Site Specific Risk Assessment Tools for Land Applied Biosolids
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Abstract:

This project compiled information on the fate, transport, and risk presented by pathogens in land-applied biosolids into a spreadsheet based risk assessment model. The model was applied to an example field. This report describes the integration of knowledge to assess microbial risks from the land application of biosolids. This knowledge has been incorporated into an environmental dispersion, exposure, and risk model, known as the Spreadsheet Microbial Assessment of Risk: Tool for Biosolids (“SMART Biosolids”). The SMART Biosolids model includes a user’s manual that enables wastewater utilities, land applicators, and regulators, to estimate microbial risk from biosolids land application under a variety of scenarios and thereby gain insight into effective management practices. In addition, this project conducted field monitoring to assess the fate and transport of microbes from land application during wet weather events.

The field monitoring did not find detectable quantities of pathogens after transport through several feet of soil in the field. However, the study did quantify some desorption of pathogens and indicators into ponded surface water, suggesting that runoff from biosolids amended fields may have trace amounts of pathogens. The risk assessment model was applied to quantify the risks such runoff might pose to surface waterbodies on a site-specific basis. The example scenarios run suggest that microbial risk due to contamination of surface waters from land application runoff would be below existing risk standards for recreational surface waters. The risk modeling estimated that exposure due to the incidental ingestion of soil appears to be the pathway of most concern and adenovirus was found to be the organism presenting the highest risk over the different pathways considered. Adenovirus is a common pathogen that is not associated with life threatening illness. The results are based on extremely limited monitoring for adenovirus (N=5). An important goal of knowledge integration efforts such as this is to identify and help prioritize knowledge gaps. The need for better information on the occurrence and persistence of adenovirus in land-applied biosolids is a key research need identified by this study.

Benefits:

♦ Compiles the latest data and knowledge from a wide variety of sources into a user-friendly tool for regulators and land applicators to perform site-specific assessments of microbial risk, including estimates of the effect of different setback requirements on microbial risk, the relative risks associated with different pathogens and exposure pathways, and the correspondence between indicator organisms and pathogens.

♦ Provides support – the user’s manual guides both novice and experienced programmers through the tool.

♦ Includes hypothetical examples and fills data gaps related to the fate and transport of microbes from land application during wet weather events.

♦ Identifies future research needs, particularly the need for information on the occurrence and persistence of adenovirus at land application sites.

Keywords: Biosolids, microbial risk assessment, pathogens, spreadsheet environment.
# TABLE OF CONTENTS

Acknowledgements ......................................................................................................................... ii  
Abstract and Benefits ..................................................................................................................... iii  
List of Tables ........................................................................................................................................ ix  
List of Figures ..................................................................................................................................... x  
Executive Summary .......................................................................................................................... ES-1

1.0 Overview and Scopes .................................................................................................................. 1-1  
1.1 Introduction .............................................................................................................................. 1-1  
1.2 Database Development .......................................................................................................... 1-1  
1.3 Model Development .............................................................................................................. 1-2  
1.4 Field Monitoring .................................................................................................................... 1-3  
1.5 Identification and Assessment of Scenarios of Concern ...................................................... 1-3  
1.6 Engagement with the Profession .......................................................................................... 1-3  
1.7 Study Conclusions ................................................................................................................. 1-4

2.0 Introduction to the Spreadsheet Model of Risk Tool for Biosolids .......................................... 2-1  
2.1 Introduction ............................................................................................................................ 2-1  
2.2 Color Coding .......................................................................................................................... 2-3  
2.3 Getting Started with the Model .............................................................................................. 2-3  
2.3.1 Running the Model .......................................................................................................... 2-4  
2.3.2 Model Outputs ................................................................................................................ 2-5  
2.3.3 Use of the Model ............................................................................................................. 2-5  
2.3.4 Limitations and Applications of the Model ....................................................................... 2-6

3.0 SMART Biosolids User Manual ............................................................................................ 3-1  
3.1 Overview of the Modeling Tool ............................................................................................... 3-1  
3.2 Function of the Program ......................................................................................................... 3-2  
3.2.1 Estimation of Risk ........................................................................................................... 3-2  
3.2.2 Direct Ingestion Pathway ................................................................................................. 3-2  
3.2.3 Air Exposure Pathway .................................................................................................... 3-2  
3.2.4 Surface Water Exposure Pathway .................................................................................. 3-3  
3.2.5 Groundwater Exposure Pathway .................................................................................... 3-4  
3.2.6 Indirect Ingestion Exposure Pathway ............................................................................. 3-6  
3.2.7 Assumptions of the Model .............................................................................................. 3-6  
3.3 Model Interface and Inputs .................................................................................................... 3-6  
3.3.1 User Interface .................................................................................................................. 3-9  
3.3.2 Risk Assessment ............................................................................................................ 3-11  
3.3.3 Direct Ingestion Pathway ............................................................................................... 3-23
3.3.4 Air Exposure Pathway ................................................................. 3-26
3.3.5 Surface Water Exposure Pathway .................................................. 3-34
3.3.6 Groundwater Exposure Pathway .................................................... 3-51
3.3.7 Indirect Ingestion Pathway ............................................................. 3-63
3.4 Interpretation of Model Results .......................................................... 3-67
3.4.1 What Do the Numbers Mean? ......................................................... 3-67
3.4.2 Is the Risk Acceptable? ................................................................. 3-67
3.4.3 Communicating About Pathogen Risk ............................................. 3-68
3.4.4 Uncertainty in Risk Estimates ......................................................... 3-68

4.0 Risk Assessment Technical Document ............................................... 4-1
4.1 Background ....................................................................................... 4-1
4.2 Risk Analysis Approach ................................................................. 4-1
4.2.1 Hazard Identification ................................................................. 4-1
4.3 Dose-Response Assessment ............................................................... 4-4
4.4 Exposure Assessment ................................................................. 4-5
4.4.1 Exposed Subpopulation ............................................................... 4-5
4.4.2 Exposure Routes ................................................................. 4-5
4.4.3 Exposed Pathogen Dose (Dose_{exp}) ........................................ 4-6
4.5 Risk Characterization ...................................................................... 4-6
4.5.1 Cumulative Risk Estimate for Long-Term Exposure ......................... 4-6
4.5.2 Risk of Infection ...................................................................... 4-7

5.0 Soil Exposure Model Technical Document ........................................... 5-1

6.0 Air Exposure Model Technical Document ........................................... 6-1
6.1 Background ....................................................................................... 6-1

7.0 Surface Water Exposure Model Technical Document ......................... 7-1
7.1 Surface Runoff Model ....................................................................... 7-1
7.1.1 Model Selection ......................................................................... 7-1
7.1.2 Joint Green-Ampt Model ............................................................. 7-1
7.2 Overland Transport and Fate of Biosolids-Associated Pathogens .......... 7-3
7.2.1 Pathogen Source ....................................................................... 7-3
7.2.2 Overland Transport of Pathogens ............................................... 7-3

8.0 Groundwater Exposure Model Technical Document ........................... 8-1
8.1 Function of the Program .................................................................. 8-1
8.2 Model Description .......................................................................... 8-2
8.2.1 Estimation of Infiltration Rate and Depth of Wetting Front ................. 8-2
<table>
<thead>
<tr>
<th>List of Tables</th>
</tr>
</thead>
<tbody>
<tr>
<td>3-1 List of SMART Biosolids Sheets Containing Input Variables, Default Parameters, and Modeling Results for Risk Assessment and Five Exposure Pathways</td>
</tr>
<tr>
<td>3-2 Input Parameters, Constants and Output Parameters Employed</td>
</tr>
<tr>
<td>3-3 Input Parameters and Output Parameters (Direct Ingestion)</td>
</tr>
<tr>
<td>3-4 List of Input Parameters Required for Running Soil Exposure Model</td>
</tr>
<tr>
<td>3-5 Snapshot of Soil Pathogen Model Showing Output Parameters</td>
</tr>
<tr>
<td>3-6 List of Input Parameters for Air Exposure Model</td>
</tr>
<tr>
<td>3-7 List of Biosolids Application-Related Constants Required for Air Exposure Model</td>
</tr>
<tr>
<td>3-8 Input Parameters, Constants, and Output Parameters Employed in Surface Water Exposure Pathway</td>
</tr>
<tr>
<td>3-9 List of Input Parameters Required for Running the Surface Water Exposure Model</td>
</tr>
<tr>
<td>3-10 Biosolids Application-Related Constants</td>
</tr>
<tr>
<td>3-11 Input Parameters, Constants, and Output Parameters Employed in the Groundwater Exposure Pathway</td>
</tr>
<tr>
<td>3-12 List of Input Parameters Required for Running the Ground Water Exposure Model</td>
</tr>
<tr>
<td>3-13 Biosolids Application-Related Constants</td>
</tr>
<tr>
<td>3-14 Input Parameters, Constants and Output Parameters Employed in the Indirect Ingestion Exposure Pathway</td>
</tr>
<tr>
<td>3-15 List of Input Parameters Required for Running the Indirect Ingestion Exposure Model (Sheet: Inputdata)</td>
</tr>
<tr>
<td>4-1 Pathogens of Concern in the Bacteria Category</td>
</tr>
<tr>
<td>4-2 Pathogens of Concern in the Virus Category</td>
</tr>
<tr>
<td>4-3 Pathogens of Concern in the Parasites Category</td>
</tr>
<tr>
<td>6-1 Aerosolize Efficiencies for Splash-Plate, Slinger, and Disk Incorporation Application</td>
</tr>
<tr>
<td>10-1 Site-Specific Conditions</td>
</tr>
<tr>
<td>10-2 Air Pathway Residential Adult, Setback Distance of 250 Feet</td>
</tr>
<tr>
<td>10-3 Incidental Ingestion of Soil, 31 Days After Application</td>
</tr>
<tr>
<td>10-4 Surface Water: Recreational Swimming, 1 in 100-Year Storm Event, Surface Water Pathway Residential Adult and Residential Children, Buffer Strip of 33 Feet</td>
</tr>
<tr>
<td>10-5 Groundwater Pathway Residential Adult and Residential Children</td>
</tr>
<tr>
<td>10-6 Indicator Organism Concentration Estimates</td>
</tr>
<tr>
<td>11-1 Initial Somatic Phage, P-22 and Adenovirus Concentration in Biosolids</td>
</tr>
<tr>
<td>11-2 Physical and Chemical Characteristics for Each Lysimeter Applied with Biosolids</td>
</tr>
<tr>
<td>11-3 Infiltration Rates, Drainage Classification, Root System of Each Lysimeter</td>
</tr>
<tr>
<td>11-4 Recovery Percentage of Chloride and P-22 from Leachate and Top Half of Lysimeter Soils</td>
</tr>
<tr>
<td>11-5 Microbial Characteristics of the Romeo Biosolids</td>
</tr>
<tr>
<td>Figure</td>
</tr>
<tr>
<td>--------</td>
</tr>
<tr>
<td>2-1</td>
</tr>
<tr>
<td>3-1</td>
</tr>
<tr>
<td>3-2</td>
</tr>
<tr>
<td>3-3</td>
</tr>
<tr>
<td>3-4</td>
</tr>
<tr>
<td>3-5a</td>
</tr>
<tr>
<td>3-5b</td>
</tr>
<tr>
<td>3-5c</td>
</tr>
<tr>
<td>3-5d</td>
</tr>
<tr>
<td>3-6</td>
</tr>
<tr>
<td>3-7</td>
</tr>
<tr>
<td>3-8a</td>
</tr>
<tr>
<td>3-8b</td>
</tr>
<tr>
<td>3-8c</td>
</tr>
<tr>
<td>3-8d</td>
</tr>
<tr>
<td>3-9a</td>
</tr>
<tr>
<td>3-9b</td>
</tr>
<tr>
<td>3-9c</td>
</tr>
<tr>
<td>3-9d</td>
</tr>
<tr>
<td>3-10a</td>
</tr>
<tr>
<td>3-10b</td>
</tr>
<tr>
<td>3-10c</td>
</tr>
<tr>
<td>3-10d</td>
</tr>
<tr>
<td>3-10e</td>
</tr>
<tr>
<td>3-11a</td>
</tr>
<tr>
<td>3-11b</td>
</tr>
</tbody>
</table>
3-12  Snapshot of User Interface of Soil Exposure Model ........................................................ 3-24
3-13  Snapshot of Soil Pathogen Model Sheet Showing Output Parameters ............................... 3-25
3-14  Snapshot of Air Constants Sheet Showing Calculation Steps ........................................... 3-29
3-15  Snapshot of Constants for Calculating Bioaerosol Concentrations ................................. 3-30
3-16a  Snapshot of AirOccupational Sheet ............................................................................... 3-32
3-16b  Snapshot of AirResAdult Sheet ....................................................................................... 3-32
3-17  Snapshot of Surface Constants Showing Constants Required for Surface Water Exposure Model ............................................................................................................. 3-42
3-18  User Interface of Overland Transport and Fate of Biosolids-Associated Pathogens Model ...................................................................................................................... 3-43
3-19  Constant Parameters for Overland Transport and Fate of Biosolids-Associated Pathogens Model .............................................................................................................. 3-44
3-20  Snapshot of SWPathogen Model Sheet Showing Calculation Steps ................................... 3-46
3-21  Information About Land Application of Biosolids for Overland Transport and Fate of Biosolids-Associated Pathogens Model .............................................................. 3-46
3-22  Snapshot of SWRain Model Sheet Showing Output Parameters Related to Total Rainfall, Runoff, Runoff Ratio, and Infiltration Volume ................................................. 3-47
3-23  Snapshot of the SWPathogen Model Sheet Showing Output Parameters Related to Pathogen Load ............................................................................................................. 3-49
3-24  Selection of the Default Group for Obtaining Different Hydrologic Information After the Rainfall Event (Sheet: SWRain Model) .............................................................. 3-50
3-25  Snapshot of the GW Pathogen Model Showing Default Pathogen Parameters for the Groundwater Exposure Model Input ........................................................................ 3-55
3-26a  Snapshot of the GW Pathogen Model Sheet Showing the Transport Phases for Scenario 1: Non-Saturating Rainfall Events ................................................................... 3-58
3-26b  Snapshot of the GW Pathogen Model Sheet Showing the Results of Infiltration Information ......................................................................................................................... 3-59
3-27  Snapshot of the GW Pathogen Model Sheet Showing the Results of Partitioning and Straining ........................................................................................................................ 3-59
3-28  Snapshot of the GW Pathogen Model Sheet Showing the Results of Subsurface Transport and Fate Model ....................................................................................................... 3-60
3-29  User Interfaces of the Detailed Output Values for the Groundwater Exposure Model (Sheet: GW Pathogen Model, Part I) ......................................................................................... 3-61
3-30  Snapshot of the VegePathogen Model Sheet Showing Output Parameters ........................... 3-66
7-1  Schematic of the Overland Transport of Sediments ................................................................. 7-5
8-1  Flow Chart for Possible Groundwater Exposure Pathway Scenarios ..................................... 8-2
11-1  Breakthrough Curves for the Chloride Tracer ...................................................................... 11-7
11-2  Breakthrough Curves of P-22 and the Chloride Tracer ............................................................ 11-9
11-3  P-22 Concentration at Different Soil Depth .......................................................................... 11-10
11-5  P-22 and Somatic Phage Levels in Surface Water Samples in 2009 ...................................... 11-11
11-6  Decay Curves of P-22 and Somatic Phage in Surface Water Samples ................................. 11-12
11-7  Meteorological Information and Wet-Weather Driven Sampling Schedule ........................ 11-18
11-8 Effects of Biosolids Application Vents on Fecal Indicator and Tetracycline-Resistance Bacteria in Biosolid-Amended Soil Samples

11-9 Effects of Biosolids Application Events on Fecal Indicator and Tetracycline-Resistance Bacteria in Tile-Drain Effluent Sample
EXECUTIVE SUMMARY

This project compiled knowledge on occurrence, environmental transport, and attenuation of pathogens into a computer model, the Spreadsheet Microbial Assessment of Risk: Tool for Biosolids (SMART Biosolids). SMART Biosolids assesses risk associated with land-applied biosolids through five pathways: 1) inhalation of aerosols from land application sites, 2) consumption of groundwater contaminated by land-applied biosolids, 3) direct ingestion of biosolids-amended soils, 4) ingestion of plants contaminated by land-applied biosolids, and 5) consumption of surface water contaminated by runoff from a land application site. The SMART Biosolids model enables wastewater utilities, land applicators, and regulators, to estimate human exposure to pathogenic microorganisms from biosolids land application under a variety of scenarios and thereby gain insight into effective management practices.

An example application found that among the five pathways considered, the incidental ingestion of soil posed the greatest risk. Risks were not computed for pathogens present at levels below detection in biosolids, which limited the risk assessment to six pathogens: adenovirus, enterovirus, *Shigella*, *Salmonella*, *Cryptosporidium*, and *Giardia*. Adenovirus showed the highest risks across the five exposure pathways; these results are based on extremely limited (N=5) adenovirus occurrence information. Of the five pathways, the incidental soil ingestion pathway presented the greatest risks. The consideration of wet weather events found that exposure by groundwater and surface water may exceed a 1 in 10,000 benchmark value for annual microbial risk associated with U.S. public drinking water supplies when a 100-year return period stormwater runoff event is considered. Nominal risk estimates do not exceed marine recreational water use risk benchmarks for any pathways although the upper bound (95th percentile risk) for incidental ingestion of soil by children of 5.6 in 100 exceeds the 1.9 in 100 risk level for marine surface water recreation. Risks for groundwater exposure are highly uncertain with upper bound risks for several pathogens exceeding the recreational water risk levels.

The field monitoring was not able to measure detectable quantities of pathogens after transport through several feet of soil in the field. The field monitoring did quantify some desorption of pathogens and indicators into ponded surface water, suggesting that runoff from biosolids amended fields may have trace amounts of pathogens. As noted above, the risk assessment model was used to quantify the risks this runoff might pose to surface waterbodies and the example application indicated that even for a 100-year storm event, the microbial risk due to contamination of surface waters from land application runoff would be below existing risk standards for recreation surface waters.

This knowledge integration effort identified the occurrence and persistence of adenovirus in land applied biosolids as a key issue warranting further research. Better data on the occurrence and persistence of *Giardia* and *Cryptosporidium* were also identified as priorities for future research. Information from future studies can readily be brought into the SMART Biosolids model so that improved risk estimates can be developed. Further applications of the model to consider alternative scenarios and exposed groups are being conducted as part of follow up work.
CHAPTER 1.0

OVERVIEW AND SCOPE

1.1 Introduction

Over the past several decades, better scientific knowledge has been developed that can help estimate the potential for exposure to pathogens associated with biosolids land application. At the time of the development of the 40 CFR Part 503 rule, *Standards for the Use and Disposal of Sewage Sludge*, allowable levels of microbial contaminants were based on treatment methods, rather than risk levels. At that time, microbial risk assessment methodologies were not sufficiently developed for the establishment of risk-based standards for pathogens in biosolids. Uncertainties such as this may have contributed to both public and technical assessments of the safety of land application. A National Research Council study (NRC, 2002) noted that there was no documented evidence of harm to human health resulting from the land application of biosolids, but also cited persistent uncertainty regarding the practice and recommended further research. Substantial research has been conducted since the National Research Council report was issued. This has included substantial field monitoring studies (Brooks et al., 2004, Brooks et al., 2005a; Brooks et al., 2005b), risk assessment (Gerba et al., 2002, Gerba et al., 2008), and the development of a framework for assessing risk from pathogens from biosolids (Eisenberg et al., 2008).

The availability of this new information created a need to consolidate available information. Such knowledge integration is beneficial on two levels. First, the compilation of available information brings into relief gaps in existing knowledge. This informs future research efforts which can then be directed towards filling the most critical gaps. Second, the compilation of knowledge facilitates the application of this knowledge in practice. Microbial risk assessment has the potential to inform a number of important practical decisions. On a policy formulation level, appropriate setbacks must be determined and risk assessments can be an important input into this decision making process. On a site-specific level, sites vary on many different parameters which may impact their suitability for land application. Certainly there is no indication that sites that comply with appropriate regulatory standards might present unacceptable risk. Nevertheless, land application is a practice subject to intense scrutiny and the ability to address specific concerns at a specific site may be helpful. It should be emphasized that the use of the model to address site-specific concerns would need to be a single component of an overall stakeholder engagement approach.

This study undertook a broad knowledge integration effort for quantitative microbial risk assessment of biosolids land application. The major components of the effort are described in the sections below.

1.2 Database Development

Realistic inputs are the starting point for a credible microbial risk assessment. This study drew on a wealth of published research on the fate and transport of pathogens from biosolids in the environment (Brooks et al., 2005a, Brooks et al., 2005b, Tanner et al., 2005, Chetochine et
Studies were evaluated to identify both averages and ranges for factors, such as bioaerosol emission rates associated with different biosolids handling operations, persistence of pathogens in the environment, and occurrence of pathogens in treated biosolids.

The values identified are summarized in the tables of model inputs provided with this report, in the default values provided with the computer model, and in a journal publication (Pepper et al., 2010).

1.3 Model Development

The parameters compiled serve as inputs to models describing the environmental fate of pathogens in biosolids, including the transport of pathogens to humans and the associated health risks to exposed individuals. These models are well established in the technical literature. This study built on the results of a previous WERF-sponsored effort which developed a framework for microbial risk assessment of land-applied biosolids (Eisenberg et al., 2006). This framework identified five pathways of concern: 1) inhalation of aerosols from land application sites, 2) consumption of groundwater contaminated by biosolids, 3) direct ingestion of biosolids, 4) ingestion of plants grown on biosolids-amended fields, and 5) consumption of water contaminated by runoff from a land application site.

This study focused on maximum reasonable exposures, in keeping with the recommendations of the National Research Council (NRC, 2002). Thus risk estimates are developed for individuals with the highest likelihood of infection. This group includes biosolids generators, biosolids land appliers, agricultural field workers, and residents of homes adjacent to sites. The research estimates their maximal exposure risks, considering risks to sensitive subpopulations, such as individuals who have not acquired immunity to various pathogens through prior exposure. Population average risks were not developed. This process recognizes the reality that the public and regulators will require land application practices to be protective of even highly exposed individuals without prior immunity.

This study developed reduced-form exposure models for all five pathways of concern. It integrated these models with human health risk assessment models. The combined models are integrated with the parameter input database described above to develop an integrated risk assessment tool. Default values are provided for a range of different site conditions (soil textures, atmospheric stability classes, etc.) and users are able to input a variety of site specific information such as setback distances, hill slope, wind speed, and others. This enables one to characterize specific sites as to their suitability for land application and to explore how differing setbacks impact microbial risk. All of this may help to inform policy development.

This risk assessment tool is included on the CD provided with this report as a Microsoft Excel spreadsheet with Visual Basic macros. An overview of this spreadsheet tool is provided in Chapter 2.0 and the user guide for the risk assessment tool is provided in Chapter 3.0 of this report. Technical documentation of the models used is provided in Chapters 4.0 through 9.0. Example results are provided in Chapter 10.0.
1.4 Field Monitoring

Even in advance of the detailed knowledge integration performed by this study, it was recognized that knowledge gaps existed and further field monitoring could help to address these gaps. A particularly important gap was that previous field monitoring had not addressed the impact of wet weather events. Wet weather events may temporarily saturate soils above the water table, potentially mobilizing microbes and entraining them as the water infiltrates to the water table. In addition, wet weather events may generate runoff that mobilizes microbes and transports them to surface waterbodies. Field monitoring was conducted to investigate the behavior of indicators and pathogens from land-applied biosolids during wet weather events. This effort directly informed the modeling by identifying occurrence values for indicators and pathogens in biosolids and estimates of the fraction of microbes that partition from biosolids into the aqueous phase during a wet weather event. In addition, the field monitoring gathered information on the fate of antibiotic resistant microbes in land-applied biosolids. An overview of the results of the field monitoring are provided in Chapter 11.0 of this report with details provided in Munir et al. (2011) and Wong et al. (2010).

1.5 Identification and Assessment of Scenarios of Concern

While previous risk assessments have considered exposures measured or extrapolated from monitoring results and concluded that risks associated with land application of biosolids are generally low (Gerba et al., 2002, Brooks et al., 2005a, Brooks et al., 2005b), these prior assessments considered typical risk, that is, risk when processes and procedures are functioning properly. In reality, there are risks that processes (such as anaerobic digestion) or program procedures (such as posting site restrictions) will not be properly implemented. Failures can radically alter the system’s microbial risk, yet there has been very little formal assessment of risk under failure scenarios. The research team is undertaking such an assessment by identifying plausible failure scenarios, conducting surveys of professionals to indentify the frequency with which different scenarios are reported to occur, and using the risk assessment tool to estimate health risks associated with the different scenarios. This approach can identify important safeguards and control strategies to incorporate into the management of biosolids land application programs. The results of this effort will be provided in an addendum to this final report.

1.6 Engagement with the Profession

The study team developed and held two workshops in conjunction with Decision Partners, the Water Environment Federation, the Mid Atlantic Biosolids Association, the Northeast Biosolids, Association, the North Carolina Water Environment Association, and a wide range of land application professionals, in which biosolids land application programs were discussed from a broad range of perspectives. These discussions included the role of the microbial risk assessment tool but went beyond this topic to consider a range of potential program elements. Survey data were collected on participants’ assessments of different program management elements, which may help to identify promising elements for inclusion into overall management programs. While this aspect of the project is outside of the study scope, efforts are underway to analyze these data and develop a journal paper. In addition, the curriculum materials used for the workshops can be made available for future efforts.
1.7 Study Conclusions

Risk assessments are always evolving in response to new information. The goal of this effort has not been to develop a definitive assessment but rather to develop an assessment framework that can accommodate and organize new information. Nevertheless, one can review available results both with respect to whether or where concerns exist and where additional research might be informative. This review and the resulting conclusions are presented in Chapter 12.0.
CHAPTER 2.0

INTRODUCTION TO THE SPREADSHEET MODEL OF RISK TOOL FOR BIOSOLIDS

2.1 Introduction

The Spreadsheet Microbial Assessment of Risk: Tool for Biosolids (SMART Biosolids) is a computational tool that will allow utilities, land appliers, regulators, and local public administrators to assess the relative pathogen risks associated with biosolids. This user manual is intended to guide novice users as well as experienced programmers through the SMART Biosolids model.

SMART Biosolids estimates risk associated with exposure to pathogens from land-applied biosolids through five pathways:

1) Inhalation of aerosols from land application sites
2) Consumption of groundwater impacted by land-applied biosolids
3) Direct ingestion of biosolids-amended soils
4) Ingestion of plants impacted by land-applied biosolids (work on this pathway is currently pending)
5) Consumption of water contaminated by runoff from a land application site
These five pathways were identified through previous research efforts that developed a framework for microbial risk assessment from land applied biosolids (Colford et al., 2003; Eisenberg et al., 2004, 2006, and 2008). SMART Biosolids assesses risk to highly exposed individuals, such as residents whose homes border land application sites. This is in keeping with the National Research Council recommendation that biosolids risk assessments focus on highly exposed individuals (NRC, 2002). This allows managers to focus on how key management decisions (set back distances) and measurement variables (pathogen and indicator concentrations) that impact risk to the most exposed individuals. Given that the public and regulators will demand that risks to such groups be minimal, this is an appropriate focus of attention. Nevertheless, it should be noted that overall impacts of these exposures may be greater than implied by SMART Biosolids, as secondary transmission of pathogens is not considered by this model. SMART Biosolids does not provided population risks associated with biosolids and is not intended for use in overall benefit-cost assessment or regulatory impact analysis.

The strategy underlying the development of the SMART Biosolids program is that each risk assessment is different. Thus, the tool is designed for flexibility. Rather than being a “black box” that maps inputs to outputs using an un-editable, compiled code, a spreadsheet interface is used. The spreadsheet environment provides a familiar interface for entering inputs and
accessing outputs while providing access to a range of post-processing tools including chart building capabilities. The environmental fate and transport models associated with each of the exposure pathways are computed in Microsoft Excel. The use of a spreadsheet interface allows the advanced user to trace the computations used and modify parameters and even change mathematical algorithms as desired. A limited amount of Visual Basic code is used to run the exposure pathway models multiple times for different pathogens and to conduct a Monte Carlo uncertainty analysis. This code is readily viewable and can be edited by the advanced user. The cost of this flexibility is that the user must learn to navigate among the different tabs of the spreadsheet to find inputs and outputs and must learn to run Visual Basic macros in the Excel environment. This user guide contains step-by-step instructions for doing this.

This chapter of the user guide presents an overview of how to use the model. Chapter 3.0 serves as a user guide for the model. Chapters 4.0 through 9.0 describe the mathematical basis of the model and are intended for readers with some background in environmental modeling and risk assessment. Chapter 4.0 describes the risk computations, and Chapters 5.0 through 9.0 describe each of the exposure pathway models in turn.

2.2 Color Coding

Each component of SMART Biosolids uses the same color-coding:

- **Input**
  - **Site-specific variables.** Blue cells are used to show the required inputs entered by the user to describe the application area, application practices, location of exposed individuals, etc. All of these required inputs are located on the Inputdata sheet of the Excel workbook.

- **Output**
  - **Modeling results.** Yellow cells are used to show values computed by the model. The equations used to derive these results are described in the Technical Documentation provided in Chapters 4.0 through 9.0 of this user guide.

- **Constants**
  - **Default values.** Green cells are used to show default parameters that have been selected based on an extensive review of published environmental and laboratory research. For important uncertain inputs, both best estimates and ranges of plausible values are given. The sources used for these default values are cited in the Excel file containing the model. The user is able to change these default variables to create outputs relevant to their needs and situation.

2.3 Getting Started with the Model

The SMART Model runs in the Microsoft Excel environment using Visual Basic Macros. It is developed as an application for use with the Microsoft Windows operating system. Its use is not supported for other operating systems. You most likely received the model as a compressed file with a .zip extension. When you double click on the icon for the .zip file, you will see an icon for a Microsoft Excel spreadsheet. Double click on this to open it. Unless you specifically enable the macros each and every time that you open the model, the model will not run properly.
To enable the macros:

1. Look for the SECURITY WARNING below the Toolbar.
2. Click ‘Options’ and select ‘Enable this content.’

Once the model is open, use the save as option to save the file to an appropriate location. You may save the file either as an Excel 2003 workbook (.xls) or as a macros-enabled Excel 2007 workbook (.xlsm).

The model consists of a series of worksheets accessed by clicking on tabs at the lower margin of the spreadsheet. The tabs for three sheets that the beginning user needs to access are highlighted in green at the left side of this display of tabs. These three tabs are Instructions, Inputdata, and Riskoutput. Before starting, click on the tab labeled Instructions which describes how to enable and run the macros required for the model. You may then enter appropriate site and application characteristics on the Inputdata sheet. You are now ready to run the model.

2.3.1 Running the Model

Simply entering different inputs into the sheet does not cause the model to automatically update. Each time different values are entered as inputs, the user must run the macros to update the model outputs.

To run the macros in Excel 2007:

1. When you open the model, look for the SECURITY WARNING below the Toolbar.
2. Click ‘Options’ and select ‘Enable this content.’
3. Make adjustments to the input parameters in the Inputdata sheet.
4. Click View and select Macros (or ALT + F8).
5. Select RiskCal macro and click RUN.
6. Wait for model to run. During this time the spreadsheet will be frozen (unresponsive to user inputs).
7. Click on RiskOutput tab to see results.

Steps 1 and 2 are required once each time the model is opened. If you wish to adjust parameters and re-run the model once it is already open with the macros enabled, you may simply repeat Steps 3 through 7.

To run the macros in Microsoft Excel 2003:

1. Click on Tools in the toolbar.
2. Click on Macro, then Macros.
3. Select Sheet2.RiskCal macro and click RUN.
4. Wait for model to run. During this time the spreadsheet will be frozen (unresponsive to user inputs).
5. Click on RiskOutput tab to see results.

The run-time for the model varies according to the computer used and the number of iterations performed for doing an uncertainty analysis, which will reduce bounds around the risk.
(cell C31 in Inputdata sheet). It is recommended that users first run the model in point estimation mode (using a single iteration). On a typical computer allow roughly 10-15 minutes for a point estimate. To run 50 iterations (provides a rough estimate of uncertainty bounds) allow several hours. To obtain more accurate uncertainty bounds, use 1000 iterations and allow the model to run for an extended period of time. Running 1000 iterations will narrow the confidence intervals for mean predictions by a factor of 4 compared to a simulation of only 50 iterations and is highly recommended for finalized results.

2.3.2 Model Outputs
The model estimates:

♦ Expected concentrations of microbes in air, soil, surface and ground water resulting from biosolids applications

♦ Expected probability of infection by these microbes for residents of nearby properties and workers applying the biosolids

2.3.3 Use of the Model

Begin by opening the model and reviewing the Instructions. Then go to the Inputdata tab and enter values for a land application site of interest to you. One major feature of the model is its consideration of wet weather events. Chose a storm of interest to you and enter its intensity (rainfall/hour) and duration in the appropriate cells. If you wish you may also enter a rough return period associated with this storm in the appropriately labeled cell.

For the first run, set the iterations to 1 so that the model will run quickly. Give the model several minutes to run, then click on the RiskOutput tab and explore the model results. Summary results are presented on the left portion of the spreadsheet with results for different pathways, health outcomes, and microbes presented in tables to the right. Be sure to scroll right and down to see the full range of results presented by the model. As you review these results consider which exposure pathway is of most concern? Which microbes present the most risk? Are any of the risks at a level that might cause concern? For some guidance on what risk levels may be of concern, you may consult Chapter 2.0 of this user guide.

Now consider a different site. Change the input parameters to reflect conditions at this site. How different are the risks? Is one site preferable to the other? Are both/neither sites appropriate for land application?

Once you have run the model for a single iteration, you may wish to explore model uncertainty. To do this, increase the number of iterations. As described above, on most computers you should allow several hours for 50 iterations which provides a very rough estimate of the possible range of model output. To more fully characterize uncertainty, set the number of iterations to at least 1000 and allow the program to run for an extended time period. The model can run a Monte Carlo analysis. A Monte Carlo uncertainty analysis uses computational algorithms to compute predictions based on repeated random sampling. It allows one to determine how random variation, lack of knowledge, or error could affect the sensitivity, performance, or reliability of the model. When reviewing the outputs of the uncertainty analysis consider aspects such as, which microbes or pathways have the greatest uncertainty associated with them (broadest range between reported 5th percentile and 95th percentile values)? Are there cases where the upper bound (95th percentile) of estimated risk may be of concern even if the

Site Specific Risk Assessment Tools for Land Applied Biosolids
best estimate is not? In these cases further assessment may be justified to reduce uncertainty and determine if the risk actually exceeds a level of concern.

2.3.4 Limitations and Applications of the Model

The user should always be mindful that this model, like many risk models, requires many assumptions. In general the approach has been to be conservative, that is, to err on the side of overestimating risk. Nevertheless, the impact of different model structural assumptions is not always clear, and model risk estimates may not be health protective in all cases. The Technical Documentation details the assumptions that are made, but several key ones are noted here as well:

♦ Risk assessments are for highly exposed individuals. Neither prior immunity nor secondary transmission is considered. These assumptions are appropriate for managing risks to important subpopulations, but the model does not quantify the overall impact of an exposure on the entire population.

♦ During wet weather events, a fixed percentage release of microbes to the water was assumed. While sorption coefficients for soil are available for at least some microbes, biosolids constitute a very different matrix and it was decided that partition coefficients developed for soil should not be used for biosolids.

♦ During surface water transport, microbes that are not attached to soil particles are assumed not to be removed by a vegetative filter strip. It was felt that the literature data on removal of microbes by such vegetative filter strips is influenced mostly by removal of suspended sediment with attached particles and that unattached microbes might pass through the filter strips.

Despite these limitations, the model may be useful for informing a number of decisions:

♦ Site specific assessments. Regulators and land application program managers may be able to use the model to review different sites and determine which sites are most appropriate for land application. Near neighbors and others concerned with land application may be involved as appropriate to consider whether appropriate sites and management practices are in use.

♦ Set back requirements. In general setback requirements have not been informed by microbial risk assessments. SMART Biosolids provides a means to evaluate how microbial risk varies as a function of setback distance. This enables program managers and regulators to assess when additional setbacks provide real benefits in terms of risk reduction and when additional setbacks offer diminishing returns. In particular, depth to groundwater has a highly non-linear effect on risk and the modeling approach used here is intended to capture differential transport of microbes in the saturated and unsaturated zone so that effects of different requirements for depth to groundwater can be explored by the user.

♦ Interpretation of indicator organism results. Monitoring of land application is based largely on measurements of indicator organisms. SMART Biosolids includes four important and widely used indicator organisms: E. coli, total coliforms, Enterococci, and coliphage. The exposure pathway models provide quantitative estimates of concentrations of these indicators in different environmental media over time which account for differences in transport and survival of indicators and pathogens. This can provide guidance as to the risk level associated with observed levels of indicators, provided that typical ratios of pathogens and indicators in biosolids are maintained, and fate and transport parameters accurately
capture differences among different microbes (see Chapter 10.0 for examples). Conversely, if SMART Biosolids estimates that risks are of concern, then follow up sampling can be conducted, and predicted concentrations of indicators compared with measured indicator concentrations to determine if the model predictions are applicable.

♦ **Failure analysis.** While land application is carefully regulated and subject to numerous controls, there is always some potential for exposures due to deviations from normal land-application practices. SMART Biosolids provides a variety of information, including typical pathogen concentrations in Class B biosolids and dose response parameters that may be helpful to understand the risks presented by such incidents and what remedial actions are appropriate. While SMART Biosolids cannot directly model all of the many potential deviations from normal practices that could occur, in many cases it may be possible to slightly modify one of the existing exposure pathways to account for unforeseen exposures. For example, the spill of biosolids during transport might generate aerosol exposures that could be modeled with the air exposure pathway once an appropriate duration and rate of release were determined. The ingestion from dermal exposure could be modeled using the direct ingestion pathway by reducing the time of ingestion after application to zero and adjusting the ingestion amount to reflect the circumstances of the release.

The results of this model cannot replace engineering judgment in assuring safety in biosolids land application programs. They are intended as a guide to the potential severity of different risks and may perhaps most usefully be interpreted as providing insight into the relative risks associated with different organisms and pathways. In particular, the broad, multi-pathway and multi-organism approach undertaken here can identify key gaps in knowledge where additional research would be most helpful.
CHAPTER 3.0

SMART BIOSOLIDS USER MANUAL

3.1 Overview of the Modeling Tool

The Spreadsheet Microbial Assessment of Risk: Tool for Biosolids (“SMART Biosolids,” hereafter) calculates risk of infection and illness per application period from exposure to biosolids-associated pathogens for different subpopulations. Five exposure routes are considered: 1) Direct ingestion of soil, 2) Inhalation of air, 3) Ingestion of surface water, 4) Ingestion of groundwater, and 5) Ingestion of vegetables grown on fields adjacent to biosolids-amended fields. Figure 3-1 shows a schematic of the information flow in SMART Biosolids. Based on site-specific user inputs, the pathogen concentrations in different exposure media (soil, air, surface water, groundwater, and vegetables) are calculated from transport and fate models which describe the direct ingestion, air, surface water, groundwater, and indirect ingestion pathways, respectively. Finally, risk of human infection and illness are calculated for various subpopulations based on the pathogen exposure dose estimated from concentrations in different environmental media provided by the five exposure pathway models, and pathogen-specific dose-response parameters.

Figure 3-1. Schematic of the Information Flow in SMART Biosolids.
3.2 Function of the Program

The SMART Biosolids model calculates pathogen concentrations in environmental media from fate and transport models developed for five exposure pathways and then estimates risk of human infection and illness for different subpopulations. Descriptions of the risk estimation method and the five exposure pathways are provided below.

3.2.1 Estimation of Risk

SMART Biosolids calculates numerical risk assessments that signify the likelihood of contracting an infectious disease from biosolids-associated pathogens over a specified application period. Risks are calculated based on pathogen-specific dose-response parameters for different subpopulations (presented in Appendix A) and on pathogen exposure concentrations calculated from fate and transport modeling of the five exposure pathways. A description of the Sheet24.RiskCal visual basic macro for calculating risk is presented in Appendix B and a detailed mathematical description of the risk calculation methods are provided in Chapter 4.0.

3.2.2 Direct Ingestion Pathway

During land-application of biosolids, biosolids are deposited on land and are mixed with soil particles. The direct ingestion model calculates the number of biosolids-associated pathogens present in soil after land-application of biosolids, and the human ingestion exposure associated with direct contact with biosolids-amended soil (Sheet: SoilPathogenModel). In addition, this model calculates the number of biosolids-associated pathogens that remain attached to the soil following a rainfall event, where a small fraction of biosolids-associated pathogens are released into the runoff water. Risk of infection and risk of illness due to exposures to these pathogens for different subpopulation are then calculated based on the time-dependent pathogen concentrations in soil. Chapter 5.0 provides information on the mathematical details of the direct ingestion pathway.

3.2.3 Air Exposure Pathway

During land-application of biosolids, some of the biosolids particles are aerosolized (termed aerosolized biosolids, hereafter), and likewise, some of the biosolids-associated pathogens are also aerosolized (termed “bioaerosols” hereafter; Brooks et al., 2004). The air exposure model calculates inhalation exposure to biosolids-associated pathogens during the land application process. Figure 3-2 shows a schematic of biosolids application for a hypothetical site. The model simulates the concentration of biosolids-associated pathogens in air for workers applying the biosolids (Sheet: AirOccupational) as well as for residential adults (AirResAdult) and children (Air ResChild) living downwind of the field to which biosolids are applied. Risk of infection and risk of illness due to exposure to these pathogens for different subpopulation types are then calculated based on airborne pathogen concentrations. The technical details of the air exposure model are presented in Chapter 6.0, including model constants and a table of model parameters.
3.2.4 Surface Water Exposure Pathway

The surface water model calculates surface runoff volume, infiltration volume, runoff ratio, and overland fate and transport of biosolids-associated pathogens for individual rain events. The model first calculates the soil water infiltration rate on a given plot of land for a given storm, which is used to calculate surface runoff volume, sediment load due to water erosion, and sediment entrainment in the runoff water. Subsequently, the model calculates the quantities of pathogens released from land-applied biosolids to the runoff water (unattached-pathogen cells, hereafter) and pathogens attached to the land-applied biosolids after the rainfall events (attached-pathogen cells, hereafter). Further, this model calculates the number of biosolids-associated pathogen cells reaching the nearest farm pond due to overland flow of the runoff water and calculates the pond-water pathogenic concentration.

Two sub-models of the Surface Water Exposure Pathway include: 1) Infiltration and runoff (Sheets: SWRainModel and SurfaceConstants), and 2) Overland fate and transport of biosolids-associated pathogens (Sheets: SWPathogenModel, Barrenplot, and VegStrip).

The objective of the infiltration and runoff sub-model is to calculate the surface infiltration rate \( q \) and the surface runoff volume \( V_{\text{runoff}} \), which are further applied to models describing the overland fate and transport of biosolids-associated pathogens. The surface runoff volume is used in the surface water transport and soil erosion models. The Green-Ampt infiltration model (Green and Ampt, 1911) was selected because it is a well-established model that has been shown to be applicable to a wide variety of conditions (U.S. EPA, 1998). For ease of use in a spreadsheet environment, a Joint Green-Ampt model was developed, which incorporates the Explicit Green-Ampt solution (Salvucci and Entekhabi, 1994) into the Constant Flux Green-Ampt model to calculate infiltration rate, cumulative infiltration, and surface runoff values.

The overland fate and transport sub-model calculates the loading of biosolids-associated pathogens to a farm pond, following land-application of biosolids (Figure 3-3). Due to the effects
of rainfall events, some of the pathogens attached to the biosolids are released into the runoff water (i.e., unattached-pathogen cells, hereafter). Biosolids and sediments are entrained in the runoff water due to erosion and transported to a nearby farm pond. Biosolids-associated pathogens reach the nearest farm pond either by means of transport of the unattached-pathogen cells in runoff water or transport of the biosolids entrained in the runoff water. The runoff water reaches the nearest farm pond via gravitational flow, and mixes with the farm pond water. During this process, pathogen cell concentrations in the runoff water are diluted due to the effect of mixing of the runoff water with the farm pond water. Finally, humans are exposed to these biosolids-associated pathogens via recreational activities in the farm pond.

Further technical details on model background and development are presented in the Surface Water Exposure Model Technical Document (Chapter 7.0). Appendix G presents a validation of the infiltration modeling.

![Figure 3-3. Runoff-infiltration Generation.](image)

### 3.2.5 Groundwater Exposure Pathway

The groundwater model estimates the number of pathogens in a well downstream from a biosolids application site following individual wet weather events, and can be used to calculate the risk of pathogen exposure through groundwater when it is coupled with the probability of an individual rainfall event. The groundwater exposure model links models of pathogen transport vertically through saturated or unsaturated infiltration, and horizontally through groundwater flow through saturated soil (Figure 3-4).

There are two primary functions of the program: 1) Determine the transport scenario during a rainfall event using an infiltration and runoff model (Sheets: GWPathogenModel and GWConstants); and 2) Predict the corresponding pathogen concentration in a downstream well using a subsurface fate and transport model (Sheet: GWTransportModel). Subsurface pathogen transport during wet weather events may be facilitated via a saturated wetting front connecting to the water table. If this saturated connection is established, there is no pathogen attenuation through the unsaturated zone buffer.

This model predicts groundwater transport by considering two distinct scenarios of transport. The scenarios depend on whether or not the infiltrating wetting front from a rainfall event saturates through to the ground water table, creating a fully saturated connection.
Scenario 1 (non-saturating rainfall event), assumes the depth to the water table is larger than wetting front depth, and pathogen attenuation includes three processes:

- Vertical transport through saturated soil above the wetting front,
- Vertical transport through unsaturated soil below the wetting front but above the water table,
- Horizontal transport through saturated soil through groundwater flow to the downstream well.

Scenario 2 (saturating rainfall event), assumes the depth to the water table is smaller than the wetting front depth during a rainfall event, and pathogens transport vertically in saturated soil above the wetting front and then join the saturated horizontal groundwater flow to the downstream well without any attenuation through unsaturated soil. Scenario 2 presents a greater risk of pathogen transport. The infiltration model used to predict the transport scenario is based on a Joint Green-Ampt model, which was developed to facilitate use in a spreadsheet environment. The model incorporates the Explicit Green-Ampt solution (Salvucci and Entekhabi, 1994) into the Constant Flux Green-Ampt model to estimate infiltration rate, cumulative infiltration, and depth of wetting front, and is described extensively in the Surface Water Exposure Model Technical Document (Chapter 7.0).

The model provides a time-dependent, pathogen concentration profile as a function of distance from the application field. The advection-dispersion equation with adsorption and decay is used for modeling vertical transport through soil saturated by the infiltrating wetting front, as well as for modeling horizontal transport with groundwater flow to a downstream drinking well at the depth of the wetting front. The cumulative number of pathogens is calculated at a specified distance downstream. The depth of the unsaturated barrier can be determined by the difference between the water table depth and the wetting front depth. Pathogen attenuation in unsaturated soil is modeled considering mass transfer across the liquid-solid and liquid-air interfaces.

A detailed description of the infiltration model is presented in Chapter 7.0, the Surface Water Exposure Model Technical Document, and the subsurface transport and fate models can be found in Chapter 8.0, the Groundwater Exposure Model Technical Document. The constants used are summarized in Appendix E, and a description of the subfactors for the groundwater exposure model is presented in Appendix F. Validation of the transport model in both saturated and unsaturated porous media is presented in Appendix G.
3.2.6 Indirect Ingestion Exposure Pathway

During land-application of biosolids, biosolids are deposited on land and are mixed with soil particles. If there is a rainfall event after the application, some of the biosolids-associated pathogens may be released to runoff water and can flow to an adjacent vegetated field. The indirect ingestion model calculates the number of biosolids-associated pathogens present on vegetables in an adjacent field after land-application of biosolids, and human exposure associated with consumption of the biosolids-contaminated vegetables (Sheet: VegePathogenModel). Risk of infection and risk of illness due to pathogen ingestion for different subpopulation types is based on pathogen concentrations on ingested lettuce leaves. Chapter 9.0 provides technical information on the mathematical details of the model.

3.2.7 Assumptions of the Model

General assumptions of the SMART Biosolids model are summarized below. Assumptions specific to the direct ingestion, air exposure, surface water, groundwater and indirect ingestion exposure models are described in the pathway-specific technical documents presented in Chapters 4.0 through 9.0, respectively.

1) Land-applied biosolids are assumed to be the only source of pathogens in this work;
2) The model assesses the risk to humans only;
3) For a given biosolids-associated pathogen, exposures from different media are independent of each other (this enables risks to be aggregated across pathogens in a straightforward manner);
4) Exposures to different biosolids-associated pathogens are independent of each other;
5) Exposure factors for different routes and subpopulations are based on values from the EPA Exposure Factor Handbook (U.S. EPA, 1997);
6) When a dose-response model is not available for the inhalation route, an ingestion-based dose-response model is used with ingested dose equal to 50% of the inhaled dose (Brooks et al., 2005b). This is a rough estimation of the fraction of microbes that deposit in the upper respiratory system during inhalation and are transferred to the digestive system through the mucociliary escalator.

3.3 Model Interface and Inputs

The SMART Biosolids model runs in the Microsoft Excel environment using Visual Basic Macros. The following section describes the user interface, input variables and constants used to build and run the model. This information is presented both for the composite SMART Biosolids model, and also for the individual spreadsheet programs that model the five exposure pathways. Risk assessment calculations are based on human exposure doses generated from predicted pathogen concentrations in environmental media (soil, air, surface water, groundwater and vegetables), as determined by the five exposure pathway models.

Risk assessment calculations are performed on a Visual Basic (VBA) platform. To open the VBA module, open the SMARTBiosolids_June29_11.xlsm file and select Enable Macros (Figure 3-5a). For Excel 2003 users, go to Tools -> Macro -> Macros (Figure 3-5b), select Sheet24.RiskCal (Figure 3-5c) (See Appendix A for more on this macro) which opens the RiskCal macro (Figure 3-5d). After entering input parameters into the Input Data Sheet (Sheet:
Inputdata) (Figure 3-6), press F5 to run the VBA module (Figure 3-5d). For Excel 2007 go to the View tab, select Macros, and then View Macros. From the dialogue box, select Sheet24.RiskCal and Run.

![Figure 3-5a. Enabling of Macros in Excel 2003.](image)

![Figure 3-5b. Opening of VBA Module in Excel 2003.](image)
Figure 3-5c. Selection of the Sheet24.RiskCal Macro and Clicking of Edit Button to Open the Visual Basic Program.
(Sheet: Visual Basic Module, Program: Sheet24.RiskCal)

![Visual Basic Program Interface](image)

Figure 3-5d. Visual Basic Program Code for Conducting Risk Assessment; Press F5 for Running the Visual Basic Program.
(Sheet: Visual Basic Module, Program: Sheet24.RiskCal)

```
Sub RiskCalc()
    'PARAMETERS INITIALIZATION
    'Activate "RiskOutput" sheet
    Sheets("RiskOutput").Activate
    Dim Starttime, Stoptime
    Starttime = Time  'Recording start time
```
3.3.1 User Interface

The user interface contains three major components: 1) input variables (highlighted in blue), representing site-specific information about land, climate, biosolids application, exposed populations, and pathogens of concern; 2) default parameter values (highlighted in green), representing default values filled in with constants considered applicable to many situations but which may be edited by the advanced user to better reflect site-specific values; and 3) modeling outputs and results (highlighted in yellow). All input data for the model are listed and entered in the sheet Inputdata (Figure 3-7). These input data are used by the submodels for each of the five exposure pathways. Many of the pathway-specific constants and default values (green cells) and modeling outputs (yellow cells) are contained in sheets specific to those exposure pathways. Table 3-1 lists the relevant sheets where input data, default parameters and modeling outputs may be found for overall risk assessment and each exposure pathway. Input variables, constants, and model outputs are described below for specific exposure pathways. Overall results from the risk assessment and information on how to interpret these results is presented in Section 3.4.

### Table 3-1. List of SMART Biosolids Sheets Containing Input Variables, Default Parameters and Modeling Results for Risk Assessment and Five Exposure Pathways.

<table>
<thead>
<tr>
<th>Exposure Pathway</th>
<th>Input Variables</th>
<th>Default Parameters</th>
<th>Modeling Results</th>
</tr>
</thead>
<tbody>
<tr>
<td>Direct Ingestion</td>
<td>Inputdata</td>
<td>SoilPathogenModel</td>
<td>SoilPathogenModel</td>
</tr>
<tr>
<td>Air</td>
<td>Inputdata</td>
<td>AirConstants</td>
<td>AirOccupational</td>
</tr>
<tr>
<td></td>
<td></td>
<td>SurfaceConstants</td>
<td>AirResAdult</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pathogen</td>
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<td></td>
<td></td>
<td>AirOccupational</td>
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<td></td>
<td>SWPathogenModel</td>
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<tr>
<td>Surface Water</td>
<td>Inputdata</td>
<td>SurfaceConstants</td>
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<td></td>
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<td>SWRainModel</td>
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<td></td>
<td></td>
<td>SWPathogenModel</td>
<td>Barrenplot</td>
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<td>Pathogen</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>SWPathogenModel</td>
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</tr>
<tr>
<td>Groundwater</td>
<td>Inputdata</td>
<td>GWPathogenModel</td>
<td>GWPathogenModel</td>
</tr>
<tr>
<td>Indirect Ingestion</td>
<td>Inputdata</td>
<td>VegePathogenModel</td>
<td>VegePathogenModel</td>
</tr>
<tr>
<td>Risk Assessment</td>
<td>Inputdata</td>
<td>RiskConstants</td>
<td>RiskOutput</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pathogen</td>
<td></td>
</tr>
</tbody>
</table>

Figure 3-6. Input Data Sheet.
(Sheet: InputData)
Figure 3-7. A Snapshot of the Inputdata Sheet Showing Different Input Parameters.
(Sheet: Inputdata).
### 3.3.2 Risk Assessment

The input parameters, constant values and output parameters used in the risk assessment are listed in Table 3-2, along with their location in the SMART Biosolids modeling tool. A more detailed explanation of the parameters follows.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Unit</th>
<th>Definition</th>
<th>Sheet Title</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Input parameter</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pathogen</td>
<td>-</td>
<td>Pathogen of interest</td>
<td>Inputdata (Cell C24)</td>
</tr>
<tr>
<td>Sub_pop</td>
<td>-</td>
<td>Exposed subpopulation</td>
<td>Inputdata (Cell C25)</td>
</tr>
<tr>
<td>Route</td>
<td>-</td>
<td>Pathway</td>
<td>Inputdata (Cell C26)</td>
</tr>
<tr>
<td>( t_{\text{Soilconc}} )</td>
<td>Days</td>
<td>Time of soil ingestion after biosolids application</td>
<td>Inputdata (Cell C28)</td>
</tr>
<tr>
<td>( t_{SW} )</td>
<td>Days</td>
<td>Time of exposure to pond water after biosolids application</td>
<td>Inputdata (Cell C29)</td>
</tr>
<tr>
<td>Iteration</td>
<td>-</td>
<td>Number of iterations required to calculate uncertainty estimates</td>
<td>Inputdata (Cell C31)</td>
</tr>
<tr>
<td>Restore</td>
<td>-</td>
<td>Restore variable data</td>
<td>Inputdata (Cell C32)</td>
</tr>
<tr>
<td>Uchoice</td>
<td>-</td>
<td>Uncertainty analysis choice</td>
<td>Inputdata (Cell C33)</td>
</tr>
<tr>
<td><strong>Constants</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Model( D-R )</td>
<td>-</td>
<td>Dose-response model</td>
<td>Pathogen (Cell W11)</td>
</tr>
<tr>
<td>( R )</td>
<td>-</td>
<td>Exponential dose-response model parameter</td>
<td>Pathogen (Cell X11)</td>
</tr>
<tr>
<td>a, b</td>
<td>-</td>
<td>Beta-poisson dose-response model parameters</td>
<td>Pathogen (Cell Y11-Z11)</td>
</tr>
<tr>
<td>Medium( \text{exp} )</td>
<td>-</td>
<td>Exposure medium</td>
<td>Technical Document</td>
</tr>
<tr>
<td>Age( subpopulation )</td>
<td>Years</td>
<td>Age of the exposed subpopulation</td>
<td>Technical Document</td>
</tr>
<tr>
<td>( E_r )</td>
<td>( \text{m}^2/\text{day or mg/day or L/day} )</td>
<td>Exposure rate</td>
<td>RiskConstants (Cell O4)</td>
</tr>
<tr>
<td>( D_{\text{exp}} )</td>
<td>h/day</td>
<td>Exposure duration</td>
<td>RiskConstants (Cell P4)</td>
</tr>
<tr>
<td>( D_{\text{exp,app}} )</td>
<td>Days/application period</td>
<td>Exposure duration/application period</td>
<td>RiskConstants (Cell Q4)</td>
</tr>
<tr>
<td>( \eta_{\text{morb,pathogen}} )</td>
<td>-</td>
<td>Pathogen morbidity rate (ratio of illness risk to infection risk)</td>
<td>Pathogen (Cell AR11)</td>
</tr>
<tr>
<td><strong>Output Parameters</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>( D_{\text{exp}} )</td>
<td>No./day</td>
<td>Exposure dose</td>
<td>Technical Document</td>
</tr>
<tr>
<td>( D_{\text{exp,50%}} )</td>
<td>No/day</td>
<td>Median effective dose (i.e., a dose required to infect 50% of the population)</td>
<td>Technical Document</td>
</tr>
<tr>
<td>RiskInf</td>
<td>-</td>
<td>Infection risk</td>
<td>Technical Document</td>
</tr>
<tr>
<td>RiskInf( \text{daily} )</td>
<td>Infection risk/day</td>
<td>Daily risk of infection</td>
<td>Technical Document</td>
</tr>
</tbody>
</table>

---

*Site Specific Risk Assessment Tools for Land Applied Biosolids* 3-11
3.3.2.1 Input Variables

i. **Results of interest (Sheet Inputdata):** Pathogen-of-interest (Pathogen, Cell: C24), Exposed Population (Sub_pop, Cell: C25), Pathway-of-interest (Route, Cell: C26): The model automatically calculates risks for the full suite of pathogens pathways and subpopulations. In some cases, identifying results for a specific pathogen from large tables of output results may be confusing. For this reason, the user has the flexibility to select results for a specific pathogen (pathogen) (-) (Cell: C24), subpopulation (Sub_pop) (-) (Cell: C25), and pathway (Route) (-) (Cell: C26). These results are then pulled from the overall results table into separate tables for easier access.

ii. **Information for Monte Carlo Uncertainty Analysis (Sheet: Inputdata):** The model performs a Monte Carlo uncertainty analysis using the Sheet24.RiskCal macro (See Appendix A for more on this macro). The model requires a user to enter number of iterations (Cell C31, Sheet: Inputdata). The Monte Carlo analysis will overwrite the nominal values for model inputs with simulated values. The user has the option to restore the nominal values by selecting *yes* for the restore option in the Cell C32 (Sheet: Inputdata). In addition, the model provides the option for conducting uncertainty analysis for all pathogens or only for a selected pathogen-of-concern (Cell C33, Sheet: Inputdata) in order to reduce model run time.

3.3.2.2 Constants

This section describes parameters for which default values are used in this study. The user has the flexibility to accept these default values or to input different values of these constants (Sheets: Pathogen and RiskConstants).

i. **Dose-Response Model (ModelD,R) (-) (Sheet: Pathogen) (Cells: A152-X179) (Figure 3-8a):** Based on the selection of a pathogen-of-interest (Pathogen) (-) and exposure route (Route) (-), the dose-response model and related model parameters (\( r \) for exponential dose-response model; \( a \) and \( b \) for beta-poisson dose-response model) are selected. Values of these constants are shown in Tables A-1 to A-3 (Appendix E). For enteroviruses, inhalation risk is calculated using an inhalation dose-response model for coxsackievirus and ingestion risk is calculated using ingestion dose-response model for Echovirus.
Inhalation Dose-response models

Parameter ("r") ("r" for exponential and "alpha/beta" for beta-poisson models)

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>Pathogen D-flip Distribution (Mean)</th>
<th>Standard Minimum</th>
<th>Minimum</th>
<th>Standard Error of mean</th>
<th>Standard Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cryptosporidium</td>
<td>1 1 0</td>
<td>4.1E-04</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Campylobacter</td>
<td>2 0 0</td>
<td>1.0E-06</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Escherichia coli</td>
<td>2 0 0</td>
<td>1.0E-07</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Vibrio cholerae</td>
<td>4 1 0</td>
<td>2.0E-02</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bacillus anthracis</td>
<td>5 0 0</td>
<td>1.0E-05</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pseudomonas aeruginosa</td>
<td>6 0 0</td>
<td>1.0E-08</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Salmonella spp.</td>
<td>7 0 0</td>
<td>1.0E-09</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Enterobacter aerogenes</td>
<td>8 2 0</td>
<td>1.0E-06</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Helicobacter pylori</td>
<td>9 0 0</td>
<td>1.0E-09</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Figure 3-8a. Dose-Response Model Parameters.**
(Sheet: Pathogen)

**ii. Exposure (Figures 3-8b and 3-8c)** (Sheet: RiskConstants): Exposure factors used to calculate doses for different subpopulations and summarized in the sheet RiskConstants (Cells: A5-I32) (Figure 3-8b). Exposure to pathogens depends on exposure rate (E_r) and exposure duration (D_exp) which are presented in the sheet RiskConstants (Cells: M1-Q31) (Figure 3-8c), the exposure medium (Mediumexp) (-), and age of the exposed subpopulation (Age_subpopulation) (years). Depending on the exposure medium and exposed subpopulation (Subpoppop), the exposure rate is selected from Tables A-2 to A-5 (Appendix A). These default exposure rates are taken from the U.S. EPA Exposure Handbook (U.S. EPA, 1997). Similar to the exposure rate, values of daily exposure duration and exposure duration per application period (D_exp_app) (days/application period) (Sheet: RiskConstants) are selected from Tables A-6 to A-7 (Appendix A).

**Figure 3-8b. Exposure Concentrations During Transport of Microorganisms from Different Exposure Routes.**
(Sheet: RiskConstants)
### Pathogen Infection and Incidence Matrix (Figure 3-8d) (Sheet: Pathogen)

This matrix indicates whether a particular pathogen is associated with a particular health effect (0=no and 1=yes), such as respiratory and gastro-enteric infection and the severity of the illness (0=no adverse effects, 1= temporarily debilitating, 2= life threatening) (Cells AK11-AQ38) (Table A-6; Appendix A).

### Morbidity Rate ($\eta_{morb}$) (Figure 3-8d) (Sheet: Pathogen)

During pathogenic exposure, only a fraction of infections result in illness, depending on factors, such as host’s age and immune status; pathogen virulence and strain type; and exposure route (Regli et al., 1991). The morbidity rate parameter ($\eta_{morb,pathogen}$; Cells AR11-AS38) is the probability of illness given that an infection has occurred. This varies with pathogen type and host type. These values can be modified depending on availability of representative morbidity rate values (Table A-7; Appendix A).

---

<table>
<thead>
<tr>
<th>Pathogen Infection and Incidence Matrix (Casman, personal communication)</th>
<th>Pathogen Infection Index (Casman, personal communication)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pathogen Infection Index (Value = &quot;Y&quot; / Value = &quot;N&quot;)</td>
<td>Incidence Index in USA (Value = &quot;Y&quot; / Value = &quot;N&quot;)</td>
</tr>
<tr>
<td>Respiratory infection</td>
<td>Gastrointestinal infection</td>
</tr>
<tr>
<td>Gastrointestinal infection</td>
<td>Respiratory infection</td>
</tr>
<tr>
<td>Through normal or broken skin</td>
<td>Through normal or broken skin</td>
</tr>
</tbody>
</table>

---

**Figure 3-8c.** Exposure Constants for Different Subpopulations for Different Exposure Routes. (Sheet: RiskConstants)

**Figure 3-8d.** Pathogen Infection and Incidence Matrix and Pathogen Morbidity Rate. (Sheet: RiskConstants)

Note: (1) See values of infection and incidence indices for respiratory and gastro-enteric infection for different microorganisms in Cells AK11-AQ38. (2) See values of morbidity rates for different microorganisms in cells AR11-AS38.
v. **Parameters for Monte Carlo Uncertainty Analysis (Figure 3-9a-d) (Sheet: Pathogen):**

For conducting Monte Carlo uncertainty analysis using the `Sheet24.RiskCal` macro (See Appendix A for more on this macro), the present version of the model provides a structure for varying the following parameters: (1) Microbial concentration in biosolids (Cells I47-Q74) (Figure 3-9a), (2) pathogen release parameter (Cells) (Figure 3-9b), (3) Virus decay constants (Figure 3-9b), and (4) Groundwater model parameters (Figure 3-9c), and (5) Dose-response model parameters (Figure 3-9d). For each of these parameters, information such as probability distribution type and values of average, standard deviation, minimum, maximum, standard error of mean and standard deviation can be entered in the *Pathogen* sheet.

![Figure 3-9a. A Snapshot of the Pathogen Sheet Showing Different Statistical Information Used for Developing Model Distributions for Microbial Concentrations in Biosolids.](image)

Note: See columns I to P used for collecting statistical information. Information shown in green cells can be updated by the user.

![Figure 3-9b. A Snapshot of the Pathogen Sheet Showing Different Statistical Information Used for Developing Model Distributions for Microbial Concentrations in Biosolids.](image)

Note: Information shown in green cells can be updated.
3.3.2.3 Reading and Interpreting the Model Output

This section presents results of SMART Biosolids (Sheet: RiskOutput and Macro: Sheet24.RiskCal). See Appendix A for more description about the visual basic macro. Detailed descriptions of different output parameters are given below.

i. **Daily Risk of Infection/Application (Risk\textsubscript{inf,daily}) (Infection risk/day) (Macro: Sheet24.RiskCal):** Daily risk of infection of the selected pathogen-of-concern is calculated using the dose-response model of the pathogen for a given exposure medium (Equation 4-1; Chapter 4.0). A detailed description of different dose-response models of different biosolids-associated pathogens is given in Table A-1 (Appendix A). For the groundwater pathway, exposure from a single application occurs gradually over time as pathogens are slowly transported through the groundwater. For this reason the daily risk of infection is not constant, but varies over time. Detailed values of daily risk over time can be found in the Sheet GWPathogenModel, Cells: A92-E1092. Risk estimates are calculated in the GWPathogenModel spreadsheet (these calculations do not use Macro programming).

ii. **Infection Risk/Application Period (Risk\textsubscript{inf,app}) (Infection risk/application period) (Sheet: RiskOutput, Cells: R6-AR175) (Figure 3-10a):** Infection risk per application period is calculated using Equation 4-9 (Chapter 4.0), assuming all events of pathogen exposure are independent of each other. This parameter depends on Risk\textsubscript{inf,daily} (Macro: Sheet24.RiskCal)
A five-point statistical summary of risk estimates (average, standard deviation, 5th, 50th, and 95th percentile values) is presented to characterize the uncertainty in the risk estimates given the uncertainties in model inputs.

Figure 3-10a. A Snapshot of the RiskOutput Sheet Showing Five-Point Statistical Summary of Estimates of Risk of Infection per Application Period from the Air Exposure Route.

Note: See estimates for four subpopulations for different pathogens.


iv. **Disease-Based Illness Risk** (Figure 3-10 a-e.) (Sheet: RiskOutput, Macro: Sheet24.RiskCal): As not all pathogens initiate all kinds of illnesses, probabilities of particular illnesses are associated with specific pathogens, such as respiratory illness, gastrointestinal (GI) illness, and dermal or ocular infection through wound or broken skin, as well as different classes of effects, temporarily debilitating, termed as minor extent, hereafter, and possibly life threatening, termed as major extent, hereafter (Riskill_app, extent, disease, pathogen) (-). Figures 3-10b and 3-10c show a five-point statistical summary for risk of major illness per application period (Cells: AT8-BR175; Sheet: RiskOutput) and risk of minor illness per application period (Cells: BV8-CT175; Sheet: RiskOutput). Also, cumulative risks of getting an illness of minor or major extent (Riskinf_app, extent, disease) (-) are calculated using Equations 4-7 and 4-8. Five-point statistical summaries of these estimates are presented in Cells: CZ7-DV71 (Sheet: RiskOutput) (Tables 3-10d and 3-10e).
This section shows statistics of major risk of illness per application period.

"-100" values indicate that calculation is not done here as dose-response model info is not available.

### Air model

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>Occupational field worker</th>
<th>Occupational truck driver</th>
<th>Residential adult</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>95% lower</td>
<td>95% upper</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Figure 3-10b. A Snapshot of the RiskOutput Sheet Showing Five-Point Statistical Summary of Estimates of Risk of Major Illness per Application Period from the Air Exposure Route.

Note: See estimates for four subpopulations for different pathogens.
This section shows statistics of minor risk of illness per application period. “-100” values indicate that calculation is not done here as dose-response model info is not available.

Air model

Pathogens          Occupational field worker          Occupational truck driver          Residential adult

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>Air model</th>
<th>Occupational field worker</th>
<th>Occupational truck driver</th>
<th>Residential adult</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Average</td>
<td>Standard Deviation</td>
<td>5% quantile</td>
</tr>
<tr>
<td></td>
<td></td>
<td>50 periods</td>
<td>100 periods</td>
<td>100 periods</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Note: See estimates for four subpopulations for different pathogens.

Figure 3-10c. A Snapshot of the Risk Output Sheet Showing Five-Point Statistical Summary of Estimates of Risk of Minor Illness per Application Period from the Air Exposure Route.
Figure 3-10d. A Snapshot of the RiskOutput Sheet Showing Five-Point Statistical Summary of Estimates of Overall Risk of Minor Illness per Application Period from Different Exposure Routes for Different Subpopulations.
3.3.2.4 Output Data

Results from the model assessing risks of human infection from different exposure routes are shown in Figures 3-11a and 3-11b (Sheets: RiskOutput). Figure 3-11a shows a snapshot of results showing estimates of risk of infection and illness per application period for a selected pathogen-of-concern. Figure 3-11b shows a snapshot of results showing estimates of overall risk of illness per application for different subpopulations from different exposure routes.
### B. Overall infection and illness risks/application period (including all pathogens)\(w/o\) LOD

<table>
<thead>
<tr>
<th>Soil texture class</th>
<th>Exposure route</th>
<th>Exposed pop</th>
<th>Exp pop_ID</th>
<th>Respiratory infection</th>
<th>Respiratory infection</th>
<th>Gastrointestinal illness</th>
<th>Gastrointestinal illness</th>
<th>Overall risks of illness/application</th>
</tr>
</thead>
<tbody>
<tr>
<td>Loam</td>
<td>Ingestion, drinkingwater</td>
<td>occupational</td>
<td></td>
<td>1.643E-00</td>
<td>1.000E+00</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Ingestion, drinkingwater</td>
<td>residential, subPA</td>
<td></td>
<td>1.233E-00</td>
<td>1.000E+00</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Inhalation</td>
<td>occupational, TIO</td>
<td></td>
<td>1.500E-09</td>
<td>1.500E+09</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Inhalation</td>
<td>residential, ch/RC</td>
<td></td>
<td>1.362E-09</td>
<td>1.500E+09</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Figure 3-11b. Overall Infection and Illness Risks for Different Subpopulations from Different Exposure Routes.**

(Sheet: RiskOutput)
3.3.3 Direct Ingestion Pathway

The input parameters, constant values and output parameters used in the direct ingestion pathway are listed in Table 3-3, along with their location in the SMART Biosolids modeling tool. A more detailed explanation of the parameters follows. The default values of different constants are obtained from literature reports, which the user has the flexibility to accept or change.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Unit</th>
<th>Definition</th>
<th>Sheet Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>$I_{\text{rainfall}}$</td>
<td>-</td>
<td>An indicator to represent if rainfall occurs after land-incorporation of biosolids</td>
<td>Inputdata (Cell I8)</td>
</tr>
<tr>
<td>$t_{\text{soil,conc}}$</td>
<td>Days</td>
<td>Time of soil ingestion after biosolids application</td>
<td>Inputdata (Cell C28)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Input Parameters</th>
</tr>
</thead>
<tbody>
<tr>
<td>$N_0$</td>
</tr>
<tr>
<td>$F$</td>
</tr>
<tr>
<td>$N_{\text{attached}}$</td>
</tr>
<tr>
<td>$N_{\text{remain}}$</td>
</tr>
<tr>
<td>$N_{\text{remain,eff}}$</td>
</tr>
<tr>
<td>$k_{\text{decay,soil}}$</td>
</tr>
</tbody>
</table>

A screenshot showing the general user interface of the Soil Pathogen Model (Sheet: *SoilPathogenModel*) is shown in Figure 3-12.
3.3.3.1 Input Variables

This section describes the input parameters required for calculating the number of biosolids-associated pathogens present in soil following land-application of biosolids.

i. Does Rainfall Occur After Land-incorporation of Biosolids? (I_{rainfall}) (-) (Sheet: Inputdata, Cell: I8): The user enters either *Yes* or *No* to indicate if rainfall occurs after land-incorporation of biosolids and before human contact with the biosolids. This...
information is important for the model, as rainfall events induce some of the biosolids-associated pathogens to be released from the soil into the runoff water, thereby decreasing the effective number of biosolids-associated pathogens remaining in the soil.

ii. **Time of Soil Ingestion After Biosolids Application** ($t_{\text{soilconc}}$) (days) (Sheet: Inputdata, Cell: C28): This parameter is used to calculate the natural decay of biosolids-associated pathogens in soil following the biosolids application event.

### 3.3.3.2 Reading and Interpreting the Output

This section describes the output parameters calculated for the Soil Exposure Model (Sheet: SoilPathogenModel) (Figure 3-3). Detailed descriptions of these parameters are given below.

i. **Remaining Number of Biosolids-Associated Pathogens** ($N_{\text{remain}}$) (No./g biosolids) (Sheet: SoilPathogenModel, Cells: B15-B42): When no rainfall occurs the parameter $N_{\text{remain}}$ is equal to the initial number of pathogens applied on land ($N_0$) (No./g biosolids) (Sheet: Pathogen, Cells: B11-B38). When rainfall occurs after the biosolids application event, the parameter $N_{\text{remain}}$ is adjusted to reflect the fraction of pathogens which are washed off by the rainfall event, which is given by the pathogen release parameter ($f$) (-) (Sheet: Pathogen, Cells: C11-C38) (Equation 5-1; Chapter 5.0: Soil Exposure Model Technical Document).

ii. **Effective Number of Biosolids-Associated Pathogens in Soil** ($N_{\text{remain,eff}}$) (No./mg soil) (Sheet: SoilPathogenModel, Cell: C15-C42): This parameter represents the effective number of biosolids-associated pathogens present in a given mass of soil and is calculated using the remaining number of biosolids-associated pathogens in biosolids (i.e., $N_{\text{remain}}$; Sheet: SoilPathogenModel, Cells: B15-B42), the time of soil ingestion after biosolids application ($t_{\text{soilconc}}$) (day) (Sheet: SoilPathogenModel, Cell: C6), and the pathogen first-order decay parameter ($k_{\text{decay,soil}}$) (1/day) (Sheet: Pathogen, Cells: I11-I38) (Equation 5-2; Chapter 5.0: Direct Ingestion Exposure Model Technical Document).

### 3.3.3.3 Output Data

Calculated numbers of biosolids-associated pathogens present on soil are shown in Figure 3-13.

<table>
<thead>
<tr>
<th></th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>Output</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>11</td>
<td><strong>Pathogen</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>12</td>
<td>$N_{\text{remain}}$</td>
<td>$N_{\text{remain,eff}}$</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>13</td>
<td>1</td>
<td>$N_{0}$</td>
<td></td>
<td>$N_{\text{remain}}$</td>
<td></td>
</tr>
<tr>
<td>14</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>15</td>
<td>Cryptosporidium</td>
<td>9.20E-19</td>
<td>6.36E-24</td>
<td></td>
<td></td>
</tr>
<tr>
<td>16</td>
<td>Cyclospora</td>
<td>9.20E-19</td>
<td>9.20E-24</td>
<td></td>
<td></td>
</tr>
<tr>
<td>17</td>
<td>Entamoeba histolytica</td>
<td>9.20E-19</td>
<td>9.20E-24</td>
<td></td>
<td></td>
</tr>
<tr>
<td>18</td>
<td>Giardia lamblia</td>
<td>9.20E+10</td>
<td>3.15E+05</td>
<td></td>
<td></td>
</tr>
<tr>
<td>19</td>
<td>Microspora</td>
<td>9.20E-19</td>
<td>3.15E-24</td>
<td></td>
<td></td>
</tr>
<tr>
<td>20</td>
<td>Campylobacter jejuni</td>
<td>9.20E-01</td>
<td>2.51E-07</td>
<td></td>
<td></td>
</tr>
<tr>
<td>21</td>
<td>Clostridium</td>
<td>3.83E+07</td>
<td>3.80E+02</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>E. coli O157</td>
<td>9.20E-01</td>
<td>4.58E-07</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Figure 3-13. A Snapshot of the SoilPathogenModel Sheet Showing Output Parameters.*
### 3.3.4 Air Exposure Pathway

The input parameters, constant values and output parameters used in the air exposure pathway are listed in Table 3-5, along with their location in the SMART Biosolids modeling tool. A more detailed explanation of the parameters follows. The default values of different constants are obtained from literature reports, which the user has the flexibility to accept or change.

Table 3-5. Input Parameters, Constants, and Output Parameters Employed in the Air Exposure Pathway.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Unit</th>
<th>Definition</th>
<th>Sheet Title</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Input parameters</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Soil texture</td>
<td>-</td>
<td>Soil texture type</td>
<td>Inputdata (Cell C7)</td>
</tr>
<tr>
<td>Area</td>
<td>Acre</td>
<td>Area of application site</td>
<td>Inputdata (Cell C8)</td>
</tr>
<tr>
<td>Slope of the plot</td>
<td>%</td>
<td>Slope of the plot</td>
<td>Inputdata (Cell C9)</td>
</tr>
<tr>
<td>Application method</td>
<td>-</td>
<td>Application method</td>
<td>Inputdata (Cell C10)</td>
</tr>
<tr>
<td>Biosolids application rate</td>
<td>dry tons/acre</td>
<td></td>
<td>Inputdata (Cell C11)</td>
</tr>
<tr>
<td>Pathogen of interest</td>
<td>-</td>
<td>Pathogen of interest</td>
<td>Inputdata (Cell C24)</td>
</tr>
<tr>
<td>Subpopulation of interest</td>
<td>-</td>
<td>Subpopulation of interest</td>
<td>Inputdata (Cell C25)</td>
</tr>
<tr>
<td>Distance of residential population from biosolids application site</td>
<td>ft</td>
<td>Distance of residential population from biosolids application site</td>
<td>Inputdata (Cell C27)</td>
</tr>
<tr>
<td>Wind velocity</td>
<td>ft/sec</td>
<td>Wind velocity</td>
<td>Inputdata (Cell C6)</td>
</tr>
<tr>
<td>Solar irradiation</td>
<td>W/m²/day</td>
<td>Solar irradiation</td>
<td>Inputdata (Cell C17)</td>
</tr>
<tr>
<td><strong>Exposed population type</strong></td>
<td>%</td>
<td>Solids content in biosolids</td>
<td>SurfaceConstants (Cell J23)</td>
</tr>
<tr>
<td>Biosolids release rate</td>
<td>lb/sec</td>
<td>Biosolids release rate</td>
<td>AirOccupational (Cell C17)</td>
</tr>
<tr>
<td>X₁FW</td>
<td>ft</td>
<td>X-distance of field worker from source</td>
<td>AirOccupational (Cell C18)</td>
</tr>
<tr>
<td>Y₁FW</td>
<td>ft</td>
<td>Y-distance of field worker from source</td>
<td>AirOccupational (Cell C19)</td>
</tr>
<tr>
<td>y and z directional dispersion coefficients</td>
<td>ft</td>
<td>y and z directional dispersion coefficients</td>
<td>AirConstants (Cell B58)</td>
</tr>
<tr>
<td>Particle removal efficiency of a cabin filter</td>
<td>%</td>
<td>Particle removal efficiency of a cabin filter</td>
<td>AirConstants (Cell B11)</td>
</tr>
<tr>
<td>Number of pathogens in biosolids</td>
<td>No/g</td>
<td>Number of pathogens in biosolids</td>
<td>Pathogen (Cell B11)</td>
</tr>
<tr>
<td>First-order decay constant of pathogens in air</td>
<td>1/day</td>
<td>First-order decay constant of pathogens in air</td>
<td>Pathogen (Cell H11)</td>
</tr>
<tr>
<td>Net resuspension factor</td>
<td>1/ft</td>
<td>Net resuspension factor</td>
<td>AirConstants (Cell C70)</td>
</tr>
<tr>
<td><strong>Constants</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Biosolids dilutions in soil</td>
<td>-</td>
<td>Biosolids dilutions in soil</td>
<td>SWPathogenModel (Cell C164)</td>
</tr>
<tr>
<td>Amount of biosolids applied per unit area</td>
<td>Kg/m²</td>
<td>Amount of biosolids applied per unit area</td>
<td>SurfaceConstants (Cell C162)</td>
</tr>
<tr>
<td>Concentrations of resuspended biosolids-amended soil particles in air</td>
<td>lb/ft³</td>
<td>Concentrations of resuspended biosolids-amended soil particles in air</td>
<td>AirConstants (Cell C71)</td>
</tr>
<tr>
<td>Inhalation height</td>
<td>ft</td>
<td>Inhalation height</td>
<td>AirOccupational (Cell C5)</td>
</tr>
<tr>
<td>Source height</td>
<td>ft</td>
<td>Source height</td>
<td>AirOccupational (Cell C6)</td>
</tr>
<tr>
<td>Source velocity</td>
<td>ft/sec</td>
<td>Source velocity</td>
<td>AirOccupational (Cell C8)</td>
</tr>
<tr>
<td>Spray width</td>
<td>ft</td>
<td>Spray width</td>
<td>AirOccupational (Cell C10)</td>
</tr>
<tr>
<td>Interval</td>
<td>ft</td>
<td>Interval</td>
<td>AirOccupational (Cell C11)</td>
</tr>
<tr>
<td>Maximum x-dimension of the plot</td>
<td>ft</td>
<td>Maximum x-dimension of the plot</td>
<td>AirOccupational (Cell C12)</td>
</tr>
<tr>
<td>Maximum y-dimension of the plot</td>
<td>ft</td>
<td>Maximum y-dimension of the plot</td>
<td>AirOccupational (Cell C13)</td>
</tr>
<tr>
<td>X-distance of a receptor from boundary</td>
<td>ft</td>
<td>X-distance of a receptor from boundary</td>
<td>AirOccupational (Cell C14)</td>
</tr>
<tr>
<td>y-distance of a receptor from boundary</td>
<td>ft</td>
<td>y-distance of a receptor from boundary</td>
<td>AirOccupational (Cell C15)</td>
</tr>
<tr>
<td>Time after bioaerosol concentration is determined</td>
<td>sec</td>
<td>Time after bioaerosol concentration is determined</td>
<td>AirOccupational (Cell C16)</td>
</tr>
</tbody>
</table>
### Parameter | Unit | Definition | Sheet Title
--- | --- | --- | ---
\( Q_{application} \) | Kg/sec or L/sec | Biosolids application rate | SurfaceConstants (Cell E23)

#### Output parameters

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Unit</th>
<th>Definition</th>
<th>Sheet Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>( C_{air_biosolids_cell} )</td>
<td>lb/ft(^3)</td>
<td>Concentration of aerosolized biosolids, generated from a model cell</td>
<td>Technical Document</td>
</tr>
<tr>
<td>( C_{air_biosolids_plot} )</td>
<td>lb/ft(^3)</td>
<td>Total concentration of aerosolized biosolids, generated from a plot</td>
<td>Technical Document</td>
</tr>
<tr>
<td>( C_{air_biosolids_FW} )</td>
<td>lb/ft(^3)</td>
<td>Total concentration of aerosolized biosolids for a field worker</td>
<td>AirOccupational (Cell C74)</td>
</tr>
<tr>
<td>( C_{air_biosolids_cabin_TD} )</td>
<td>lb/ft(^3)</td>
<td>Total concentration of aerosolized biosolids for a truck driver</td>
<td>AirOccupational (Cell C75)</td>
</tr>
<tr>
<td>( C_{air_biosolids_RA} )</td>
<td>lb/ft(^3)</td>
<td>Total concentration of aerosolized biosolids for a residential-adult</td>
<td>AirResAdult (Cell C74)</td>
</tr>
<tr>
<td>( C_{air_biosolids_RC} )</td>
<td>lb/ft(^3)</td>
<td>Total concentration of aerosolized biosolids for a residential-child</td>
<td>AirResChild (Cell C74)</td>
</tr>
<tr>
<td>( C_{bioaerosols_FW} )</td>
<td>No./ft(^3)</td>
<td>Concentration of bioaerosols for a field worker</td>
<td>AirOccupational (Cell B81)</td>
</tr>
<tr>
<td>( C_{bioaerosols_TD} )</td>
<td>No./ft(^3)</td>
<td>Concentration of bioaerosols for a truck driver</td>
<td>AirOccupational (Cell C81)</td>
</tr>
<tr>
<td>( C_{bioaerosols_RA} )</td>
<td>No./ft(^3)</td>
<td>Concentration of bioaerosols for a residential-adult</td>
<td>AirResAdult (Cell C80)</td>
</tr>
</tbody>
</table>

### 3.3.4.1 Input Variables

The model should be customized to describe site-specific conditions and the method of biosolids application the user is contemplating. All the information that the user should supply to the Air Model is found in Table 3-6. The last column of this table is left blank so the user can fill it in with his or her choices before attempting to run the model. The cell locations refer to the worksheet named *Inputdata*. After compiling the list of values, the user should enter the values in the *Inputdata* worksheet. Some worksheet cells may already contain default values. These are supplied for those users who do not have location-specific information. Neglecting to replace default values with location-specific information will produce results that may not be reflective of actual site-specific conditions. The following section describes the input variables required by the model.
Table 3-6. List of Input Parameters for the Air Exposure Model.
(Sheet: Inputdata)

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Symbol/Unit</th>
<th>Cell Location</th>
<th>User Input</th>
</tr>
</thead>
<tbody>
<tr>
<td>Soil texture class (sand, loamy sand, sandy loam, etc.)</td>
<td>S Texture</td>
<td>Cell C7</td>
<td></td>
</tr>
<tr>
<td>Area of application site</td>
<td>A (acre)</td>
<td>Cell C8</td>
<td></td>
</tr>
<tr>
<td>Slope of the plot</td>
<td>Grade (%)</td>
<td>Cell C9</td>
<td></td>
</tr>
<tr>
<td>Application method (slinging, manure spreading, spraying through tank,</td>
<td>App_method (-)</td>
<td>Cell C10</td>
<td></td>
</tr>
<tr>
<td>and spray irrigation)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Biosolids application rate</td>
<td>B (dry tons biosolids/acre)</td>
<td>Cell C11</td>
<td></td>
</tr>
<tr>
<td>Pathogen-of-interest</td>
<td>Pathogen (-)</td>
<td>Cell C24</td>
<td></td>
</tr>
<tr>
<td>Subpopulation-of-interest (occupational worker, residential adults,</td>
<td>Sub_pop (-)</td>
<td>Cell C25</td>
<td></td>
</tr>
<tr>
<td>and residential children)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Distance of residential population to field</td>
<td>Ddist_res (ft)</td>
<td>Cell C27</td>
<td></td>
</tr>
<tr>
<td>Wind velocity</td>
<td>Vwind (ft/sec)</td>
<td>Cell I6</td>
<td></td>
</tr>
<tr>
<td>Solar irradiation</td>
<td>I, W/m²/day</td>
<td>Cell I7</td>
<td></td>
</tr>
<tr>
<td>Consider resuspension for occupational workers during biosolids</td>
<td>Resuspension (-)</td>
<td>Cell C30</td>
<td></td>
</tr>
</tbody>
</table>

i. **Field Conditions (Sheet: Inputdata, Cells: C7-C9):** Information about field conditions, such as soil texture (Cell C7), area (A; unit: Acre; Cell C8), and plot slope (Grade; unit: %; Cell C9) are required for characterizing the application area. The list of soil texture classes (Cell C7) includes sand, loamy sand, sandy loam, loam, silty loam, sandy clay loam, clay loam, silt clay loam, silty clay, clay, sandy clay, and silt. Information about plot area (A; Cell C8) is required for calculating plot dimensions.

ii. **Application Method (App_method) (-) (Cell: C10, Sheet: Inputdata):** The user provides information about the biosolids application method, such as slinging, splash-plate spraying, and disk incorporation, and biosolids application rate (B) (dry tons biosolids/acre) (Cell: C11, Sheet: Inputdata). This information is useful for calculating pathogen concentrations in biosolids at the source.

iii. **Wind Velocity (Sheet: Inputdata):** Aerosolization of biosolids and biosolids-associated pathogens depends on wind velocity (vwind, ft/sec) (Sheet: Inputdata, Cell: I6).

iv. **Solar Irradiation (I,) (-) (Figure 3-15):** The exact value of solar irradiation (I, W/m²/day) (Sheet: Inputdata, Cell: I7) is not used in the computations. Instead the specified value is used to place the solar irradiation into one of three categories, slight (<350 W/m²/day), moderate (350-700 W/m²/day), and high (>700 W/m²/day). This classification is governed by both the solar altitude (i.e., the vertical angle between the horizontal and the sun) and cloudiness. The Strong category relates to a condition when a solar altitude is greater than 60° with clear sky conditions in midsummer. The Slight category relates to a similar condition in midwinter or to a solar altitude from 15 to 30° with clear skies in midsummer.
v. **Consideration of Resuspension for Occupational Workers (Resuspension)** (-) *(Sheet: Inputdata, Cell: C30)*: Resuspension of biosolids-amended soils in air is also assumed due to wind activities and mechanical stresses (i.e., movement of vehicles on a plot with dry soil). The model provides the option of considering resuspension for occupational workers (Cell C30; InputData). This aspect is not considered for residential populations as they live at least 250 ft or 75 m from the application site and pathogen exposure concentrations due to these resuspended particles are assumed to be low. Upon selection of consideration for resuspension, a resuspension factor (RF) (1/ft) is calculated in the AirConstant sheet (Cell 70; Figure 3-14) and concentration of air-borne biosolids-amended soil is calculated (lb/ft³; AirConstants).

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
<th>F</th>
<th>G</th>
</tr>
</thead>
<tbody>
<tr>
<td>61</td>
<td><strong>Resuspension factor (RF) (1/ft)</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>62</td>
<td>Component</td>
<td>Mean</td>
<td>Min.</td>
<td>Max.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>63</td>
<td>Wind resuspension</td>
<td>4.55E-05</td>
<td>2.73E-11</td>
<td>9.09E-05</td>
<td></td>
<td></td>
</tr>
<tr>
<td>64</td>
<td>Mechanical stress</td>
<td>6.06E-03</td>
<td>3.03E-11</td>
<td>1.21E-02</td>
<td></td>
<td></td>
</tr>
<tr>
<td>66</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>67</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>68</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>69</td>
<td>Biosolids-amended soil (surface conc.)</td>
<td>lb/ft²</td>
<td>0.00128449</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>70</td>
<td>Net resuspension factor (RF_net)</td>
<td>1/ft</td>
<td>0.00060561</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>71</td>
<td>Biosolids-amended soil (air-borne conc.)</td>
<td>lb/ft³</td>
<td>7.78E-06</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>72</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Figure 3-14. A Snapshot of the AirConstants Sheet Showing Calculation Steps for Resuspension Factor and Concentrations of Air-Borne Biosolids Amended Soil.*

Note: Resuspension factor depends on wind velocity and mechanical stress due to vehicle motion on a field.

### 3.3.4.2 Constants

Certain constants are required to calculate concentrations of aerosolized biosolids and bioaerosols after application of biosolids on land. The default values for these constants are intended as good ballpark assumptions that do not require precise adjustments for most scenarios. In some cases, these values are automatically generated by the model when related choices on the Inputdata worksheet are entered. The following section presents descriptions of these constants used in the air exposure model.

i. **Inhalation Height (H_{inhalation}) (ft)** *(Figure 3-15)*: A default value of 6 feet is used as an inhalation height for occupational workers (Cell: C5, Sheet: AirOccupational) (Figure 3-15) and residential adults (Cell: C5, Sheet: AirResAdult). For residential children, a default value of 4 feet is used as an inhalation height (Cell C5, Sheet: AirResChild).

ii. **Biosolids Application** *(Figure 3-15)*: Based on the user-selected biosolids application method from the Inputdata sheet (Cell C10), values of related parameters for Air Exposure Model are auto-filled. These parameters are: height of the applicator equipment (i.e., source Height, H_{source}, ft) (Sheet: AirOccupational, Cell: C6), source velocity of the applicator equipment (i.e., v_{source}, ft/sec) (Sheet: AirOccupational, Cell: C8), spray width (i.e., W_{spray}, ft) (Sheet: AirOccupational, Cell: C10), and biosolids release rate (i.e., Q_{biosolids}, lb/sec) (Sheet: AirOccupational, Cell: C17). Here, source height refers to the height of the nozzle...
spraying biosolids after initial stabilization of the biosolids-plume, and source velocity is equal to the velocity of the applicator. Spray width is the width of ground covered by dispersion of biosolids in one pass, which corresponds to the dimension of one model grid cell along the x-direction (Figure 3-2). These values are intended to be common across different exposed individuals for a given exposure scenario and are obtained from the SurfaceConstants sheet (Table 3-7). To ensure that consistent values are used for both occupation and residential populations (Sheets: AirResAdult and AirResChild), values of these parameters for the residential populations are taken from the AirOccupational sheet.

**Figure 3-15. A Snapshot of Different Constants Used for Calculating Bioaerosol Concentrations for Occupational Workers.**

(Sheet: AirOccupational)

Note: The green cells represent either input parameters obtained from the Inputdata sheet or constant values obtained from the AirConstants sheet. The default values of different constants are obtained from the scientific literature and the user may change these values. Similar sets of constants are used for the AirResAdult and AirResChild sheets as well.

**Table 3-7. List of Biosolids Application-Related Constants Required for Air Exposure Model**

(Cells H23-P28; Sheet: SurfaceConstants) (Brooks et al., 2004; Kumar et al., in prep).
iii. **Plot Characteristics (Figure 3-15):** This study assumes a square plot (Figure 3-2). The user provides information about plot area (Sheet: *Inputdata*, Cell: C11), which is used to calculate length (i.e., maximum x-dimension \(X_{\text{max}} \text{ ft}\); Cell: C12) and width (i.e., maximum y-dimension \(Y_{\text{max}} \text{ ft}\); Cell: C13) (Sheet: *AirOccupational*; Figures 3-2). For residential populations (Sheets: *AirResAdult* and *AirResChild*), values of these parameters are taken from the *AirOccupational* sheet. Maximum x-dimension is the length of the application field along the x-axis, which is assumed to be perpendicular to the direction of the applicator’s back and forth travel across the field (Figure 3-2).

iv. **Interval Size (Size) (ft) (Figure 3-15):** This parameter (Sheet: *AirOccupational*, Cell: C11) is a dimension of each cell in the y-direction (Figure 3-2), which influences the precision of the calculation. Cell interval size is assumed to be equal to spray width (Cell: C10, Sheet: *AirOccupational*). In addition, the maximum number of cells may not exceed 2,500 and there can be no more than 50 cells along any axis in this version. The same value of interval size is used for residential populations and is taken from the *AirOccupational* sheet.

v. **Location of Receptor (Figure 3-15):** The x-distance of a receptor from the boundary \(X_{\text{rec-b}} \text{ ft}\) (Sheet: *AirOccupational*, Cell: C14) is the distance between the exposed person and the edge of the application field along the x-axis (Figure 3-2), which corresponds to the downwind distance of the exposed person (Sheet: *AirOccupational*). The y-distance from the boundary \(Y_{\text{rec-b}}\) is the distance between the western edge of the application field (or the left side of the generated grid). A residential adult or child is assumed to be standing outdoors, at the minimum distance \(\text{Dist}_{\text{res}} \text{ ft}\) (Sheet: *Inputdata*, Cell: C27) from the application site on X-axis (i.e., \(X_{\text{rec-b}} = \text{Dist}_{\text{res}} \text{ and } Y_{\text{rec-b}} = 0\)). A field worker is assumed to work behind the moving source at a constant distance \(X_{\text{FW}} = 6.6 \text{ ft, } Y_{\text{FW}} = 6.6 \text{ ft}\). A truck driver is assumed to move with the source.

### 3.3.4.3 Modeling Results

Once the constant values are entered into the *AirOccupational* sheet, a grid of the specified size is entered between cells C22 and AZ71. Each cell emits aerosols only during the time the applicator is located in that cell. This results in a traveling plume capable of producing intermittent spikes at a downfield site. The coordinates of each cell’s center point are displayed in blue, with the x-coordinates in column B and the y-coordinates in row 21 (*AirOccupational*). The origin \((x = 0, y = 0)\) is located at the bottom left of the grid (i.e., Cell B71, Sheet: *AirOccupational*). The model assumes that the applicator will start in the upper left corner of the grid (i.e., Cell B21, Sheet: *AirOccupational*) and will move left and right while working down toward the exposed individual (Figure 3-2). The remaining cells indicate the concentration of bioaerosols at the point of inhalation due to the contribution of that particular cell.

### 3.3.4.4 Reading and Interpreting the Output

This section describes the output parameters for occupational workers (Sheet: *AirOccupational* (Figures 3-16a) and residential population (Sheets: *AirResAdult* and *AirResChild*) (Figures 3-16b).
Figure 3-16a. A Snapshot of the AirOccupational Sheet Showing Concentrations of Aerosolized Biosolids and Aerosolized Pathogens for Occupational Field Workers and Truck Driver.
(Sheet: AirOccupational)

i. **Aerosolized Biosolids Particles (lb/ft³) (Figure 3-16):** The concentration of aerosolized biosolids particles is calculated separately for occupational workers (Sheet: AirOccupational) (Figure 3-16a), for adults in the residential population (C_{air,biosolids,RA}) (Cell: C74, Sheet: AirResAdult) (Figure 3-16b), and for children in the residential population (C_{air,biosolids,RC}) (Cell: C74, Sheet: AirResChild). The total concentration of aerosolized biosolids particles inside the truck cabin (C_{air,biosolids,cabin,TD}) (lb/ft³) (Cell: C75, Sheet: AirOccupational) includes the effect of cabin filters in removing particles (size > 3μm, Tanner et al., 2008) with particle filtration efficiency (η_{filter}, Cell: P4, Sheet: AirConstants). Airborne concentrations of resuspended biosolids-amended soils are calculated for occupational workers and added to concentrations of aerosolized biosolids (see Chapter 10.0 for details).

Figure 3-16b. A Snapshot of the AirResAdult Sheet Showing Concentrations of Aerosolized Biosolids and Aerosolized Pathogens for Residential Adults.
(Sheet: AirResAdult)

Note: Similar output parameters are also calculated for residential children (AirResChild).
ii. **Bioaerosols (C\textsubscript{bioaerosols} (No./ft\textsuperscript{3})):** Concentrations of aerosolized biosolids-associated pathogens, i.e., bioaerosols, depend on concentrations of aerosolized biosolids particles (\(C_{\text{air biosolids}}\) (lb/ft\textsuperscript{3})) (Cells: C74-75, Sheet: *AirOccupational*), pathogen concentrations in biosolids (\(N_0\) (No./g biosolids)) (Cells: B11-38, Sheet: *Pathogen*), and decay rate of pathogens in air (inactivation rate in air: \(k_{\text{decay,air}}\) (1/day)) (Cell: H11-38, Sheet: *Pathogen*). No pathogen decay is assumed for occupational workers due to the short transport distance (*AirOccupational*, Cells: B81-C108). For the residential population, concentrations of bioaerosols consider the effect of inactivation of pathogens in air, and are shown in sheets (*AirResAdult*, Cells: B80-107) and (*AirResChild*, Cells: B80-107), respectively.

### 3.3.4.5 Output Data

Output data in terms of concentrations of aerosolized pathogens are shown in *AirOccupational*, *AirResAdult*, and *AirResChild*. These concentrations are subsequently used in the *RiskModel* for calculating inhalation risks due to biosolids-associated pathogens (discussed in Chapter 4.0).
3.3.5 Surface Water Exposure Pathway

The input parameters, constant values and output parameters used in the surface water exposure pathway are listed in Table 3-8, along with their location in the SMART Biosolids modeling tool. A more detailed explanation of the parameters follows. The default values of different constants are obtained from literature reports, which the user has the flexibility to accept or change.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Unit</th>
<th>Definition</th>
<th>Sheet Title</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Input Parameters</strong></td>
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<tr>
<td>$T_{\text{storm}}$</td>
<td>Years</td>
<td>Storm return period</td>
<td>Inputdata (Cell C5)</td>
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<tr>
<td>$N_{\text{rain}}$</td>
<td>-</td>
<td>Number of rain events</td>
<td>Inputdata (Cell C12)</td>
</tr>
<tr>
<td>$T$</td>
<td>°F</td>
<td>Surface temperature</td>
<td>Inputdata (Cell C6)</td>
</tr>
<tr>
<td>$S_{\text{texture}}$</td>
<td>-</td>
<td>Soil texture class</td>
<td>Inputdata (Cell C7)</td>
</tr>
<tr>
<td>$A$</td>
<td>Acre</td>
<td>Area of application site</td>
<td>Inputdata (Cell C8)</td>
</tr>
<tr>
<td>Grade</td>
<td>%</td>
<td>Slope of the plot</td>
<td>Inputdata (Cell C9)</td>
</tr>
<tr>
<td>App_method</td>
<td>-</td>
<td>Application method</td>
<td>Inputdata (Cell C10)</td>
</tr>
<tr>
<td>$B$</td>
<td>Tons/acre</td>
<td>Biosolids application rate</td>
<td>Inputdata (Cell C11)</td>
</tr>
<tr>
<td>$L_{\text{VS}}$</td>
<td>ft</td>
<td>Length of a vegetative strip</td>
<td>Inputdata (Cell C17)</td>
</tr>
<tr>
<td>Grade$_{\text{VS}}$</td>
<td>%</td>
<td>Grade of a vegetative strip</td>
<td>Inputdata (Cell C18)</td>
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<td>$I_{\text{VS}}$</td>
<td>-</td>
<td>Indicator for presence of a vegetative strip</td>
<td>Inputdata (Cell C16)</td>
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<td>$L_{\text{ch}}$</td>
<td>ft</td>
<td>Length of a channel</td>
<td>Inputdata (Cell C20)</td>
</tr>
<tr>
<td>$W_{\text{ch}}$</td>
<td>ft</td>
<td>Width of a channel</td>
<td>Inputdata (Cell C21)</td>
</tr>
<tr>
<td>Grade$_{\text{ch}}$</td>
<td>%</td>
<td>Grade of a channel</td>
<td>Inputdata (Cell C22)</td>
</tr>
<tr>
<td>$I_{\text{ch}}$</td>
<td>-</td>
<td>Indicator for presence of a channel</td>
<td>Inputdata (Cell C19)</td>
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<tr>
<td>$I_{\text{im}}$</td>
<td>-</td>
<td>Indicator for presence of a farm pond</td>
<td>Inputdata (Cell C23)</td>
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<td>Pathogen</td>
<td>-</td>
<td>Pathogen-of-interest</td>
<td>Inputdata (Cell C24)</td>
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<td>sub_pop</td>
<td>-</td>
<td>Subpopulation-of-interest</td>
<td>Inputdata (Cell C25)</td>
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<tr>
<td>Route</td>
<td>-</td>
<td>Pathway-of-interest</td>
<td>Inputdata (Cell C26)</td>
</tr>
<tr>
<td>$Pa$</td>
<td>inches</td>
<td>Annual precipitation</td>
<td>Inputdata (Cell I4)</td>
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<td>inches/hr</td>
<td>Maximum 30-minute intensity</td>
<td>Inputdata (Cell I5)</td>
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<tr>
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<td>Inputdata (CellIC8)</td>
</tr>
<tr>
<td><strong>Constants</strong></td>
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<td></td>
<td></td>
</tr>
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<td>Form$_{\text{biosolids}}$</td>
<td>-</td>
<td>Form of biosolids</td>
<td>SurfaceConstants (Cell I23)</td>
</tr>
<tr>
<td>$Q_{\text{application}}$</td>
<td>Kg/s or L/s</td>
<td>Biosolids application rate</td>
<td>SurfaceConstants (Cell L23)</td>
</tr>
<tr>
<td>$f_{\text{biosolids}}$</td>
<td>%</td>
<td>Solid content in biosolids</td>
<td>SurfaceConstants (Cell J23)</td>
</tr>
<tr>
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<td>cm/h</td>
<td>Saturated hydraulic conductivity</td>
<td>SWRainModel (Cell C6)</td>
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<td>$\Lambda$</td>
<td>-</td>
<td>Pore size index</td>
<td>SWRainModel (Cell C7)</td>
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<td>-</td>
<td>Exponent of the Brooks-Corey conductivity model.</td>
<td>Technical Document</td>
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<td>cm</td>
<td>Air-entry head</td>
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<tr>
<td>$h_e$</td>
<td>cm</td>
<td>Air-exit head</td>
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<td>$\eta$</td>
<td>-</td>
<td>Capillary pressure at the wetting front</td>
<td>Technical Document</td>
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<td>$\theta_s$</td>
<td>cm$^3$/cm$^3$</td>
<td>Saturated volumetric content</td>
<td>SWRainModel (Cell B9)</td>
</tr>
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Table 3-8. Input Parameters, Constants, and Output Parameters Employed in the Surface Water Exposure Pathway.
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<th>Unit</th>
<th>Definition</th>
<th>Sheet Title</th>
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<td>Residual volumetric water content</td>
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<td>R</td>
<td>cm/h</td>
<td>Rainfall rate</td>
<td>SWRainModel (Cell B14)</td>
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<tr>
<td>T</td>
<td>Hours</td>
<td>Rainfall duration</td>
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<td>Cm</td>
<td>Ponding depth</td>
<td>SWRainModel (Cell B16)</td>
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<td>$t_0$</td>
<td>h</td>
<td>Time when surface saturation occurs</td>
<td>SWRainModel (Cell H20)</td>
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<tr>
<td>$\Delta t$</td>
<td>day</td>
<td>Duration for calculating remaining pathogen concentration in farm pond</td>
<td>SWPathogenModel (Cell C7)</td>
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<td>$R_{eq}$</td>
<td>EI unit</td>
<td>Equivalent erosivity values for cold weather conditions</td>
<td>Technical Document</td>
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<td>Indicator for considering the effects of cold weather conditions on sediment erosion</td>
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<td>-</td>
<td>Ponding subfactor</td>
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<td>$p_d$</td>
<td>-</td>
<td>Subsurface drainage subfactor</td>
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<td>Farm pond volume</td>
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<td>$V_{runoff,land}$</td>
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<td>Runoff volume on land</td>
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<td>$\sin \theta$</td>
<td>%</td>
<td>Sine of angle of plot with horizontal</td>
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<td>S</td>
<td>-</td>
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<td>Slope exponent factor</td>
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<td>$\beta$</td>
<td>-</td>
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<td>$s_c$</td>
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<td>ton/acre. EI unit</td>
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<td>Texture subfactor</td>
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<td>Soil profile permeability</td>
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<td>Canopy subfactor</td>
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<td>Groundcover subfactor</td>
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<td>Soil subsurface subfactor</td>
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<td>Ridge height subfactor</td>
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<td>$E$</td>
<td>hundreds of foot-ton/acre</td>
<td>Total storm energy</td>
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<td>Ton/acre</td>
<td>Combined surface factor for land</td>
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<td>$B_{total}$</td>
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<td>Initial pathogen load in biosolids</td>
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<td>Fraction of biosolids in biosolids-soils matrix</td>
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<td>-</td>
<td>Release parameter</td>
<td>Pathogen (Cell C11)</td>
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<td>$P_{si}$</td>
<td>%</td>
<td>Percentage silt fraction</td>
<td>SWPathogenModel (Cell C15)</td>
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<tr>
<td>$P_{sd}$</td>
<td>%</td>
<td>Percentage sand fraction</td>
<td>SWPathogenModel (Cell C16)</td>
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<tr>
<td>$P_{cl}$</td>
<td>%</td>
<td>Percentage clay fraction</td>
<td>SWPathogenModel (Cell C18)</td>
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<tr>
<td>$P_{vfs}$</td>
<td>%</td>
<td>Percentage of very fine sand</td>
<td>SWPathogenModel (Cell C17)</td>
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<tr>
<td>$O_m$</td>
<td>%</td>
<td>Percentage organic matter</td>
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<td>Soil profile permeability rating</td>
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<td>Soil roughness due to the soil disturbing operation</td>
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<td>Tillage intensity</td>
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<tr>
<td>$B$</td>
<td>1/percent</td>
<td>Relative effectiveness of groundcover</td>
<td>Technical Document</td>
</tr>
<tr>
<td>$k_a$</td>
<td>1/day</td>
<td>Overall inactivation constant in water</td>
<td>Pathogen (Cell E11)</td>
</tr>
<tr>
<td>$B_a$</td>
<td>lb./(acre.in.)</td>
<td>Mass of the live and dead root biomass averaged over 10&quot;</td>
<td>Technical Document</td>
</tr>
<tr>
<td>$B_r$</td>
<td>lb./(acre.in.)</td>
<td>Amount of buried residue</td>
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<td>Canopy shape</td>
<td>-</td>
<td>Canopy shape</td>
<td>Technical Document</td>
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<tr>
<td>Locsurfarea</td>
<td>-</td>
<td>Location of surface area concentration</td>
<td>Technical Document</td>
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<tr>
<td>$h_{top}$</td>
<td>ft</td>
<td>Height of the top of canopy</td>
<td>Technical Document</td>
</tr>
<tr>
<td>$h_{bot}$</td>
<td>ft</td>
<td>Height of the bottom of canopy</td>
<td>Technical Document</td>
</tr>
<tr>
<td>$a_s$</td>
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<td>Shape coefficient</td>
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<td>$a_g$</td>
<td>-</td>
<td>Groundcover coefficient</td>
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<td>Manning’s constant</td>
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<td>$b_2$</td>
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<td>-</td>
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<td>SWPathogenModel (Cell C56)</td>
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<td>$V_f$</td>
<td>ft/sec</td>
<td>Fall velocity of sediments of a kth particle class in still water</td>
<td>SurfaceConstants (Cell V51)</td>
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<td>$f_{SDR}$</td>
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<td>Surface delivery ratio</td>
<td>Technical Document</td>
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<tr>
<td>$C_0$</td>
<td>No./L</td>
<td>Initial pathogen concentration in farm pond</td>
<td>Pathogen (Cell D11)</td>
</tr>
<tr>
<td>$s_u$</td>
<td>-</td>
<td>Slope of the segment with higher Manning’s constant</td>
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</tr>
<tr>
<td>$s_i$</td>
<td>-</td>
<td>Slope of the segment with lower Manning’s constant</td>
<td>Technical Document</td>
</tr>
<tr>
<td>$q_{inf}$</td>
<td>cm/h</td>
<td>Infiltration rate</td>
<td>SWRainModel (Cell C21)</td>
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<tr>
<td>$I$</td>
<td>cm</td>
<td>Cumulative infiltration</td>
<td>SWRainModel (Cell C22)</td>
</tr>
<tr>
<td>$r_{total}$</td>
<td>cm</td>
<td>Total rainfall</td>
<td>SWRainModel (Cell C23)</td>
</tr>
<tr>
<td>$V_{runoff}$</td>
<td>cm</td>
<td>Runoff</td>
<td>SWRainModel (Cell C24)</td>
</tr>
<tr>
<td>$f_{runoff}$</td>
<td>-</td>
<td>Surface runoff ratio</td>
<td>SWRainModel (Cell C25)</td>
</tr>
<tr>
<td>$V_{inf}$</td>
<td>m³</td>
<td>Infiltration volume</td>
<td>SWRainModel (Cell C26)</td>
</tr>
<tr>
<td>$V_{rain}$</td>
<td>m³</td>
<td>Rainfall volume</td>
<td>SWRainModel (Cell C27)</td>
</tr>
<tr>
<td>$V_{runoff}$</td>
<td>m³</td>
<td>Runoff volume</td>
<td>SWRainModel (Cell C28)</td>
</tr>
<tr>
<td>$g_i$</td>
<td>lb/sec/ft</td>
<td>Sediment load leaving the ith segment</td>
<td>Barrenplot (Cell J11)</td>
</tr>
<tr>
<td>$D_{ii}$</td>
<td>lb/sec/ft²</td>
<td>Sediment load produced per unit segment length due to interrill erosion in the ith segment</td>
<td>Barrenplot (Cell J11)</td>
</tr>
<tr>
<td>Parameter</td>
<td>Unit</td>
<td>Definition</td>
<td>Sheet Title</td>
</tr>
<tr>
<td>-----------</td>
<td>------</td>
<td>------------</td>
<td>-------------</td>
</tr>
<tr>
<td>(D_{\text{drop}}(i))</td>
<td>lb/sec/ft²</td>
<td>Sediment load either detached from surface (with a &quot;+&quot; sign) or deposited to the surface (with a &quot;-&quot; sign) per unit segment length</td>
<td>Technical Document</td>
</tr>
<tr>
<td>(T_{ci-1})</td>
<td>lb/sec/ft</td>
<td>Sediment transport capacity</td>
<td>Barrenplot (Cell G11)</td>
</tr>
<tr>
<td>(\Psi_k)</td>
<td>-</td>
<td>Mass fraction of sediment in the kth sediment class.</td>
<td>SurfaceConstants (Cell F51)</td>
</tr>
<tr>
<td>(K_T)</td>
<td>-</td>
<td>Transportability coefficient for sediments</td>
<td>Technical Document</td>
</tr>
<tr>
<td>(\zeta)</td>
<td>-</td>
<td>Extent of effect of hydraulic resistance on sediment transport capacity</td>
<td>Technical Document</td>
</tr>
<tr>
<td>(\sigma_i)</td>
<td>ft²/s</td>
<td>Excess rainfall in that segment</td>
<td>Technical Document</td>
</tr>
<tr>
<td>(D_{\text{combined}})</td>
<td>lb/sec/ft²</td>
<td>Total amount of sediment eroded due to the effects of interrill and rill erosion</td>
<td>Technical Document</td>
</tr>
<tr>
<td>(D)</td>
<td>lb/sec/ft²</td>
<td>Sediment transport capacity</td>
<td>Barrenplot (Cell BJ11)</td>
</tr>
<tr>
<td>(\Delta x_b)</td>
<td>ft</td>
<td>Backwater length</td>
<td>SWPathogenModel (Cell C115)</td>
</tr>
<tr>
<td>(\theta_{ch})</td>
<td>-</td>
<td>Angle of the channel with horizontal</td>
<td>Technical Document</td>
</tr>
<tr>
<td>(g_{ch,k})</td>
<td>lb/sec/ft</td>
<td>Amount of sediment of a kth particle class leaving the channel</td>
<td>SWPathogenModel (Cell I135)</td>
</tr>
<tr>
<td>(g_{ch,total})</td>
<td>lb/sec/ft</td>
<td>Total sediment load in channel</td>
<td>SWPathogenModel (Cell V135)</td>
</tr>
<tr>
<td>(d_{ch,biosolids})</td>
<td>lb/L/day/(ft plot width)</td>
<td>Concentration of biosolids-associated particles in channel</td>
<td>SWPathogenModel (Cell AE135)</td>
</tr>
<tr>
<td>(g_{im,k})</td>
<td>lb/L/day/(ft plot width)</td>
<td>Amount of sediment load of kth particle class in farm pond after settling of particles</td>
<td>SWPathogenModel (Cell A143)</td>
</tr>
<tr>
<td>(C_i)</td>
<td>sec/ft</td>
<td>Trapping efficiency of farm pond for sediment particles</td>
<td>Technical Document</td>
</tr>
<tr>
<td>(g_{im,total})</td>
<td>lb/L/day/(ft plot width)</td>
<td>Total sediment load in farm pond</td>
<td>SWPathogenModel (Cell F143)</td>
</tr>
<tr>
<td>(d_{im,biosolids})</td>
<td>lb/L/day/(ft plot width)</td>
<td>Concentration of biosolids-associated particles in farm pond</td>
<td>SWPathogenModel (Cell N143)</td>
</tr>
<tr>
<td>(N_{\text{total}})</td>
<td>No.</td>
<td>Total pathogen applied on land</td>
<td>SWPathogenModel (Cell B151:178)</td>
</tr>
<tr>
<td>(N_R)</td>
<td>No.</td>
<td>Pathogen released from biosolids due to runoff</td>
<td>SWPathogenModel (Cell C151:178)</td>
</tr>
<tr>
<td>(N_{\text{attached}})</td>
<td>No.</td>
<td>Pathogen attached on biosolids after initial release</td>
<td>SWPathogenModel (Cell D151:178)</td>
</tr>
<tr>
<td>(ED_{\text{unattached}})</td>
<td>No.</td>
<td>Effective delivery of unattached-pathogen cells</td>
<td>SWPathogenModel (Cell E151:178)</td>
</tr>
<tr>
<td>(C_{\text{pathogen,im}})</td>
<td>No./L</td>
<td>Pathogen concentration in farm pond after mixing of runoff water with the farm pond water</td>
<td>SWPathogenModel (Cell H151:178)</td>
</tr>
<tr>
<td>(C_{\text{eff,pathogen,im}})</td>
<td>No./L</td>
<td>Effective pathogen concentration in farm pond after mixing of runoff with the farm pond water</td>
<td>SWPathogenModel (Cell I151:178)</td>
</tr>
<tr>
<td>(d_{\text{biosolids}})</td>
<td>No./L</td>
<td>Biosolid-sediment concentration in runoff water</td>
<td>Technical Document</td>
</tr>
<tr>
<td>(ED_{\text{attached}})</td>
<td>No.</td>
<td>Effective delivery of attached-pathogen cells</td>
<td>SWPathogenModel (Cell F151:178)</td>
</tr>
</tbody>
</table>
3.3.5.1 Input Variables

All the information that the user should supply to the Surface Water Exposure Model is found in Table 3-9. The last column of this table is left blank so the user can fill it in with his or her choices before attempting to run the model. The cell addresses refer to the worksheet named Inputdata. After compiling the list of values, the user should enter the values in the worksheet. Some worksheet cells may already contain default values. These are supplied for those users who do not have location-specific information. Neglecting to replace default values with location-specific information may produce output that is not relevant to conditions at a particular site. Detailed descriptions of different components are summarized below. Some of the constants, described in Appendix A and Appendix E, are hidden in the model. The user can see these hidden cells (highlighted in the gold color) by going to the Format menu, selecting Row and clicking the Unhide option in the sheet. All input parameters are shown in the Inputdata worksheet.
Table 3-9. List of Input Parameters Required for Running the Surface Water Exposure Model.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Symbol/Unit</th>
<th>Cell Location</th>
<th>User Input</th>
</tr>
</thead>
<tbody>
<tr>
<td>Location</td>
<td>Cell C3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Time between biosolids application and the onset of rain</td>
<td>$t_{rain}$ (days)</td>
<td>Cell C4</td>
<td></td>
</tr>
<tr>
<td>Return period</td>
<td>years</td>
<td>Cell C5</td>
<td></td>
</tr>
<tr>
<td>Temperature</td>
<td>$T$ (°C)</td>
<td>Cell C6</td>
<td></td>
</tr>
<tr>
<td>Soil texture class (sand, loamy sand, sandy loam, loam, silty loam, sandy clay loam, clay loam, silt clay loam, silty clay, clay, sandy clay, and silt)</td>
<td>$s_{texture}$</td>
<td>Cell C7</td>
<td></td>
</tr>
<tr>
<td>Area of application site</td>
<td>A (acre)</td>
<td>Cell C8</td>
<td></td>
</tr>
<tr>
<td>Slope of the plot</td>
<td>Grade (%)</td>
<td>Cell C9</td>
<td></td>
</tr>
<tr>
<td>Application method (slinging, manure spreading, spraying through tank, and spray irrigation)</td>
<td>App_method (-)</td>
<td>Cell C10</td>
<td></td>
</tr>
<tr>
<td>Biosolids application rate</td>
<td>B (dry tons/acre)</td>
<td>Cell C11</td>
<td></td>
</tr>
<tr>
<td>Water table depth</td>
<td>$h$ (ft)</td>
<td>Cell C13</td>
<td></td>
</tr>
<tr>
<td>Distance to well</td>
<td>L (ft)</td>
<td>Cell C14</td>
<td></td>
</tr>
<tr>
<td>Hydraulic gradient</td>
<td>$i$ (-)</td>
<td>Cell C15</td>
<td></td>
</tr>
<tr>
<td>Indicator for presence of a buffer zone</td>
<td>$l_{VS}$ (-)</td>
<td>Cell C16</td>
<td></td>
</tr>
<tr>
<td>Indicator for presence of a channel</td>
<td>$l_{O}$ (-)</td>
<td>Cell C19</td>
<td></td>
</tr>
<tr>
<td>Channel length</td>
<td>$L_{ch}$ (ft)</td>
<td>Cell C20</td>
<td></td>
</tr>
<tr>
<td>Channel width</td>
<td>$W_{ch}$ (ft)</td>
<td>Cell C21</td>
<td></td>
</tr>
<tr>
<td>Channel grade</td>
<td>$Grade_{ch}$ (-)</td>
<td>Cell C22</td>
<td></td>
</tr>
<tr>
<td>Indicator for presence of a farm pond</td>
<td>$l_{im}$ (-)</td>
<td>Cell C22</td>
<td></td>
</tr>
<tr>
<td>Pathogen-of-interest</td>
<td>Pathogen (-)</td>
<td>Cell C24</td>
<td></td>
</tr>
<tr>
<td>Subpopulation-of-interest (occupational worker, residential adults, and residential children)</td>
<td>Sub_pop (-)</td>
<td>Cell C25</td>
<td></td>
</tr>
<tr>
<td>Time of exposure after biosolids application</td>
<td>$t_{SW}$ (day)</td>
<td>Cell C29</td>
<td></td>
</tr>
<tr>
<td>Storm intensity</td>
<td>cm/h</td>
<td>Cell I9</td>
<td></td>
</tr>
<tr>
<td>Storm duration</td>
<td>$h$</td>
<td>Cell I10</td>
<td></td>
</tr>
<tr>
<td>Annual precipitation</td>
<td>Pa (inches)</td>
<td>Cell I4</td>
<td></td>
</tr>
<tr>
<td>Maximum 30-minute intensity</td>
<td>$I_{30}$ (inches/hr)</td>
<td>Cell I5</td>
<td></td>
</tr>
<tr>
<td>Does the rainfall occurs after biosolids application</td>
<td>$I_{rainfall}$ (-)</td>
<td>Cell I8</td>
<td></td>
</tr>
</tbody>
</table>

i. **Rainfall Characteristics (Sheet: Inputdata):** The user enters the location information in Cell C3 (Sheet: Inputdata), information about return period in Cell C5, storm intensity in Cell I9, and storm duration in Cell I10 ($N_{rain}$ (-) (Cell: C12). Further, the user selects if the rainfall occurs after biosolids application ($I_{rainfall}$ (-) (Cell: I8) and inputs time between biosolids application and the onset of rain ($t_{rain}$ (days)) in Cell C4 of the Inputdata sheet. In addition, the user needs to enter values for annual precipitation (Pa) (inches) (Cell: I4) which is used to calculate the slope exponent factor, and maximum 30-minute intensity ($I_{30}$) (inches/hr) (Cell I5) which is used to calculate the erosivity subfactor. If this cell is left blank then the rainfall intensity is used.
ii. **Temperature (T) (°C) (Sheet: Inputdata, Cell: C6):** Daily surface temperature is required to calculate rate of pathogen inactivation due to temperature.

iii. **Soil Texture Class (Stexture) (Sheet: Inputdata, Cell: C7):** The list of soil texture classes includes sand, loamy sand, sandy loam, loam, silty loam, sandy clay loam, clay loam, silt clay loam, silty clay, clay, sandy clay, and silt.

iv. **Area of Application Site (A) (Acre) (Sheet: Inputdata, Cell: C8):** The user needs to provide the area of the farm land where biosolids are applied. The model assumes a square plot. For runoff estimation and sediment routing purposes the length and width of the plot can be changed in Cells I11-I12 of the Inputdata sheet, keeping the plot area consistent (Cell C8, Inputdata sheet).

v. **Slope of the Plot (Grade) (%) (Sheet: Inputdata, Cell: C9):** The user inputs the slope of the plot of the land. This value is required to calculate natural slope of the land and slope-length factor, required for calculating sediment load.

vi. **Biosolids Application (Sheet: Inputdata):** The user provides information about the application method (Appl_method) (-) (Cell: C10) (i.e., instrument) used for applying biosolids on land, such as slinger, manure spreader, spray tanker, and spray irrigation and biosolids application rate (B) (dry tons biosolids/acre) (Cell: C11). Based on the user-selected biosolids application method from the Inputdata sheet (Cell C10), values of related parameters are auto-filled from Table 3-10.

<table>
<thead>
<tr>
<th>Application Method</th>
<th>Biosolid Material</th>
<th>Solids</th>
</tr>
</thead>
<tbody>
<tr>
<td>App_method</td>
<td>Formbiosolids</td>
<td>f_biosolids (%)</td>
</tr>
<tr>
<td>Surface spreading</td>
<td>Liquid</td>
<td>5.7</td>
</tr>
<tr>
<td>Spray irrigation</td>
<td>Liquid</td>
<td>5.7</td>
</tr>
<tr>
<td>Slinger</td>
<td>Cake</td>
<td>20</td>
</tr>
<tr>
<td>Manure spreader</td>
<td>Cake</td>
<td>20</td>
</tr>
</tbody>
</table>

vii. **Water Table Depth (h) (ft) (Sheet: Inputdata, Cell: C13):** The user inputs depth to water table which is used in the groundwater model (GWPathogenModel and GWTransportModel sheets) for calculating transport of pathogens in the saturated and unsaturated subsurface.

viii. **Distance to well (L) (ft) (Sheet: Inputdata, Cell: C14):** This information is required to calculate horizontal transport of pathogens in subsurface soil and is used in the groundwater model.
ix. **Hydraulic gradient (i) (-) (Sheet: Inputdata, Cell: C15):** Hydraulic gradient is needed to calculate groundwater velocity.

x. **Buffer Zone (Sheet: Inputdata):** This model allows for the presence of a buffer zone between the plot and a farm pond (indicator: I_{vS}) (-) (Cell: C16). The user has the flexibility to select or deselect the presence of a vegetative strip at the end of the barren plot.

xi. **Interceptor (Sheet: Inputdata):** This model allows for the presence of an interceptor, i.e. a channel, (indicator: I_{ch}) (-) (Cell: C19) after the water runs off the field and through the VFS (if the VFS is present). The channel (ch) length (L_{ch}) (ft) (Cell: C20), width (W_{ch}) (ft) (Cell: C21), and grade (Grade_{ch}) (-) (Cell: C22) are all user inputs. Following the channel, a farm pond (im) is assumed to be present (indicator: I_{im}) (-) (Cell: C23).

xii. **Time of Exposure after Biosolids Application (Sheet: Inputdata):** The model requires the user to input time of exposure for people drinking the farm pond water after the biosolids application event (i.e., t_{SW} (day), Cell: C29).

### 3.3.5.2 Constants

**Estimation of Surface Infiltration Rate and Surface Runoff Values** The following section describes constant parameters, used in estimating surface infiltration and runoff volumes. Values of these constants are summarized in the sheet *SurfaceConstants* (Figure 3-17). The user has the flexibility to accept these default values or to input different values of these soil properties in the sheet *SurfaceConstants*.

<table>
<thead>
<tr>
<th>N1</th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
<th>F</th>
<th>G</th>
<th>H</th>
<th>I</th>
<th>J</th>
<th>K</th>
</tr>
</thead>
</table>
| 1  | Constants for Surface Water Modeling | Red colored  
East Lansing, Ingham County, MI | | | | | | | | | |
| 2  | Constants for Surface Water (Joint Green-Ampt Model) | Information for creating highest runoff (based on net rainfall) | | | | | | | | | |
| 3  | Fallon, 1997 | | | | | | | | | | |
| 4  | | Sand, s_{sand} | 3.5 | 3.46 | 0.38 | 0.37 | Sand | | | | |
| 5  | | Loam, s_{loam} | 3.9 | 3.46 | 0.44 | 0.33 | Loam | | | | |
| 6  | | Clay, s_{clay} | 4.9 | 3.51 | 0.49 | 0.32 | Clay | | | | |
| 7  | | Clay-loam, s_{clay-loam} | 4.9 | 3.51 | 0.49 | 0.32 | Clay-loam | | | | |
| 8  | | Loam-clay, s_{loam-clay} | 4.9 | 3.51 | 0.49 | 0.32 | Loam-clay | | | | |
| 9  | | Clay-sandy, s_{clay-sandy} | 4.9 | 3.51 | 0.49 | 0.32 | Clay-sandy | | | | |
| 10 | | Sand, s_{sand} | 3.5 | 3.46 | 0.38 | 0.37 | Sand | | | | |
| 11 | | Loam, s_{loam} | 3.9 | 3.46 | 0.44 | 0.33 | Loam | | | | |
| 12 | | Clay, s_{clay} | 4.9 | 3.51 | 0.49 | 0.32 | Clay | | | | |
| 13 | | Clay-loam, s_{clay-loam} | 4.9 | 3.51 | 0.49 | 0.32 | Clay-loam | | | | |
| 14 | | Loam-clay, s_{loam-clay} | 4.9 | 3.51 | 0.49 | 0.32 | Loam-clay | | | | |
| 15 | | Clay-sandy, s_{clay-sandy} | 4.9 | 3.51 | 0.49 | 0.32 | Clay-sandy | | | | |
| 16 | | Clay, s_{clay} | 4.9 | 3.51 | 0.49 | 0.32 | Clay | | | | |
| 17 | | Sand, s_{sand} | 3.5 | 3.46 | 0.38 | 0.37 | Sand | | | | |
| 18 | | Loam, s_{loam} | 3.9 | 3.46 | 0.44 | 0.33 | Loam | | | | |
| 19 | | Clay, s_{clay} | 4.9 | 3.51 | 0.49 | 0.32 | Clay | | | | |
| 20 | | Clay-loam, s_{clay-loam} | 4.9 | 3.51 | 0.49 | 0.32 | Clay-loam | | | | |
| 21 | | Loam-clay, s_{loam-clay} | 4.9 | 3.51 | 0.49 | 0.32 | Loam-clay | | | | |
| 22 | | Clay-sandy, s_{clay-sandy} | 4.9 | 3.51 | 0.49 | 0.32 | Clay-sandy | | | | |
| 23 | | Loam, s_{loam} | 3.9 | 3.46 | 0.44 | 0.33 | Loam | | | | |
| 24 | | Clay, s_{clay} | 4.9 | 3.51 | 0.49 | 0.32 | Clay | | | | |
| 25 | | Clay-loam, s_{clay-loam} | 4.9 | 3.51 | 0.49 | 0.32 | Clay-loam | | | | |
| 26 | | Loam-clay, s_{loam-clay} | 4.9 | 3.51 | 0.49 | 0.32 | Loam-clay | | | | |
| 27 | | Clay-sandy, s_{clay-sandy} | 4.9 | 3.51 | 0.49 | 0.32 | Clay-sandy | | | | |
| 28 | | Loam, s_{loam} | 3.9 | 3.46 | 0.44 | 0.33 | Loam | | | | |
| 29 | | Clay, s_{clay} | 4.9 | 3.51 | 0.49 | 0.32 | Clay | | | | |
| 30 | | Clay-loam, s_{clay-loam} | 4.9 | 3.51 | 0.49 | 0.32 | Clay-loam | | | | |
| 31 | | Loam-clay, s_{loam-clay} | 4.9 | 3.51 | 0.49 | 0.32 | Loam-clay | | | | |

Figure 3-17. A Snapshot of the SurfaceConstants Sheet Showing Different Constants Required for the Surface Water Exposure Model.
i. **Soil Properties (Sheet: SWRainModel, Cells: A6-D10):** Selection of a particular soil texture class (Sheet: Inputdata, Cell C7) auto-fills the values of different soil parameters, such as saturated hydraulic conductivity (K_s; cm/h), pore size index (λ; -), air-entry head (h_b; cm), saturated volumetric content (θ_s; cm^3/cm^3), and residual volumetric water content (θ_0; cm^3/cm^3). The model references three studies (i.e., Brakensiek et al., 1981; Pajian, 1987; Carsel and Parrish, 1988) to obtain values of these parameters, which are summarized in Tables E-1 and E-2 (Appendix E) and also shown in the sheet SurfaceConstants.

ii. **Rainfall Characteristics (Sheet: SWRainModel, Cells: B14-B15):** Rainfall characteristics for the SWRainModel sheet are obtained from the Inputdata sheet (Cells: C5, I9, and I10).

iii. **Ponding Depth (h_p; cm) (Sheet: SWRainModel, Cell: B16):** Default value of the ponding depth is assumed to be zero for this study. This model assumes that no ponding occurs and excess rainfall infiltrates into the subsurface.

**Overland Transport and Fate of Biosolids-Associated Pathogens** The following section presents a description of constant parameters used in the overland transport and fate of biosolids-associated pathogens model (Sheets: SWPathogenModel, SurfaceConstants, Barrenplot, and VegStrip). The default values of these parameters are obtained from reviewing literature publications and eliciting opinions of experts in the field, and both values and citations to references for the sources of these are stored in the sheet SurfaceConstants (Figure 3-17). The user has the flexibility to accept these default values or to input different values of these parameters.

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**Figure 3-18. User Interface of the Overland Transport and Fate of Biosolids-Associated Pathogens Model Collecting Input Parameters and Constants.**

(Sheet: SWPathogenModel)

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iv. **R_{eq}-Area Indicator for Considering Effects of Cold Weather Conditions (I_{Req} (-), Sheet: SWPathogenModel, Cell: C11):** Cold weather conditions influence the extent of sediment erosion from the soil surface and increase soil erodibility (Foster, 2005). The effect of cold weather conditions on soil erodibility is more pronounced in the northwestern part of the U.S. where the erodibility of soil, especially of cropland and other highly disturbed soils, increases during winter months. The standard erosivity relationships do not hold for these regions and therefore, R_{eq} values are used for calculating soil erosivity. This study does not
consider the effect of cold weather conditions in estimating sediment erosion and the default value of this indicator ($I_{req}$) is chosen to be "0" (Figure 3-18).

ii. **Land Use (Sheet: SWPathogenModel) (Figure 3-18):** Land characteristics play an important role during the erosion of sediments from the soil surface due to the effects of rainfall events. For land, the default value of this indicator ($I_{landuse}$, Cell: C12) is chosen to be No, indicating that only the effects of slope of the land, soil erosivity, and erodibility are used in calculating the value of sediment erosion. The effects of all other land management subfactors, such as cover management subfactor ($C_{mgmt}$), contouring subfactor ($p_c$), ponding subfactor ($p_r$), and subsurface drainage subfactor ($p_d$) are not included and assumed to be equal to one. Detailed descriptions of these subfactors are given in the Surface Water Exposure Model Technical Document. Contouring subfactors, ponding subfactor, and subsurface drainage subfactor are combined and represented as Other subfactors ($O_{subfactors}$) (-) (Cell: C80), equal to 1.

iii. **Farm Pond Volume ($V_{im}$) (L) (Sheet: SWPathogenModel, Cell: C13):** Farm pond volume is calculated by multiplying impoundment depth (i.e., 9’ or 2.73m) by its surface area, which is assumed to be 20% of the total drainage area (i.e., plot area) (U.S. EPA, 2003) (Figure 3-18).

<table>
<thead>
<tr>
<th>TABLE</th>
<th>Constant Parameters for the Overland Transport and Fate of Biosolids-Associated Pathogens Model.</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Land</strong></td>
<td><strong>Vegetation</strong></td>
</tr>
<tr>
<td>Sine (angle of the overland path w/ north)</td>
<td>Sine (angle of vegetative strip w/ north)</td>
</tr>
<tr>
<td>$\pi_{ang}$</td>
<td>$\pi_{veg}$</td>
</tr>
<tr>
<td>4.000-02</td>
<td>0.04</td>
</tr>
<tr>
<td>Width of a plane</td>
<td>Length of the unit plot</td>
</tr>
<tr>
<td>$w_{pk}$</td>
<td>$l_{pk}$</td>
</tr>
<tr>
<td>938.83</td>
<td>72.30</td>
</tr>
<tr>
<td>Assume a square plot; unless given</td>
<td>Assume a square plot; unless given</td>
</tr>
<tr>
<td><strong>Factors</strong></td>
<td><strong>Slope steepness factor</strong></td>
</tr>
<tr>
<td>Soil consolidation subfactor</td>
<td>Soil biomass subfactor</td>
</tr>
<tr>
<td>$c_s$</td>
<td>$s_b$</td>
</tr>
<tr>
<td>1.00</td>
<td>1</td>
</tr>
</tbody>
</table>

Figure 3-19. Constant Parameters for the Overland Transport and Fate of Biosolids-Associated Pathogens Model. (Sheet: SWPathogenModel)
iv. **Plot Characteristics** (Sheet: SWPathogenModel, Cells: C27-C31) (Figure 3-19): Plot characteristics, such as steepness of the overland path with the horizontal ($\alpha$) (Sheet: SWPathogenModel, Cell: C27) (-) is used to calculate slope steepness subfactor (S) (-) (Sheet: SWPathogenModel, Cell: C72) (Equations 7-9, 7-10, 7-11). Assuming a square plot of area (A) (Sheet: Inputdata, Cell: C8) (acre), plot dimensions, such as total length ($L_{plot}$) (Sheet: SWPathogenModel, Cell: C28) (ft) and width ($W_{plot}$) (Sheet: SWPathogenModel, Cell: C29) (ft) are calculated. However, length and width of the plot can be changed by the user. The length of the unit plot ($\lambda_u$) is assumed to be 72.6 ft (Sheet: SWPathogenModel, Cell: C30).

v. **Net Ground Cover** ($f_{gn,plot}$) (-) (Sheet: SWPathogenModel, Cell: C37) (Figure 3-19): Land vegetation plays an important role during the erosion of sediments from the soil surface due to the effects of rainfall events, and decreases the extent of soil erosion. This study assumes that biosolids are applied on a barren plot and thus, it does not incorporate the effect of land vegetation on sediment erosion. The default value of net ground cover is assumed to be “0”. At the end of a barren plot, a vegetative filter strip may be present (at the option of the user) with net ground cover ($f_{gn,VS}$) (-) (Sheet: SWPathogenModel, Cell: C43) (Figure 3-19) of “1”.

vi. **Slope Exponent Factor** (m) (-) (Sheet: SWPathogenModel, Cell: C58) (Figure 3-19): This factor is a function of the ratio of rill to interrill erosion ($\beta$); Equation 7-12 and is calculated using Equation 7-11 (for all areas except the $R_{eq}$ zone, where $m = 0.5$). The ratio of rill to interrill erosion depends on the ratio of their erodibility, below ground effect, ground cover, and slope steepness values (Equations 7-13 to 7-17). This study assumes no ground cover on land (i.e., $f_{gn} = 0$) and no effects of soil consolidation (i.e., $s_c = 1$; Sheet: SWPathogenModel, Cell: C51) and soil biomass ($s_b = 1$; Sheet: SWPathogenModel, Cell: C52). Detailed descriptions of calculations of these subfactors are given in Chapter 7.0.

vii. **Soil Erodibility Subfactor** ($K$) (ton/(acre. E1 unit)) (Sheet: SWPathogenModel, Cell: C66) (Figure 3-19): This subfactor is calculated using texture subfactor ($k_t$) (Cell: C62; a hidden-cell), organic matter subfactor ($k_o$) (Cell: C63; a hidden-cell), soil structure subfactor ($k_s$) (Cell: C64; a hidden cell), and soil profile permeability subfactor ($k_p$) (Cell: C65; a hidden cell). A detailed description of calculation of this subfactor is given in Chapter 7.0.

viii. **Cover Management Factor** ($C_{mgmt_land}$) (-) (Sheet: SWPathogenModel, Cell: C69) (Figure 3-19): This factor depends on canopy subfactor ($c_c$), ground cover subfactor ($g_c$), soil subsurface subfactor ($s_s$), ridge height subfactor ($r_h$), soil biomass subfactor ($s_b$), soil consolidation subfactor ($s_c$), and antecedent effect subfactor ($s_m$). Detailed descriptions of calculations of these subfactors are given in Chapter 7.0. The default value of the cover management factor is assumed to be 1.

ix. **Slope Steepness Factor** (S) (-) (Sheet: SWPathogenModel, Cell: C72): This factor depends on slope of the plot and influences the sediment erosion load.
The soil erosivity factor is computed by multiplying the storm’s energy (E) (hundreds of foot-ton/acre) (Cell: C76) by its maximum 30-minute intensity (I₃₀) (in./h) (Cell: C75).

The combined surface factor is calculated by multiplying effects of different subfactors, such as erosivity, erodibility, steepness, and other subfactors (Cell: C80).

The biosolids application rate (B) is set equal to the value supplied by the user on the input sheet. The application rate is required to calculate the quantity of biosolids applied on a given plot of land (Bₜₒₜ₉; Cell: C89). Biosolids land application rates depend on several factors, including the quality of biosolids, environmental conditions, and objective of the biosolids application, and can range from 2 to 100 dry tons/acre (or 0.5 to 25 dry kg/m²) with an approximate average value of 5 dry tons/acre (or 1.25 dry kg/m²) (Gerba et al., 2008; McFarland, 2009; Ippolito et al., 2001; Wong et al., 2010).

The fraction of biosolids in the biosolids-soil matrix is required to determine the quantity of biosolids reaching the nearest farm pond and is assumed to be 0.01 (Gerba et al., 2008). Also, the mass of biosolids in soil (Mₜₒₜₚₒᵦₑᵦ; Cell: C91) (lb/ft plot width) is calculated.
3.3.5.3 Reading and Interpreting the Modeling Output

*Estimation of Surface Infiltration Rate and Surface Runoff Values* The output parameters of the infiltration and runoff model are infiltration rate ($q_{\text{inf}}$), cumulative infiltration ($I$), total rainfall ($r_{\text{total}}$), surface runoff ratio ($f_{\text{runoff}}$), infiltration volume ($V_{\text{inf}}$), total rainfall volume ($V_{\text{rain}}$), and runoff volume ($V_{\text{runoff}}$) for the given field (Figure 3-22). Values of these parameters are calculated using soil characteristics obtained from three different studies. Detailed descriptions of these parameters are given below.

<table>
<thead>
<tr>
<th>A2</th>
<th></th>
<th>B2</th>
<th>C2</th>
<th>D2</th>
<th>E2</th>
<th>F2</th>
<th>G2</th>
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<tr>
<td>O</td>
<td>Results</td>
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</tr>
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<td></td>
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<td></td>
<td></td>
<td></td>
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<tr>
<td>22</td>
<td>Brekenhake et al., 1981</td>
<td>q=</td>
<td>4.0375931449 cm/h</td>
<td>Infiltration rate</td>
<td>to=</td>
<td>0.4423903</td>
<td></td>
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<tr>
<td>23</td>
<td></td>
<td>I=</td>
<td>7.15390238 cm</td>
<td>Cumulative infiltration</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>24</td>
<td></td>
<td>Total rainfall</td>
<td>7.3152 cm</td>
<td>Total rainfall amount</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>25</td>
<td></td>
<td>Runoff=</td>
<td>0.161230762 cm</td>
<td>Surface runoff</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>26</td>
<td></td>
<td>Runoff rate=</td>
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<td>Surface runoff ratio</td>
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<td></td>
<td></td>
</tr>
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<td>27</td>
<td></td>
<td>Infiltration volume</td>
<td>42.97281838 m3</td>
<td>Infiltration volume for the given field</td>
<td></td>
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<td>28</td>
<td></td>
<td>Total rainfall volume</td>
<td>42.89282894 m3</td>
<td>Total rainfall volume for the given field</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>29</td>
<td></td>
<td>Runoff volume=</td>
<td>0.95354361 m3</td>
<td>Runoff volume for the given field</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>30</td>
<td></td>
<td>q=</td>
<td>2.822999126 cm/h</td>
<td>Infiltration rate</td>
<td>to=</td>
<td>0.164436</td>
<td></td>
</tr>
<tr>
<td>31</td>
<td></td>
<td>I=</td>
<td>4.710839584 cm</td>
<td>Cumulative infiltration</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>32</td>
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<td>Total rainfall</td>
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<td>Total rainfall amount</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>33</td>
<td></td>
<td>Runoff=</td>
<td>2.69430416 cm</td>
<td>Surface runoff</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>34</td>
<td></td>
<td>Runoff rate=</td>
<td>0.359920398</td>
<td>Surface runoff ratio</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>35</td>
<td></td>
<td>Infiltration volume</td>
<td>28.26444693 m3</td>
<td>Infiltration volume for the given field</td>
<td></td>
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</tr>
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<td>36</td>
<td></td>
<td>Total rainfall volume</td>
<td>43.8028294 m3</td>
<td>Total rainfall volume for the given field</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>37</td>
<td></td>
<td>Runoff volume=</td>
<td>15.6525836 m3</td>
<td>Runoff volume for the given field</td>
<td></td>
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<td></td>
</tr>
<tr>
<td>38</td>
<td></td>
<td>q=</td>
<td>3.025589955 cm/h</td>
<td>Infiltration rate</td>
<td>to=</td>
<td>0.2030701</td>
<td></td>
</tr>
<tr>
<td>39</td>
<td></td>
<td>I=</td>
<td>5.121217622 cm</td>
<td>Cumulative infiltration</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>40</td>
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<td>Total rainfall</td>
<td>7.3152 cm</td>
<td>Total rainfall amount</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>41</td>
<td></td>
<td>Runoff=</td>
<td>2.193982378 cm</td>
<td>Surface runoff</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>42</td>
<td></td>
<td>Runoff rate=</td>
<td>0.299921038</td>
<td>Surface runoff ratio</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>43</td>
<td></td>
<td>Infiltration volume</td>
<td>30.75566371 m3</td>
<td>Infiltration volume for the given field</td>
<td></td>
<td></td>
<td></td>
</tr>
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<td>44</td>
<td></td>
<td>Total rainfall volume</td>
<td>43.4928294 m3</td>
<td>Total rainfall volume for the given field</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>45</td>
<td></td>
<td>Runoff volume=</td>
<td>13.1631922 m3</td>
<td>Runoff volume for the given field</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Figure 3-22. A Snapshot of the SWRainModel Sheet Showing Output Parameters Related to Total Rainfall, Runoff, Runoff Ratio, and Infiltration Volume.**

**i. Infiltration Rate ($q_{\text{inf}}$) (cm/h) (Sheet: SWRainModel, Cell: C21 or C30 or C39) (Figure 3-22):** This value represents the rate of water infiltrated per unit area of land.

**ii. Cumulative Infiltration ($I$) (cm) (Sheet: SWRainModel, Cell: C22 or C31 or C40) (Figure 3-22):** This parameter represents the total depth of rainfall water infiltrated per unit area of land.

**iii. Total Rainfall ($r_{\text{total}}$) (cm) (Sheet: SWRainModel, Cell: C23 or C32 or C41) (Figure 3-22):** This value represents the total depth of rainfall per unit area of land.

**iv. Runoff ($V_{\text{runoff}}$) (cm) (Sheet: SWRainModel, Cell: C24 or C33 or C42) (Figure 3-22):** The value of this parameter is the difference between total rainfall and cumulative infiltration.
v. **Surface Runoff Ratio ($f_{runoff}$) (-)** (Sheet: SWRainModel, Cell: C25 or C34 or C43) (Figure 3-22): This value is a fraction of total rainfall resulting in runoff.

vi. **Infiltration Volume ($V_{inf}$) (m$^3$)** (Sheet: SWRainModel, Cell: C26 or C35 or C44) (Figure 3-22): This parameter is calculated by multiplying infiltration depth to total area of application site ($A$) (Sheet: SWRainModel, Cell: B17), and represents the total volume of water infiltrate.

vii. **Total Rainfall Volume ($V_{rain}$) (m$^3$)** (Sheet: SWRainModel, Cell: C27 or C36 or C45) (Figure 3-22): This parameter is calculated by multiplying rainfall depth by total area of application site.

viii. **Runoff Volume ($V_{runoff}$) (m$^3$)** (Sheet: SWRainModel, Cell: C28 or C37 or C46) (Figure 3-22): This parameter is calculated by multiplying runoff ($V_{runoff}$) by the total area of application site.

**Overland Transport and Fate of Biosolids-Associated Pathogens**

i. **Pathogens** (Sheet: SWPathogenModel) (Figure 3-23): Total number of pathogens applied on land ($N_{total}$) (No.) (Cell: B151) is calculated by multiplying total biosolids applied on land (Sheet: SWPathogenModel, Cell: C89) by pathogen concentration in biosolids (Sheet: Pathogen, Cell: B11). Concentrations of different pathogens, generally found in biosolids, are given in the sheet Pathogen (Cells: A11-B38). Concentrations of pathogens released due to the effect of water erosion on land-applied biosolids ($N_R$) (No.) (Sheet: SWPathogenModel, Cell: C151) are calculated by multiplying total pathogens applied on land by release parameter ($f$) for a given pathogen type (Equation 7-6; Chapter 7.0). Further, concentrations of pathogens remaining attached to biosolids ($N_{attached}$) (No.) (Sheet: SWPathogenModel, Cell: D151) are calculated using Equation 7-7 (Chapter 7.0) and stored in Cells D151-178 (Sheet: SWPathogenModel).
Effective Delivery of Pathogens to a Farm Pond (Sheet: SWPathogenModel) (Figure 3-23): Effective delivery of unattached-pathogen cells to a farm pond water (ED_{unattached,im}) (No.) (Cells: E151:178) is calculated for each pathogen using Equation 7-8 (Chapter 11.0) based on the assumption that pathogens do not decay during their overland transport and considering that all unattached cells reach the impoundment. Effective delivery of attached-pathogens (ED_{attached,im}) (No.) (Cells: F151:178) is calculated for each pathogen using Equation 7-36 (Chapter 7.0) considering the amount of suspended biosolids in the impoundment (d_{imp,biosolids}) (lb/ft width) (Cell: N143). Total pathogen accumulation in the impoundment water (ED_{pathogen,im}) (No.) (Cells: G151:178) is calculated by adding values of ED_{unattached,im} and ED_{attached,im}.

Pathogen Concentration in Farm Pond Water (Sheet: SWPathogenModel): Pathogen concentration in farm pond water (C_{pathogen,im}) (No./L) (Sheet: SWPathogenModel, Cells: H151:178) represents the concentration of individual pathogens in farm pond water after mixing of runoff water with the farm pond water. It depends on pond volume (V_{im}), pathogen numbers in runoff (ED_{pathogen,im}) (No.) (Sheet: SWPathogenModel, Cells: G151:178) and initial pathogen concentrations in farm pond water (C_{0}) (No./L) (Sheet: Pathogen, Cells: D11-D38). In this study, initial pathogen concentrations in the pond are assumed to be zero to calculate excess risks associated with biosolids-associated pathogens. However, the user has the flexibility to update the pathogen concentration database (i.e., Pathogen sheet) reflecting field conditions. A mass balance of pathogens in the pond water.

Figure 3-23. A Snapshot of the SWPathogenModel Sheet Showing Output Parameters Related to Pathogen Load.
is used to calculate pathogen concentrations (Equation 7-37; Chapter 7.0). The effective concentration of pathogen cells in farm pond water (C_{eff,pathogen,im}) (No./L) (Sheet: SWPathogenModel, Cells: I151:178) after time (Δt) (days) (Sheet: SWPathogenModel, Cell: C7) is calculated using Equation 7-38 (Chapter 7.0) using a first-order decay rate (k_a) (1/day) (Sheet: Pathogen, Cells: E11-E38).

### 3.3.5.4 Output Data

Estimates of surface infiltration rate and surface runoff values are presented for three separate data input sets (Cells A22-H47; Sheet: SWRainModel). In addition, time-dependent variation of different hydrologic parameters, such as infiltration rate, cumulative infiltration, total rainfall amount, runoff, and runoff ratio are presented in tabular format (Cells A51-Q75; Sheet: SWRainModel). The user has the option to increase the extent of total rainfall duration (i.e., number of rows) and obtain the time-dependent variation of different hydrologic parameters. In addition, the user can also plot the variation of these parameters with time by selecting the data column and clicking Insert in the menu and then choosing Chart and Chart Type.

A comparison of values of runoff ratio, obtained from the Joint Green-Ampt model using three groups of soil hydraulic properties (i.e., Brakensiek et al., 1981; Pajian, 1987; Carsel and Parrish, 1988) (Appendix D) indicated that the highest runoff ratio (or least infiltration) occurs when soil hydraulic properties from the Pajian (1987) study were used. For calculating maximum risk of pathogen exposure from the surface water route, highest runoff ratio (or highest runoff volume) is required and thus, the use of soil hydraulic properties from the Pajian (1987) study is recommended and set as default (Figure 3-24). However, the user has the option of selecting either of these data input sets and related results (Figure 3-22).

![Table of runoff values](Sheet: SWRainModel)

**Figure 3-24. Selection of the Default Group for Obtaining Different Hydrologic Information after the Rainfall Event.**

(Sheet: SWRainModel)
3.3.6 Groundwater Exposure Pathway

The input parameters, constant values and output parameters used in the groundwater exposure pathway are listed in Table 3-11, along with their location in the SMART Biosolids modeling tool. A more detailed explanation of the parameters follows. The default values of different constants are obtained from literature reports, which the user has the flexibility to accept or change.

### Table 3-11. Input Parameters, Constants, and Output Parameters Employed in the Groundwater Exposure Pathway.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Unit</th>
<th>Definition</th>
<th>Sheet Title</th>
</tr>
</thead>
<tbody>
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<td><strong>Input Parameters</strong></td>
<td></td>
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<td></td>
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<tr>
<td>$T_{\text{storm}}$</td>
<td>years</td>
<td>Storm return period</td>
<td>Inputdata, Cell: C5</td>
</tr>
<tr>
<td>r</td>
<td>cm/hr</td>
<td>Rainfall intensity</td>
<td>Inputdata, Cell: I9</td>
</tr>
<tr>
<td>t</td>
<td>hr</td>
<td>Rainfall duration time</td>
<td>Inputdata, Cell: I10</td>
</tr>
<tr>
<td>T</td>
<td>Fahrenheit</td>
<td>Temperature</td>
<td>Inputdata, Cell: C6</td>
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<tr>
<td>$S_{\text{texture}}$</td>
<td>-</td>
<td>Soil texture class</td>
<td>Inputdata, Cell: C7</td>
</tr>
<tr>
<td>A</td>
<td>acre</td>
<td>Area of application site</td>
<td>Inputdata, Cell: C8</td>
</tr>
<tr>
<td>B</td>
<td>Dry tons biosolids/acre</td>
<td>Biosolids application rate</td>
<td>Inputdata, Cell: C11</td>
</tr>
<tr>
<td>h</td>
<td>cm</td>
<td>Water table depth</td>
<td>Inputdata, Cell: C13</td>
</tr>
<tr>
<td>L or L</td>
<td>cm</td>
<td>Distance from nearest field edge to downstream well</td>
<td>Inputdata, Cell: C14</td>
</tr>
<tr>
<td>i</td>
<td>-</td>
<td>Hydraulic gradient</td>
<td>Inputdata, Cell: C15</td>
</tr>
<tr>
<td>Pathogen</td>
<td>-</td>
<td>Pathogen of interest</td>
<td>Inputdata, Cell: C24</td>
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<td><strong>Constants</strong></td>
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<td>cm/hr</td>
<td>Vertical saturated hydraulic conductivity</td>
<td>GWPathogenModel, Cell: B6</td>
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<td>cm/hr</td>
<td>Horizontal saturated hydraulic conductivity</td>
<td>GWPathogenModel, Cell: B7</td>
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<tr>
<td>$\alpha_x$</td>
<td>cm</td>
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<td>GWPathogenModel, Cell: B9</td>
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<td>$\lambda$</td>
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<td>Pore size index</td>
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<td>$h_b$</td>
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<td>Air-entry head</td>
<td>GWPathogenModel, Cell: B11</td>
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<td>$\theta_s$</td>
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<td>Saturated volumetric water content</td>
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<td>$\theta_o$</td>
<td>cm$^3$/cm$^3$</td>
<td>Initial volumetric water content</td>
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<td>cm$^3$/cm$^3$</td>
<td>Volumetric water content for unsaturated soil</td>
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<td>-</td>
<td>Water retention curve fitting parameter</td>
<td>GWPathogenModel, Cell: B16</td>
</tr>
<tr>
<td>$\alpha$</td>
<td>/m</td>
<td>Water retention curve fitting parameter</td>
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<td>Average radius of soil particles</td>
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<td>Ponding depth</td>
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<td>Inactivation rate for soil-sorbed pathogens</td>
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<td>Radius of the pathogens</td>
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</tr>
<tr>
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<td>cm$^3$/g</td>
<td>Equilibrium distribution coefficient</td>
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</tr>
<tr>
<td>$k_{str}$</td>
<td>/hr</td>
<td>Straining coefficient</td>
<td>GWPathogenModel, Cell: B34</td>
</tr>
<tr>
<td>$h_{str}$</td>
<td>cm</td>
<td>The distance</td>
<td>GWPathogenModel, Cell: B35</td>
</tr>
<tr>
<td>Parameter</td>
<td>Unit</td>
<td>Definition</td>
<td>Sheet Title</td>
</tr>
<tr>
<td>-----------</td>
<td>-----------------------</td>
<td>-----------------------------------------------------------------------------</td>
<td>-------------------------------------------------</td>
</tr>
<tr>
<td><strong>Constants</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$N_0$</td>
<td>number/g dry biosolids</td>
<td>Initial pathogens load in unit of biosolids</td>
<td>GWPathogenModel, Cell: B36</td>
</tr>
<tr>
<td>$f_{\text{release}}$</td>
<td>-</td>
<td>Release parameter (percentage of pathogens leached out of the biosolid-soil matrix)</td>
<td>GWPathogenModel, Cell: B38</td>
</tr>
<tr>
<td><strong>Output parameters</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$q$</td>
<td>cm/hr</td>
<td>Infiltration rate</td>
<td>GWPathogenModel, Cell: B57</td>
</tr>
<tr>
<td>$I$</td>
<td>cm</td>
<td>Cumulative infiltration</td>
<td>GWPathogenModel, Cell: B58</td>
</tr>
<tr>
<td>$Z_{\text{potential}}$</td>
<td>cm</td>
<td>The calculated depth of wetting front</td>
<td>GWPathogenModel, Cell: B59</td>
</tr>
<tr>
<td>$M$, $M_1$ and $M_2$</td>
<td>Number/cm$^2$</td>
<td>Pathogens load in transport with water</td>
<td>GWPathogenModel, Cells: B64, B69, and B76</td>
</tr>
<tr>
<td>$v$</td>
<td>cm/hr</td>
<td>Pore water velocity of groundwater flow</td>
<td>GWPathogenModel Cell: B19</td>
</tr>
<tr>
<td>$t$</td>
<td>hour</td>
<td>Transport time duration</td>
<td>GWPathogenModel, Cells: B67, B74, and B81</td>
</tr>
<tr>
<td>$Z_{\text{actual}}$</td>
<td>cm</td>
<td>The actual transport distance above wetting front</td>
<td>GWPathogenModel, Cell: B68</td>
</tr>
<tr>
<td>$C_p$</td>
<td>Number/L</td>
<td>Peak concentration in well water</td>
<td>GWPathogenModel, Cell: B83</td>
</tr>
</tbody>
</table>

### 3.3.6.1 Input Variables

Table 3-12 lists input parameters required for running this model and their locations in the biosolids model (Sheet: Inputdata). The user may use this table to organize information about different parameters before running the model. Detailed descriptions of different components are summarized below.
Table 3-12. List of Input Parameters Required for Running the Ground Water Exposure Model.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Symbol/Unit</th>
<th>Cell Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>Location</td>
<td>-</td>
<td>Cell C3</td>
</tr>
<tr>
<td>Time between biosolids application and the onset of rain</td>
<td>t&lt;sub&gt;rain&lt;/sub&gt; (days)</td>
<td>Cell C4</td>
</tr>
<tr>
<td>Return period</td>
<td>T&lt;sub&gt;storm&lt;/sub&gt; (years)</td>
<td>Cell C5</td>
</tr>
<tr>
<td>Temperature</td>
<td>T (°C)</td>
<td>Cell C6</td>
</tr>
<tr>
<td>Soil texture class (sand, loamy sand, sandy loam, loam, silty loam, sandy clay loam, clay loam, silt clay loam, silty clay, clay, sandy clay, and silt)</td>
<td>S&lt;sub&gt;texture&lt;/sub&gt;</td>
<td>Cell C7</td>
</tr>
<tr>
<td>Area of application site</td>
<td>A (acre)</td>
<td>Cell C8</td>
</tr>
<tr>
<td>Slope of the plot</td>
<td>Grade (%)</td>
<td>Cell C9</td>
</tr>
<tr>
<td>Application method (slinging, manure spreading, spraying through tank, and spray irrigation)</td>
<td>App_method (-)</td>
<td>Cell C10</td>
</tr>
<tr>
<td>Biosolids application rate</td>
<td>B (tons/acre)</td>
<td>Cell C11</td>
</tr>
<tr>
<td>Water table depth</td>
<td>h (ft)</td>
<td>Cell C13</td>
</tr>
<tr>
<td>Distance to well</td>
<td>L (ft)</td>
<td>Cell C14</td>
</tr>
<tr>
<td>Hydraulic gradient</td>
<td>i(-)</td>
<td>Cell C15</td>
</tr>
<tr>
<td>Indicator for presence of a buffer zone</td>
<td>I&lt;sub&gt;VS&lt;/sub&gt; (-)</td>
<td>Cell C16</td>
</tr>
<tr>
<td>Indicator for presence of a channel</td>
<td>I&lt;sub&gt;ch&lt;/sub&gt; (-)</td>
<td>Cell C19</td>
</tr>
<tr>
<td>Channel length</td>
<td>L&lt;sub&gt;ch&lt;/sub&gt; (ft)</td>
<td>Cell C20</td>
</tr>
<tr>
<td>Channel width</td>
<td>W&lt;sub&gt;ch&lt;/sub&gt; (ft)</td>
<td>Cell C21</td>
</tr>
<tr>
<td>Channel grade</td>
<td>Grade&lt;sub&gt;ch&lt;/sub&gt; (-)</td>
<td>Cell C22</td>
</tr>
<tr>
<td>Indicator for presence of a farm pond</td>
<td>I&lt;sub&gt;im&lt;/sub&gt; (-)</td>
<td>Cell C23</td>
</tr>
<tr>
<td>Pathogen-of-interest</td>
<td>Pathogen (-)</td>
<td>Cell C24</td>
</tr>
<tr>
<td>Subpopulation-of-interest (occupational worker, residential adults, and residential children)</td>
<td>Sub_pop (-)</td>
<td>Cell C25</td>
</tr>
<tr>
<td>Time of exposure after biosolids application</td>
<td>t&lt;sub&gt;SW&lt;/sub&gt; (day)</td>
<td>Cell C29</td>
</tr>
<tr>
<td>Storm intensity</td>
<td>r (cm/h)</td>
<td>Cell I9</td>
</tr>
<tr>
<td>Storm duration</td>
<td>t (h)</td>
<td>Cell I10</td>
</tr>
<tr>
<td>Annual precipitation</td>
<td>Pa(inches)</td>
<td>Cell I4</td>
</tr>
<tr>
<td>Maximum 30-minute intensity</td>
<td>I&lt;sub&gt;30&lt;/sub&gt; (inches/h)</td>
<td>Cell I5</td>
</tr>
<tr>
<td>Does the rainfall occurs after biosolids application</td>
<td>I&lt;sub&gt;rainfall&lt;/sub&gt; (-)</td>
<td>Cell I8</td>
</tr>
</tbody>
</table>

All input parameters are included in the Inputdata worksheet. The following section describes only the input parameters required by the subsurface transport and fate model.
i. Rainfall Characteristics (Sheet: Inputdata): The user enters the location information in Cell C3 (Sheet: Inputdata) and enters information about return period in Cell C5, storm intensity in Cell I9, and storm duration in Cell I10 for a single rain event \(N_{\text{rain}}\) (\(-\)) (Cell: C12). Further, the user selects if the rainfall occurs after biosolids application \(I_{\text{rainfall}}\) (\(-\)) (Cell: I8) and inputs time between biosolids application and the onset of rain \(t_{\text{rain}}\) (days) in Cell C4 of the Inputdata sheet. The user must also enter values for annual precipitation \(P_a\) (inches) (Cell: I4) and maximum 30-minute intensity \(I_{\text{30}}\) (inches/hr) (Cell I5).

ii. Temperature \((T)\) \(^{\circ}\text{F}\) (Sheet: Inputdata, Cell: C6): Daily surface temperature is required to calculate rate of pathogen inactivation due to temperature.

iii. Soil Texture Class \((S_{\text{texture}})\) (Sheet: Inputdata, Cell: C7): The list of soil texture classes includes sand, loamy sand, sandy loam, loam, silty loam, sandy clay loam, clay loam, silt clay loam, silty clay, clay, sandy clay, and silt. Once selected, the selected soil type auto-fills hydraulic parameters (Sheet: GWPathogenModel, Cells B6 to B24) for soil characteristics.

iv. Area of application site \((A)\) (Acre) (Sheet: Inputdata, Cell: C8): The user needs to provide the area of the farm land where biosolids are applied. The model assumes a square plot for horizontal groundwater transport estimation, and the length of biosolids application field is autofilled (Sheet: GWPathogenModel, Cell: B23).

v. Biosolids Application (Sheet: Inputdata, Cells: C10-C11): These parameters are used to calculate pathogen load at the soil surface. The user provides information about the application method \((\text{Appl_method})\) (-) (Cell: C10) (i.e., instrument) used for applying biosolids on land, such as slinger, splash-plate spray applicator, and disk incorporation and biosolids application rate \((B)\) (dry tons biosolids/acre) (Cell: C11). Based on the user-selected biosolids application method from the Inputdata sheet (Cell: C10), values of related parameters are auto-filled from Table 3-13.

<table>
<thead>
<tr>
<th>Application Method</th>
<th>Biosolid Material</th>
<th>Solids</th>
</tr>
</thead>
<tbody>
<tr>
<td>Surface spreading</td>
<td>Liquid</td>
<td>5.7</td>
</tr>
<tr>
<td>Spray irrigation</td>
<td>Liquid</td>
<td>5.7</td>
</tr>
<tr>
<td>Slinger</td>
<td>Cake</td>
<td>NA</td>
</tr>
<tr>
<td>Manure spreader</td>
<td>Cake</td>
<td>NA</td>
</tr>
</tbody>
</table>

*NA-Information is not included in this version.

vi. Water Table Depth \((h)\) (feet) (Sheet: Inputdata, Cell: C13): The user inputs depth to water table and this parameter is compared to the calculated wetting front depth (Sheet: GWPathogenModel, Cell: B59) from the Joint Green-Ampt Model in order to determine if the wetting front reaches the water table and the depth of unsaturated soil.
vii. **Distance to Well (L) (feet) (Sheet: Inputdata, Cell: C14):** This parameter is the distance from the nearest field edge to downstream well. This information is required to calculate horizontal transport of pathogens in subsurface soil.

viii. **Hydraulic Gradient (i) (Sheet: Inputdata, Cell: C15):** This parameter is used to estimate interstitial water velocity for horizontal groundwater flow.

![Figure 3-25. A Snapshot of the GWPathogenModel Showing Default Pathogen Parameters for the Groundwater Exposure Model Input.](image)

### 3.3.6.2 Constants

All default values for parameters used in estimating subsurface fate and transport are summarized in the *GWConstants* sheet, and constants for a selected pathogen of concern are shown in the *GWPathogenModel* worksheet Part I Cell A2 to G18. The following section describes these parameters and which model they are used for. The Groundwater Exposure Model Technical Document (Chapter 8.0) gives a detailed description of the subsurface transport and fate model, and the Surface Water Exposure Model Technical Document (Chapter 7.0) gives a detailed description of the Joint Green-Ampt infiltration model.

**Hydraulic parameters** The hydraulic parameters are determined by soil texture and are summarized in the sheet *GWPathogenModel*.
i. **Vertical saturated hydraulic conductivity (K_{sz}) and horizontal saturated hydraulic conductivity (K_{sx}) (cm/hr)** (Sheet: GWPathogenModel, Cell: B6 and B7): This parameter is a coefficient that describes the rate at which water can move through saturated soil, which is determined by soil texture. Different values were estimated for vertical and horizontal transport, respectively. The horizontal saturated hydraulic conductivity (K_{sx}) was assumed to be six times the vertical hydraulic conductivity (K_{sz}) (Sawyer and Lieuallen-Dulam, 1998). Vertical hydraulic conductivity, K_{sz}, is required in the Joint Green-Ampt infiltration model to estimate the wetting front depth, and horizontal hydraulic conductivity, K_{sx}, is required in the subsurface transport and fate model in saturated and unsaturated soil.

ii. **Vertical dispersivity (\alpha_z) and horizontal dispersivity (\alpha_x) (cm)** (Sheet: GWPathogenModel, Cell: B8 and B9): These parameters are used to calculate the vertical and horizontal dispersion coefficients, and are required in the saturated and unsaturated subsurface transport and fate models. Detailed information can be found in Appendix F.

iii. **Pore size index (\lambda) (unitless)** (Sheet: GWPathogenModel, Cell: B10): This parameter is the exponent of the Brooks-Corey water retention model, and is used to calculate capillary pressure head at the wetting front h_f (Equation 3-1). It is required in the Joint Green-Ampt infiltration model to estimate the wetting front depth.

\[ h_f = \eta/(\eta-1) h_e \]  

(3-1)

where \( \eta \) is the exponent of the Brooks-Corey water retention model, which is calculated as \((2+3\lambda)\); \( h_e \) is the air exit head (cm), which may be taken as equal to one half of the air entry head \( h_b \).

iv. **Air-entry head (h_b) (cm)** (Sheet: GWPathogenModel, Cell: B11): This parameter is used to calculate capillary pressure head at the wetting front \( h_f \) (Equation 3-1). It is required in the Joint Green-Ampt infiltration model to estimate the wetting front depth.

v. **Saturated volumetric water content (\theta_s) (cm^3/cm^3)** (Sheet: GWPathogenModel, Cell: B12): The saturated volumetric water content is the water-filled fraction of the total soil volume when all pores are filled with water. This parameter is used to estimate the water content of the soil above wetting front, which is saturated by the infiltrated rainfall water. It is required in the Joint Green-Ampt infiltration model to estimate the wetting front depth and subsurface transport and fate model in unsaturated soil.

vi. **Residual volumetric water content (\theta_0) (cm^3/cm^3)** (Sheet: GWPathogenModel, Cell: B13): This parameter defines the volumetric water content at the start of the simulation. It is used to estimate the water content of the soil before the rainfall events. It is required in the Joint Green-Ampt infiltration model to estimate the wetting front depth and in the subsurface transport and fate model for unsaturated soil.

vii. **Volumetric water content for unsaturated soil (\theta_m) (cm^3/cm^3)** (Sheet: GWPathogenModel, Cell: B14): This parameter defines the volumetric water content for unsaturated soil and is equal to the volume of water divided by the total volume. It is required in the Joint Green-Ampt infiltration model to estimate the wetting front depth and in the subsurface transport and fate model for unsaturated soil.
viii. Bulk density of the soil ($\rho_b$) (g/cm$^3$) (Sheet: GWPathogenModel, Cell: B15): This parameter defines the mass of dry soil relative to the bulk volume of soil. It is required in the subsurface transport and fate model for saturated and unsaturated soil.

ix. Water retention curve fitting parameter ($n_v$) (unitless) (Sheet: GWPathogenModel, Cell: B16): The van Genuchten parameter required to estimate the air-water interfacial area using derived equations from Rose and Bruce (1949). This parameter is required in the subsurface transport and fate model for unsaturated soil.

x. Water retention curve fitting parameter ($\alpha$) (m$^{-1}$) (Sheet: GWPathogenModel, Cell: B17): The van Genuchten parameter required to estimate the air-water interfacial area using derived equations from Rose and Bruce (1949). This parameter is required in the subsurface transport and fate model in unsaturated soil.

xi. Average radius of soil particles ($r_s$) (cm) (Sheet: GWPathogenModel, Cell: B18): This parameter is used to calculate the liquid to liquid-solid interface mass transfer rate $k_s$ (Sheet: GWTransportModel, Cell: B30) and is required in the subsurface transport and fate model in unsaturated soil. This parameter is also required for estimation of the straining coefficient (Sheet: GWTransportModel, Cell: B30).

xii. Pore water velocity of groundwater flow ($v$) (cm/hr) (Sheet: GWPathogenModel, Cell: B19): This parameter is estimated by the hydraulic gradient $i$ (Sheet: Inputdata, Cell: C15), horizontal saturated hydraulic conductivity $K_{sx}$ (Sheet: GWPathogenModel, Cell: B7), and saturated water content $\theta_s$ (Sheet: GWPathogenModel, Cell: B12) (Equation 6-3). It is required in the subsurface transport and fate model in unsaturated soil.

$$v=K_{sx}\times i/\theta_s$$

Pathogen parameters The pathogen parameters are summarized in the sheet GWPathogenModel (Figure 3-25).

i. Inactivation rate for suspended pathogens ($\lambda_l$) (h$^{-1}$) (Sheet: GWPathogenModel, Cell: B28) and inactivation rate for soil-sorbed pathogens ($\lambda_s$) (h$^{-1}$) (Sheet: GWPathogenModel, Cell: B29): These parameters are used for estimation of pathogen decay in the liquid phase and on the surface of the soil particles, respectively. They are required in the subsurface transport and fate model in saturated and unsaturated soil.

ii. Liquid to liquid-solid interface mass transfer coefficient ($k_s$) (cm h$^{-1}$) (Sheet: GWPathogenModel, Cell: B30) and liquid to air-solid interface mass transfer coefficient ($k_a$) (cm h$^{-1}$) (Sheet: GWPathogenModel, Cell: B31): These parameters are used for estimation of pathogen attachment, and are required in the subsurface transport and fate model in unsaturated soil. A detailed description of these parameters can be found in Appendix F.

iii. Radius of the pathogens ($r_p$) (cm) (Sheet: GWPathogenModel, Cell: B32): This parameter is used for estimation of pathogen attachment, and is required in the subsurface transport and fate model in unsaturated soil. It is also required for the straining prediction.
iv. **Equilibrium distribution coefficient (K_d) (cm³/g)** (Sheet: GWPathogenModel, Cell: B33): This parameter is the linear partition coefficient, which describes the relative distribution of the pathogens between that which is sorbed to the solid phase and that which is dissolved in water. It is required in the subsurface transport and fate model for saturated and unsaturated soil.

v. **Straining coefficient (k_str) (h⁻¹)** (Sheet: GWPathogenModel, Cell: B34) and **distance for straining (h_str) (cm)** (Sheet: GWPathogenModel, Cell: B35): These parameters are used to estimate the microbial removal fraction due to straining. A detailed description of this estimation approach can be found in Appendix F.

vi. **Release parameter (f_release)** (Sheet: GWPathogenModel, Cell: B38): The release parameter represents the fraction of pathogens released from biosolids to water due to rainfall events.

### 3.3.6.3 Modeling Results

Output results for a specific pathogen or indicator of concern from the subsurface fate and transport model are shown in the *GWPathogenModel* sheet Part I, and the output summary for all pathogens and indicators of concern is presented in the *GWPathogenModel* sheet Part III.

### 3.3.6.4 Transport Scenarios

Two possible transport scenarios are determined based on the rainfall rate, duration, and a comparison between the water table depth and wetting front depth (Sheet: *GWPathogenModel*) (Figure 3-26a).

![Figure 3-26a. A Snapshot of the GWPathogenModel Sheet Showing the Transport Phases for Scenario 1: Non-Saturating Rainfall Events.](image-url)
3.3.6.5 Reading and Interpreting the Output

*Estimation of infiltration rate and depth of wetting front* According to the user-input information, results show the value of the infiltration rate, cumulative infiltration, and depth of the wetting front, as determined by the Joint Green-Ampt infiltration model (Figure 3-26b).

![Figure 3-26b. A Snapshot of the GW PathogenModel Sheet Showing the Results of Infiltration Information.](image)

1. **Infiltration rate (q) (cm/h) (Sheet: GWPathogenModel, Cell: B57):** This value represents the rate of water infiltrated per unit area of a land. It is used for the subsurface transport and fate model in saturated soil above the wetting front.

2. **Cumulative infiltration (I) (cm) (Sheet: GWPathogenModel, Cell: B58):** This parameter represents the total depth of rainfall water infiltrated per unit area of a land. It is used to calculate depth of wetting front Z (Equation 8-1).

3. **The potential depth of wetting front (Z_potential) (cm) (Sheet: GWPathogenModel, Cell: B59):** This parameter is calculated from Equation 8-1. It is compared to water table depth h (Sheet: Inputdata, Cell: B13) in order to determine the possible scenario for the rainfall events and to determine the actual vertical transport distance in saturated soil (Z-actual) (Sheet: GWPathogenModel, Cells: B68) and the vertical transport distance in unsaturated soil (h-Z) (Sheet: GWPathogenModel, Cells: B75).

*Estimation of partitioning and straining* Microorganisms may be removed from the water column due to partitioning and straining. The pathogen load in water transported to the water table (M) (number/cm²) (Sheet: GWPathogenModel, Cell: B64) is estimated and displayed (Figure 3-27).

![Figure 3-27. A Snapshot of the GWPathogenModel Sheet Showing the Results of Partitioning and Straining.](image)
Subsurface transport and fate of biosolids-associated pathogens in saturated and unsaturated soil  The results of pathogen attenuation are summarized in GWPathogenModel sheet Part I for a single pathogen (Figure 3-28) and Part III for all pathogens (Figure 3-29).

Figure 3-28. A Snapshot of the GWPathogenModel Sheet Showing the Results of Subsurface Transport and Fate Model.
Figure 3-29. User Interfaces of the Detailed Output Values (specific for one pathogen or indicator) for the Groundwater Exposure Model.
(Sheet: GWPathogenModel, Part I)

i. **Peak concentration in well water (C) (number/L)** (Sheet: GWPathogenModel Part I, Cell: B83 and B90) (Sheet: GWPathogenModel Part III, Column J): This value is the peak microbial concentration in well water after transport through saturated and unsaturated soil. The total mass of biosolids-associated pathogens reaching the water table is assumed to be an instantaneous source for horizontal transport. As the slug moves downstream, it spreads and the concentration is estimated using the subsurface fate and transport model. Governing equations and a detailed description are presented in the Groundwater Exposure Model Technical Document (Chapter 8.0).

ii. **Transport time (t) (hour)** (Sheet: GWPathogenModel, Cells: B67, B74, and B81): These values represent the transport time in soil for each transport phase: through the saturated wetting front, through unsaturated soil, and through saturated groundwater flow, respectively. Transport time is used to calculate cumulative pathogen mass transport through each media based on the time-dependent concentration profile.

iii. **The actual depth of wetting front (Z_actual) (cm), thickness of the unsaturated soil (h-Z) (cm) and distance to well (L1) (cm)** (Sheet: GWPathogenModel, Cells: B68, B75, and B82): These values are pathogen vertical transport distances in saturated soil above the water table and in unsaturated soil, and horizontal transport distance in saturated soil with groundwater flow, respectively.
iv. Pathogen total number in water (M₁ and M₂) (Number/cm²) (Sheet: GWPathogenModel, Cell: B69 and B76): These values represent the cumulative number of pathogens in water at the end of each transport phase.

v. Pathogen attenuation (M₁/M, M₂/M₁, and Attenuation) (Unitless) (Sheet: GWPathogenModel, Cell: B70, B77, and B84): The attenuation factor is the fraction of the total number of pathogens in water at the end of each transport phase to the value at the beginning of that transport phase.

vi. Log removal (Unitless) (Sheet: GWPathogenModel, Cell: B71, B78, and B85): The log removal is equal to the negative value of log (attenuation factor) for each transport phase.
3.3.7 Indirect Ingestion Exposure Pathway

The input parameters, constant values and output parameters used in the indirect ingestion exposure pathway are listed in Table 3-14, along with their location in the SMART Biosolids modeling tool. A more detailed explanation of the parameters follows. The default values of different constants are obtained from literature reports, which the user has the flexibility to accept or change.

Table 3-14. Input Parameters, Constants, and Output Parameters Employed in the Indirect Ingestion Exposure Pathway.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Unit</th>
<th>Definition</th>
<th>Sheet Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>Input Parameters</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$t_{vegeconc}$</td>
<td>Days</td>
<td>Time of vegetables ingestion after biosolids application</td>
<td>Inputdata (Cell C34)</td>
</tr>
<tr>
<td>$n_{leaf}$</td>
<td></td>
<td>Number of ingested vegetable leaves from the contaminated field</td>
<td>Inputdata (Cell C35)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Constants</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$V_{runoff}$</td>
<td>ft³</td>
<td>Volume of runoff water</td>
<td>VegePathogenModel (Cell C6)</td>
</tr>
<tr>
<td>$A_{per_leaf}$</td>
<td>in²</td>
<td>Surface area of each lettuce leaf</td>
<td>VegePathogenModel (Cell C7)</td>
</tr>
<tr>
<td>$h_{water_storage}$</td>
<td>mm</td>
<td>The surface storage capacity of each individual leaf</td>
<td>VegePathogenModel (Cell C8)</td>
</tr>
<tr>
<td>$V_{per_leaf}$</td>
<td>ft³</td>
<td>Volume of water deposited on each vegetable leaf</td>
<td>VegePathogenModel (Cell C9)</td>
</tr>
<tr>
<td>$V_{on_vegetable}$</td>
<td>ft³</td>
<td>Total volume of water deposited on vegetables ingested</td>
<td>VegePathogenModel (Cell C10)</td>
</tr>
<tr>
<td>$k_{decay,soil}$</td>
<td>1/day</td>
<td>Pathogen first order decay rate in soil</td>
<td>Pathogen (Cell I11-I38)</td>
</tr>
<tr>
<td>$ED_{pathogen,im}$</td>
<td>No.</td>
<td>The total number of pathogen cells entering the field</td>
<td>VegePathogenModel</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>(Cells B19-B46)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Constants</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$N_{field}$</td>
<td>No./L</td>
<td>The concentration of pathogens in the runoff water entering the field</td>
<td>VegePathogenModel (Cells C19-C46)</td>
</tr>
<tr>
<td>$ED_{on_vegetable}$</td>
<td>No.</td>
<td>Number of biosolids-associated pathogens on lettuce surface</td>
<td>VegePathogenModel (Cells D19-D46)</td>
</tr>
</tbody>
</table>

3.3.7.1 Input Variables

This section describes the input parameters required for calculating the number of biosolids-associated pathogens present on lettuce leaves following land-application of biosolids. All the information that the user should supply to the Indirect Ingestion Exposure Model is found in Table 3-15. The last column of this table is left blank so the user can fill it in with his or her choices before attempting to run the model. The cell locations refer to the worksheet named Inputdata. After compiling the list of values, the user should enter the values in the worksheet. Some worksheet cells may already contain default values. These are supplied for those users who do not have location-specific information. Neglecting to replace default values with location-specific information produces results that are less specific to the particular site being considered. The following section describes each of the input variables required by the model.
Table 3-15. List of Input Parameters Required for Running the Indirect Ingestion Exposure Model.
(Sheet: Inputdata)

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Symbol/Unit</th>
<th>Cell Location</th>
<th>User Input</th>
</tr>
</thead>
<tbody>
<tr>
<td>Time of vegetables ingestion after biosolids application</td>
<td>t&lt;br&gt;vegeconc&lt;br&gt;(days)</td>
<td>Cell C34</td>
<td></td>
</tr>
<tr>
<td>Number of ingested vegetable leaves from the contaminated field</td>
<td>n&lt;br&gt;leaf</td>
<td>Cell C35</td>
<td></td>
</tr>
</tbody>
</table>

i. **Time of vegetable ingestion after biosolids application**<br>\( t_{vegeconc} \) (days) (Sheet: **Inputdata, Cell: C34**): This is time duration after biosolids application and ingestion of vegetables assuming there is a rainfall event directly after the application. This parameter is used to calculate the natural decay of biosolids-associated pathogens on lettuce leaves following the biosolids application event.

ii. **Number of ingested vegetable leaves from the contaminated field**<br>\( n_{leaf} \) (Sheet: **Inputdata, Cell: C35**): This parameter and the volume of water deposited on each lettuce leaf \( V_{per\_leaf}, ft^3 \) (Sheet: **VegePathogenModel, Cell: C9**) are used to calculate the total volume of water deposited on ingested vegetables \( V_{on\_vegetable}, ft^3 \) (Sheet: **VegePathogenModel, Cell: C10**).

iii. **Volume of runoff water**<br>\( V_{runoff}, ft^3 \) (Sheet: **VegePathogenModel, Cell: C6**): This parameter and the total number of pathogen cells entering the field \( ED_{pathogen,im} \) (No.) (Sheet: **VegePathogenModel, Cells: B19-B46**) are used to calculate the concentration of pathogens in the runoff water \( N_{field}, No./L \) (Sheet: **VegePathogenModel, Cells: C19 to C46**) assuming that pathogens are completely mixed with the overflow water. This value has been assumed to be same as the runoff volume calculated from the Surface Water Exposure Model (Sheet: **SWRainModel, Cell: C91**).

iv. **Surface area of each lettuce leaf**<br>\( A_{per\_leaf}, in^2 \) (Sheet: **VegePathogenModel, Cell: C7**): This parameter and the surface storage capacity of each individual leaf \( h_{water\_storage}, mm \) (Sheet: **VegePathogenModel, Cell: C8**) are used to calculate the volume of water deposited on each lettuce leaf \( V_{per\_leaf}, ft^3 \) (Sheet: **VegePathogenModel, Cell: C9**). The default values for each lettuce leaf have been set as 7.5 inch tall and 4 inch width (USDA, 2010).

v. **The surface storage capacity of each individual leaf**<br>\( h_{water\_storage}, mm \) (Sheet: **VegePathogenModel, Cell: C8**): This parameter and the surface area of each lettuce leaf \( A_{per\_leaf}, in^2 \) (Sheet: **VegePathogenModel, Cell: C7**) are used to calculate the volume of water deposited on each lettuce leaf \( V_{per\_leaf}, ft^3 \) (Sheet: **VegePathogenModel, Cell: C9**). The default value has been set to be 0.2 mm based on a study by Barfied, 1973.

vi. **Volume of water deposited on each vegetable leaf**<br>\( V_{per\_leaf}, ft^3 \) (Sheet: **VegePathogenModel, Cell: C9**): This parameter is used to calculate the total volume of water deposited on vegetables ingested \( V_{on\_vegetable}, ft^3 \) (Sheet: **VegePathogenModel, Cell: C10**) It is calculated by multiplying the surface area of each lettuce leaf \( A_{per\_leaf}, in^2 \) (Sheet: **VegePathogenModel, Cell: C7**) by the surface storage capacity of each individual leaf \( h_{water\_storage}, mm \) (Sheet: **VegePathogenModel, Cell: C8**).
vii. **Total volume of water deposited on vegetables ingested (\(V_{on\_vegetable}\)) (\(ft^3\)) (Sheet: VegePathogenModel, Cell: C10):** This parameter is used to calculate the number of biosolids-associated pathogens on lettuce surfaces (\(ED_{on\_vegetable}\))(No.) (Sheet: VegePathogenModel, Cells: D19 to D46). It is calculated by the volume of water deposited on each vegetable leaf (\(V_{per\_leaf}\)) (\(ft^3\)) (Sheet: VegePathogenModel, Cell: C9) and the number of ingested vegetable leaves from the contaminated field (\(n_{leaf}\)) (Sheet: Inputdata, Cell: C35).

### 3.3.7.2 Reading and Interpreting the Output

This section describes the output parameters calculated for the Indirect Ingestion Exposure Model (Sheet: VegePathogenModel) (Figure 3-30). Detailed descriptions of these parameters are given below.

i. **The total number of pathogen cells entering the field (\(ED_{pathogen,im}\)) (No.) (Sheet: VegePathogenModel, Cells: B19-B46) (Figure 3-30):** This parameter is assumed to be the same as the total number of pathogen cells reaching the farm pond (\(ED_{pathogen,im}\)) (No.) (Sheet: SWPathogenModel, Cells: G151-G178) calculated from the Surface Water Exposure Model.

ii. **The concentration of pathogens in the runoff water entering the field (\(N_{field}\)) (No./L) (Sheet: VegePathogenModel, Cells: C19-C46) (Figure 3-30):** This parameter is calculated from the total number of pathogen cells entering the field (\(ED_{pathogen,im}\)) (No.) (Sheet: VegePathogenModel, Cells: B19-B46) and the overflow water volume (\(V_{runoff}\)) (\(ft^3\)) (Sheet: VegePathogenModel, Cell: C6).

iii. **The number of biosolids-associated pathogens on lettuce surface (\(ED_{on\_vegetable}\)) (No.) (Sheet: VegePathogenModel, Cells: D19 to D46) (Figure 3-30):** This parameter is determined by the concentration of pathogens in the runoff water entering the field (\(N_{field}\); No./L) (Sheet: VegePathogenModel, Cells: C19-C46), the total volume of water deposited on ingested vegetables (\(V_{on\_vegetable}\); \(ft^3\)) (Sheet: VegePathogenModel, Cell: C10), the decay rate in soil (\(k_{decay,soil}\); 1/day) (Sheet: Pathogen, Cells: I11 to I38), and the time of ingestion after biosolids application (\(t_{vegeconc}\); days) (Sheet: Inputdata, Cell: C34).
3.3.7.3 Output Data

Calculated numbers of biosolids-associated pathogens on lettuce leaves are shown in Figure 3-30.
3.4 Interpretation of Model Results

SMART Biosolids calculates numerical risk assessments that signify the likelihood of contracting an infectious disease over a specified time frame. It produces risk estimates for exposed adults and children residing near land application sites, as well as workers with occupational exposure to biosolids, assuming all have normal immune function. The microbial risk probabilities, though based on a thorough review of available scientific information, depend on many different uncertain inputs and modeling assumptions. Risk estimates can easily be off by several orders of magnitude (factors of 10).

No matter how far the exposed individual is removed in distance or time from the application, the models used in this tool will always estimate a non-zero risk (although in some cases the numbers may be too small to compute). This brings up the question of whether a risk estimate is “high enough” to merit some concern. This section is intended to familiarize the user with interpreting risk estimates and with some factors that influence whether a risk is acceptable.

3.4.1 What Do the Numbers Mean?

If the risk is 1, the exposed individual has 100% chance of getting infected. Most people would agree that 1 is an unacceptable level of risk. A risk of 1E-1 (scientific notation for 0.1) means that the risk is 1 in 10, 1E-2 means 1 in 100, and so on. The larger the negative exponent (the number after “E-“), the smaller the risk, so 1E-30 means 1 chance of infection in 100,000,000,000,000,000,000,000,000,000 (a negligibly small risk).

3.4.2 Is the Risk Acceptable?

People do not accept risks in isolation; they accept options with attendant risks. Knowing the magnitude and severity of a risk helps one evaluate the options. The term, acceptable risk, means a conscious decision between risky options based on some balance of good and bad consequences. In the context of biosolids application and microbial risk, this implies that some small level of increased disease incidence may be associated with land application of biosolids. The question is: what is that small level and how should it be evaluated?

There is no universal acceptable risk level. Sometimes the background level of a risk is considered to be acceptable, the logic being that the community standards and norms are reflected in their efforts to manage the background level of the risk. This is the case for the current EPA standard for potable drinking water, where the acceptable risk is defined as one additional infection per 10,000 people in a single year. One can argue against this benchmark, as it is based on background incidence, and rather than representing a conscious decision, it may really represent a passive acceptance of a risk, and the lack of an obvious, easy, or affordable alternative.

Nevertheless, the value of a number such as one non-fatal infection per 10,000 exposed people a year (1E-4) helps us understand the space between a risk of one and the risk of 1E-30. Microbial risks larger than 1E-4 exceed the small but real risks posed by drinking treated tap water. For this reason the value of one in 10,000 has become widely used a benchmark for microbial risk estimates, despite the lack of a strong societal endorsement of this value or theoretical justification for its use.
While the authors do not mean to imply that because you accept some level of risk for drinking water, you should take on another risk of the same magnitude from another source of infection, they say that if you consider the drinking water risk to be negligible, you may also be comfortable with that level of risk from biosolids applied near your dwelling. In reality, acceptable risks are determined by a wide range of factors, such as the benefits provided by an activity, the availability of lower risk alternatives, whether the risks are borne by the beneficiaries of the activity, and whether the risks are accepted voluntarily. In EPA’s recreational water program much higher risk targets, 8 in 1000 for freshwater and 1.9 in 100 for marine waters (EPA, 2011). The use of different standard for recreation compared to drinking water may be justified by considering the more voluntary nature of swimming compared to drinking, but may also reflect the smaller population involved and the lack of single responsible party for ambient water quality, as well as non-uniform attitudes towards risk that are common in societal decision making.

3.4.3 Communicating About Pathogen Risk

Effectively communicating about pathogen risk to stakeholders, particularly community members who are not experts, is a complex undertaking. It requires understanding how those stakeholders will interpret the technical information (for example the risk estimates and their attendant uncertainties). More importantly, it requires understanding what they want to know about the risk and how they want to use the information. How people interpret and use risk information is unique to the stakeholder and their circumstances.

As part of this Research Challenge, the research team collaborated with researchers who adapted a strategic risk communications process to fit the unique communication needs of biosolids program managers. For a description of the process and how it was applied in case studies, one may review the WERF SRSK2R08 Research Challenge Report entitled: *A Strategic Risk Communications Process for Outreach and Dialogue on Biosolids Land Application*. This report provides guidance to utilities that want to improve their risk communications efforts. While the process in this report, and its supporting tools, has been developed for program managers to use as they plan outreach and dialogue on biosolids land applications, it can be applied to address the range of issues, including communicating effectively about health risks associated with biosolids, including pathogens. The authors specifically outline in their final chapter of that report how the process can be used for these purposes.

3.4.4 Uncertainty in Risk Estimates

As noted above there are many uncertainties associated with a complex microbial risk assessment. To get an idea of how uncertain these risk estimates are, you can run the model for multiple iterations. You simply enter a value greater than one in cell C31 of the Inputdata sheet. Determining the number of iterations to run requires a tradeoff between the precision of the result and the required computing time. Fifty iterations will give you a rough estimate of uncertainty and will require several hours of model run time. 1000 iterations will give a much better estimate (roughly four times the precision offered by 50 iterations) but may require days for the model to run.

When running the model for more than one iteration, SMART Biosolids will randomly pick different inputs from ranges of plausible values and compute the risks associated with these different inputs. SMART Biosolids will then compile these values and show the 5th percentile, 95th percentile, median, mean, and standard deviation of the range of risk estimates. The range
between the 5th percentile and the 95th percentiles accounts for 90% of the estimates and gives a rough idea of where most of the computed risk estimates lie. If the mean or median are 1E-4 but the 95th percentile is 1E-1 and the 5th percentile is 1E-7 then the uncertainty spans 6 orders of magnitude from 1 in 10 to 1 in 10,000,000. A risk of 1 in 10,000,000 would be considered negligible by many while a risk of 1 in 10 would likely be considered unacceptable. In many cases risks due to biosolids may be so low that even the upper bound (95th percentile in this case) remains below the target risk. In other cases, one might seek to gather information that would reduce the uncertainty range for the risk. For example, one might analyze for pathogens in the biosolids produced by a given treatment plant and substitute the measured values for the default values used by SMART Biosolids (given in the Pathogen sheet). Typically, bringing more detailed site specific information to bear will reduce the uncertainty range and clarify whether there is a potential to exceed the risk target.

This explanation is intended to illustrate the subjective nature of microbial risk assessment, the interpretation of uncertainty estimates in the prediction, and how to tell a big risk from a small one.
CHAPTER 4.0

RISK ASSESSMENT
TECHNICAL DOCUMENT

4.1 Background

Biosolids may have trace levels of different types of pathogens, such as bacteria, parasites, and viruses, depending on the types of physicochemical- and biological-processes and the extent of treatment used. The objective of the Spreadsheet Microbial Assessment of Risk: Tool for Biosolids (i.e., “SMART Biosolids”, hereafter) is to calculate risks of human infection due to land application of biosolids.

The following sections present descriptions of the overall risk assessment approach used in this work, which consists of 1) Hazard Identification, 2) Dose-Response Assessment, 3) Exposure Assessment, and 4) Risk Characterization (Maier et al., 2008; Haas et al., 1999).

4.2 Risk Analysis Approach

4.2.1 Hazard Identification

To identify pathogens of concern from biosolids in different categories, such as bacteria, viruses, and parasites, an expert elicitation process was conducted in the fall of 2008 by constituting an expert panel. Experts were identified from the WERF Issue Area Team and Research Council. The expert panel was presented the list of possible pathogens of concerns from biosolids, including bacteria, viruses, and parasites and was asked to prioritize bacterial, viral, and parasitic pathogens for inclusion in a list of present pathogens of concern (i.e., identifying pathogens-of-immediate-concern) or inclusion in a list of future pathogens of concern (i.e., identifying pathogens not of established but of emerging concern) to human health.

Summaries of pathogens of concern from bacteria, viruses, and parasites categories are shown in Tables 4-1 through 4-3, respectively. Among bacteria, Campylobacter jejuni, E. coli O157:H7, non-typhi Salmonella, antibiotic resistant Campylobacter jejuni, Shigella spp., Legionella, Vibrio cholerae, Clostridium spp., Yersinia spp., Helicobacter, and Listeria are noted as bacterial pathogens of concern (Table 4-1). Among viruses, Adenovirus 4, Enteroviruses (a group consists of poliovirus, coxsackie virus, echo virus, and enterovirus types 68-71), Norovirus, Rotavirus, Hepatitis A and E, and Astrovirus are noted as viral pathogens of concern (Table 8-2). Among parasites, Cryptosporidium, Giardia lamblia, Ascaris, Toxoplasma gondii, Cyclosporida, Entamoeba histolytica, and Microsporidia are noted as parasitic pathogens of concern (Table 4-3), out of which Toxoplasma gondii, Cyclosporida, and Microsporidia are highlighted as “emerging pathogens of concern.”
<table>
<thead>
<tr>
<th>Pathogen</th>
<th>Priority</th>
<th>% Response for Inclusion (Present/Future) (N =7)</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Campylobacter jejuni</td>
<td>1</td>
<td>29/71</td>
<td>Literature data available. High percentage of votes as a future concern.</td>
</tr>
<tr>
<td>E.coli O157:H7</td>
<td>1</td>
<td>100/86</td>
<td>High percentage of votes. Data are available on anaerobic digested solids</td>
</tr>
<tr>
<td>Non-typhi Salmonella</td>
<td>1</td>
<td>57/71</td>
<td>High percentage of votes. Abundant data available.</td>
</tr>
<tr>
<td>Shigella spp.</td>
<td>2</td>
<td>14/43</td>
<td>Data are available in literature. Higher percentage of votes as an area of uncertainty.</td>
</tr>
<tr>
<td>Legionella</td>
<td>3</td>
<td>14/14</td>
<td>Legionella is known to be carried in aerosols. It is usually associated with warm water. Persistence would be key to whether this could be an issue in biosolids. If there is data on occurrence in sewage sludge it is limited.</td>
</tr>
<tr>
<td>Vibrio cholerae</td>
<td>3</td>
<td>14/14</td>
<td>There has not been a waterborne or non-seafood cases in this country for over 100 years. However, non-01 V. cholerae causes skin GI infections and we do have cases in the U.S.</td>
</tr>
<tr>
<td>Clostridium spp.</td>
<td>3</td>
<td>0/0</td>
<td>C. difficile is a growing problem in hospitals and is spreading to the community. Questions regarding sewage sludge have already come up among the public. Antibiotic resistant forms may be an issue if they persist in the environment. No data on occurrence in sewage sludge is available that we know of.</td>
</tr>
<tr>
<td>Yersinia spp.</td>
<td>3</td>
<td>14/14</td>
<td>The organism has been detected in sewage sludge, but data are limited. A waterborne and foodborne problem in Europe, but not much concern in the U.S. as outbreaks is rare.</td>
</tr>
<tr>
<td>Helicobacter</td>
<td>3</td>
<td>0/29</td>
<td>No data available</td>
</tr>
<tr>
<td>Listeria</td>
<td>3</td>
<td>0/29</td>
<td>This organism is a major concern of the food industry. As long as you do not apply to land with no food crops it is not likely to be a problem.</td>
</tr>
</tbody>
</table>
Table 4-2. Pathogens of Concern in the Virus Category.

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>Priority</th>
<th>% Response for Inclusion (Present/Future) (N =7)</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adenovirus 4</td>
<td>1</td>
<td>29/57</td>
<td>Data are available. Relatively little existing work but received a fairly high percentage of votes.</td>
</tr>
<tr>
<td>Enteroviruses</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Types 68-71</td>
<td>1</td>
<td>0/0</td>
<td>Enteroviruses are well established as a concern in the literature and the existing regulatory framework. Data on occurrence are available.</td>
</tr>
<tr>
<td>Coxsackievirus</td>
<td>1</td>
<td>14/29</td>
<td>For enterovirus, inhalation risk is calculated using inhalation dose-response model of coxsackievirus and ingestion risk is calculated using ingestion dose-response model of Echovirus.</td>
</tr>
<tr>
<td>Echovirus</td>
<td>1</td>
<td>14/14</td>
<td></td>
</tr>
<tr>
<td>Poliovirus</td>
<td>1</td>
<td>0/43</td>
<td></td>
</tr>
<tr>
<td>Norovirus</td>
<td>1</td>
<td>43/43</td>
<td>No data on viability or reduction by treatment processes.</td>
</tr>
<tr>
<td>Rotavirus</td>
<td>1</td>
<td>29/57</td>
<td>Highest Dose-Response function known</td>
</tr>
<tr>
<td>Hepatitis A</td>
<td>2</td>
<td>14/29</td>
<td>No occurrence data. Fairly high percentage of votes as future concern</td>
</tr>
<tr>
<td>Hepatitis E</td>
<td>2</td>
<td>14/43</td>
<td>No occurrence data. Higher percentage of votes as future concern.</td>
</tr>
<tr>
<td>Astroviruses</td>
<td>3</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Table 4-3. Pathogens of Concern in the Parasites Category.

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>Priority</th>
<th>% Response for Inclusion (Present/ Future) (N = 7)</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cryptosporidium</td>
<td>1</td>
<td>29 (Present)/43 (Future)</td>
<td>Some data available in the literature. Fairly high percentage of votes</td>
</tr>
<tr>
<td>Giardia lamblia</td>
<td>1</td>
<td>43/71</td>
<td>High percentage of votes. Existing data is on presence of cysts, but not viability. Some data on reduction by digestion. Dose response data available.</td>
</tr>
<tr>
<td>Ascaris</td>
<td>2</td>
<td>0/29</td>
<td>Good data base on occurrence and recent published dose response model</td>
</tr>
<tr>
<td>Toxoplasma gondii*</td>
<td>3</td>
<td>14/0</td>
<td>No data on occurrence that we are aware of in wastewater or sludge. Dose response data for cats might be available. Waterborne outbreaks have occurred and it is now believe that other animals besides felines may serve as reservoirs. No method available for detection in biosolids. It may be a good one to include, but might require additional funding.</td>
</tr>
<tr>
<td>Cyclosporidia*</td>
<td>3</td>
<td>0/14</td>
<td>No data base on occurrence or infectivity.</td>
</tr>
<tr>
<td>Entamoeba histolytica</td>
<td>3</td>
<td>0/14</td>
<td>Not a problem in the U.S. Dose response data available.</td>
</tr>
<tr>
<td>Microsporidia*</td>
<td>3</td>
<td>0/14</td>
<td>Some data on occurrence in biosolids, but no infectivity data that we are aware of</td>
</tr>
</tbody>
</table>

*Emerging pathogen-of-concern

4.3 Dose-Response Assessment

Risk of infection (Risk$_{inf}$) depends on exposed dose (Dose$_{exp}$), pathogen type (Pathogen), and pathogen-specific dose-response model (Model$_{D-R}$) (Equation 8-1). Different dose-response models exist for different pathogen-exposure route pairs. In general, two dose-response models: 1) Exponential model (Equation 4-2), and 2) Beta-Poisson model (Equation 4-3) have been extensively used to calculate the risk of infection from microbial exposure (Maier et al., 2008; Haas et al., 1999; Teunis et al., 1996; Eisenberg et al., 2008). The exponential model has only one parameter (i.e., $r$: fraction of the ingested microorganisms that survive to initiate infections or host-microorganisms interaction probability). The Beta-Poisson model has two parameters (i.e., a and b), which can be related to the median effective dose (Dose$_{exp,50%}$, i.e., a dose required to infect 50% of the population) (Equation 4-3b). Dose-response model parameters for different microorganism-exposure route pairs are obtained from the literature (e.g., Haas et al., 1999) and summarized in Appendix A.

\[
Risk_{inf} = f (Dose_{exp}, Model_{D-R}, Pathogen_{exp})
\]

\[
Risk_{inf,exp,tl} = 1 - e^{-r \times Dose_{exp}}
\]
As noted above, for pathogens for which a dose-response model for the inhalation route is not available, the ingestion-based dose-response model is used an ingested dose equal to 50% of the inhaled dose (Brooks et al., 2005b).

4.4 Exposure Assessment

4.4.1 Exposed Subpopulation

The total population is subdivided into three subpopulation types: 1) Residential-adult, 2) Residential-child, and 3) Occupational-worker (U.S. EPA, 1997; Brooks et al., 2005a and 2005b; Eisenberg et al., 2008; Gerba et al., 2002 and 2008), which have different exposure rates for different exposure media (U.S. EPA, 1997). The exposure duration depends on exposed subpopulation type, exposure media, and proximity to the pollutant source (in this case: land-applied biosolids).

4.4.2 Exposure Routes

This chapter calculates risks of infection/illness from ingesting surface or groundwater, indirectly ingesting biosolids-amended soils, and inhaling air contaminated with biosolids-associated pathogens.

4.4.2.1 Ingestion of Surface Water

During land application of biosolids, biosolids either fall on the soil surface or aerosolize in air. The biosolids and biosolids-associated pathogens that fall on the soil surface remain on the soil surface until the rainfall event when some of the biosolids-associated pathogens are released in the runoff water and some of the biosolids along with soil sediments are entrained in the runoff water. These biosolids-associated pathogens and sediments, which are entrained in the runoff water, travel and mix with water in the nearest agricultural farm pond. The exposure to these biosolids-associated pathogens from the agricultural farm pond water during recreational activities is termed as Exposure of biosolids-associated pathogens via ingestion of surface water. Pathogen concentration in the surface water medium is calculated using the surface water exposure model (Sheets: SWPathogenModel, SWRainModel, Barrenplot, Vegstrip, and Sheet24.RiskCal).

4.4.2.2 Ingestion of Groundwater

During the rainfall event, part of the water could infiltrate into the ground and thus, biosolids-associated pathogens that fall on the soil surface could also infiltrate into the soil with rainfall water and travel through saturated and unsaturated aquifers to the nearby well. Exposure to these biosolids-associated pathogens occurs through the ingestion of contaminated groundwater from a well. Pathogen concentrations in the groundwater medium are calculated using the groundwater exposure model (Sheets: GWPathogenModel and GWTransportModel).
4.4.2.3 Direct Ingestion of Biosolids-Amended Soils

Direct ingestion of biosolids-amended soils occurs during accidental exposures to biosolids-amended soil. Pathogen concentrations in the biosolids-amended soils are calculated using the soil exposure model (SoilPathogenModel and Sheet24.RiskCal).

4.4.2.4 Inhalation of Air

During land-application of biosolids, aerosolized biosolids (and also biosolids-associated pathogens) remain in the air and are transported away from the source by wind until they fall on the soil surface due to gravitational forces. Pathogen concentrations in the air are calculated using the air exposure model and a VBA code (Sheets: AirOccupational, AirResAdult, AirResChild, and Sheet24.RiskCal).

4.4.3 Exposed Pathogen Dose (Dose$_{exp}$)

Exposed pathogen dose is calculated using environmental concentrations of pathogens (N$_{path}$) (Equation 4-4), where $E_r$ represents exposure rate. Environmental concentrations of pathogens depend on initial pathogen concentration and environmental decay with time.

$$ Dose_{exp} = N_{path}E_r $$  \hspace{1cm} (4-4)

For the groundwater case, the pathogens transport with groundwater flow and were not assumed to be cumulative in well water. Instead, daily risk calculations were made for the exposure specific to each day. Overall risk was calculated as described below using Equation 4-8 below (start from Row 92 in the Sheet: GWPathogenModel).

4.5 Risk Characterization

4.5.1 Cumulative Risk Estimate for Long-Term Exposure

SMART Biosolids calculates microbial risk given the occurrence of particular events, such as rare storm and flooding events. To calculate the cumulative risk of probability events over long time periods, the risk estimate for time $t$ (Risk$_t$) is first calculated using risk at day 0 (Risk$_0$) (i.e., the output from SMART Biosolids) and pathogen decay rate ($k_{decay}$) using Equation 4-5a:

$$ Risk_t = Risk_0e^{-k_{decay}t} $$  \hspace{1cm} (4-5a)

For low estimates of risk, these estimates for different time periods can be added (assuming that their interactions are small) forming a geometric series which can be simplified as Equation (4-5b):

$$ Risk_{ex} \approx \sum_{t=0}^{\infty} Risk_0e^{-k_{decay}t} \approx \frac{e^{-Nk_{decay}} - e^{-k_{decay}}Risk_0}{1 - e^{-k_{decay}}} $$  \hspace{1cm} (4-5b)

For large N, the exp(-kN) term tends to zero which further simplifies Equation (4-5b) to Equation (4-5c):

$$ Risk \approx \frac{e^{-k_{decay}}Risk_0}{e^{-k_{decay}} - 1} \approx \frac{Risk_0}{1 - e^{-k_{decay}}} $$  \hspace{1cm} (4-5c)
4.5.2 Risk of Infection

Infection indices shown in Table A-6 (Appendix A) indicate if there is the possibility of getting a particular type of disease (i.e., respiratory illness, gastrointestinal illness) from a particular pathogen.

To calculate daily risk of infection, daily dose ($D_{\text{exp}}$) (No.) is used for risk estimation. For calculating risks of infection from biosolids-associated enteric viruses, dose-response model parameters of ingestion of Echovirus 12 are used to characterize risk of infection from enteric viruses (Brooks et al., 2005a and b). For inhalation risk of enteric viruses, dose-response parameters of Coxsackie virus 12 virus are used to characterize risk of infection from enteric viruses (Brooks et al., 2005a and b).

Daily risk of infection from a particular pathogen for a given exposure route is further categorized into two different extents of illness: (a) Temporarily debilitating (termed as minor extent, hereafter) and (2) Possibly life threatening (termed as major extent, hereafter) as per the classification of incidence of illness given in Table A-6 and denoted as $\text{Risk}_{\text{inf, daily, extent, disease, pathogen}}$ (-).

During pathogenic exposure, only a fraction of infections result in illness, depending on factors, such as host’s age and immune status; pathogens virulence and strain type; and exposure route (Regli et al., 1991). Estimates of daily risk of infection could be used further to calculate estimates of daily risk of illness ($\text{Risk}_{\text{ill, daily, extent, disease, pathogen}}$ (-) using morbidity rates of pathogens ($\eta_{\text{morb, pathogen}}$), obtained from epidemiological data (Equation 4-6).

$$\text{Risk}_{\text{ill, daily, extent, disease, pathogen}} = \eta_{\text{morb, pathogen}} \times \text{Risk}_{\text{inf, daily, extent, disease, pathogen}} \tag{4-6}$$

Cumulative daily risk of getting a particular type of illness at minor or major extent ($\text{Risk}_{\text{ill, daily, extent, disease}}$) (-) is a combination of pathogen-specific risk of illness and can be calculated using Equation (4-7):

$$\text{Risk}_{\text{ill, daily, extent, disease}} = 1 - \prod_{i=1}^{N} \left(1 - \text{Risk}_{\text{ill, daily, extent, disease, pathogen, i}}\right) \tag{4-7}$$

Illness risk per application period ($\text{Risk}_{\text{ill, app, pathogen, medium}}$) (-) is calculated using Equation (4-8), where $D_{\text{exp, app}}$ represents duration of application period (days) (assuming all events of pathogen exposure are independent to each other). For ingestion of groundwater, the $D_{\text{exp, app}}$ is the duration through which biosolids-associated pathogens are observed in drinking wells.

$$\text{Risk}_{\text{ill, app, pathogen, medium}} = 1 - \prod_{i=1}^{D_{\text{exp, app}}} \left(1 - \text{Risk}_{\text{ill, daily, pathogen, medium, i}}\right) \tag{4-8}$$
During land-application of biosolids, biosolids are deposited on land and are mixed with soil particles, causing a dilution in the number of biosolids-associated pathogens per mass of soil (Gerba et al., 2002 and 2008). In addition, during rainfall events, some of the biosolids-associated pathogens are released to the runoff water while some remain attached to the soil (attached-pathogen cells, hereafter). The following section describes calculation of the number of biosolids-associated pathogens present in a given mass of a soil. Assumptions of this model are summarized below:

1) Land-applied biosolids are assumed to be the only source of pathogens in this work;
2) After a rainfall event, a fraction of the biosolids-associated pathogens remain attached to soil surfaces;
3) Biosolids particles are completely mixed with native soil particles so that their concentration is diluted during incorporation of biosolids into soil (Gerba et al., 2002; 2008). Gerba et al., (2002) reported that the usual practice of land application of biosolids is to plow fields within a day of surface spreading of biosolids, which results in the dilution of the biosolids in the soil matrix.

Let’s assume that $N_0$ is the initial number of pathogens present in the applied biosolids (No./g biosolids). Also, during rainfall events, a fraction of the pathogens are released in the runoff water and the remaining pathogens remain attached to the biosolids (attached-pathogen cells, hereafter). Let us assume that $N_{attached}$ is the number of attached-pathogens in biosolids (No./g biosolids) and is calculated using the following Equation (5-1), where $f$ is the fraction of pathogens released from the biosolids-soil matrix.

$$N_{attached} = (1 - f)N_0 \quad (5-1)$$

Remaining number of pathogens after biosolids application event ($N_{remain}$; No./mg soil) is assumed to be equal to $N_0$ if rainfall does not occur immediately after the biosolids application event or equal to $N_{attached}$ (Equation 5-1), if rainfall occurs immediately after the biosolids application event.

The effective number of biosolids-attached pathogens ($N_{remain,eff}$) (No./mg soil) is calculated using the remaining biosolids-associated pathogens ($N_{remain}$)(No./g biosolids), biosolids dilution in soil ($f_{soil}$) (-) (assumed to be 0.01, Gerba et al., 2008), time of soil ingestion after biosolids application ($t_{soilconc}$) (days), and pathogen first-order decay parameter ($k_{decay,soil}$) (1/day) as per the following Equation (5-2):

$$N_{remain,eff} = \frac{1}{1000} f_{soil} N_{remain} \exp(-k_{decay,soil} \times t_{soilconc}) \quad (5-2)$$
6.1 Background

Most of the mechanistic air transport models involve a form of the Gaussian plume or area source dispersion models, which assume constant stationary sources. However, land application usually involves a moving tractor, which conflicts with these assumptions. When passing by a receptor or human, this moving source will produce a large intermittent spike in concentration, which may be obscured by time-averaged exposure models (Low et al., 2007). To better account for these intermittent spikes, the researchers have modeled a traveling Gaussian plume, which incorporates the changing position of the emission source.

Biosolids emission rates can be varied depending on application method (Appl_method), such as slinging, spraying, and disk incorporation (Brooks et al., 2004). The biosolids emission rate \( Q_{\text{biosolids}} \) (lb/sec) is calculated by multiplying biosolids application rate in air \( Q_{\text{application}} \) (lb/sec) by the solid content in biosolids \( f_{\text{biosolids}} \) (%). The biosolids application rate in air \( Q_{\text{application}} \) (lb/sec) is the production of the total biosolids sprayed \( B \) (dry tons biosolids/acre), source velocity \( v_{\text{source}} \) (m/s), source width \( W_{\text{spray}} \) (m), and aerosolization efficiency factor \( E \).

The aerosolization efficiency \( E \) is the fraction of the material applied that results in aerosols that can be advected downwind. This parameter varies with the type of application methods and certain meteorological parameters, such temperature, wind speed, and solar radiation. The default values have been estimated for different application methods, such as slinger, splash-plate spray applicator, and disk incorporation application (Table 6-1). The reason for the lower \( E \) values from liquid biosolids relative to cake biosolids may be due to the fact that drier material is more likely to be aerosolized than wet material. The higher \( E \) values from diskin compared to slinging is consistent to field findings that loading or disturbing the material always provided the most aerosolization relative to any other method of application. The detailed calculation can be found in Appendix C.

<table>
<thead>
<tr>
<th>Slinger</th>
<th>Splash-plate</th>
<th>Disk</th>
</tr>
</thead>
<tbody>
<tr>
<td>Biosolids froms</td>
<td>Cake</td>
<td>Liquid</td>
</tr>
<tr>
<td>Aerosolize efficiencies</td>
<td>1.81E-6</td>
<td>3.3E-7</td>
</tr>
</tbody>
</table>

The biosolids emission rate \( Q_{\text{biosolids}} \) (lb/sec), emission height \( H_{\text{source}} \) (ft), and source velocity \( v_{\text{source}} \) (ft/sec) are used to define the Gaussian plume and to calculate aerosolized biosolids-associated pathogens (i.e., bioaerosols). The Gaussian plume model (Equation 6-1a), consists of a source term (i.e., bioaerosol emission term: \( Q_{\text{term}} \)) and dispersion terms for the \( y \)- and \( z \)-directions (\( y_{\text{term}} \) and \( z_{\text{term}} \), respectively).
\[ C_{\text{air biosolids,cell}} = (Q_{\text{term}}) \times (y_{\text{term}}) \times (z_{\text{term}}) \] (6-1a)

The bioaerosol emission term \( Q_{\text{term}} \) depends on the biosolids emission rate \( Q_{\text{biosolids}} \) (lb/sec), wind velocity \( v_{\text{wind}} \) (ft/sec), and related dispersion (Equation 6-1b). Dispersions in the y- and z-directions depend on the respective distance (y or z), dispersion coefficient \( \sigma_y \) or \( \sigma_z \), and source height \( H_{\text{source}} \) (ft) (Equations 6-1c and 6-1d, respectively for y- and z-dispersion terms).

\[ Q_{\text{term}} = \frac{Q_{\text{biosolids}}}{2\pi v_{\text{wind}} \sigma_y \sigma_z} \] (6-1b)

\[ y_{\text{term}} = \exp\left( \frac{-0.5 y^2}{\sigma_y^2} \right) \] (6-1c)

\[ z_{\text{term}} = \left[ \exp\left( \frac{-0.5(z - H_{\text{source}})^2}{\sigma_z^2} \right) + \exp\left( \frac{-0.5(z + H_{\text{source}})^2}{\sigma_z^2} \right) \right] \] (6-1d)

The y- and z-directional dispersion constants depend on distance from the source, wind velocity, and atmospheric stability conditions (Six categories: A, B, C, D, E, and F; Seinfeld, 1986) and are calculated using Equations (6-1e and 6-1f), respectively. Tables 6-1 and 6-2 show different stability classes and dispersion constants for different wind velocity and solar irradiation categories (Seinfeld, 1986).

\[ \sigma_y = R_y \times x^{r_y} \] (6-1e)

\[ \sigma_z = R_z \times x^{r_z} \] (6-1f)

Equation (6-1a) is used to calculate concentrations of aerosolized biosolids particles, emitted from cells of the model grid, which are added together to calculate total concentration of aerosolized biosolids particles \( C_{\text{air biosolids,plot}} \) (lb/ft\(^3\)) (Equation 6-2).

\[ C_{\text{air biosolids,plot}} = \sum_{i=1}^{n_{\text{cells}}} C_{\text{air biosolids,cell}_i} \] (6-2)

In addition to calculating concentrations of aerosolized biosolids particles during an application event, concentrations of biosolids-amended soil particles resuspended in air due to wind activities and mechanical stresses (Sehmel, 1980) are also calculated and added to concentrations of aerosolized biosolids particles for occupational workers only. No resuspension of biosolids-amended soil particles are assumed for residential populations as they live at least 250 ft (or 75 m) from application sites and pathogen exposure concentrations due to these resuspended particles are assumed to be low.

For calculating concentrations of resuspended biosolids-amended soil particles in air \( C_{\text{air biosolids, resus}} \) (lb/ft\(^3\)), the net resuspension factor \( RF_{\text{net}} \) (1/ft) due to wind activity and
mechanical stresses (Table B-3) is multiplied by the amount of biosolids applied per unit land area (B; kg/m²) and biosolids dilutions in soil (f_{soil}) (-) (assumed to be 0.01, Gerba et al., 2002) (Equation 6-3). Resuspension due to wind activity is only considered for wind velocities exceeding the critical wind velocity of 19.8 ft/sec (Sehmel, 1980).

\[ C_{air\_biosolids, resus} = RF_{net} f_{soil} B \left( \frac{1000}{454 \times 3.3^3} \right) \]  

(6-3)

For residential populations, Equations (6-1 and 6-2) are used to calculate total concentration of aerosolized biosolids particles for residential-adult (C_{air\_biosolids,RA}) (lb/ft³) and residential-child (C_{air\_biosolids,RC}) populations (lb/ft³), respectively.

Two different types of occupational workers are assumed: (a) A field worker and (b) An operator driving the application vehicle (termed truck driver, hereafter). For a field worker working at a constant distance from the moving source (x-distance: X_{FW}, y-distance: Y_{FW}) (ft), total concentration of aerosolized biosolids particles (C_{air\_biosolids,FW})(lb/ft³) is calculated using Equation (6-4), assuming that aerosolized particles are uniformly distributed in a rectangular control volume of height (H_{inhalation}) (ft), length (v_{wind}) (ft/sec), and width (maximum of W_{spray} and 2Y_{FW}) (ft).

\[ C_{air\_biosolids,FW} = \frac{Q_{biosolids}}{v_{wind} H_{inhalation} W_{spray} (2 * Y_{FW})} + C_{air\_biosolids, resus} \]  

(6-4)

For a truck driver, concentration of aerosolized biosolids particles inside a truck cabin (C_{air\_biosolids,TD})(lb/ft³) is calculated using a similar approach (Equation 6-5). However, inhalation height is adjusted to reflect the height of the truck driver. Also, aerosolized concentration inside the cabin is reduced due to the effect of filtration of cabin filters on aerosolized biosolids particles (particle size > 3μm) (Tanner et al., 2008):

\[ C_{air\_biosolids,cabin,TD} = \left( \frac{Q_{biosolids}}{v_{wind} H_{inhalation} W_{spray}} + C_{air\_biosolids, resus} \right) (1 - \eta_{filter}) \]  

(6-5)

where, \( \eta_{filter} \) represents filtration efficiency (-) of particles of size > 3 μm (Tanner et al., 2008). In this case, the truck driver is always positioned at a constant distance of X_{FW} from the source (as both are moving at a constant source velocity, i.e., v_{source}). The assumption of complete mixing in the control volume is not intended to be a physically realistic representation of concentrations at any point in time but rather to reflect the time-averaged exposure as variations in wind and in the relative positions of the applicator and the receptor over time will tend to average out exposures to the plume of bioaerosols.

Concentrations of aerosolized biosolids-associated pathogens, i.e., bioaerosols \( (C_{bioaerosols}) \) (No./ft³) for different pathogen types are calculated using the initial pathogen concentrations in biosolids (N_0) (No./g) and the concentration of aerosolized biosolids (C_{air\_biosolids}) (Equation 6-6).

\[ C_{bioaerosols} = N_0 C_{air\_biosolids} \]  

(6-6)

As pathogens decay in the environment due to the effects of meteorological conditions, their concentrations at time (t, day) are calculated using a first-order exponential decay model (Equation 10-A-7):
\[ C_{\text{bioaerosols, decay}} = C_{\text{bioaerosols}} \exp\left(-k_{\text{decay, air}} \times t\right) \]  

(6-7)

where, \( C_{\text{bioaerosols, decay}} \) represents concentration of bioaerosols after decay (No/ft\(^3\)) and \( k_{\text{decay, air}} \) represents first-order decay constant for bioaerosols in air (1/day). As occupational workers are exposed to bioaerosols very shortly after emission \( (t \rightarrow 0) \); Tanner et al., 2008), no pathogen decay is assumed for calculating concentration of bioaerosols for occupational workers. However, pathogen decay over time is assumed for calculating the concentration of bioaerosols for residential populations as this subpopulation generally lives at a distance of at least 250 ft or 75 m (i.e., setback distance) from the biosolids application site.
CHAPTER 7.0

SURFACE WATER EXPOSURE MODEL
TECHNICAL DOCUMENT

7.1 Surface Runoff Model

7.1.1 Model Selection

The objective of this model is to calculate: 1) soil water infiltration rate, and 2) surface water runoff volume which are used to calculate the overland transport and fate of biosolids-associated pathogens (Figure 1-1). The following assumptions were made in this model:

1) The soil profile is homogeneous;
2) Rainfall is applied directly and uniformly to the site;
3) No surface ponding is considered;
4) Surface runoff is calculated as excess infiltration.

7.1.2 Joint Green-Ampt Model

The explicit Green-Ampt model for determining infiltration rate \( q_{\text{inf}}(t) \) (cm/h) and cumulative infiltration \( I(t) \) (cm) was developed by Salvucci and Entekhabi (1994) as a straightforward and accurate estimation of infiltration as a function of time. The constant flux Green-Ampt model can be applied to calculate infiltration for non-ponding conditions (Equations 7-1 to 7-3). The Joint Green-Ampt model was developed by incorporating the explicit Green-Ampt Model into the Constant Flux Green-Ampt Model (Swartzendruber, 1974), which can also be applied for non-ponding conditions.

When rainfall rate \( r \) (cm/h) is smaller than the saturated hydraulic conductivity \( K_s \) (cm/h) of the soil, Equation 1 is used to calculate values of infiltration rate and cumulative infiltration.

When rainfall rate is larger than the saturated hydraulic conductivity, values of infiltration rate and cumulative infiltration depend on the time when surface saturation occurs \( t_0 \) (h). When time for calculating infiltration rate and cumulative infiltration \( t \) (h) is smaller than \( t_0 \), Equation 7-2 is used to calculate values of infiltration rate and cumulative infiltration and when \( t \) is larger than \( t_0 \), Equation 7-3 is used to calculate these values.

\[
\begin{align*}
(i) \quad & \text{When } r < K_s \\
q_{\text{inf}}(t) &= r \\
I(t) &= rt \\
\end{align*}
\]
(ii) When $r > K_s$ and $t < t_0$

$$q_{inf}(t) = r$$

$$I(t) = rt \quad (7-2)$$

When $r > K_s$ and $t > t_0$

$$q_{inf}(t) = K_s \left( \frac{2^{0.5}}{2} \tau^{-0.5} + \frac{2}{3} - \frac{2^{0.5}}{6} \tau^{0.5} + \frac{1 - 2^{0.5}}{3} \tau \right) \quad (7-3a)$$

$$I(t) = K_s \left( \frac{1 - 2^{0.5}}{3} \tau + \frac{2^{0.5}}{3} \left( \lambda t + \chi \right)^{0.5} \ln \left( \frac{t + \chi}{\chi} \right) + \frac{2^{0.5}}{3} \chi \left[ \frac{1 + 0.5 \chi + \left( \lambda t + 0.5 \chi \right)^{0.5}}{0.5 \chi} \right] \right) \quad (7-3b)$$

$$\chi = \frac{(h_s - h_f)(\theta_s - \theta_0)}{K_s} \quad (7-3c)$$

$$\tau = \frac{t}{t + \chi} \quad (7-3d)$$

$$t_0 = \frac{-K_s h_f (\theta_s - \theta_0)}{r(r - K_s)} \quad (7-3e)$$

In Equation (7-3), $\theta_s$ represents the saturated volumetric water content (cm$^3$/cm$^3$), $\theta_0$ represents the initial volumetric water content (cm$^3$/cm$^3$), $h_s$ represents the ponding depth and is set to zero, assuming no ponding case. The capillary pressure ($h_f$) at the wetting front is calculated using Equation (7-4), where, $h_e$ is air exit head (cm), $\lambda$ is the exponent of the Brooks-Corey water retention model, and $\eta$ is the exponent of the Brooks-Corey conductivity model. The air exit head ($h_e$) depends on the air entry head and is calculated using Equation (7-4c). In the absence of initial moisture content, the residual volumetric water constant ($\theta_r$)(cm$^3$/cm$^3$) is used (Equation 7-5). Typical values of these parameters are provided in Tables E-1 and E-2 (Appendix E).

$$h_f = \frac{\eta}{\eta + 1} h_e \quad (7-4a)$$

$$\eta = 2 + 3 \lambda \quad (7-4b)$$

$$h_e = 0.5 h_b \quad (7-4c)$$

$$\theta_0 = \theta_r \quad (7-5)$$
Model validation of the developed *SWRainModel* is presented in Appendix G.

### 7.2 Overland Transport and Fate of Biosolids-Associated Pathogens

#### 7.2.1 Pathogen Source

Biosolids may be applied on land using different application methods (Appl_method, Sheet), such as slinging, manure spreading, and spraying (Brooks et al., 2004) at different biosolids application rates ($Q_{\text{application}}$, kg/s for cake form and L/s for liquid form of biosolids material), biosolids application durations per unit area ($\Delta t_{\text{application}}$, s/m²), and solid contents ($f_{\text{biosolids}}$; g/g for cake form (> 7%) and g/mL for liquid form (< 7%)). Assuming that biosolids are applied on a plot of land area ($A$, m²), the amount of biosolids applied per unit land area ($B$; kg/m² or L/m² depending on form of biosolids material) can be calculated by multiplying $Q_{\text{application}}$ by $\Delta t_{\text{application}}$ (i.e., $B = Q_{\text{application}} \times \Delta t_{\text{application}}$). The amount of total biosolids applied ($B_{\text{total}}$; kg or L depending on form of biosolids material) can be calculated using the following equation: $B_{\text{total}} = B \times A$.

The amount of dry biosolids applied on land ($Q_{\text{biosolids}}$, g) can be calculated by multiplying $B_{\text{total}}$ by $f_{\text{biosolids}}$. Assuming $N_0$ is the initial number of pathogens present in the applied biosolids (No./g dry biosolids), the total number of pathogens applied to the land ($N_{\text{total}}$, No.) can be calculated by multiplying $Q_{\text{biosolids}}$ by $N_0$ (i.e., $N_{\text{total}} = Q_{\text{biosolids}} \times N_0$), where a constant value of 1000 represents a conversion factor used to convert total mass of dry biosolids applied on the plot from kilograms to grams.

Due to rainfall events, some pathogens are released into the water at the rate of $f$ (-) from the biosolids-soil matrix. The number of pathogens released (termed as unattached-pathogen cells, hereafter; $N_R$, No.) is given by Equation (7-6). The number of pathogen cells remaining attached to the biosolids ($N_{\text{attached}}$, termed attached-pathogen cells, hereafter) (No.) is given by Equation (7-7).

$$N_R = f(N_{\text{total}}) \quad (7-6)$$

$$N_{\text{attached}} = (1 - f)N_{\text{total}} \quad (7-7)$$

#### 7.2.2 Overland Transport of Pathogens

The following sections describe the fate and transport of unattached- and attached-pathogen cells during overland flow of runoff water from a barren plot of land to the nearest farm pond, via transport over a buffer zone between the barren plot and a farm pond (termed as a vegetative filter strip, VFS in this study). The following assumptions are made:

1) Detachment and deposition during overland flow in rill areas cannot occur simultaneously at a point.

2) Both rill and interrill erosion are non-selective (i.e., during erosion, detached sediment particles contain all particle classes).

3) Interrill detachment occurs simultaneously with deposition in rill areas.

4) Distribution of transport capacity of a particle class is proportional to its mass fraction.

5) All sediments are equally transferable and a single value of sediment transportability is used to calculate transport capacity of runoff in the rill areas.
6) Distribution of sediment mass among sediment particle classes at the point of detachment depends primarily on the soil’s clay content.

7) Detachment is a non-selective process but deposition is a selective process and depends on sediment particle’s settling velocity (i.e., function of particle diameter and density).

8) A combination of a barren land plot, a vegetative filter strip (VFS), a channel, and a farm pond is assumed for developing this model. In addition, other combinations, such as (i) land, followed by a channel, (ii) land, followed by a pond, and (iii) land, followed by VFS and channel or pond are possible.

9) For a VFS, runoff water is assumed to enter irrespective of the relative row grade along the upper edge of the VFS barrier.

10) Sediment loads in a channel are calculated assuming a uniform channel grade, where sediment input from the overland flow area is uniform along the channel length. Sediment deposition for a particulate particle class occurs when incoming sediment load exceeds the sediment transport capacity.

11) Sediment transport capacity of a pond is assumed to be zero and it is treated as a fixed length settling basin.

12) Unattached-pathogen cells are assumed to remain in suspension. However, attached-pathogen cells are removed at different parts of the overland flow path.

7.2.2.1 Unattached-pathogen Cells

Effective delivery of unattached-pathogen cells (i.e., $ED_{unattached}$) (No.) reaching the farm pond from a given plot of land is given by Equation (7-8):

$$ED_{unattached} = f_{SDR,unattached} N_R$$

where, $f_{SDR,unattached}$ is a fraction of total number of pathogens released due to runoff, reaching the nearest farm pond (-) and is assumed to be 1 in this study indicating no pathogen loss during their overland transport to the nearest farm pond.

7.2.2.2 Attached-Pathogen Cells

During runoff events, biosolids along with soil sediments are entrained in runoff water and transported to the nearest farm pond via overland transport on a barren plot of land, a VFS, and a channel. Along with these biosolids particles, attached-pathogen cells on biosolids also travel to the nearest farm pond and add to the total concentration of pathogens in the pond water.

Overland transport of biosolids is assumed to be similar to that of sediments. During overland transport of sediments (or biosolids), this study does not consider the effects of land management practices on sediment erosion (i.e., a barren plot of land is assumed). Further, a VFS and a channel are assumed to be present at the end of the plot of land, which influence the delivery of sediments (and also biosolids) to the farm pond. The amount of biosolids entrained in runoff water depends on the amount of sediment eroded from the soil surface during overland flow of runoff water. This study models overland transport of sediments (and also, biosolids-associated pathogens) on a barren plot of land, followed by a VFS, a channel, and a farm pond in separate segments.
Throughout the transport pathways, no pathogen decay is assumed in these sub-systems, which might result in overestimations of the number of attached-pathogen cells entrained in runoff water, thereby providing conservative risks of pathogen exposure. The following sections describe overland transport of sediments (and biosolids-associated pathogens) in these segments separately.

![Figure 7-1. A Schematic of the Overland Transport of Sediments.](image)

**Barren Plot** A schematic of the overland transport of sediments is given in Figure 7-1. This model spatially integrates sediment loads of every particle class from different segments on an overland flow path (this process is known as “sediment routing”). For sediment routing purposes, a barren plot is modeled as a series of small segments ($N_{seg}$). Segment length ($L_{seg}$) (ft) is calculated by dividing the length of the plot by the number of segments.

Amount of sediment load leaving from the $i^{th}$ segment of length ($\Delta x = x_i - x_{i-1}$) at the lower end ($g_i$) (lb/sec/ft plot width) is calculated using Equation (7-9):

$$g_i = g_{i-1} + \left[D_{i(i)} + D_{rorp(i)}\right] \left(x_i - x_{i-1}\right)$$

(7-9)

in which $g_{i-1}$ is amount of sediment load entering the $i^{th}$ segment at the upper end (lb/sec/ft plot width), $D_{i(i)}$ is amount of sediment produced per unit segment length due to interrill erosion in the $i^{th}$ segment (lb/sec/ft segment length/ft plot width), and $D_{rorp(i)}$ is amount of sediment either detached ($D_r$) from the rill surface (with a “+” sign) or deposited ($D_p$) to the surface (with a “-” sign) per unit segment length (lb/sec/ft segment length/ft plot width), which depends on sediment transport capacity ($T_{ci-1}$)(lb/sec/ft plot width) and sediment load ($g_{i-1,k}$) of the runoff water.

Based on the total sediment load in a given $i^{th}$ segment ($g_{i,i}$), sediment load of each sediment class ($g_{k,i}$)(lb/sec/ft plot width) is also calculated using Equation (7-10),

$$g_{k,i} = \Psi_k g_{i,i}$$

(7-10)

where $\Psi_k$ represents mass fraction of sediment in the $k^{th}$ sediment class (-) as summarized in Appendix E.

The following sections present brief descriptions of mechanisms of sediment detachment (interrill and rill erosion) and deposition. Deposition of sediments primarily depends on sediment transport capacity and influences overall sediment load for a particular $i^{th}$ segment. Sediment transport capacity ($T_c$) for the $i^{th}$ segment (lb/sec/ft plot width) is calculated using Equation (7-
where $K_T$ represents a transportability coefficient for sediments (-), $\theta$ is the angle which the plot of the land makes with horizontal (°), $q$ represents overland flow rate per unit width ($\text{ft}^3/\text{sec}/\text{ft plot width}$) (Equation 7-12), and $\zeta$ indicates the extent that an increased hydraulic resistance influences sediment transport capacity (-) (varies between 0 and 1).

$$T_c = K_T \zeta q \times \sin \theta$$  \hspace{1cm} (7-11)

$$q_i = q_{i-1} + (\sigma_i) \Delta x$$  \hspace{1cm} (7-12)

The overland flow rate per unit width ($q_i$) depends flow received from the previous segment ($q_{i-1}$) and on segment length and excess rainfall in that segment ($\sigma_i$) ($\text{ft}^2/\text{sec}/\text{ft width}$), which depends on rainfall and infiltration rates in that segment. This model, similar to RUSLE2, assumes that all sediments are equally transportable and thus have the same transportability coefficient ($\zeta$), i.e., 250,000, calculated using the RUSLE2 model (Equation 7-13) (RUSLE, 2008). The transportability coefficient depends on hydraulic roughness of surface which depends on form (i.e., soil surface, vegetation, and ground cover) and grain (i.e., individual soil particles and aggregates at the soil flow interface) roughness values and given by Equation (7-11).

$$\zeta = 0.0008n_t^{-1.5}$$  \hspace{1cm} (7-13)

In Equation (7-13), $n_t$ represents Manning’s total roughness value (-) (>0.01) and depends on soil surface roughness, ground cover, live vegetation biomass, and standing biomass residue presented in Appendix E.

Sediment detachment over the entire segment occurs for the case when the transport capacity at the upper end of the segment ($T_{ci-1}$) is greater than the incoming segment load ($g_{i-1}$) and the transport capacity at the lower end of the segment ($T_{ci}$). Amount of sediment load at the lower end of the segment ($g_i$) for the case of no deposition is calculated using Equation (7-14), derived from Equation (7-9) for the condition: $D_{p(i)}=0$:

$$g_i = g_{i-1} + D_{t,combined(i)}(x_i - x_{i-1})$$  \hspace{1cm} (7-14)

In Equation (7-14), $D_{t,combined}$ represents total amount of sediment eroded due to the effects of interrill and rill erosion ($\text{lb/sec/ft segment length/ft plot width}$) (i.e., total sum of $D_{t(i)}$ and $D_{r(i)}$ terms from Equation 11-9). This parameter is calculated using the modified Universal Soil Loss Equation (USLE; Foster, 2005), which was developed for erosion of sediments for non-uniform overland flow paths, where soil, steepness, and cover management practices vary depending on the overland flow path (Equation 7-15).

$$D_{t,combined} = (m + 1)RKSC_{mgmt}O_{subfactors} \left( \frac{x}{\lambda_u} \right)^m$$  \hspace{1cm} (7-15)

where $m$ represents the slope length exponent (-), $R$ represents the erosivity subfactor (EI unit: hundreds of foot-ton.in/acre/h), $K$ represents subfactor for erodibility of soil (ton/acre/EI unit), $S$ is the slope steepness subfactor (-), $C_{mgmt}$ is the cover management factor (-), $O_{subfactors}$ is a combined subfactor (-) representing the combined effects of ponding, contouring, and subsurface drainage on sediment erosion, $x$ represents the distance from the origin of the overland flow path.
for calculating the net detachment (ft), and \( \lambda_u \) is the length of the unit plot (ft). The term RK in the Equation (7-15) represents the daily erosion of the unit plot\(^1\) and the term SC\(_{mgmtO_{subfactors}}\) represents the combined effects of slope length, cover management, slope steepness, surface contours, subsurface drainage, and soil erosivity on sediment erosion from soil surface. For calculating sediment erosion from a plot of land, this study only considers the effects of land slope, soil erosivity, and erodibility, and does not include the effects of cover management subfactor, ponding subfactor, contouring subfactor, and subsurface drainage subfactor (assumed to be equal to 1 in this study).

Sediment deposition occurs, when the incoming sediment load \( g_{i-1} \) exceeds the transport capacity of the runoff water at the upper end of the segment \( (T_{c_i-1}) \) and the segment is short or when the amount of sediment detached exceeds the increase in transport capacity within the segment (i.e., \( D > dT_c/dx \)). The amount of sediment load at the lower end of the segment \( (g_i) \) for the deposition case is calculated using Equation (11-16), derived from Equation (7-9) for the condition when rill erosion \( (D_{r(i)}) = 0 \):

\[
g_i = g_{i-1} + \left[ D_{i(i)} + D_{p(i)} \right] \left( x_i - x_{i-1} \right)
\]

(7-16)

where, \( D_{i(i)} \) represents the amount of sediment detached due to interrill erosion (lb/sec/ft segment length/ft plot width) and \( D_{p(i)} \) represents the amount of sediment deposited on land (lb/sec/ft segment length/ft plot width). The amount of sediment detached due to interrill erosion in the \( i^{th} \) segment \( (D_{i(i)}) \) (lb/sec/ft segment length/ft plot width) is given by Equation (7-17):

\[
D_{i(i)} = 0.5RKSC_{mgmtO_{subfactors}}
\]

(7-17)

where all parameters are same as those for calculating amount of sediments detached due to combined rill and interrill erosions, except slope steepness factor \( (S_i) \) which is specific to interrill erosion.

In general, the amount of sediment deposited at the upper end of the \( i^{th} \) segment \( (D_{p,i}) \) (lb/sec/ft segment length/ft plot width) is calculated by summing the sediments deposited for different sediment classes \( (D_{p,k,i}) \) (lb/sec/ft segment length/ft plot width) (Equation 7-18):

\[
D_{p,i} = \sum_{k=1}^{5} D_{p,k,i}
\]

(7-18a)

\[
D_{p,k,i} = \left[ \left( \frac{a_dV_{f,k}}{q_i} \right) \left( T_{c_{i-1}} - g_{i-1} \right) \right]
\]

(7-18b)

In Equation (11-18b), \( a_d \) is a deposition coefficient and determined by calibration and is equal to 3 for the US unit system, \( V_{f,k} \) is fall velocity of sediments of a \( k^{th} \) particle class in still water (ft/sec), \( g_{c-1} \) is sediment load (lb/sec/ft plot width) (described more in the following section), and all other parameters have been described earlier. Fall velocities of different particle classes are

---

\(^1\) A plot of the land of 72.6 ft length (\( \lambda_u \)) on a 9% slope, maintained in continuous fallow, tilled to a seedbed condition up and down hill periodically to control weeds and break crusts that form on the soil surface.
calculated using their respective diameter and specific density values. The first term in bracket of Equation (7-18b) reflects the effect of settling velocity on sediment deposition. It imparts the capability to model the more rapid deposition of coarser sediments.

The preceding sections provided information about fundamentals of sediment routing. The following sections present application of these fundamentals for estimation of loads of total sediment and biosolids-associated sediments.

For the first segment, specific considerations are made following the RUSLE approach due to no inflow boundary conditions and the fact that sediment leaving the first segment should be equal to that calculated by the USLE. Thus, the first segment of the RUSLE2 matches the uniform slope assumptions of the USLE. For the case when $dT/dx > D_i$, no deposition occurs and total sediment load is given by Equation (7-19) and sediment loads of individual particle classes are calculated using initial mass fractions of different sediment classes at the time of detachment as detachment is a non-selective process.

$$g_{t,1} = (m+1)R K S C_{mgmt} O_{subfactors} \left( \frac{x}{\lambda_u} \right)^m \left( x_1 - x_0 \right)$$ (7-19)

For the case of $dT/dx < D_i$, the transport capacity is not sufficient to carry the entire amount of eroded soil and thus, not all sediment can be transported. Equal amounts of different size fractions erode, but heavier size fractions preferentially deposit. RUSLE2 calculates “quasi-deposition”, essentially deposition occurring within a given segment, to account for the enrichment of fine sediments along the course of the first segment as coarser sediments are eroded and deposit within the segment. The quasi-deposition amounts for different sediment size classes are calculated using Equation (7-20):

$$D_{q,k,1} = \left( 1 + \frac{q_1 / x_1}{3V_{f,k}} \right)^{-1} \left\{ \left[ \left( \frac{dT_c}{dx} \right)_{1} - D_{t,1} \right] \Psi_k \right\}$$ (7-20)

where $D_{t,1}$ is interrill erosion load (lb/sec/ft segment length/ft plot width), $T_c$ is sediment carrying capacity (lb/sec/ft plot width), $T_{c,1}$ is sediment carrying capacity at the lower end of the segment, $q_1$ is discharge rate (ft$^3$/sec/ft plot width), $g_{q,k,1}$ is quasi-class-sediment load (lb/sec/ft plot width) and $D_{q,k,1}$ is quasi-class-deposition load of the $k^{th}$ sediment class in the first segment (lb/sec/ft segment length/ft plot width), and $\Psi_k$ is mass fraction of $k^{th}$ sediment class (-). For this condition, the remaining quasi-sediment loads of different sediment classes for the first segment are calculated using Equation (7-21):

$$g_{q,k,1} = \Psi_k T_{c,1} - \left( \frac{q_1 D_{q,k,1}}{3V_{f,k}} \right)$$ (7-21)

Equations (7-20) and (7-21) are developed by solving Equations (7-11 to 7-13), (7-16), and (7-18b). Here, for the first segment only sediment transport capacity and interrill erosion load are known, thus quasi-class sediment loads (Equation 7-21) are calculated using sediment transport capacity of the first segment at lower end and quasi-class deposition load. In both of these equations, the constant “3” represents deposition coefficient (from the Equation 17-18b) for the
U.S. unit system. In this case also, total sediment load remains the same and is given by Equation
(7-19). Using quasi-sediment load of each sediment class (i.e., $g_{q,k,1}$), mass-fraction of each
sediment class is re-calculated using Equation (7-22), where $\Psi_{q,k,1}$ represents mass fraction of
sediment in the $k^{th}$ sediment class and is used to calculate sediment load in each sediment class.

$$
\Psi_{q,k,1} = \frac{g_{q,k,1}}{\sum_{k=1}^{5} g_{q,k,1}} \tag{7-22}
$$

In general, for all segments, sediment load at the lower end of a segment ($g_i$) is compared
with sediment transport capacity at the lower end of the segment ($T_{l,i}$) to determine if sediment
deposition occurs within segment. In the case of sediment deposition, the class-sediment
deposition load is calculated using Equation (7-18b).

The sediment transport rate at the end of the overland flow path ($g_i$) (lb/sec/ft width) is
used to estimate total sediment load ($d_{segment}$) (lb/ft width) using Equation (7-23), where $t_0$
represents time to saturation (h) and $t$ represents cumulative rainfall duration (h). Here, a
constant value of 3600 represents a conversion factor used to convert time in hours to time in
seconds.

$$
d_{segment} = g_i \times (3600 \times (t - t_0)) \tag{7-23}
$$

Sediment load of a particular segment ($d_{segment}$) (lb/ft width) is used to estimate biosolids
load at the end of the segment ($d_{segment,biosolids}$) (lb/ft width) using biosolids mass fraction
($f_{biosolids,segment}$) (-) (Equation 7-24). The biosolids mass fraction parameter depends on the initial
fraction of biosolids in the soil-biosolids matrix, i.e., equal to $f_{bio,segment}$ (-). In Equation (7-24a), the
parameter, $d_{segment,biosolids}$, is less than or equal to the amount of biosolids applied on the field, i.e.,
$M_{BS-soil}$ (lb/ft width). Subsequently, loads of biosolids associated with different particle classes
($BS_{exit,k}$) (lb/ft plot width) are also calculated using respective mass fractions of different particle
classes ($\Psi_k$) (-) (Equation 7-24b).

$$
d_{segment,biosolids} = d_{segment} \times f_{biosolids,segment} \tag{7-24a}
$$

$$
BS_{exit,k} = d_{segment,biosolids} \times \Psi_k \tag{7-24b}
$$

Biosolids-associated deposited sediment loads for each sediment class ($d_{BS,dep,k}$) (lb/ft width)
are calculated using Equation (7-25), where $D_k$ represents class-deposition load of the $k^{th}$
sediment class (lb/sec/ft segment length/ft plot width). All other parameters have been described
earlier.

$$
d_{BS,dep,k} = f_{biosolids,segment} \times D_k \times \Delta x \times (3600 \times (t - t_0)) \tag{7-25}
$$

Vegetative Filter Strip A vegetative filter strip (VFS) is a buffer zone between a barren plot and
a farm pond. It offers higher hydraulic resistance than the overland flow path immediately
upslope of the barrier, resulting in deposition of sediment between a barren plot and the VFS.
The effect of a backwater process on sediment deposition is incorporated by adding a backwater length ($\Delta x_b$) (ft) (Equation 7-26) to the length of a VFS and subtracting that from the length of the barren segment. In Equation (7-26), $s_u$ and $q_b$ represent slope (-) and discharge rate of the segment ($\text{ft}^3/\text{sec}/\text{plot ft width}$) with higher Manning’s $n_t$ value (-) (i.e., of a VFS in this case), respectively and $s_l$ represents the slope (-) of the segment with lower Manning’s $n_t$ value (i.e., of a barren segment in this case).

$$
\Delta x_b = \left( \frac{3.44}{s_u} \right) \left[ \frac{n_t q_b}{1.49 s_l^{0.5}} \right]^{0.6} \quad (7-26)
$$

The amount of sediment coming out from backwater or VFS ($g_{\text{VFS}}$) (lb/sec/ft plot width) is calculated using Equation (7-27) (Parajuli et al., 2008). In Equation (7-27), $L_{VS}$ is width of either VFS or backwater (i.e., $\Delta x_b$) and $g_{\text{barren plot}}$ is sediment load coming out from a barren plot.

Using estimates of $g_{\text{VFS}}$, amounts of biosolids-associated suspended and deposited sediments are calculated using expressions similar to Equations (7-24 and 7-25). This approach is also used to route sediments in backwater between the barren plot and VFS.

$$
g_{\text{VFS}} = g_{\text{barren plot}} \left[ -0.367 \left( L_{VS} \right)^{0.2967} \right] \quad (7-27)
$$

**Interceptor Barriers**

**Channel.** Deposition of sediments in a channel occurs when the incoming sediment load to the channel exceeds the sediment transport capacity of flow in the channel. The amount of sediments deposited for a $k^{th}$ particle class per unit channel length along the channel length ($D_{p,k}$) (lb/sec/ft channel length/ft plot width) is calculated using the following Equation (7-28), where $\Psi_k$ is mass fraction of sediment of the $k^{th}$ particle class (-), coming from the overland flow area, $T$ is sediment transport capacity of flow in the channel (lb/sec/ft plot width), $x$ is distance along the channel (ft), $V_{f,k}$ is the fall velocity of the $k^{th}$ particle class in water (ft/sec) (Table 5-A-12) (Appendix 5-A, Chapter 5.0), and $q_0$ is the discharge rate at the end of the overland flow path ($\text{ft}^3/\text{sec}/\text{ft channel length/ft plot width}$).

$$
D_{p,k} = \Psi_k \left( \frac{4000000V_{f,k}}{4000000V_{f,k} + q_0} \right) \left( \frac{dT}{dx} - g_0 \right) \quad \text{when} \quad \frac{dT}{dx} < g_0
$$

$$
D_{p,k} = 0 \quad \text{when} \quad \frac{dT}{dx} \geq g_0
$$

A change in sediment transport capacity with distance ($dT/dx$) (lb/sec/ft channel length/ft plot width) is calculated using Equation (7-29), where $\theta_{ch}$ represents the angle of the channel with horizontal and all other variables are defined previously.

$$
\frac{dT}{dx} = 450 q_0 \left( \sin \theta_{ch} \right)^{1.16} \quad (7-29)
$$
The amount of sediment of a $k^{th}$ particle class leaving the channel ($g_{ch,k}$) (lb/sec/ft channel length/ft plot width) is calculated using Equation (7-30) and is used to calculate total sediment load in channel ($g_{ch,total}$) (lb/sec/ft channel length/ft plot width) (Equation 7-31).

$$g_{ch,k} = g_{0,k} - D_{p,k}$$  \hspace{1cm} (7-30)

$$g_{ch,total} = \sum_{k=1}^{5} g_{ch,k}$$  \hspace{1cm} (7-31)

Total sediment load leaving the channel is used to calculate concentrations of biosolids-associated particles in the channel ($d_{ch,biosolids}$) (lb/ft plot width) (Equation 7-32), similar to that used in Equation (7-24).

$$d_{ch,biosolids} = f_{biosolids,ch} \times g_{ch,total} \times L_{ch} \times \left(3600(t - t_0)\right)$$  \hspace{1cm} (7-32)

Here, $L_{ch}$ is channel length (ft) and $f_{biosolids,ch}$ is a fraction of mass of biosolids in total suspended sediments in the channel, which is assumed to be equal to that of the biosolids-particles in sediments coming from the overland flow path.

Further, loads of biosolids associated with different particle classes in the channel $BS_{exit,k}$ (lb/ft plot width) are calculated using relationships similar to that used in Equation (7-24), using mass fractions of different particle classes in the channel.

Farm Pond. When sediment particles reach the farm pond which has a volume denoted by $V_{im}$ (L) and contains no pathogens (i.e., pathogen concentration: $C_0$ (No./L) =0), situated at the end of the overland flow path, sediment particles deposit depending on their fall velocities (Appendix E).

The sediment load of the $k^{th}$ particle class in the pond after settling of particles ($g_{im,k}$) (lb/sec/ft plot width) is given by Equation (7-33), based on the assumption that a farm pond does not have any sediment transport capacity (RUSLE, 2008). In Equation (7-33), $g_{im,0,k}$ is the input sediment load of the $k^{th}$ particle class to the farm pond, $V_{fk}$ is the fall velocity of sediment of the $k^{th}$ particle class (ft/sec) (Table 3-8), and $C_i$ is the trapping efficiency of the farm pond (sec/ft).

$$g_{im,k} = g_{im,0,k} \exp\left(-C_iV_{f,k}\right)$$  \hspace{1cm} (7-33)

The value of $C_i$ depends on sediment trapping ratio of a farm pond and is calculated with a value of 10,000 sec/ft for $C_i$ of silt loam soil, determined by fitting Equation (7-33) to experimental data for a farm pond (RUSLE, 2008). This value was observed to range between 10,000 and 1,700 sec/ft corresponding to sediment trapping ratios ranging from 6.4% to 25% (RUSLE, 2008). To be on a conservative side to protect human health, a constant value of 10,000 sec/ft corresponding to a 6.4% sediment trapping ratio was assumed in this study to achieve high value of sediment delivery ratio and a conservative estimate of human health risk.

The total sediment load in the pond ($g_{im,total}$)(lb/sec/ft plot width) (Equation 7-34) is calculated by adding individual sediment loads of different particle classes. This parameter is
used to calculate the concentration of biosolids-associated particles in the pond \((d_{im,biosolids})\) (lb/ft plot width) (Equation 7-35).

\[
g_{im,total} = \sum_{k=1}^{5} g_{im,k} \tag{7-34}
\]

\[
d_{im,biosolids} = f_{biosolids,im} g_{im,total} (t - t_0) \tag{7-35}
\]

In addition, loads of biosolids associated with different particle classes in the farm pond \((BS_{exit,k})\) (lb/ft plot width) are also calculated using relationships similar to that shown in Equation (7-24b), using mass fractions of different particle classes in the farm pond.

### 7.2.3 Pathogen Concentrations in a Farm Pond

Effective deliveries of unattached-pathogen cells (i.e., \(ED_{unattached}\)) (No.) and attached-pathogen cells (\(ED_{attached}\)) (No.) to a farm pond from a given plot of land via surface runoff are given by Equations (7-8) and (7-36), respectively. In Equation (7-36), \(W\) represents plot width (ft), \(N_0\) is the initial number of pathogens present in biosolids applied on land (No./g biosolids), \(d_{im,biosolids}\) is the amount of biosolids reaching the farm pond attached to sediments (lb/ft width), and \(f\) is the fraction of pathogens released from the biosolids-soil matrix (-). A constant value of 454 represents conversion of mass of biosolids in pounds to grams.

\[
ED_{attached,im} = 454d_{im,biosolids} WN_0 (1 - f) \tag{7-36}
\]

The total number of pathogen cells, reaching the farm pond (i.e., \(ED_{pathogen,im} = ED_{unattached,im} + ED_{attached,im}\)) (No.) is diluted due to mixing of the runoff water (volume: \(V_{runoff,land}\)) with the farm pond water (volume: \(V_{im}\)), and is calculated using Equation (7-37), where \(C_{pathogen,im}\) is the pathogen concentration in the farm pond (No./L).

\[
C_{pathogen,im} = \frac{C_0 V_{im} + ED_{unattached,im} + ED_{attached,im}}{V_{im} + V_{runoff,land}} \tag{7-37}
\]

The effective concentration of pathogen-cells in the farm pond \((C_{eff,pathogen,im})\) (No./L) after time \((t^*)\) (day) is calculated using a first-order pathogen decay model (Equation 7-38), where \(k_a\) represents the decay rate of pathogens in water.

\[
C_{eff,pathogen,im} = C_{pathogen,im} \exp(-k_a t^*) \tag{7-38}
\]
CHAPTER 8.0

GROUNDWATER EXPOSURE MODEL
TECHNICAL DOCUMENT

8.1 Function of the Program

There are two primary functions of the program: 1) Determine the transport scenario during a rainfall event using an infiltration and runoff model; and 2) Predict the corresponding pathogen concentration in a downstream well using a subsurface fate and transport model. The transport scenario depends on whether or not the infiltrating wetting front from the rainfall event saturates through to the ground water table, creating a fully saturated connection. Figure 8-1 illustrates how to determine the transport scenario based on rainfall information. Scenario 1 (non-saturating rainfall event): if the depth to the water table, h, is larger than wetting front depth, Z, pathogen attenuation includes three processes: vertical transport through saturated soil above the wetting front, vertical transport in unsaturated soil below the wetting front but above the water table, and horizontal transport in saturated soil through groundwater flow to the downstream well. Scenario 2 (saturating rainfall event): if the depth to the water table, h, is smaller than the wetting front depth, Z, during a rainfall event, pathogens transport vertically in saturated soil above the wetting front and then join the saturated horizontal groundwater flow to the downstream well without any attenuation through unsaturated soil. Scenario 2 presents a greater risk of pathogen transport.

This chapter presents a brief descriptions of the Groundwater Exposure Model (Sheets: GWConstants, GWPathogenModel, and GWTransportModel), including definitions of input variables and constants, and how to read and interpret the output data. The mathematical details of the model are also presented. The constants used are summarized in Appendix F. Validation of the transport model in both saturated and unsaturated porous media is presented in Appendix G.
8.2 Model Description

8.2.1 Estimation of Infiltration Rate and Depth of Wetting Front

Pathogen transport during wet weather events may be facilitated via a saturated wetting front connecting to the water table. If this saturated connection is established, there is no pathogen attenuation through the unsaturated zone buffer. In order to predict pathogen transport and fate following precipitation, infiltration rate and depth of the saturated wetting front need to be estimated.

The infiltration model is based on a Joint Green-Ampt model, which was developed to facilitate use in a spreadsheet environment. The model incorporates the Explicit Green-Ampt solution (Salvucci and Entekhabi, 1994) into the Constant Flux Green-Ampt model to estimate infiltration rate, cumulative infiltration, and depth of wetting front, and is described extensively in the Surface Water Exposure Model Technical Document (Chapter 7.0).
The depth of the wetting front is calculated by:

\[ Z = \frac{I}{(\theta_s - \theta_0)} \]  

(8-1)

where \( Z \) is depth of wetting front (cm); \( I \) is cumulative infiltration (cm); \( \theta_s \) and \( \theta_0 \) are saturated and initial water content (cm\(^3/cm^3\)), respectively.

8.2.2 Subsurface Transport and Fate of Biosolids-Associated Pathogens through Saturated Soil

Based on the Advection-Dispersion Equation with adsorption and decay, the model provides a time-dependent, pathogen concentration profile as a function of distance. This equation is used for modeling vertical transport through soil saturated by the infiltrating wetting front, as well as for modeling horizontal transport with groundwater flow to a downstream drinking well at the depth of the wetting front. The cumulative number of pathogens is calculated at a specified distance downstream.

8.2.3 Subsurface Transport and Fate of Biosolids-Associated Pathogens through Unsaturated Soil

The depth of the unsaturated barrier can be determined by the difference between the water table depth (\( h \)) and the wetting front depth (\( Z \)), i.e. (\( h - Z \)). Pathogen attenuation in unsaturated soil is modeled considering mass transfer across the liquid-solid and liquid-air interfaces.

Assumptions of this model are summarized below:

1) Land-applied biosolids are assumed to be the only source of pathogens.
2) There is a rainfall event directly after the biosolids application.
3) Model calculations are done for a square plot.
4) Rainfall and biosolids are applied directly and uniformly to the site.
5) The soil profile is homogeneous.
6) The infiltration rate is assumed to be constant during and after the rainfall events.
7) Vertical flow is through uniform layers of porous media without preferential flow pathways.
8) The effects of inactivation, straining, air-water and water-solid interaction are all irreversible, and they follow first-order rate laws; the effects of attachment is described by the retardation factor.
9) A potable water well is located directly down gradient of the biosolids application site.
10) A one-dimensional transport model is appropriate both vertically and horizontally.
11) Ingestion of ground water occurs over the entire period when the number of biosolids-associated pathogens in well water is non-zero.
12) Only risk to humans is considered, and secondary transmission risks are not addressed by this model.

13) The exposure to biosolids-associated pathogens from subsurface transport is independent of other pathways, such as consumption of contaminated runoff, inhalation of aerosols from land application sites, direct ingestion of biosolids, or ingestion of contaminated plants.

14) Exposures to different biosolids-associated pathogens are independent of each other.

15) Exposure from ingestion of contaminated well water is assumed to be the same for all subpopulations.

8.3 Background

The groundwater exposure model links models of pathogen transport vertically through the saturated wetting front and unsaturated soil, and horizontally through saturated ground-water flow. For the vertical transport phase, two cases are considered. For the first scenario, non-saturating rainfall events, an analytical solution to the advection-dispersion equation with sorption and decay is used to model vertical pathogen migration through saturated soil in the infiltrating wetting front. Next, pathogen attenuation through the unsaturated zone below the wetting front is modeled using equations considering mass transfer across the liquid-solid and liquid-air interfaces (Faulkner, et al., 2002). For the second scenario, saturating rainfall events, in which the infiltrating wetting front reaches the underlying ground-water table, an analytical solution to the advection-dispersion equation (Bedient, et al., 1997) is used to predict pathogen attenuation. Horizontal transport through the saturated zone to a downstream well is modeled for both scenarios using an analytical solution to the advection-dispersion equation, incorporating the effects of adsorption to soil and pathogen decay.

8.4 Model Selection

8.4.1 Subsurface Fate and Transport of Biosolids-Associated Pathogens in Saturated Soil

The governing equation for microbial transport through saturated soil, both for vertical wetting zone transport and horizontal groundwater flow, is the one-dimensional advection-dispersion model with an instantaneous source and including effects of adsorption to soil and first-order inactivation of pathogens (Bedient, et al., 1997).

\[
D_x \frac{\partial^2 C}{\partial x^2} - v_x \frac{\partial C}{\partial x} - \lambda C = \frac{C}{\partial t} R
\]  

(8-2)

where \( D_x \) is coefficient of hydrodynamic dispersion (cm²/h) (= \( \alpha v_x \), where \( \alpha \) is dispersivity), \( v_x \) is the average seepage velocity (cm/h), \( \lambda \) is the first order inactivation rate (/h), and \( R \) is the retardation factor. The retardation factor is defined as \( 1 + (\rho_b / n)K_d \), where \( \rho_b \) is the bulk dry mass density (g/cm³), \( n \) is porosity, and \( K_d \) is the equilibrium distribution coefficient (cm³/g).

The analytical solution was derived for the injection of a tracer pulse at \( x=0 \) with background concentration equal to zero, as the slug moves downstream with \( v_x \) in the +x direction:
\[ C(x, t) = \frac{M}{(\frac{4\pi D_x t}{R})^\frac{1}{2}} \exp \left( -\frac{R(x-v_xt)^2}{4D_x t} \right) \exp (-\lambda t) \] (8-3)

where \( M \) is the injected mass per unit cross-sectional area.

Assumptions:
1) The tracer is ideal, with constant density and viscosity;
2) The fluid is incompressible;
3) The medium is homogeneous and isotropic;
4) Only saturated flow is considered;
5) The background concentration is equal to zero.

### 8.4.2 Subsurface Fate and Transport of Biosolids-associated Pathogens in the Unsaturated Zone (Faulkner, et al., 2002)

Transport in unsaturated porous media is governed by the following equation:

\[
\frac{\partial (\rho C_l)}{\partial t} + \frac{\partial (\rho \theta C_l)}{\partial x} + \frac{\partial (\rho \theta C_s)}{\partial z} = \frac{\partial}{\partial x} \left( \theta D \frac{\partial C_l}{\partial x} \right) - \lambda_l \theta C_l - \lambda_s \rho C_s - \lambda_a \theta C_a
\] (8-4)

where \( C_l, C_s, \) and \( C_a \) are the concentration in the liquid, liquid-solid interface, and air-liquid interface, respectively; \( \rho \) is the bulk density of the solid matrix; \( \theta \) is the volumetric moisture content; \( \lambda_l, \lambda_s, \) and \( \lambda_a \) are the inactivation rate coefficients of pathogen suspended in the liquid, pathogen sorbed at the liquid-solid interface, and pathogen sorbed at the air-liquid interface, respectively.

The attenuation factor \( A \) is calculated as

\[ A = e^{\Gamma_2(\gamma)L} \] (8-5)

where \( L \) is the thickness of the barrier (cm) and components of \( A \) are calculated as follows (cm\(^{-1}\)):

\[ \Gamma_2(\gamma) = \frac{\sqrt{\gamma^2 + 4D_z \gamma}}{2D_z} \] (8-6)

A target value of \( A=0.0001 \), meaning “4-log attenuation”, translates to 99.99% attenuation of active viruses.

Velocity is estimated by the following relationships:

\[ v = \frac{q}{\theta_m} \] (8-7)

\[ q = K(\theta_m) \] (8-8)

\[ K(\theta_m) = K_\infty S_e \left[ \frac{1}{n} \left( 1 - \frac{S_e^{1-n}}{S_e^{1-n} - S_n^{1-n}} \right)^{\frac{1}{n}} \right]^2 \] (8-9)

\[ S_e = \frac{\theta_m - \theta_r}{\theta_s - \theta_r} \] (8-10)
Dispersión se estima por las siguientes relaciones:

\[ D_z = \alpha_z \frac{q}{\theta_m} + D_e \]  
\[ D_e = \frac{D}{\tau} \]  
\[ \tau = \begin{cases} \frac{\theta_m^{11/5}}{\theta_m^{11/5}} & \text{si } \theta_m \leq 2 \\ \frac{\theta_m^{11/5}}{\theta_m^{11/5}} & \text{de otra manera} \end{cases} \]  
\[ D = \frac{k_b T}{6\pi \mu r_v} \]

Decay and mass transfer are estimated by the following relationships:

\[ \gamma = \lambda_1 + \frac{\lambda_1 \rho}{\theta_m \lambda s \rho} + k_a \]  
\[ K_s = k_s \alpha_{ts} \]  
\[ \alpha_{ts} = \frac{3(1-\theta_s)}{r_p} \]  
\[ K_a = k_a \alpha_{ta} \]  
\[ \alpha_{ta} = \rho_{wg} \frac{\theta_m}{\alpha \sigma} [(S_e^{-1})^{1-1/n} - 1]^{1/n} \]

where \( v \) is the average velocity of the percolating water (cm/hr); \( q \) is the specific discharge (cm/hr); \( K(\theta_m) \) is the unsaturated hydraulic conductivity (cm/hr); \( S_e \) is the effective saturation (unitless); \( \theta_m \) is the moisture content (cm\(^3\)/cm\(^3\)); \( K_{sz} \) is the vertical saturated hydraulic conductivity (cm/hr); \( n \) is the water retention curve fitting parameter; \( \theta_r \) is the residual soil water content (cm\(^3\)/cm\(^3\)); \( \theta_s \) is the moisture content of a saturated porous medium (cm\(^3\)/cm\(^3\)); \( D_z \) is the vertical hydrodynamic dispersion coefficient (cm\(^2\)/hr); \( D_e \) is the effective molecular diffusion coefficient (cm\(^2\)/hr); \( \alpha_z \) is the vertical dispersivity (cm); \( \tau \) is the tortuosity coefficient; \( k_b \) is Boltzmann’s constant (J/K); \( \mu \) is the viscosity of water (g/cm h); \( r_v \) is the radius of the pathogens (cm); \( \lambda_1 \) is the inactivation rate coefficient of pathogens in the liquid phase (/hr); \( \lambda_s \) is the inactivation rate coefficient of pathogens sorbed at the liquid-solid interface (/hr); \( \rho \) is the bulk density of the soil (g/cm\(^3\)); \( K_d \) is the equilibrium distribution coefficient (cm\(^3\)/g); \( K_s \) is the liquid to liquid-solid interface mass transfer rate (/hr); \( k_s \) is the liquid to liquid-solid interface mass transfer coefficient (cm/hr); \( r_p \) is the average radius of soil particles (cm); \( K_a \) is the liquid to air-liquid interface mass transfer rate (/hr); \( k_a \) is the liquid to air-liquid interface mass transfer coefficient (cm/hr); \( \rho_{wg} \) is the density of water (kg/m\(^3\)); \( g \) is the acceleration due to gravity (m/s\(^2\)); \( \sigma \) is the surface tension of water (g/hr\(^2\)); \( \alpha \) is water retention curve fitting parameter (/m); \( \alpha_{ts} \) is the liquid-solid interfacial area (/cm); \( \alpha_{ta} \) is the air-liquid interfacial area (/cm); \( T \) is temperature (K).
CHAPTER 9.0

INDIRECT INGESTION MODEL TECHNICAL DOCUMENT

During land-application of biosolids, biosolids are deposited on land and are mixed with soil particles. If there is a rainfall event after the application, some of the biosolids-associated pathogens may be released to runoff water and can flow to an adjacent vegetated field. The following section describes calculation of the number of biosolids-associated pathogens present on the surface of ingested lettuce leaves. Assumptions of this model are summarized below:

1) Land-applied biosolids are assumed to be the only source of pathogens in this work.
2) There is a rainfall event directly after the biosolids application.
3) After a rainfall event, a fraction of the biosolids-associated pathogens release to runoff water, flow through a buffer zone and enter an adjacent vegetated field.
4) The overflow water is evenly deposited on the surface of the lettuce.
5) Biosolids-associated pathogens are completely mixed with the overflow water and are evenly deposited on the lettuce.
6) The raw vegetables are ingested following harvest from the contaminated field without further rinsing.

The concentration of pathogens in the runoff water entering the vegetated field \( N_{field}; \text{No./L} \) is calculated from the total number of pathogen cells reaching the farm pond \( E_{pathogen,im}; \text{No.} \) and the overflow water volume \( V_{runoff}; \text{ft}^3 \), both of which are calculated by the Surface Water Exposure Model (Chapters 7.0).

The number of biosolids-associated pathogens on the surface of ingested lettuce leaves \( E_{on\_vegetable}; \text{No.} \) is thus determined from the concentration of pathogens in the runoff water entering the field \( N_{field}; \text{No./L} \), the total volume of water deposited on ingested vegetables \( V_{on\_vegetable}; \text{ft}^3 \), calculated by Equations 9-3 and 9-3), the decay rate in soil \( k_{decay,soil}; \text{1/day} \), and the time of ingestion after biosolids application \( t_{vege\_conc}; \text{days} \) (Equation 9-2).

\[
N_{field} = \frac{E_{pathogen,im}}{(28.3 L / ft^3) V_{runoff}} \quad (9-1)
\]

\[
E_{on\_vegetable} = N_{field} V_{on\_vegetable} \exp(-k_{decay,soil} \times t_{vege\_conc}) \quad (9-2)
\]

\[
V_{on\_vegetable} = V_{per\_leaf} \times n_{leaf} \quad (9-3)
\]

\[
V_{per\_leaf} = h_{water\_storage} \times A_{per\_leaf} \quad (9-4)
\]
where $V_{\text{per \_ leaf}}$ (ft$^3$) is the volume of water deposited on each lettuce leaf; $n_{\text{leaf}}$ (number) is the number of ingested lettuce leaves from the contaminated field; $h_{\text{water \_ storage}}$ (mm) is the surface storage capacity of each individual leaf (assumed to be 0.2 mm for lettuce leaf, Barfield, 1973); and $A_{\text{per \_ leaf}}$ (in$^2$) is the surface area of each lettuce leaf.
CHAPTER 10.0

APPLYING THE MODEL

10.1 Introduction

This chapter presents example results of the SMART Biosolids model. This is not intended as a comprehensive risk assessment but rather as a demonstration of the types of results that the model can generate. Comparisons across pathogens and pathways are presented, as are evaluations of the effects of different setback requirements. However, it should be kept in mind that all of these results are specific to the conditions evaluated in the model.

10.2 Site-Specific Conditions

Tables 10-1a and 10-1b summarize the site conditions modeled in this chapter. These inputs do not correspond rigorously to any particular site but were developed after consideration of typical applications observed in Michigan as part of the field monitoring for this project. Any deviations from these input parameters are specifically noted when the model results are presented.
Table 10-1. Site-Specific Conditions.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
<th>Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>Time of start of rain after biosolids application</td>
<td>0</td>
<td>days</td>
</tr>
<tr>
<td>Temperature</td>
<td>83</td>
<td>Fahrenheit</td>
</tr>
<tr>
<td>Soil texture class</td>
<td>sandy_loam</td>
<td>-</td>
</tr>
<tr>
<td>Area of application site</td>
<td>625</td>
<td>acre</td>
</tr>
<tr>
<td>Slope of the plot</td>
<td>4.00</td>
<td>%</td>
</tr>
<tr>
<td>Application method</td>
<td>Slinger</td>
<td>none</td>
</tr>
<tr>
<td>Biosolids application rate</td>
<td>2.57</td>
<td>dry tons biosolids/acre</td>
</tr>
<tr>
<td>Water Table Depth</td>
<td>3</td>
<td>ft</td>
</tr>
<tr>
<td>Distance to Well</td>
<td>100</td>
<td>ft</td>
</tr>
<tr>
<td>Hydraulic Gradient</td>
<td>0.04</td>
<td>-</td>
</tr>
<tr>
<td>Presence of buffer strip between field and ditch (VS)</td>
<td>1</td>
<td>1(Yes) or 0(No)</td>
</tr>
<tr>
<td>Length of buffer strip</td>
<td>33</td>
<td>ft</td>
</tr>
<tr>
<td>Slope of buffer strip</td>
<td>4.00</td>
<td>%</td>
</tr>
<tr>
<td>Presence of channel after VS</td>
<td>0</td>
<td>1(Yes) or 0(No)</td>
</tr>
<tr>
<td>Presence of pond</td>
<td>1</td>
<td>1(Yes) or 0(No)</td>
</tr>
<tr>
<td>Distance of residential population to field</td>
<td>250</td>
<td>ft</td>
</tr>
<tr>
<td>Time of soil ingestion after biosolids application</td>
<td>31</td>
<td>days</td>
</tr>
<tr>
<td>Time for exposure to pond water after biosolids application</td>
<td>0.0000001</td>
<td>days</td>
</tr>
<tr>
<td>Consider resuspension for occupational workers during biosolids application</td>
<td>1</td>
<td>1(Yes) or 0(No)</td>
</tr>
<tr>
<td>Time of vegetable ingestion after biosolids application</td>
<td>5</td>
<td>days</td>
</tr>
<tr>
<td>Number of ingested vegetable leaves</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>Computational Reporting Threshold</td>
<td>1.00E-20</td>
<td>Lowest level of risk reported</td>
</tr>
<tr>
<td>Annual precipitation</td>
<td>18</td>
<td>inches</td>
</tr>
<tr>
<td>Maximum 30-minute intensity</td>
<td>NA</td>
<td>in/h</td>
</tr>
<tr>
<td>Wind velocity(for air model)</td>
<td>2.62</td>
<td>ft/sec</td>
</tr>
<tr>
<td>Solar irradiation (three categories are used, slight is below 350, moderate is 350-700, strong &gt;700)</td>
<td>550</td>
<td>W/m²/day</td>
</tr>
<tr>
<td>Does rainfall occur after land-incorporation of biosolids?</td>
<td>Yes</td>
<td>-</td>
</tr>
<tr>
<td>Rainfall rate</td>
<td>7.3</td>
<td>cm/h</td>
</tr>
<tr>
<td>Rainfall duration time</td>
<td>1</td>
<td>h</td>
</tr>
<tr>
<td>Total length of the field</td>
<td>5248.23</td>
<td>ft</td>
</tr>
<tr>
<td>Width of the field</td>
<td>5248.23</td>
<td>ft</td>
</tr>
</tbody>
</table>
10.3 Results for Different Pathogens and Pathways

This section summarizes the results obtained for each of the five pathways given the inputs listed in Section 10.2 for a typical adult residing near a land application site. These summary results do not include all subgroups of interest (e.g., children, individuals with occupational exposures). The intent is to provide a common reference group for comparisons across pathways and pathogens under typical land application conditions.

Table 10-2 summarizes the results for the air pathway. No risks are computed for parasites as inhalation has not been shown to be a pathway of transmission for these organisms. Sufficient information is available to calculate risks for two bacteria (Shigella and Salmonella) and two viruses (adenovirus and enterovirus). Risks are larger for the disk incorporation than for the slinger application, as aerosolization rates are higher during disk incorporation. The use of a spray plate applicator would result in lower risks than the slinger applicator (results not shown) as fewer biosolid particles are aerosolized. Of the different organisms shown, adenovirus has the highest risk, but overall the risks do not appear to be of concern. The highest upper bound is 8.9 in 1 million for adenovirus, which is associated with a common and non-fatal illness. Risks for Shigella, which can induce a potentially fatal illness, are orders of magnitude lower (Shigella has an infection risk of roughly 5.2 in 1 billion with and upper bound of 9.1 in 100 million).

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>Slinger Application</th>
<th>Disk Incorporation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Parasites</td>
<td>Risk by the inhalation route has not been documented for parasites.</td>
<td></td>
</tr>
<tr>
<td>Salmonella</td>
<td>1.78 x 10^{-15}</td>
<td>5.17 x 10^{-13}</td>
</tr>
<tr>
<td></td>
<td>(NA – 1.15 x 10^{-12})</td>
<td>(2.77 x 10^{-15} – 6.47 x 10^{-10})</td>
</tr>
<tr>
<td>Shigella</td>
<td>1.73 x 10^{-11}</td>
<td>5.18 x 10^{-9}</td>
</tr>
<tr>
<td></td>
<td>(1.29 x 10^{-11} – 2.96 x 10^{-10})</td>
<td>(2.12 x 10^{-9} – 9.08 x 10^{-8})</td>
</tr>
<tr>
<td>Adenovirus</td>
<td>1.16 x 10^{-8}</td>
<td>3.46 x 10^{-6}</td>
</tr>
<tr>
<td></td>
<td>(2.17 x 10^{-9} – 3.10 x 10^{-8})</td>
<td>(8.88 x 10^{-7} – 8.85 x 10^{-6})</td>
</tr>
<tr>
<td>Enteroviruses</td>
<td>4.8 x 10^{-12}</td>
<td>1.25 x 10^{-9}</td>
</tr>
<tr>
<td></td>
<td>(6.11 x 10^{-13} – 7.05 x 10^{-11})</td>
<td>(7.24 x 10^{-11} – 1.70 x 10^{-8})</td>
</tr>
</tbody>
</table>

Values displayed are based on nominal input parameter values with 5-95th percentiles of a Monte Carlo simulation given in parentheses. Splash plate applicator risks are lower.

Table 10-3 shows the risks associated with incidental ingestion of soil when accessing the site 31 days after the biosolids are applied (i.e., the 30 day site restriction provided for by the Part 503 regulations has been respected). For this pathway risks for two parasites, Cryptosporidium and Giardia are calculated as well as risks for the two bacteria (Salmonella and Shigella) and two viruses (adenovirus and enterovirus) considered above. Risks are shown for both children and adults. The risks for children are higher than for adults because of an assumed higher ingestion rate for soil (480 mg/day for children compared to 50 mg/day for adults). For adults, adenovirus risk (nominal estimate of 9.6 in 10,000 and an upper bound of 6.0 in 1000)
exceeds the 1 in 10,000 value sometimes used as a benchmark for drinking water microbial risk. The upper bound for *Giardia* also exceeds the 1 in 10,000 benchmark (3.2 in 10,000).

The adenovirus risk estimate for children has a nominal value of 9.2 in 1,000 which is between the risk associated with freshwater and marine water recreational standards (8 in 1000 and 1.9 in 100, respectively). The 95th percentile of the adenovirus risk (5.6 in 100) exceeds even the marine recreational water risk level. The nominal estimate for *Cryptosporidium* (1.7 in 10,000) exceeds the 1 in 10,000 benchmark, as do the upper bounds for *Giardia* and *Shigella* (3.1 in 1,000 and 8.7 in 10,000) with *Shigella* presenting a particular concern because of its potential for serious, even fatal, illness.

In summary, risks for the soil ingestion pathway are generally greater than for the air pathway. Risks for children due to adenovirus are in the range associated with recreational water guidelines (an upper bound estimates of this risk exceed these guidelines). However, risks for this pathway are confined to the application site which may be an influence on how acceptable these risks are judged to be.

Table 10-3. Incidental Ingestion of Biosolids-Amended Soil, 31 Days after Application.

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>Adult Risk Estimate</th>
<th>Child Risk Estimate</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Parasites</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Cryptosporidium</em></td>
<td>$1.75 \times 10^{-5}$</td>
<td>$1.68 \times 10^{-4}$</td>
</tr>
<tr>
<td></td>
<td>($1.49 \times 10^{-10} - 9.04 \times 10^{-5}$)</td>
<td>($1.44 \times 10^{-9} - 8.68 \times 10^{-4}$)</td>
</tr>
<tr>
<td><em>Giardia</em></td>
<td>$7.32 \times 10^{-6}$</td>
<td>$7.02 \times 10^{-5}$</td>
</tr>
<tr>
<td></td>
<td>(NA – 3.23 x 10^{-4})</td>
<td>(NA – 3.1 x 10^{-3})</td>
</tr>
<tr>
<td><strong>Bacteria</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Salmonella</em></td>
<td>$8.45 \times 10^{-13}$</td>
<td>$8.11 \times 10^{-12}$</td>
</tr>
<tr>
<td></td>
<td>(NA – 1.69 x 10^{-6})</td>
<td>(NA – 1.62 x 10^{-7})</td>
</tr>
<tr>
<td><em>Shigella</em></td>
<td>$4.02 \times 10^{-7}$</td>
<td>$3.86 \times 10^{-6}$</td>
</tr>
<tr>
<td></td>
<td>(NA – 7.01 x 10^{-5})</td>
<td>(NA – 6.73 x 10^{-4})</td>
</tr>
<tr>
<td><strong>Viruses</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Adenovirus</em></td>
<td>$9.64 \times 10^{-4}$</td>
<td>$9.22 \times 10^{-3}$</td>
</tr>
<tr>
<td></td>
<td>($1.83 \times 10^{-9} - 5.98 \times 10^{-3}$)</td>
<td>($1.76 \times 10^{-9} - 5.6 \times 10^{-2}$)</td>
</tr>
<tr>
<td><em>Enteroviruses</em></td>
<td>$2.45 \times 10^{-9}$</td>
<td>$2.35 \times 10^{-8}$</td>
</tr>
<tr>
<td></td>
<td>(NA – 1.14 x 10^{-6})</td>
<td>(NA – 1.05 x 10^{-5})</td>
</tr>
</tbody>
</table>

Values displayed are based on nominal input parameter values with 5-95th percentiles of a Monte Carlo simulation given in parentheses. NA – not available as value was below reporting threshold of $10^{-20}$.

Table 10-4 shows risks associated with recreational use of a pond receiving runoff from a 1 in 100 year storm event. The adenovirus has an estimated risk of 1.3 in 1000 (95th percentile of 4.2 in 1000) with all other estimates being orders of magnitude lower. The nominal estimate for adenovirus and the upper bound for Giardia (3.5 in 10,000) exceed the 1 in 10,000 benchmark associated with drinking water but not the 8 in 1000 or 1.9 per 100 levels associated with other recreational water exposures (EPA, 2011). It should be noted that these estimates are conditioned on a fairly low probability event, a 100-year storm event immediately after biosolids application.
Table 10-4. Surface Water Recreational Swimming, 1 in 100-Year Storm Event, Buffer Strip of 33 Feet.

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>Risk Estimate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Parasites</td>
<td></td>
</tr>
<tr>
<td>Cryptosporidium</td>
<td>$2.06 \times 10^{-5}$ (NA, $8.6 \times 10^{-5}$)</td>
</tr>
<tr>
<td>Giardia lamblia</td>
<td>$4.49 \times 10^{-5}$ (NA, $3.05 \times 10^{-4}$)</td>
</tr>
<tr>
<td>Bacteria</td>
<td></td>
</tr>
<tr>
<td>Salmonella</td>
<td>$3.85 \times 10^{-10}$ (NA, $7.36 \times 10^{-9}$)</td>
</tr>
<tr>
<td>Shigella</td>
<td>$3.86 \times 10^{-6}$ (NA, $5.58 \times 10^{-5}$)</td>
</tr>
<tr>
<td>Viruses</td>
<td></td>
</tr>
<tr>
<td>Adenovirus</td>
<td>$1.29 \times 10^{-3}$ (NA, $4.23 \times 10^{-3}$)</td>
</tr>
<tr>
<td>Enteroviruses</td>
<td>$3.68 \times 10^{8}$ (NA, $1.03 \times 10^{-6}$)</td>
</tr>
</tbody>
</table>

Values displayed are based on nominal input parameter values with 5-95th percentiles of a Monte Carlo simulation given in parentheses. NA – not available as value was below reporting threshold of $10^{-2}$.

Table 10-5 shows risks associated with groundwater consumption from the same storm event as described above for the surface water pathway. Nominal estimates of most risks are quite low, but the estimate for adenovirus of 3.78 in 1,000 exceeds the 1 in 10,000 baseline for U.S. annual potable water risk. This risk would be associated with consumption of water at the water table depth of 3 feet, and few potable wells would be so shallow. Additional pathogen attenuation would be expected with extraction of groundwater from deeper wells. In addition, this risk is associated with rare storm event. For these reasons the risk may well be judged to be acceptable. This pathway has the greatest uncertainty in model predictions with, for example, predictions for adenovirus covering a range from 1 (certain infection) to below the reporting level of 1 in $10^{20}$. Uncertainties in both the transport model and decay model are substantial. As a result the peak of the microbial contamination can arrive very quickly (high hydraulic conductivity) or slowly (low hydraulic conductivity) and concentrations at the well vary exponentially with both the time to arrival of the microbes and the decay constant of the microbes.
Table 10-5. Groundwater Pathway Residential Adult and Residential Children, Setback Distance to Well of 100 Feet.

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>Risk Estimate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Parasites</td>
<td></td>
</tr>
<tr>
<td>Cryptosporidium</td>
<td>$3.50 \times 10^{-5}$ (NA, $1.97 \times 10^{-2}$)</td>
</tr>
<tr>
<td>Giardia lamblia</td>
<td>$8.50 \times 10^{-9}$ (NA, $2.11 \times 10^{-1}$)</td>
</tr>
<tr>
<td>Bacteria</td>
<td></td>
</tr>
<tr>
<td>Salmonella</td>
<td>NA (NA, $4.13 \times 10^{-9}$)</td>
</tr>
<tr>
<td>Shigella</td>
<td>$1.39 \times 10^{-9}$ (NA, $1.33 \times 10^{-2}$)</td>
</tr>
<tr>
<td>Viruses</td>
<td></td>
</tr>
<tr>
<td>Adenovirus</td>
<td>$3.78 \times 10^{-3}$ (NA, $7.87 \times 10^{-1}$)</td>
</tr>
<tr>
<td>Enteroviruses</td>
<td>$2.18 \times 10^{-12}$ (NA, $2.97 \times 10^{-4}$)</td>
</tr>
</tbody>
</table>

Values displayed are based on nominal input parameter values with 5-95th percentiles of a Monte Carlo simulation given in parentheses.

Results for the vegetable ingestion pathway are all below the reporting threshold of 1 in $10^{-20}$.

Comparing across pathways, the soil ingestion pathway appears to be of the greatest concern. The vegetable ingestion pathway did not produce risks above the reporting threshold. The air pathway did not appear to produce significant risks for residents of neighboring properties. However, this analysis did not include occupational exposures which may in some cases be significant. The groundwater and surface water pathways produced risks that may be of some concern, but the best estimates do not exceed the bounds of what has been considered acceptable risk for recreational water use. Groundwater risks are very uncertain and at the upper bound may exceed both drinking water and recreational standards, but these risks would be associated with very shallow groundwater (depth of 3 feet), which would not typically be used as a potable water source. The soil ingestion pathway produced the highest risks. Nominal risks do not exceed the highest of the recreational use risk benchmarks (the 1.9 in 100 value associated with marine recreational standards, EPA 2011) for any pathways although the upper bound for soil ingestion by children does exceed this value.

Adenovirus presented the greatest risk across the different pathways. Current estimates of adenovirus occurrence levels are based on a single study (Pepper et al., 2010) with a sample size of only 5 observations. Better data on the occurrence of adenovirus and its persistence over the required site restriction period is a key data gap that warrants future research. Cryptosporidium produced the next highest risk levels by the soil ingestion pathway. While Giardia has lower nominal risks than Cryptosporidium by this pathway, its upper bound was actually higher than the upper bound for Cryptosporidium risk due to the large amount of uncertainty in the parameter estimates for Giardia. Better information on the occurrence and persistence of these pathogens in land-applied biosolids are also high priorities for future research.

While these results do suggest some areas of concern for which future research is appropriate, it should be noted that the greatest risks are associated with adenovirus which does not cause a life threatening disease and the population exposed via the soil ingestion pathway
would be a fairly small sector of the public. Individuals having contact with soil at land application sites would most likely include the site owners and their families. This sector of the public should be readily reached by stakeholder engagement efforts, should follow up be required.

In addition to predictions of risk, the model predicts indicator organism concentrations, which are shown in Table 10-6. Results are not shown for the groundwater pathway (indicator and pathogens may move at different speeds and there is not a unique correspondence between indicator and pathogen levels), nor for the vegetable ingestion pathway (levels were below the model computational threshold). In general indicators would be very difficult to measure in air. Of the indicators considered, fecal coliforms would appear to be the most promising but hundreds of cubic feet of air would need to be filtered in order to obtain measureable levels. In contrast, levels in pond water appear measureable, as do levels in soil for coliphage. These indicators do not derive uniquely from biosolids and their presence could not establish the presence of biosolids contamination. However, their absence would provide some evidence of lack of contamination. This conclusion is sensitive to the decay rates used for indicators and pathogens and the relative release fractions of indicators and pathogens from biosolids. Further work following indicator and pathogen ratios over time will help to better establish the value of these indicator measurements.

Table 10-6. Indicator Organism Concentration Estimates.

<table>
<thead>
<tr>
<th>Indicators</th>
<th>Air Concentration (per m³)</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Slinger</td>
<td>Disking</td>
</tr>
<tr>
<td>Coliphage</td>
<td>2.94 x 10⁻⁶</td>
<td>1.32 x 10⁻³</td>
<td></td>
</tr>
<tr>
<td>Fecal Coliforms</td>
<td>1.79 x 10⁴</td>
<td>8 x 10²</td>
<td></td>
</tr>
<tr>
<td>E. Coli</td>
<td>4.44 x 10⁶</td>
<td>1.99 x 10⁵</td>
<td></td>
</tr>
<tr>
<td>Enterococci</td>
<td>1.79 x 10⁻⁷</td>
<td>8 x 10⁶</td>
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</table>

<table>
<thead>
<tr>
<th>Indicators</th>
<th>Pond Water Concentration (per L)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Coliphage</td>
<td>3.61 x 10²</td>
</tr>
<tr>
<td>Fecal Coliforms</td>
<td>2.19 x 10⁴</td>
</tr>
<tr>
<td>E. Coli</td>
<td>5.46</td>
</tr>
<tr>
<td>Enterococci</td>
<td>2.19 x 10¹</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Indicators</th>
<th>Soil Concentration (per mg soil)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Coliphage</td>
<td>0.24</td>
</tr>
<tr>
<td>Fecal Coliforms</td>
<td>1 x 10⁻⁴</td>
</tr>
<tr>
<td>E. Coli</td>
<td>1.6 x 10⁻¹¹</td>
</tr>
<tr>
<td>Enterococci</td>
<td>9.56 x 10⁻⁹</td>
</tr>
</tbody>
</table>
CHAPTER 11.0

FIELD MONITORING

11.1 Introduction

This chapter presents an overview of the field monitoring. In addition to the summary provided here, detailed studies have been published of the occurrence of indicators and pathogens in biosolids (Wong et al., 2010) and on the behavior of antibiotic resistance genes during land application (Munir et al., 2011).

Two field sites were monitored and both sites were located in Michigan, in order to represent wet climates. Site A was located at the Kellogg Biological Station at MSU Extension and was a controlled site with lysimeters and a portable rainfall simulator. Site B was located in Imlay City and was an actual case-study site in a tiled field. The overall objective of the field study in Site A was the evaluation of leaching and ponding of viral contaminants following land application of biosolids on sandy-loam soil. The overall objective of the field study in site B was to describe a case study of wet-weather-driven fate of biosolids associated contaminants.

In site A, mesophilic anaerobic digested (MAD) biosolids were applied at 56,000 L/ha on a sandy-loam soil over large containment lysimeters seeded to perennial covers of orchardgrass (*Dactylis glomerata* L.), switchgrass (*Panicum virgatum*), or planted annually to maize (*Zea mays* L.). Portable rainfall simulators were used to evaluate the transport of viral contaminants under nearly saturated (90%, volumetric basis) conditions. Lysimeter leachate and surface ponded water samples were collected and analyzed for somatic phage, adenoviruses, and anionic (chloride) and microbial (P-22 bacteriophage) tracers. Neither adenovirus nor somatic phage was recovered from the leachate samples. P-22 bacteriophage was found in the leachate of three lysimeters (removal rates ranged from 1.8 to 3.2 log<sub>10</sub>/m). Although the peak of the anionic tracer breakthrough occurred at a similar pore volume in each lysimeter (around 0.3 pore volume), the peak of P-22 breakthrough varied between lysimeters (<0.1, 0.3 and 0.7 pore volume). The early time to peak breakthrough of anionic and microbial tracers indicated preferential flow paths, presumably from soil cracks, root channels, worm holes or other natural phenomena. The concentration of viral contaminants collected in ponded surface water ranged from 1 to 10% of the initial concentration in the applied biosolids. The die off of somatic phage and P-22 in the surface water was fit to a first order decay model and somatic phage reached background levels at about day ten. Viral pollution from runoff following significant rainfall events is likely when biosolids remain on the soil surface.

In site B, wet-weather sampling was conducted for 80 days between June to September (2009) after biosolids application in a natural setting (i.e., without modifying site characteristics and arrangement) and analyzed for biosolids-associated contaminants. Fecal coliforms, *E. coli*, enterococci, somatic coliphage; *Salmonella*; adenovirus 40/41, total adenovirus, enterovirus, hepatitis A virus; tetracycline-resistance bacteria, and tetracycline-resistance genes were monitored. Due to small surface runoff volumes, fate of biosolids-associated contaminants in surface runoff water could not be studied. After the biosolids application event, no significant difference in microbial quality (indicator microorganisms; tetracycline-resistance bacteria and tetracycline-resistance genes) of soil and tile-drain effluent samples was observed (p-value
>0.05). No pathogens were observed in environmental media after biosolids application. These findings indicated that the biosolids application event did not appear to contribute additional contamination to environmental media under the conditions studied. More site-specific monitoring studies, such as the one presented here, are recommended to understand combined effects of field conditions and biosolids application events on fate of biosolids-associated contaminants.

### 11.2 Site A

#### 11.2.1 Methods

**Lysimeters.** Six stainless steel containment lysimeters enclosing a monolith of undisturbed soil were installed in large experimental plots (600 m²) on a *Kalamazoo fine-loamy, mixed mesic Typic Hapludalf* soil at the Kellogg Biological Station of Michigan State University (MSU) in southwest Michigan. The lysimeters were used from 1994 to 1999 in a study of nitrate movement to groundwater in a rotation of corn (*Zea mays* L.) and alfalfa (*Medicago sativa* L.) with various treatments of compost, manure or inorganic fertilizer (Basso and Ritchie, 2005). They have not been used for experimental work since that time. From 2000 to 2003, continuous corn was grown on all plots and the lysimeter leachate was evacuated annually. No manure or compost has been applied to the plots since 1999.

The lysimeters are 1.5 m wide and 2.1 m deep. A drainage tube extends from the bottom of each lysimeter to the plot edge to avoid unnecessary disturbance of the cropped area. The bulk density of the soil ranged from 1.5-1.6 g/cm³ (Basso and Ritchie, 2005) and the porosity was approximately 40% on a volumetric basis. The pore volume of each lysimeter was approximately 1.48m³ based on a particle density of 2.65g/cm³.

**Biosolids.** Biosolids from the Plainwell (2008) and St. Clair (2009) wastewater treatment (WWTP) plants (Michigan, U.S.) were applied to the surface (56,100 L/ha) of the lysimeters during the growing season. The biosolids were received from the WWTP within 24 hr of application and stored at 4°C. Immediately before application the biosolids were spiked with P-22 bacteriophage to a concentration of 3.00×10¹¹ and 1.25×10¹⁰ PFU/100ml in 2008 and 2009, respectively (Table 11-1). Subsamples were analyzed within 24 hr for concentrations of somatic phage (2009), adenovirus, P-22, and percent total solids (Table 11-1). One mole of anionic tracer (potassium chloride) was mixed in 4L of water and applied uniformly to the surface of each lysimeter followed by 12.7 mm simulated rainfall on the day before the biosolids were applied.

<table>
<thead>
<tr>
<th>Year of Study</th>
<th>% Solid</th>
<th>Somatic Phage (PFU/100ml)</th>
<th>P-22 (PFU/100ml)</th>
<th>Adenovirus (copies/100ml)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2008</td>
<td>5.0</td>
<td>NA</td>
<td>3.00×10¹¹</td>
<td>4.20×10⁸</td>
</tr>
<tr>
<td>2009</td>
<td>6.0</td>
<td>8.00×10⁴</td>
<td>1.25×10¹⁰</td>
<td>3.30×10⁷</td>
</tr>
</tbody>
</table>

**Lysimeter experiments:** Six lysimeters were used: lysimeter numbers L1 to L3 in August, 2008 and L4 to L6 in May, 2009. Biosolids were applied on all lysimeters except L3, which was a control. Leachate samples were collected in 2008 and 2009; surface water and core soil samples were collected in 2009. Leachate and surface samples were monitored for somatic phage (2009), P-22 and adenovirus. The anionic tracer was only monitored in leachate samples. The biosolids
were applied uniformly (9.9 L/lysimeter) to the soil surface and allowed to remain undisturbed for 12 hours prior to simulated rainfall. The uniformity of the application was controlled by using small containers to evenly distribute the biosolids on the lysimeter surface. The rainfall simulator applied water at a rate of 5 cm/h on a semi-continuous (on-off) basis controlled by the operator to minimize surface ponding. A rain gauge was used to monitor the amount of water applied on each lysimeter and the water application rate was approximately 8 to 10 cm per day. Irrigation and water sampling continued on a daily basis for about 12 h/day until about 1.7 pore volumes of leachate was collected from each lysimeter.

The average ambient temperature during the 2008 and 2009 study was 13.3°C (ranging from 7.2 to 19.4°C) and 15.0°C (ranging from 8.3 to 20°C), respectively. The average surface soil temperature during the 2008 and 2009 study was 10.0°C (range from 5.0 to 16.8°C) and 11.3°C (range from 5.9 to 19.2°C), respectively. Three sensors (5TM Soil Moisture and Temperature Sensor, Decagon Devices Inc.) were installed in each lysimeter at the depth of 10 cm, 30 cm, and 100 cm to monitor soil moisture. The water saturation in each lysimeter soil was about 90% (volumetric basis) during the study period.

Leachate samples (3.9L) were drawn from the bottom of the lysimeters with a peristaltic pump every 0.1 pore volumes (148 L) and stored in sterilized containers, placed on ice and transported to the laboratory for analysis. The leachate collected between each 0.1 pore volume sample was discharged downslope and at least 5 m from the lysimeters. The leachate volume was recorded in a graduated 18.9 L container. Approximately 0.1 pore volume of water leached through each lysimeter for every 24 to 36h. In 2009, leachate samples were also collected once a month for three consecutive months after completion of 1.7 pore volumes sampling.

A circular, galvanized steel ring (137 cm by 30cm) was placed on the soil surface over the lysimeter on L4, L5 and L6 to retain ponded surface water. Ponded surface water samples were collected daily during the sampling period. Samples (3.9L) were collected in sterilized containers, stored on ice and transported to the laboratory for analysis each day.

**Infiltration rate:** The *in situ* water infiltration rate was measured with a double-ring infiltrometer upon completion of the experiment and before the soil cores were removed from the lysimeters.

**Chloride analysis:** Chloride concentration in the leachate samples was analyzed with an ion selective electrode (model no. 27502-13, Cole Parmer). The electrode was calibrated by plotting the millivoltage reading versus three standard chloride solutions on a semi-log scale. The developed calibration curve was used to determine the chloride concentration of the leachate samples.

**P-22 propagation and phage analysis:** Salmonella phage (P-22) was used as a microbial tracer. The P-22 was propagated by infecting its host strain *S. typhimurium* overnight in Tryptic Soy Broth (TSB; Difco) at 37°C and isolated by filtering through 0.45µm cellulose ester-based membrane (Millipore, MA) to remove cell debris. Somatic phage and P-22 were analyzed by the double layer agar method (U.S. EPA method 1602). The host cell for somatic phage was *E. coli* CN13. All dilutions were made with sterilized phosphate buffer water (PBW).

**Adenovirus analysis:** Water samples were concentrated to achieve a larger equivalent volume during the qPCR reaction for adenovirus detection. The concentration method developed by Haramoto et al. (2005) was used with the following modification: Amicon Ultra (Millipore, Billerica MA) rather than Centriprep YM-50 was used to concentrate the NaOH eluent.
filtered volume for surface and groundwater was 100 ml and 2 L, respectively. The final volume of concentrated eluent was around 140 µL and it was stored at -80°C for DNA extraction. The primers and probe were adopted from Heim et al. (2003). Each qPCR reaction mix included 10 µL of 2X LightCycler 480 TaqMan Master Mix; 1.0 µL of each forward and reverse primer (each final concentration was 500 nM); 0.6 µL of 10 µM TaqMan probe (final conc. = 300 nM); 2.7 µL of PCR-grade water and 5 µL of DNA sample or standard. The real-time PCR running program (all thermocycles were performed at a temperature transition rate of 20°C/s) was 95°C for 15 min followed by 45 cycles at 95°C for 3 sec; 55°C for 10 sec; 65°C for 60 sec and 30 sec at 40°C. The fluorescent signal was detected after each extension cycle.

**Viral analysis of soil samples:** Intact soil cores (3.8 cm diameter) were extracted to a depth of about 90 cm after completion of the rainfall simulation experiments in 2009 (volumes of soil core ranged from 6.9-10.3×10² cm³). The soil probe was only able to extract the soils above the 90 cm depth since the soil below that depth was primarily unconsolidated sand and the probe was not able to retain an intact core. The soil cores were subdivided based on identifiable changes in soil color or texture. Soil physical and chemical properties and residual virus concentrations (L4, L5, L6) were analyzed. No virus analyses were performed on L1 and L2 soil samples because the core soil samples were taken more than one year after the completion of the 2008 experiments. Analysis of the soil physical and chemical properties (Table 11-2) was done by the Soil and Plant Nutrient Laboratory at MSU.

Viruses were eluted from the soil samples by stirring 50 grams of soil in 50mL of 10% beef extract for 30 minutes (Williamson et al., 2003). The solid phase of the mixture was spun down by centrifugation at 10,000 x g for 30 minutes at 4°C and the supernatant was retained for virus analysis.

**Recovery of the Cl tracer and removal rate of P-22:** Mass recovery of anionic and microbial tracer was calculated by the trapezoidal rule whereby the area under the curve of the effluent concentration (virus/L) versus pore volume (0.1 pore volume = 148L) was measured and normalized with the initial mass input to the system.

The removal rate of P-22 was calculated using Equation 11-1 which describes the relative log-reduction in microbial concentration per unit of distance traveled (Pang, 2009).

\[
\lambda = \frac{-\ln \text{(mass recovery)}}{x}
\]  

(11-1)

Where:
- \(\lambda\) is the removal rate (log₁₀/m)
- \(x\) is the soil depth (m)
- mass recovery is (unitless)

**Recovery of P-22 from soil:** The recovery of P-22 from the soil cores (depth of 76 to 91 cm) was calculated as the sum of P-22 recovered from each soil layer normalized with the initial mass of P-22 applied to the soil surface. The P-22 recovered in each layer of soil was calculated as:

\[
M_{\text{soil}} = \frac{\left(A \times D \times (1 - \theta) \times B \times C_{\text{soil}}\right)}{0.26}
\]

(11-2)
Where:

- $M_{soil}$ is the P-22 recovered in each soil layer (PFU)
- $A$ is the surface area of the lysimeter (cm²)
- $D$ is the thickness of each layer of core soil samples (cm)
- $\Theta$ is the soil porosity ($V_{pore}/V_{total}$) = 0.40
- $B$ is the bulk density (1.6 g/cm³)
- $C_{soil}$ is the P-22 concentration in each layer (PFU/g)
- 0.26 is the recovery of virus from soils with beef extract (Williamson et al., 2003).

Equation 11-2 assumes a homogenous distribution of P-22 in each soil layer. Porosity and soil bulk density values are based on Basso and Ritchie, 2005).

**Decay analysis:** The P-22 concentration in the ponded surface water was fit to a first order decay model (Equation 11-3):

$$\ln \left( C_t \right) = -Kt + \ln \left( C_0 \right)$$

Where:

- $C_t$ is the microorganism concentration (pfu/100ml)
- $t$ is time from application (days)
- $C_0$ is the phage concentration (pfu/100ml) at time zero
- $k$ is the decay coefficient (d⁻¹).

### 11.2.2 Results

**Soil properties:** The physical and chemical properties of the soil are listed in Table 11-2. The soil series was a Kalamazoo Loam (*Kalamazoo fine-loamy, mixed mesic Typic Hapludalfs*). The near-surface soil texture was typically a sandy-loam although most of the lysimeters had a sandy-clay-loam layer at depths ranging from 20 to 40 cm. The sand content generally increased at greater depth.

The Natural Resource Conservation Service (NRCS) drainage classification for the soil series was ‘poor’. Measured infiltration rates ranged from 3.6 to 8 mm/h for the lysimeters (L1-L5) containing orchardgrass or switchgrass (Table 11-3). The measured infiltration rates for L6 (corn) was unrealistically low (1.0 mm/h) and was not consistent with the flow rate through the lysimeter during the water sampling period. There was no crop residue, no vegetative cover and no active root system to protect the soil from the impact of the simulated rainfall. After the soil dried the resulting soil compaction and loss of pore space restricted the infiltration rate.
Table 11-2. Physical and Chemical Characteristics for Each Lysimeter Applied with Biosolids.

<table>
<thead>
<tr>
<th>Lysimeter depth (cm)</th>
<th>pH</th>
<th>CEC (meq/100g)</th>
<th>OM  (%)</th>
<th>Sand (%)</th>
<th>Silt (%)</th>
<th>Clay (%)</th>
<th>Soil classification</th>
<th>P (ppm)</th>
<th>K (ppm)</th>
<th>Mg (ppm)</th>
<th>Ca (ppm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>L1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>0-25</td>
<td>6.4</td>
<td>7.7</td>
<td>1.8</td>
<td>55.2</td>
<td>35</td>
<td>9.8</td>
<td>Sandy loam</td>
<td>54</td>
<td>131</td>
<td>165</td>
<td>1196</td>
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<tr>
<td>25-46</td>
<td>7.1</td>
<td>7.7</td>
<td>1.4</td>
<td>53.2</td>
<td>35</td>
<td>11.8</td>
<td>Sandy loam</td>
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<td>69</td>
<td>157</td>
<td>1235</td>
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<td>46-61</td>
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<td>9.1</td>
<td>1.1</td>
<td>56.4</td>
<td>28.8</td>
<td>14.8</td>
<td>Sandy loam</td>
<td>52</td>
<td>95</td>
<td>180</td>
<td>1474</td>
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<tr>
<td>61-91</td>
<td>7.1</td>
<td>8.7</td>
<td>0.6</td>
<td>71.8</td>
<td>9.4</td>
<td>19.8</td>
<td>Sandy loam</td>
<td>28</td>
<td>18.1</td>
<td>79.1</td>
<td>1372</td>
</tr>
<tr>
<td>L2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>0-25</td>
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<td>8.2</td>
<td>1.1</td>
<td>62.4</td>
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<td>13.8</td>
<td>Sandy loam</td>
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<td>95</td>
<td>196</td>
<td>1273</td>
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<td>25-43</td>
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<td>8.8</td>
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<td>29.4</td>
<td>15.8</td>
<td>Sandy loam</td>
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<td>83</td>
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<td>43-76</td>
<td>6.9</td>
<td>11</td>
<td>0.9</td>
<td>67.8</td>
<td>9.4</td>
<td>22.8</td>
<td>Sandy clay loam</td>
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<td>120</td>
<td>238</td>
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<td>L3</td>
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<td></td>
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</tr>
<tr>
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<td>1.8</td>
<td>53.2</td>
<td>31.8</td>
<td>15.0</td>
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<td>15-36</td>
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<td>36-51</td>
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<td>9.6</td>
<td>1.1</td>
<td>57.4</td>
<td>13.8</td>
<td>28.8</td>
<td>Sandy clay loam</td>
<td>31</td>
<td>92</td>
<td>312</td>
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<td>51-61</td>
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<td>79.9</td>
<td>5.7</td>
<td>14.4</td>
<td>Sandy clay loam</td>
<td>43</td>
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<td></td>
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<td></td>
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<td></td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
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<td>7.2</td>
<td>9.1</td>
<td>2.1</td>
<td>52.4</td>
<td>36.8</td>
<td>10.8</td>
<td>Sandy loam</td>
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<td>111</td>
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<td>0.9</td>
<td>68.8</td>
<td>12.8</td>
<td>18.4</td>
<td>Sandy loam</td>
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<td>0.5</td>
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<td>Loamy sand</td>
<td>35</td>
<td>54</td>
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<td></td>
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<td></td>
<td></td>
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<tr>
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<td>8</td>
<td>2.2</td>
<td>53.8</td>
<td>35.8</td>
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<td>Sandy loam</td>
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<td>126</td>
<td>201</td>
<td>1210</td>
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<td>20-36</td>
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<td>6.9</td>
<td>11.7</td>
<td>1.1</td>
<td>47.8</td>
<td>25.4</td>
<td>26.8</td>
<td>Sandy clay loam</td>
<td>29</td>
<td>127</td>
<td>303</td>
<td>1769</td>
</tr>
<tr>
<td>51-66</td>
<td>6.9</td>
<td>8.6</td>
<td>0.8</td>
<td>73.9</td>
<td>7.7</td>
<td>18.4</td>
<td>Sandy loam</td>
<td>30</td>
<td>77</td>
<td>166</td>
<td>1399</td>
</tr>
<tr>
<td>66-84</td>
<td>7</td>
<td>4.5</td>
<td>0.5</td>
<td>88.1</td>
<td>2.5</td>
<td>9.4</td>
<td>Loamy sand</td>
<td>37</td>
<td>38</td>
<td>92</td>
<td>733</td>
</tr>
<tr>
<td>L6</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>0-15</td>
<td>6.6</td>
<td>7</td>
<td>2</td>
<td>51.2</td>
<td>36</td>
<td>12.8</td>
<td>Sandy loam</td>
<td>50</td>
<td>104</td>
<td>171</td>
<td>1062</td>
</tr>
<tr>
<td>15-25</td>
<td>6.9</td>
<td>6.6</td>
<td>1.3</td>
<td>51.4</td>
<td>33.8</td>
<td>14.8</td>
<td>Sandy loam</td>
<td>56</td>
<td>57</td>
<td>162</td>
<td>1016</td>
</tr>
<tr>
<td>25-46</td>
<td>7.1</td>
<td>9.3</td>
<td>1.2</td>
<td>52.4</td>
<td>32.8</td>
<td>14.8</td>
<td>Sandy loam</td>
<td>64</td>
<td>90</td>
<td>242</td>
<td>1415</td>
</tr>
<tr>
<td>46-61</td>
<td>7</td>
<td>7.7</td>
<td>0.8</td>
<td>54.8</td>
<td>21.4</td>
<td>23.8</td>
<td>Sandy Clay Loam</td>
<td>41</td>
<td>67</td>
<td>200</td>
<td>1164</td>
</tr>
<tr>
<td>61-74</td>
<td>7.1</td>
<td>8</td>
<td>0.6</td>
<td>69.8</td>
<td>11.4</td>
<td>18.8</td>
<td>Sandy loam</td>
<td>40</td>
<td>75</td>
<td>210</td>
<td>1205</td>
</tr>
<tr>
<td>74-91</td>
<td>7.1</td>
<td>7.5</td>
<td>0.6</td>
<td>63.8</td>
<td>16.4</td>
<td>19.8</td>
<td>Sandy loam</td>
<td>39</td>
<td>68</td>
<td>188</td>
<td>1155</td>
</tr>
</tbody>
</table>

CEC = Cation exchange capacity; OM = Organic matter; P = Phosphorus; K = Potassium;
Mg = Magnesium; Ca=Calcium
a = 1:1 soil:water ratio
b = Ammonium acetate method (Thomas et al., 1982)
c = Dichromate method (Nelson and Sommers, 1982)
d = Bray P1 method (Frank et al., 1998)
Table 11-3. Infiltration Rates, Drainage Classification, Root System of Each Lysimeter.

<table>
<thead>
<tr>
<th>Lysimeter</th>
<th>Infiltration Rate (mm/hr)</th>
<th>Drainage Class</th>
<th>Crop</th>
</tr>
</thead>
<tbody>
<tr>
<td>L1</td>
<td>5.9</td>
<td>poor</td>
<td>orchard grass</td>
</tr>
<tr>
<td>L2</td>
<td>3.6</td>
<td>poor</td>
<td>orchard grass</td>
</tr>
<tr>
<td>L3 (control)</td>
<td>8.0</td>
<td>poor</td>
<td>orchard grass</td>
</tr>
<tr>
<td>L4</td>
<td>7.7</td>
<td>poor</td>
<td>switch grass</td>
</tr>
<tr>
<td>L5</td>
<td>4.3</td>
<td>poor</td>
<td>switch grass</td>
</tr>
<tr>
<td>L6</td>
<td>1.0</td>
<td>poor</td>
<td>corn</td>
</tr>
</tbody>
</table>

**Lysimeter effluent:** The break through curve (BTC) of the chloride tracer revealed differences in the flow characteristics of each lysimeter (Figure 11-1). This variability was expected given the variation in soil texture and vegetation. The peak concentration occurred near 0.3 PV for all lysimeters and remained above background levels throughout the sampling period. Chloride recovery ranged from about 33 to 99% (Table 11-4).

![Breakthrough Curves for the Chloride Tracer](image-url)
Table 11-4. Recovery Percentage of Chloride and P-22 from Leachate and Top Half of Lysimeter Soils.

<table>
<thead>
<tr>
<th>Lysimeter</th>
<th>Leachate</th>
<th>Soil</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Chloride</td>
<td>P-22</td>
</tr>
<tr>
<td>L1</td>
<td>71.3</td>
<td>ND</td>
</tr>
<tr>
<td>L2</td>
<td>74.2</td>
<td>0.59</td>
</tr>
<tr>
<td>L3</td>
<td>32.6</td>
<td>NA</td>
</tr>
<tr>
<td>L4</td>
<td>99.3</td>
<td>ND</td>
</tr>
<tr>
<td>L5</td>
<td>74.2</td>
<td>0.12</td>
</tr>
<tr>
<td>L6</td>
<td>51.2</td>
<td>2.14</td>
</tr>
</tbody>
</table>

ND = not detected; NA = not available

a = no chloride analysis on soil samples

No adenovirus or somatic phage was recovered from the leachate samples. P-22 was recovered from L2 (orchardgrass), L5 (switchgrass) and L6 (continuous corn) leachate, but none was detected in L1 (orchard grass) or L4 (switchgrass). The P-22 breakthrough curves of L2, L5 and L6 are shown in Figure 11-2. The peak breakthrough in L2, L5 and L6 occurred at 0.7, 0.3 and <0.1 pore volumes (PV), respectively. The rapid breakthrough in L6 may indicate the potential for preferential flow through transient flow paths when biosolids are applied to an annual crop such as maize whereby the root system decays leaving channels for preferential flow. There was a three- to four-log reduction of P-22 from the initial concentration in the spiked biosolids to the peak concentration in the leachate. The recoveries of P-22 in L2, L5 and L6 leachate were 0.59, 0.12 and 2.14% of the initial concentration (Table 11-3), respectively. The P-22 removal rate (λ) for L2, L5 and L6 was 2.4, 3.2 and 1.8 log/m, respectively.
Figure 11-2. Breakthrough Curves of P-22 and the Chloride Tracer in L2, L5 and L6 Leachate. Error Bars Represent the Standard Deviation of the Duplicate Measurements from Each Sample.
**Viral levels in soil samples:** The soil cores extracted from (L4, L5 and L6) were evaluated for P-22, somatic phage and adenovirus. No somatic phage or adenovirus was detected, but P-22 was detected in all samples. Interestingly, no P-22 was detected in L4 leachate, but the concentration of P-22 extracted from the L4 soil samples was greater than in L5 and L6 at nearly every depth (Figure 11-3).

![Figure 11-3. P-22 Concentration at Different Soil Depths; No Somatic Phage or Adenovirus Were Detected.](image)

**Surface water:** The somatic phage and P-22 concentration in the ponded surface water is shown in Figure 11-4. Somatic phage reached non-detectable levels around day ten. Adenoviruses were detected in all surface water samples but no decay trend was observed. The average concentration of adenovirus in the surface water from all sampling events was $2.94 \pm 3.05 \times 10^3$ copies/100ml, about 4 logs lower than the initial concentration in biosolids. It took longer for P-22 to reach non-detectable levels (>21 days), likely because the initial concentration was 6 logs greater than the concentration of somatic phage.

The greatest viral concentration in the ponded water was at the start of the simulated rainfall and the samples with the greatest concentration were about 1-10% of the initial concentration in the spiked biosolids. The reduction of viruses in the ponded water samples over time was fit to a first order decay model (Figure 11-5) and the resulting decay coefficients of somatic phage and P-22 were similar (slightly less than 0.40/day).
Figure 11-5. P-22 and Somatic Phage Levels in Surface Water Samples in 2009.
The dotted-line indicates the detection limit. Error bars indicate one standard deviation from the mean of L4, L5, and L6.
11.2.3 Discussion

To the best of the researchers’ knowledge, the leaching of biosolid-associated pathogens through undisturbed soil in large-scale lysimeters with soil depths greater than 100 cm has not been reported. The results obtained from the freely drained lysimeters in this study may be particularly applicable to artificially drained cropland.

The rapid, peak breakthrough of the anionic and microbial tracers (<1PV) indicated transport through preferential flow paths. Preferential flow was reported in earlier lysimeter work (Aislabie et al., 2001; McLeod et al., 2001, 2003, 2004; Pang et al., 2008; Jiang et al., 2008). The transport rate measured in laboratory scale experiments may be considerably lower than the transport rate in the natural environment because the preferential flow pathways allow contaminants to bypass the soil matrix. Beside natural soil cracks and fissures, the root systems of vegetative covers improve infiltration by providing root channels for preferential flow.

Differences in BTCs and recoveries between the anionic and microbial tracer may be due to differences in sorption behavior. Also, even though the size of individual viruses is small (less than 100 nanometers), aggregation may take place under some pH values and ionic strengths favoring neutralization of virus surface charge (Gutierrez et al., 2010; da Silva et al., 2011). Larger sizes of virus aggregates may be more effectively removed by subsurface soil compared to individual viruses or anionic tracer.

The removal of the P-22 bacteriophage in three of the lysimeters (1.83 to 3.21 log/m) was similar to the removal rate reported by Jiang et al. (2008; 1.92 to 2.80 log/m) and Carlander et al. (2000; 3.76 log/m). Manure-associated fecal coliform were detected in the leachate samples reported by Jiang et al. (2008) but no biosolids-associated somatic phage or HAdV were detected.
in the leachate from the lysimeters, likely because of the greater depth of soil (2.1 m versus 0.4 to 1.0 m). The results of the researchers’ work with the application of biosolids on a sandy loam soil confirm the results of Jiang et al. (2008) and Carlander et al. (2000) with dairy manure on similar soils. This indicates that a sandy loam soil with a vegetative cover can be an effective filter for removing enteric viruses for water quality protection, but depth of the soil profile is important.

The low recovery of P-22 from the leachate and soil cores (Table 11-4) indicates that most viruses are sorbed to organic matter or soil particles and are retained in the soil matrix or die-off. There was a three- to four-log reduction in the P-22 from the initial concentration in the spiked biosolids to the peak concentration in the leachate. The initial concentration of somatic phage in the biosolids was relatively lower (8.00×10² PFU /ml) and somatic phage was effectively retained in the soil matrix.

The adenovirus genome concentration in the biosolids was about 3 logs greater than the somatic phage and the equivalent volume of each qPCR reaction was about 50 ml but adenoviruses were not detected. This is consistent with the results reported by Chetochine et al. (2006) that observed most of the indigenous phage remained in the solid pellet after a series of extractions, and the results reported by Gerba et al. (1980) whereby enteroviruses formed strong attachments to sludge particles and were difficult to elute. Sano et al. (2004) reported that the virus-binding proteins (VBPs) in a bacterial culture from activated sludge play a key role in attaching indigenous viruses to sludge particles. It is likely that adenoviruses formed a stronger attachment to the sludge solids than the spiked P-22 and were more readily sorbed and retained in the soil. Additionally, the low recovery of adenoviruses may be influenced by the sampling process. In recently published work (Fong et al., 2010), the recovery of adenovirus in MilliQ water and a river water matrix ranged from 0.17 to 6.98% using HA filtration, much lower than the 30-74% recovery reported earlier (Haramoto et al., 2005). The results indicate that there is a need for a better understanding of the transport, retention and die-off of indigenous viruses in the natural environment as opposed to spiked viral indicators.

Because rain drops break down soil particles upon impact there was mixing of water, soil and biosolids at the soil surface during the simulated rainfall. The ponded water samples included viruses attached to soil particles, waste or slurry particles, and unattached cells or clumps. Each of these are sources of contaminants that can be transported in overland flow (Tyrrel and Quinton, 2003; Muirhead et al., 2005). Based on the results of the researchers’ work, the virus concentration in ponded surface water can be as great as 1-10% of the initial virus concentration in the biosolids. These virus concentrations represent a considerable threat to water quality from surface runoff if biosolids are allowed to remain on the soil surface after application. The biosolid-associated pathogens may exist for several days under wet conditions. In earlier work (Pourcher et al., 2007), no enteroviruses in sludge contaminated soil were detected beyond 14 days after application, but adenovirus was detected after 20 days in this study. The greater survival in the researchers’ work may have been due to the strong UV resistance of adenoviruses and the presence of vegetation, crop residue and soil particles that can create a protective micro-environment.

The results of this work can be used to develop best management practices for the land application of manure and biosolids on drained land. Some of the management practices that may help protect water quality are: 1) pre-tillage to disrupt the continuity of macro-pores, 2) controlled (low) application rates, and 3) timing biosolids/manure application rates to avoid
application on wet ground, when tiles are flowing, or when there is a chance of significant rainfall (> 0.5 inches) within the next few days.

11.3 Site B
11.3.1 Methods

Study Design: An agricultural farm (loam soil with a 2-6% natural surface slope) containing a network of tile-drains, situated in Imlay city (Michigan, U.S.A.), was selected to study environmental fate of BACs after land application of class B biosolids. Table 11-5 shows concentration levels of BACs in the Romeo biosolids. Only part of the plot was used for biosolids application (termed as “biosolids plot”; 80,936 m² total available area for biosolids application), which was surrounded by a buffer strip from all sides to protect the nearby ditch (termed as “ditch buffer”; width: 45.5 m) and house (buffer width: 45.5 m)

Table 11-5. Microbial Characteristics of the Romeo Biosolids.
(Salmonella was not detected using both culture and molecular methods; Hepatitis A was not detected using molecular methods).

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Sampling Events</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>May 29th, 2009</td>
</tr>
<tr>
<td>Dry solids (%)</td>
<td>12.14%</td>
</tr>
<tr>
<td>Pathogen indicators</td>
<td></td>
</tr>
<tr>
<td>Fecal coliforms (MPN/g)</td>
<td>1.97×10²</td>
</tr>
<tr>
<td>E.coli (MPN/g)</td>
<td>7.41×10¹</td>
</tr>
<tr>
<td>Enterococci (MPN/g)</td>
<td>5.11×10¹</td>
</tr>
<tr>
<td>Coliphage (PFU/g)</td>
<td>1.32×10⁴</td>
</tr>
<tr>
<td>Human enteric viruses</td>
<td></td>
</tr>
<tr>
<td>Enteric viruses (MPN/4g) (BGM)</td>
<td>6.8</td>
</tr>
<tr>
<td>Total adenovirus (copies/g)</td>
<td>3.27×10⁶</td>
</tr>
<tr>
<td>Adenovirus 40/41 (copies/g)</td>
<td>4.63×10⁴</td>
</tr>
<tr>
<td>Enterovirus (copies/g)</td>
<td>3.53×10⁴</td>
</tr>
<tr>
<td>Antibiotic-resistance bacteria (ARB)</td>
<td></td>
</tr>
<tr>
<td>Tetracycline-resistance bacteria (CFU/g)</td>
<td>4.12×10⁴</td>
</tr>
<tr>
<td>Total bacterial count without antibiotics (CFU/g)</td>
<td>3.71×10⁶</td>
</tr>
<tr>
<td>Antibiotic-resistance gene (ARG)</td>
<td></td>
</tr>
<tr>
<td>Tet-W genes (copies/g)</td>
<td>3.22×10⁴</td>
</tr>
<tr>
<td>16S rRNA genes (copies/g)</td>
<td>2.91×10¹³</td>
</tr>
</tbody>
</table>

CFU-Colony forming units; copies/g-Genomic copies/g; MPN-Most probable number; PFU-Plaque forming units

Biosolid Application Events: Class B biosolids were applied on land and periodic environmental samples were collected after rain events for a total of three months and analyzed for different fecal indicators, salmonella, enteric viruses, TRB and Tet-W genes. It is important to note that this study was an observational study instead of a controlled study, and thus, no field amendments were made before the start of the study and during the monitoring period.

The monitoring study began on June 23rd, 2009 with application of class B biosolids, obtained from the Romeo wastewater treatment plant (WWTP) in Michigan (U.S.A.). The Romeo WWTP receives raw wastewater at an average flow rate of 0.8 million gallons per day (MGD) with a maximum capacity of 2.2 MGD. The plant uses rotating biological contactors for
BOD and COD removal and uses a mesophilic anaerobic digestion (MAD) process for producing class B biosolids.

Biosolids application events were conducted by BioTech Agronomics, Inc. (Beulah, MI, U.S.A.) on June 23rd, 2009 (termed as “BS1” event), August 1st, 2009 (termed as “BS2” event), and August 3rd, 2009 (termed as “BS3” event). Before the application event, biosolids were collected from the Romeo WWTP holding tank in one liter Nalgene autoclaved bottles and transported to the Water Quality Laboratory at Michigan State University (East Lansing, MI, U.S.A.) on ice and characterized for microbial parameters and dry solids. In addition, biosolids and field soil samples were analyzed for nutrient contents and dry solids for determining biosolids application rates. During the first BS1 event, biosolids (5.7% solids) were applied to the soil surface (i.e., using spreading method) at the application rate of 10.2 liters/m². During subsequent BS2 and BS3 events, biosolids were injected into the soil at the application rates of 5.91 liters/m² (solids content: 5.2%) and 2.34 liters/m² (solids content: 7.8% solids), respectively. Subsequently, biosolids were allowed to sit on the soil before incorporating it into soil.

Sampling: Wet-weather sampling (i.e., sampling immediately after the rain event) was conducted in response to rainfall events following BS application. Information on rainfall intensity, duration, and temperature were obtained from the nearby weather station (IDNS45; Latitude: N 43° 3' 8", Longitude: W 83° 0' 43"; http://www.wunderground.com/). Field sampling was conducted on June 9th and June 18th (2009) to determine background concentrations of pathogens, antibiotic-resistance bacteria and genes in two types of samples: 1) Soil samples, and 2) Tile-drain effluent samples. Tile-drain effluent samples from the biosolids plot were collected. The tile drain is discharging water to the nearby ditch. Sampling volumes for water samples depended on tile-drain effluent flow rates.

Sample Collection and Initial Processing for Fecal Indicators, Salmonella and Viruses: All soil samples were collected in 100 mL specimen cups and water samples for analysis of bacterial indicators, somatic coliphage, and Salmonella were collected in autoclaved 3.78 liters volume collapsible carboys. All collected samples were analyzed within 2-4 hours after the collection.

Soil samples, collected for analysis of fecal indicators and Salmonella were also used for virus analysis. The virus elution and concentration were performed according to the ASTM D 4994-89 method (ASTM, 2002). Approximately, 30-50 gallons (i.e., 113.4-189 liters) tile-drain effluent samples were collected at every sampling time, if possible depending on flow rate and transferred to the Water Quality Laboratory. Upon arrival, these samples were filtered with 1MDS (Cuno) electropositive filters immediately using the sampling apparatus explained in the U.S. EPA (2001a). After every filtration, the apparatus was then disinfected using a 0.167% bleach solution for a total of 20 minutes of contact time and then de-chlorinated using a 2% sodium thiosulfate (U.S. EPA, 2006). After the all samples were filtered they were placed in a 4°C cooler for no longer than 24 hours. Further, all filtered samples were eluted 24 hours according to the methodology presented in the U.S. EPA manual (U.S. EPA, 2006) and Xagoraraki et al. (2007) study.

Sample Collection and Initial Processing for Tetracycline-resistance Bacteria and Tet-W Genes: Soil samples, collected for indicator analysis, were also analyzed for TRB and Tet-W genes. For TRB and Tet-W genes analysis, water samples were collected in 3.78 liters collapsible pre-disinfected carboys and processed within 48hrs of sample collection. The samples were concentrated by filtration onto 0.45µm HA filters (MF™; Millipore) using different
sampling volumes (ranging between 500 and 1500 mL) depending upon turbidity of water samples. The filters were collected in 50 mL tubes with phosphate buffer water and vortexed for 5 minutes to allow filtrate to dissolve in the water. The 50mL tubes were then centrifuged for 20 minutes at 4500 rpm. Supernatant was discarded and the concentrates were stored at –80°C until DNA extraction was performed for molecular analysis. Copies of Tet-W and 16SrRNA genes were determined using the qPCR method.

**Analytical Methods:** Fecal coliforms were analyzed according to the U.S. EPA method 1680 (U.S. EPA, 2002). *E. coli* and enterococci were analyzed using the IDEXX methods (IDEXX, 2009). Somatic phage was analyzed by the double layer agar method (EPA method 1602) (U.S. EPA, 2001b). *Salmonella* was determined using the Semisolid Rappaport-Vassiliadis medium method described in US EPA method 1682 (U.S. EPA, 2006). All dilutions were prepared with sterilized phosphate buffer water. Concentrations of tetracycline-resistant bacteria and heterotrophic plate count (HPC) in different samples were determined using the methodology described in Brooks et al. (2007). Concentrations of enteric viruses, salmonella and ARG in the environmental samples were quantified using qPCR methods used previously (Suzuki et al., 2000; Aminov et al., 2001; Xagoraraki et al., 2007; Dierseen et al., 2007; Jothikumar et al., 2005; Novinscak et al., 2007).

**Mathematical Methods:** To study effects of biosolids application on occurrence of different BACs in biosolid-amended soil and tile-drain effluent samples, analysis of variance analysis (ANOVA) test was conducted on log-transformed concentrations for two groups: 1) Group A-Samples collected during first 34 days including BS1 event and 2) Group B-Samples collected between 35th and 80th day (including BS2 and BS3 events) (i.e., α = 0.05). Log-transformation of concentrations was conducted to meet normality requirements of ANOVA. Surface water samples were not statistically analyzed due to small number of samples. Association between concentrations of BACs in biosolid-amended soil and tile-drain effluent samples were determined by calculating values of Spearman rank-correlation coefficients (α = 0.05). All mathematical analyses were conducted using the Statistical Package for Social Sciences (SPSS) software (SPSS Inc., Chicago, IL, U.S.).

11.3.2 Results

Table 11-5 shows concentration levels of BACs in the Romeo biosolids. None of the pathogens was observed in any of the environmental samples. However, fecal indicators, TRB, and Tet-W genes were observed in biosolid-amended soil and tile-drain effluent samples. Following sections present findings for soil and tile-drain effluent samples.

The background soil samples were not observed to be contaminated with any of the pathogens evaluated in this study. After the BS1 event, none of these pathogens and somatic coliphage was observed in biosolid-amended soil samples, except for bacterial fecal indicators. Concentrations of bacterial fecal indicators were initially observed to increase followed by decrease in concentration. For example, after the third day of BS1 event, concentrations of the bacterial fecal indicators were observed to be ~2-3 logs higher compared to the background soil concentrations; however, these concentrations were observed to decrease after the seventh day of the BS1 event (i.e., ~ 2 log reduction relative to the third day concentration values). Similar trends were also found after the BS2 and BS3 events.

Before the BS1 event, total bacterial population grown on the R2A media plates without adding any tetracycline antibiotic, was observed to be $2.33 \times 10^7$ cfu/g. After the BS1 event,
Concentration of total bacterial population was observed to range between $1.57 \times 10^7$ cfu/g and $9.91 \times 10^7$ cfu/g, slightly higher than the background concentration level, but in the same order of magnitude.

Concentration of TRB in soil samples was found to be $6.15 \times 10^5$ cfu/g before the BS1 event, which was observed to increase first and then decrease over time. For example, TRB concentration was observed to be $1.56 \times 10^6$ cfu/g after the third day of the BS1 event (i.e., higher than the background concentration level), which decreased to $8.66 \times 10^5$ cfu/g after 34th day of the BS1 event (i.e., reaching to the background concentration levels). After the BS2 and BS3 events, concentration of TRB was not observed to increase above the background concentration levels.

The statistical analysis for testing significance of difference in concentrations of BACs for pre- and post-BS1 events could not be conducted due to small sample size and nature of sampling schedule. After the BS2 and BS3 events, only concentrations of TRB in Group A biosolid-amended soil samples (i.e., samples collected during first 34 days including BS1 event) and Group B biosolid-amended soil samples (i.e., samples collected between 35th and 80th day including BS2 and BS3 events) were observed to be statistically different (p-value = 0.037) with 95% confidence. However, concentrations of all other BACs were not observed to be statistically different between two groups with 95% confidence. These comparisons are presented in Figure 11-7.

The background tile-drain effluent samples had $1.50 \times 10^5$ CFU/100 mL fecal coliforms, $1.12 \times 10^5$ MPN/100 mL E. coli, and $9.59 \times 10^3$ MPN/100 mL enterococci (in samples collected five days before the BS1 event). After the BS1 event, concentrations of these bacterial indicators in samples collected on the third day after the BS1 event were observed to be lower compared to that in background tile-drain effluent samples.

Before the BS1 event, total bacterial population grown on the R2A media without any addition of tetracycline antibiotic in tile-drain effluent samples was observed to be $1.12 \times 10^6$ cfu/100 mL. After the BS1 event, concentrations of total bacterial population were observed to vary between $1.7 \times 10^6$ cfu/100 mL and $2.2 \times 10^6$ cfu/100mL values, comparable to that before the BS1 event. Similar trend of variation of total bacterial concentration was also observed after the BS2 and BS3 events. During the whole study duration, total bacterial population was observed to vary between $8.0 \times 10^5$ cfu/100 mL and $3.75 \times 10^7$ cfu/100 mL, with highest value observed during the BS2 and BS3 events.

The tetracycline-resistant bacterial concentration was observed to be equal to $4.6 \times 10^4$ cfu/100 mL before the BS1 event and vary between $8.0 \times 10^3$ cfu/100 mL and $1.3 \times 10^4$ cfu/100mL for the first 34 days after the BS1 event. Concentrations of TRB were observed to increase during the BS2 and BS3 events (concentration range: $2.0 \times 10^3$ cfu/100 mL to $1.05 \times 10^6$ cfu/100 mL), with highest value observed on 46th day after the BS1 event, approximately two-log higher than the TRB concentration observed on 34th day after the BS2 event.

In general, no apparent effect of BS1 event on microbial quality of tile-drain effluent samples was observed (Figure 11-8). Only concentrations of fecal coliforms and enterococci between Groups A and B samples were observed to be statistically different with 95% confidence (p-value = 0.017 and 0.049 for fecal coliforms and enterococci, respectively). Concentrations of all other BACs were not observed to be statistically different between Group A and B samples (p-value >0.05).
Figure 11-7. Meteorological Information and Wet-weather Driven Sampling Schedules (Year 2009):
(a) Precipitation trend, biosolids application events, and sampling schedules for Plot #1 and
(b) Temperature. Bg1-2: Background sampling events; BS1, BS2, and BS3: Biosolids application events;
S1-S9: Sampling events after biosolids application
Figure 11-8. Effects of Biosolids Application Vents on (a) Fecal Indicator and (b) Tetracycline-resistance Bacteria in Biosolid-Amended Soil Samples. (Average ± one standard deviation values are shown here)

Group A- Samples between 0 and 34 days; Group B-Samples between 35 and 80 days after the first biosolids application event; R2Aw/oAB: Bacteria grown on R2A media plates in the absence of tetracycline antibiotics; TetR2A: Tetracycline-resistance bacteria grown on R2A media plates; Tet –W: Tetracycline-resistance Tet-W genes; 16SrRNA: Total genes of bacteria culturable on R2A media plates.

Note: In Figure 11-8a, all indicators are expressed as MPN/g. In Figure 11-8b, TetR2A and R2Aw/oAB are expressed as CFU/g; Tet-W and 16SrRNA are expressed as copies/g. Error bars shown for genomic concentrations represent error between two replicate PCR assays.
11.3.3 Discussion

This study observed a typical trend of initial increase followed by decrease in concentrations of bacterial fecal indicators and TRB in soil after the BS event, as also observed previously (Pourcher et al., 2007). Manure was occasionally observed to be applied on the Imlay City field buffer zone during the study. There is a possibility that the indicators in the tile drains originated from manure application.

Observed higher concentrations of TRB in Group A biosolid-amended soil samples and fecal coliforms and enterococci in Group A tile-drain effluent samples compared to their
respective Group B samples indicated that the surface spreading method appeared to influence microbial quality more compared to surface injection method for some of the parameters studied. Gottschall et al. (2009) also observed similar effect of surface spreading application method on microbial concentration in surface water samples compared to that due to surface injection method. However, for tile-drain effluent samples, they observed differently, which could be attributed to differences in nature of the study and prior pollution levels of the studied site. The present study was an observational case study with prior history of fecal contamination due to manure application versus the Gottschall et al. (2009) study which was designed to monitor fate of biosolids-associated fecal indicators and pathogens in environment after land application of dewatered biosolids on a field site without any prior fecal contamination.

Although biosolids were applied in three different stages with two stages being surface injection, no effect of BS application on concentrations of bacterial fecal indicators and TRB in tile-drain effluent samples was observed, probably due to either discontinuous flow of water between tile-drains and soil surface or short sampling duration. Calculations of rank-based Spearman correlation coefficients did not show any statistically significant relationship between soil samples and tile-drain effluent samples for any of the BACs studied (p-value > 0.05), supporting the possibility that water flow might be disconnected between tile-drains and soil surface. No information was available on connectivity of water flow between tile-drain and soil surface or depth of tile-drain from soil surface, presenting a limitation to the present study. However, it also represents a field-related issue of monitoring of BACs in infiltrated water from an undisturbed field during an observation-based study. Further, this study was terminated after 80 days of observations due to observed no increase in BAC levels; however, long-term monitoring may provide information about long-term fate of BACs in soil and tile-drain effluent samples.

Although the present study provided insights about environmental fate of BACs and its effect on environmental media, findings of this study are site-specific (loam soil; class B biosolids; surface spreading and surface injection application methods) and should be used with caution for other biosolids application events. Site-specific long-term monitoring is required to understand combined effect of field conditions and BS events on fate of bacterial fecal indicators, TRB, and Tet-W genes in soil and water.
CHAPTER 12.0

SUMMARY AND CONCLUSIONS

This project compiled information on the fate, transport, and risk presented by pathogens in land-applied biosolids into a spreadsheet based risk assessment model. The model was applied to an example field. Adenovirus was the pathogen that presented the greatest risk across the different pathways considered. The incidental ingestion of soil was found to present the highest risk of the pathways considered. Risks for adenovirus by this pathway were higher for children (9.2 in 1,000) than adults (9.6 in 10,000) due to the greater soil ingestion rate used for children. There is substantial uncertainty in these estimates with 5th to 95th percentile ranges varying over several orders of magnitude. The adenovirus estimates are based on a sample size of only 5, indicating that there is substantial uncertainty in the national occurrence distribution for this pathogen.

There is no societally acknowledged threshold for acceptable microbial risk. Nominal risks for the residential population considered here were generally found to be within or below the range of microbial risk standards for recreational water use which are 8 per 1,000 for freshwater and 1.9 per 100 for marine waters. Some exceedances of the 1:10,000 benchmark associated with annual risk form U.S. public water supplies were observed. How these risks will be perceived and whether they will be judged to be acceptable is a matter for societal discussion and reflection. Factors which might contribute to these risks being judged acceptable include 1) adenovirus, which accounts for most of the risk found here, is not associated with life threatening illnesses, 2) the highest risks were presented by ingestion of soil on the site, rather than offsite migration of pathogens. However, exposure to biosolids may be considered a risk imposed by outsiders to a community rather than a voluntarily accepted risk which would tend to decrease the acceptability of this risk.

This project conducted field monitoring to address knowledge gaps on the behavior of microorganisms from land applied biosolids during wet weather events. Based on the results observed in Site A (controlled site with lysimeters and a rainfall simulator), no indigenous adenoviruses or somatic phage were detected in leachate samples following the application of biosolids and simulated rainfall on a sandy-loam soil planted to orchard grass, switchgrass or maize. The microbial tracer (P-22) removal rates obtained in this study ranged from 1.8 log/m to complete removal. Early breakthrough of P-22 indicates preferential flow plays a critical role in terms of virus transport in the subsurface. The movement of anionic tracer cannot predict the movement of viruses and this may be due to differences in sorption behavior and physical size. Somatic phage and P-22 were detected in ponded surface water for at least two weeks, which indicates that immediate runoff after land application can be a considerable threat to water quality.

Based on the results observed in Site B (case study of biosolids application followed by wet weather conditions), concentrations of bacterial fecal indicators, TRB, and Tet-W genes in soil and tile-drain effluent samples were observed to increase immediately after the BS event followed by subsequent decrease over time, indicating an initial influence of BS application on
microbial quality of environmental samples. However, the BS event did not appear to contribute significantly to the microbial quality of environmental samples, under the conditions studied.

The field monitoring did not measure detectable quantities of pathogens after transport through several feet of soil in the field. This tends to confirm the model predictions that groundwater exposures will be modest. However, the field monitoring did quantify some desorption of pathogens and indicators into ponded surface water, suggesting that runoff from biosolids amended fields may have trace amounts of pathogens. This desorption percentage was used in the risk assessment model and as described above the risks associated with recreational use of waterbodies impacted by runoff from a biosolids amended field did not exceed existing recreational water use risk levels. The field monitoring documented the persistence of a qPCR signal for adenovirus over several weeks. The viability of the adenovirus has not been established.

Based on these results, the following recommendations are made:

1. Additional research on pathogen occurrence in biosolids is warranted. Additional data for adenovirus is a critical data need as adenovirus accounted for most of the risk found here yet only 5 observations of adenovirus concentrations were available. *Cryptosporidium* and *Giardia* occurrence are also high priority research needs, as they presented the next highest risks for the soil ingestion pathway.

2. Additional data on the persistence of viable and infectious agents in land applied biosolids over time is also a high priority research need. The risks estimated here for soil ingestion were based on first order decay over a 31-day period. As deviations from first order decay are commonly observed, additional data on attenuation rates over realistic site access restriction time periods would improve the risk assessment. Data for adenovirus, *Cryptosporidium*, and *Giardia* would again be the highest priorities.

3. Nominal estimates of risks are neither completely negligible nor in excess of microbial risks tolerated in another context, that of surface water recreation. In such cases one might search for reasonable ways to mitigate risks. Further consideration of site restrictions and setback distances using the SMART Biosolids model is planned as part of an addendum to this final report. As additional information on pathogen occurrence and persistence in biosolids become available such efforts should be repeated. The SMART Biosolids model could be updated with the additional information and used for such future assessments.

This project is working on several efforts that are not documented in this report. As noted in item #3 above, the project will explore additional exposure scenarios, including a set of scenarios of concern that were identified through a survey of biosolids professionals. The modeling results will be used to prioritize the scenarios of concern and identify appropriate program management practices for managing the high priority risks. These results will be summarized in an addendum to this report.

Recognizing that programmatic changes must be informed by the knowledge of practicing professionals, the project has also developed and implemented interactive workshops in which input from land application practitioners has been collected through facilitated discussions and structured surveys. The input from these practitioners will be summarized in a separate paper.

In concluding this report, one should note that the SMART Biosolids model developed here is not intended as a definitive risk assessment but rather as an organizing framework for the
application of quantitative microbial risk assessment to biosolids. While the current version of
the model included with this report represents the research team’s best effort to compile
information from a broad range of sources, it necessarily remains a snapshot of current
knowledge in the field. The use of a spreadsheet format allows for users to edit parameters as
appropriate to different sites and to update and extend the tool as additional information becomes
available. Thus, the model may provide a framework for organizing future information on land
application or even microbial risk assessment in general. Information such as dose response
parameters and environmental attenuation rates are widely used in quantitative microbial risk
assessment, making the information compiled in this model potentially useful in domains other
than land application, such as risk assessment of land-applied manures, environmental transport
of human wastes in areas lacking appropriate sanitation, and dispersion of intentionally released
pathogens.
## A.1 Dose-Response Models for Biosolids-Associated Bacteria

Table A-1. Dose-Response Models for Different Biosolids-Associated Bacteria.

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>D-R Type</th>
<th>DR-Type</th>
<th>Mean</th>
<th>UF</th>
<th>UB</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cryptosporidum</td>
<td>1.00E+00</td>
<td>4.19E-03</td>
<td>1.81E+00</td>
<td>95\textsuperscript{th}: 7.57E-03</td>
<td>Haas et al. (1999)</td>
<td></td>
</tr>
<tr>
<td>Cyclosporidium</td>
<td>1.00E+00</td>
<td>2.19E-02</td>
<td>3.16E+00</td>
<td>90\textsuperscript{th}: 6.93E-02</td>
<td>Chacin-Bonilla (2010)</td>
<td></td>
</tr>
<tr>
<td>Entamoeba histolytica</td>
<td>1.00E+00</td>
<td>4.90E-02</td>
<td>1.41E+00</td>
<td>90\textsuperscript{th}: 6.93E-02</td>
<td>Asano et al. (2007)</td>
<td></td>
</tr>
<tr>
<td>Giardia lamblia</td>
<td>1.00E+00</td>
<td>2.00E-02</td>
<td>2.84E-02</td>
<td>95\textsuperscript{th}: 5.66E-02</td>
<td>Teunis et al. (1996); Haas et al (1999)</td>
<td></td>
</tr>
<tr>
<td>Microsporidia</td>
<td>0.00E+00</td>
<td>0.00E+00</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Campylobacter jejuni</td>
<td>2.00E+00</td>
<td>1.91E-02</td>
<td>2.32E+00</td>
<td>95\textsuperscript{th}: 4.43E-02</td>
<td>Haas et al. (1999); Teunis et al. (1996)</td>
<td></td>
</tr>
<tr>
<td>Clostridium spp.</td>
<td>1.00E+00</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>E.coli O157</td>
<td>2.00E+00</td>
<td>1.00E-07</td>
<td>1.00E+01</td>
<td>90\textsuperscript{th}: 1.00E-06</td>
<td>Haas et al. (1999)</td>
<td></td>
</tr>
<tr>
<td>Helicobacter</td>
<td>1.00E+00</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Clapham et al. (2004)</td>
</tr>
<tr>
<td>Listeria</td>
<td>1.00E+00</td>
<td>1.76E-08</td>
<td>1.08E+01</td>
<td>95\textsuperscript{th}: 1.91E-07</td>
<td>Smith et al. (2008)</td>
<td></td>
</tr>
<tr>
<td>Salmonella spp.</td>
<td>2.00E+00</td>
<td>2.71E-06</td>
<td>1.14E+02</td>
<td>90\textsuperscript{th}: 3.09E-04</td>
<td>Soller et al. (2004)</td>
<td></td>
</tr>
<tr>
<td>Shigella spp.</td>
<td>2.00E+00</td>
<td>4.90E-03</td>
<td>1.00E+01</td>
<td>90\textsuperscript{th}: 4.90E-02</td>
<td>Haas et al. (1999); Soller et al. (2004)</td>
<td></td>
</tr>
<tr>
<td>Vibrio cholera</td>
<td>2.00E+00</td>
<td>1.54E-02</td>
<td>2.73E+00</td>
<td>95\textsuperscript{th}: 4.21E-02</td>
<td>Haas et al. (1999)</td>
<td></td>
</tr>
<tr>
<td>Yersinia spp.</td>
<td>1.00E+00</td>
<td>1.02E-03</td>
<td>1.00E+01</td>
<td>90\textsuperscript{th}: 1.02E-02</td>
<td>Lathem (2005)</td>
<td></td>
</tr>
<tr>
<td>Adenovirus</td>
<td>1.00E+00</td>
<td>4.17E-01</td>
<td></td>
<td>90\textsuperscript{th}: 1E+00</td>
<td>Haas et al. (1999)</td>
<td></td>
</tr>
<tr>
<td>Ascaris</td>
<td>1.00E+00</td>
<td>9.49E-02</td>
<td>1.00E+01</td>
<td>90\textsuperscript{th}: 1E+00</td>
<td>Mara and Sleigh (2010)</td>
<td></td>
</tr>
<tr>
<td>Coliphage (Somatic)</td>
<td>0.00E+00</td>
<td>0.00E+00</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Enteroviruses</td>
<td>1.00E+00</td>
<td>2.00E-03</td>
<td></td>
<td></td>
<td></td>
<td>Regli et al. (1991) (for Echovirus12: ingestion route); For inhalation: Tanner et al. (2008) ; Brooks et al. (2005a,b) ; Haas et al. (1999) (using Coxsackievirus B5 dose-response model)</td>
</tr>
<tr>
<td>Hepatitis A virus</td>
<td>1.00E+00</td>
<td>5.49E-01</td>
<td></td>
<td>90\textsuperscript{th}: 19E+00</td>
<td>Haas et al. (1999)</td>
<td></td>
</tr>
<tr>
<td>Hepatitis E</td>
<td>1.00E+00</td>
<td>1.30E-02</td>
<td>1.00E+01</td>
<td>90\textsuperscript{th}: 1.30E-01</td>
<td>Bouwknecht et al. (2009)</td>
<td></td>
</tr>
<tr>
<td>Astrovirus</td>
<td>1.00E+00</td>
<td>6.06E-07</td>
<td>1.00E+01</td>
<td>90\textsuperscript{th}: 6.06E-06</td>
<td>Commission on Life Sciences et</td>
<td></td>
</tr>
<tr>
<td>Pathogen</td>
<td>D-R Type DR-Type (“1” for Exp, “2” for Beta, “0” for Not Available)</td>
<td>Mean</td>
<td>UF</td>
<td>UB</td>
<td>Reference</td>
<td></td>
</tr>
<tr>
<td>----------------</td>
<td>-----------------------------------------------------------------</td>
<td>--------</td>
<td>--------</td>
<td>--------</td>
<td>----------------------------</td>
<td></td>
</tr>
<tr>
<td>Legionella</td>
<td>1.00E+00 6.00E-02</td>
<td>1.00E+01</td>
<td>90(^{th}): 6.00E-01</td>
<td>Armstrong and Haas (2007)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Norovirus</td>
<td>1.00E+00 2.78E-04</td>
<td></td>
<td></td>
<td></td>
<td>Teunis et al. (2008)</td>
<td></td>
</tr>
<tr>
<td>Rotavirus</td>
<td>1.00E+00 6.19E-01</td>
<td></td>
<td></td>
<td>90(^{th}): 1E+00</td>
<td>Regli et al. (1991); Haas et al (1999)</td>
<td></td>
</tr>
<tr>
<td>Toxoplasma</td>
<td>0.00E+00 0.00E+00</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Fecal coliforms 0.00E+00 0.00E+00

E. coli 0.00E+00 0.00E+00

Enterococci 0.00E+00 0.00E+00

### A.2 Default Values

**Table A-2. Default Values for Inhalation Exposure Route.**

<table>
<thead>
<tr>
<th>Exposed Subpopulation</th>
<th>Exposure Rate (m³/day)*</th>
<th>Exposure Duration (h/day)</th>
<th>Exposure Duration per Application Period (days)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Residential-adult</td>
<td>19.92</td>
<td>24</td>
<td>3</td>
</tr>
<tr>
<td>Residential-child</td>
<td>19.92</td>
<td>24</td>
<td>3</td>
</tr>
<tr>
<td>Occupational</td>
<td>19.92</td>
<td>8</td>
<td>3</td>
</tr>
</tbody>
</table>


**Table A-3. Default Values for Direct Ingestion Exposure Route.**

<table>
<thead>
<tr>
<th>Exposed Subpopulation</th>
<th>Exposure Rate (mg/day) *</th>
<th>Exposure Duration (h/day)</th>
<th>Exposure Duration per Application Period (days)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Residential-adult</td>
<td>50</td>
<td>Calculated from the AirModel</td>
<td>3</td>
</tr>
<tr>
<td>Residential-child</td>
<td>480</td>
<td>Calculated from the AirModel</td>
<td>3</td>
</tr>
<tr>
<td>Occupational</td>
<td>50</td>
<td>8</td>
<td>3</td>
</tr>
</tbody>
</table>

* U.S. EPA (1997) for all values except for exposure duration values for residential population
### Table A-4. Default Values for Ingestion of Ground Water Exposure Route.

<table>
<thead>
<tr>
<th>Exposed Subpopulation</th>
<th>Exposure Rate (L/d)*</th>
<th>Exposure Duration (h/day)</th>
<th>Exposure Duration per Application Period (days)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Residential-adult</td>
<td>2</td>
<td>24</td>
<td>1</td>
</tr>
<tr>
<td>Residential-child</td>
<td>2</td>
<td>24</td>
<td>1</td>
</tr>
<tr>
<td>Occupational</td>
<td>2</td>
<td>24</td>
<td>3</td>
</tr>
</tbody>
</table>


### Table A-5. Default Values for Ingestion of Surface Water Exposure Route.

<table>
<thead>
<tr>
<th>Exposed Subpopulation</th>
<th>Exposure Rate (L/d)*</th>
<th>Exposure Duration (h/day)</th>
<th>Exposure Duration per Application Period (days)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Residential-adult</td>
<td>0.1</td>
<td>24</td>
<td>1</td>
</tr>
<tr>
<td>Residential-child</td>
<td>0.1</td>
<td>24</td>
<td>1</td>
</tr>
<tr>
<td>Occupational</td>
<td>0.1</td>
<td>24</td>
<td>3</td>
</tr>
</tbody>
</table>


### A.3 Infection and Incidence Indexes

### Table A-6. Indexes for Pathogen-Wise Infections and Incidences of Different Diseases.

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>Infection Index</th>
<th>Incidence Index</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Respiratory infection</td>
<td>GI illness</td>
</tr>
<tr>
<td>Cryptosporidium</td>
<td>1*</td>
<td>1*</td>
</tr>
<tr>
<td>Cyclosporidia</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Entamoeba histolytica</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Giardia lamblia</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Microsporidia</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Campylobacter jejuni</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Clostridium spp.</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>E.coli O157</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>helicobacter</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Listeria</td>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>
### Pathogen Infection Index Incidence Index

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>Infection Index</th>
<th>Incidence Index</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Respiratory</td>
<td>GI illness</td>
</tr>
<tr>
<td>Salmonella spp.</td>
<td>1 1 0</td>
<td>2 2 0</td>
</tr>
<tr>
<td>Shigella spp.</td>
<td>1 1 0</td>
<td>2 2 0</td>
</tr>
<tr>
<td>Vibrio cholerae</td>
<td>1 1 0</td>
<td>2 2 0</td>
</tr>
<tr>
<td>Yersinia spp.</td>
<td>1 1 0</td>
<td>2 2 0</td>
</tr>
<tr>
<td>Adenovirus</td>
<td>1 1 0</td>
<td>1 0 0</td>
</tr>
<tr>
<td>Ascaris</td>
<td>1 1 0</td>
<td>1 1 0</td>
</tr>
<tr>
<td>Colipage</td>
<td>0 0 0</td>
<td>0 0 0</td>
</tr>
<tr>
<td>Enteroviruses</td>
<td>1 1 0</td>
<td>2 1 0</td>
</tr>
<tr>
<td>Hepatitis A virus</td>
<td>1 1 0</td>
<td>1 1 0</td>
</tr>
<tr>
<td>Hepatitis E</td>
<td>1 1 0</td>
<td>1 1 0</td>
</tr>
<tr>
<td>Astrovirus</td>
<td>1 1 0</td>
<td>1 1 0</td>
</tr>
<tr>
<td>Legionella</td>
<td>1 0 0</td>
<td>1 0 0</td>
</tr>
<tr>
<td>Norovirus</td>
<td>1 1 0</td>
<td>1 1 0</td>
</tr>
<tr>
<td>Rotavirus</td>
<td>1 1 0</td>
<td>1 1 0</td>
</tr>
<tr>
<td>Toxoplasma</td>
<td>1 1 0</td>
<td>1 1 0</td>
</tr>
<tr>
<td>Fecal coliforms</td>
<td>0 0 0</td>
<td>0 0 0</td>
</tr>
<tr>
<td>E. coli</td>
<td>0 0 0</td>
<td>0 0 0</td>
</tr>
<tr>
<td>Enterococci</td>
<td>0 0 0</td>
<td>0 0 0</td>
</tr>
</tbody>
</table>

*Value of “1” indicates possibility of getting an infection from a particular exposure route and value of “0” indicates no possibility of getting an infection from a particular exposure route. **Value of “0” indicates no relation with any disease, value of “1” indicates possible relation to temporarily debilitating disease, and value of “2” indicates possible relationship to a life-threatening disease.

### A.4 Morbidity Rate Values
Table A-7. Values of Morbidity Rates ($\eta_{morb}$),
Indicating the Development of Illness Following Infection for Different Microorganisms.
(A default value of 1.0 is assumed for all pathogens and 0 value for indicators)

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>GI Illness</th>
<th>Respiratory Illness</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cryptosporidium</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Cyclosporidia</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Entamoeba histolytica</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Giardia lamblia</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Microsporidia</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Campylobacter jejuni</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Clostridium spp.</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>E.coli O157</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>helicobacter</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Listeria</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Salmonella spp.</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Shigella spp.</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Vibrio cholerae</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Yersinia spp.</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Adenovirus</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Ascaris</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Enteroviruses</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Hepatitis A virus</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Hepatitis E</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Astrovirus</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Legionella</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Norovirus</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Rotavirus</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Toxoplasma</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Fecal coliforms, E.coli, enterococci, coliphage</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>
## A.5 Pathogen Occurrence Values

Table A-8. Compilation of Occurrence by Pathogen. Items in Red are Data Gaps.

<table>
<thead>
<tr>
<th>Pathogen</th>
<th>Distribution Type (&quot;1&quot; for Normal,&quot;2&quot; for Uniform, &quot;0&quot; for not applicable)</th>
<th>Mean</th>
<th>Standard Deviation</th>
<th>Minimum</th>
<th>Maximum</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cryptosporidium</td>
<td>2.00E+00</td>
<td>2.80E+01</td>
<td>1.90E+01</td>
<td>1.30E+01</td>
<td>6.40E+01</td>
<td>Guzman et al. (2007)</td>
</tr>
<tr>
<td>Cyclosporidia</td>
<td>1.00E+00</td>
<td>1.00E-18</td>
<td>2.00E-19</td>
<td>1.00E-20</td>
<td>1.00E-17</td>
<td></td>
</tr>
<tr>
<td>Entamoeba histolytica</td>
<td>1.00E+00</td>
<td>1.00E-18</td>
<td>2.00E-19</td>
<td>1.00E-20</td>
<td>1.00E-17</td>
<td></td>
</tr>
<tr>
<td>Giardia lamblia</td>
<td>2.00E+00</td>
<td>1.28E+01</td>
<td>2.00E-19</td>
<td>2.50E-13</td>
<td>2.82E+01</td>
<td>Chauret et al. (1999)</td>
</tr>
<tr>
<td>Microsporidia</td>
<td>1.00E+00</td>
<td>1.00E-18</td>
<td>2.00E-19</td>
<td>1.00E-20</td>
<td>1.00E-17</td>
<td></td>
</tr>
<tr>
<td>Campylobacter jejuni</td>
<td>2.00E+00</td>
<td>&lt;1.00E+00</td>
<td>2.00E-01</td>
<td>1.00E-20</td>
<td>1.00E+01</td>
<td>Pepper et al. (2010)</td>
</tr>
<tr>
<td>Clostridium spp.</td>
<td>2.00E+00</td>
<td>4.16E+07</td>
<td>1.86E+08</td>
<td>3.98E+04</td>
<td>8.53E+08</td>
<td>Pepper et al. (2010)</td>
</tr>
<tr>
<td>E.coli O157</td>
<td>2.00E+00</td>
<td>&lt;1.00E+00</td>
<td>2.00E-01</td>
<td>1.00E-20</td>
<td>1.00E+01</td>
<td>Pepper et al. (2010)</td>
</tr>
<tr>
<td>Helicobacter</td>
<td>1.00E+00</td>
<td>1.00E-18</td>
<td>2.00E-19</td>
<td>1.00E-20</td>
<td>1.00E-17</td>
<td></td>
</tr>
<tr>
<td>Listeria</td>
<td>1.00E+00</td>
<td>1.00E-18</td>
<td>2.00E-19</td>
<td>1.00E-20</td>
<td>1.00E-17</td>
<td></td>
</tr>
<tr>
<td>Salmonella spp.</td>
<td>2.00E+00</td>
<td>8.10E-01</td>
<td>2.60E+00</td>
<td>2.50E-21</td>
<td>3.35E-01</td>
<td>Pepper et al. (2010)</td>
</tr>
<tr>
<td>Shigella spp.</td>
<td>2.00E+00</td>
<td>4.49E+00</td>
<td>5.37E+01</td>
<td>1.00E-20</td>
<td>2.00E+00</td>
<td>Pepper et al. (2010)</td>
</tr>
<tr>
<td>Vibrio cholera</td>
<td>1.00E+00</td>
<td>1.00E-18</td>
<td>2.00E-19</td>
<td>1.00E-20</td>
<td>1.00E-17</td>
<td></td>
</tr>
<tr>
<td>Yersinia spp.</td>
<td>1.00E+00</td>
<td>1.00E-18</td>
<td>2.00E-19</td>
<td>1.00E-20</td>
<td>1.00E-17</td>
<td></td>
</tr>
<tr>
<td>Adenovirus</td>
<td>2.00E+00</td>
<td>1.76E+00</td>
<td>1.33E+01</td>
<td>3.70E+00</td>
<td>2.26E+01</td>
<td>Pepper et al. (2010)</td>
</tr>
<tr>
<td>Ascaris</td>
<td>2.00E+00</td>
<td>&lt;2.50E-01</td>
<td>5.00E-02</td>
<td>2.50E-21</td>
<td>2.50E+00</td>
<td>Pepper et al. (2010)</td>
</tr>
<tr>
<td>Coliphage (Somatic)</td>
<td>2.00E+00</td>
<td>8.40E+08</td>
<td>3.38E+12</td>
<td>1.00E-20</td>
<td>1.92E+07</td>
<td>Pepper et al. (2010)</td>
</tr>
<tr>
<td>Enteroviruses</td>
<td>2.00E+00</td>
<td>1.05E-01</td>
<td>2.00E-01</td>
<td>1.38E-02</td>
<td>8.00E-01</td>
<td>Pepper et al. (2010)</td>
</tr>
<tr>
<td>Hepatitis A virus</td>
<td>1.00E+00</td>
<td>1.00E-18</td>
<td>2.00E-19</td>
<td>1.00E-20</td>
<td>1.00E-17</td>
<td></td>
</tr>
<tr>
<td>Hepatitis E</td>
<td>1.00E+00</td>
<td>1.00E-18</td>
<td>2.00E-19</td>
<td>1.00E-20</td>
<td>1.00E-17</td>
<td></td>
</tr>
<tr>
<td>Astrovirus</td>
<td>1.00E+00</td>
<td>1.00E-18</td>
<td>2.00E-19</td>
<td>1.00E-20</td>
<td>1.00E-17</td>
<td></td>
</tr>
<tr>
<td>Legionella</td>
<td>1.00E+00</td>
<td>1.00E-18</td>
<td>2.00E-19</td>
<td>1.00E-20</td>
<td>1.00E-17</td>
<td></td>
</tr>
<tr>
<td>Norovirus</td>
<td>1.00E+00</td>
<td>1.00E-18</td>
<td>2.00E-19</td>
<td>1.00E-20</td>
<td>1.00E-17</td>
<td></td>
</tr>
<tr>
<td>Rotavirus</td>
<td>1.00E+00</td>
<td>1.00E-18</td>
<td>2.00E-19</td>
<td>1.00E-20</td>
<td>1.00E-17</td>
<td></td>
</tr>
<tr>
<td>Toxoplasma</td>
<td>1.00E+00</td>
<td>1.00E-18</td>
<td>2.00E-19</td>
<td>1.00E-20</td>
<td>1.00E-17</td>
<td></td>
</tr>
<tr>
<td>Fecal coliforms</td>
<td>2.00E+00</td>
<td>1.27E+07</td>
<td>3.62E+07</td>
<td>5.17E+01</td>
<td>1.58E+08</td>
<td>Pepper et al. (2010)</td>
</tr>
<tr>
<td>Enterococci</td>
<td>2.00E+00</td>
<td>3.16E+03</td>
<td>2.00E+01</td>
<td>6.05E+00</td>
<td>1.12E+06</td>
<td>Wong et al. (2010)</td>
</tr>
</tbody>
</table>

1 Densities per 10 g of DM; All initial values have been divided by 10.
2 Cake Product -Organisms per 100g of wet sludge; Counts corrected to account for dewatering; All initial value have been divided by 100.
3 This is the detection limit
4 All samples were below detection (<1).
5 Some samples were below detection (<1); MLE values used.
6 Organism per 4g; Minimum value was below detection (<1); All initial values have been divided by 4.
7 Utilized values of Fecal streptococcus; Minimum value was below detection (<1).
### A.6 Macro for SMART Biosolids

**Macro for Sheet.24.RiskCal**

'The "Riskfunc" calculates risk using exponential model relationship

Public Function riskfunc(dose, r)
    riskfunc = 1 - Exp(-r * dose) 'Without low-dose approximation
End Function

'The "Riskfunc1" calculates risk using exponential (kind=1) or beta-poisson (kind=2) dose-response model

Public Function riskfunc1(kind, dose, r, a, b)
    If kind = 1 Then
        'riskfunc1 = r * dose 'An expression for low-dose approximation case
        riskfunc1 = 1 - Exp(-r * dose) 'Without low-dose approximation
    ElseIf kind = 2 Then
        'riskfunc1 = a * dose / b 'An expression for low-dose approximation case
        riskfunc1 = 1 - Excel.WorksheetFunction.Power((1 + (dose / b)), (-a)) 'Without low-dose approximation
    End If
End Function

Function Stat(data() As Single, datastat() As Single, Iteration As Long)

    Call Sort1(data, Iteration)
    datastat(1) = Mean(Iteration, data)
    datastat(2) = StdDev(Iteration, data)
    datastat(3) = Percentile(data, 0.05, Iteration)
    datastat(4) = Percentile(data, 0.5, Iteration)
datastat(5) = Percentile(data, 0.95, Iteration)
End Function

'************************************************************************
'************************************************************************
Function Mean(k As Long, arr() As Single)
    Dim Sum As Single
    Dim i As Integer

    Sum = 0
    For i = 1 To k
        Sum = Sum + arr(i)
    Next i

    Mean = Sum / k
End Function

'************************************************************************
'************************************************************************
Function StdDev(k As Long, arr() As Single)
    Dim i As Integer
    Dim avg As Single, SumSq As Single
avg = Mean(k, arr)
For i = 1 To k
    SumSq = SumSq + (arr(i) - avg)^2
Next i

StdDev = Sqr(SumSq / (k - 1))

End Function

'***********************************************************************
'* Return random numbers from Normal Distribution *
'***********************************************************************

Function Normal(MeanX, SdX)
Dim x As Double
Dim fac As Double, r As Double, V1 As Double, V2 As Double

x = gauss * SdX + MeanX
Normal = x

End Function

'***********************************************************************
'* Return random numbers from Standard Normal Distribution *
'***********************************************************************

Function gauss()
Dim fac As Double, r As Double, V1 As Double, V2 As Double

10   V1 = 2 * Rnd - 1
    V2 = 2 * Rnd - 1
    r = V1 ^ 2 + V2 ^ 2
    If (r >= 1) Then GoTo 10
    fac = Sqr(-2 * Log(r) / r)
    gauss = V2 * fac
End Function

'***********************************************************************
'* Return random numbers from uniform Distribution  *
'***********************************************************************


Function Uni(MinX, MaxX)
'Dim x As Double
Dim x As Single

    x = (MaxX - MinX) * Rnd + MinX

    Uni = x
End Function

Function Percentile(arr() As Single, k As Single, m As Long)

    Dim i As Long, n As Long, j1 As Long

    'N = UBound(arr)
    n = m
Call Sort1(arr, m)

x = (n - 1) * k + 1

For i = 1 To n
    If i > x Then j1 = i - 1: i = n + 1
Next i

Percentile = arr(j1) + (x - j1) * (arr(j1 + 1) - arr(j1))

End Function

Sub Sort1(arr() As Single, m As Long)

    Dim Temp As Single
    Dim i As Long
    Dim j As Long

    For j = 2 To m
        'MsgBox "Hello"
        Temp = arr(j)
        For i = j - 1 To 1 Step -1
            If (arr(i) <= Temp) Then GoTo 10
            arr(i + 1) = arr(i)
        Next i
        arr(i + 1) = arr(i)
        Next i
        i = 0

Site Specific Risk Assessment Tools for Land Applied Biosolids A-11
10   arr(i + 1) = Temp
    Next j
End Sub

Sub RiskCal()
'Probability of rain is assumed to be 100% (See Cell C5; Inputdata )

'PARAMETERS INITILIZATION

'Activate RiskOutput sheet
Sheets(RiskOutput).Activate

Dim Starttime, Stoptime
Starttime = Time 'Recording stop time
Sheets(RiskOutput).Cells(1, 9).Value = Starttime

Dim i As Integer, j As Integer, j1 As Integer, k As Integer, m As Integer, y As Integer, restore As Integer
Dim Iteration As Long, i1 As Long 'Determine the number of iterations

Dim kind As Integer  'An index for dose-response model type: Value=1 for exponential and 2 for beta-poisson dose-response models

ReDim datastat(5) As Single 'Mean, standard deviation, 5th percentile, 50th percentile, and 95th percentile values from cell 1 to 5

'Pathogen info
Dim Number As Double, n As Double 'Number of pathogens
Dim PathogenInterest As Integer 'Getting ID of pathogen of interest from the InputData sheet
Dim UChoice As Integer 'Getting user choice for conducting uncertainty analysis for pathogen of interest (Choice: 1) or all pathogens (Choice:0)
Dim UPathogen(28, 1) As Integer 'An array to indicate user choice for selecting a pathogen of interest for uncertainty analysis
ReDim Pmatrix(28, 40) 'Dose-response data matrix
ReDim PInMatrix(28, 3) 'Pathogen infection matrix, decides if infection occurs from a particular exposure route; j=1 for respiratory, j=2 for gastroenteritis, and j=3 for ocular infection
ReDim PIncidence(28, 3) 'Pathogen incidence matrix decides if minor or major illness happens; j=1 for respiratory, j=2 for gastroenteritis, and j=3 for ocular infection; Value =1 for minor and 2 for major illness
ReDim Pdecay(28, 4) 'Pathogen decay constant: Column 1-For suspended pathogens in water; Column 2- For bioaerosols; Column 3-For soil-sorbed pathogens (ALL UNITS ARE: 1/DAY)
ReDim Pdist(28, 10, 20) 'Distribution matrix for k= 1 for pathogen conc., 2 for release parameter, 3 for decay in air, 4 for decay in suspension,
'k=5 for liquid to liquid-solid interface mass transfer coefficient, k=6 for liquid to air-liquid interface mass transfer coefficient, k=7 for pathogen radius,
'k=8 fr equilibrium partitioning coefficient between biosolids and groundwater, k=9 for first dose-response model parameter ("r" or "alpha"), k=10 for second dose-response model parameter ("beta")
ReDim PSim(28, 5000, 20) 'Simulated distribution matrix for k= 1 to 20 as discussed for "Pdist" matrix
ReDim Soildist(12, 7, 7) 'Distribution matrix for six soil-related parameters (k=1 for hydraulic conductivity, 2 for pore-size index, 3 for residual moisture content, 4 for % sand, 5 for %clay, 6 for % silt,
'and 7 for saturated water content)
ReDim SoilSim(12, 5000, 7) 'Simulated distribution matrix for six soil-related parameters (k=1 for hydraulic conductivity, 2 for pore-size index, 3 for moisture content, 4 for % sand, 5 for %clay, 6 for % silt,
'and 7 for saturated water content)
ReDim Airdist(5, 3) 'Distribution matrix for three air-related parameters (j=1 for aerosolization efficiency, 2 for mechanical stress, and 3 for cabin filtration efficiency)
ReDim AirSim(5000, 3) 'Simulated distribution matrix for three air-related parameters (j=1 for aerosolization efficiency, 2 for mechanical stress, and 3 for cabin filtration efficiency)
ReDim Attackrate(28, 3) ' First column: Attack rate for GI illness from infection; Second column: Attack rate for inhalation based illness from infection

Dim TRain As Integer ' Time to storm after biosolids application

Dim RTRain As Double 'Return period of a storm event (years)

Dim pRain As Double 'Daily probability of happening of a rainfall event (between 0 and 1)

ReDim TIng(2, 2) 'Time elapsed before ingestion of either soil-biosolids composite or pond water; unit: 1/day

'Air model

ReDim Pconc(8, 30) 'Pathogen environmental conc. at receptor for a single iteration

ReDim InhExp(4, 4) ' For row=1 to 4 for field worker, truck driver, residential adult and residential children

ReDim InhDose(28, 5000, 4)

ReDim InhDInfRisk(28, 5000, 4) 'Daily risk of infection

ReDim InhDIllRisk(28, 5000, 4) 'Daily risk of illness

ReDim InhApInfRisk(28, 5000, 4) 'Risk of infection per application period

ReDim InhApIllRisk(28, 5000, 4) 'Risk of illness per application period

ReDim InhInitialRisk(28, 5000, 4) 'Initial inhalation risk of infection

ReDim InhInitialIllRisk(28, 5000, 4) 'Initial ingestion risk of illness

ReDim InhCumRisk(28, 5000, 4) 'Cumulative risk of infection during periodic exposure

ReDim InhCumIllRisk(28, 5000, 4) 'Cumulative risk of illness during periodic exposure

ReDim InhApInfMinorRisk(28, 5000, 4) ' Minor inhalation risk of infection per application period

ReDim InhApInfMajorRisk(28, 5000, 4) ' Major inhalation risk of infection per application period

ReDim InhApIllMinorRisk(28, 5000, 4) ' Minor inhalation risk of illness per application period

ReDim InhApIllMajorRisk(28, 5000, 4) ' Major inhalation risk of illness per application period

ReDim AirApRiskstat(28, 5, 4) As Single '28 pathogens * 5 statistics * 4 population for risk of illness

ReDim AirApIllMajorRiskstat(28, 5, 4) As Single '28 pathogens * 5 statistics * 4 population for risk of major illness
ReDim AirApIllMinorRiskstat(28, 5, 4) As Single '28 pathogens * 5 statistics * 4 population for risk of minor illness

ReDim NoRespRisk(4, 2, 5000) 'Matrix of no respiratory risk of illness (i=1 to 4 for four subpopulation and j=1 to 2 for minor and major types of risk

ReDim CumRespRisk(4, 2, 5000) 'Matrix of respiratory risk of illness (i=1 to 4 for four subpopulation and j=1 to 2 for minor and major types of risk

ReDim CumRespRiskstat(4, 2, 5) 'Matrix of stats for respiratory risk of illness (i=1 to 4 for four subpopulation; j=1 to 2 for minor and major types of risk; k=1 to 5 for five-point summary statistics

Dim Airtemp(4, 5000) As Single, Airtempminor(4, 5000) As Single, Airtempmajor(4, 5000) As Single 'temp for calculation

'SWmodel

ReDim IngSWExp(2, 4)

ReDim IngSWDose(28, 5000, 2) 'Single pathogen dose

ReDim IngSWInitialRisk(28, 5000, 2) 'Initial ingestion risk of infection

ReDim IngSWInitialIllRisk(28, 5000, 2) 'Initial ingestion risk of illness

ReDim IngSWCumRisk(28, 5000, 2) 'Cumulative risk of infection during periodic exposure

ReDim IngSWCumIllRisk(28, 5000, 2) 'Cumulative risk of illness during periodic exposure

ReDim IngSWApInfRisk(28, 5000, 2) 'Ingestion risk of infection per application period

ReDim IngSWApIllRisk(28, 5000, 2) 'Ingestion risk of illness per application period

ReDim IngSWApInfMinorRisk(28, 5000, 2) ' Minor SW GI risk of infection per application period

ReDim IngSWApInfMajorRisk(28, 5000, 2) ' Major SW GI risk of infection per application period

ReDim IngSWApIllMinorRisk(28, 5000, 2) ' Minor SW GI risk of illness per application period

ReDim IngSWApIllMajorRisk(28, 5000, 2) ' Major SW GI risk of illness per application period

ReDim SWApRiskstat(28, 5, 2) As Single '28 pathogens * 5 statistics * 2 population for risk of illness

ReDim SWApIllMajorRiskstat(28, 5, 2) As Single '28 pathogens * 5 statistics * 2 population for risk of major illness
ReDim SWApIllMinorRiskstat(28, 5, 2) As Single '28 pathogens * 5 statistics * 2 population for risk of minor illness

ReDim NoSWGIRisk(2, 2, 5000) 'Matrix of no SW GI risk of illness (i=1 to 2 for two residential subpopulations and j=1 to 2 for minor and major types of risk

ReDim CumSWGIRisk(2, 2, 5000) 'Matrix of SW GI risk of illness (i=1 to 2 for two residential subpopulations and j=1 to 2 for minor and major types of risk

ReDim CumSWGIRiskstat(2, 2, 5) 'Matrix of stats for gastroenteritis risk of illness (i=1 to 2 for residential adults and children; j=1 to 2 for minor and major types of risk; k=1 to 5 for five-point summary statistics

Dim SWtemp(2, 5000) As Single, SWtempminor(2, 5000) As Single, SWtempmajor(2, 5000) As Single 'temp for calculation

'Soilmodel

ReDim IngSoilExp(3, 4)

ReDim IngSoilDose(28, 5000, 3) 'Single pathogen dose

ReDim IngSoilInitialRisk(28, 5000, 3) 'Initial ingestion risk of infection

ReDim IngSoilInitialIllRisk(28, 5000, 3) 'Initial ingestion risk of illness

ReDim IngSoilCumRisk(28, 5000, 3) 'Cumulative risk of infection during periodic exposure

ReDim IngSoilCumIllRisk(28, 5000, 3) 'Cumulative risk of illness during periodic exposure

ReDim IngSoilApInfRisk(28, 5000, 3) 'Ingestion risk of infection per application period

ReDim IngSoilApIllRisk(28, 5000, 3) 'Ingestion risk of illness per application period

ReDim IngSoilApInfMinorRisk(28, 5000, 3) 'Minor Soil GI risk of infection per application period

ReDim IngSoilApInfMajorRisk(28, 5000, 3) 'Major Soil GI risk of infection per application period

ReDim IngSoilApIllMinorRisk(28, 5000, 3) 'Minor Soil GI risk of illness per application period

ReDim IngSoilApIllMajorRisk(28, 5000, 3) 'Major Soil GI risk of illness per application period

ReDim SoilApRiskstat(28, 5, 3) As Single '28 pathogens * 5 statistics * 3 population for risk of illness

ReDim SoilApIllMajorRiskstat(28, 5, 3) As Single '28 pathogens * 5 statistics * 3 population for risk of major illness

ReDim SoilApIllMinorRiskstat(28, 5, 3) As Single '28 pathogens * 5 statistics * 3 population for risk of minor illness
ReDim NoSoilGIRisk(3, 2, 5000) 'Matrix of no Soil GI risk of illness (i=1 to 3 for res_adults, res_children and occupational workers and j=1 to 2 for minor and major types of risk

ReDim CumSoilGIRisk(3, 2, 5000) 'Matrix of Soil GI risk of illness (i=1 to 3 for res_adults, res_children and occupational workers and j=1 to 2 for minor and major types of risk

ReDim CumSoilGIRiskstat(3, 2, 5) 'Matrix of stats for gastroenteritis risk of illness (i=1 for residential adult, 2 for residential children, and 3 for occupational workers; j=1 to 2 for minor and major types of risk; k=1 to 5 for five-point summary statistics

Dim Soiltemp(3, 5000) As Single, Soiltempminor(3, 5000) As Single, Soiltempmajor(3, 5000) As Single 'temp for calculation

'Groundwater model

ReDim IngGWCumRisk(28, 5000) As Double 'Cumulative risk of infection during periodic exposure

ReDim IngGWCumIllRisk(28, 5000) As Double 'Cumulative risk of illness during periodic exposure

ReDim IngGWAplnRisk(28, 5000) As Double 'Ingestion risk of infection per application period

ReDim IngGWAplnllRisk(28, 5000) As Double 'Ingestion risk of illness per application period

ReDim IngGWAplnminorRisk(28, 5000) As Double 'Minor Soil GI risk of infection per application period

ReDim IngGWAplnmajorRisk(28, 5000) As Double 'Major Soil GI risk of infection per application period

ReDim IngGWAplnllminorRisk(28, 5000) As Double 'Minor GW GI risk of illness per application period

ReDim IngGWAplnllmajorRisk(28, 5000) As Double 'Major GW GI risk of illness per application period

'ReDim IngGWlflllminorRisk(28, 5000) 'Minor GW GI risk of illness per lifetime

'ReDim IngGWlflllmajorRisk(28, 5000) 'Major GW GI risk of illness per lifetime

ReDim NoGWGIRisk(2, 5000) 'Matrix of no GW GI risk of illness per application period (i=1 to 2 for minor and major types of risk)

ReDim CumGWGIRisk(2, 5000) 'Matrix of GW GI risk of illness per application period (i=1 to 2 for minor and major types of risk)
ReDim CumGWGIRiskstat(2, 5) 'Matrix of stats for gastroenteritis risk of illness (i=1 to 2 for minor and major types of risk; k=1 to 5 for five-point summary statistics

'ReDim NoGWLifeGIRisk(2, 5000) 'Matrix of no GW GI risk of illness per lifetime (i=1 to 2 for minor and major types of risk)

'ReDim CumGWLifeGIRisk(2, 5000) 'Matrix of GW GI risk of illness per lifetime (i=1 to 2 for minor and major types of risk)

ReDim GWApRiskstat(28, 5) As Single '28 pathogens * 5 statistics for risk of infection

ReDim GWApIllMajorRiskstat(28, 5) As Single '28 pathogens * 5 statistics for risk of major illness

ReDim GWApIllMinorRiskstat(28, 5) As Single '28 pathogens * 5 statistics for risk of minor illness

Dim GWtemp(5000) As Single, GWtempminor(5000) As Single, GWtempmajor(5000) As Single 'temp for calculation


'Ingestion of food crops model

ReDim IngVegExp(2, 4)

ReDim IngVegDose(28, 5000, 2) 'Single pathogen dose

ReDim IngVegInitialRisk(28, 5000, 2) 'Initial ingestion risk of infection

ReDim IngVegInitialIllRisk(28, 5000, 2) 'Initial ingestion risk of illness

ReDim IngVegCumRisk(28, 5000, 2) 'Cumulative risk of infection during periodic exposure

ReDim IngVegCumIllRisk(28, 5000, 2) 'Cumulative risk of illness during periodic exposure

ReDim IngVegApInfRisk(28, 5000, 2) 'Ingestion risk of infection per application period

ReDim IngVegApIllRisk(28, 5000, 2) 'Ingestion risk of illness per application period

ReDim IngVegApInfMinorRisk(28, 5000, 2) 'Minor Vegetable GI risk of infection per application period

ReDim IngVegApInfMajorRisk(28, 5000, 2) 'Major Vegetable GI risk of infection per application period

ReDim IngVegApIllMinorRisk(28, 5000, 2) 'Minor Vegetable GI risk of illness per application period
ReDim IngVegApIllMajorRisk(28, 5000, 2) ' Major Vegetable GI risk of illness per application period
ReDim VegApRiskstat(28, 5, 2) As Single ' 28 pathogens * 5 statistics * 2 population for risk of illness
ReDim VegApIllMajorRiskstat(28, 5, 2) As Single ' 28 pathogens * 5 statistics * 2 population for risk of major illness
ReDim VegApIllMinorRiskstat(28, 5, 2) As Single ' 28 pathogens * 5 statistics * 2 population for risk of minor illness
ReDim NoVegGIRisk(2, 2, 5000) ' Matrix of no Vegetable GI risk of illness (i=1 to 2 for res_adults, and res_children and j=1 to 2 for minor and major types of risk
ReDim CumVegGIRisk(2, 2, 5000) ' Matrix of Vegetable GI risk of illness (i=1 to 2 for res_adults, and res_children and j=1 to 2 for minor and major types of risk
ReDim CumVegGIRiskstat(2, 2, 5) ' Matrix of stats for gastroenteritis risk of illness (i=1 for residential adult, and 2 for residential children; j=1 to 2 for minor and major types of risk; k=1 to 5 for five-point summary statistics
Dim Vegtemp(2, 5000) As Single, Vegtempminor(2, 5000) As Single, Vegtempmajor(2, 5000) As Single ' temp for calculation

'GW MODEL for part III: compile intermediate results (mean values only) for all pathogens

' Read pathogen names from GWPathogenModel Cell I53:180 and assigned to Cell B26 on GWPathogenModel sheet
For i = 1 To 28
Sheets(GWPathogenModel).Cells(26, 2).Value = Sheets(GWPathogenModel).Cells(52 + i, 9).Value

' Record results for each pathogen on GWPathogenModel Column J to M
Sheets(GWPathogenModel).Cells(52 + i, 10).Value = Sheets(GWPathogenModel).Cells(90, 2).Value ' peak pathogen concentration in water
Sheets(GWPathogenModel).Cells(52 + i, 11).Value = Sheets(GWPathogenModel).Cells(90, 3).Value ' total dose per application period
Sheets(GWPathogenModel).Cells(52 + i, 12).Value = Sheets(GWPathogenModel).Cells(90, 4).Value 'total risk per application period

Sheets(GWPathogenModel).Cells(52 + i, 13).Value = Sheets(GWPathogenModel).Cells(90, 5).Value 'cumulative risk over time

Next i

'GW MODEL ENDS

****************************************************************************
**
Iteration = Sheets(Inputdata).Cells(31, 3).Value 'Number of iteration points from the Inputdata sheet

restore = Sheets(Inputdata).Cells(32, 3).Value 'Number of iteration points from the Inputdata sheet

Number = 28 'Pathogen number

UChoice = Sheets(Inputdata).Cells(33, 3).Value 'Getting user choice for conducting uncertainty analysis for pathogen of interest (Choice: 1) or all pathogens (Choice:0)

PathogenInterest = Sheets(RiskOutput).Cells(2, 5).Value 'Taking ID of pathogen of interest; Pathogen ID info is available in the Cells U11-U38 of the Pathogen sheet

'READING TIME TO INGESTION INFO FROM Inputdata sheet

TIng(1, 1) = Sheets(Inputdata).Cells(28, 3).Value 'unit: day 'Time elapsed before soil ingestion

TIng(2, 1) = Sheets(Inputdata).Cells(29, 3).Value 'unit: day'Time elapsed before ingestion of pond water

'READING STORM EVENT INFO FROM Inputdata sheet

TRain = Sheets(Inputdata).Cells(4, 3).Value 'unit: day'Time to storm after biosolids application

'Probability of happening a storm event

RTRain = Sheets(Inputdata).Cells(5, 3).Value
'pRain = 1 / (365 * RTRain) 'Daily probability of happening a storm event
pRain = 1 'Assuming that rain occurs

'READING PATHOGEN INFO FROM Pathogen SHEET

For i = 1 To 28 ' Total number of pathogens: 28

'Read Pathogen dose-response info from the Pathogen sheet and record in the "Pmatrix" array

' For j = 1 To 7
' Pmatrix(i, j) = Sheets(Pathogen).Cells(10 + i, 47 + j).Value
'Sheets(Pathogen).Cells(10 + i, 62 + j).Value = Pmatrix(i, j)
'Next j

' Read Pathogen Infection and Incidence Indexes info from the Pathogen sheet and record in the "PImatrix" and "PIncidence" array, respectively

For j = 1 To 3
    PImatrix(i, j) = Sheets(Pathogen ).Cells(10 + i, 37 + j).Value
    PIncidence(i, j) = Sheets(Pathogen ).Cells(10 + i, 41 + j).Value
Next j

'Read Pathogen attack rate matrix

For j = 1 To 2
    Attackrate(i, j) = Sheets(Pathogen ).Cells(10 + i, 44 + j).Value 'Currently set at 100%; Column 1 for GI illness from infection and column 2 for inhalation based illness from infection
Next j
Next i

'REad in exposure factors table

For j = 1 To 4
    'Air model
For i = 1 To 4 'For row=1 to 4 for field worker, truck driver, residential adult and residential children
    InhExp(i, j) = Sheets("RiskConstants").Cells(3 + i, 13 + j).Value
Next i 'done reading in exposure factors table

'Surface water model
For i = 1 To 2 'i=1 for residential adult, i=2 for residential children
    IngSWExp(i, j) = Sheets("RiskConstants").Cells(17 + i, 13 + j).Value
Next i 'done reading exposure factor table

'Soil model
For i = 1 To 3 'For row=1 to 3 for residential adult, residential children, and occupational population
    IngSoilExp(i, j) = Sheets("RiskConstants").Cells(11 + i, 13 + j).Value
Next i 'done reading in exposure factors table

'Ingestion of food crops model
For i = 1 To 2 'i=1 for residential adult, i=2 for residential children
    IngVegExp(i, j) = Sheets("RiskConstants").Cells(28 + i, 13 + j).Value
Next i 'done reading in exposure factors table
Next j
For $i_1 = 1$ To Iteration:

'PATHOGEN-RELATED PARAMETERS
'Assign values for input parameters according to distributions for every microorganism

For $n = 1$ To Number:

For $j = 1$ To 7 'Collecting seven-point model information

$P_{\text{dist}}(n, j, 1) = \text{Sheets}(\text{Pathogen}).\text{Cells}(46 + n, 8 + j).\text{Value}$ 'Pathogen conc. in biosolids

$P_{\text{dist}}(n, j, 2) = \text{Sheets}(\text{Pathogen}).\text{Cells}(82 + n, 1 + j).\text{Value}$ 'Pathogen release parameter

$P_{\text{dist}}(n, j, 3) = \text{Sheets}(\text{Pathogen}).\text{Cells}(82 + n, 23 + j).\text{Value}$ 'Pathogen decay in air

$P_{\text{dist}}(n, j, 4) = \text{Sheets}(\text{Pathogen}).\text{Cells}(82 + n, 11 + j).\text{Value}$ 'Pathogen decay in water suspension

$P_{\text{dist}}(n, j, 5) = \text{Sheets}(\text{Pathogen}).\text{Cells}(115 + n, 1 + j).\text{Value}$ 'Pathogen liquid to liquid-solid mass transfer coefficient

$P_{\text{dist}}(n, j, 6) = \text{Sheets}(\text{Pathogen}).\text{Cells}(115 + n, 11 + j).\text{Value}$ 'Pathogen liquid to air-liquid mass transfer coefficient

$P_{\text{dist}}(n, j, 7) = \text{Sheets}(\text{Pathogen}).\text{Cells}(115 + n, 23 + j).\text{Value}$ 'Pathogen radius

$P_{\text{dist}}(n, j, 8) = \text{Sheets}(\text{Pathogen}).\text{Cells}(151 + n, 3 + j).\text{Value}$ 'Pathogen simplified inhalation-related dose-response model parameter

$P_{\text{dist}}(n, j, 9) = \text{Sheets}(\text{Pathogen}).\text{Cells}(151 + n, 16 + j).\text{Value}$ 'Pathogen simplified ingestion-related dose-response model parameter

Next $j$

For $k = 1$ To 9 'For all $k$ unknown pathogen-related parameters

  If Iteration = 1 Then 'Use only mean/median values for point estimation

  If UChoice = 0 Then
\[ \text{PSim}(n, i1, k) = \text{Pdist}(n, 2, k) \]

ElseIf UChoice = 1 Then 'Get value for the pathogen-of-interest and assign zero to other pathogens

\[
\begin{align*}
\text{If } n &= \text{PathogenInterest} \text{ Then} \\
\text{PSim}(n, i1, k) &= \text{Pdist}(n, 2, k)
\end{align*}
\]

End If

\[
\begin{align*}
\text{If } n &> \text{PathogenInterest} \text{ Then} \\
\text{PSim}(n, i1, k) &= 0
\end{align*}
\]

ElseIf n < PathogenInterest Then

\[
\begin{align*}
\text{PSim}(n, i1, k) &= 0
\end{align*}
\]

End If

End If

ElseIf Iteration > 1 Then

\[
\begin{align*}
\text{If } UChoice &= 0 \text{ Then 'Get distribution for all pathogens} \\
\text{If } \text{Pdist}(n, 1, k) &= 1 \text{ Then} \\
\text{PSim}(n, i1, k) &= \text{Pdist}(n, 2, k) \times \text{Exp}(\text{Normal}(0, \text{Pdist}(n, 7, k)))
\end{align*}
\]

'Return random numbers from Truncated Normal distribution, using 10 as factor for left and right limits

ElseIf Pdist(n, 1, k) = 2 Then

\[
\begin{align*}
\text{PSim}(n, i1, k) &= \text{Uni}(\text{Pdist}(n, 4, k), \text{Pdist}(n, 5, k))
\end{align*}
\]

'Return random numbers from uniform distribution

ElseIf Pdist(n, 1, k) = 0 Then 'If no model is available, mean value is returned.

\[
\begin{align*}
\text{PSim}(n, i1, k) &= \text{Pdist}(n, 2, k)
\end{align*}
\]

End If

ElseIf UChoice = 1 Then 'Get distribution for only pathogen-of-interest and assign zero to other pathogens

\[
\begin{align*}
\text{If } n &= \text{PathogenInterest} \text{ Then} \\
\text{If } \text{Pdist}(n, 1, k) &= 1 \text{ Then} \\
\text{PSim}(n, i1, k) &= \text{Pdist}(n, 2, k) \times \text{Exp}(\text{Normal}(0, \text{Pdist}(n, 7, k)))
\end{align*}
\]
'Return random numbers from Truncated Normal distribution, using 10 as factor for left and right limits

ElseIf Pdist(n, 1, k) = 2 Then

PSim(n, i1, k) = Uni(Pdist(n, 4, k), Pdist(n, 5, k))

'Return random numbers from uniform distribution

ElseIf Pdist(n, 1, k) = 0 Then 'If no model is available, mean value is returned.

PSim(n, i1, k) = Pdist(n, 2, k)

End If

End If

If n > PathogenInterest Then

PSim(n, i1, k) = 0

ElseIf n < PathogenInterest Then

PSim(n, i1, k) = 0

End If

End If

End If

Next k

'Assigning simulated values in the BSmodel

Sheets(Pathogen).Cells(46 + n, 2).Value = PSim(n, i1, 1) 'Simulated conc. value in biosolids as initial pathogen conc. in biosolids in pathogen sheet

Sheets(Pathogen).Cells(10 + n, 3).Value = PSim(n, i1, 2) 'Simulated release parameter in the model

Sheets(Pathogen).Cells(10 + n, 8).Value = 24 * PSim(n, i1, 3) 'Simulated decay constant for pathogens in air

Sheets(Pathogen).Cells(10 + n, 10).Value = PSim(n, i1, 4) 'Simulated decay constant for pathogens in water suspension

Sheets(Pathogen).Cells(10 + n, 12).Value = PSim(n, i1, 5) 'Simulated pathogen liquid to liquid-solid mass transfer coefficient
Sheets(Pathogen).Cells(10 + n, 13).Value = PSim(n, i1, 6) 'Simulated pathogen liquid to air-liquid mass transfer coefficient

Sheets(Pathogen).Cells(10 + n, 14).Value = PSim(n, i1, 7) 'Simulated pathogen radius

Sheets(Pathogen).Cells(10 + n, 55).Value = PSim(n, i1, 8) 'Simulated inhalation-related simplified dose-response model parameter

Sheets(Pathogen).Cells(10 + n, 52).Value = PSim(n, i1, 9) 'Simulated ingestion-related simplified dose-response model parameter

Next n

For i = 1 To 28 ' Total number of pathogens: 28

'Pathogen decay (Pdecay; unit: 1/day)

Pdecay(i, 1) = Sheets(Pathogen).Cells(10 + i, 5).Value 'For suspended pathogens; unit: 1/day

Pdecay(i, 2) = Sheets(Pathogen).Cells(10 + i, 8).Value 'For bioaerosols; unit: 1/day

Pdecay(i, 3) = Sheets(Pathogen).Cells(10 + i, 9).Value 'For suspended pathogens used for soil digestion case; unit: 1/day

'Read Pathogen dose-response info from the Pathogen sheet and record in the Pmatrix array

For j1 = 1 To 7

Pmatrix(i, j1) = Sheets(Pathogen).Cells(10 + i, 48 + j1).Value

'Sheets(Pathogen).Cells(10 + i, 62 + j).Value = Pmatrix(i, j)

Next j1

Next i

'SOIL PARAMETERS

'Assign values for input parameters according to distributions of soil-related parameters for every soil

For n = 1 To 12:

For j = 1 To 7 'Collecting seven-point model information

Soildist(n, j, 1) = Sheets(SurfaceConstants).Cells(100 + n, 21 + j).Value 'Soil hydraulic conductivity (cm/hr)
Soildist(n, j, 2) = Sheets("SurfaceConstants").Cells(100 + n, 1 + j).Value 'Soil pore size index

Soildist(n, j, 3) = Sheets("SurfaceConstants").Cells(100 + n, 11 + j).Value 'Soil residual moisture content

Soildist(n, j, 4) = Sheets("SurfaceConstants").Cells(100 + n, 31 + j).Value 'Percentage sand

Soildist(n, j, 5) = Sheets("SurfaceConstants").Cells(100 + n, 41 + j).Value 'Percentage silt

Soildist(n, j, 6) = Sheets("SurfaceConstants").Cells(100 + n, 51 + j).Value 'Percentage clay

Soildist(n, j, 7) = Sheets("SurfaceConstants").Cells(100 + n, 61 + j).Value 'Saturated water content

Next j

'Determining random values of k unknown soil-related parameters

For k = 1 To 7
    If Iteration = 1 Then 'Use only mean/median values for point estimation
        SoilSim(n, i1, k) = Soildist(n, 2, k)
    ElseIf Iteration > 1 Then
        If Soildist(n, 1, k) = 1 Then
            SoilSim(n, i1, k) = Soildist(n, 2, k) * Exp(Normal(0, Soildist(n, 7, k)))
        ElseIf Soildist(n, 1, k) = 2 Then
            SoilSim(n, i1, k) = Uni(Soildist(n, 4, k), Soildist(n, 5, k))
        ElseIf Soildist(n, 1, k) = 0 Then 'If no model is available, mean value is returned.
            SoilSim(n, i1, k) = Soildist(n, 2, k)
        End If
    End If
Next k

'Assigning simulated soil-related parameter values in the BSmodel
Sheets(SurfaceConstants).Cells(50 + n, 2).Value = SoilSim(n, i1, 1) 'Soil simulated hydraulic conductivity (cm/hr)

Sheets(SurfaceConstants).Cells(4 + n, 2).Value = SoilSim(n, i1, 2) 'Soil simulated Pajian (1987) pore size index

Sheets(SurfaceConstants).Cells(4 + n, 5).Value = SoilSim(n, i1, 3) 'Soil simulated Pajian (1987) residual moisture content

Sheets(SurfaceConstants).Cells(50 + n, 3).Value = SoilSim(n, i1, 4) 'Soil simulated percentage sand content

Sheets(SurfaceConstants).Cells(50 + n, 4).Value = SoilSim(n, i1, 5) 'Soil simulated percentage silt content

Sheets(SurfaceConstants).Cells(50 + n, 5).Value = SoilSim(n, i1, 6) 'Soil simulated percentage clay content

Sheets(SurfaceConstants).Cells(4 + n, 4).Value = SoilSim(n, i1, 7) 'Soil simulated saturated water content

Next n

'AIR-RELATED PARAMETERS

'Assign values for input parameters according to distributions of air-related parameters

For j = 1 To 5 'Collecting five-point model information

   Airdist(j, 1) = Sheets(SurfaceConstants).Cells(38, 18 + j).Value 'Aerosolization efficiency for picked application method

   Airdist(j, 2) = Sheets(AirConstants).Cells(5, 16 + j).Value 'Mechanical stress-related resuspension factor

   Airdist(j, 3) = Sheets(AirConstants).Cells(4, 16 + j).Value 'Cabin filtration efficiency

Next j

'Determining random values of 3 unknown air-related parameters

For k = 1 To 3

   If Iteration = 1 Then 'Use only mean/median values for point estimation

   AirSim(i1, k) = Airdist(2, k)

   ElseIf Iteration > 1 Then

   If Airdist(1, k) = 1 Then
AirSim(i1, k) = Normal(Airdist(2, k), Airdist(3, k))

'Return random numbers from Truncated Normal distribution, using 10 as factor for
left and right limits

ElseIf Airdist(1, k) = 2 Then
AirSim(i1, k) = Uni(Airdist(4, k), Airdist(5, k))

'Return random numbers from uniform distribution

ElseIf Airdist(1, k) = 0 Then 'If no model is available, mean value is returned.
AirSim(i1, k) = Airdist(2, k)
End If

End If

Next k

'Assigning simulated soil-related parameter values in the BSmodel

Sheets("SurfaceConstants").Cells(26, 16).Value = AirSim(i1, 1) 'Simulated aerosolization
efficiency for picked application method

Sheets("AirConstants").Cells(64, 2).Value = AirSim(i1, 2) 'Simulated mechanical stress-
related resuspension factor

Sheets("AirConstants").Cells(4, 16).Value = AirSim(i1, 3) 'Simulated cabin filtration
efficiency

'FOR DIFFERENT EXPOSURE ROUTES

For m = 1 To 28

' Read pathogen conc. at receptor info from the RiskConstants sheet and record in the
"Conc." array

For j = 1 To 8
Pconc(j, m) = Sheets("RiskConstants").Cells(4 + m, 1 + j).Value
Next j

'(A) INHALATION RISK CALCULATION FOR i1th ITERATION

'For inhalation of enterovirus scenario, use dose-response model parameters of
Coxsackievirus for calculating inhalation risk
'Check if inhalation dose-response model is available

For j = 1 To 4  'FW, TD, RA, and RC

'Put default values in when no inhalation dose-response model is available

    InhDInfRisk(m, i1, j) = -100  'Condition not applicable
    'Sheets(Pathogen).Cells(10 + m, 76).Value = InhDInfRisk(m, i1, 1)
    InhApInfRisk(m, i1, j) = -100  'Condition not applicable
    InhApInfMajorRisk(m, i1, j) = 0
    InhApInfMinorRisk(m, i1, j) = 0
    InhDIIIRisk(m, i1, j) = -100  'Condition not applicable
    InhApIllRisk(m, i1, j) = -100  'Condition not applicable
    InhApIllMajorRisk(m, i1, j) = 0
    InhApIllMinorRisk(m, i1, j) = 0
    'Sheets(RiskOutput).Cells(1 + m, 129).Value = InhApIllMajorRisk(m, i1, 1)

'Single dose and one-time risk

    InhInitialRisk(m, i1, j) = -100 ' Condition not applicable
    InhInitialIllRisk(m, i1, j) = -100 ' Condition not applicable

'Cumulative risk

    InhCumRisk(m, i1, j) = -100 'Condition not applicable
    InhCumIllRisk(m, i1, j) = -100 'Condition not applicable

If Pmatrix(m, 6) > 0 Then  'Inhalation dose-response model is available

    'Number of pathogens = Conc. in air * Inhalation rate* Daily exposure(hours of exposures per day)
    InhDose(m, i1, j) = PImatrix(m, 1) * (Pconc(j, m)) * InhExp(j, 2) * InhExp(j, 3) * (1 / 24)
    'Sheets(Pathogen).Cells(10 + m, 74).Value = InhDose(m, i1, 1)
'Sheets(Pathogen).Cells(10 + m, 75).Value = Pmatrix(m, 7)

InhDInfRisk(m, i1, j) = riskfunc(InhDose(m, i1, j), Pmatrix(m, 7))

'InhDInfRisk(m, i1, j) = riskfunc(Pmatrix(m, 8), InhDose(m, i1, j), Pmatrix(m, 9), Pmatrix(m, 10), Pmatrix(m, 11))

'Sheets(Pathogen).Cells(10 + m, 76).Value = InhDInfRisk(m, i1, 1)

InhApInfRisk(m, i1, j) = 1 - Excel.WorksheetFunction.Power((1 - (InhDInfRisk(m, i1, j))), (InhExp(j, 4)))

InhDIllRisk(m, i1, j) = Attackrate(m, 2) * InhDInfRisk(m, i1, j) 'Risk of infection * Attack rate

InhApIllRisk(m, i1, j) = 1 - Excel.WorksheetFunction.Power((1 - (InhDIllRisk(m, i1, j))), (InhExp(j, 4)))

'Single dose and one-time risk

InhInitialRisk(m, i1, j) = InhDInfRisk(m, i1, j) 'Initial inhalation risk of infection

InhInitialIllRisk(m, i1, j) = InhDIllRisk(m, i1, j) 'Initial inhalation risk of illness

'Cumulative risk

InhCumRisk(m, i1, j) = (InhInitialRisk(m, i1, j)) 'Infection

InhCumIllRisk(m, i1, j) = (InhInitialIllRisk(m, i1, j)) 'Illness

If Pdecay(m, 2) > 0 Then

InhCumRisk(m, i1, j) = (InhInitialRisk(m, i1, j)) / (1 - Exp(-Pdecay(m, 2))) 'Infection

InhCumIllRisk(m, i1, j) = (InhInitialIllRisk(m, i1, j)) / (1 - Exp(-Pdecay(m, 2))) 'Illness
End If

'Calculating major and minor risks of illness

If PIncidence(m, 1) = 1 Then 'Minor risk of illness is possible

InhApIllMajorRisk(m, i1, j) = 0

InhApIllMinorRisk(m, i1, j) = InhApIllRisk(m, i1, j)
ElseIf PIncidence(m, 1) = 2 Then 'Major risk of illness is possible

    InhApIllMajorRisk(m, i1, j) = InhApIllRisk(m, i1, j)
    InhApIllMinorRisk(m, i1, j) = 0

End If

'Sheets(RiskOutput).Cells(1 + m, 129).Value = InhApIllMajorRisk(m, i1, 1)

End If

Next j

'(B): SURFACE WATER RISK CALCULATION
(All ingested pathogens result in infection)

'For ingestion of enterovirus scenario, use dose-response model parameters of Echovirus 12 for calculating ingestion risk

For j = 1 To 2

'Put default values in when ingestion dose-response model is not available

'Single dose and one-time risk
IngSWInitialRisk(m, i1, j) = -100 ' Condition not applicable
'Sheets(Pathogen).Cells(10 + m, 79).Value = IngSWInitialRisk(m, i1, 1)

IngSWInitialIllRisk(m, i1, j) = -100 ' Condition not applicable

'Risk per application period
IngSWApInfRisk(m, i1, j) = -100 'Condition not applicable
IngSWApIllRisk(m, i1, j) = -100 'Condition not applicable

'Cumulative risk
IngSWCumRisk(m, i1, j) = -100 'Condition not applicable
IngSWCumIllRisk(m, i1, j) = -100 'Condition not applicable
IngSWApInfMajorRisk(m, i1, j) = 0
IngSWApInfMinorRisk(m, i1, j) = 0
IngSWApIllMajorRisk(m, i1, j) = 0
IngSWApIllMinorRisk(m, i1, j) = 0

If Pmatrix(m, 3) > 0 Then 'Ingestion dose-response model is available

'Single dose and one-time risk
IngSWDose(m, i1, j) = pRain * PImatrix(m, 2) * 1 * (Pconc(6, m)) * IngSWExp(j, 2) * IngSWExp(j, 3) * (1 / 24)
IngSWInitialRisk(m, i1, j) = riskfunc(IngSWDose(m, i1, j), Pmatrix(m, 4)) 'Infection

'Sheets(Pathogen).Cells(10 + m, 77).Value = IngSWDose(m, i1, 1)
'Sheets(Pathogen).Cells(10 + m, 78).Value = Pmatrix(m, 4)
'Sheets(Pathogen).Cells(10 + m, 79).Value = IngSWInitialRisk(m, i1, 1)

'IngSWInitialRisk(m, i1, j) = riskfunc(Pmatrix(m, 3), IngSWDose(m, i1, j), Pmatrix(m, 4), Pmatrix(m, 5), Pmatrix(m, 6)) 'Infection
IngSWInitialIllRisk(m, i1, j) = Attackrate(m, 1) * IngSWInitialRisk(m, i1, j) 'Illness

'Risk per application period
IngSWApInfRisk(m, i1, j) = 1 - Excel.WorksheetFunction.Power((1 - (IngSWInitialRisk(m, i1, j))), (IngSWExp(j, 4))) 'Infection
IngSWApIllRisk(m, i1, j) = 1 - Excel.WorksheetFunction.Power((1 - (IngSWInitialIllRisk(m, i1, j))), (IngSWExp(j, 4))) 'Illness

'Cumulative risk
If Pdecay(m, 1) = 0 Then
IngSWCumRisk(m, i1, j) = (IngSWInitialRisk(m, i1, j)) 'Infection
IngSWCumIllRisk(m, i1, j) = (IngSWInitialIllRisk(m, i1, j)) 'Illness
ElseIf Pdecay(m, 1) > 0 Then
IngSWCumRisk\(m, i1, j\) = \(\frac{\text{IngSWInitialRisk}\(m, i1, j\)}{1 - \text{Exp}\(-P\text{decay}\(m, 1\))}\) 'Infection

IngSWCumIllRisk\(m, i1, j\) = \(\frac{\text{IngSWInitialIllRisk}\(m, i1, j\)}{1 - \text{Exp}\(-P\text{decay}\(m, 1\))}\) 'Illness

End If

'Calculating major and minor risks of illness

If PIncidence\(m, 2\) = 1 Then 'Minor risk is possible

IngSWApIllMajorRisk\(m, i1, j\) = 0

IngSWApIllMinorRisk\(m, i1, j\) = IngSWApIllRisk\(m, i1, j\)

ElseIf PIncidence\(m, 2\) = 2 Then 'Major risk is possible

IngSWApIllMajorRisk\(m, i1, j\) = IngSWApIllRisk\(m, i1, j\)

IngSWApIllMinorRisk\(m, i1, j\) = 0

End If

End If

Next j

'(C) DIRECT SOIL INGESTION

For j = 1 To 3

'Put default values in when ingestion dose-response model is not available

'Single dose and one-time risk

IngSoilInitialRisk\(m, i1, j\) = -100 'Condition not applicable

IngSoilInitialIllRisk\(m, i1, j\) = -100 'Condition not applicable

'Risk per application period

IngSoilApInfRisk\(m, i1, j\) = -100 'Condition not applicable

IngSoilApIllRisk\(m, i1, j\) = -100 'Condition not applicable
'Cumulative risk
IngSoilCumRisk(m, i1, j) = -100 'Condition not applicable
IngSoilCumIllRisk(m, i1, j) = -100 'Condition not applicable

IngSoilApInfMajorRisk(m, i1, j) = 0
IngSoilApInfMinorRisk(m, i1, j) = 0
IngSoilApIllMajorRisk(m, i1, j) = 0
IngSoilApIllMinorRisk(m, i1, j) = 0

If Pmatrix(m, 3) > 0 Then

'Single dose and one-time risk
IngSoilDose(m, i1, j) = pRain * PImatrix(m, 2) * 1 * (Pconc(5, m)) * IngSoilExp(j, 2) * IngSoilExp(j, 3) * (1 / 24)
IngSoilInitialRisk(m, i1, j) = riskfunc(IngSoilDose(m, i1, j), Pmatrix(m, 4)) 'Infection
IngSoilInitialIllRisk(m, i1, j) = Attackrate(m, 1) * IngSoilInitialRisk(m, i1, j) 'Illness

'Risk per application period
IngSoilApInfRisk(m, i1, j) = 1 - Excel.WorksheetFunction.Power((1 - (IngSoilInitialRisk(m, i1, j))), (IngSoilExp(j, 4))) 'Infection
IngSoilApIllRisk(m, i1, j) = 1 - Excel.WorksheetFunction.Power((1 - (IngSoilInitialIllRisk(m, i1, j))), (IngSoilExp(j, 4))) 'Illness

'Cumulative risk
If Pdecay(m, 3) = 0 Then
    IngSoilCumRisk(m, i1, j) = (IngSoilInitialRisk(m, i1, j)) 'Infection
    IngSoilCumIllRisk(m, i1, j) = (IngSoilInitialIllRisk(m, i1, j)) 'Illness
ElseIf Pdecay(m, 3) > 0 Then

IngSoilCumRisk(m, i1, j) = (IngSoilInitialRisk(m, i1, j)) / (1 - Exp(-Pdecay(m, 3)))
'Infection

IngSoilCumIllRisk(m, i1, j) = (IngSoilInitialIllRisk(m, i1, j)) / (1 - Exp(-Pdecay(m, 3)))
'Illness

End If

'Calculating major and minor risks of illness
If PIncidence(m, 2) = 1 Then 'Minor risk is possible
  IngSoilApIllMajorRisk(m, i1, j) = 0
  IngSoilApIllMinorRisk(m, i1, j) = IngSoilApIllRisk(m, i1, j)
ElseIf PIncidence(m, 2) = 2 Then 'Major risk is possible
  IngSoilApIllMajorRisk(m, i1, j) = IngSoilApIllRisk(m, i1, j)
  IngSoilApIllMinorRisk(m, i1, j) = 0
End If
End If
Next j

'(D) RISK CALCULATION FOR GROUNDWATER INGESTION FOR i1th ITERATION
'Read pathogen names from GWPathogenModel Cell I53:I80 and assigned to Cell B26 on GWPathogenModel sheet
Sheets(GWPathogenModel).Cells(26, 2).Value = Sheets(GWPathogenModel).Cells(52 + m, 9).Value

'Put default values in when ingestion dose-response model is not available
'Single dose and one-time risk is not available since conc changes during time
'Risk per application period
IngGWApInfRisk(m, i1) = -100 'Condition not applicable
IngGWApIllRisk(m, i1) = -100 'Condition not applicable

'Cumulative risk
IngGWCumRisk(m, i1) = -100 'Condition not applicable
IngGWCumIllRisk(m, i1) = -100 'Condition not applicable

IngGWAPlInfMajorRisk(m, i1) = 0
IngGWAPlInfMinorRisk(m, i1) = 0
IngGWAPlIllMajorRisk(m, i1) = 0
IngGWAPlIllMinorRisk(m, i1) = 0

If Pmatrix(m, 3) > 0 Then
' Single dose and one-time risk is not available since conc changes during time

' Risk per application period
IngGWAPlInfRisk(m, i1) = "sheet.Cells(90, 4).Value 'Infection
IngGWAPlIllRisk(m, i1) = "sheet.Cells(90, 4).Value * Attackrate(m, 1) 'Illness

' Cumulative risk
IngGWCumRisk(m, i1) = "sheet.Cells(90, 5).Value 'Infection
IngGWCumIllRisk(m, i1) = "sheet.Cells(90, 5).Value * Attackrate(m, 1) 'Illness

' Calculating major and minor risks of illness per application period
If PIncidence(m, 2) = 1 Then 'Minor risk is possible
IngGWAPlIllMajorRisk(m, i1) = 0
IngGWAPlIllMinorRisk(m, i1) = IngGWAPlIllRisk(m, i1)
ElseIf PIncidence(m, 2) = 2 Then 'Major risk is possible
IngGWAPlIllMajorRisk(m, i1) = IngGWAPlIllRisk(m, i1)
IngGWAPlIllMinorRisk(m, i1) = 0
End If
End If

'(E) RISK CALCULATION FOR INGESTION OF FOOD CROPS FOR i1th Iteration

For j = 1 To 2

'Put default values in when ingestion dose-response model is not available

'Single dose and one-time risk
IngVegInitialRisk(m, i1, j) = -100 'Condition not applicable
IngVegInitialIllRisk(m, i1, j) = -100 'Condition not applicable

'Risk per application period
IngVegApInfRisk(m, i1, j) = -100 'Condition not applicable
IngVegApIllRisk(m, i1, j) = -100 'Condition not applicable

'Cumulative risk
IngVegCumRisk(m, i1, j) = -100 'Condition not applicable
IngVegCumIllRisk(m, i1, j) = -100 'Condition not applicable
IngVegApInfMajorRisk(m, i1, j) = 0
IngVegApInfMinorRisk(m, i1, j) = 0
IngVegApIllMajorRisk(m, i1, j) = 0
IngVegApIllMinorRisk(m, i1, j) = 0

If Pmatrix(m, 3) > 0 Then

'Single dose and one-time risk
IngVegDose(m, i1, j) = pRain * Plmatrix(m, 2) * 1 * (Pconc(8, m)) * IngVegExp(j, 2) * IngVegExp(j, 3) * (1 / 24)
IngVegInitialRisk(m, i1, j) = riskfunc(IngVegDose(m, i1, j), Pmatrix(m, 4)) 'Infection

'IngSoilInitialRisk(m, i1, j) = riskfunc(Pmatrix(m, 3), IngSoilDose(m, i1, j), Pmatrix(m, 4), Pmatrix(m, 5), Pmatrix(m, 6)) 'Infection
IngVegInitialIllRisk(m, i1, j) = Attackrate(m, 1) * IngVegInitialRisk(m, i1, j) 'Illness

'Risk per application period
IngVegApInfRisk(m, i1, j) = 1 - Excel.WorksheetFunction.Power((1 - (IngVegInitialRisk(m, i1, j))), (IngVegExp(j, 4))) 'Infection
IngVegApIllRisk(m, i1, j) = 1 - Excel.WorksheetFunction.Power((1 - (IngVegInitialIllRisk(m, i1, j))), (IngVegExp(j, 4))) 'Illness

'Cumulative risk
If Pdecay(m, 3) = 0 Then
    IngVegCumRisk(m, i1, j) = (IngVegInitialRisk(m, i1, j)) 'Infection
    IngVegCumIllRisk(m, i1, j) = (IngVegInitialIllRisk(m, i1, j)) 'Illness
ElseIf Pdecay(m, 3) > 0 Then
    IngVegCumRisk(m, i1, j) = (IngVegInitialRisk(m, i1, j)) / (1 - Exp(-Pdecay(m, 3))) 'Infection
    IngVegCumIllRisk(m, i1, j) = (IngVegInitialIllRisk(m, i1, j)) / (1 - Exp(-Pdecay(m, 3))) 'Illness
End If

'Calculating major and minor risks of illness
If PIncidence(m, 2) = 1 Then 'Minor risk is possible
    IngVegApIllMajorRisk(m, i1, j) = 0
    IngVegApIllMinorRisk(m, i1, j) = IngVegApIllRisk(m, i1, j)
ElseIf PIncidence(m, 2) = 2 Then 'Major risk is possible
    IngVegApIllMajorRisk(m, i1, j) = IngVegApIllRisk(m, i1, j)
    IngVegApIllMinorRisk(m, i1, j) = 0
End If
End If
Next j
For i1 = 1 To Iteration

'To calculate overall minor and major risk of illness for a given subpopulation

'AIR model

For j = 1 To 4  'Four subpopulation (FW, TD, RA, and RC)
    NoRespRisk(j, 1, i1) = 1 'No minor risk
    NoRespRisk(j, 2, i1) = 1 'No major risk
    For m = 1 To Number
        NoRespRisk(j, 1, i1) = NoRespRisk(j, 1, i1) * (1 - InhApIllMinorRisk(m, i1, j))
        NoRespRisk(j, 2, i1) = NoRespRisk(j, 2, i1) * (1 - InhApIllMajorRisk(m, i1, j))
    Next m
    CumRespRisk(j, 1, i1) = 1 - (NoRespRisk(j, 1, i1)) 'Minor respiratory risk of illness
    CumRespRisk(j, 2, i1) = 1 - (NoRespRisk(j, 2, i1)) 'Major respiratory risk of illness
Next j

'SW model

For j = 1 To 2  'Two subpopulations
    NoSWGIRisk(j, 1, i1) = 1 'No minor risk
    NoSWGIRisk(j, 2, i1) = 1 'No major risk
    For m = 1 To Number
        NoSWGIRisk(j, 1, i1) = NoSWGIRisk(j, 1, i1) * (1 - IngSWApIllMinorRisk(m, i1, j))
        NoSWGIRisk(j, 2, i1) = NoSWGIRisk(j, 2, i1) * (1 - IngSWApIllMajorRisk(m, i1, j))
    Next m
CumSWGIRisk(j, 1, i1) = 1 - (NoSWGIRisk(j, 1, i1)) 'Minor GI risk of illness
CumSWGIRisk(j, 2, i1) = 1 - (NoSWGIRisk(j, 2, i1)) 'Major GI risk of illness
Next j

'GW model

'For all subpopulations (overall risk per application period)
NoGWGIRisk(1, i1) = 1 'No minor risk
NoGWGIRisk(2, i1) = 1 'No major risk
For m = 1 To Number
   NoGWGIRisk(1, i1) = NoGWGIRisk(1, i1) * (1 - IngGWApIllMinorRisk(m, i1))
   NoGWGIRisk(2, i1) = NoGWGIRisk(2, i1) * (1 - IngGWApIllMajorRisk(m, i1))
Next m
CumGWGIRisk(1, i1) = 1 - (NoGWGIRisk(1, i1)) 'Minor GI risk of illness
CumGWGIRisk(2, i1) = 1 - (NoGWGIRisk(2, i1)) 'Major GI risk of illness

'Soil model

For j = 1 To 3 'Three subpopulations
   NoSoilGIRisk(j, 1, i1) = 1 'No minor risk
   NoSoilGIRisk(j, 2, i1) = 1 'No major risk
For m = 1 To Number
   NoSoilGIRisk(j, 1, i1) = NoSoilGIRisk(j, 1, i1) * (1 - IngSoilApIllMinorRisk(m, i1, j))
   NoSoilGIRisk(j, 2, i1) = NoSoilGIRisk(j, 2, i1) * (1 - IngSoilApIllMajorRisk(m, i1, j))
Next m
CumSoilGIRisk(j, 1, i1) = 1 - (NoSoilGIRisk(j, 1, i1)) 'Minor GI risk of illness
CumSoilGIRisk(j, 2, i1) = 1 - (NoSoilGIRisk(j, 2, i1)) 'Major GI risk of illness
Next j
'Veg model
For j = 1 To 2  'Two subpopulations
    NoVegGIRisk(j, 1, i1) = 1 'No minor risk
    NoVegGIRisk(j, 2, i1) = 1 'No major risk
For m = 1 To Number
    NoVegGIRisk(j, 1, i1) = NoVegGIRisk(j, 1, i1) * (1 - IngVegApIllMinorRisk(m, i1, j))
    NoVegGIRisk(j, 2, i1) = NoVegGIRisk(j, 2, i1) * (1 - IngVegApIllMajorRisk(m, i1, j))
Next m
CumVegGIRisk(j, 1, i1) = 1 - (NoVegGIRisk(j, 1, i1)) 'Minor GI risk of illness
CumVegGIRisk(j, 2, i1) = 1 - (NoVegGIRisk(j, 2, i1)) 'Major GI risk of illness
Next j

Next i1

'++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
+++++++++++++++++++++++++
'CALCULATION OF STATISTICS FOR RISK OF ILLNESS PER APPLICATION PERIOD
FOR DIFFERENT EXPOSURE ROUTES

For n = 1 To Number:  'No of pathogens

    If Iteration = 1 Then  'No of iterations
        For k = 1 To 5 '5-point risk statistic
            'Air model
            For j = 1 To 4 'Four subpopulations:FW, TD, RA, and RC
                If k = 1 Then
                    AirApRiskstat(n, k, j) = InhApInfRisk(n, Iteration, j) 'Mean value is equal to point estimate
                    AirApIllMajorRiskstat(n, k, j) = InhApIllMajorRisk(n, Iteration, j) 'Mean value is equal to point estimate
                Next j
            Next k
        Next i1
    Next n
AirApIllMinorRiskstat(n, k, j) = InhApIllMinorRisk(n, Iteration, j) 'Mean value is equal to point estimate

ElseIf k > 1 Then
    AirApRiskstat(n, k, j) = 0 'All other statistics are assigned to zero value
    AirApIllMajorRiskstat(n, k, j) = 0 'All other statistics are assigned to zero value
    AirApIllMinorRiskstat(n, k, j) = 0 'All other statistics are assigned to zero value
End If

Next j

'SW model

For j = 1 To 2 'Two subpopulations
    If k = 1 Then
        SWApRiskstat(n, k, j) = IngSWApInfRisk(n, Iteration, j) 'Mean value is equal to point estimate
        SWApIllMajorRiskstat(n, k, j) = IngSWApIllMajorRisk(n, Iteration, j) 'Mean value is equal to point estimate
        SWApIllMinorRiskstat(n, k, j) = IngSWApIllMinorRisk(n, Iteration, j) 'Mean value is equal to point estimate
    ElseIf k > 1 Then
        SWApRiskstat(n, k, j) = 0 'All other statistics are assigned to zero value
        SWApIllMajorRiskstat(n, k, j) = 0 'All other statistics are assigned to zero value
        SWApIllMinorRiskstat(n, k, j) = 0 'All other statistics are assigned to zero value
    End If

Next j

'GW model

If k = 1 Then
    GWApRiskstat(n, k) = IngGWApInfRisk(n, Iteration) 'Mean value is equal to point estimate
    GWApIllMajorRiskstat(n, k) = IngGWApIllMajorRisk(n, Iteration) 'Mean value is equal to point estimate
GWApIllMinorRiskstat(n, k) = IngGWApIllMinorRisk(n, Iteration) 'Mean value is equal to point estimate

ElseIf k > 1 Then
    GWApRiskstat(n, k) = 0 'All other statistics are assigned to zero value
    GWApIllMajorRiskstat(n, k) = 0
    GWApIllMinorRiskstat(n, k) = 0
End If

'Soil model
For j = 1 To 3 'Three subpopulations
    If k = 1 Then
        SoilApRiskstat(n, k, j) = IngSoilApInfRisk(n, Iteration, j) 'Mean value is equal to point estimate
        SoilApIllMajorRiskstat(n, k, j) = IngSoilApIllMajorRisk(n, Iteration, j) 'Mean value is equal to point estimate
        SoilApIllMinorRiskstat(n, k, j) = IngSoilApIllMinorRisk(n, Iteration, j) 'Mean value is equal to point estimate
    ElseIf k > 1 Then
        SoilApRiskstat(n, k, j) = 0 'All other statistics are assigned to zero value
        SoilApIllMajorRiskstat(n, k, j) = 0 'All other statistics are assigned to zero value
        SoilApIllMinorRiskstat(n, k, j) = 0 'All other statistics are assigned to zero value
    End If
Next j

'Ingestion of food crops model
For j = 1 To 2 'Two subpopulations
    If k = 1 Then
        VegApRiskstat(n, k, j) = IngVegApInfRisk(n, Iteration, j) 'Mean value is equal to point estimate
        VegApIllMajorRiskstat(n, k, j) = IngVegApIllMajorRisk(n, Iteration, j) 'Mean value is equal to point estimate
    End If
Next j
VegApIllMinorRiskstat(n, k, j) = IngVegApIllMinorRisk(n, Iteration, j) 'Mean value is equal to point estimate
ElseIf k > 1 Then
VegApRiskstat(n, k, j) = 0 'All other statistics are assigned to zero value
VegApIllMajorRiskstat(n, k, j) = 0 'All other statistics are assigned to zero value
VegApIllMinorRiskstat(n, k, j) = 0 'All other statistics are assigned to zero value
End If
Next j
Next k

ElseIf Iteration > 1 Then
For i = 1 To Iteration:
'Air model
For j = 1 To 4 'Four subpopulations: FW, TD, RA, and RC
Airtemp(j, i) = InhApInfRisk(n, i, j)
Airtempmajor(j, i) = InhApIllMajorRisk(n, i, j)
Airtempminor(j, i) = InhApIllMinorRisk(n, i, j)
Next j

'SW model
For j = 1 To 2
SWtemp(j, i) = IngSWApInfRisk(n, i, j)
SWtempmajor(j, i) = IngSWApIllMajorRisk(n, i, j)
SWtempminor(j, i) = IngSWApIllMinorRisk(n, i, j)
Next j

'GW model
GWtemp(i) = IngGWApInfRisk(n, i)
GWtempmajor(i) = IngGWApIllMajorRisk(n, i)
GWtempminor(i) = IngGWApIllMinorRisk(n, i)

'Soil model
For j = 1 To 3
    Soiltemp(j, i) = IngSoilApInfRisk(n, i, j)
    Soiltempmajor(j, i) = IngSoilApIllMajorRisk(n, i, j)
    Soiltempminor(j, i) = IngSoilApIllMinorRisk(n, i, j)
Next j
Next i

'Ingestion of food crops model
For j = 1 To 2
    Vegtemp(j, i) = IngVegApInfRisk(n, i, j)
    Vegtempmajor(j, i) = IngVegApIllMajorRisk(n, i, j)
    Vegtempminor(j, i) = IngVegApIllMinorRisk(n, i, j)
Next j

'CALCULATING STATISTICS
ReDim Temp1(Iteration) As Single
ReDim Tempmajor(Iteration) As Single
ReDim Tempminor(Iteration) As Single

'Air model
For j = 1 To 4 'Four subpopulations: FW, TD, RA, and RC

    For i = 1 To Iteration
        Temp1(i) = Airtemp(j, i)
    Next i
Next j
Tempmajor(i) = Airtempmajor(j, i)
Tempminor(i) = Airtempminor(j, i)
Next i

Call Stat(Temp1, dataset, Iteration) ' Calculates data statistics from data stored in "Temp" matrix and output in the "dataset" matrix
For k = 1 To 5
AirApRisk(n, k, j) = dataset(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

Call Stat(Tempmajor, dataset, Iteration) ' Calculates data statistics from data stored in "Tempmajor" matrix and output in the "dataset" matrix
For k = 1 To 5
AirApIllMajorRisk(n, k, j) = dataset(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

Call Stat(Tempminor, dataset, Iteration) ' Calculates data statistics from data stored in "Tempminor" matrix and output in the "dataset" matrix
For k = 1 To 5
AirApIllMinorRisk(n, k, j) = dataset(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

For i = 1 To Iteration
Tempminor(i) = CumRespRisk(j, 1, i)
Tempmajor(i) = CumRespRisk(j, 2, i)
Next i

Call Stat(Tempminor, dataset, Iteration) ' Calculates data statistics for cumulative minor risk of illness
For \( k = 1 \) To 5

\[
\text{CumRespRiskstat}(j, 1, k) = \text{datastat}(k) \quad \text{for mean, stdev, 5th, 50th, and 95th percentile}
\]

Next \( k \)

Call Stat(Tempmajor, datastat, Iteration) \('\) Calculates data statistics for cumulative major risk of illness

For \( k = 1 \) To 5

\[
\text{CumRespRiskstat}(j, 2, k) = \text{datastat}(k) \quad \text{for mean, stdev, 5th, 50th, and 95th percentile}
\]

Next \( k \)

Next \( j \)

'SW model

For \( j = 1 \) To 2

For \( i = 1 \) To Iteration

\[
\text{Temp1}(i) = \text{SWtemp}(j, i)
\]

\[
\text{Tempmajor}(i) = \text{SWtempmajor}(j, i)
\]

\[
\text{Tempminor}(i) = \text{SWtempminor}(j, i)
\]

Next \( i \)

Call Stat(Temp1, datastat, Iteration) \('\) Calculates data statistics from data stored in "Temp" matrix and output in the "datastat" matrix

For \( k = 1 \) To 5

\[
\text{SWApRiskstat}(n, k, j) = \text{datastat}(k) \quad \text{for mean, stdev, 5th, 50th, and 95th percentile}
\]

Next \( k \)

Call Stat(Tempmajor, datastat, Iteration) \('\) Calculates data statistics from data stored in "Tempmajor" matrix and output in the "datastat" matrix

For \( k = 1 \) To 5
SWApIllMajorRiskstat(n, k, j) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

Call Stat(Tempminor, datastat, Iteration) ' Calculates data statistics from data stored in "Tempminor" matrix and output in the "datastat" matrix
For k = 1 To 5
SWApIllMinorRiskstat(n, k, j) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

'Calculating statistics for cumulative gastroenteritis risk of minor and major risk of illness
For i = 1 To Iteration
Tempminor(i) = CumSWGIRisk(j, 1, i)
Tempmajor(i) = CumSWGIRisk(j, 2, i)
Next i

Call Stat(Tempminor, datastat, Iteration) ' Calculates data statistics for cumulative minor risk of illness
For k = 1 To 5
CumSWGIRiskstat(j, 1, k) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

Call Stat(Tempmajor, datastat, Iteration) ' Calculates data statistics for cumulative major risk of illness
For k = 1 To 5
CumSWGIRiskstat(j, 2, k) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k
'GW model

For i = 1 To Iteration
    Temp1(i) = GWtemp(i)
    Tempmajor(i) = GWtempmajor(i)
    Tempminor(i) = GWtempminor(i)
Next i

Call Stat(Temp1, datastat, Iteration) ' Calculates data statistics from data stored in "Temp" matrix and output in the "datastat" matrix

For k = 1 To 5
    GWApRiskstat(n, k) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

Call Stat(Tempmajor, datastat, Iteration) ' Calculates data statistics from data stored in "Tempmajor" matrix and output in the "datastat" matrix

For k = 1 To 5
    GWApIllMajorRiskstat(n, k) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

Call Stat(Tempminor, datastat, Iteration) ' Calculates data statistics from data stored in "Tempminor" matrix and output in the "datastat" matrix

For k = 1 To 5
    GWApIllMinorRiskstat(n, k) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

'Calculating statistics for cumulative gastroenteritis risk of minor and major risk of illness

For i = 1 To Iteration
Tempminor(i) = CumGWGIRisk(1, i)
Tempmajor(i) = CumGWGIRisk(2, i)
Next i

Call Stat(Tempminor, datastat, Iteration) ' Calculates data statistics for cumulative minor risk of illness
For k = 1 To 5
   CumGWGIRiskstat(1, k) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

Call Stat(Tempmajor, datastat, Iteration) ' Calculates data statistics for cumulative major risk of illness
For k = 1 To 5
   CumGWGIRiskstat(2, k) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

'Soil model
For j = 1 To 3
   For i = 1 To Iteration
      Temp1(i) = Soiltemp(j, i)
      Tempmajor(i) = Soiltempmajor(j, i)
      Tempminor(i) = Soiltempminor(j, i)
   Next i
   Call Stat(Temp1, datastat, Iteration) ' Calculates data statistics from data stored in "Temp" matrix and output in the "datastat" matrix
   For k = 1 To 5
SoilApRiskstat(n, k, j) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

Call Stat(Tempmajor, datastat, Iteration) ' Calculates data statistics from data stored in "Tempmajor" matrix and output in the "datastat" matrix
For k = 1 To 5
    SoilApIllMajorRiskstat(n, k, j) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

Call Stat(Tempminor, datastat, Iteration) ' Calculates data statistics from data stored in "Tempminor" matrix and output in the "datastat" matrix
For k = 1 To 5
    SoilApIllMinorRiskstat(n, k, j) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

'Calculating statistics for cumulative gastroenteritis risk of minor and major risk of illness
For i = 1 To Iteration
    Tempminor(i) = CumSoilGIRisk(j, 1, i)
    Tempmajor(i) = CumSoilGIRisk(j, 2, i)
Next i

Call Stat(Tempminor, datastat, Iteration) ' Calculates data statistics for cumulative minor risk of illness
For k = 1 To 5
    CumSoilGIRiskstat(j, 1, k) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k
Call Stat(Tempmajor, datastat, Iteration) ' Calculates data statistics for cumulative major risk of illness
For k = 1 To 5
    CumSoilGIRiskstat(j, 2, k) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
    Next k
Next j

' Ingestion of food crops model
For j = 1 To 2
    For i = 1 To Iteration
        Temp1(i) = Vegtemp(j, i)
        Tempmajor(i) = Vegtempmajor(j, i)
        Tempminor(i) = Vegtempminor(j, i)
        Next i
    Call Stat(Temp1, datastat, Iteration) ' Calculates data statistics from data stored in "Temp" matrix and output in the "datastat" matrix
    For k = 1 To 5
        VegApRiskstat(n, k, j) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
        Next k
    Call Stat(Tempmajor, datastat, Iteration) ' Calculates data statistics from data stored in "Tempmajor" matrix and output in the "datastat" matrix
    For k = 1 To 5
        VegApIllMajorRiskstat(n, k, j) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
        Next k
    Call Stat(Tempminor, datastat, Iteration) ' Calculates data statistics from data stored in "Tempminor" matrix and output in the "datastat" matrix
    For k = 1 To 5
VegApIllMinorRiskstat(n, k, j) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile

Next k

'Calculating statistics for cumulative gastroenteritis risk of minor and major risk of illness
For i = 1 To Iteration
    Tempminor(i) = CumVegGIRisk(j, 1, i)
    Tempmajor(i) = CumVegGIRisk(j, 2, i)
Next i

Call Stat(Tempminor, datastat, Iteration) 'Calculates data statistics for cumulative minor risk of illness
For k = 1 To 5
    CumVegGIRiskstat(j, 1, k) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k

Call Stat(Tempmajor, datastat, Iteration) 'Calculates data statistics for cumulative major risk of illness
For k = 1 To 5
    CumVegGIRiskstat(j, 2, k) = datastat(k) 'k=1 to 5 for mean, stdev, 5th, 50th, and 95th percentile
Next k
Next j
End If
Next n

'PRINTING STATISTICS FOR RISK PER APPLICATION FOR 4 SUBPOPULATIONS
If UChoice = 0 Then 'Print for all pathogens
    For i = 1 To 28
        'Air model
m = 0
For k = 1 To 4 'Four subpopulations: FW, TD, RA, and RC
    For j = 1 To 5
        Sheets("RiskOutput").Cells(7 + i, 19 + j + m).Value = AirApRiskstat(i, j, k)
        Sheets("RiskOutput").Cells(7 + i, 47 + j + m).Value = AirApIllMajorRiskstat(i, j, k)
        Sheets("RiskOutput").Cells(7 + i, 76 + j + m).Value = AirApIllMinorRiskstat(i, j, k)
    Next j
    m = k * j
Next k

' SW model
m = 0
For k = 1 To 2
    For j = 1 To 5
        Sheets("RiskOutput").Cells(42 + i, 19 + j + m).Value = SWApRiskstat(i, j, k)
        Sheets("RiskOutput").Cells(42 + i, 47 + j + m).Value = SWApIllMajorRiskstat(i, j, k)
        Sheets("RiskOutput").Cells(42 + i, 76 + j + m).Value = SWApIllMinorRiskstat(i, j, k)
    Next j
    m = k * j
Next k

' GW model
For j = 1 To 5
    Sheets("RiskOutput").Cells(112 + i, 19 + j).Value = GWApRiskstat(i, j)
    Sheets("RiskOutput").Cells(112 + i, 47 + j).Value = GWApIllMajorRiskstat(i, j)
    Sheets("RiskOutput").Cells(112 + i, 76 + j).Value = GWApIllMinorRiskstat(i, j)
Next j
'Soil model

m = 0

For k = 1 To 3
    For j = 1 To 5
        Sheets(RiskOutput).Cells(77 + i, 19 + j + m).Value = SoilApRiskstat(i, j, k)
        Sheets(RiskOutput).Cells(77 + i, 47 + j + m).Value = SoilApIllMajorRiskstat(i, j, k)
        Sheets(RiskOutput).Cells(77 + i, 76 + j + m).Value = SoilApIllMinorRiskstat(i, j, k)
    Next j
    m = k * j
Next k

'Ingestion of food crops model

m = 0

For k = 1 To 2
    For j = 1 To 5
        Sheets(RiskOutput).Cells(147 + i, 19 + j + m).Value = VegApRiskstat(i, j, k)
        Sheets(RiskOutput).Cells(147 + i, 47 + j + m).Value = VegApIllMajorRiskstat(i, j, k)
        Sheets(RiskOutput).Cells(147 + i, 76 + j + m).Value = VegApIllMinorRiskstat(i, j, k)
    Next j
    m = k * j
Next k
Next i

ElseIf UChoice = 1 Then 'Print for only selected pathogens and assign "Not selected" for others
    For i = 1 To 28
        If i = PathogenInterest Then
'Air model

m = 0

For k = 1 To 4 'Four subpopulations: FW, TD, RA, and RC
    For j = 1 To 5
        Sheets("RiskOutput").Cells(7 + i, 19 + j + m).Value = AirApRiskstat(i, j, k)
        Sheets("RiskOutput").Cells(7 + i, 47 + j + m).Value = AirApIllMajorRiskstat(i, j, k)
        Sheets("RiskOutput").Cells(7 + i, 76 + j + m).Value = AirApIllMinorRiskstat(i, j, k)
    Next j
    m = k * j
    Next k

'SW model

m = 0

For k = 1 To 2
    For j = 1 To 5
        Sheets("RiskOutput").Cells(42 + i, 19 + j + m).Value = SWApRiskstat(i, j, k)
        Sheets("RiskOutput").Cells(42 + i, 47 + j + m).Value = SWApIllMajorRiskstat(i, j, k)
        Sheets("RiskOutput").Cells(42 + i, 76 + j + m).Value = SWApIllMinorRiskstat(i, j, k)
    Next j
    m = k * j
    Next k

'GW model

For j = 1 To 5
    Sheets("RiskOutput").Cells(112 + i, 19 + j).Value = GWApRiskstat(i, j)
    Sheets("RiskOutput").Cells(112 + i, 47 + j).Value = GWApIllMajorRiskstat(i, j)
    Sheets("RiskOutput").Cells(112 + i, 76 + j).Value = GWApIllMinorRiskstat(i, j)
Next j
'Soil model

m = 0

For k = 1 To 3
    For j = 1 To 5
        Sheets("RiskOutput").Cells(77 + i, 19 + j + m).Value = SoilApRiskstat(i, j, k)
        Sheets("RiskOutput").Cells(77 + i, 47 + j + m).Value = SoilApIllMajorRiskstat(i, j, k)
        Sheets("RiskOutput").Cells(77 + i, 76 + j + m).Value = SoilApIllMinorRiskstat(i, j, k)
    Next j
    m = k * j
    Next k

'Ingestion of food crops model

m = 0

For k = 1 To 2
    For j = 1 To 5
        Sheets("RiskOutput").Cells(147 + i, 19 + j + m).Value = VegApRiskstat(i, j, k)
        Sheets("RiskOutput").Cells(147 + i, 47 + j + m).Value = VegApIllMajorRiskstat(i, j, k)
        Sheets("RiskOutput").Cells(147 + i, 76 + j + m).Value = VegApIllMinorRiskstat(i, j, k)
    Next j
    m = k * j
    Next k

End If

If i > PathogenInterest Then

'Air model
'SW model
m = 0
For k = 1 To 2
  For j = 1 To 5
    Sheets(RiskOutput).Cells(42 + i, 19 + j + m).Value = "NC"
    Sheets(RiskOutput).Cells(42 + i, 47 + j + m).Value = "NC"
    Sheets(RiskOutput).Cells(42 + i, 76 + j + m).Value = "NC"
  Next j
  m = k * j
Next k

'GW model
For j = 1 To 5
  Sheets(RiskOutput).Cells(112 + i, 19 + j).Value = "NC"
  Sheets(RiskOutput).Cells(112 + i, 47 + j).Value = "NC"
  Sheets(RiskOutput).Cells(112 + i, 76 + j).Value = "NC"
Next j
'Soil model

m = 0

For k = 1 To 3
    For j = 1 To 5
        Sheets("RiskOutput").Cells(77 + i, 19 + j + m).Value = "NC"
        Sheets("RiskOutput").Cells(77 + i, 47 + j + m).Value = "NC"
        Sheets("RiskOutput").Cells(77 + i, 76 + j + m).Value = "NC"
    Next j
    m = k * j
    Next k

'Ingestion of food crops model

m = 0

For k = 1 To 2
    For j = 1 To 5
        Sheets("RiskOutput").Cells(147 + i, 19 + j + m).Value = "NC"
        Sheets("RiskOutput").Cells(147 + i, 47 + j + m).Value = "NC"
        Sheets("RiskOutput").Cells(147 + i, 76 + j + m).Value = "NC"
    Next j
    m = k * j
    Next k

End If

If i < PathogenInterest Then

'Air model

m = 0

For k = 1 To 4 'Four subpopulations: FW, TD, RA, and RC
    For j = 1 To 5

A-60
Sheets("RiskOutput").Cells(7 + i, 19 + j + m).Value = "NC"
Sheets("RiskOutput").Cells(7 + i, 47 + j + m).Value = "NC"
Sheets("RiskOutput").Cells(7 + i, 76 + j + m).Value = "NC"

Next j
m = k * j
Next k

'SW model
m = 0
For k = 1 To 2
   For j = 1 To 5
      Sheets("RiskOutput").Cells(42 + i, 19 + j + m).Value = "NC"
      Sheets("RiskOutput").Cells(42 + i, 47 + j + m).Value = "NC"
      Sheets("RiskOutput").Cells(42 + i, 76 + j + m).Value = "NC"
   Next j
   m = k * j
   Next k

'Soil model
m = 0
For k = 1 To 3
   For j = 1 To 5
      Sheets("RiskOutput").Cells(77 + i, 19 + j + m).Value = "NC"
      Sheets("RiskOutput").Cells(77 + i, 47 + j + m).Value = "NC"
      Sheets("RiskOutput").Cells(77 + i, 76 + j + m).Value = "NC"
   Next j
   m = k * j
   Next k
'GW model
For j = 1 To 5
    Sheets("RiskOutput").Cells(112 + i, 19 + j).Value = "NC"
    Sheets("RiskOutput").Cells(112 + i, 47 + j).Value = "NC"
    Sheets("RiskOutput").Cells(112 + i, 76 + j).Value = "NC"
Next j

'Ingestion of food crops model
m = 0
For k = 1 To 2
    For j = 1 To 5
        Sheets("RiskOutput").Cells(147 + i, 19 + j + m).Value = "NC"
        Sheets("RiskOutput").Cells(147 + i, 47 + j + m).Value = "NC"
        Sheets("RiskOutput").Cells(147 + i, 76 + j + m).Value = "NC"
    Next j
    m = k * j
Next k

End If
Next i
End If

'PRINTING STATS OF CUMULATIVE RISK OF ILLNESS

'Air model
m = 0
For k = 1 To 4 'Four subpopulations:FW, TD, RA, and RC
    For j = 1 To 5
        Sheets("RiskOutput").Cells(7, 104 + j + m).Value = CumRespRiskstat(k, 1, j) 'stats for minor risk of illness
Sheets(RiskOutput).Cells(48, 104 + j + m).Value = CumRespRiskstat(k, 2, j) 'stats for major risk of illness
    Next j
    m = k * j
    Next k

'SW model

    m = 0
    For k = 1 To 2 'Two subpopulations: RA and RC
        For j = 1 To 5
            Sheets(RiskOutput).Cells(13, 104 + j + m).Value = CumSWGIRiskstat(k, 1, j) 'stats for minor risk of illness
            Sheets(RiskOutput).Cells(54, 104 + j + m).Value = CumSWGIRiskstat(k, 2, j) 'stats for major risk of illness
        Next j
        m = k * j
        Next k

'GW model

    For j = 1 To 5
        Sheets(RiskOutput).Cells(24, 104 + j).Value = CumGWGIRiskstat(1, j) 'stats for minor risk of illness
        Sheets(RiskOutput).Cells(65, 104 + j).Value = CumGWGIRiskstat(2, j) 'stats for major risk of illness
    Next j

'Soil model

    m = 0
    For k = 1 To 3 'Three subpopulations: RA, RC, and Occupational workers
For j = 1 To 5
    Sheets(RiskOutput).Cells(19, 104 + j + m).Value = CumSoilGIRiskstat(k, 1, j) 'stats for minor risk of illness
    Sheets(RiskOutput).Cells(60, 104 + j + m).Value = CumSoilGIRiskstat(k, 2, j) 'stats for major risk of illness
    Next j
    m = k * j
    Next k
'Ingestion of food crops model
    m = 0
    For k = 1 To 2 'Two subpopulations: RA, and RC
        For j = 1 To 5
            Sheets(RiskOutput).Cells(30, 104 + j + m).Value = CumVegGIRiskstat(k, 1, j) 'stats for minor risk of illness
            Sheets(RiskOutput).Cells(71, 104 + j + m).Value = CumVegGIRiskstat(k, 2, j) 'stats for major risk of illness
            Next j
            m = k * j
        Next k
    Next k

For i = 1 To 175
    For j = 1 To 111
        If Sheets(RiskOutput).Cells(i, j + 18).Value < 0 Then Sheets(RiskOutput).Cells(i, j + 18).Value = "Not available"
    Next j
    Next i

'RESETTING DEFAULT AVERAGE VALUES FOR ALL UNCERTAIN PARAMETERS
If restore = 1 Then
'Pathogen-related parameters
For n = 1 To 28
    Sheets("Pathogen").Cells(46 + n, 2).Value = Pdist(n, 2, 1) 'Pathogen initial conc. in biosolids in model
    Sheets("Pathogen").Cells(10 + n, 3).Value = Pdist(n, 2, 2) 'Pathogen release parameter for pathogens in model
    Sheets("Pathogen").Cells(10 + n, 8).Value = Pdist(n, 2, 3) 'Decay constant for pathogens in air in model
    Sheets("Pathogen").Cells(10 + n, 10).Value = Pdist(n, 2, 4) 'Decay constant for pathogens in water suspension in model
    Sheets("Pathogen").Cells(10 + n, 12).Value = Pdist(n, 2, 5) 'Pathogen liquid to liquid-solid mass transfer coefficient
    Sheets("Pathogen").Cells(10 + n, 13).Value = Pdist(n, 2, 6) 'Pathogen liquid to air-liquid mass transfer coefficient
    Sheets("Pathogen").Cells(10 + n, 14).Value = Pdist(n, 2, 7) 'Pathogen radius
    Sheets("Pathogen").Cells(10 + n, 55).Value = Pdist(n, 2, 8) 'Inhalation-related simplified dose-response model parameter
    Sheets("Pathogen").Cells(10 + n, 52).Value = Pdist(n, 2, 9) 'Ingestion-related simplified dose-response model parameter
Next n

'Air model parameters
Sheets("SurfaceConstants").Cells(26, 16).Value = Airdist(2, 1) 'Aerosolization efficiency for picked application method
Sheets("AirConstants").Cells(64, 2).Value = Airdist(2, 2) 'Mechanical stress-related resuspension factor
Sheets("AirConstants").Cells(4, 16).Value = Airdist(2, 3) 'Cabin filtration efficiency

'Soil parameters
For m = 1 To 12:
    Sheets("SurfaceConstants").Cells(50 + m, 2).Value = Soildist(m, 2, 1) 'Soil simulated hydraulic conductivity (cm/hr)
Sheets(SurfaceConstants).Cells(4 + m, 2).Value = Soildist(m, 2, 2) 'Soil simulated Pajian (1987) pore size index

Sheets(SurfaceConstants).Cells(4 + m, 5).Value = Soildist(m, 2, 3) 'Soil simulated Pajian (1987) residual moisture content

Sheets(SurfaceConstants).Cells(50 + m, 3).Value = Soildist(m, 2, 4) 'Soil simulated percentage sand content

Sheets(SurfaceConstants).Cells(50 + m, 4).Value = Soildist(m, 2, 5) 'Soil simulated percentage silt content

Sheets(SurfaceConstants).Cells(50 + m, 5).Value = Soildist(m, 2, 6) 'Soil simulated percentage clay content

Next m


'Set microorganism info. for pathogen of concern specifically from inputdata sheet

End If

Stoptime = Time 'Recording stop time

Sheets(RiskOutput).Cells(1, 11).Value = Stoptime

'RISK CALCULATION ENDS

'*******************************************************************************

End Sub
APPENDIX B

AIR CONSTANTS

Table B-1. Pasquill Stability Classes (Seinfeld, 1986).

<table>
<thead>
<tr>
<th>Wind (m/sec)</th>
<th>Strong</th>
<th>Moderate</th>
<th>Slight</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>A</td>
<td>A</td>
<td>B</td>
</tr>
<tr>
<td>1</td>
<td>A</td>
<td>B</td>
<td>B</td>
</tr>
<tr>
<td>2</td>
<td>A</td>
<td>B</td>
<td>C</td>
</tr>
<tr>
<td>3</td>
<td>B</td>
<td>B</td>
<td>C</td>
</tr>
<tr>
<td>4</td>
<td>B</td>
<td>B</td>
<td>C</td>
</tr>
<tr>
<td>5</td>
<td>B</td>
<td>C</td>
<td>D</td>
</tr>
<tr>
<td>6</td>
<td>C</td>
<td>C</td>
<td>D</td>
</tr>
<tr>
<td>7</td>
<td>C</td>
<td>D</td>
<td>D</td>
</tr>
</tbody>
</table>

Table B-2. Dispersion Constants (Seinfeld, 1986).

<table>
<thead>
<tr>
<th>Stability Class</th>
<th>Ry</th>
<th>Ry</th>
<th>Rz</th>
<th>rz</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>0.469</td>
<td>0.903</td>
<td>0.017</td>
<td>1.38</td>
</tr>
<tr>
<td>B</td>
<td>0.306</td>
<td>0.885</td>
<td>0.072</td>
<td>1.021</td>
</tr>
<tr>
<td>C</td>
<td>0.23</td>
<td>0.855</td>
<td>0.076</td>
<td>0.879</td>
</tr>
<tr>
<td>D</td>
<td>0.219</td>
<td>0.764</td>
<td>0.14</td>
<td>0.727</td>
</tr>
<tr>
<td>E</td>
<td>0.237</td>
<td>0.691</td>
<td>0.217</td>
<td>0.61</td>
</tr>
<tr>
<td>F</td>
<td>0.273</td>
<td>0.594</td>
<td>0.262</td>
<td>0.5</td>
</tr>
</tbody>
</table>

Table B-3. Resuspension Factor (1/m) (Sehmel, 1980).

<table>
<thead>
<tr>
<th>Component</th>
<th>Mean</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wind resuspension</td>
<td>1.50×10^{-4}</td>
<td>9.00×10^{-11}</td>
<td>3.00×10^{-2}</td>
</tr>
<tr>
<td>Mechanical stress</td>
<td>2.00×10^{-2}</td>
<td>1.00×10^{-10}</td>
<td>4.00×10^{-2}</td>
</tr>
</tbody>
</table>
APPENDIX C

AEROSOLIZATION EFFICIENCY ESTIMATION

In papers, to find out 1) the application rate of biosolids $Q_{\text{application}}$ (unit in g/s for dry biosolids, and ml/s for liquid biosolids), 2) the emission rate $Q_{\text{Emission}}$ (unit in microorganisms/s),

Calculate the aerosolize efficiency by

$$
E = \frac{Q_{\text{Emission}}}{Q_{\text{application}} \times N_0 \times f}
$$

Where $N_0$ is the occurrence number in biosolids (microorganisms/g for dry biosolids, and microorganisms/ml for liquid biosolids); $f$ is the solids content in biosolids (%).

C.1 Biosolids Applied by Spash-Plate Spray Applicator

For coliforms/\textit{E.coli}, Table 3 of Tanner et al. (2005) reports emission rate is $3.9 \times 10^1$ CFU/s (defined as “flux” term by authors), Table 2 of the same source reports occurrence number in liquid biosolids is $2.0 \times 10^5$ CFU/mL, and $f$ is estimated to be around 8%.

The application rate of biosolids $Q_{\text{application}}$ can be calculated as $V/(L/v)$, where $V$ is the capacity of the splash-plate spray applicator (=1.61×10⁴ L = 1.61×10⁷ mL), $L$ is the travel distance of the spray-tanker (=1000m), and $v$ is the approximated travel speed (=2.2m/s). The result is $Q_{\text{application}}=7.32 \times 10³$ mL/s.

Thus, $E = \frac{(3.9 \times 10^1 \text{CFU/s})}{(7.32 \times 10³ \text{mL/s}) \times (2 \times 10^5 \text{CFU/mL}) \times (8\%)} = 3.3 \times 10^{-7}$

C.2 Biosolids Applied by a Side Discharge Slinger

For coliforms, Table 1 of Paez-Rubio et al. (2007) reports the bulk biosolids concentration is $1.5 \times 10^6$ CFU/dry g, Table 1 also reports the emission rate is $4.9 \times 10^3$ CFU/s, $f$ is estimated to be 25% (range is 20-30%), and the dewatered biosolids were spread onto land at a rate of 110 dry kg/min (=1.8×10⁵ g/s).

Since the application rate is reported in unit of dry kg/min, the $f$ term was eliminated here.

Thus, $E = \frac{(4.9 \times 10^3 \text{CFU/s})}{(1.8 \times 10^5 \text{g/s}) \times (1.5 \times 10^6 \text{CFU/g})} = 1.81 \times 10^{-6}$

C.3 Biosolids Applied by the Disk Incorporation

For total coliforms, Table 1 of Paez-Rubio (2006) reports the bulk biosolids concentration is $8.56 \times 10^4$ CFU/dry g, Table 1 of the same source also reports the emission rate is $3.64 \times 10^4$ CFU/s, and $f$ is estimated to be 25% (range is 20-30%).

The averaged application rate is calculated as $B \times v \times W$, where $B$ is the application rate (=1.2×10⁴ kg/ha=1.2×10³ g/m²) (Ranged from 0.8×10⁴ kg/ha to 1.6×10⁴ kg/ha), $v$ is the average
velocity of the tractor (=1.3 m/s) (Low, Paez-Rubio et al., 2007), and W is the width of the disking apparatus (=6 m). The result is \( Q_{\text{application}} = 9.36 \times 10^3 \text{ g/s} \).

Thus, 
\[
E = \frac{(3.64 \times 10^4 \text{ CFU/s})}{(9.36 \times 10^3 \text{ g/s}) \times (8.56 \times 10^4 \text{ CFU/g})} = 4.5 \times 10^{-5}
\]
JOINT GREEN-AMPT MODEL VALIDATION

D.1 Comparison of Joint Green-Ampt Model with Constant Flux Green Ampt

The Joint Green-Ampt Model was compared with and validated against the Constant Flux Green-Ampt model, which can be applied under non-ponding conditions.

When rainfall rate ($r$) is smaller than saturated hydraulic conductivity ($K_s$), infiltration rates and cumulative infiltration ($I$) for both models are always the same. Infiltration rate is equal to rainfall rate and cumulative infiltration is equal to rainfall amount. This section compares these two models for the case when rainfall rate is greater than saturated hydraulic conductivity.

When results from the two models differ, the researchers compare the coefficient of determination ($R^2$) for infiltration rate and cumulative infiltration to assess how well the two models compare.

1. When soil type is sand, compare the infiltration rate and cumulative infiltration for $r=22\text{cm/h}$ and $r=26\text{cm/h}$, respectively ($K_s=21\text{cm/h}$).

![Figure D-1. Comparison of Infiltration Rate and Cumulative Infiltration in Sand by the Constant Flux Green-Ampt Model (red) and the Joint Green-Ampt Model (blue) with Rainfall Rates of 22cm/h (top) and 26cm/h (bottom).](image-url)
For 22 cm/h rainfall rate, coefficients of determination for infiltration rate and cumulative infiltration were calculated to be 0.71 and 0.99, respectively (Figure D-1). When rainfall rate=26cm/h, R² for infiltration rate =0.96.

(2) When soil type is loam, compare the infiltration rate and cumulative infiltration under \( r=2 \text{cm/h} \) and \( r=5 \text{cm/h} \), respectively (\( K_s=1.32 \text{cm/h} \)).

![Figure D-2. Comparison of Infiltration Rate and Cumulative Infiltration in Loam by the Constant Flux Green-Ampt Model (red) and the Joint Green-Ampt Model (blue) with Rainfall Rates of 2cm/h (top) and 5cm/h (bottom).](image)

For 2 cm/h rainfall rate, coefficients of determination for infiltration rate and cumulative infiltrations were calculated to be 0.63 and 0.92, respectively (Figure D-2).

(3) When soil type is clay, compare the infiltration rate and cumulative infiltration under \( r=0.5 \text{cm/h} \) and \( r=3 \text{cm/h} \), respectively (\( K_s=0.06 \text{cm/h} \)).
Figure D-3. Comparison of Infiltration Rate and Cumulative Infiltration in Clay by the Constant Flux Green-Ampt Model (red) and the Joint Green-Ampt Model (blue) with Rainfall Rates of 0.5cm/h (top) and 3cm/h (bottom).

For 0.5 cm/h rainfall rate, coefficients of determination for infiltration rate and cumulative infiltrations were calculated to be 0.96 and 0.96, respectively (Figure D-3).

For graphs with obvious differences, the researchers calculated the coefficient of determination. From the researchers’ results, all $R^2$ value were greater than 0.5. Most $R^2$ values were even close to 1, indicating that the Joint Green-Ampt model fits well the result obtained by the Constant Flux Green-Ampt model.

### D.2 Comparison of Runoff Ratio from Different Parameter Groups

This section presents the comparison of values of surface runoff ratio ($f_{\text{runoff}}$), obtained from the Joint Green-Ampt model using three groups of soil hydraulic properties (i.e., Brakensiek et al., 1981; Pajian, 1987; Carsel and Parrish, 1988) (Figures 11-A-4 and 11-A-5). This comparison indicates that the highest runoff ratio occurs when soil hydraulic properties from Pajian (1987) study were used.

For calculating the maximum risk of pathogen exposure from the surface water route, the highest runoff ratio is required. To obtain highest runoff ratio, the use of soil hydraulic properties from the Pajian (1987) study is recommended.
(1) When rainfall rate $r=5\text{cm/h}$

Figure D-4. Runoff Ratio with Different Parameters for Each Soil Type When Rainfall Rate $r=5\text{cm/h}$.

Runoff Ratio with the Pajian Study Parameters is the Highest.
(2). When rainfall rate =10cm/h

Figure D-5. Runoff Ratio with Different Parameters for Each Soil Type When Rainfall Rate r=10cm/h. Runoff Ratio Using the Pajian Study Parameters is the Highest.
### APPENDIX E

### CONSTANTS

Table E-1. Typical Hydraulic Parameter Values for Various Soil Texture Classes.
Saturated Hydraulic Conductivity ($K_s$), Pore Size Index ($\lambda$), Air-entry Head ($h_b$), Saturated Volumetric Water Content ($\theta_s$), Residual Volumetric Water Content ($\theta_r$), Bulk Density of the Soil ($\rho_b$), Water Retention Curve Fitting Parameter ($n$), Water Retention Curve Fitting Parameter ($\alpha$), and Average Radius of Soil Particles ($r_s$). (Carsel and Parrish, 1988).

<table>
<thead>
<tr>
<th>Soil texture class</th>
<th>$K_s$ (cm/hr)</th>
<th>$\lambda$ (cm)</th>
<th>$h_b$ (cm)</th>
<th>$\theta_s$ (cm$^3$/cm$^3$)</th>
<th>$\theta_r$ (cm$^3$/cm$^3$)</th>
<th>$\rho_b$ (g/cm$^3$)</th>
<th>$n$ (m$^{-1}$)</th>
<th>$\alpha$ (cm$^{-1}$)</th>
<th>$r_s$ (cm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sand</td>
<td>29.7</td>
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<td>-6.9</td>
<td>0.43</td>
<td>0.045</td>
<td>1.51</td>
<td>2.68</td>
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<tr>
<td>Loamy_sand</td>
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<td>0.057</td>
<td>1.56</td>
<td>2.28</td>
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<td>Sandy_loam</td>
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<td>1.89</td>
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<td>Loam</td>
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<td>1.56</td>
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<td>1.41</td>
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<td>1.48</td>
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<td>0.06</td>
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<td>1.56</td>
<td>1.31</td>
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<td>Silt_clay_Loam</td>
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<td>$\lambda_s$ (hr)</td>
<td>$k_s$ (cm/hr)</td>
<td>$k_a$ (cm/hr)</td>
<td>$r_p$ (cm)</td>
<td>$N_0$ (number/g dry biosolids)</td>
<td>$f$ (unitless)</td>
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Table E-3. Typical Values of Saturated Hydraulic Conductivity and Percentage Fractions of Sand, Silt, and Clay of Different Texture Classes.

<table>
<thead>
<tr>
<th>Texture Class</th>
<th>% Sand</th>
<th>%Silt</th>
<th>%Clay</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sand</td>
<td>90</td>
<td>6</td>
<td>4</td>
</tr>
<tr>
<td>Loamy Sand</td>
<td>82</td>
<td>12</td>
<td>6</td>
</tr>
<tr>
<td>Sandy Loam</td>
<td>65</td>
<td>25</td>
<td>10</td>
</tr>
<tr>
<td>Loam</td>
<td>41</td>
<td>41</td>
<td>18</td>
</tr>
<tr>
<td>Silt Loam</td>
<td>20</td>
<td>65</td>
<td>15</td>
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<tr>
<td>Sandy Clay Loam</td>
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<td>27</td>
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<td>Clay Loam</td>
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<tr>
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<td>Clay</td>
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<td>20</td>
<td>60</td>
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<td>Sandy Clay</td>
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<td>Silt</td>
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<td>87</td>
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(Source: U.S. EPA, 1998)

Table E-4. Typical Values of Porosity (n) (cm\(^3\)/cm\(^3\)) (Morris and Johnson, 1967).

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<th>Soil Texture Class</th>
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</tr>
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<td>Sand Coarse</td>
<td>0.39</td>
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<td>Sand Fine</td>
<td>0.43</td>
</tr>
<tr>
<td>Loam</td>
<td>0.45</td>
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<td>Silt</td>
<td>0.46</td>
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<tr>
<td>Clay</td>
<td>0.42</td>
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Table E-5. Typical Values of Bulk Density ($\rho_b$) (g/cm$^3$) (Leij et al., 1996).

<table>
<thead>
<tr>
<th>Soil texture class</th>
<th>Bulk density</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sand Coarse</td>
<td>1.58</td>
</tr>
<tr>
<td>Sand Fine</td>
<td>1.58</td>
</tr>
<tr>
<td>Loam</td>
<td>1.43</td>
</tr>
<tr>
<td>Silt</td>
<td>1.43</td>
</tr>
<tr>
<td>Clay</td>
<td>1.29</td>
</tr>
</tbody>
</table>

Table E-6. Mass-Fraction (-) of Different Particle Classes (RUSLE, 2008).

<table>
<thead>
<tr>
<th>Texture class</th>
<th>Primary Clay</th>
<th>Small Aggregate</th>
<th>Primary Silt</th>
<th>Small Aggregate</th>
<th>Primary Sand</th>
<th>Large Aggregate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sand</td>
<td>0.0104</td>
<td>0.072</td>
<td>0.0001</td>
<td>0.0599</td>
<td>0.7338</td>
<td>0.1958</td>
</tr>
<tr>
<td>Loamy_sand</td>
<td>0.0156</td>
<td>0.108</td>
<td>0.012</td>
<td>0.108</td>
<td>0.6018</td>
<td>0.2626</td>
</tr>
<tr>
<td>Sandy_loam</td>
<td>0.026</td>
<td>0.18</td>
<td>0.07</td>
<td>0.18</td>
<td>0.3838</td>
<td>0.3402</td>
</tr>
<tr>
<td>Loam</td>
<td>0.0468</td>
<td>0.324</td>
<td>0.086</td>
<td>0.324</td>
<td>0.1520</td>
<td>0.3912</td>
</tr>
<tr>
<td>Silty_loam</td>
<td>0.039</td>
<td>0.27</td>
<td>0.38</td>
<td>0.27</td>
<td>0.0887</td>
<td>0.2223</td>
</tr>
<tr>
<td>Sandy_clay_loam</td>
<td>0.0702</td>
<td>0.438</td>
<td>0.0001</td>
<td>0.1299</td>
<td>0.1244</td>
<td>0.6754</td>
</tr>
<tr>
<td>Clay_loam</td>
<td>0.0884</td>
<td>0.396</td>
<td>0.0001</td>
<td>0.3299</td>
<td>0.0413</td>
<td>0.5403</td>
</tr>
<tr>
<td>Silt_clay_loam</td>
<td>0.0884</td>
<td>0.396</td>
<td>0.164</td>
<td>0.396</td>
<td>0.0125</td>
<td>0.3391</td>
</tr>
<tr>
<td>Silty clay</td>
<td>0.1222</td>
<td>0.318</td>
<td>0.152</td>
<td>0.318</td>
<td>0.0025</td>
<td>0.4053</td>
</tr>
<tr>
<td>Clay</td>
<td>0.156</td>
<td>0.36</td>
<td>0.0001</td>
<td>0.1999</td>
<td>0.0020</td>
<td>0.6420</td>
</tr>
<tr>
<td>Sandy clay</td>
<td>0.1144</td>
<td>0.336</td>
<td>0.0001</td>
<td>0.0499</td>
<td>0.0280</td>
<td>0.8075</td>
</tr>
<tr>
<td>Silt</td>
<td>0.013</td>
<td>0.09</td>
<td>0.78</td>
<td>0.09</td>
<td>0.0619</td>
<td>0.0551</td>
</tr>
</tbody>
</table>
Table E-7. Manning’s Constants (Water Depth < 30 mm).

<table>
<thead>
<tr>
<th>Surface description</th>
<th>Manning’s n-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cultivated soil w/ residue</td>
<td>0.06 (0.05-0.17)</td>
</tr>
<tr>
<td>Grass*</td>
<td>0.195 (0.13-0.41)</td>
</tr>
</tbody>
</table>

*Including constant values for short grass prairie, dense grass, Bermuda, and natural grasses. Source: SCS (1986).

Table E-8. Diameter (mm) of Different Particle Classes (RUSLE, 2008).

<table>
<thead>
<tr>
<th>Texture class</th>
<th>Primary clay</th>
<th>Primary silt</th>
<th>Primary sand</th>
<th>Small aggregate</th>
<th>Large aggregate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sand</td>
<td>0.002</td>
<td>0.01</td>
<td>0.3</td>
<td>0.03</td>
<td>0.3</td>
</tr>
<tr>
<td>Loamy_sand</td>
<td>0.002</td>
<td>0.01</td>
<td>0.3</td>
<td>0.03</td>
<td>0.3</td>
</tr>
<tr>
<td>Sandy_loam</td>
<td>0.002</td>
<td>0.01</td>
<td>0.3</td>
<td>0.03</td>
<td>0.3</td>
</tr>
<tr>
<td>Loam</td>
<td>0.002</td>
<td>0.01</td>
<td>0.3</td>
<td>0.03</td>
<td>0.36</td>
</tr>
<tr>
<td>Silty_loam</td>
<td>0.002</td>
<td>0.01</td>
<td>0.3</td>
<td>0.03</td>
<td>0.3</td>
</tr>
<tr>
<td>Sandy_clay_loam</td>
<td>0.002</td>
<td>0.01</td>
<td>0.3</td>
<td>0.034</td>
<td>0.54</td>
</tr>
<tr>
<td>Clay_loam</td>
<td>0.002</td>
<td>0.01</td>
<td>0.3</td>
<td>0.048</td>
<td>0.68</td>
</tr>
<tr>
<td>Silt_clay_loam</td>
<td>0.002</td>
<td>0.01</td>
<td>0.3</td>
<td>0.048</td>
<td>0.68</td>
</tr>
<tr>
<td>Silty clay</td>
<td>0.002</td>
<td>0.01</td>
<td>0.3</td>
<td>0.074</td>
<td>0.94</td>
</tr>
<tr>
<td>Clay</td>
<td>0.002</td>
<td>0.01</td>
<td>0.3</td>
<td>0.1</td>
<td>1.2</td>
</tr>
<tr>
<td>Sandy clay</td>
<td>0.002</td>
<td>0.01</td>
<td>0.3</td>
<td>0.068</td>
<td>0.88</td>
</tr>
<tr>
<td>Silt</td>
<td>0.002</td>
<td>0.01</td>
<td>0.3</td>
<td>0.03</td>
<td>0.3</td>
</tr>
</tbody>
</table>
Table E-9. Specific Density (RUSLE, 2008).

<table>
<thead>
<tr>
<th>Texture class</th>
<th>Primary clay</th>
<th>Primary silt</th>
<th>Primary sand</th>
<th>Small aggregate</th>
<th>Large aggregate</th>
</tr>
</thead>
<tbody>
<tr>
<td>All texture classes</td>
<td>2.6</td>
<td>2.65</td>
<td>2.65</td>
<td>1.8</td>
<td>1.6</td>
</tr>
</tbody>
</table>

Table E-10. Calculated Fall Velocity (ft/sec) in Water.

<table>
<thead>
<tr>
<th>Texture class</th>
<th>Primary clay</th>
<th>Primary silt</th>
<th>Primary sand</th>
<th>Small aggregate</th>
<th>Large aggregate</th>
</tr>
</thead>
<tbody>
<tr>
<td>All texture classes</td>
<td>1.15E-05</td>
<td>2.96E-04</td>
<td>2.66E-01</td>
<td>1.29E-03</td>
<td>9.67E-02</td>
</tr>
</tbody>
</table>
APPENDIX F

SUBFACTORS FOR GROUNDWATER EXPOSURE MODEL

F.1 Critical Rainfall Information (Teng, Kumar, et al., 2010)

This section describes how to estimate the rainfall intensity and duration associated with different probabilities of runoff and infiltration.

F.1.1 Approach and Results

Generalized precipitation-frequency maps provided by the U.S. Weather Bureau provide return periods for rainfall intensities associated with different durations. However, the probabilities of different amounts of runoff and infiltration are not directly available. Teng et al., present an approach to derive these probabilities by identifying the maximum runoff and the maximum infiltration associated with a given return period (Teng, Kumar et al., 2010). The critical rainfall events (i.e., intensities and durations), identified in this manner, can be used to calculate infiltration depth and runoff volumes for use in exposure and infection risk models. The inverse of the return period of the critical rainfall event provides the probabilities of infiltration and runoff produced by that rainfall. The calculated exposure risk of infection is conditional on the occurrence of this amount of infiltration and runoff. Table F-1 presents the probabilities of critical rainfall events, and their associated infiltration depths, for East Lansing (Michigan, U.S.). The default values for intensity and duration are in Sheet GWConstants Row 8 to Row 17.

Table F-1. Precipitation Parameter Values Estimated by (Carsel and Parrish, 1988).

<table>
<thead>
<tr>
<th>Return Period (year)</th>
<th>Probability of Occurrence in One Day</th>
<th>Duration (h)</th>
<th>Intensity (cm/h)</th>
<th>Wetting Front Depth (cm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>1.37×10⁻³</td>
<td>0.5</td>
<td>5.18</td>
<td>9.74</td>
</tr>
<tr>
<td>5</td>
<td>5.48×10⁻⁴</td>
<td>1</td>
<td>4.26</td>
<td>14.55</td>
</tr>
<tr>
<td>10</td>
<td>2.74×10⁻⁴</td>
<td>1</td>
<td>4.92</td>
<td>14.55</td>
</tr>
<tr>
<td>25</td>
<td>1.10×10⁻⁴</td>
<td>1</td>
<td>5.36</td>
<td>14.55</td>
</tr>
<tr>
<td>50</td>
<td>5.48×10⁻⁵</td>
<td>2</td>
<td>2.84</td>
<td>16.16</td>
</tr>
<tr>
<td>100</td>
<td>2.74×10⁻⁵</td>
<td>2</td>
<td>3.20</td>
<td>22.14</td>
</tr>
</tbody>
</table>

F.1.2 Dispersivity Estimation

Dispersivity is an important hydraulic parameter in the subsurface transport and fate model (Groundwater Exposure Model User Manual Chapter 6 Constants section). Vertical dispersivity (αz; unit in cm; Sheet: GWPathogenModel, Cell: B8) and horizontal dispersivity (αx; unit in cm; Sheet: GWPathogenModel, Cell: B9) are estimated.
Dispersivity, including vertical dispersivity ($\alpha_z$) and horizontal dispersivity ($\alpha_x$) were found to increase with increasing transport distance and scale of the experiment (Vanderborght and Vereecken, 2007). A proposed relationship to estimate dispersivity based on the length of the flow path is presented by Xu and Eckstein (Xu and Eckstein, 1995). Results were compared with literature values, as shown in Table F-2. Reported data show a larger range of values than estimated by the calculations, but the average values were close. The average dispersivity was calculated based on transport distance taken from inputs to the spreadsheet model.

$$\alpha = 0.83 (\log L)^{2.414} \quad (F-1)$$

where $\alpha$ is the dispersivity, and $L$ is the length of the flow path.

Table F-2. Comparison of Dispersivity Values (cm) Reported from Literature and Calculated from Equation F-1.

<table>
<thead>
<tr>
<th>Travel Distance</th>
<th>Data from Review Paper (Vanderborght and Vereecken, 2007)</th>
<th>Results from Calculation (Xu and Eckstein, 1995)</th>
</tr>
</thead>
<tbody>
<tr>
<td>81-200 cm</td>
<td>5-10</td>
<td>3.95-6.2</td>
</tr>
<tr>
<td>31-80 cm</td>
<td>2.5-15</td>
<td>2.18-3.92</td>
</tr>
<tr>
<td>0-30 cm</td>
<td>1.5-10</td>
<td>0.83-2.13</td>
</tr>
</tbody>
</table>

F.1.3 Mass Transfer Coefficients

Mass transfer coefficients for liquid-solid and air-liquid mass transfer are input parameters to the subsurface transport and fate model, and are determined by pathogen type and soil texture. Since there are few established correlations for the liquid-solid mass transfer coefficient ($k_s$; unit in cm/hr; Sheet: GWPathogenModel, Cell: B30) or air-liquid mass transfer coefficient ($k_a$; unit in cm/hr; Sheet: GWPathogenModel, Cell: B31), the researchers rely on results estimated from Anders (2009).

According to Equations 8-15 and 8-17, the mass transfer rate ($K_s$ for liquid-solid and $K_a$ for air-liquid) and interfacial area ($\alpha_{ts}$ for liquid-solid and $\alpha_{ta}$ for air-liquid) are required for estimation of the mass transfer coefficients. Model parameters (Anders, 2009, Table 1) and breakthrough curve fitted data in experiment 3 for MS2 (Anders, 2009, Table 2) were used for this back-calculation.

$$k_s = \frac{K_s}{\alpha_{ts}} = \frac{0.0033 h^{-1}}{1.392 cm^{-1}} = 2.37 \times 10^{-5} \left(\frac{cm}{h}\right) \quad (F-2)$$

$$k_a = \frac{K_a}{\alpha_{ta}} = \frac{0.012 h^{-1}}{95.3 cm^{-1}} = 1.26 \times 10^{-4} \left(\frac{cm}{h}\right) \quad (F-3)$$

F.1.4 Straining Coefficient Calculation

The straining mechanism was included in the model to capture pathogen removal due to physical straining and is particularly relevant for larger microbes, such as bacteria and protozoa. The straining removal is determined by the coefficient ($k_{str}$) (h$^{-1}$) (Sheet: GWPathogenModel,
Cell: B34) and the distance for straining (h_{str}) (cm) (Sheet: GWPathogenModel, Cell: B35). The details of the approach are discussed below.

**F.2 Model Development**

The formula below was used to predict the concentration of strained microorganisms (Tufenkji, 2007)

\[
\frac{C}{C_0} = \exp \left( - \frac{k_{str}}{v} L \right)
\]

where \( C \) is the effluent concentration and \( C_0 \) is the influent concentration, \( k_{str} \) is the straining coefficient, \( v \) is the interstitial microbe velocity, and \( L \) is transport distance. The fraction of strained microorganisms is calculated as \((1-C/C_0)\).

**F.3 Parameter Estimation**

Bradford et al. (2004) report that straining occurs when the ratio of the organism size to the median grain diameter is larger than 0.5%. Values for \( k_{str} \) were estimated using a correlation based on the microorganism grain size ratio (Bradford, Simunek et al., 2003).

\[
k_{str} = 269.7 \left( \frac{d_p}{d_{50}} \right)^{1.42}
\]

where \( d_p \) is microorganism size and \( d_{50} \) is the median porous medium grain diameter.

Foppen found that straining took place over the entire column length, but there was more strained material near the column inlet (especially for the first 1 cm length) than further away (Foppen, Van Herwerden et al., 2007). The researchers assumed that straining only occurs in the first 1 centimeter, which is \( L=2 \) cm.

**F.4 Results and Discussion**

The applicability of the straining model is shown by calculating the straining removal for bacteria (0.5-5 micron) and protozoa (10-50 micron). The interstitial velocity \( v \) was assumed to be constant as 0.05 cm/s based on Foppen’s research (Foppen, Van Herwerden et al., 2007). The straining coefficient values \( (k_{str}) \) and calculated strained fractions calculated in this model for bacteria and protozoa in various soils are shown in Table F-3.

**F.4.1 Bacteria**

Values for \( k_{str} \) were reported for *Escherichia coli* in saturated columns (Foppen, Van Herwerden et al., 2007). The \( k_{str} \) for grain sizes of 75-90 µm was 0.0334, which is consistent with the researchers’ prediction for bacterial transport in silty clay and silt soil (soil particle size of 81.36 µm and 90.52 µm, respectively). The percentage of strained bacteria during transport in fine grained soil, such as silt, was found to be 10.58-94.73% of the total number applied. This result is consistent with the 15-21% straining reported in Foppen’s study (Foppen, Van Herwerden et al., 2007).

**F.4.2 Protozoa**

Estimation of \( k_{str} \) (equation F-2) was based on column studies using colloid sizes of 0.45 to 3.2 µm, a size range which is comparable to that of bacteria. Confidence in the prediction of \( k_{str} \) and thereby strained fraction, for protozoa or protozoan-sized microspheres based on these estimates is not very high. However, physical straining may play a significant role for larger
microorganisms and was therefore included in the model to capture some of the aspects of relative risk among organisms of different sizes. Below are results from published literature to verify the model predictions.

a) The removal for Cryptosporidium parvum Oocysts was approximately 41% during transport in a 7.1 cm column packed with clean quartz grains (with average grain diameter of 210 μm, comparable size to silty loam) (Tufenkji, Miller et al., 2004). The researchers’ prediction for strained small protozoa by silty loam is 52.92%.

b) Harvey studied the transport of flagellates in column experiments and found no elution of large microspheres (diameter of 6.2 μm) and minimal elution of smaller microspheres (diameter of 2.8-μm) through 0.6 m of sediment (500 to 1000 μm grain size) (Harvey, Kinner et al., 1995). The researchers’ predictions for straining of protozoa in sandy clay (soil particle size of 530.4 μm) range between 21.26% and 99.81%.

A large fraction (45-73%) of protozoan microsporidia (diameters ranging between 1 and 5 μm) was not recovered in the effluent from 7cm long sandy columns (Brusseau, Oleen et al., 2005). The researchers’ prediction of protozoa strained by sand is 10.03-93.8%.

Table F-3. kstr and Calculated Strained Fraction of Microorganisms.

<table>
<thead>
<tr>
<th>Soil texture</th>
<th>kstr</th>
<th>Strained fraction ((1-C/C_0))</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Bacteria</td>
<td>Protozoa</td>
</tr>
<tr>
<td></td>
<td>min</td>
<td>Max</td>
</tr>
<tr>
<td>Sand</td>
<td>0.0001</td>
<td>0.002642</td>
</tr>
<tr>
<td>Loamy sand</td>
<td>0.000118</td>
<td>0.003108</td>
</tr>
<tr>
<td>Sandy loam</td>
<td>0.000163</td>
<td>0.004291</td>
</tr>
<tr>
<td>Loam</td>
<td>0.000307</td>
<td>0.008073</td>
</tr>
<tr>
<td>Silty loam</td>
<td>0.000716</td>
<td>0.018834</td>
</tr>
<tr>
<td>Sandy clay loam</td>
<td>0.000184</td>
<td>0.004838</td>
</tr>
<tr>
<td>Clay loam</td>
<td>0.000435</td>
<td>0.011454</td>
</tr>
<tr>
<td>Silt clay loam</td>
<td>0.001979</td>
<td>0.052048</td>
</tr>
<tr>
<td>Silty clay</td>
<td>0.003254</td>
<td>0.085602</td>
</tr>
<tr>
<td>Clay</td>
<td>0.000914</td>
<td>0.024038</td>
</tr>
<tr>
<td>Sandy clay</td>
<td>0.000227</td>
<td>0.005975</td>
</tr>
<tr>
<td>silt</td>
<td>0.002797</td>
<td>0.073568</td>
</tr>
</tbody>
</table>
G.1 Verification by Eisenberg et al. (2006)

The transport models were compared to simulation results from Eisenberg et al. (2006). The spreadsheet models for transport in saturated and unsaturated soil were run separately.

G.1.1 Pathogen Transport Model in the Saturated Zone

Table G-1 shows the input parameter definitions and values used to validate the saturated transport model. Table G-2 shows point estimates for log removal predicted from the spreadsheet model, as compared to results from Monte Carlo simulations presented by Eisenberg et al. (2006) (Figure G-1). Log removal estimates from the spreadsheet model are higher than the upper bound values estimated by Eisenberg et al. (2006).

| Table G-1. Input Parameters for the Saturated Model. |
|---------------------------------|---------------------------------|--------------------------------------------------|
| Parameter | Values | Description |
| α (cm) | 0.43 | Vertical hydrodynamic dispersivity |
| v (cm/h) | 14.58 | Velocity |
| λ (h⁻¹) | 1.875E⁻³ | Inactivation rate for free pathogens |
| Kₐ (cm³ g⁻¹) | 17.8 | Equilibrium distribution coefficient |

<p>| Table G-2. Output of Log Removal Estimations for Saturated Model. |
|---------------------------------------------------------|-----------------|-----------------|</p>
<table>
<thead>
<tr>
<th>Distance (m)</th>
<th>Estimations from Eisenberg et al., 2006</th>
<th>Output from Spreadsheet Model</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>SD</td>
</tr>
<tr>
<td>5</td>
<td>1.23</td>
<td>0.09</td>
</tr>
<tr>
<td>15</td>
<td>3.68</td>
<td>0.27</td>
</tr>
<tr>
<td>30</td>
<td>7.35</td>
<td>0.53</td>
</tr>
</tbody>
</table>
The steady-state conditions assumed by Eisenberg et al. (2006) would be reached during maximum breakthrough concentration, which assumes long-term, continual input of pathogens and may be seen as the worst-case scenario. The transient, instantaneous source model predicts a slightly lower level of pathogen breakthrough compared with the steady-state solution. Results from the spreadsheet model showed higher, but acceptable, log removal rates compared to previous estimates run under steady-state conditions. Although slightly less conservative, the instantaneous source model was used since its analytical solution is easier to implement in a spreadsheet environment, and it corresponds to the realistic situation of a single input of biosolids to a field per growing season.

### G.1.2 Pathogen Transport Model in the Unsaturated Zone

Table G-3 shows the input parameter values used to validate the unsaturated zone model. Table G-4 shows the output for log removal, comparing results from the spreadsheet model to estimates presented by Eisenberg et al. (2006) (Figure G-2).
### Table G-3. Input Parameter Value Distributions for the Unsaturated Model.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Distribution</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>log $K_s$ (log m h$^{-1}$)</td>
<td>N(-6.91E-1, 2.18E+1)</td>
<td>Saturated hydraulic conductivity</td>
</tr>
<tr>
<td>$\theta_s$ (cm$^3$ cm$^{-3}$)</td>
<td>N(3.67E-1, 3.20E-2)</td>
<td>Saturated soil moisture content</td>
</tr>
<tr>
<td>$\theta_r$ (cm$^3$ cm$^{-3}$)</td>
<td>N(5.00E-2, 3.00E-3)</td>
<td>Residual soil water content</td>
</tr>
<tr>
<td>$\rho$ (g m$^{-3}$)</td>
<td>N(1.58E+6, 1.42E+5)</td>
<td>Soil bulk density</td>
</tr>
<tr>
<td>log n (unitless)</td>
<td>N(4.82E-1, 7.70E-2)</td>
<td>Water retention curve fitting parameter</td>
</tr>
<tr>
<td>log $\alpha$ (log m$^{-1}$)</td>
<td>N(5.31E-1, 3.40E-2)</td>
<td>Water retention curve fitting parameter</td>
</tr>
<tr>
<td>$\kappa$ (m)</td>
<td>N(5.59E-3, 1.00E-4)</td>
<td>Vertical hydrodynamic dispersivity</td>
</tr>
<tr>
<td>$r_p$ (m)</td>
<td>N(4.71E-4, 1.60E-5)</td>
<td>Mean soil particle radius</td>
</tr>
<tr>
<td>$T$ (°Celsius)</td>
<td>N(1.17E+1, 7.38E+0)</td>
<td>Temperature</td>
</tr>
<tr>
<td>log $\lambda_l$ (log h$^{-1}$)</td>
<td>N(-2.406E-0, 1.62E-1)</td>
<td>Inactivation rate for suspended pathogens</td>
</tr>
<tr>
<td>log $\lambda_s$ (log h$^{-1}$)</td>
<td>N(-2.684E-0, 1.62E-1)</td>
<td>Inactivation rate for soil-sorbed pathogens</td>
</tr>
<tr>
<td>$k_s$ (m h$^{-1}$)</td>
<td>N(1.34E-3, 1.80E-3)</td>
<td>Suspended to solid sorbed pathogen mass transfer coefficient</td>
</tr>
<tr>
<td>$k_a$ (m$^{-1}$)</td>
<td>N(9.27E-3, 1.80E-3)</td>
<td>Suspended to air sorbed pathogen mass transfer coefficient</td>
</tr>
<tr>
<td>$r_v$ (m)</td>
<td>N(1.38E-10, 1.00E-11)</td>
<td>Pathogen radius</td>
</tr>
<tr>
<td>$K_d$ (m$^3$ g$^{-1}$)</td>
<td>N(7.44E-1, 2.53E-3)</td>
<td>Equilibrium distribution coefficient</td>
</tr>
<tr>
<td>$\theta_m$ (cm$^3$ cm$^{-3}$)</td>
<td>2.00E-1</td>
<td>Moisture content</td>
</tr>
<tr>
<td>$K_b$ (J K$^{-1}$)</td>
<td>1.38E-23</td>
<td>Boltzmann's constant</td>
</tr>
<tr>
<td>$\mu$ (g m$^{-1}$ h$^{-1}$)</td>
<td>4.72E+3</td>
<td>Viscosity of water</td>
</tr>
<tr>
<td>$\sigma$ (g h$^{-2}$)</td>
<td>9.62E+8</td>
<td>Surface tension of water</td>
</tr>
<tr>
<td>$g$ (m s$^{-2}$)</td>
<td>9.8E+0</td>
<td>Acceleration due to gravity</td>
</tr>
<tr>
<td>$\rho_w$ (kg m$^{-3}$)</td>
<td>1.00E+3</td>
<td>Density of water</td>
</tr>
</tbody>
</table>

N(mean, standard deviation) - normal distribution.

### Table G-4. Output of Log Removal of Pathogens through the Unsaturated Zone.

<table>
<thead>
<tr>
<th>Distance (m)</th>
<th>Mean</th>
<th>SD</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.25</td>
<td>19.2</td>
<td>18.1</td>
<td>0.05</td>
<td>289.2</td>
</tr>
<tr>
<td>0.5</td>
<td>37.8</td>
<td>34.4</td>
<td>0.08</td>
<td>320.8</td>
</tr>
<tr>
<td>1</td>
<td>72.7</td>
<td>58.8</td>
<td>0.24</td>
<td>323.3</td>
</tr>
</tbody>
</table>
G.2 Verification by Anders et al. (2009)

Results from the spreadsheet transport model were compared to experimental results from Anders et al. (2009). MS2 and PRD1 were selected as model viruses and their transport behavior through columns packed with sand was studied. The spreadsheet models for transport in saturated and unsaturated soil were run separately. Table G-5 shows the input parameter values used in this exercise.

Table G-5. Input Parameters for Saturated (100% Saturation) and Unsaturated (76% and 54% Saturation) Model.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Values</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>100% saturation</td>
<td>76% saturation</td>
</tr>
<tr>
<td>$r_p$ (cm)</td>
<td>0.0125</td>
<td></td>
</tr>
<tr>
<td>$l$ (cm)</td>
<td>15.2</td>
<td></td>
</tr>
<tr>
<td>$\theta_s$ (cm$^3$ cm$^{-3}$)</td>
<td>0.409</td>
<td></td>
</tr>
<tr>
<td>$\theta_r$ (cm$^3$ cm$^{-3}$)</td>
<td>0.003</td>
<td></td>
</tr>
<tr>
<td>$v$ (cm/h)</td>
<td>MS2 37.8 PRD1 41.4</td>
<td>24.6 25.2</td>
</tr>
<tr>
<td>$D$ (cm$^2$/h)</td>
<td>MS2 5.46 PRD1 2.92</td>
<td>2.2 4.27</td>
</tr>
<tr>
<td>$K_D$ (cm$^3$/g)</td>
<td>MS2 33.72 PRD1 36.17</td>
<td>380.9 40.75</td>
</tr>
<tr>
<td>$\lambda_l$ (h$^{-1}$)</td>
<td>MS2 2.5E-3 PRD1 8.75E-5</td>
<td></td>
</tr>
<tr>
<td>$\lambda_s$ (h$^{-1}$)</td>
<td>MS2 2.75E-3 PRD1 8.5E-5</td>
<td></td>
</tr>
</tbody>
</table>
Using the inputs from Table G-5 in the spreadsheet model, the cumulative number of pathogens recovered at the end of the transport distance was reported, and the recovery fractions were calculated. These values were in good agreement with the recovery fractions reported in breakthrough curves from the Anders et al. (2009) column study (Table G-6).

### Table G-6. Comparison of Model-Predicted Pathogen Recovery Fractions with Experimental Data.

<table>
<thead>
<tr>
<th>Water saturation</th>
<th>100%</th>
<th></th>
<th>76%</th>
<th></th>
<th>54%</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Biosolids model</td>
<td>Column study</td>
<td>Biosolids model</td>
<td>Column study</td>
<td>Biosolids model</td>
<td>Column study</td>
</tr>
<tr>
<td>MS2</td>
<td>1</td>
<td>1</td>
<td>0.989</td>
<td>1</td>
<td>0.892</td>
<td>0.890</td>
</tr>
<tr>
<td>PRD1</td>
<td>1</td>
<td>1</td>
<td>0.998</td>
<td>1</td>
<td>0.940</td>
<td>0.950</td>
</tr>
</tbody>
</table>

### Table G-7. Partitioning Values.

<table>
<thead>
<tr>
<th>Microorganisms</th>
<th>Mean</th>
<th>SD</th>
<th>UF</th>
<th>Min</th>
<th>Max</th>
<th>Reference</th>
<th>Remarks</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adenovirus</td>
<td>2.5%</td>
<td>2%</td>
<td>4%</td>
<td>Xagoraraki, 2010</td>
<td>Percentage of virus desorbed from soil (with 8% organic matter) by the first extraction.</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>&lt;1%</td>
<td></td>
<td></td>
<td>Xagoraraki, 2010</td>
<td>Percentage of virus desorbed from soil (with 2% organic matter) by the first extraction.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Coliphage</td>
<td>7.4%</td>
<td></td>
<td></td>
<td>Chetochine, 2006</td>
<td>Recovery from column transport studies with 7% biosolids.</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>4.3%</td>
<td>3.3%</td>
<td>5.3%</td>
<td>Chetochine, 2006</td>
<td>Recovery from column transport studies with 2% biosolids.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Poliovirus and echovirus</td>
<td>0%</td>
<td></td>
<td></td>
<td>Bitton, 1984</td>
<td>Percentage of virus in soil leachates collected after natural rainfall</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Salmonella enterica ssp.</td>
<td>30%</td>
<td>13.88%</td>
<td>52.26%</td>
<td>Horswell, 2008</td>
<td>Percentage of salmonella in leachate from sewage sludge (200 kg N ha⁻¹) (study for New Zealand)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Enterica serovar</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Thphimurium-lux</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adenovirus</td>
<td>0.077</td>
<td>0.043</td>
<td>0.121</td>
<td>Horswell, 2008</td>
<td>Percentage of adenovirus in leachate from sewage sludge (200 kg N ha⁻¹) (study for New Zealand)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pathogen</td>
<td>Mean</td>
<td>SD</td>
<td>UF</td>
<td>Min</td>
<td>Max</td>
<td>Reference</td>
<td>Remarks</td>
</tr>
<tr>
<td>--------------------------</td>
<td>---------</td>
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<td>-------</td>
<td>--------</td>
<td>--------</td>
<td>-------------------</td>
<td>-------------------------------------------------------------------------</td>
</tr>
<tr>
<td>Cryptosporidium</td>
<td>1.58E-03</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Medema, 1998</td>
<td>Survival in water from sedimentation experiments at 23°C (approximated from Figure 1B in the reference paper)</td>
</tr>
<tr>
<td>Cyclosporidia</td>
<td>0.00E+00</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Erickson, 2006</td>
<td>0% inactivation in 7 days at 20-25°C</td>
</tr>
<tr>
<td>Entamoeba histolytica</td>
<td>4.80E-03</td>
<td>3.20E-03</td>
<td>6.40E-03</td>
<td></td>
<td></td>
<td>Feachem, 1983</td>
<td>Survival for 15 to 30 days in fresh water at 20-30°C (assumed to be 90% inactivation)</td>
</tr>
<tr>
<td>Giardia lamblia</td>
<td>3.80E-03</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Medema, 1998</td>
<td>Survival in water from sedimentation experiments at 23°C (approximated from Figure 1B in the reference paper)</td>
</tr>
<tr>
<td>Microsporidia</td>
<td>1.31E-04</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Koudela, 1999</td>
<td>Survival of Encephalitozoon cuniculi Levaditi in distilled water at 4°C for 2 years</td>
</tr>
<tr>
<td>Campylobacter jejuni</td>
<td>3.36E-02</td>
<td>2.59E-03</td>
<td></td>
<td></td>
<td></td>
<td>Cook, 2007</td>
<td>Decay for LR underground river (from Table 2 in the reference paper)</td>
</tr>
<tr>
<td></td>
<td>2.3E-02</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Azevedo, 2008</td>
<td>Survival in water (assumed to be 90% inactivation) at 25°C in the absence of light (approximated from Figure 1 in the reference paper)</td>
</tr>
<tr>
<td>Clostridium spp.</td>
<td>2.50E-04</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Filip, 1988</td>
<td>Survival of clostridium perfringens in groundwater (approximated from Figure 1 in the reference paper)</td>
</tr>
<tr>
<td>E.coli O157</td>
<td>2.88E-02</td>
<td>3.84E-02</td>
<td>9.59E-04</td>
<td>1.44E-01</td>
<td></td>
<td>John, 2005</td>
<td>Assumed to be same as coliform bacteria at temp from 3-37°C (from Table 2 in the reference paper)</td>
</tr>
<tr>
<td>Pathogen</td>
<td>Mean</td>
<td>SD</td>
<td>UF</td>
<td>Min</td>
<td>Max</td>
<td>Reference</td>
<td>Remarks</td>
</tr>
<tr>
<td>------------------</td>
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<td>-------</td>
<td>-----------</td>
<td>-------------------------------------------------------------------------</td>
</tr>
<tr>
<td>Helicobacter</td>
<td>3.1E-02</td>
<td>1.4E-02</td>
<td>4.8E-02</td>
<td>Azevedo, 2008</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Survival in water (assumed to be 90% inactivation) at 25°C in the absence of light. Minimum from H. pylori 968, and maximum from H. mustelae and H. muridarum (approximated from Figure 1 in the reference paper)</td>
<td></td>
<td></td>
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<td></td>
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<td></td>
</tr>
<tr>
<td></td>
<td>2.45E-01</td>
<td>3E-02</td>
<td>4.6E-01</td>
<td>Adams, 2003</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Survival time under temperature from 16°C to 23°C in natural fresh water environment (assumed to be 90% inactivation) (approximated from Figure 3 in the reference paper)</td>
<td></td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>Listeria</td>
<td>3.43E-03</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Kim, 2010</td>
<td>Survival of 28 days in manure-based compost (assumed to be 90% inactivation)</td>
</tr>
<tr>
<td>Salmonella spp.</td>
<td>9.59E-03</td>
<td>1.91E-02</td>
<td>2.88E-03</td>
<td>5.75E-02</td>
<td>John, 2005</td>
<td>At temperature range from 10 to 22°C (from Table 2 in the reference paper)</td>
<td></td>
</tr>
<tr>
<td>Shigella spp.</td>
<td>4.40E-03</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Henis, 1987</td>
<td>Survival time is 22 days in wells (assumed to be 90% inactivation)</td>
</tr>
<tr>
<td>Vibrio cholera</td>
<td>2.27E-03</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Ramaiah, 2004</td>
<td>Survival in natural, filtered seawater (from starvation duration of 75 days in Table 3 of the reference paper)</td>
</tr>
<tr>
<td>Yersinia spp.</td>
<td>5.00E-04</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Filip, 1988</td>
<td>Yersinia enterocolitica in groundwater (Approximated from Figure 1 in the reference paper)</td>
</tr>
<tr>
<td>Adenovirus</td>
<td>1.75E-03</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Enriquez, 1995</td>
<td>Persistence in secondary sewage effluent at 15°C Average of adeno 40 and 41 (from Table 3 in the reference paper)</td>
</tr>
<tr>
<td>Pathogen</td>
<td>Mean</td>
<td>SD</td>
<td>UF</td>
<td>Min</td>
<td>Max</td>
<td>Reference</td>
<td>Remarks</td>
</tr>
<tr>
<td>--------------</td>
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<td>-------------------------------------</td>
<td>-------------------------------------------------------------------------</td>
</tr>
<tr>
<td>Ascaris</td>
<td>7.67E-05</td>
<td>6.57E-05</td>
<td>8.76E-05</td>
<td>Jackson, 1977 &amp; Griffiths, 1978</td>
<td>Survival of 3 to 4 years in soil (assumed to be 90% inactivation)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Coliphage</td>
<td>2.88E-03</td>
<td>2.88E-03</td>
<td>2.30E-10</td>
<td>9.58E-03</td>
<td>John, 2005</td>
<td>At temperature from 0-10°C (from Table 3 in the reference paper)</td>
<td></td>
</tr>
<tr>
<td>Enteroviruses</td>
<td>5.00E-03</td>
<td></td>
<td></td>
<td></td>
<td>Lyon &amp; Chattopadhyay, 2001</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hepatitis A virus</td>
<td>1.92E-03</td>
<td>3.84E-03</td>
<td>2.30E-10</td>
<td>7.66E-03</td>
<td>John, 2005</td>
<td>At temperature from 0-10°C (from Table 3 in the reference paper)</td>
<td></td>
</tr>
<tr>
<td>Hepatitis E virus</td>
<td>1.92E-03</td>
<td>3.84E-03</td>
<td>2.30E-10</td>
<td>7.66E-03</td>
<td>John, 2005</td>
<td>Assumed to be same and HAV-A</td>
<td></td>
</tr>
<tr>
<td>Astrovirus</td>
<td>2.4E-03</td>
<td></td>
<td></td>
<td></td>
<td>Espinosa, 2008</td>
<td>Survival in groundwater (approximated from Figure 2 in the reference paper)</td>
<td></td>
</tr>
<tr>
<td>Norovirus</td>
<td>3E-04</td>
<td>1.6E-04</td>
<td>4.39E-04</td>
<td>Ngazoa, 2007</td>
<td>Survival in river at 4°C (from viral reduction at 20 days and 30 days in Table 2 of the reference paper)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rotavirus</td>
<td>1.14E-03</td>
<td></td>
<td></td>
<td></td>
<td>Espinosa, 2008</td>
<td>Survival in groundwater (approximated from Figure 1 in the reference paper)</td>
<td></td>
</tr>
<tr>
<td>Toxoplasma</td>
<td>8.75E-03</td>
<td>1.5E-03</td>
<td>1.6E-02</td>
<td>Dubey, 1998</td>
<td>Survival at temperature from 35-55°C (assumed to be 90% inactivation) (from Table 1 in the reference paper)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fecal coliforms</td>
<td>1.88E-02</td>
<td></td>
<td></td>
<td></td>
<td>McFeters, 1974</td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>E. coli</em></td>
<td>2.88E-02</td>
<td>3.84E-02</td>
<td>9.59E-04</td>
<td>1.44E-01</td>
<td>John, 2005</td>
<td>Table 2. Assumed to be same as coliform bacteria, temp range is 3-37°C</td>
<td></td>
</tr>
<tr>
<td>Enterococci</td>
<td>2.88E-02</td>
<td>2.88E-02</td>
<td>9.58E-04</td>
<td>7.67E-02</td>
<td>John, 2005</td>
<td>Table 2. Assumed to be same as coliform bacteria, temp range is 3-22°C</td>
<td></td>
</tr>
<tr>
<td>Organism</td>
<td>Mean</td>
<td>Standard deviation</td>
<td>UF</td>
<td>Minimum</td>
<td>Maximum</td>
<td>Reference</td>
<td>Remarks</td>
</tr>
<tr>
<td>---------------------------</td>
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<td>-----</td>
<td>---------</td>
<td>---------</td>
<td>-----------</td>
<td>----------------------------------------------</td>
</tr>
<tr>
<td>Crypto sporidium</td>
<td>N/A</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Parasites are not an issue in aerosols</td>
</tr>
<tr>
<td>Cyclo sporidia</td>
<td>N/A</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Parasites are not an issue in aerosols</td>
</tr>
<tr>
<td>Entamoeba histolytica</td>
<td>N/A</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Parasites are not an issue in aerosols</td>
</tr>
<tr>
<td>Giardia lambila</td>
<td>N/A</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Parasites are not an issue in aerosols</td>
</tr>
<tr>
<td>Micro sporidia</td>
<td>N/A</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Parasites are not an issue in aerosols</td>
</tr>
<tr>
<td>Campylobacter jejuni</td>
<td>3.11</td>
<td></td>
<td>0.97</td>
<td>5.24</td>
<td></td>
<td>Cox, 1968</td>
<td>Assumed to be same as E.coli</td>
</tr>
<tr>
<td>Clostridium spp.</td>
<td>3.11</td>
<td></td>
<td>0.97</td>
<td>5.24</td>
<td></td>
<td>Cox, 1968</td>
<td>Assumed to be same as E.coli</td>
</tr>
<tr>
<td>E.coli O157</td>
<td>4.79</td>
<td></td>
<td>4.45</td>
<td>5.13</td>
<td></td>
<td>Cox, 1970</td>
<td>Survival for E.coli B at 40-60% RH at aerosol age of 2 min and 15 min (approximated from Figure 4 in the reference paper)</td>
</tr>
<tr>
<td></td>
<td>3.11</td>
<td></td>
<td>0.97</td>
<td>5.24</td>
<td></td>
<td>Cox, 1968</td>
<td>Survival for E.coli K12 HfrC at 50-60% RH at 26.5°C at aerosol age of 2 min and 15 min (approximated from Figure 1 and Figure 2 in the reference paper)</td>
</tr>
<tr>
<td>Helicobacter</td>
<td>3.11</td>
<td></td>
<td>0.97</td>
<td>5.24</td>
<td></td>
<td>Cox, 1968</td>
<td>Assumed to be same as E.coli</td>
</tr>
<tr>
<td>Listeria</td>
<td>3.11</td>
<td></td>
<td>0.97</td>
<td>5.24</td>
<td></td>
<td>Cox, 1968</td>
<td>Assumed to be same as E.coli</td>
</tr>
<tr>
<td>Salmonella spp.</td>
<td>3.11</td>
<td></td>
<td>0.97</td>
<td>5.24</td>
<td></td>
<td>Cox, 1968</td>
<td>Assumed to be same as E.coli</td>
</tr>
<tr>
<td>Shigella spp.</td>
<td>3.11</td>
<td></td>
<td>0.97</td>
<td>5.24</td>
<td></td>
<td>Cox, 1968</td>
<td>Assumed to be same as E.coli</td>
</tr>
<tr>
<td>Vibrio cholera</td>
<td>3.11</td>
<td></td>
<td>0.97</td>
<td>5.24</td>
<td></td>
<td>Cox, 1968</td>
<td>Assumed to be same as E.coli</td>
</tr>
<tr>
<td>Yersinia spp.</td>
<td>3.11</td>
<td></td>
<td>0.97</td>
<td>5.24</td>
<td></td>
<td>Cox, 1968</td>
<td>Assumed to be same as E.coli</td>
</tr>
<tr>
<td>Adenovirus</td>
<td>1</td>
<td></td>
<td>9.8E-2</td>
<td>1.92</td>
<td></td>
<td>Harper, 1961</td>
<td>Assumed to be same as enteroviruses</td>
</tr>
<tr>
<td>Virus</td>
<td>Mean</td>
<td>Standard deviation</td>
<td>UF</td>
<td>Minimum</td>
<td>Maximum</td>
<td>Reference</td>
<td>Remarks</td>
</tr>
<tr>
<td>---------------</td>
<td>------</td>
<td>--------------------</td>
<td>----</td>
<td>---------</td>
<td>---------</td>
<td>----------------------------------</td>
<td>---------------------------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>Ascaris</td>
<td>N/A</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Helminth worms are not an issue in aerosols</td>
</tr>
<tr>
<td>Coliphage</td>
<td>3.39</td>
<td></td>
<td></td>
<td>2.51</td>
<td>4.26</td>
<td>Benbough, 1971</td>
<td>Survival for T7 coliphage at 50-60% RH at aerosol age of 5 min and 1 hour (approximated from Figure 7 in the reference paper)</td>
</tr>
<tr>
<td></td>
<td>0.35</td>
<td></td>
<td></td>
<td>0.28</td>
<td>0.42</td>
<td>Warren, 1969</td>
<td>Survival for T3 coliphage at 50% RH at 21°C at aerosol age of 5 min, 30 min, 60 min, 120 min, and 180 min (approximated from Table 4 in the reference paper)</td>
</tr>
<tr>
<td>Entero viruses</td>
<td>0.8</td>
<td></td>
<td></td>
<td>0.72</td>
<td>0.87</td>
<td>Ehrlich, 1964</td>
<td>Survival for T3 coliphage at 48-76% RH from 2 min to 30 min (approximated from Figure 1 in the reference paper)</td>
</tr>
<tr>
<td>Entero viruses</td>
<td>2.1</td>
<td></td>
<td></td>
<td>1.51</td>
<td>2.7</td>
<td>Benbough, 1971</td>
<td>Survival for polioviruses at 35-65% RH at 23 hours after spray (approximated from Table 1 in the reference paper)</td>
</tr>
<tr>
<td>Hepatitis A virus</td>
<td>1</td>
<td>9.8E-2</td>
<td></td>
<td>1.92</td>
<td></td>
<td>Harper, 1961</td>
<td>Assumed to be same as enteroviruses</td>
</tr>
<tr>
<td>Hepatitis E</td>
<td>1</td>
<td>9.8E-2</td>
<td></td>
<td>1.92</td>
<td></td>
<td>Harper, 1961</td>
<td>Assumed to be same as enteroviruses</td>
</tr>
<tr>
<td>Astrovirus</td>
<td>1</td>
<td>9.8E-2</td>
<td></td>
<td>1.92</td>
<td></td>
<td>Harper, 1961</td>
<td>Assumed to be same as enteroviruses</td>
</tr>
<tr>
<td>Norovirus</td>
<td>2</td>
<td>2.86E-01</td>
<td></td>
<td>1.42E-01</td>
<td>7.92</td>
<td>Boone and Gerba, 2007</td>
<td></td>
</tr>
<tr>
<td>Rotavirus</td>
<td>8E-02</td>
<td></td>
<td></td>
<td>3E-02</td>
<td>1.2E-1</td>
<td>Sattar and Ijaz, 1984</td>
<td>Survival for rotavirus SA11 at 20-55% RH at 20±1°C (approximated from Figure 1 in the reference paper)</td>
</tr>
<tr>
<td></td>
<td>1.43</td>
<td></td>
<td></td>
<td>1.34</td>
<td>1.51</td>
<td>Ijaz and Sattar, 1985</td>
<td>Survival for rotavirus at 50±5% RH after aerosol stabilization period of 15 min (approximated</td>
</tr>
<tr>
<td></td>
<td>Mean</td>
<td>Standard deviation</td>
<td>UF</td>
<td>Minimum</td>
<td>Maximum</td>
<td>Reference</td>
<td>Remarks</td>
</tr>
<tr>
<td>------------------</td>
<td>------</td>
<td>--------------------</td>
<td>----</td>
<td>---------</td>
<td>---------</td>
<td>----------</td>
<td>----------</td>
</tr>
<tr>
<td>Toxo plasma</td>
<td>N/A</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Cox, 1968</td>
<td>Parasites are not an issue in aerosols</td>
</tr>
<tr>
<td>Fecal coliforms</td>
<td>3.11</td>
<td>0.97</td>
<td>5.24</td>
<td></td>
<td></td>
<td>Cox, 1968</td>
<td>Assumed to be same as E.coli</td>
</tr>
<tr>
<td>E. coli</td>
<td>3.11</td>
<td>0.97</td>
<td>5.24</td>
<td></td>
<td></td>
<td>Cox, 1968</td>
<td>Assumed to be same as E.coli</td>
</tr>
<tr>
<td>Entero cocci</td>
<td>3.11</td>
<td>0.97</td>
<td>5.24</td>
<td></td>
<td></td>
<td>Cox, 1968</td>
<td>Assumed to be same as E.coli</td>
</tr>
</tbody>
</table>
APPENDIX H

HIDDEN CELLS

This section presents the description of those parameters which are kept as hidden cells in the model describing the overland transport and fate of biosolids-associated pathogens (Sheets: SWPathogenModel, Barrenplot, and VegStrip). The user can see these hidden cells by going to the Format menu, selecting Row and clicking Unhide option in the sheet (Figure H-1).

![Figure H-1. A Snapshot of the SWPathogenModel Showing Steps to Unhide the Hidden Cells.](image)

Note: See commands to unhide hidden cells (highlighted in gold color).

The following section presents descriptions of different parameters.

1. **Soil Characteristics (Sheet: SWPathogenModel, Cells: C15-C25) (Figure 5-C-1):**
   Percentage fractions of silt (P$_d$) (%) (Cell: C15), sand (P$_ad$)(%)(Cell: C16), very fine sand (P$_vd$)(%) (Cell: C17), clay (P$_cl$)(%) (Cell: C18), and organic matter (O$_m$) (%) (Cell: C19) are calculated based on the selection of the soil texture class. The soil profile permeability rating (P$_r$) (-) (Cell: C21) is used for calculating the soil profile permeability subfactor. The soil structure class (S$_s$) (-) (Cell: C22) is used to calculated the soil structure subfactor (k$_s$). The texture subfactor (k$_t$) (-) (Cells: C24-C25) is used to calculate the soil texture subfactor.
2. Mechanical Soil Disturbance (Sheet: SWPathogenModel) (Figure 5-C-2): This study assumes that the land-application of biosolids occurs immediately after the mechanical soil disturbance and thus, time since last mechanical soil disturbance (\(t_d\)) (days) (Cell: C32) is assumed to be “0”. This parameter is required to calculate the effects of mechanical disturbance on soil surface and its sediment erosion potential. After the mechanical soil disturbance, roughness left by a soil disturbing operation depends on the existing roughness at the time of the operation (\(R_{a_{\text{existing}}}\)) (in.) (assumed to be 0.24 inches; RUSLE, 2008) and roughness caused by the soil disturbing operation (i.e., \(R_{ib}\)) (in.) (assumed to be 0.24 inches; RUSLE, 2008). The roughness left by the soil disturbing operation depends on its tillage intensity (\(\xi\)) (-), which indicates the aggressiveness of the soil disturbing operation and ranges between 0 and 1 (The tillage intensity of 1 indicates a very aggressive soil disturbing operation such that existing surface roughness does not have any effect on the roughness left by the operation). This study assumes that the default value of the tillage intensity is “0”, indicating that the surface roughness remains the same before and after the soil disturbing operation. The adjusted soil roughness (\(R_{a_{\text{adj}}}\)) (in.) (Cell: C38) is calculated using Equation (H-1).

\[
R_{a_{\text{adj}}} = (1 - \xi) \left( R_{a_{\text{existing}}} - R_{ib} \right) + R_{ib}
\] (H-1)

3. Vegetation (Sheet: SWPathogenModel, Cells: C39-C45) (Figure H-2): This study assumes that biosolids are applied on a barren plot and thus, it does not incorporate the effect of land vegetation on sediment erosion. Thus, the default values of mass of live and dead root biomass averaged over 10” \((B_{rt})\) (lb. / (acre. in.)) and mass of buried residue in the soil \((B_{rs})\) (lb. / (acre. in.)) are assumed to be “0”. The relative effectiveness of ground cover for reducing erosion \((b)\) (-) is set to “0.06”. The default shape of canopy \((\text{Canopy}_{\text{shape}})\) (-) is assumed to be “Triangle”, making the value of the shape coefficient \((a_{s})\) (-) and the effective height of the canopy the smallest. For “Triangle” canopy, values of shape coefficient and groundcover coefficient \((a_{g})\) are 0.25 and 0.75, respectively (RUSLE, 2008). The location of the surface area concentration within the canopy \((\text{Loc}_{\text{surfarea}})\) (-) is assumed to be at the bottom of the canopy, indicating that the bottom of the canopy is heavily concentrated and closer to the soil surface compared to the top portion of canopy. As no vegetation is assumed on the plot of land, default values of the height of the top of canopy \((h_{top})\) (ft) and bottom of
canopy (h<sub>bot</sub>) (ft), and percent cover (f<sub>c</sub>) (%) are assumed to be “0”. Using the vegetation characteristics, Manning’s constant (n<sub>t</sub>) (-) (Sheet: SWPathogenModel, Cell: C39) is obtained from the scientific literature (Cells: I66-Q79, Sheet: SurfaceConstants).

4. **Subfactors for Calculating Cover Management Factor (Sheet: SWPathogenModel)**: The cover management factor (C<sub>mgmt</sub>) (-) (Cell: C69) (Equation H-2) depends on the canopy subfactor (c<sub>c</sub>)(-), the ground cover subfactor (g<sub>c</sub>)(-), the soil subsurface subfactor (s<sub>r</sub>)(-), the soil biomass subfactor (s<sub>b</sub>)(-), the soil consolidation subfactor (s<sub>c</sub>)(-), the ridge height subfactor (t<sub>r</sub>)(-), and the antecedent effect subfactor (s<sub>m</sub>)(-). No effect of ridge height and antecedent soil conditions (for no-Req area) on sediment erosion is assumed in this study and thus, the default values of ridge height subfactor and antecedent effect subfactor are assumed to be “1”.

\[
C_{mgmt} = c_c g_c s_r t_h s_b s_c s_m \quad \text{(H-2)}
\]

\[
c_c = 1 - \left[ f_c (1 - f_{gn}) \exp \left[ -0.1 (h_{bot} + a_s a_g \left( h_{top} - h_{bot} \right) ) \right] \right] \quad \text{(H-3)}
\]

\[
g_c = \exp \left[ -bf_{gn} \left( \frac{0.24}{Ra} \right)^{0.08} \right] \quad \text{(H-4)}
\]

\[
s_r = 1 - \exp \left[ -0.66(Ra - 0.24) \right] \quad \text{(H-5)}
\]

![Figure H-3. A Snapshot of the SWPathogenModel Sheet Showing Values of Different Sediment Erosion-Related Parameters for a Barren Plot and a Vegetative Filter Strip.](image)

5. **Barren Plot (Sheets: SWPathogenModel, and Barrenplot)** (Figures H-3 to H-9): Sediment erosion loads exiting from a barren plot, calculated in the Barrenplot sheet, are presented in the SWPathogenModel sheet. The whole barren plot is subdivided into small segments (N<sub>seg</sub>) (-) (Sheet: SWPathogenModel, Cell: B103) for calculation purposes. Based on a sensitivity analysis for effect of number of segments on sediment erosion loads, one hundred segments were found to result in convergence on the sediment erosion loads exiting...
from a barren plot. Using number of segments and length of a barren plot, segment length is calculated ($L_{seg}$) (ft) (Sheet: SWPathogenModel, Cell: B109).

To calculate the amount of sediment load in runoff water due to detachment of sediments from a barren plot, the sediment load of a segment is compared with the sediment transport capacity of the segment as presented in Cells: E11-K11 (Sheet: Barrenplot) (Figure H-4). The interrill erosion load is calculated (Cell: J11, Barrenplot) (Figure H-4) and potential sediment load is calculated (Cell: K11, Barrenplot) (Figure H-4). When the incoming sediment load ($g_{i-1}$) (lb/sec/ft plot width) (Sheet: Barrenplot, Cell: I11) exceeds the transport capacity of the runoff water at the upper end of the segment ($T_{c_{i-1}}$) (lb/sec/ft plot width) (Sheet: Barrenplot, Cell: E11) or when the amount of sediment detached ($D$) (lb/sec/ft/ft plot width) (Sheet: Barrenplot, Cell: K11) exceeds the increase in transport capacity within the segment (i.e., $dT_{c}/dx$) (lb/sec/ft/ft plot width) (Sheet: Barrenplot, Cell: H11), sediment deposition occurs.

Based on comparisons of potential sediment load with sediment transport capacity and interrill erosion loads, three indexes are calculated (Figure H-4):

♦ An index for potential sediment deposition for the first segment ($I_{dep1}$) (-) (Sheet: Barrenplot, Cell: L11).
♦ An index for potential sediment detachment in the whole segment for segments other than the first segment ($I_{detach}$) (-) (Sheet: Barrenplot, Cell: M11).
♦ An index for potential sediment deposition in the whole segment for segments other than the first segment ($I_{dep}$) (-) (Sheet: Barrenplot, Cell: N11).

The amount of sediment detached/deposited for a particular particle class is calculated based on its initial mass fraction, settling velocity, and sediment load in runoff water (shown in Cells: P11-BA1010; Sheet: Barrenplot) (Figure H-4). Using number of segments and length of a barren plot, segment length is calculated ($L_{seg,veg}$) (ft) (Sheet: SWPathogenModel, Cell: B183) (Figure H-3). Sediment load at the end of the overland flow path ($g_i$) (lb/sec/ft width) (Sheet: Barrenplot, Cell: BC11) (Figure H-5) is used to estimate sediment load ($d_{segment}$) (lb/ft width) (Sheet: Barrenplot, Cell: BJ11). Biosolids load at the end of the segment ($d_{segment,biosolids}$) (lb/ft width) is given in Cell BL11 (Sheet: Barrenplot). Loads of biosolids associated with different particle classes exiting from a barren plot ($BS_{exit,k}$) (lb/ft plot width) are shown in Cells: BM11-BQ11 (Sheet: Barrenplot) (Figure 5-C-5). Remaining loads of deposited biosolids-associated sediments with different particle classes ($d_{BS,dep}$) (lb/ft width) are shown in Cells: BR11-BQ11 (Sheet: Barrenplot) (Figure 5-C-6). Overall summary of these calculations for barren plot are shown in Figures H-7 and H-8.

---

**Figure H-4. A Snapshot of the Barrenplot Sheet Showing Calculation Steps for Sediment Erosion Loads.**
Site Specific Risk Assessment Tools for Land Applied Biosolids

H-5

Figure H-5. A Snapshot of the Barrenplot Sheet Showing Calculation Steps for Loads of Different Sediment Classes.

Figure H-6. A Snapshot of the Barrenplot Sheet Showing Calculation Steps for Exiting Loads of Different Biosolids-associated Sediment Classes.

Figure H-7. A Snapshot of the Barrenplot Sheet Showing Calculation Steps Deposited Loads of Different Biosolids-Associated Sediment Classes.

Figure H-8. A Snapshot of the SWPathogenModel Sheet Showing Presentation of Biosolids-Associated Sediment Erosion Loads.
6. Vegetative Filter Strip (Sheet: VegStrip) (Figures C-10): Here, segment length is modified by subtracting the backwater length ($\Delta x_b$) (ft) (Cell: B11) (Figure H-10). Removal of sediments in backwater or VFS is shown in Cell E11 and is used to calculate sediment load exiting the segment (Cell F11). Subsequently, amount of biosolids-associated suspended and deposited sediments are shown in Cells Q11-AK12 (Figure H-10).

7. Interceptor Barriers (Sheets: SWPathogenModel): Sediment loads of individual particle classes in the channel and in the farm pond are shown in Cells: A127-AL143 (Figure H-11).
APPENDIX I

SUBFACTORS FOR CALCULATING SEDIMENT LOAD

The following sections present description of different subfactors used in calculating sediment load during overland flow of runoff water.

I.1 Erosivity Subfactor (R) (hundreds of foot-ton.in/(acre.h))

This factor indicates the combined effects of storm energy and intensity on a particle’s entrainment in the runoff water and is calculated by multiplying the storm’s energy (E) (foot-tons/acre) by its maximum 30-minute intensity (I_{30}) (inches/h) (i.e., the average intensity over the continuous 30-minute interval with the highest rainfall in the storm (rainfall amount > 0.5 in. or 12 mm, known as erosive rainfall)) (Equation I-1; Wischmeier and Smith, 1978). The total storm energy is calculated using Equation (I-2) and is represented in terms of hundreds of foot-toms/ (acre) (U.S. Customary unit for storm’s energy). The value of the erosivity factor is represented in terms of hundreds of foot-ton.in/ (acre.h), the U.S. customary unit for energy intensity. A limit of 3 inches/hr is used here as median rain drop size does increase does not increase further as higher intensity values.

\[
R = E I_{30} \quad \text{(I-1)}
\]

\[
E = 916 + 331 \times \log_{10} I \quad \text{for} \quad I < 3 \text{ inches/h}
\]

\[
E = 1074 \quad \text{for} \quad I \geq 3 \text{ inches/h} \quad \text{(I-2)}
\]

For this study, probability values of erosion index (EI) for Ingham County over a 22-year precipitation period were obtained from the Wischmeier and Smith (1978) study and are shown in Table I-1.
Table I-1. Statistics of Erosion Index (EI) for Michigan (U.S.A.), Calculated Using a 22-Year Precipitation Period.

<table>
<thead>
<tr>
<th>Location</th>
<th>Observed 22-Year Range</th>
<th>50th Percentile</th>
<th>20th Percentile</th>
<th>5th Percentile</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alpena</td>
<td>14-124</td>
<td>57</td>
<td>85</td>
<td>124</td>
</tr>
<tr>
<td>Detroit</td>
<td>56-179</td>
<td>100</td>
<td>134</td>
<td>177</td>
</tr>
<tr>
<td>East Lansing</td>
<td>35-161</td>
<td>86</td>
<td>121</td>
<td>166</td>
</tr>
<tr>
<td>Grand Rapids</td>
<td>33-203</td>
<td>84</td>
<td>123</td>
<td>178</td>
</tr>
</tbody>
</table>

*Source: Wischmeier and Smith (1978)

EI values are also available for other U.S. states in the Wischmeier and Smith (1978) study, and may be used. If the EI value for a particular city is not available from the Wischmeier and Smith (1978) study, average values of median ELs (i.e., 50th percentile values) at different locations in that particular state may be used instead. For calculating EI of a particular storm, Equations (I-1 and I-2) are used instead of the estimated median EI value from the Wischmeier and Smith (1978) study (Table I-1 for Michigan). Further, expected values of EI for different return periods in Michigan, calculated using a 22-year precipitation period data is shown in Table I-2.

Table I-2. Expected Value of Single-Storm Erosion Index Values for Michigan (U.S.A.), Calculated Using a 22-Year Precipitation Period.

<table>
<thead>
<tr>
<th>Location</th>
<th>Index Values Normally Exceeded Once in</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Year 1</td>
</tr>
<tr>
<td>--------------</td>
<td>--------</td>
</tr>
<tr>
<td>Alpena</td>
<td>14</td>
</tr>
<tr>
<td>Detroit</td>
<td>21</td>
</tr>
<tr>
<td>East Lansing</td>
<td>19</td>
</tr>
<tr>
<td>Grand Rapids</td>
<td>24</td>
</tr>
</tbody>
</table>

*Source: Wischmeier and Smith (1978)

1.2 Erodibility Subfactor (K)((ton/acre)/EI unit)

The erodibility subfactor is calculated using Equation (I-3) (RUSLE, 2008):

\[
K = \left( k_t k_o + k_s + k_p \right) / 100
\]

(I-3)
where \( k_t \) is texture subfactor, \( k_o \) is organic matter subfactor, \( k_s \) is soil structure subfactor, and \( k_p \) is soil profile permeability subfactor. The texture subfactor is calculated using Equations (I-4 to I-5), where \( k_{tb} \) is texture subfactor when total sum of silt and very fine sand fractions (\( P_{sl} \) and \( P_{vfs} \), respectively; expressed as %) is less than 68% (Equation I-4), and \( P_{cl} \) and \( P_{sd} \) represents the fractions of clay and sand, respectively (expressed as %). Percentage fractions of silt, clay, and sand of different texture classes are summarized in Table A-8 (Appendix A, Chapter 1).

\[
P_{vfs} = (0.74 - 0.0062 P_{sd}) P_{sd}
\]

(I-4)

\[
k_{tg} = 0.00021(P_{sl} + P_{vfs} (100 - P_{cl}))^{1.14} \text{ for } (P_{sl} + P_{vfs}) \leq 68\%
\]

(I-5a)

\[
k_t = k_{tb} - \left[ 0.67 \times (k_{tb} - (0.00021)[68(100 - P_{cl})]^{1.14})^{0.82} \right]
\]

for \((P_{sl} + P_{vfs}) \geq 68\%
\]

(I-5b)

The organic subfactor \((k_o)\) depends on organic matter content \((O_m)\) (%) and is calculated using Equation (I-6). The soil subfactor is calculated using Equation (I-7), where soil structure class \((S_s)\) is divided into four categories: 1) Very fine granular, 2) Fine granular, 3) Medium or coarse granular and 4) Blocky, platy, or massive.

\[
k_o = 12 - O_m
\]

(I-6)

\[
k_s = 3.25(S_s - 2) \text{ for } (k_t k_o + k_s) \geq 7
\]

(I-7a)

\[
k_s = 7 - k_t k_o \text{ for } (k_t k_o + k_s) < 7
\]

(I-7b)

The soil profile subfactor is calculated using Equation (I-8), where \( P_r \) is soil profile permeability rating and ranges from 1 (i.e., very low runoff potential; sandy to gravelly soils, no layering) to 6 (i.e., very high runoff potential; high clay content and poor aggregation). Other permeability class values are 2 for moderate to rapid runoff potential (sandy loam), 3 for moderate runoff potential (loam, silt loam soils), 4 for slow to moderate runoff potential (clay loam, silt soils), and 5 for slow runoff potential (high clay content or compacted soils of other textural groups).

\[
k_p = 2.5(P_r - 3)
\]

(I-8)

### I.3 Slope Steepness Subfactor (S) (-)

The slope steepness subfactor, which depends on the angle which a plot of land forms with the horizontal (\( \theta \) (°)), is calculated using Equations (I-9 and I-10) (RUSLE, 2008). Here, Equation I-9 calculates slope steepness subfactor for all areas except the \( R_{eq} \) zone, and Equation I-10 calculates slope steepness subfactor for areas within the \( R_{eq} \) zone. The \( R_{eq} \) zone represents
the northwestern part of the U.S. where erodibility of soil, especially of cropland and other highly disturbed soils, increases during winter months.

\[
S = 0.03 + 10.8 \sin \theta \quad \text{for } 100 \tan \theta < 9\% \quad (I-9a)
\]

\[
S = -0.5 + 16.8 \sin \theta \quad \text{for } 100 \tan \theta \geq 9\% \quad (I-9b)
\]

\[
S = \left( \frac{\sin \theta}{0.0896} \right)^{0.6} \quad \text{for } 100 \tan \theta \geq 9\% \quad (I-10)
\]

### I.4 Slope Length Exponent (m)

The slope length exponent is a function of ratio of rill to interrill erosion (\(\beta\)) (-) and is calculated using Equations (I-11 and I-12) (valid for all areas except the \(R_{eq}\) zone, where \(m = 0.5\)). The slope length exponent varies about 0.5 as the value of \(\beta\) varies about 1 (Equation I-12). The \(f_{ge}\) parameter represents the fraction of ground cover (%), and \(s\) represents the sine of the slope angle (\(\theta\)).

\[
m = \left( \frac{\beta}{1 + \beta} \right) \quad (I-11)
\]

\[
\beta = \left( \frac{K_r}{K_i} \right) \left( \frac{C_{pr}}{C_{pi}} \right) \left( \exp\left(-0.05f_{ge}\right) \right) \left( \frac{s / 0.0896}{3(s / 0.0896)^{0.8} + 0.56} \right) \quad (I-12)
\]

In Equation (5-B-12), \((K_r/K_i)\) represents the ratio of rill and interrill soil erodibility and depends on percentage fractions of sand, silt, and clay for a given soil texture class (Equation I-13).

\[
\frac{K_r}{K_i} = \frac{0.01P_{sd}[1 - \exp(-0.05P_{sd})] + 2.7(0.01P_{sd})^2[1 - \exp(-0.05P_{sd})] + 0.0035P_{sd}[1 - \exp(-0.05P_{sd})]}{0.01P_{sd}[1 - \exp(-0.05P_{sd})] + 2.7(0.01P_{sd})^2[1 - \exp(-0.05P_{sd})] + 0.0035P_{sd}[1 - \exp(-0.05P_{sd})]} \quad (I-13)
\]

The value of the ratio of the effects of soil consolidation and soil biomass on rill and interrill erosion \((C_{pr}/C_{pi})\) is calculated using Equation (I-14). The soil consolidation subfactor \((s_c\)) (-), depends on time since last mechanical soil disturbance \((t_d)\) (days) and time to soil consolidation \((t_c)\) (days) (Equation I-15).

\[
\frac{C_{pr}}{C_{pi}} = 0.45 + 1.55(s_c s_b)^2 \quad (I-14)
\]

\[
s_c = 0.45 + \exp\left[-3.314\left(0.1804 + \left(\frac{t_d}{t_c}\right)^{1.439}\right)\right] \quad (I-15)
\]
The time to soil consolidation depends on annual precipitation ($P_a$) (in.) (Equation I-16). The soil biomass subfactor ($s_b$) (-) depends on biomass present of soil surface and buried within soil (Equation B-17). In Equation (I-17), $B_{rt}$ represents the sum of the live and dead root biomass averaged over a 10” depth (in.) and $B_{rs}$ represents the amount of buried residue averaged over a 10” depth (in.).

\[
\begin{align*}
t_c &= 20 & P_a < 10 & \text{(I-16a)} \\
t_c &= 26.5 - 0.65P_a + 0.5 & 10 \leq P_a \leq 30 & \text{(I-16b)} \\
t_c &= 7 & 30 < P_a & \text{(I-16c)} \\
\end{align*}
\]

\[
\begin{align*}
s_b &= 0.951 \exp \left( -0.0026B_{rt} - 0.0006 \frac{B_{rs}}{s_c^{0.5}} \right) & s_b \leq 0.9035 & \text{(I-17a)} \\
s_b &= \exp \left[ -1.9785 \left( 0.0026B_{rt} + 0.0006 \frac{B_{rs}}{s_c^{0.5}} \right) \right] & s_b \geq 0.9035 & \text{(I-17b)}
\end{align*}
\]
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