



Review

Modeling fate and transport of fecally-derived microorganisms at the watershed scale: State of the science and future opportunities



Kyung Hwa Cho ^a, Yakov A. Pachepsky ^{b,*}, David M. Oliver ^c, Richard W. Muirhead ^d,
Yongun Park ^b, Richard S. Quilliam ^c, Daniel R. Shelton ^b

^a School of Urban and Environmental Engineering, Ulsan National Institute of Science and Technology, Ulsan, 689-798, South Korea

^b USDA-ARS, Environmental Microbial and Food Safety Laboratory, 10300 Baltimore Ave. Building 173, BARC-EAST, Beltsville, MD 20705, USA

^c Biological & Environmental Sciences, University of Stirling, Stirling, FK9 4LA, UK

^d Land & Environment, AgResearch Ltd, Invermay Research Centre, Private Bag 50034, Mosgiel 9053, New Zealand

ARTICLE INFO

Article history:

Received 3 February 2016

Received in revised form

27 April 2016

Accepted 28 April 2016

Available online 29 April 2016

Keywords:

Fecal indicator organism (FIO)

Catchment scale

Fate and transport model

Non-point source pollution

Pathogens

ABSTRACT

Natural waters serve as habitat for a wide range of microorganisms, a proportion of which may be derived from fecal material. A number of watershed models have been developed to understand and predict the fate and transport of fecal microorganisms within complex watersheds, as well as to determine whether microbial water quality standards can be satisfied under site-specific meteorological and/or management conditions. The aim of this review is to highlight and critically evaluate developments in the modeling of microbial water quality of surface waters over the last 10 years and to discuss the future of model development and application at the watershed scale, with a particular focus on fecal indicator organisms (FIOs). In doing so, an agenda of research opportunities is identified to help deliver improvements in the modeling of microbial water quality draining through complex landscape systems. This comprehensive review therefore provides a timely steer to help strengthen future modeling capability of FIOs in surface water environments and provides a useful resource to complement the development of risk management strategies to reduce microbial impairment of freshwater sources. Published by Elsevier Ltd. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

Contents

1. Introduction	39
2. Components and compartments of current watershed models	40
2.1. Survival in manure and animal waste	44
2.2. Survival in soil	44
2.3. Sorption in the soil reservoir	44
2.4. Transport in the soil column	44
2.5. Release from animal waste and manure reservoirs	44
2.6. Release from the soil reservoir	46
2.7. FM delivery to streams via overland transport	46
2.8. In-stream processes	47
2.9. Transport in groundwater	47
2.10. Parameter ranges in watershed models	47
3. Process-based models to address less common conditions and special cases	47
3.1. Release from the above ground fecal reservoir	47
3.2. Survival in the aboveground fecal reservoir	47
3.3. Retention in the soil reservoir	48
3.4. Survival in soil reservoir	48
3.5. Mobilization of FM from soil to runoff	49

* Corresponding author.

3.6.	Survival in the water column	49
3.7.	Survival in streambed sediments	50
3.8.	Transient storage and hyporheic exchange	50
4.	Future needs and feasibilities of watershed scale modeling of microbial water quality	51
4.1.	Effects of hydrological regimes on FM fate and transport	51
4.2.	In-stream processes	51
4.3.	Processes on land surface	52
4.4.	Effects of scale and scaling	52
4.5.	Model performance evaluation and comparison	52
4.6.	Model reliability	53
5.	Conclusions	53
	Acknowledgements	54
	References	54

1. Introduction

Natural waters serve as habitat for a wide range of microorganisms, a proportion of which may be derived from fecal material. The presence of fecally-derived microorganisms (FMs) in an aquatic environment indicates that a contamination pathway has connected a fecal source in the landscape to the water environment. FMs include pathogens, and microbes that are not pathogenic but do indicate the presence of fecal contamination, e.g. *Escherichia coli* and enterococci, commonly referred to as fecal indicator organisms (FIOs) (Ashbolt et al., 2001; Noble et al., 2003). The presence of FIOs does not confirm the presence of pathogenic microorganisms in the water (Pachepsky et al., 2014); however, the presence of FIOs is an indicator of the hygienic status of an aquatic environment and they are used globally as a proxy in water quality standards. FIOs are correlated with an increased risk to human health when detected in higher concentrations in waters used for recreation, irrigation, agricultural product processing, shellfish production, fishing and domestic use. Public health risks are related to the presence of microorganisms that are pathogenic to humans, for example, *E. coli* O157:H7, *Campylobacter jejuni* and *Cryptosporidium parvum*, among others, which can cause a variety of medical conditions leading in some cases to death. Therefore, microbial quality of waters is an issue of global concern both in terms of environmental standards and the protection of health and wellbeing (WHO, 2014; CDC, 2015).

Microbial contamination of water sources is influenced by surrounding land use, and both point and nonpoint sources are of importance (Alderisio and DeLuca, 1999; Cho et al., 2010a, 2010b, 2012; Guber et al., 2006; Pachepsky and Shelton, 2011; Oliver et al., 2015). Various management practices have been developed to improve microbial water quality, such as preventing direct input, overland transport, and subsurface movement of FMs to water sources. Laboratory and field experimentation and on-farm adoption of such practices have shown that their efficiency is a complex function of environmental and management conditions, and can vary both spatially and temporally (Karim et al., 2004; Reinoso et al., 2008). Therefore, various combinations of microbial fate and transport controls have led to the development of mathematical models capable of generating “what if” responses to a range of on-farm scenarios. Currently, the use of such models is an important component in helping to guide microbial water quality evaluation and decision-making in order to meet those regulatory requirements associated with water quality protection and management (Gronewold, 2009; Bougeard et al., 2011; Shoemaker et al., 2005).

Before the last decade a number of comprehensive reviews of modeling practices and perspectives have been published

(Jamieson et al., 2004; Benham et al., 2006; Pachepsky et al., 2006). Recent legislative activity however, such as revisions to both the EU Bathing Water and Shellfish Waters Directives (EUPC, 2006a, 2006b), and The Food Safety and Modernization Act (FSMA), which requires the U. S. Food Drug Administration to establish the FSMA Rule for Produce Safety (USFDA, 2011), has encouraged the use of modeling as part of wider programs of integrated catchment management. The current version of the FSMA rule has a provision on microbial water quality that requires fresh produce farmers to carry out (a) a baseline survey of the quality of their irrigation water, (b) annual surveys, and (c) re-establishing a baseline in case of significant contamination events outside of the farmer's control. Some commodity groups and larger companies have established their own requirements to safeguard the microbial quality of irrigation water, e.g. in the UK in 2004, the retailer Marks & Spencer released a new code of practice called “Field to Fork” that required all of their growers to test irrigation water for *E. coli* (Monaghan, 2006). Others, such as the restaurant chain McDonalds, use ‘Good Agricultural Practices’ to set microbial standards for irrigation water used for their produce (Allende and Monaghan, 2015). Commodity groups in California created the Leafy Green Products Handler Marketing Agreement (LGMA) that adopted irrigation water quality standards based on *E. coli* concentrations (CSFSGLLGSC, 2006). Watershed-scale fate and transport modeling has the potential to help determine whether these standards can be met under site specific weather and management conditions, and clearly offers advantages to drive forward the research agenda associated with microbial quality of irrigation water (Pachepsky et al., 2011). In addition, recent developments in quantitative microbial risk assessment (QMRA) of surface water quality can provide an alternative modeling approach that is specifically linked to human exposure. Thus, QMRA can explicitly include the watershed-scale water quality models to project human exposure to contaminated bathing water (Whelan et al., 2014; Schijven et al., 2015). All regulations and guidance regarding irrigation, recreational, and shellfish water quality continue to be based on concentrations of fecal coliforms, *E. coli* and in some cases enterococci; subsequently, the overwhelming majority of watershed-scale modeling work also involves this limited number of FIOs.

The aim of this review is to highlight and critically evaluate developments in modeling of microbial water quality over the last 10 years, and to discuss directions for model development and application, with a particular focus on FIOs (although considering wider FMs where appropriate). Specifically, our objective is to review progress in model development by focusing on a range of fecal sources and subsequent FIO survival in soil, water and manure matrices; release and transport of FIOs in runoff; processes in receiving waters that affect FIO survival; and ultimately how

modeled outputs relate to water quality standards. We first review existing modeling systems, then consider components that had recently become the subject of research for improvements, and finally suggest an outlook of research needs and application feasibility for modeling microbial quality of surface waters.

2. Components and compartments of current watershed models

Watershed-scale modeling can include a range of components from simulating surface runoff from soil through to FM fate and transfer dynamics within a series of complex environmental matrices (Fig. 1). The origin of fecal material in a watershed includes fresh fecal material deposited directly by livestock and wild animals, and farm wastes such as manure and slurry that often contains a mixture of feces, urine and bedding material, (Oliver et al., 2007; Hutchison et al., 2005). Feces can be directly defecated into waterbodies by animals (Sunohara et al., 2012), and manure or effluent can accidentally be delivered to water via spreading equipment (Oliver et al., 2007). However, the application of fecal material to land is the primary pathway for the deposition of FMs to the soil surface. Following rainfall or irrigation, FMs can be mobilized from their fecal source and partitioned into either particle-associated or soil solution fractions, and be routed through or across the soil via a range of different hydrological pathways, with their persistence then determined by a range of biotic and abiotic factors within the soil-feces mixture. Upon delivery to receiving waters, FM concentrations are influenced by additional factors, i.e. release from resuspension of streambed sediments and hyporheic exchange, and die-off and settling. We first review existing components and compartments of current watershed models for simulating the fate and transport of FMs in terms of FM behavior in animal waste and soil, the processes of FM release and transport in runoff, and in-stream processing of FM in receiving waters. Models that will be reviewed are listed in Table 1. Some model acronyms below refer to models with the FM transport component whereas others refer to the hydrological model that serves as a driver for the FM fate and transport model providing necessary water flow and hydrological routing in the wider FM modeling framework.

The Soil and Water Assessment Tool (SWAT) is a simulation watershed-scale model that operates on a daily time step. This

model divides a watershed into sub-basins using digital elevation model (DEM) data with both stream network and sub-basin outlets. Subsequently, sub-basins are subdivided into hydrologic response units (HRUs). A single land use type, soil type, and management regime are assigned to each HRU. The HRUs can be used to simulate water flow, sediment transport, and fate and transport of nutrients, pesticides and FM affecting water quality. For the latter, Sadeghi and Arnold (2002) developed the FM sub model that enabled SWAT to identify and estimate FM source loading in watersheds (Bougeard et al., 2011; Coffey et al., 2010). Others have developed SWAT further with the inclusion of an in-stream module to account for in-stream processing of FMs (Cho et al., 2012; Kim et al., 2010; Pandey et al., 2012), and fit-for-purpose testing of model applicability in site-specific environments (Coffey et al., 2013; Iudicello and Chin, 2013; Niazi et al., 2015; Tang et al., 2011). Using SWAT for watershed modeling produces variable results depending on the size of the watershed. SWAT has been deployed across HRUs ranging in area from <math><0.01\text{ km}^2</math> to

The Hydrological Simulation Program Fortran (HSPF) is a continuous simulation, lumped parameter, watershed-scale model. Any time step (minimum of 1 min) that divides equally into one day can be used, although the typical time step used is 1 h. The sub-basin is sub-divided into HRUs, defined as relatively homogeneous areas based on land use and hydrologic properties of both pervious and impervious land, which HSPF can simulate separately. This model was developed and applied to model fate and transport of FIOs in watersheds to quantify the concept of the Total Maximum Daily Load (TMDL) (Benham et al., 2006; Brannan et al., 2002; Chin, 2011; Desai et al., 2011; Hall et al., 2008) and source identification (LaWare and Rifai, 2006; Moyer and Hyer, 2003; Petersen et al., 2011; Rolle et al., 2012). The HSPF performance in establishing TMDL has been evaluated, where the size of watersheds in simulations of FIO fate and transport ranged from

The generalized watershed loading function (GWLf) model is a continuous simulation, lumped parameter, watershed-scale model that operates on daily (for weather and water balance calculations)

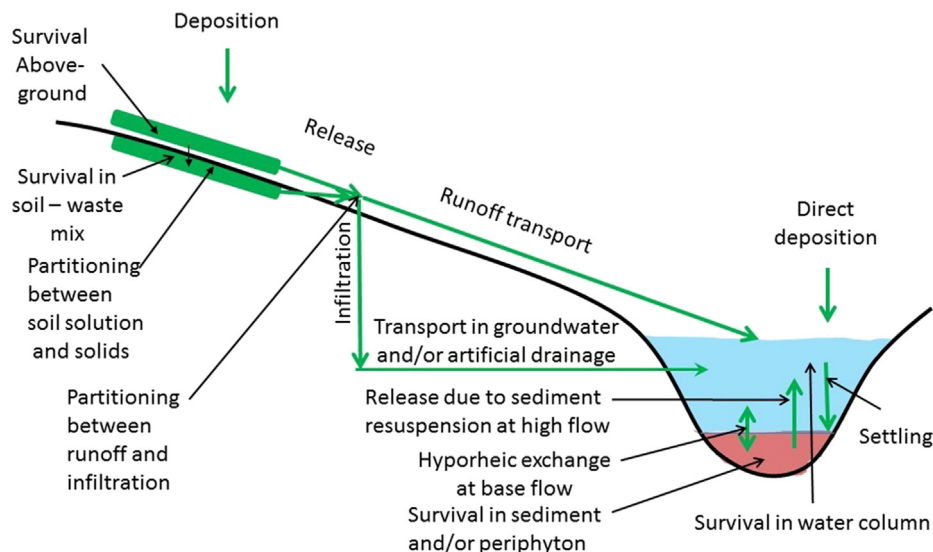


Fig. 1. Pathway of fecal microorganisms including surface runoff from soil to survival in surface water bodies; green lines represent the pathway of fecal microorganism release and transport and black lines point to specific fate-related process that need to be modeled.

and monthly (for nutrient loads calculations) time steps. Sub-basins are primary HRUs that are delineated based on different land uses. This model was applied to simulate FM fate, and transport of microorganisms specifically for the purpose of source identification and quantification of *Cryptosporidium parvum* (Walker and Stedinger, 1999) in the Catskill-Delaware watershed that is part of the New York City water supply system.

The watershed assessment model (WAM) is a continuous, geographical information system-based, watershed model that operates on a daily time step. The entire watershed is sub-divided into a regular rectangular array of cells according to user-defined cell size. The GIS based version of the model was developed recently (Bottcher et al., 2012). This model has been used to predict FIO concentrations in streams in order to improve land management strategies to reduce fecal contamination of waterways (Collins and Rutherford, 2004; Tian et al., 2002). The size of watersheds in these applications of WAM were 2.6 km² (Collins and Rutherford, 2004) and 1.4 km² (Tian et al., 2002).

The pathogen catchment budget (PCB) model is a watershed-scale model that quantifies FM contamination from primary sources, including livestock and domestic animals, wildlife and wastewater, i.e. wastewater treatment plant and on-site septic tanks (Ferguson et al., 2007). The watershed in the model is subdivided into sub-catchments, which are basic mass balance units defined by slope of area, soil type, elevation, stream density and land use. Different governing equations are used for different dominant weather conditions. Ferguson et al. (2007) combined the PCB model with a hydrological model to estimate pathogen budgets for a large catchment (9050 km²) and to rank those sub-catchments that would contribute the highest pathogen loads in dry weather, and in intermediate and large wet weather events.

The RIVERSTRAHLER/EC model is a continuous simulation watershed-scale model that operates on a daily time step (Ruelland et al., 2007). The entire watershed is divided into connected directional basins within the drainage network layer. Each cell is sub-divided into an elementary watershed (EW) layer (derived by DEM) based on land use and soil type. This model, coupled with the fate and transport model SENEQUE-EC, was used to simulate seasonal and spatial variations of microbial water quality in rivers in order to assess the impact of land use and wastewater management on *E. coli* concentrations (Ouattara et al., 2013; Servais et al., 2007). The size of watershed in those two applications was 20,000 km² and 75,000 km², respectively. Ouattara et al. (2013) also coupled the SENEQUE-EC model with a hydrodynamic model capable of simulating *E. coli* fate and transport in estuarine and ocean domains (de Brauwere et al., 2014).

The SIMHYD model is a continuous simulation, lumped-conceptual, watershed-scale hydrological model that operates with a daily time step. It incorporates three stores: an interception store, soil/vadose zone store and a groundwater store. This model was combined with the fate and transport model which simulates the *E. coli* build up in a watershed governed by the amount of fecal material deposited by animals or humans and the reduction in *E. coli* numbers due to desiccation, predation, or other factors. The runoff of *E. coli* from a catchment is modeled as a function of the kinetic energy of rainfall dispersing the fecal material and the resulting flow removing *E. coli* from the watershed. The resultant SIMHYD-EG model was applied to predict *E. coli* export from large watersheds (Haydon and Deletic, 2006) and source identification (Holz, 2010). The size of watersheds modeled ranged from 0.12 km² to 119 km².

The storm water management model (SWMM) simulates surface runoff quantity and quality driven by a single rainfall event or continuous rainfall events on an hourly or daily time step (Rossman, 2010). The model represents a watershed as a series of

hydrologically connected sub-watersheds. This model has been applied in simulations of fate and transport of FIOs in different watersheds in TMDL development (Bai et al., 2006). The watershed sizes ranged from 0.36 km² to 223 km², with average sizes of the hydrological response unit reported as being 0.73 km² (USEPA, 2000).

WATFLOOD is a continuous simulation, flood flow forecasting, watershed-scale, hydrological model that operates on time steps ranging from 1 h to several weeks (Kouwen and Mousavi, 2002). The entire watershed is divided into grid cells, which are then grouped by land use. The hydrologic response is obtained by calculating the response for each of the land cover classes within a cell and then weighting the response by land cover area fractions within the grid cell. This model, coupled with a pathogen fate and transport model, was used to simulate fate and transport of pathogens for the purpose of source identification in watersheds used for drinking water supply (Dorner et al., 2006) and to determine the magnitude of FM contributions from sediments (Wu et al., 2009). The size of watersheds in these studies was 130 km² and 186.7 km², respectively.

The framework for risk analysis in multimedia environmental systems (FRAMES) is a component-based, software framework for integrating models (e.g., watershed model, groundwater model, surface water model, and exposure/risk model) and environmental databases such as meteorological data, population statistics, geographical information, chemical toxicity, and exposure parameter (Rose et al., 1987; Roser et al., 2006; Soller et al., 2006). QMRAs based on FRAMES were applied to evaluate potential health risk by exposure to recreational waters affected by microbial contamination originating from further up the watershed (Whelan et al., 2014). The size of watersheds used to evaluate the model was highly variable according to the literature ranging from 0.72 km² to 1561.6 km².

Wilkinson et al. (2011) developed a continuous simulation model that emphasized the role of the streambed for transferring FIOs to the water column during storm flow events. This model, unlike most of above models, used very short time steps – from a quarter of an hour to 1 h – in order to more accurately capture storm flow dynamics and the corresponding release of FIOs from stream sediment storage. The model considered *E. coli* fate and transport in riparian pasture, stream water, and streambed sediments. The entire watershed is divided into sub-catchments as the basic calculation unit, and the time step increases as the simulated area increases. The dynamics of *E. coli* in rivers is determined differently for dry and wet weather conditions as die-off rates are controlled by, among other things, sunlight intensity, UV radiation and temperature. The size of the watershed used in this model was 2074 km² and the size of the basic calculation unit was 109.2 km² (Wilkinson et al., 2011).

The commercially available code MIKE SHE has the pathogen fate and transport add-on; however we are not aware of peer-reviewed publications where that code has been used in watershed-scale microbial fate and transport modeling. QMRA-catch is a continuous simulation model that simulates microbial water quality in an environmental system containing a floodplain and main river, where the floodplain can receive feces from direct deposition and receive overflow from the river. Human, wildlife and bird fecal deposits at the floodplain are considered, and all fecal deposits are re-suspended when flooding occurs. Bank filtration is accounted for, and infection risk assessment computations are included. This model was used at the site at the River Danube near Vienna, Austria (Schijven et al., 2015).

The WALRUS model is a parametric conceptual rainfall-runoff model that is suitable for lowlands where shallow groundwater and surface water influence runoff generation. The model consists

Table 1
Fecal organism modeling approaches in most used watershed scale models.

Model	Processes in animal waste and soil				Processes of release and transport in runoff			Processes in receiving water				
	Survival in manure and animal waste	Survival in soil	Sorption in soil	Transport in soil and unsaturated zone	Release from the animal waste or manure reservoir	Release from the soil reservoir	Delivery to stream with overland flow	Fate in stream water column	Fate in sediment	Exchange between sediment and water column	In-stream microbial transport	Transport via ground-water
Original SWAT ^(a)	Die-off with first order kinetics	Die-off with first order kinetics	Linear partitioning between solid and liquid soil phases	Loss from the soil mixing layer proportional to bacteria concentration and infiltration	Wash-off fraction	Release of planktonic bacteria proportional to the bacteria number on the surface and runoff depth	Released bacteria are partitioned into the fraction delivered to main channel and the fraction and stored for the future delivery	Die-off with the first order kinetics	None	None	Convective	None
Modified SWAT ^(b)	Same as above		Same as above	Same as above	Same as above	Same as above	Same as above	Same as above	Sine function of time	Release with resuspended bottom sediment and deposition	Convective	None
Modified SWAT ^(c)	Same as above		Same as above	Same as above	Same as above	Same as above	Same as above	Same as above	Temperature-dependent growth	Release with resuspended bottom sediment and deposition	Convective	None
Hydrologic Simulation Program in FORTRAN (HSPF) ^(d)	None	Daily removal rate	Linear partitioning between solid and liquid soil phases	None	None	bacterial release estimated by the amount of overland flow generated and the susceptibility of the bacteria to wash-off	Released bacteria are partitioned into the fraction delivered to main channel & the fraction & stored for the future delivery	Die off with the first order kinetics	None	None	Convective	Release from active ground-water discharge
Watershed Assessment Model (WAM) ^(e)	None	Die-off with the first-order kinetics	None	None	Release proportional to the bacteria number on the surface and runoff depth	None	The fraction of released bacteria that is delivered is proportional to the runoff volume	Die-off with the first order kinetics	None	None	Convective	None
WATFLOOD ^(f)	None	Die-off with first order kinetics.	None	Mass balance in unsaturated zone	None	The power law function of the shear stress	All released bacteria are delivered on the same time step	Die-off with the first order kinetics	None	Deposition	Convective	Accumulation in ground-water without effect on stream-water
SWMM ^(g)	None	None	None	None	Release proportional to the power law function of the runoff & to the bacteria number on the soil surface.	None	All released bacteria are delivered on the same time step	None	None	None	Convective	None

Pathogen Catchment Budgets (PCB) ^(h)	Die-off with the first order kinetics.	Die-off with first order kinetics	Linear partitioning between solid and liquid soil phases	None	Release proportional to the amount of manure on the surface & effective rainfall	None	All released bacteria are delivered on the same time step	Die-off with the first order kinetics	None	Deposition or bind	Convective	None
FC-RIVERSTRAHLER ⁽ⁱ⁾	None	None	None	None	Release depends on the landuse class	None	All released bacteria are delivered on the same time step	Die-off with the first order kinetics	None	None	Convective	None
GWLF-OOCYST MODEL ^(j)	Die-off with the first order kinetics	None	None	None	Fraction of manure left after release decreases exponentially with the runoff above threshold	None	All released bacteria are delivered on the same time step	Die-off with the first order kinetics	None	Settling	Convective	None
FRAMES ^(k)	None	Die-off with first order kinetics	Linear partitioning between solid and liquid soil phases	None	None	Release proportional to concentration in the liquid phase and peak runoff rate	All released bacteria are delivered on the same time step	Die-off with the first order kinetics	None	None	Convective - dispersive	None
SIMHYD-EG ^(l)	None	Die-off with first order kinetics	None	Loss from the soil mixing layer proportional to bacteria concentration & infiltration	Release proportional to the power law function of the runoff & to the bacteria number on the soil surface	None	All released bacteria are delivered on the same time step	Not reported	None	None	Convective	None
Wilkinson et al. (2011) ^(m)	Die-off with first order kinetics	None	None	None	Release proportional to the bacteria number in the pasture area and the annual runoff yield	None	All released bacteria are directly delivered on the same time step	Die-off with first order kinetics	Die-off with first order kinetics	Release from the bottom sediment and settling	Dispersion simulated as a result of mixing	None
QMRAcatch ⁽ⁿ⁾	Die-off with first order kinetics	None	None	Not reported	Wash-off fraction	None	Released bacteria are partitioned into the fraction delivered to floodplain river and the fraction stored for the future delivery	Die-off with the first order kinetics	None	None	Convective	Log removal via bank filtration
WALRUS ^(o)	Die-off with first order kinetics	None	None	None	Bradford-Schilven model	None	Partitioned to quick flow and surface water supply	Die-off with the first order kinetics	None	None	Convective	None

Sources (a) Bougeard et al., 2011, Coffey et al., 2010, 2013, Sadeghi and Arnold, 2002, Iudicello and Chin, 2013, Niazi et al., 2015, Tang et al., 2011, (b) Kim et al., 2010, (c) Pandey et al., 2016, (d) Brannan et al., 2002, Benham et al., 2006, Moyer and Hyer, 2003, Paul et al., 2004, Im et al., 2004, LaWare and Rifai, 2006, Hall et al., 2008, Petersen et al., 2011, Chin, 2011, Desai et al., 2011, Seong et al., 2013, Rolle et al., 2012, (e) Collins and Rutherford, 2004, (f) Dorner et al., 2006, (g) Gautam et al., 2006, (h) Ferguson et al., 2007, (i) Servais et al., 2007, (j) Walker and Stedinger, 1999, (k) Whelan et al., 2014, (l) Haydon and Deletic, 2006, (m) Wilkinson et al., 2011, (n) Schijven et al. (2015), (o) Sterk et al. (2016).

of three reservoirs, soil, quick flow and surface water. This model was supplemented with FM fate and transport modules and applied to evaluate effects of climate change on *Cryptosporidium* and *Campylobacter* runoff within small watersheds in the Netherlands (Sterk et al., 2016).

2.1. Survival in manure and animal waste

FIO survival in manure or animal waste is simulated as the net result of simultaneous growth and inactivation, which leads to the rate of overall die-off. All watershed-scale models listed in Table 1 use the first order kinetics equation known as Chick's law:

$$\frac{dN}{dt} = -kN \quad (1)$$

where N is the total mass or count of microorganisms, k is the survival rate (d^{-1}), and t is time, (days). Here and below, units of mass or counts of microorganisms (N) is defined by the analytical procedure, e.g. N can be the number of colony forming units (CFU) or the most probable number (MPN).

The commonly used finite-difference analog of the Eq. (1) is

$$N(t) = N(t-1)(1-\omega) \quad (2)$$

where t is time (days), w is the daily die-off fraction ($-$), $\omega = \exp(-k)$. Various watershed quality models handle differently the dependencies of the survival rates on the environmental conditions. In particular, the PCB model (Ferguson et al., 2007) does not account for the effect of temperature on FM survival rates. Walker and Stedinger (1999) applied the GWLF- OOCYST model in which they used the power-law dependence of the survival rate of *Cryptosporidium parvum* in the form:

$$k = 10^{0.058T-2.68} \quad (3)$$

where T is temperature ($^{\circ}\text{C}$). As shown by Blaustein et al. (2013), all power-law dependencies of the survival rate on temperature are approximations of the Arrhenius-type equation

$$k = k_{20}\theta^{T-20} \quad (4)$$

where k_{20} is the survival rate at 20°C , θ is the temperature correction parameter ($-$). Presentation of Eq. (2) in the form of Eq. (3) results in values of $\theta = 1.143$, $k_{20} = 0.030$. The reported survival rate (k) values range from 0.016 to 0.200 d^{-1} (Table 2).

2.2. Survival in soil

The HSPF and PCB models define the daily removal rate (or fraction removed daily) to estimate FIO die-off, while Eq. (1) is the most common model used in simulation of FIOs in soils (Table 1). The differences between different watershed scale models are in the way the survival rate k is related to environmental conditions. The SWAT model uses Eq. (4) to describe the temperature effect. The value of θ is an adjustable parameter. Different values of k_{20} can be used for adsorbed and planktonic (free-floating) microorganisms. The WAM model (Collins and Rutherford, 2004) employs the dependence of k on both temperature and solar radiation in the form:

$$k = \frac{R}{K_R} + \frac{T}{K_T} \quad (5)$$

where K_R ($\text{MJ m}^{-2} \text{ d}^{-1}$) and K_T ($^{\circ}\text{C}$) are constants. Another method

of combining radiation and temperature conditions to estimate the survival rate was suggested by the authors of the SIMHYD model (Haydon and Deletic, 2006) who set the k value to be a power-law function of the potential evapotranspiration. The above approaches lead to daily changes in values of k . However, less variable survival rates have also been utilized. The WATFLOOD model (Dorner et al., 2006) was successfully applied to predict *Cryptosporidium* oocyst transport with values of k that varied by season. Applications of Eq. (1) with the year-round constant value of k can also be found (e.g. Whelan et al., 2014). Table 2 shows the substantial variability among the reported kinetic constant values used in this model, ranging from 0.002 d^{-1} to 3.99 d^{-1} .

2.3. Sorption in the soil reservoir

Linear partitioning is a commonly used method to distribute FMs between solid and liquid soil phases, as shown in Table 1, but some difference is found among models with regard to using this method. The method used in SWAT is not a common application of the adsorption model because no redistribution between solid and liquid phases occurs after partitioning as concentrations in both phases change during die-off (Benham et al., 2006). SWAT does not have user controls to regulate the distribution of FMs between adsorbed and liquid phases. The PCB model assumes that the total number of FMs adsorbed by particles is the same as that of the liquid phase. The FRAMES model (Whelan et al., 2014) uses linear partitioning, where land application, grazing cattle and microbial loading is accounted for as storage in the solid phase until the next storm event, at which time it is linearly partitioned between solid and liquid phases:

$$Mc_w = \frac{Mc_T}{1 + K'_d} = \frac{Mc_T}{1 + \frac{Mc_s}{Mc_w}} \quad (6)$$

where Mc_T , Mc_w , and Mc_s are total, liquid phase, and solid phase microbial concentrations, respectively, and K'_d is the dimensionless distribution coefficient.

2.4. Transport in the soil column

Water infiltration through soil can transfer FMs from the soil surface down to the subsurface zone, although few watershed models simulate this transport mechanism (Table 1). SWAT and SIMHYD-EG models estimate FM loss from the soil mixing layer as being proportional to the FM concentration as a product of the water infiltration rate. The default proportionality coefficient of 0.15 has been suggested (Arnold et al., 2011). The WATFLOOD (Dorner et al., 2006) model includes mass balance for *Cryptosporidium* oocysts in three soil storage layers: the saturated upper zone storage, the unsaturated intermediate zone storage, and the saturated lower zone storage. This model assumes convective transport of FMs from one layer to another, and states that only a fraction of water fluxes from layer to layer carries oocysts.

2.5. Release from animal waste and manure reservoirs

A general conceptualization of FM release and removal at field or pasture scale is shown in Fig. 2. In general, two FM reservoirs can be considered: the aboveground reservoir ① releases FMs in suspension to the soil reservoir and to runoff (pathways a and b in Fig. 2, respectively); and the soil reservoir can release FMs to runoff in suspension from soil solution and with soil particles (pathways c and d in Fig. 2, respectively). Parts of the soil reservoir may also receive FMs from runoff with infiltrating suspension and settling

Table 2
Examples of FIO survival rates above ground, and in soils, water column, and sediment.

Authors	Linked model	Microorganism group	Bacteria survival above ground and in soil	Bacteria survival in water	Bacteria survival in sediment
Bougeard et al. (2011)	Original SWAT	fecal coliforms	0.016 d ⁻¹ (foliage)	0.35–1.030 d ⁻¹	–
Chin (2011)		fecal coliforms	0.023–2.010 d ⁻¹ (soil)		
Coffey et al. (2013)	Modified SWAT	<i>E. coli</i>	0.2 d ⁻¹ (foliage)	0.06 d ⁻¹	–
Iudicello and Chin (2013)		fecal coliforms	0.06 d ⁻¹ (soil)		
Niazi et al. (2015)	Hydrologic Simulation Program in FORTRAN (HSPF)	fecal coliforms	0.00–3.99 d ⁻¹	0.00–0.128 d ⁻¹	–
Tang et al. (2011)		<i>E. coli</i>	0.3–0.5 (E. coli)		
Kim et al. (2010)	Modified SWAT	<i>Cryptosporidium</i>	0.02 d ⁻¹ (foliage)	–	–
Cho et al. (2012)		<i>E. coli</i>	1.4 d ⁻¹ (soil)		
Pandey (2012)	Watershed Assessment Model (WAM)	<i>E. coli</i>	–	–	Sinusoidal functions
Moyer and Hyer (2003)		Fecal coliforms	–		
Paul et al. (2004)	WATFLOOD	<i>E. coli</i>	–	Solar intensity coefficient [m ² /MJ/day]	0.003–0.13 d ⁻¹
Im et al. (2004)		fecal coliforms	0.1 d ⁻¹		
LaWare and Rifai (2006)	SWMM	fecal coliforms	–	1.1 d ⁻¹	–
Hall et al. (2008)		fecal coliforms	–		
Petersen et al. (2011)	PCB	fecal coliforms	–	0.70–2.35 d ⁻¹	–
Chin (2011)		fecal coliforms	–		
Desai et al. (2011)	RIVERSTRAHLER-EC	fecal coliforms	–	0.75–1.15 d ⁻¹	–
Seong et al. (2013)		<i>E. coli</i>	–		
Iudicello and Chin (2013)	RIVERSTRAHLER/FC	fecal coliforms	–	4.2 d ⁻¹	–
Rolle et al. (2012)		<i>E. coli</i>	–		
Collins and Rutherford (2004)	GWLF- OOCYST MODEL	fecal coliforms	–	1.15 d ⁻¹	–
Dorner et al. (2006)		fecal coliforms	–		
Gautam et al. (2006)	FRAMES	fecal coliforms	–	2.5 d ⁻¹	–
Ferguson et al. (2007)		<i>E. coli</i>	0.15–0.5 d ⁻¹		
Servais et al. (2007)	SWMM	<i>Cryptosporidium</i>	0.01–0.06 d ⁻¹	0.01–0.06 d ⁻¹	–
Servais et al. (2007)		<i>Giardia</i>	0.02–0.05 d ⁻¹		
Walker and Stedinger (1999)	PCB	<i>Campylobacter</i>	0.08 d ⁻¹	0.04–0.08 d ⁻¹	–
Whelan et al., 2014		<i>E. coli</i>	0.01–0.02 d ⁻¹		
Whelan et al., 2014	PCB	<i>E. coli</i> O157:H7	0.01–0.02 d ⁻¹	0.05–4.0 d ⁻¹	–
Whelan et al., 2014		<i>Cryptosporidium</i>	0.02 d ⁻¹		
Whelan et al., 2014	PCB	<i>E. coli</i>	–	–	–
Whelan et al., 2014		<i>Giardia</i>	–		
Whelan et al., 2014	PCB	<i>E. coli</i>	–	0.54 d ⁻¹ at 20 °C	0.108 d ⁻¹ at 20 °C
Whelan et al., 2014		Fecal coliforms	1.08 d ⁻¹ at 20 °C		
Whelan et al., 2014	PCB	<i>Cryptosporidium</i>	0.002–0.003 d ⁻¹	0.011–0.013 d ⁻¹	–
Whelan et al., 2014		<i>E. coli</i> O157:H7	0.16		
Whelan et al., 2014	PCB	<i>Salmonella</i>	0.23	1.30	–
Whelan et al., 2014		<i>Cryptosporidium</i>	0.04		

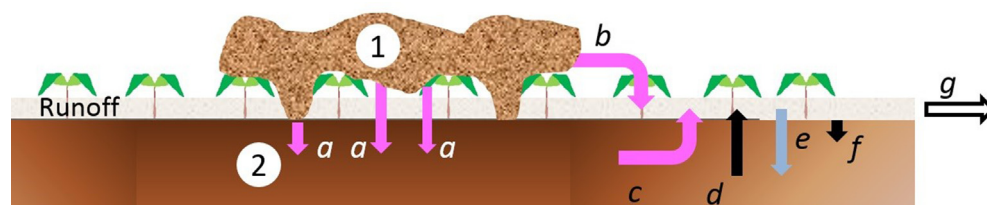


Fig. 2. Pathways of microorganism release and removal; ① and ② - above ground and belowground (soil) reservoir, respectively.; a - release in suspension to soil, b - release in suspension to runoff, c - release in suspension from soil to runoff, d - release adsorbed microorganisms with soil particles to runoff, e - infiltration with runoff suspension, f - settling with sediment particles, g - overall removal (or export) from the application site.

sediment (pathways e and f in Fig. 2, respectively), but these pathways are not usually considered in watershed-scale models.

Watershed-scale models are mostly concerned with the total FM removal flux (g in Fig. 2), which enters receiving waters or buffer vegetation. Several watershed-scale models consider a single fecal reservoir that combines FMs in soil and aboveground manure or animal waste. One argument in favor of this simplification is that, although the two-reservoir representation may provide a better qualitative reproduction of microbial release kinetics, it may be difficult to calibrate the two-reservoir model without having a high correlation of the parameters of the different pathways in Fig. 2 (Muirhead and Monaghan, 2012).

In the SWAT model the aboveground reservoir also represents FIOs on foliage. The daily wash-off fraction f is the parameter to simulate FIO release according to this pathway in Fig. 2. This parameter is not affected by the rainfall intensity or duration. SWAT does not simulate pathway b (Fig. 2). The WAM model does not have the belowground reservoir and simulates FIO release during runoff (pathway b) as:

$$f = \begin{cases} \frac{R}{K}, & R < K \\ 1, & R \geq K \end{cases} \quad (7)$$

where f is the fraction of FIO in aboveground reservoir released (–), R is the daily runoff depth (mm), K is the parameter (mm day^{-1}), FIOs are fully removed if runoff exceeds the value of K . The SWMM model simulates only pathway b and employs the power-law dependence of the release fraction f on the runoff rate r in the form $f = C_1 r^{C_2}$. Calibration of this model produced the value of $C_2 = 1.1$ for agricultural areas (Gautam et al., 2006), and therefore the linear approximation $f = C_1 r$ might be applicable in such areas. Such linear approximation is adopted in the PCB model which mobilizes FIOs from manure in proportion to the effective rainfall rather than to the runoff depth. The effective rainfall is defined as the rainfall that relates to stream flow, and can generally be larger than the runoff volume. The GWLF-OOCYST model computes the fraction of the manure left after release, i.e.

$$1 - f = 1 - \exp[-\alpha(R - R_0)] \quad (8)$$

where R is the daily runoff (mm), and R_0 is the threshold daily runoff value below which no manure and *Cryptosporidium* oocysts are washed off. Table 1 in the work of Walker and Stedinger (1999) indicates that the product $\alpha(R - R_0)$ can be small enough to apply the Taylor expansion in the Eq. (8) that again leads to linear dependence;

$$f \cong \alpha(R - R_0) \quad (9)$$

This appears to be the only release model which uses explicit dependencies of the release parameters α and R_0 on the age of manure. The model SIMHYD-EG simulates the release with the power-law dependence of the released fraction as a fraction of the overland flow input in total flow. The exponent value in this power law dependence has not been reported, and it is not clear whether the linear relationship between the fraction of released FIOs and runoff was acceptable in case studies.

Overall, the majority of models use the linear dependence of the released fraction of FIOs on runoff depth or on runoff rate. In a large scale study in a watershed of over 75,000 km^2 , the RIVER-STRAHLER/FC model (Servais et al., 2007) assumed microbial concentration in runoff to be a function of land use type, rather than a function of the application rate of a specific manure or animal waste. The FIO concentrations by land use were 100 per 100 ml in forests and on cultivated lands, 1000 per 100 ml on pastures, and

5000 per 100 ml in urban areas (Servais et al., 2007).

2.6. Release from the soil reservoir

Export of FMs from manure or animal waste deposited on soil is mostly modeled as microbial release to surface runoff, i.e. cells in suspension in soil solution or bound to sediment particles. The linear relationship between the microbial fraction released in soil solution and the runoff depth is adopted in the SWAT model. The fraction of FIOs removed from the soil solution mixing layer near the soil surface is defined as:

$$s = R/(\rho d \kappa) \quad (10)$$

where R is the daily runoff depth (mm), ρ and d are soil bulk density (mg m^{-3}) and thickness of the soil surface mixing layer (mm), κ is the microorganism-soil partitioning coefficient (–). In the HSPF model, the fraction removed from the surface storage is estimated as

$$s = 1 - \exp(-\beta R) \quad (11)$$

where R is runoff depth, and β is the parameter that characterizes the susceptibility of microorganisms to runoff (mm^{-1}). When βR is small, the HSPF formulation leads to the approximate expression

$$s \cong \beta R \quad (12)$$

Therefore, results of application of SWAT and HSPF expressions should be similar if $\beta = 1/(\rho d \kappa)$. Both models also account for FIOs attached to sediment particles that subsequently become suspended in runoff. The WATFLOOD model relates microbial release from particles to the dominant shear stress, which in turn appears to be a function of the land slope and runoff water layer thickness. Whereas the model FRAMES relates the released microbial fractions to the peak runoff rate rather than to total runoff.

The specific release of FIOs in runoff suspension attached to sediment is simulated in models that distinguish microorganisms in pore solutions and microorganisms attached to soil particles.

In particular, the SWAT model utilizes the loading function defined as

$$b = \varepsilon B S \quad (13)$$

where b is the mass or count of microorganisms removed in sediment from unit area (N m^{-2}), B is the mass or count of attached microorganisms in soil mixing layer per unit of soil mass (N mg^{-1}) S is the sediment yield per unit area (mg m^{-2}), ε is the enrichment ratio estimated as a power law function of the concentration of sediment in runoff (–):

$$\varepsilon = 0.78 \left(10^3 \frac{B}{R} \right)^{-0.25} \quad (14)$$

where R is the runoff depth (mm).

2.7. FM delivery to streams via overland transport

Watershed models mostly assume that all FMs are released from the soil surface layer and are delivered to stream channels on the same time step. However, the SWAT, HSPF and WAM models apply partitioning to estimate (a) the portion of released FIOs delivered to main channels on the day of release, and (b) the portion of FIOs stored for future delivery to stream channels. The most elaborate approach is taken in the WAM model where the delivery of FIOs is determined by slope, proximity to stream, and flow accumulation.

2.8. In-stream processes

The majority of watershed models determine the fate of in-stream FIOs with the application of the first-order kinetic, which is influenced by meteorological conditions, i.e., temperature and/or radiation. The SIMHYD-EG model estimates microbial die-off expressed as a function of the potential evapotranspiration (PET), as this variable influences factors affecting die-off rate (Haydon and Deletic, 2006). The HSPF and SWAT use the first order kinetic equation to estimate die-off, which is adjustable by changing temperature (Cho et al., 2016). The WAM model also considers the dependence of k on both temperature and solar radiation, whilst the WATFLOOD model differentiates between the die-off constants for different seasons. The RIVERSTRAHLER/EC model gives a die-off rate of $45 \times 10^{-3} \text{ d}^{-1}$ for a large drainage network at 20°C , but corrects this value for other temperatures T ($^\circ\text{C}$) and specific flow rates q (L s^{-1}) using the composite variable $q \cdot \exp(-(T - 25)^2/400)$. The die-off rate values in the GWLF-OOCYST and FRAMES models do not have any dependencies on meteorological conditions.

The result of simultaneous action of growth and die-off in sediments was simulated by Kim et al. (2010) who assumed sinusoidal *E. coli* dynamics in streambeds and improved the accuracy of SWAT in a pasture-dominant watershed. The streambed sediment *E. coli* concentrations sampled at three sites were fitted as a sinusoidal function as follows;

$$\log C = c_1 \cdot \sin\left(c_2 \cdot \frac{\text{days} - c_3}{366} \cdot \pi\right) + c_4 \quad (15)$$

where $c_1 = 1.543$ is the amplitude, $c_2 = 2.194$ is the angular frequency, $c_3 = 187$ is the phase, and $c_4 = 3.870$ is the bias. Substantial improvement was achieved in *E. coli* concentration simulations. Pandey et al. (2016) proposed the first model of FIO growth rate in sediments in the form:

$$g = \mu_{\max} [C_{T1}(T - T_{\min}) * (1 - \exp(C_{T2}(T - T_{\max})))^2] \quad (16)$$

where μ_{\max} is the maximum growth rate (day_1); C_{T1} and C_{T2} are coefficients; T_{\min} and T_{\max} are the minimum and maximum growth temperatures ($^\circ\text{C}$); and T is stream water temperature ($^\circ\text{C}$).

Some watershed models include microbial exchange between sediment and the water column as a result of deposition or re-suspension. The modified version of the SWAT model proposed by Kim et al. (2010) included an exchange module to estimate the impact of the streambed sediment re-suspension or deposition on microbial water quality. The PCB model utilizes a parameter (F) which controls the probability of FM being deposited or bound to streambed sediment. In contrast, the GWLF-OOCYST model simply assumed the value of settling velocity of *Cryptosporidium* oocyst to estimate the amount of oocysts likely to settle. The model of Wilkinson et al. (2011) computes the remobilization of *E. coli* from the streambed storage on rising flows with the rate proportional to the flow increment and the content of FIOs in the sediment reservoir; the model also considers the rate of settling proportional to the water depth. In-stream transport is most often simulated as convective transport in the majority of watershed-scale models. The FRAMES model explicitly includes convective-dispersive transport and the Wilkinson et al. (2011) model simulates mixing.

2.9. Transport in groundwater

Among the surveyed watershed models (Table 1), the HSPF and WATFLOOD models both account for microbial transport through groundwater. The HSPF model includes the contribution of groundwater transport on microbial concentration during

baseflow, while the WATFLOOD simulates the accumulation of microorganisms in aquifers, but does not consider the microbial transport in groundwater to stream water.

2.10. Parameter ranges in watershed models

The important feature of parameter values in watershed models is the large range of variation of site-specific parameters describing the same process. Two orders of magnitude appear to be a typical range. For example, using default values of $k = 175$, $d = 10$, and assuming $\rho = 1.5$, the removal fraction from Eq. (12) gives $s = 0.00038R$. On the other hand, using the default value of 25 for K in Eq. (7), one obtains the microbial removal fraction $f = 0.04R$. High variability has been found for FIO die-off rate kinetics (Table 2). A similar range of variation was reported in meta-analysis works for *E. coli* survival in soils (Park et al., 2016), water (Blaustein et al., 2013), and livestock waste (Franz et al., 2008). *E. coli* adsorption to soil particles occurs with widely varying partitioning coefficients from $2 \text{ m}^3 \text{ kg}^{-1}$ in sandy soils to $60 \text{ m}^3 \text{ kg}^{-1}$ in clay soils (Pachepsky et al., 2006).

3. Process-based models to address less common conditions and special cases

Rates of processes in the existing suite of watershed models are often considered to be independent of a number of environmental variables such as salinity, solar radiation, pH, rainfall duration and turbidity. This assumption tends to hold true if those environmental variables stay in typical ranges. However, if these variables appear to be outside of typical ranges, the rates of processes affecting FM fate and transport become dependent on these variables. This section provides examples of this and discusses some of the trends found for such dependencies.

3.1. Release from the above ground fecal reservoir

Surface applied manure and livestock waste deposited on pasture contribute to an aboveground fecal reservoir. In watershed scale modeling, the release of FMs from a fecal reservoir or matrix is generally described using the exponential model (Eq. (1)). However, there are environmental conditions under which the exponential model fails to perform as a satisfactory predictor. Such environmental conditions include short, high intensity rainfall events and very long rainfalls of moderate intensity (Blaustein et al., 2015a,b,c). During these type of events, the Bradford-Shijven model

$$\frac{N}{N_0} = 1 - \frac{1}{(1 + k_p \beta W)^{\frac{1}{\beta}}} \quad (17)$$

provides better results (Blaustein et al., 2015a, 2015b). In Eq. (17), N_0 is the initial total count of FMs in applied animal waste, N is the total count of released FMs, W is the rainfall depth (mm), k_p (mm^{-1}) and β (–) are release parameters. This model and its modifications (Whelan et al., 2014; Guber et al., 2007, 2013) performed better than the exponential release model when investigating FM release using small plot studies but it has also been tested at larger watershed scales when accommodated within the WALRUS model (Sterk et al., 2016).

3.2. Survival in the aboveground fecal reservoir

Fecal reservoirs accumulate on grazed pasture due to the substantial amounts of livestock waste that are deposited over time through direct excretion (e.g. cowpats). This is different from

manure applications where the presence of a significant fecal reservoir above the soil surface can be ignored. This is because manure applications are usually followed by incorporation (e.g. ploughing into soil) for solid manures or infiltration for liquid manures and slurry.

Biphasic kinetics have been reported for FIO survival in fecal reservoirs. [Oliver et al. \(2010\)](#) reported that the use of first-order kinetic equations could result in an underestimation of *E. coli* burden attributed to the land reservoir, mainly because of growth and re-growth of *E. coli* in feces post-defecation. The survival model suggested by [Oliver et al. \(2010\)](#) was:

$$E_{(x)} = E_{in(x)} + E_{(x-1)} \times e^{-b(x)} + ER_{(x)} \quad (18)$$

where $E_{(x)}$ is the total number of the *E. coli* stored at a pasture on day x (CFU or MPN), E_{in} is the *E. coli* input of fresh deposits (CFU or MPN), b is the die-off rate on day x (–), and ER is the magnitude of daily *E. coli* growth for the same day (CFU or MPN). [Martinez et al. \(2013\)](#) indicated that the net difference between daily FIO growth and die-off appears to be a function of temperature. Using data from [Martinez et al. \(2013\)](#), the daily change in $\log_{10}C$ can be computed as:

$$\Delta \log_{10}C = (-0.394 + 0.073T - 4.20e-3T^2 + 1.01e-4T^3 - 8.63e-7T^4)(1.48)^{(T-20)/10} \quad (19)$$

where T is temperature ($^{\circ}C$). The R^2 value of Eq. (19) was 0.80 within the temperature range from -10 to 22 $^{\circ}C$.

Meteorological factors other than temperature affect long term FM survival in cowpats under field conditions. [Soupir et al. \(2008\)](#) explored both first-order and higher-order approximations to estimate *E. coli* and enterococci die-off coefficients impacted by weather variables under field conditions. Their study demonstrated that a higher-order approximation with inclusion of weather variables was better for modeling the re-growth and die-off trends of FIOs. Data from this work, shown in [Table 3](#), suggest that the meteorological variables (temperature, relative humidity, rainfall, and solar radiation) can have the opposite effect on FIO survival during different seasons, though it is noted that the initial FIO growth was ignored in the regression analysis developed by [Soupir et al. \(2008\)](#).

Presence of shade appears to be an important factor that can influence FIO die-off in the field. [Van Kessel et al. \(2007\)](#) compared the die-off rates of fecal coliforms and *E. coli* within shaded and unshaded cowpats under field conditions, and concluded that in shaded cowpats, the die-off of FIOs was significantly slower, relative to the unshaded cowpats. This may have significant implications with respect to wildlife sources of FIOs, and FMs in general,

Table 3

Best estimates of seasonal *E. coli* die-off (natural logarithm of *E. coli* (CFU (g dry weight) $^{-1}$)) by higher-order approximation and including weather parameters ([Soupir et al., 2008](#)).

Variable ^a	Spring	Summer	Fall	Winter
Intercept	7.269	10.57	18.22	18.19
t	0.2502	-0.1066	-0.2226	0.4381
t ²	-1.20E-02	2.90E-04	1.53E-03	-6.97E-03
t ³	1.32E-04	0	-3.72E-06	2.79E-05
t ⁴	-4.57E-07	0	0	0
Temperature, $^{\circ}C$	0.1839	0.3842	0	-0.1881
Relative humidity (%)	6.18E-02	-6.93E-02	0	0
Rainfall (cm)	-8.89E-02	0.4536	0	0.3509
Solar radiation (MJ)	0	0	0	-3.493

^a Temperature, previous week high; relative humidity, previous week average; rainfall, previous week total; solar radiation (MJ), previous week high, t – time, days.

due to the likely deposition of fecal material in shaded riparian areas.

In some cases, watershed modeling uses die-off rates derived from laboratory studies carried out at constant temperature. [Van Kessel et al. \(2007\)](#) concluded that *E. coli* die-off rates were significantly lower under laboratory conditions relative to variable field conditions. It has been suggested that temperature oscillations typical of field conditions may speed up FIO inactivation since under such conditions FIOs would likely have to use additional resources to adapt to the continuously changing environment ([Semenov et al., 2007](#)). Exploring the impacts of environmental fluctuations on FIO persistence under more controlled conditions would provide useful evidence to support or reject this hypothesis.

3.3. Retention in the soil reservoir

Watershed-scale models have to simulate fate and transport of FMs that, after being released to soil, can remain in upper soil surface layers for potential entrainment into surface runoff when hydrological conditions are sufficient to detach or remobilize cells. Attachment of FMs to organic and inorganic particles is one of the mechanisms that is likely to promote FM retention on the soil surface.

The linear isotherm equation

$$S = K_d c \quad (20)$$

is widely used to model attachment of FIOs to such particles ([Ling et al., 2003](#); [McGechan and Vinten, 2004](#)). Here, S is the concentration of FIOs attached to particles (CFU 100 ml $^{-1}$), K_d is a distribution coefficient (CFU mg $^{-1}$) and c is particle concentration in solution (mg 100 ml $^{-1}$). Coefficient K_d is related to the clay percentage in soil as $K_d = A(\text{CLAY})^B$ where $\text{CLAY} < 50$, and parameters $A = 10^{-1.6 \pm 0.9}$, and $B = 1.98 \pm 0.7$ for *E. coli* ([Pachepsky et al., 2006](#)). [Guzman et al. \(2012\)](#) found that the Freundlich isotherm may be more accurate for modeling FIO attachment when the concentrations of cells in the solution are in excess of 10^4 per ml. The Freundlich exponent reported in the [Guzman et al. \(2012\)](#) study was ~ 0.5 suggesting that K_d in Eq. (20) would decrease with increasing cell concentrations. These authors also noted that the build-up of alkalinity and a corresponding increase in pH can result in decreased attachment of *E. coli* to soil due to soil dispersion.

Exploring the relationship between FM partitioning coefficients and soil texture may be useful in soil that is relatively poor in organic matter. In organic-rich top soils, sand particles covered with organic matter may adsorb *E. coli* with the same K_d as clay particles ([Guber et al., 2007](#)). Because attachment is not controlled by solely soil texture, the approach of [Zhao et al. \(2015\)](#) may be preferable; here a linear model was derived to estimate the partition coefficient (K_d) of *Streptococcus suis* on soil particles as a function of pH and cation exchange capacity (CEC) rather than as a function of soil texture.

3.4. Survival in soil reservoir

[Park et al. \(2016\)](#) assembled and analyzed a large database from published data on *E. coli* survival in soils. Within this database it was clear that a two-stage (biphasic) survival kinetic was often evident, whereby two phases of distinctly different population change rates would occur, i.e. periods of rapid and slow die-off, or growth versus death. Subsequently, decision trees to determine the conditions and factors affecting the occurrence, durations, and rates of the first survival phase were developed ([Park et al., 2016](#)). An example of this decision tree analysis is shown in [Fig. 3](#) and relates the occurrence of the first stage of survival to a number of

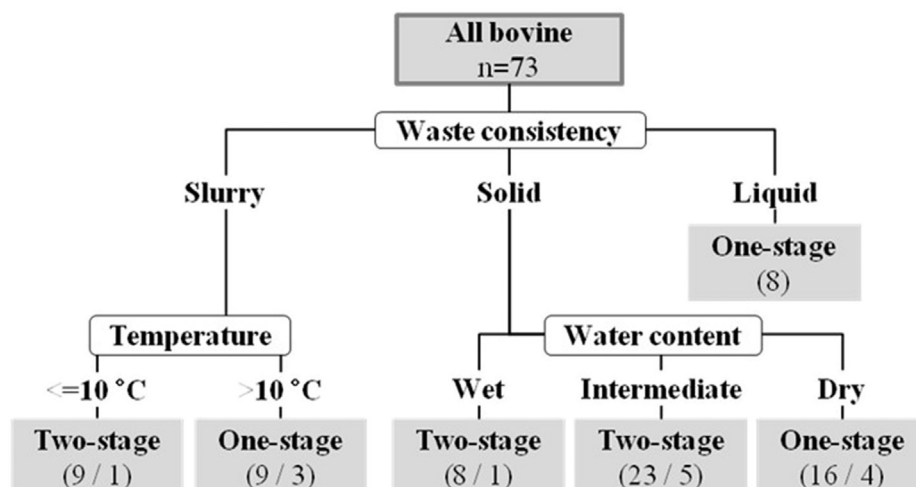


Fig. 3. The decision tree to predict the type of the survival kinetics for *E. coli* in bovine animal waste in soil. Numbers in parentheses mean “total number of datasets with the kinetics stated above/the number of datasets where the opposite type of kinetics occurs” (Park et al., 2016).

environmental and management factors.

Fig. 3 suggests that the animal waste consistency, i.e. solid, slurry, or liquid form, is the lead factor in determining the typology of kinetics that describe FIO survival. Temperature controls the type of FIO survival kinetics in slurries, whereas the type of FIO survival kinetics for solid waste is influenced heavily by soil water content.

3.5. Mobilization of FM from soil to runoff

Pasturelands were used to infer the transition of FMs to runoff from soils and livestock waste deposited during grazing events. For the soil reservoir, Muirhead and Monaghan (2012) presented data on the relationship between *E. coli* concentrations in soil E_s (CFU m^{-2}) and concentrations of *E. coli* in runoff C_r (CFU 100 ml^{-1}) that can be modeled with the power law relationship:

$$C_r = 6.44 E_s^{0.245} \quad (21)$$

We note that the soil reservoir was limited to a 1 cm thick surface layer in this work and the recent work of Stocker et al. (2015) indicated that this assumption is acceptable given that most *E. coli* and enterococci released from soil runoff under simulated rainfall in their study was derived from this layer.

3.6. Survival in the water column

Many models have been proposed to predict FM dynamics in water bodies (Benham et al., 2006) and the linear semi-logarithmic (LSL) inactivation, or Chick's law (Chick, 1908), is widely used to simulate fate of FIOs in waters. Blaustein et al. (2013) found that the performance of the LSL inactivation model was satisfactory only in about 25% of a large *E. coli* database in waters. A variety of models, including expressions developed by Veltz, Weibull, Gompertz, Frost, and Streeter among others, have been recommended to fit *E. coli* inactivation data in which different stages of survival with distinctly different die-off rates were observed (Easton et al., 2005). The application of the Weibull model has been proposed as the superior model to predict FIO inactivation in waters (Stocker et al., 2014).

Temperature is a known controller of FM inactivation. The Arrhenius equation, the Q_{10} model, and the power-law dependence are approximations of each other and simulate the increase in the

inactivation rate of FMs (Blaustein et al., 2013). However, changes in other environmental factors can also impact on FM inactivation rates. Such special cases are briefly considered below.

Salinity is an important factor of FIO survival in estuarine and sea waters. Mancini (1978) summarized data of fecal coliform survival rates in marine waters. His data are shown in Fig. 4a and demonstrate that salinity influences can be neglected at saline concentrations less than 15 $g L^{-1}$, but that these influences become substantial when salinity levels approach concentrations characteristic of marine waters. Rozen and Belkin (2001) reviewed the effects of salinity on survival of *E. coli* in seawater and concluded that the hostile situation encountered by FIOs in seawater can trigger cells to enter a viable-but-non-culturable state.

The pH level can also influence survival, with the effects on FIO die-off in surface waters being most significant either below 6 or above 8, for example, Curtis et al. (1992) observed a 5-fold difference between the numbers of surviving FIOs in dark and in light conditions in water from a waste stabilization pond with a pH up to 9, and became more pronounced as pH exceeded 9 (Fig. 4b).

Dissolved oxygen concentrations substantially affect FM populations in the presence of light. In particular, within eutrophic waters, algae may reduce or enhance the damage to FM cells caused by sunlight, since they both impede light penetration and increase oxygen concentrations. Fig. 4c demonstrates the exponential decrease in FIO concentrations as the concentration of dissolved oxygen increases.

Solar radiation however, is the most influential factor in promoting die-off of FMs in the water column. Previous studies have been conducted to investigate the effect of different parts of solar spectrum, namely, visible light (400–775 nm) and UV radiation (280–400 nm) (Mancini, 1978; Fujioka et al., 1981; Auer and Niehaus, 1993) on the decline of FMs. The UVA range of wavelengths (i.e. range from 320 through to 400 nm), is considered to be the most bactericidal (Jozic et al., 2014). A UVA radiation level of 60–70 $W m^{-2}$ was sufficient to reduce the T_{90} for *E. coli* to a fraction of a day in sea water despite the large difference in T_{90} for two strains when their die-off was studied under dark conditions (Fig. 4d). The type of aquatic ecosystem is also influential in regulating the magnitude of the sunlight effect on FM survival. Mancini (1978) noted that although the effect of sunlight on *E. coli* decay rates in sea water has been known for a long time (Mancini, 1978), similar data on the effect of sunlight on *E. coli* survival in brackish

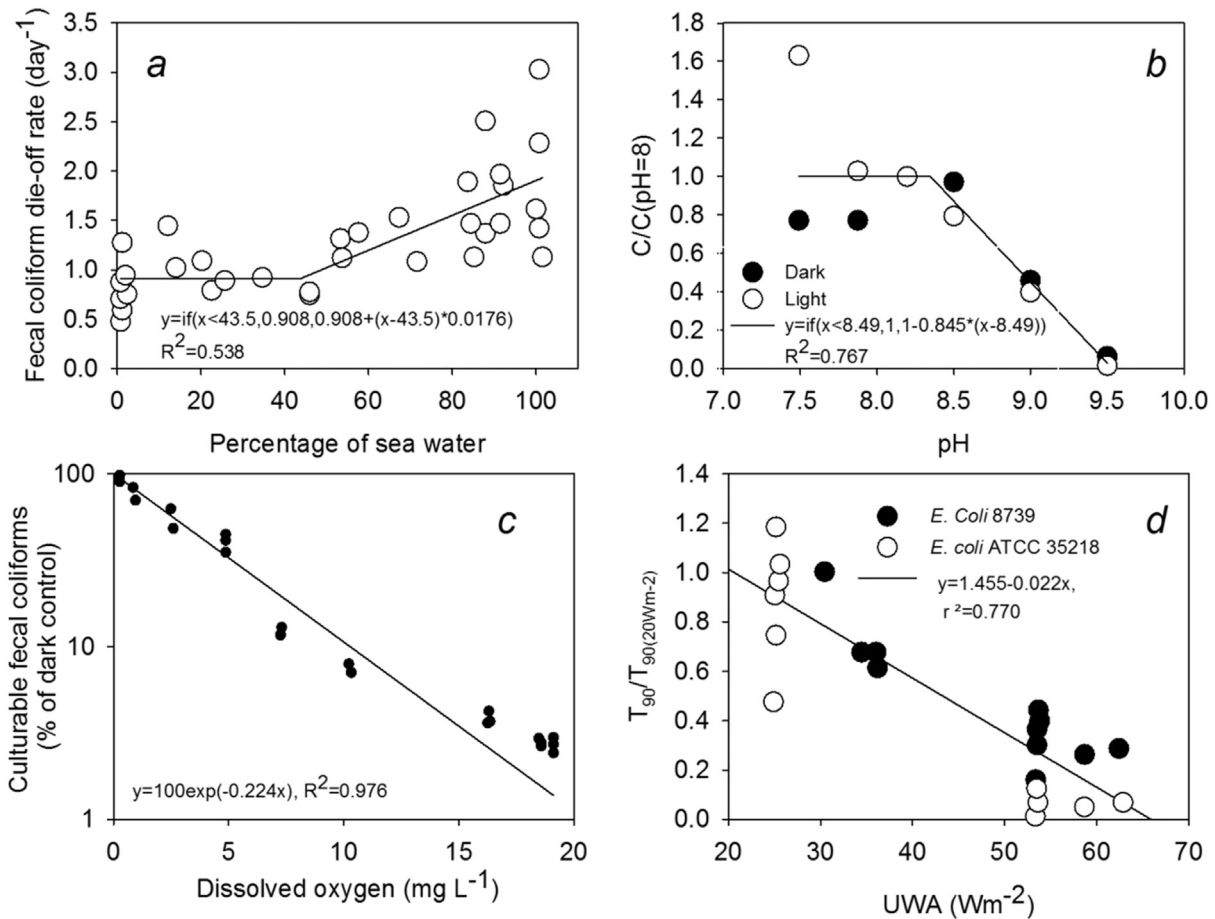


Fig. 4. Environmental effects on *E. coli* survival. (a) Effect of water salinity on coliform survival (data from Mancini, 1978); (b) effect of pH on bacteria survival in light and dark conditions in waters from the waste stabilization pond (experimental data from Curtis et al., 1992); (c) effect of oxygen concentration on the impact of light on bacteria concentrations; the samples (pH 8.8) received 7.83 MJ m⁻² for 136 min (=960 W m⁻²) (experimental data from Curtis et al., 1992); (d) decrease in relative T₉₀ with the increase in UV radiation level for two strains of *E. coli* in water from retention pond (data from Jozic et al., 2014).

and freshwater has only recently been published (Perkins et al., in press).

A linear relationship

$$k_S = a_R R_S \quad (22)$$

was suggested by Mancini (1978). Here, k_S is the mortality rate (d⁻¹), R_S is the radiation (W m⁻²), and $a_R = 11.3$ for low light conditions normally anticipated in natural environments. Sinton et al. (2007) confirmed the possibility of using cumulative global solar radiation (insolation) to estimate the FM die-off rates and proposed that the seasonality of daylight inactivation may need to be accounted for.

Dissolved or suspended organic matter can positively affect *E. coli* survival in water. Waters accommodating high organic content have, in the majority of cases, resulted in *E. coli* survival patterns whereby the first stage of survival following inoculation exhibited either growth or just no tangible decrease of cell concentration (Blaustein et al., 2013). Using a standard one-stage kinetics equation to model cell decline under such conditions may lead to a significant deviation from observed *E. coli* persistence patterns.

3.7. Survival in streambed sediments

The ability of *E. coli* to survive and to grow in streambed

sediments has been demonstrated (Pachepsky and Shelton, 2011). In the absence of nutrient inputs the linear semilogarithmic (Chick's) model was shown to accurately represent *E. coli* persistence. However, when the overlying water column was enriched with nutrients it resulted in a period of growth of approximately one order of magnitude in the *E. coli* population residing in the streambed sediments. The subsequent rate of die-off was equivalent to the same temperature dependent rate observed before nutrient enrichment (Shelton et al., 2014).

3.8. Transient storage and hyporheic exchange

The transient storage (TS) associated with watercourses is replenished during high flow events, and may then provide a continuous source of chemical or FM concentrations to the overlying water column after such events (Bencala and Walters, 1983; Gooseff et al., 2008). Yakirevich et al. (2013) used a one-dimensional stream solute transport model to combine existing understanding of FIO fate and transport with a TS module where a linear kinetic equation assuming the first-order mass transfer was used to simulate the FIO exchange with TS. In doing so, the combined model was able to simulate the elevated FIO concentrations in a monitored watercourse long after an artificial high-flow event subsided, thus highlighting the contributions of FIOs from TS. Hyporheic exchange refers to the advectively driven bidirectional exchange of water between the stream and the streambed (Buss

et al., 2015). Grant et al. (2011) examined the rate constant that characterizes the exchange of water between the stream and its storage zone. The volumetric flux of water between the stream and its storage zone could be estimated from the product of the first-order exchange rate ($\alpha = 4 \times 10^{-3} \text{ s}^{-1}$) and a measure of the stream's water depth ($R = 0.6 \text{ m}$) (Bencala and Walters, 1983). Little research has focused on quantifying the specific attenuation and release mechanisms of FIOs within the hyporheic zone and the role of groundwater influx and upwelling in contributing to FIO loading of streams under low flow conditions.

4. Future needs and feasibilities of watershed scale modeling of microbial water quality

4.1. Effects of hydrological regimes on FM fate and transport

The results of fate and transport modeling are controlled by underlying hydrological modeling results. The hydrologic modules of watershed models are calibrated using measurements of stream or river discharge values. The same values of discharge may correspond to different values of total volume of water in a reach, stage, and surface area for a reach. The assumed relationship between the hydraulic variables appears to have a profound impact on long-term average FM concentrations, FM die-off as related to the residence time within streams, and water quality criterion violation rates (Hall et al., 2008). Observed and simulated low-flow conditions often occur in small, low-order, upland streams, which can approach zero flow during dry weather conditions. In these streams, modeling limitations often result when attempting to predict small flow rates when, in reality within the stream reach, either no flow is occurring or flow is discontinuous, i.e., water collects in pools within the reach. The role of streambed sediment as a reservoir supporting FM persistence in such low flow conditions is currently unknown.

Another challenge relates to understanding the impacts of water abstraction, e.g. irrigation, on FM dynamics in watershed modeling (Monaghan et al., 2009). Studies have shown that *E. coli* loading in irrigation water can be high (McDowell et al., 2008) and there is evidence to link contaminant signatures in water quality in a large catchment to irrigation practices on pastoral land (McDowell and Kitto, 2013). These effects are important to consider given that the irrigation season typically occurs during summer, coinciding with the key recreational water use periods for swimming and fishing. In New Zealand, conversion from traditional flood irrigation systems to more modern and efficient spray irrigation systems reduced, but did not eliminate, *E. coli* losses from farmed land (McDowell and Kitto, 2013). The ability to incorporate irrigation practices into watershed scale models of FM dynamics will be important for future application in many agricultural areas.

Particular soil water regimes, including those created by irrigation, can result in special conditions for FM transport in and through soils. The proportion of FMs transported through the soil column is highly dependent on the physical structure of the soils and soil water saturation (Smith et al., 1985; McLeod et al., 2008). Furthermore, soil structure and transport pathways can be significantly modified by artificial drainage of soils (Oliver et al., 2005; Monaghan et al., 2016). So far there have been few attempts to quantitatively model these spatially variable processes (McGeachan and Vinten, 2004).

4.2. In-stream processes

FIOs are routinely found in streambed sediments, stream bank soils, and other environmental and man-made media that are exposed to surface water environments. Modeling can play an

important role in helping to apportion FM contributions from land sources and direct deposition to water from FM contributions from such contact media. For example, advances have been made in modeling FIO release with re-suspended sediment and its retention in transient storage (Kim et al., 2010; Yakirevich et al., 2013; Pandey and Soupir, 2013; Pandey et al., 2016). However, little progress has been made in modeling (or indeed observing in detail) FIO influx from sediment by groundwater influx during baseflow and yet high FIO concentrations during baseflow are routinely observed in some waterbodies (e.g., Kim et al., 2010). Comparison of the genetic make-up of *E. coli* in water and in sediment has shown that a substantial (17–21% according to Piorkowski et al., 2014, and possibly 36% according to Brinkmeyer et al., 2015) percentage of the in-stream *E. coli* population can originate from the streambed sediment. There is also a possibility that some FIOs are brought to the stream with groundwater flow itself, rather than from disturbance of the contaminated sediments via upwelling (Dorner et al., 2006; Schijven et al., 2015). Of course, residual runoff, seepage from springs and hydrological lag-times have also been offered as an explanation of high FIO concentrations in receiving waters long after the waterway has returned to antecedent conditions (Desai et al., 2011; Collins and Rutherford, 2004). Overall there is a need to increase research attention on FIO inputs to streams during base flow conditions. This appears to be critical since such inputs may preclude bringing stream water quality to the regulatory limits by land-based management practices. Addressing this research gap will be challenging because many base flow inputs to streams are independent of rainfall hydrology (Muirhead et al., 2011) and thus requires separate modeling that is detached from rainfall-runoff processes within watershed models.

Given the importance of streambed sediment as an FIO source it is critical to understand the variety of factors (e.g. grain sediment size, nutrient conditions) that can influence and support FIO persistence and growth in these environments. Such regrowth has been observed under field conditions (Evanson and Ambrose, 2006; Muirhead et al., 2004; Henson et al., 2007), and has been shown in laboratory microcosm experiments (Shelton et al., 2014), but has not been simulated in watershed scale modeling. Data from microcosm studies show that nutrient concentrations in water have a nonlinear effect on FIO regrowth (Shelton et al., 2014). Therefore, simulations of in-stream nutrient dynamics may need to be coupled with in-stream FIO fate and transport simulations to bring about effective modeling of FIO behavior in streambed sediments in response to nutrient inputs.

Presence of carbon-rich substances in the water column may affect FM die-off rates in waters. Blaustein et al. (2013) demonstrated both qualitative and quantitative differences in FIO die-off rates observed in surface waters from different sources. For example, the persistence profile of *E. coli* in sewage-affected waters demonstrated a period of growth followed by a second phase of exponential inactivation. Little is known, however, about this effect in natural waterways. If this effect exists at the scale of streams and rivers, it could partially explain the improvement in SWAT modeling obtained after assuming seasonal differences in survival rates that include growth in warm seasons and accelerated die-off in cold seasons (Cho et al., 2016).

We note that in-stream processes are lumped together in the majority of watershed-scale models, and as a result a few parameters are often used to simulate much of the complexity of watershed processes (e.g. in-stream processing). For example, FM die-off rates are affected both by radiation and temperature, and yet a single dependence on temperature is often implemented to describe FM die-off. The outcome of process lumping or aggregation is a high degree of sensitivity in modeled outputs attributed to lumped in-stream parameters (Iudicello and Chin, 2013). It will be

beneficial to the modeling community to determine which in-stream processes create this sensitivity. However, it is likely that the importance of these factors will vary with stream morphology and watershed hydrological functioning, making it difficult to incorporate such nuanced detail into lumped models. Over-parameterization of models provides another challenge for in-stream process modeling. For example, the SWAT model can accommodate the presence of two populations of the same bacterium with different survival rates. However, at the current time we cannot populate such parameter values because investigations are not yet robust enough to effectively determine rate constants for both bacteria populations.

4.3. Processes on land surface

Land deposition of fecal material on grazing lands can affect *E. coli* concentrations in runoff long after the deposition occurred. Legacy impacts on runoff water quality extending up to 1300 days post deposition have been recorded (Muirhead and Monaghan, 2012). The authors suggested that an environmental reservoir of *E. coli* exists on grazing lands that needs to be treated as a separate FIO source compartment in watershed-scale models and requires further investigation to determine its role and importance in contributing to non-point source pollution. Aging of livestock waste is another related, but also poorly understood, control of *E. coli* concentrations in runoff from grazing land, although the effect of such aging on *E. coli* mobilization is currently not well known (McDowell et al., 2008). Differences in the physical, chemical and biological composition of fecal matrices, e.g. livestock manures versus livestock waste deposits, are profound and may create a number of differences in FM mobilization and subsequent transport behavior, which may also vary as the fecal matrix ages over time. Fortunately, these knowledge gaps are now beginning to attract research attention (Blaustein et al., 2015a,b,c).

Partitioning microbial cells in runoff into those that are freely suspended and those that are moving in association with solid particles is currently poorly understood, with empirical observations varying widely in published research. Muirhead et al. (2006) noted that FIOs were not attached to soil particles when carried in runoff generated at field plot scales. However, when unattached cells were inoculated into the turbid water flow, the *E. coli* appeared to attach predominantly to small particles (<2 μm) and hence remain unattenuated during transport. Soupir and Mostaghimi (2011) studied transport of FIO from fresh manure and found that the majority of *E. coli* and enterococci were transported from fresh manure sources in an unattached state with only 4.8% of *E. coli* and 13% of enterococci associated with particles. Their second experiment, which compared partitioning in runoff from both highly and sparsely vegetated land covers, found lower FIO attachment rates: the average *E. coli* percent attached was 0.06% from plots with highly vegetated cover and 2.8% from plots with sparsely vegetated cover, while the corresponding values for enterococci were 0.98% and 1.23%, respectively. In contrast, Soupir et al. (2010) tested three different soil textures (silty loam, silty clay loam, and loamy fine sand) to investigate the FIO partitioning release under simulated rainfall conditions and observed similar patterns among three soil textures, showing that 28–49% of *E. coli* were attached to particles in runoff. One reason for such discrepancies may be the assumption that centrifugation is a robust method of estimating adsorption of viable cells to soil particles. This assumption needs to be verified since living bacteria may be affected by acceleration and solid particle bombardment. The importance of understanding FIO partitioning to soil particles is reinforced when considering scale effects of sediment transport across a watershed. Sediment export with runoff per unit area is known to decrease as the size of the

study area increases (Delmas et al., 2012) and so if cells are associating with soil particles this might help to explain observed decreases of *E. coli* concentrations in waterways of different orders (Harmel et al., 2010).

4.4. Effects of scale and scaling

An important question is whether the parameters used in FM fate and transport modeling need to vary with scale of model application. Upscaling from individual fields, land use practices and management systems to obtain a single homogeneous soil, land use, and management parameters across HRUs introduces unavoidable uncertainty. However, this aggregation helps to deliver manageable and interpretable modeling results across large areas of interest. In response, more research is needed to improve and justify the formulation of rules to enable such upscaling (lumping). Insights can be obtained from modeling FM responses at finer scales and upscaling modeling results, but such attempts still remain scarce.

4.5. Model performance evaluation and comparison

Increased attention to model performance evaluation is necessary. Model performance metrics, such as root-mean-squared error, Nash-Sutcliffe efficiency, are often applied without accounting for underlying data uncertainty. The temporal uncertainty in FIO concentrations observed in environmental matrices can be very high. Bougeard et al. (2011) report values of 0.33 and 0.70 for standard deviations of the decimal logarithm of FIO concentrations measured diurnally during both low and high rainfall, respectively, and yet the daily time step of models cannot reproduce such sub-grid variations (Im et al., 2004). Therefore, diurnal variations have to be properly compared with model errors to avoid reporting accuracy of model predictions that are higher than the accuracy of the data used to inform the model.

Critical evaluation of model performance needs to be targeted to the model application rather than to the abstract accuracy of the model. Microbial water quality standards are typically characterized by statistical measures from a population, such as medians and percentile values, rather than point estimates. Thus, model performance should be evaluated by the accuracy of reproducing the distribution of expected values rather than point-to-point comparison statistics (Muirhead et al., 2001; Stott et al., 2011). An example is given in the work of Bougeard et al. (2011) who investigated microbial water quality in shellfish producing waters and used the results of a comparison of cumulative distributions in computed concentrations to derive the conclusions about their model performance. Coffey et al. (2013) concluded that the SWAT model was adequate to assess the magnitude of various FM sources within catchments but capability to replicate daily observations was hindered by uncertainty. Nevertheless, outputs from those models could provide adequate data to help develop more robust approaches to human exposure assessment and assist policy-makers in developing appropriate risk management strategies across watersheds.

The modeling of FM loads versus FM concentrations also provides an interesting contrast with respect to model performance. When loads, i.e. cumulative masses, are considered, regular model performance metrics show much better performance than when computed and simulated concentrations are compared (Haydon and Deletic, 2006). In this example it was suggested that the computation of loads reduced the effect of any one individual measurement. Ultimately the performance of the model should be measured against the purpose of the model and so a model developed to predict concentrations of FIOs in rivers is appropriate

for understanding water quality targets in the river but it may be more appropriate to focus on loads when the purpose of the model is predicting riverine inputs to a larger receiving water body.

A large number of watershed scale models are available (see e.g. Table 1 and references therein), and so the end-users of models, e.g. policy-makers, scientists, watershed stakeholders, have considerable choice in terms of which model to deploy. Choosing the right model to deliver on the watershed management objective at hand is essential and this reinforces a critical need for the development of specific criteria to guide model selection and adoption by watershed stakeholders (Oliver et al., 2016). Those with past experience of modeling approaches may tend to re-use models with which they are familiar, or choose those that have been developed with a 'user-friendly' interface. These are undoubtedly important factors for guiding model choice, but other aspects may be of larger significance. Some models may overlook fate and transport of site-specific importance, such as hyporheic mass exchange in shallow water sources, algal growth that harbors FIOs, adequate accommodation of watercourse impoundments in model structure. There is of course the possibility of adopting code from one model to be used in a different model. However, not all source codes are available, and modularity and description of some codes leave much to be desired.

Model transferability across international borders is another issue that can influence model selection by end-users. Models that accommodate empirical equations that link to environmental databases and classifications specific for the country it was developed for create compatibility issues for exploring trans-boundary modeling of FMs. It is, of course, inherently challenging to use a model framework developed in one country and translate it to a different country without harmonizing classifications, which is far from trivial. An example is the use of field capacity of soils where the value of hydraulic head for field capacity appears to be country-specific. It is -5 kPa in United Kingdom and France, -6 kPa in Brazil, -10 kPa in Australia and Sweden, -33 kPa in US (Nemes et al., 2011). Therefore the blind use of the pressure head of -33 kPa to determine water contents at field capacity values from US may lead to a gross underestimation of soil water storage in applications in other countries.

We concede that this review is limited to continuous simulation models that employ daily or shorter time steps and use the results from the previous time step as initial values to make the next time step. Models of other types have been developed and applied. For example, Muirhead (2015) developed a model to characterize FM concentrations in agricultural systems at the annual scale and the development and application of statistical models of FM concentrations in freshwater sources have been reported (e.g., Nnane et al., 2011). Comparison of accuracy, reliability and utility of different model structures, as well as intercomparison of different continuous simulation models presents scope for interesting and exciting future developments in the field of watershed modeling of FMs.

4.6. Model reliability

The wide range of site-specific values that can be used to populate the same parameters in models is a significant issue (section 2.10). This may be caused by environmental factors that are not accounted for, for example, differences in scale, lumped representation of several processes, uncertainty in data used for calibration. Insights into the breadth of parameter range distributions are needed to be able to make modeled predictions of FM fate and transfer in un-gauged watersheds.

A fundamental problem with watershed-scale FIO fate and transport modeling is due to the inherent uncertainty in some essential parameter inputs (Niazi et al., 2015). In particular, levels of

fecal loading from wildlife is commonly unknown, although has the potential to contribute a substantial fraction to the total FIO load to the wider environment (Parajuli et al., 2009; Rolle et al., 2012), and can be responsible for 100% of the FIO load in stream headwaters in forested areas (Guber et al., 2014). The state of on-site water treatment systems is usually unknown, and, although failing septic tank systems were shown to not have a strong effect on FIO concentrations in the study of Coffey et al. (2010), they may be more influential in different environmental contexts. The relationship between point source wastewater release of FIOs and the biological oxygen demand estimated as 1.2×10^9 CFU per g BOD may be helpful (Servais et al., 2007), but the degree of its generality is unknown. Livestock waste deposition both on land and in streams is not well defined in terms of spatial and temporal patterns of loading, and concentrations of FIO in livestock waste and manure vary widely. Such uncertainty does not preclude model use and deployment, but suggests increased value of adopting modeling approaches that accommodate multiple simulations while varying the uncertain inputs within realistic ranges and reporting the cumulative probability distributions of the output variables, rather than their single values (Muirhead et al., 2011).

A significant challenge for modeling specific pathogen dynamics in catchment systems is the scarcity of pathogen data to underpin model calibration and testing. The costs for large scale sampling campaigns and subsequent quantification of a suite of different pathogens in environmental matrices can be prohibitive (Dorner et al., 2006). Another challenge is presented by the lack of existing data (LaWare and Rifai, 2006). Since the assessment of microbial water quality remains complex and expensive (relative to, for example, nutrients), the current challenge is to develop monitoring strategies to help improve our modeling capability while recognizing the need for efficient use of resources spent on sampling. Sampling 'hot-spots' of FIO loading will be important for future modeling efforts but is fraught with challenges. For example, sampling locations in the vicinity of wildlife colonies and sampling in stagnant flow zones would yield interesting information for modeling, but such targeted sampling is likely to be prone to sampling errors, although the magnitude of the error has not been researched. The same applies to sampling where sediment may be affected by frequent inflows of FIO-rich turbid waters. Finally, the sensitivity of different parameters on modeling results will vary across different hydrological states of the system (e.g. rising and falling limb of hydrographs, baseflow), and therefore monitoring has to target different hydrological states to strengthen the impact and validity of modeling results for different watershed stakeholders, e.g. recreational water users, those reliant on abstraction and those in the aquaculture industry.

5. Conclusions

- With greater awareness of microbial water quality issues in watershed systems there is growing impetus for predictions of fecal microorganism concentrations, fluxes, and loads in different types of water bodies to inform policy development and guide future water quality control activities.
- The uncertainty reduction in modeling results has to be targeted and can be achieved via active experimentation with and monitoring of overland, groundwater, and underlying bed sediment-related fate and transport of fecal microorganisms in heterogeneous hydrological mass balance units over the range of scales.
- Complexity and variability of microbial fate and transport processes and environments as well as differences in modeling purposes warrant further development of different watershed-scale microbial fate and transport models that collectively will

provide tools for microbial water quality management on the changing planet.

Acknowledgements

This research was supported by the Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (NRF-2014R1A1A2059680). DMO & RSQ received funding from the UK Natural Environment Research Council (NERC) as part of the 'PRACTICAL Modelling' project (NE/M005860/1). YP, YP, and DRS were funded via the USDA-ARS project "Pathogenic microorganisms in irrigation waters". RWM was supported by the Clean Water, Productive Land research programme (C10x1006) funded by the New Zealand Ministry for Business, Innovation and Employment.

References

- Alderisio, K.A., DeLuca, N., 1999. Seasonal enumeration of fecal coliform bacteria from the feces of ring-billed gulls (*Larus delawarensis*) and Canada geese (*Branta canadensis*). *Appl. Environ. Microbiol.* 65 (12), 5628–5630.
- Allende, A., Monaghan, J., 2015. Irrigation water quality for leafy crops: a perspective of risks and potential solutions. *Int. J. Environ. Res. Public Health* 12 (7), 7457–7477.
- Arnold, J., Kiniry, J., Srinivasan, R., Williams, J.R., Haney, E.B., Neitsch, S.L., 2011. Soil and Water Assessment Tool Input/Output File Documentation Version 2009. Texas Water Resources Institute Technical Report No. 365.
- Ashbolt, N.J., Grabow, W.O.K., Snozzi, M., 2001. Indicators of microbial water quality. In: Fewtrell, L., Bartram, J. (Eds.), *Water Quality: Guidelines, Standards and Health: Risk Assessment and Management for Water Related Infectious Diseases*. IWA Publishing, London, pp. 289–316.
- Auer, M.T., Niehaus, S.L., 1993. Modeling fecal-coliform bacteria. 1. Field and laboratory determination of loss kinetics. *Water Res.* 27 (4), 693–701.
- Bai, S., Morton, M., Parker, A., 2006. Modeling enterococci in the tidal Christina River. *Estuary and Coastal Modeling*. In: Spaulding, M.L., et al. (Eds.), *Proceedings of the Ninth International Conference Estuarine and Coastal Modeling*. ASCE, pp. 305–318.
- Bencala, K.E., Walters, R.A., 1983. Simulation of solute transport in a mountain pool-and-riffle stream: a transient storage model. *Water Resour. Res.* 19, 718–724.
- Benham, B.L., Baffaut, C., Zeckoski, R.W., Pachepsky, Y.A., Mankin, K.R., Sadeghi, A.M., Brannan, K.M., Soupir, M.L., Habersack, M.J., 2006. Modeling pathogen fate and transport in watersheds to support TMDLs. *Trans. ASABE* 49, 987–1002.
- Blaustein, R.A., Pachepsky, Y.A., Hill, R.L., Shelton, D.R., 2015a. Solid manure as a source of fecal indicator microorganisms: release under simulated rainfall. *Environ. Sci. Technol.* 49 (13), 7860–7869.
- Blaustein, R.A., Hill, R.L., Micallef, S., Shelton, D.R., Pachepsky, Y.A., 2015b. Rainfall intensity effects on removal of fecal indicator bacteria from solid dairy manure applied over grass-covered soil. *Sci. Total Environ.* 539 (1), 583–591.
- Blaustein, R.A., Pachepsky, Y.A., Shelton, D.R., Hill, R.L., 2015c. Release and removal of microorganisms from land-deposited animal waste and animal manures: a review of data and models. *J. Environ. Qual.* 44 (5), 1338–1354.
- Blaustein, R.A., Pachepsky, Y., Hill, R.L., Shelton, D.R., Whelan, G., 2013. *E. coli* survival in waters: temperature dependence. *Water Res.* 47 (2), 569–578.
- Bottcher, A.B., Whiteley, B.J., James, A.L., Hiscock, J.G., 2012. Watershed assessment model (WAM): model use, calibration, and validation. *Trans. ASABE* 55 (4), 1367–1383.
- Bougeard, M., Le Saux, J.C., Teillon, A., Belloir, J., Le Mennec, C., Thome, S., Durang, G., Pompepy, M., 2011. Combining modeling and monitoring to study fecal contamination in a small rural catchment. *J. Water Health* 9 (3), 467–482.
- Brannan, K.M., Mostaghimi, S., Dillaha, T.A., Heatwole, C.D., Wolfe, M.L., 2002. Fecal Coliform TMDL for Big Otter River, Virginia: a case study. In: Saleh, A. (Ed.), *Total Maximum Daily Load (TMDL) Environmental Regulations: Proceedings of March 11–13, 2002, Conference*, pp. 367–376. ASAE Publication Number 701P0102.
- Brinkmeyer, R., Amon, R.M., Schwarz, J.R., Saxton, T., Roberts, D., Harrison, S., Ellis, N., Fox, J., DiGuardi, K., Hochman, M., Duan, S., Stein, R., Elliott, C., 2015. Distribution and persistence of *Escherichia coli* and Enterococci in stream bed and bank sediments from two urban streams in Houston, TX. *Sci. Total Environ.* 502, 650–658.
- Buss, S., Cai, Z., Cardenas, B., Fleckenstein, J., Hannah, D., Heppell, K., Hulme, P., Ibrahim, T., Kaeser, D., Krause, S., Lawler, D., Lerner, D., Mant, J., Malcolm, I., Old, G., Parkin, G., Pickup, R., Pinay, G., Porter, J., Rhodes, G., Richie, A., Riley, J., Robertson, A.L., Sear, D., Shields, B., Smith, J., Tellam, J., Wood, P., 2015. *The hyporheic handbook: a handbook on the groundwater-surface-water interface and the hyporheic zone for environmental managers*. Environ. Agency Sci. Rep. SC0 50070.
- Centers for Disease Control and Prevention, 2015. *Surveillance Reports for Recreational Water-associated Disease & Outbreaks*. Available from URL: <http://www.cdc.gov/healthywater/surveillance/rec-water-surveillance-reports.html>.
- Chick, H., 1908. An investigation of the laws of disinfection. *J. Hyg.* 8 (01), 92–158.
- Cho, K.H., Pachepsky, Y.A., Kim, J.H., Kim, J.W., Park, M.H., 2012. The modified SWAT model for predicting fecal coliforms in the Wachusett Reservoir Watershed, USA. *Water Res.* 46 (15), 4750–4760.
- Cho, K.H., Cha, S.M., Kang, J.H., Lee, S.W., Park, Y., Kim, J.W., Kim, J.H., 2010a. Meteorological effects on the levels of fecal indicator bacteria in an urban stream: a modeling approach. *Water Res.* 44 (7), 2189–2202.
- Cho, K.H., Pachepsky, Y., Kim, J.H., Guber, A., Shelton, D., Rowland, R., 2010b. Release of *Escherichia coli* from the bottom sediment in a first-order creek: experiment and reach-specific modeling. *J. Hydrology* 391 (3), 322–332.
- Cho, K.H., Pachepsky, Y.A., Kim, M., Pyo, J.C., Park, M.H., Kim, J.W., Kim, J.H., 2016. Modeling seasonal variability of fecal coliform in natural surface waters using the modified SWAT. *J. Hydrology* 535, 377–385.
- Chin, D.A., 2011. Quantifying pathogen sources in streams by hydrograph separation. *J. Environ. Eng* 137 (9), 770–781.
- Coffey, R., Cummins, E., O'Flaherty, V., Cormican, M., 2010. Pathogen sources estimation and scenario analysis using the Soil and Water Assessment Tool (SWAT). *Hum. Ecol. Risk Assess.* Int. J. 16 (4), 913–933.
- Coffey, R., Dorai-Raj, S., O'Flaherty, V., Cormican, M., Cummins, E., 2013. Modelling of pathogen indicator organisms in a small-scale agricultural catchment using SWAT. *Hum. Ecol. Risk Assess.* Int. J. 19 (1), 232–253.
- Collins, R., Rutherford, K., 2004. Modelling bacterial water quality in streams draining pastoral land. *Water Res.* 38 (3), 700–712.
- CSFSGLLGSC, 2006. *Commodity Specific Food Safety Guidelines for the Lettuce and Leafy Greens Supply Chain*, first ed. Available from: <http://www.fda.gov/downloads/Food/GuidanceRegulation/UCM169008.pdf> (last accessed 25.03.14.).
- Curtis, T.P., Mara, D.D., Silva, S.S., 1992. Influence of pH, oxygen, and humic substances on ability of sunlight to damage fecal coliforms in waste stabilization pond water. *Appl. Environ. Microbiol.* 58 (4), 1335–1343.
- de Brauwere, A., Gourgue, O., de Brye, B., Servais, P., Ouattara, N.K., Deleersnijder, E., 2014. Integrated modelling of faecal contamination in a densely populated river-sea continuum (Scheldt River and Estuary). *Sci. Total Environ.* 468, 31–45.
- Delmas, M., Pak, L.T., Cerdan, O., Souchère, V., Le Bissonnais, Y., Couturier, A., Sorel, L., 2012. Erosion and sediment budget across scale: a case study in a catchment of the European loess belt. *J. Hydrology* 420, 255–263.
- Desai, A., Rifai, H.S., Petersen, T.M., Stein, R., 2011. Mass balance and water quality modeling for load allocation of *Escherichia coli* in an urban watershed. *J. Water Resour. Plan. Manag.* 137 (5), 412–427.
- Dorner, S.M., Anderson, W.B., Slawson, R.M., Kouwen, N., Huck, P.M., 2006. Hydrologic modeling of pathogen fate and transport. *Environ. Sci. Technol.* 40 (15), 4746–4753.
- Easton, J.H., Gauthier, J.J., Lalor, M.M., Pitt, R.E., 2005. Die-off of pathogenic *E. coli* O157:H7 in sewage contaminated waters. *J. Am. Water Resour. Assoc.* 41 (5), 1187–1193.
- EUPC, 2006a. The European Parliament and the Council, Directive 2006/113/EC of the European Parliament and of the Council of 12 December 2006 on the quality required of shellfish waters. *Official J. Eur. Union L* 376, 14.
- EUPC, 2006b. The European Parliament and the Council, Directive 2006/7/EC of the European Parliament and of the Council of 15 February 2006 concerning the management of bathing water quality and repealing directive 76/160/EEC. *Official J. Eur. Union L* 64, 37.
- Evanson, M., Ambrose, R.E., 2006. Sources and growth dynamics of fecal indicator bacteria in a coastal wetland system and potential impacts to adjacent waters. *Water Res.* 40, 475–486.
- Ferguson, C.M., Croke, B.F.W., Beatson, P.J., Ashbolt, N.J., Deere, D.A., 2007. Development of a process-based model to predict pathogen budgets for the Sydney drinking water catchment. *J. Water Health* 5 (2), 187–208.
- Franz, E., Semenov, A.V., Termorshuizen, A.J., De Vos, O.J., Bokhorst, J.G., Van Bruggen, A.H.C., 2008. Manure-amended soil characteristics affecting the survival of *E. coli* O157:H7 in 36 Dutch soils. *Environ. Microbiol.* 10 (2), 313–327.
- Fujioka, R.S., Hashimoto, H.H., Siwak, E.B., Young, R.H.F., 1981. Effect of sunlight on survival of indicator bacteria in seawater. *Appl. Environ. Microbiol.* 41 (3), 690–696.
- Gautam, B., Kasi, M., Lin, W., 2006. Determination of fecal coliform loading and its impact on river water quality for TMDL development. In: *The Water Environment Federation's Technical Exhibition and Conference (WEFTEC® 06)*, October 21–25, Dallas, TX, pp. 3851–3874.
- Gooseff, M.N., Bencala, K.E., Wondzell, S.M., 2008. Solute transport along stream and river networks. In: Rice, S.P., Roy, A.G., Rhoads, B.L. (Eds.), *River Confluences, Tributaries and the Fluvial Network*. John Wiley & Sons, Ltd. Ch. 18.
- Grant, S.B., Litton-Mueller, R.M., Ahn, J.H., 2011. Measuring and modeling the flux of fecal bacteria across the sediment-water interface in a turbulent stream. *Water Resour. Res.* (5), 47.
- Gronewold, A.D., 2009. *Water Quality Models for Supporting Shellfish Harvesting Area Management by Water Quality Models for Supporting Shellfish Harvesting Area Management* (Doctoral dissertation). Available from URL: <http://dukespace.lib.duke.edu/dspace/handle/10161/898>.
- Guber, A.K., Pachepsky, Y.A., Shelton, D.R., Yu, O., 2007. Effect of bovine manure on fecal coliform attachment to soil and soil particles of different sizes. *Appl. Environ. Microbiol.* 73 (10), 3363–3370.
- Guber, A.K., Pachepsky, Y.A., Dao, T.H., Shelton, D.R., Sadeghi, A.M., 2013. Evaluating manure release parameters for nonpoint contaminant transport model KINEROS2/STWIR. *Ecol. Model* 263, 126–138.

- Guber, A.K., Shelton, D.R., Pachepsky, Y.A., Sadeghi, A.M., Sikora, L.J., 2006. Rainfall-induced release of fecal coliforms and other manure constituents: comparison and modeling. *Appl. Environ. Microbiol.* 72 (12), 7531–7539.
- Guber, A.K., Williams, D.M., Quinn, A.C.D., Tamrakar, S.B., Rose, J.B., Porter, W.F., 2014. SWAT-SIR model for predicting fate and transport of manure borne pathogens in fragmented agriculture forest ecosystems. In: Proceedings of the 7th International Congress on Environmental Modelling and Software: Bold Visions for Environmental Modeling, iEMSS, vol. 3, pp. 1474–1481.
- Guzman, J.A., Fox, G.A., Penn, C.J., 2012. Sorption of *Escherichia coli* in agricultural soils influenced by swine manure constituents. *Trans. ASABE* 55 (1), 61–71.
- Hall, K.M., Zeckoski, R.W., Brannan, K.M., Benham, B.L., 2008. FTABLE generation method effects on instream fecal bacteria concentrations simulated with HSPF. *J. Am. Water Resour. Assoc.* 44 (2), 489–495.
- Harmel, R.D., Karthikeyan, R., Srinivasan, G.T., 2010. Effects of agricultural management, land use, and watershed scale on *E. coli* concentrations in runoff and streamflow. *Trans. ASABE* 53 (6), 1833–1841.
- Haydon, S., Deletic, A., 2006. Development of a coupled pathogen-hydrologic catchment model. *J. Hydrol.* 328 (3–4), 467–480.
- Henson, S.A., Ahearn, D.S., Dahlgren, R.A., Van Nieuwenhuysse, E., Tate, K.W., Fleenor, W.E., 2007. Water quality response to a pulsed-flow event on the Mokelumne River, California. *River Res. Appl.* 23, 185–200.
- Holz, G.K., 2010. Sources and processes of contaminant loss from an intensively grazed catchment inferred from patterns in discharge and concentration of thirteen analyses using high intensity sampling. *J. Hydrology* 383 (3), 194–208.
- Hutchison, M.L., Walters, L.D., Avery, S.M., Munro, F., Moore, A., 2005. Analysis of livestock production, waste storage, and pathogen levels and prevalences in farm manures. *Appl. Environ. Microbiol.* 71 (3), 1231–1236.
- Im, S., Brannan, K.M., Mostaghimi, S., Cho, J., 2004. Simulating fecal coliform bacteria loading from an urbanizing watershed. *J. Environ. Sci. Health. Part A, Toxic/Hazardous Subst. Environ. Eng.* 39 (3), 663–679.
- Iudicello, J.J., Chin, D.A., 2013. A multi-model, multiple watershed examination of in-stream bacteria modeling. *J. Environ. Eng.* 139 (5), 719–727.
- Jamieson, R., Gordon, R., Joy, D., Lee, H., 2004. Assessing microbial pollution of rural surface waters: a review of current watershed scale modeling approaches. *Agric. Water Manag.* 70 (1), 1–17.
- Jozic, S., Morovic, M., Solic, M., Krstulovic, N., Ordulj, M., 2014. Effect of solar radiation, temperature and salinity on the survival of two different strains of *Escherichia coli*. *Fresenius Environ. Bull.* 23 (8), 1852–1859.
- Karim, M.R., Manshadi, F.D., Karpiscak, M.M., Gerba, C.P., 2004. The persistence and removal of enteric pathogens in constructed wetlands. *Water Res.* 38 (7), 1831–1837.
- Kim, J.W., Pachepsky, Y.A., Shelton, D.R., Coppock, C., 2010. Effect of streambed bacteria release on *E. coli* concentrations: monitoring and modeling with the modified SWAT. *Ecol. Model.* 221 (12), 1592–1604.
- Kouwen, N., Mousavi, S.F., 2002. WATFLOOD/SPL9 hydrological model and flood forecasting system. In: Singh, V.P., Frevert, D.K. (Eds.), *Mathematical Models of Large Watershed Hydrology*. Water Resource Publications, Highlands Ranch, Colorado, pp. 649–685.
- LaWare, P., Rifai, H.S., 2006. Modeling fecal coliform contamination in the Rio Grande I. *J. Am. Water Resour. Assoc.* 42 (2), 337–356.
- Ling, T.Y., Achberger, E.C., Drapcho, C.M., Bengtson, R.L., 2003. Quantifying adsorption of an indicator bacteria in a soil-water system. *Trans. ASAE* 45 (3), 669–674.
- Mancini, J.L., 1978. Numerical estimates of coliform mortality-rates under various conditions. *J. Water Pollut. Control Fed.* 50 (11), 2477–2484.
- Martinez, G., Pachepsky, Y.A., Shelton, D.R., Whelan, G., Zepp, R., Molina, M., Panhorst, K., 2013. Using the Q10 model to simulate *E. coli* survival in cowpats on grazing lands. *Environ. Internat* 54, 1–10.
- McDowell, R.W., Kitto, J.A., 2013. Assessment, modelling and management of land use and water quality in the upper Taieri River catchment. *N. Z. J. Agric. Res.* 56 (4), 261–278.
- McDowell, R.W., Houlbrooke, D.J., Muirhead, R.W., Muller, K., Shepherd, M., Cuttle, S.P., 2008. *Grazed Pastures and Surface Water Quality*. Nova Science Publishers Inc, New York, 238 pp.
- McLeod, M., Aislabie, J., Ryburn, J., McGill, A., 2008. Regionalizing potential for microbial bypass flow through New Zealand soils. *J. Environ. Qual.* 37 (5), 1959–1967.
- McGechan, M.B., Vinten, A.J.A., 2004. Simulation of transport through soil of *E. coli* derived from livestock slurry using the MACRO model. *Soil Use Manag.* 19 (4), 321–330.
- Monaghan, J.M., 2006. United Kingdom and European approach to fresh produce safety and security. *Hort. Technol.* 16 (4), 559–562.
- Monaghan, R.M., Carey, P.L., Wilcock, R.J., Drewry, J.J., Houlbrooke, D.J., Quinn, J.M., Thorrold, B.S., 2009. Linkages between land management activities and stream water quality in a border dyke-irrigated pastoral catchment. *Agric. Ecosyst. Environ.* 129 (1), 201–211.
- Monaghan, R.M., Smith, L.C., Muirhead, R.W., 2016. Pathways of contaminant transfers to water from and artificially-drained soil under intensive grazing by dairy cows. *Agric. Ecosyst. Environ.* 220, 76–88.
- Moyer, D.L., Hyer, K.E., 2003. Use of the Hydrological Simulation Program - FORTRAN and Bacterial Source Tracking for Development of the Fecal Coliform Total Maximum Daily Load (TMDL) for Accotink Creek, Fairfax County, Virginia, Water Resource Investigation Report 03-4160.
- Muirhead, R., 2015. A farm-scale risk-index for reducing fecal contamination of surface waters. *J. Environ. Qual.* 44 (1), 248–255.
- Muirhead, R.W., Monaghan, R.M., 2012. A two reservoir model to predict *Escherichia coli* losses to water from pastures grazed by dairy cows. *Environ. Int.* 40 (1), 8–14.
- Muirhead, R.W., Elliott, A.H., Monaghan, R.M., 2011. A model framework to assess the effect of dairy farms and wild fowl on microbial water quality during base-flow conditions. *Water Res* 45 (9), 2863–2874.
- Muirhead, R.W., Collins, R.P., Bremer, P.J., 2006. Interaction of *Escherichia coli* and soil particles in runoff. *Appl. Environ. Microbiol.* 72 (5), 3406–3411.
- Muirhead, R.W., Davies-Colley, R.J., Donnison, A.M., Nagels, J.W., 2004. Fecal bacteria yields in artificial flood events: quantifying in-stream stores. *Water Res.* 38, 1215–1224.
- Nemes, A., Pachepsky, Y.A., Timlin, D.J., 2011. Toward improving global estimates of field soil water capacity. *Soil Sci. Soc. Am. J.* 75, 807–812.
- Nnane, D.E., Ebdon, J.E., Taylor, H.D., 2011. Integrated analysis of water quality parameters for cost-effective faecal pollution management in river catchments. *Water Res.* 45 (6), 2235–2246.
- Niazi, M., Obropta, C., Miskewitz, R., 2015. Pathogen transport and fate modeling in the Upper Salem River Watershed using SWAT model. *J. Environ. Manag.* 151, 167–177.
- Noble, R., Moore, D.F., Leecaster, M.K., McGee, C.D., Weisberg, S.B., 2003. Comparison of total coliform, fecal coliform, and enterococcus bacterial indicator response for ocean recreational water quality testing. *Water Res.* 37 (7), 1637–1643.
- Oliver, D.M., Heathwaite, A.L., Hodgson, C.J., Chadwick, D.R., 2007. Mitigation and current management attempts to limit pathogen survival and movement within farmed grassland. *Adv. Agron.* 93, 95–152.
- Oliver, D.M., Heathwaite, L., Haygarth, P.M., Clegg, C.D., 2005. Transfer of *Escherichia coli* to water from drained and undrained grassland after grazing. *J. Environ. Qual.* 34 (3), 918–925.
- Oliver, D.M., Page, T., Heathwaite, A.L., Haygarth, P.M., 2010. Re-shaping models of *E. coli* population dynamics in livestock feces: increased bacterial risk to humans. *Environ. Int.* 36, 1–7.
- Oliver, D.M., Porter, K.D.H., Heathwaite, A.L., Zhang, T., Quilliam, R.S., 2015. Impact of low intensity summer rainfall on *E. coli* discharge event dynamics with reference to sample acquisition and storage. *Environ. Monit. Assess.* 187 (7), 1–13.
- Oliver, D.M., Porter, K.D.H., Pachepsky, Y.A., Muirhead, R.W., Reaney, S.M., Coffey, R., Kay, D., Milledge, D.G., Hong, E., Anthony, S.G., Page, T., Bloodworth, J.W., Mellander, P.-E., Carbonneau, P.E., McGrane, S.J., Quilliam, R.S., 2016. Predicting microbial water quality with models: over-arching questions for managing risk in agricultural catchments. *Sci. Total Environ.* 544, 39–47.
- Ouattara, N.K., de Brauwere, A., Billen, G., Servais, P., 2013. Modelling faecal contamination in the Scheldt drainage network. *J. Mar. Syst.* 128, 77–88.
- Pachepsky, Y., Shelton, D.R., McLain, J.E.T., Patel, J., Mandrell, R.E., 2011. Irrigation waters as a source of pathogenic microorganisms in produce. *Rev. Adv. Agron* 113, 73–138.
- Pachepsky, Y., Shelton, D., Dorner, S., Whelan, G., 2014. Can *E. coli* or thermotolerant coliform concentrations predict pathogen presence or prevalence in irrigation waters? *Crit. Rev. Microbiol.* 7828, 1–10.
- Pachepsky, Y.A., Shelton, D.R., 2011. *Escherichia coli* and fecal coliforms in freshwater and estuarine sediments. *Crit. Rev. Environ. Sci. Technol.* 41 (12), 1067–1110.
- Pachepsky, Y.A., Sadeghi, A.M., Bradford, S.A., Shelton, D.R., Guber, A.K., Dao, T., 2006. Transport and fate of manure-borne pathogens: Modeling perspective. *Agric. Water Manag* 86 (1–2), 81–92.
- Pandey, P.K., Soupir, M.L., 2013. Assessing the impacts of *E. coli* laden streambed sediment on *E. coli* loads over a range of flows and sediment characteristics. *J. Am. Water Resour. Assoc.* 49 (6), 1261–1269.
- Pandey, P.K., Soupir, M.L., Rehmann, C.R., 2012. A model for predicting resuspension of *Escherichia coli* from streambed sediments. *Water Res* 46 (1), 115–126.
- Pandey, P.K., Soupir, M.L., Ikenberry, C.D., Rehmann, C.R., 2016. Predicting streambed sediment and water column *Escherichia coli* levels at watershed scale. *J. Am. Water Resour. Assoc.* 52 (1), 184–197.
- Parajuli, P.B., Mankin, K.R., Barnes, P.L., Rosssi, C.G., 2009. Fecal bacteria source characterization and sensitivity analysis of swat 2005. *Trans. ASABE* 52 (6), 1847–1858.
- Park, Y., Pachepsky, Y., Shelton, D., Jeong, J.M., Whelan, G., 2016. Survival of manure-borne *Escherichia coli* and fecal coliforms in soil: temperature dependence as affected by site-specific factors. *J. Environ. Qual.* 45 (3), 949–957.
- Paul, S., Haan, P.K., Matlock, M.D., Mukhtar, S., Pillai, S.D., 2004. Analysis of the HSPF water quality parameter uncertainty in predicting peak in stream fecal coliform concentrations. *Trans. ASAE* 47 (1), 69–78.
- Perkins, T.L., Perrow, K., Rajko-Nenow, P., Jago, C.F., Jones, D.L., Malham, S.K., McDonald, J.E., 2016. Decay rates of faecal indicator bacteria from sewage and ovine faeces in brackish and freshwater microcosms with contrasting suspended particulate matter concentrations. *Sci. Total Environ.* <http://dx.doi.org/10.1016/j.scitotenv.2016.03.076>.
- Petersen, C.M., Rifai, H.S., Villarreal, G.C., Stein, R., 2011. Modeling *Escherichia coli* and its sources in an Urban Bayou with Hydrologic Simulation Program—FORTRAN. *J. Environ. Eng* 137 (6), 487–503.
- Piorkowski, G., Jamieson, R., Bezanson, G., Truelstrup, H.L., Yost, C., 2014. Reach specificity in sediment *E. coli* population turnover and interaction with water-borne populations. *Sci. Total Environ.* 496, 402–413.
- Reinoso, R., Torres, L.A., Bécarea, E., 2008. Efficiency of natural systems for removal of bacteria and pathogenic parasites from wastewater. *Sci. Total Environ.* 395 (2–3), 80–86.
- Rolle, K., Gitau, M.W., Chen, G., Chauhan, A., 2012. Assessing fecal coliform fate and

- transport in a coastal watershed using HSPF. *Water Sci. Technol.* 66 (5), 1096–1102.
- Rose, J.B., Mullinax, R.L., Singh, S.N., Yates, M.V., Gerba, C.P., 1987. Occurrence of rotaviruses and enteroviruses in recreational waters of Oak Creek, Arizona. *Water Res* 21 (11), 1375–1381.
- Roser, D.J., Davies, C.M., Ashbolt, N.J., Morison, P., 2006. Microbial exposure assessment of an urban recreational lake: a case study of the application of new risk-based guidelines. *Water Sci. Technol* 54 (3), 245–252.
- Rossman, L.A., 2010. Storm Water Management Model User's Manual, Version 5.0, EPA/600/R-05/040, United States Environment Protection Agency.
- Rozen, Y., Belkin, S., 2001. Survival of enteric bacteria in seawater. *Fems Microbiol. Rev.* 25 (5), 513–529.
- Ruelland, D., Billen, G., Brunstein, D., Garnier, J., 2007. SENEQUE: a multi-scaling GIS interface to the Riverstrahler model of the biogeochemical functioning of river systems. *Sci. Total Environ.* 375 (1), 257–273.
- Sadeghi, A.M., Arnold, J.G., 2002. A SWAT/microbial sub-model for predicting pathogen loadings in surface and groundwater at watershed and basin scales. Total Maximum Daily Load (TMDL): Environmental Regulations. In: Proceedings of the March 11–13, 2002 Conference, (Fort Worth, Texas, USA) 701P0102, pp. 56–63. <http://dx.doi.org/10.13031/2013.7529>.
- Schijven, J., Derr, J., de Roda Husman, A.M., Blaschke, A.P., Farnleitner, A.H., 2015. QMRACatch: microbial quality simulation of water resources including infection risk assessment. *J. Environ. Qual.* 44 (5), 1491–1502.
- Semenov, A.V., Van Bruggen, A.H., Van Overbeek, L., Termorshuizen, A.J., Semenov, A.M., 2007. Influence of temperature fluctuations on *Escherichia coli* O157: H7 and *Salmonella enterica* serovar Typhimurium in cow manure. *FEMS Microbiol. Lett* 60 (3), 419–428.
- Seong, C.H., Benham, B.L., Hall, K.M., Kline, K., 2013. Comparison of alternative methods to simulate bacteria concentrations with HSPF under low-flow conditions. *Appl. Eng. Agric.* 29 (6), 917–931.
- Servais, P., Billen, G., Goncalves, A., Garcia-Armisen, T., 2007. Modelling microbiological water quality in the Seine river drainage network: past, present and future situations. *Hydrology Earth Syst. Sci. Discuss.* 4 (3), 1153–1184.
- Shelton, D.R., Pachepsky, Y.A., Kiefer, L.A., Blaustein, R.A., McCarty, G.W., Dao, T.H., 2014. Response of coliform populations in streambed sediment and water column to changes in nutrient concentrations in water. *Water Res.* 59, 316–324.
- Shoemaker, L., Dai, T., Koenig, J., Hantush, M., 2005. TMDL Model Evaluation and Research Needs. EPA/600/R-05/149.
- Sinton, L., Hall, C., Braithwaite, R., 2007. Sunlight inactivation of *Campylobacter jejuni* and *Salmonella enterica*, compared with *Escherichia coli*, in seawater and river water. *J. Water Health* 5 (3), 357–365.
- Smith, M.S., Thomas, G.W., White, R.E., Ritonga, D., 1985. Transport of *Escherichia coli* through intact and disturbed soil columns. *J. Environ. Qual.* 14 (1), 87–91.
- Soller, J.A., Eisenberg, J., DeGeorge, J., Cooper, R., Tchobanoglous, G., Olivieri, A., 2006. A public health evaluation of recreational water impairment. *J. Water Health* 4 (1), 1–19.
- Soupir, M.L., Mostaghimi, S., Lou, J., 2008. Die-off of *E. coli* and enterococci in dairy depositions. *Trans. ASABE* 51, 1987–1996.
- Soupir, M.L., Mostaghimi, S., 2011. *Escherichia coli* and enterococci attachment to particles in runoff from highly and sparsely vegetated grassland. *Water, Air, & Soil Pollut.* 216 (1–4), 167–178.
- Soupir, M.L., Mostaghimi, S., Dillaha, T., 2010. Attachment of *Escherichia coli* and Enterococci to particles in runoff. *J. Environ. Qual.* 39 (3), 1019–1027.
- Sterk, A., Schijven, J., de Roda Husman, A.M., de Nijs, T., 2016. Effect of climate change on runoff of *Campylobacter* and *Cryptosporidium* from land to surface water. *Water Res.* 95, 90–102.
- Stocker, M.D., Pachepsky, Y.A., Shelton, D.R., 2014. Performance of Weibull and linear semi-logarithmic models in simulating inactivation in waters. *J. Environ. Qual.* 43 (5), 1559–1565.
- Stocker, M.D., Pachepsky, Y.A., Hill, R.L., Shelton, D.R., 2015. Depth dependent survival of *Escherichia coli* and enterococci in soil after manure application and simulated rainfall. *Appl. Environ. Microbiol.* 81 (14), 4801–4808.
- Stott, R., Davies-Colley, R., Nagels, J., Donnison, A., Ross, C., Muirhead, R., 2011. Differential behaviour of *Escherichia coli* and *Campylobacter* spp. in a stream draining dairy pasture. *J. Water Health* 9 (1), 59–69.
- Sunohara, M.D., Topp, E., Gottschall, N., Neumann, N., Ruecker, N., Jones, T.H., Edge, T.A., Marti, R., Lapen, D.R., 2012. Impact of riparian zone protection from cattle on nutrient, bacteria, F-coliphage, *Cryptosporidium*, and *Gardia* loading of an intermittent stream. *J. Environ. Qual.* 41 (4), 1301–1314.
- Tang, J., McDonald, S., Peng, X., Samadder, S.R., Murphy, T.M., Holden, N.M., 2011. Modelling *Cryptosporidium* oocysts transport in small ungauged agricultural catchments. *Water Res* 45 (12), 3665–3680.
- Tian, Y.Q., Gong, P., Radke, J.D., Scarborough, J., 2002. Spatial and temporal modeling of microbial contaminants on grazing farmlands. *J. Environ. Qual.* 31 (3), 860–869.
- USEPA, 2000. Total Maximum Daily Load (TMDL) for Fecal Coliform Bacteria in the Waters of Duck Creek in Mendenhall Valley, Alaska.
- U.S. Food and Drug Administration, 2011. Standards for the Growing, Harvesting, Packing, and Holding of Produce for Human Consumption. Available from URL: <http://www.fda.gov/Food/GuidanceRegulation/FSMA/ucm334114.htm>.
- Van Kessel, J.S., Pachepsky, Y.A., Shelton, D.R., Karns, J.S., 2007. Survival of *Escherichia coli* in depositions in pasture and in laboratory conditions. *J. Appl. Microbiol.* 103 (4), 1122–1127.
- Walker, F.R., Stedinger, J.R., 1999. Fate and transport model of *Cryptosporidium*. *J. Environ. Eng.* 125 (4), 325–333.
- Whelan, G., Kim, K., Pelton, M.A., Soller, J.A., Castleton, K.J., Molina, M., Pachepsky, Y., Zepp, R., 2014. An integrated environmental modeling framework for performing quantitative microbial risk assessments. *Environ. Model. Softw.* 55, 77–91.
- Wilkinson, R.J., McKergow, L.A., Davies-Colley, R.J., Ballantine, D.J., Young, R.G., 2011. Modelling storm-event *E. coli* pulses from the Motueka and Sherry Rivers in the South Island, New Zealand. *N. Z. J. Mar. Freshw. Res.* 45 (3), 369–393.
- World Health Organization, 2014. Food Safety. Fact Sheet N°399. Available from URL: <http://www.who.int/mediacentre/factsheets/fs399/en/>.
- Wu, J., Rees, P., Storrer, S., Alderisio, K., Dorner, S., 2009. Fate and Transport Modeling of potential pathogens: the contribution from sediments. *JAWRA J. Am. Water Resour. Assoc.* 45 (1), 35–44.
- Yakirevich, A., Pachepsky, Y.A., Guber, A.K., Gish, T.J., Shelton, D.R., Cho, K.H., 2013. Modeling transport of *Escherichia coli* in a creek during and after artificial high-flow events: three-year study and analysis. *Water Res.* 47 (8), 2676–2688.
- Zhao, W., Liu, X., Huang, Q., Cai, P., 2015. *Streptococcus suis* sorption on agricultural soils: Role of soil physico-chemical properties. *Chemosphere* 119, 52–58.