



Capturing microbial sources distributed in a mixed-use watershed within an integrated environmental modeling workflow



Gene Whelan^{a,*}, Keewook Kim^{b,1}, Rajbir Parmar^a, Gerard F. Laniak^a, Kurt Wolfe^a, Michael Galvin^a, Marirosa Molina^a, Yakov A. Pachepsky^c, Paul Duda^d, Richard Zepp^a, Lourdes Prieto^a, Julie L. Kinzelman^e, Gregory T. Kleinheinz^f, Mark A. Borchardt^g

^a U.S. Environmental Protection Agency, Office of Research and Development, Athens, GA, USA

^b Idaho Falls Center for Higher Education, University of Idaho, Idaho Falls, ID, USA

^c U.S. Department of Agriculture, Agricultural Research Service, Beltsville, MD, USA

^d AQUA TERRA Consultants, A Division of RESPEC, INC, Decatur, GA, USA

^e Public Health Department, Racine, WI, USA

^f Department of Engineering Technology, University of Wisconsin Oshkosh, Oshkosh, WI, USA

^g U.S. Department of Agriculture, Agricultural Research Service, Marshfield, WI, USA

ARTICLE INFO

Article history:

Received 28 November 2016

Received in revised form

17 June 2017

Accepted 8 August 2017

Keywords:

Integrated environmental modeling

QMRA

Risk assessment

Pathogens

Manure

Watershed modeling

ABSTRACT

Many watershed models simulate overland and instream microbial fate and transport, but few provide loading rates on land surfaces and point sources to the waterbody network. This paper describes the underlying equations for microbial loading rates associated with 1) land-applied manure on undeveloped areas from domestic animals; 2) direct shedding (excretion) on undeveloped lands by domestic animals and wildlife; 3) urban or engineered areas; and 4) point sources that directly discharge to streams from septic systems and shedding by domestic animals. A microbial source module, which houses these formulations, is part of a workflow containing multiple models and databases that form a loosely configured modeling infrastructure which supports watershed-scale microbial source-to-receptor modeling by focusing on animal- and human-impacted catchments. A hypothetical application – accessing, retrieving, and using real-world data – demonstrates how the infrastructure can automate many of the manual steps associated with a standard watershed assessment, culminating in calibrated flow and microbial densities at the watershed's pour point.

Published by Elsevier Ltd.

1. Introduction

The United States Environmental Protection Agency (EPA) is interested in characterizing, managing, and minimizing the risks of human exposure to pathogens in water resources impacted by effluents and runoff from both agricultural activities and built infrastructure. EPA (2016a) indicates that 52.8% of the assessed river and stream miles are impaired, with pathogens being the main cause followed by sediment contamination and nutrients. The designation “pathogen” is used in the broadest sense based upon detection of fecal indicator bacteria (FIB), *Escherichia coli* (*E. coli*),

and fecal coliforms. Monitoring for the presence of pathogens in manure- and sewage-contaminated waters is extremely challenging, as pathogen concentrations in water samples are often low. Such low concentrations make detection unfeasible, unless large volumes of water are analyzed. Most monitoring approaches and microbial water quality regulations are based on indicator bacteria, since they are easier to sample and quantify (EPA, 2012, 2015), although good correlations between indicators and pathogens may be suspect. For example, Haack and Duris (2013) note that “... there is a widely acknowledged variable relationship between FIB and pathogen concentrations (Field and Samadpour, 2007; Savichtcheva et al., 2007).” Therefore, states might avail themselves of water quality criteria, if they can demonstrate an equivalent level of public health protection with higher indicator concentrations.

Agriculture is one of the most likely causes of pollution, affecting almost 13% of the total river miles assessed, since applying manure

* Corresponding author. U.S. Environmental Protection Agency, Office of Research and Development, Athens, GA 30605, USA.

E-mail address: Whelan.Gene@epa.gov (G. Whelan).

¹ Current address: Busan Development Institute, Busan, South Korea.

for crop nutrition and production and animal shedding due to grazing are common practices. Manure applications may carry environmental contaminants such as pathogens, organic chemical residues and heavy metals (Edwards and Daniel, 1992). These contaminants adversely affect water quality mainly due to runoff-producing rainfall events. Among the various animal fecal sources, poultry are responsible for 44% of the total feces production in the United States, followed by cattle (31%) and swine (24%) (Kellogg et al., 2000). In comparison, humans contribute only a small fraction (0.7%) on an equal weight basis; however, human sewage/wastewater is generally thought to constitute a much higher risk to public health due to the likelihood of viral pathogen presence (Soller et al., 2010; Schoen et al., 2011; Dufour, 1984).

Models can play a role in assessing the distribution of microbes in a mixed-use watershed and the potential risks associated with both measured and predicted indicator concentrations (i.e., degree to which concentrations indicate threats to public health under varying circumstances). Assessment of potential risks is critical in determining the appropriateness of waivers to criteria and concentration standards based on site-specific environmental settings and source conditions. Site surveys, coupled with modeling tools, are a basic way to identify sources, characterizing them, associate a level of infectivity with the source, and assess its level of impact at the point of exposure.

A Quantitative Microbial Risk Assessment (QMRA) is a source-to-receptor modeling approach that integrates disparate data – such as fate/transport, exposure, and human health effect relationships – to characterize the distribution of indicator and pathogenic microbes within a watershed, and the potential health impacts/risks from exposure to pathogenic microorganisms (Soller et al., 2010; Whelan et al., 2014a, 2014b; Haas et al., 1999; Hunter et al., 2003). As Whelan et al. (2014b) note, a QMRA's conceptual design fits well within an integrated, multi-disciplinary modeling perspective which describes the problem statement; data access retrieval and processing [e.g., D4EM (EPA, 2013a; Wolfe et al., 2007)]; software frameworks for integrating models and databases [e.g., FRAMES (Whelan et al., 2014b; Johnston et al., 2011)]; infrastructures for performing sensitivity, variability, and uncertainty analyses [e.g., SuperMUSE (Babendreier and Castleton, 2005)]; and risk quantification. Coupling modeling results with epidemiology studies allows policy-related issues (EPA, 2010; EPA and USDA, 2012; for example) to be explored. An important aspect of the integrated environmental modeling (IEM) (Laniak et al., 2013) microbial workflow is its ability to define spatial and temporal microbial loadings from human and animal sources within a mixed-use watershed. Multiple software tools have been developed to estimate microbial source loadings to a watershed, such as MWASTE, COLI, SEDMOD, modifications to SWAT, SELECT, BIT, and BSLC.

Moore et al. (1989) developed MWASTE to simulate waste generation and calculate bacterial concentrations in runoff from the land-applied waste of various animals and management techniques. MWASTE only considers animal-borne bacteria and allows only one animal per execution, so multiple runs are required for the consideration of different animal species.

Walker et al. (1990) developed the COLI model to predict bacteria concentration in runoff resulting from a single storm occurring immediately after land application of manure. It uses a Monte Carlo simulation to combine a deterministic relationship with rainfall and temperature variations and calculates maximum and minimum bacteria concentration in runoff.

Fraser et al. (1996) developed a GIS-based Spatially Explicit Delivery Model (SEDMOD) that estimates spatially-distributed delivery ratios for eroded soil and associated nonpoint source pollutants. The model predicts fecal coliform loading in rivers and

calculates pollutant loadings in streams by multiplying livestock fecal coliform output and a delivery ratio, estimated for each watershed cell, to predict the proportion of eroded sediment (or other non-point source pollutant) transported from the cell to the stream channel.

Parajuli (2007) manually estimated fecal bacterial loading – considering different sources such as livestock (manure application, grazing), human (septic), and wildlife – for the SWAT bacteria sub-model. Guber et al. (2016) followed this up with a limited effort that integrated infection and recovery of white-tailed deer and cattle into the watershed model SWAT. It predicted pathogen transmission between livestock and deer by considering seasonal changes in deer population, habitat, and foliage consumption; ingestion of pathogens with water, foliage, and grooming soiled hide by deer and grazing cattle; infection and recovery of deer and co-grazing cattle; pathogen shedding by infected animals; survival of pathogens in manure; and kinetic release of pathogens from applied manure and fecal material.

Teague et al. (2009) developed the Spatially Explicit Load Enrichment Calculation Tool (SELECT) to identify potential *E. coli* sources in Plum Creek Watershed in Texas; SELECT is a grid-based load assessment tool that considers multiple point and non-point sources (wastewater treatment plant, livestock, pets, wildlife, septic, urban). Riebschleager et al. (2012) automated SELECT within ArcGIS and added the Pollutant Connectivity Factor component which is based on potential pollutant loading, runoff potential, and travel distance. SELECT has been used to identify *E. coli* (Teague et al., 2009; McKee et al., 2011; Riebschleager et al., 2012; McFarland and Adams, 2014; Borel et al., 2015) and enterococci (Borel et al., 2015) sources in multiple watersheds in Texas.

The Bacterial Indicator Tool (BIT) estimates microbial loading from domestic animals, wildlife, and human activities to a mixed-use watershed (EPA, 2000). It accounts for land-application of manure and direct shedding from certain domestic animals to pasture and cropland, and from wildlife to cropland, pasture, and forest. It also estimates point source loadings from septic system failures and direct shedding to the stream from certain domestic animals. Finally, it accounts for loading in urban (built-up) areas such as residential, commercial, transportation, etc. BIT uses Microsoft Excel for calculations and considers only 10 sub-watersheds when distributing loads. Land-applied loading rates are adjusted for die-off. All loadings vary monthly, except for those from wildlife, in urban areas, and from septic systems which use constant loading rates to the stream based on the fraction of septic systems that fail. Urbanized areas include categories such as commercial, mixed-urban or built-up, residential, and roadways. Loading rates to urbanized areas are supplied by the user, although default values are suggested. Stormwater runoff through drainage pipes and combined and non-combined sewer systems are not accounted for.

In a similar manner to BIT, the Bacterial Source Load Calculator (BSLC) was designed to organize and process bacterial inputs for a Total Maximum Daily Load (TMDL) bacterial impairment analysis (Zeckoski et al., 2005). BSLC calculates bacterial loads based on animal numbers and default values for manure and bacterial production rates, accounting for die-off and the fraction of domestic animal confinement. It uses externally-generated, user-supplied inputs of watershed delineations, and land-use distribution, as well as domestic animal, wildlife, and human population estimates to suggest monthly land-based and hourly stream-based bacterial loadings. Neither BIT nor BSLC offer software that supports data collection to meet model input requirements, although their documentation suggests some default values.

Prior to allocating microbial sources within a watershed, the watershed must first be delineated into subwatersheds which are

Download English Version:

<https://daneshyari.com/en/article/6962288>

Download Persian Version:

<https://daneshyari.com/article/6962288>

[Daneshyari.com](https://daneshyari.com)