An integrated environmental modeling framework for performing Quantitative Microbial Risk Assessments

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ABSTRACT

Standardized methods are often used to assess the likelihood of a human-health effect from exposure to a specified hazard, and inform opinions and decisions about risk management and communication. A Quantitative Microbial Risk Assessment (QMRA) is specifically adapted to detail potential human-health risks from exposure to pathogens; it can include fate and transport models for various media, including the source zone (initial fecal release), air, soil/land surface, surface water, vadose zone and aquifer. The analysis step of a QMRA can be expressed as a system of computer-based data delivery and modeling that integrates interdisciplinary, multiple media, exposure and effects models and databases. Although QMRA does not preclude using source-term and fate and transport models, it is applied most commonly where the source-term is represented by the receptor location (i.e., exposure point), so the full extent of exposure scenarios has not been rigorously modeled. An integrated environmental modeling infrastructure is, therefore, ideally suited to include fate and transport considerations and link the risk assessment paradigm between source and receptor seamlessly. A primary benefit of the source-to-outcome approach is that it allows an expanded view of relevant cause-and-effect relationships, which facilitate consideration of management options related to source terms and their fate and transport pathways. The Framework for Risk Analysis in Multimedia Environmental Systems (FRAMES) provides software technology for analysts to insert appropriate models and databases that fit the problem statement and design and construct QMRAs that are reproducible, flexible, transferable, reusable, and transparent. A sample application using different models and databases registered with FRAMES is presented. It illustrates how models are linked to assess six different manure-based contaminant sources, following three pathogens (*Salmonella eterica*, *Cryptosporidium* spp., and *Escherichia coli* O157:H7) to a receptor where exposures and health risk impacts are then evaluated. The modeling infrastructure demonstrates how analysts could use the system to discern which pathogens might be important and when, and which sources could contribute to their importance.

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1. Introduction

Contamination of recreational/bathing waters by excessive amounts of fecal bacteria is known to indicate increased risk of pathogen-induced illness (from bacteria, protozoa, and viruses) to humans and represents a problem throughout the world. In the United States alone, EPA (2002) revealed that 35% of impaired rivers and streams were polluted by fecal bacteria (generally indicated by fecal coliforms, *Enterococci*, or *Escherichia coli*) which could indicate the presence of pathogens. Epidemiology studies have linked swimming-associated gastrointestinal illnesses with fecal indicator bacteria (FIB) densities in sewage-impacted recreational waters (Pruss, 1998; Wade et al., 2003; Zmirou et al., 2003); in those studies, elevated FIB levels correspond to possible fecal contamination (NRC, 2004).

The numbers of pathogenic organisms are often few and difficult to identify and isolate, partly due to their highly varied in characteristic or type (EPA, 2012a, 2001; NRC, 2004; Savichtcheva

and Okabe, 2006). Scientists and public health officials, therefore, typically monitor non-pathogenic bacteria that are associated with fecal contamination and more easily sampled and measured, and regulators impose limits on the amount of microorganisms allowed in waters where humans could potentially be infected (e.g. EPA, 2012a; WHO, 2011). The presence of pathogens in manures could be highly site- and season-specific and varies greatly by animal host. E. coli O157:H7 can be found in cattle of different ages, and it is more abundant in cattle than it is in pigs. In addition, it has wide regional variations (Zhao et al., 1995; Low et al., 2005). For instance, in a study that screened calves of different ages across the United States, E. coli O157:H7 was present in calves sampled in 11 out of 14 states (Zhao et al., 1995). Presence and associated concentration of Salmonella in beef cattle manures are generally low (<10% and <3 MPN g^{-1} of feces, respectively), although shedding of up to 3×10^3 MPN g^{-1} of feces has been reported (Fegan et al., 2004). In dairy cattle, shedding of Salmonella in feces seems to be a little higher, with numbers ranging from <10 to at least 20% presence depending on calf age (Huston et al., 2002; Lailler et al., 2005; Berge et al., 2006). Cryptosporidium is typically found at higher concentrations in calves <4 months old, and although it is also found in adult cattle, the prevalence is rather low in cattle ≥12 months old (Atwill et al., 1999).

Understanding and simulating how such pathogens get into, travel through, and eventually infect humans is a challenging problem that involves many different aspects of the environment. To allow regulators to undertake quantified risk assessments, these processes have to be combined flexibly in any software system.

1.1. Quantitative Microbial Risk Assessment for waters

A Quantitative Microbial Risk Assessment (QMRA) characterizes potential human health risk using four pieces of information: average pathogen densities, mean water ingestion for the exposure scenario, dose–response relationships for pathogens and conditional probability of illness (Haas et al., 1999; Hunter et al., 2003). The risk assessment approach differs from epidemiological approaches (Calderon et al., 1991; Colford et al., 2012; Haile et al., 1999) in that the latter seek to associate levels of self-reported disease (e.g., in a group of swimmers) with the water quality measured by fecal indicator bacteria, and not the etiological agent(s) responsible for the disease. Epidemiology studies implicitly characterize the source of fecal contamination, fate and transport kinetics of the microbes, the natural variability of the microbes in the environmental matrix, the etiological agent(s) and exposure scenario studied, while QMRA deals explicitly with these components. Transparent treatment of these components within the risk assessment framework offer considerable benefits to decision-making and to risk communication and management. QMRAs complement epidemiological studies (Pruss, 1998; Zmirou et al., 2003) with better interpretation of ambiguous epidemiological results and generating estimates of human-health risk in waters where it would be impractical to conduct an epidemiological study.

QMRAs have been used to assess potential health risks from (1) exposure to recreational waters (Ashbolt et al., 2010; Rose et al., 1987; Roser et al., 2006; Soller et al., 2006, 2003); (2) waters containing seagull excreta and primary sewage effluent (Schoen and Ashbolt, 2010); (3) human enteric viruses (Soller et al., 2010a); (4) the relative contribution of FIB and pathogens when a mixture of human sources impact a recreational waterbody (Schoen et al., 2011); and (5) fresh gull, chicken, cattle, and swine feces (Soller et al., 2010b). Although QMRAs do not preclude using source-term, fate, and transport models (Benham et al., 2006; Bradford and Schijven, 2002; Bradford et al., 2006; Bulygina et al., 2009; Guber et al., 2009, 2006; Kim et al., 2010; Kouznetsov et al., 2007,

2004; Pachepsky et al., 2006a,b; Shelton et al., 2003), including linkages to exposure/risk at the exposure point (Ferguson et al., 2007a,b; Muirhead et al., 2006; Signor et al., 2007, 2005; Stout et al., 2005), they most commonly address exposure/risk by assuming that fresh manure was deposited directly into a recreational water (Soller et al., 2010b), without fully characterizing the potential attenuation during transport of pathogens and FIB from the source of release to the point of exposure and impact (McBride et al., 1998; Soller et al., 2006, 2003).

1.2. Relative and forward QMRAs

EPA (2010) describes two approaches for implementing a QMRA: relative and forward. A forward QMRA has also been referred to as conventional or traditional. A relative QMRA compares risks from exposure to animal-impacted waters to those associated with human sources (Schoen and Ashbolt, 2010; Soller et al., 2010b). Each fecal source is assumed to contribute enough contamination that the hypothetical waterbody contains FIB equal to a predetermined reference density. By setting the reference density at a level associated with a known incidence of human-health effects, the risks between animal- and human-based contamination are compared. QMRA results can then be used to draw inferences about risks in water impacted by human and animal wastes.

A forward QMRA characterizes the risk of illness associated with exposure (EPA, 2010), based on pathogen densities determined through monitoring activities, or by modeling microbial release from sources of contamination and fate and transport to the receptor location. The risk of illness is estimated using pathogen doses and dose–response models (Haas, 2002; Haas et al., 1999). The forward QMRA approach is implemented in this study.

1.3. Integrated environmental modeling

The complexity and uncertainty of a QMRA with its different sources of pathogens, pathways, and receptors is highly demanding and requires an integrated approach. The nascent field of integrated environmental modeling (IEM) has recognized this problem and has been developing solutions by representing and linking models, databases, and visualizations tools in various ways to provide comprehensive and flexible solutions to these complex environmental problems (Laniak et al., 2013).

The QMRA studies listed earlier indicate that multiple models with varying degrees of scale and resolution were configured with databases to construct IEM paradigms. Laniak et al. (2013) note that IEM helps to solve increasingly complex, real-world problems involving the environment and its relationship to human systems and activities. The complexity and interrelatedness of real-world problems require higher-order systems thinking and holistic solutions (EPA, 2008a,b; MEA, 2005; Parker et al., 2002). IEM provides a science-based structure or framework that develops and organizes multi-disciplinary knowledge and applies it to explore, explain, and forecast environmental system responses to natural and human-induced stressors. The QMRA framework can be considered a microbial version of the existing chemical risk paradigm (EPA, 2012b, 2005a, 2000, 1989, 1986a): (1) problem formulation, including problem definition and data collection; (2) occurrence, fate, transport, and exposure assessment of the pathogens; (3) health effects assessment including dose–response relationships and health endpoints; and (4) risk characterization including sensitivity, variability, and uncertainty analyses, and evaluation of decision points.

One big difference between chemicals and microbes is that microbes are living organisms, resulting in variability and