Modelling microbial pathogens risk in the stream network

Department of Agricultural and Biosystems Engineering

Pramod K Pandey and Michelle L Soupir

Agricultural and Biosystems Engineering Department, Iowa State University, USA (pkpandey@iastate.edu)

Introduction

Contamination, such as water borne microbial pathogens, is a serious concern [1] in developed as well as developing countries. For example, 900,000 illness and 900 deaths each year are reported in the U.S. because of water borne diseases [2]. In developing countries such as Africa, waterborne diseases infect millions [3]. Managing the threats caused by water borne pathogens requires improving the security of water (i.e., drinking as well as recreational water). Improving our understanding of fate and transport of water borne pathogens at the watershed scale will help improving water security. Modeling microbial pathogens distribution at watershed scale supports identification of the source of contamination as well as it can be used as a tool to asses public health risk. Here, we have developed a watershed-scale pathogen transport model to predict water borne *E. coli* (a pathogen indicator) in streams.

Methods

Figure 1 shows the conceptual pathogen transport model developed for predicting in-stream waterborne *E. coli* concentrations. In-stream processes such as resuspension, deposition, overland transport, growth, and in-stream routing of *E. coli* were modeled. To predict the levels of *E. coli*, an existing hydrologic model, SWAT, was modified, and the predictions of modified model were tested by implementing it on the Squaw Creek Watershed [Fig. 2] in Iowa, USA.

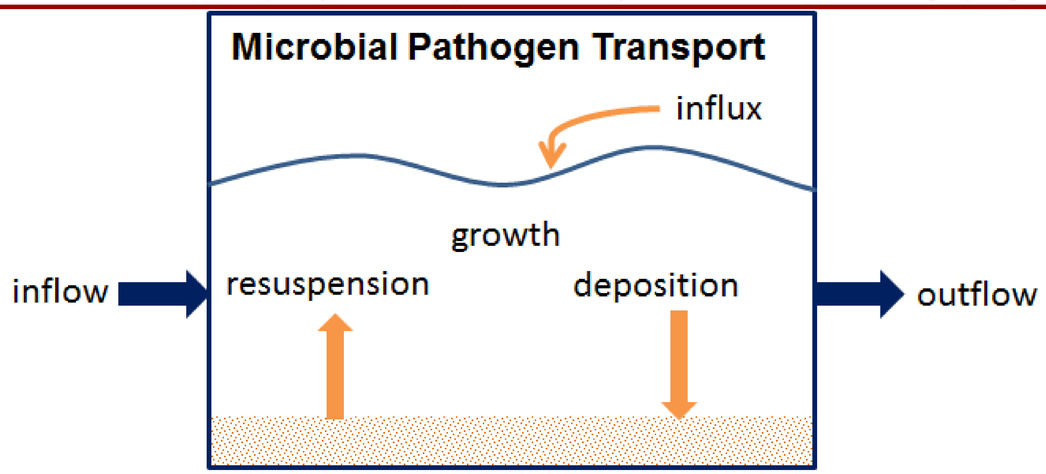


Figure 1. Conceptual in-stream microbial pathogen transport model

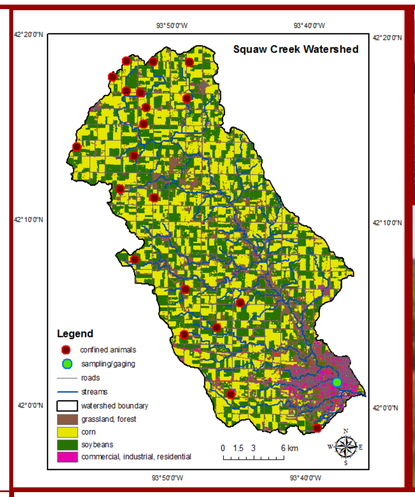


Figure 2. Study area

Input data

- Digital Elevation Model (DEM)
- Land cover
- Soil types
- Confined animal units
- Manure applications
- Rainfall
- Temperature
- Point source pollution

Output

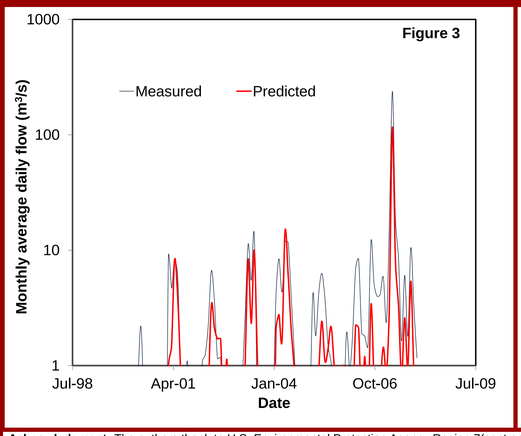
- Stream flow
- *E. coli* levels in stream water

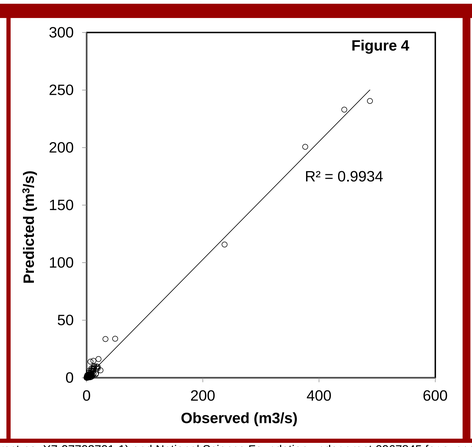
Analysis

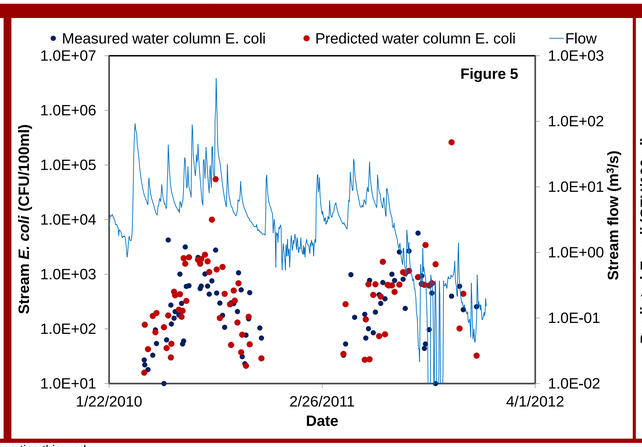
- Risk potential
- Identifying the source of contamination
- Management plan

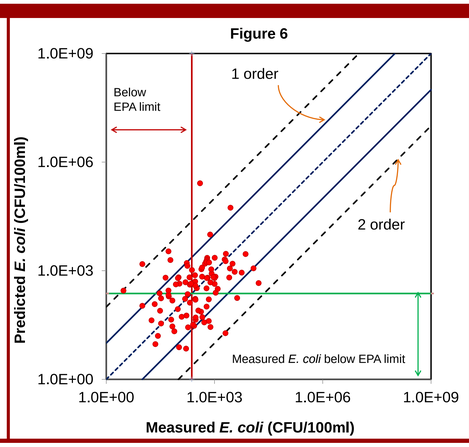
Results and Discussion

Comparison between measured and predicted flow is shown in Figures 3 and 4. Predictions of in-stream waterborne *E. coli* concentrations is shown in Figure 5. Comparison between measured and predicted *E. coli* concentrations is shown in Figure 6. Predicted and measured data, which exceeds the EPA water quality criteria is shown in Figure 6.. The R^2 and NSE values of monthly average daily stream flow were 0.0.99 and 0.75. Approximately 82 and 15% of the predicted *E. coli* concentrations in water were below 1 and 2 order of magnitude of measured values, respectively. About 60% of the both measured and predicted data exceedsEPA criteria of water quality standard (i.e., E. coli <235/100 ml), which indicates that model performed well.









Conclusions: The microbial pathogen transport model developed here performed well in assessing the risk of elevated pathogen levels. The model was tested at watershed scale. The approach developed here can be useful in predicting the scenario when stream pathogens will potentially exceed the water quality standard. In addition, the model will be useful in identifying the source of pathogen contamination and support developing a management plan for controlling the microbial pathogens in stream water.

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References: [1] US Environmental Protection Agency (US EPA) (2012). Impaired waters and total maximum daily loads. http://water.epa.gov/lawsregs/lawsguidance/cwa/tmdl/index.cfm. [2] Arnone, R.D. and Walling, J.P. (2007) Waterborne pathogens in urban watersheds. Journal of Water and Health 5(1), 149-162. [3] Fenwick, A. (2006) Waterborne Infectious Diseases-Could they be consigned to History? Science. 313, 1077-1081.