

STATISTICAL MODEL FOR ESTIMATING PATHOGENIC BACTERIA IN STREAMS

P. K. Pandey¹, M. L. Soupir¹, M. Majumder² and M. S. Kaiser²

¹Department of Agricultural and Biosystems Engineering, Iowa State University, Ames, Iowa 50014, USA

²Department of Statistics & Statistical Laboratory, Iowa State University, Ames, IA 50014, USA

1 INTRODUCTION

Pathogenic bacteria in ambient water bodies are a serious concern for the environment and public health.¹ According to the EPA's national summary of impaired waters, approximately 40,235 water bodies are impaired; approximately 15% of the total 71,363 impairments are due to water borne pathogens.^{1, 2} In the United States (as of 2011), the EPA had assessed 1,550,689 km of streams and found that 53 percent were impaired.^{3,4} The estimation of the World Health Organization (WHO) indicates that approximately 3.2 million deaths each year are associated with water contamination. This accounts for about 6% of all deaths globally.⁵

Pathogens in water have been linked to various diseases, including diarrhea, malaria, yellow fever, dengue, hepatitis A, Hepatitis E, and typhoid fever. For example, approximately 37.5% of diarrhea cases in developing countries are due to contaminated water.^{6,7} Even in the United States, approximately 60% of the total diarrhea cases are attributable to unsafe water, sanitation and hygiene.⁸ According to the World Bank (2011) estimation, US\$23 billion per year are required to develop the necessary infrastructure to provide safe water to the public.⁹

To evaluate public health risks caused by pathogenic bacteria in streams, watershed scale models capable of predicting in stream pathogen levels are required.^{10, 11} Previous studies have developed hydrological and water quality models to predict pathogen indicator such as *E. coli* levels in streams.¹⁰⁻¹⁵ Here we have proposed a statistical model for predicting in-stream *E. coli* levels.

2 METHODS AND RESULTS

Pathogenic bacteria indicator, *E. coli*, levels measured at the Squaw Creek Watershed, Iowa, were used to develop the model. The *E. coli* levels were measured at sixteen sampling locations shown in the Figure 1.

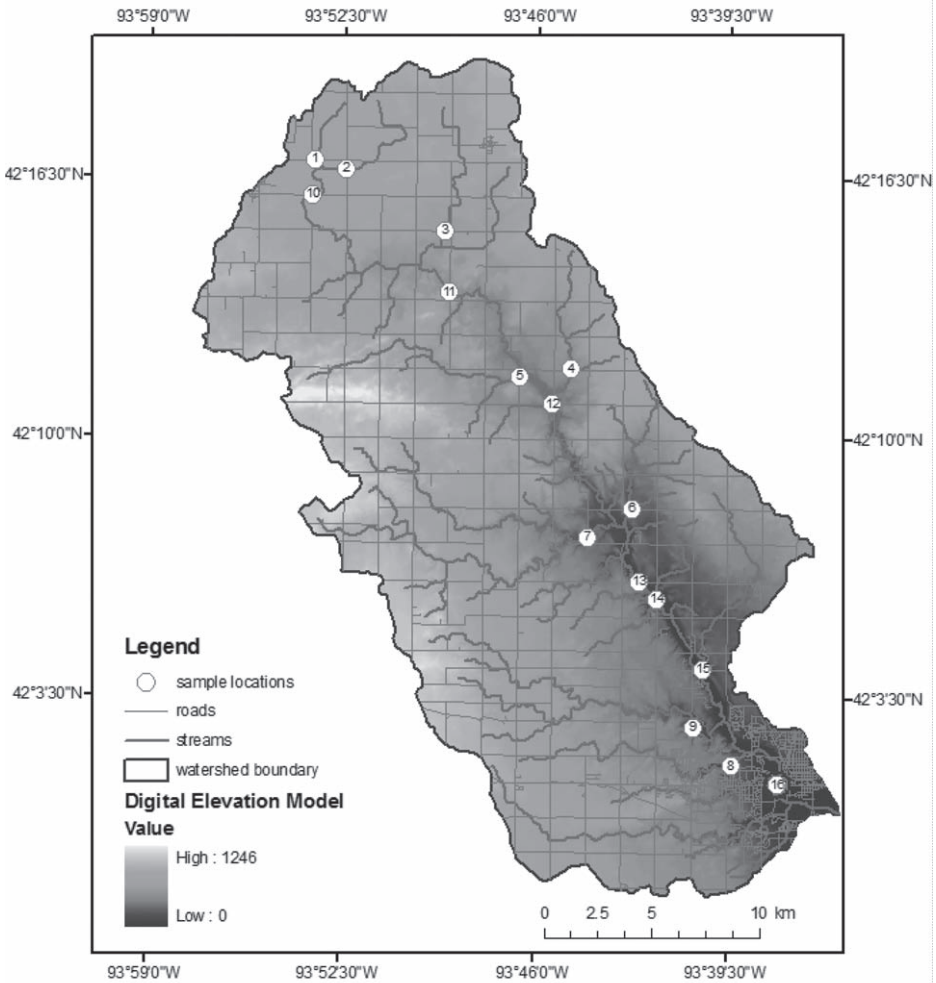


Figure 1 Sampling locations (1 – 16), streams, roads, watershed boundary, and elevations.

The watershed has a total drainage area of 592.39 sq km and average slope of 2.01%. In the watershed, the main channel length is approximately 60.46 km. Approximately 74% of the watershed is under agriculture: corn 41% and soybeans 33%. Forest cover is about 2.71%, and the total grassland is about 17% of the total watershed.

The conditionally specified model used in this study is:

Let $s_i \equiv (l, t)$ where l is sampling locations (1–16), and t is sampling event.

$$Y \equiv \{Y(s_i) : i = 1, \dots, 64\}$$

$$= \{Y(l, t) : l = 1, \dots, 16; t = 1, \dots, 4\}$$

We assume that the distributions of *E. coli* at a station, conditional on all stations upstream depends only on the closest upstream stations. To obtain the estimates of these parameters we apply maximum likelihood method. The two independent parameters water temperature ($^{\circ}\text{C}$) and stream water depth (m) were used for predicting the dependent variable, *E. coli* concentration. The approach used in this study is described elsewhere.¹⁶

Predicted and measured *E. coli* levels for eight different locations in the watershed are shown in the Figure 2. Figure 2A indicates stream water temperature and stream water depth variations, while Figure 2B shows the average of measured and predicted *E. coli* levels in eight different locations. The stream water temperature varied from 20.10 to 24.60 $^{\circ}\text{C}$ with mean of 22.45 (± 1.40) $^{\circ}\text{C}$. The stream water depth varied from 0.15 to 0.84 m with mean of 0.52 (± 0.24) m. Measured *E. coli* levels varied from 122 to 658 CFU/100 ml with mean of 400 (± 193) CFU/100 ml. The predicted *E. coli* levels varied from 187 to 416 CFU/100 ml with mean of 341 (± 79) CFU/100 ml. The difference between mean predicted and measured *E. coli* levels was within 2 factors (i.e., the mean of predicted *E. coli* levels was 85% of the mean of measured *E. coli* levels). The minimum *E. coli* level predicted by the model was slightly greater than the measured *E. coli* level, while the maximum *E. coli* level predicted by the model was slightly lower than the observed *E. coli* level. For example, observed minimum *E. coli* level was 80% of the predicted minimum *E. coli* level, while predicted maximum *E. coli* level was 63% of the observed maximum *E. coli* level. The model and results presented here will be useful for advancing the studies intended for modelling in-stream *E. coli* levels.

3 CONCLUSION

Here we have proposed a statistical model for predicting in-stream pathogenic bacteria indicator (i.e., *E. coli*) levels. The approach was used to predict *E. coli* levels in Squaw Creek Watershed, Iowa, USA. Predicted *E. coli* levels were compared with measured *E. coli* levels. The results shows that the model proposed here can be useful to estimate *E. coli* levels in stream water column.

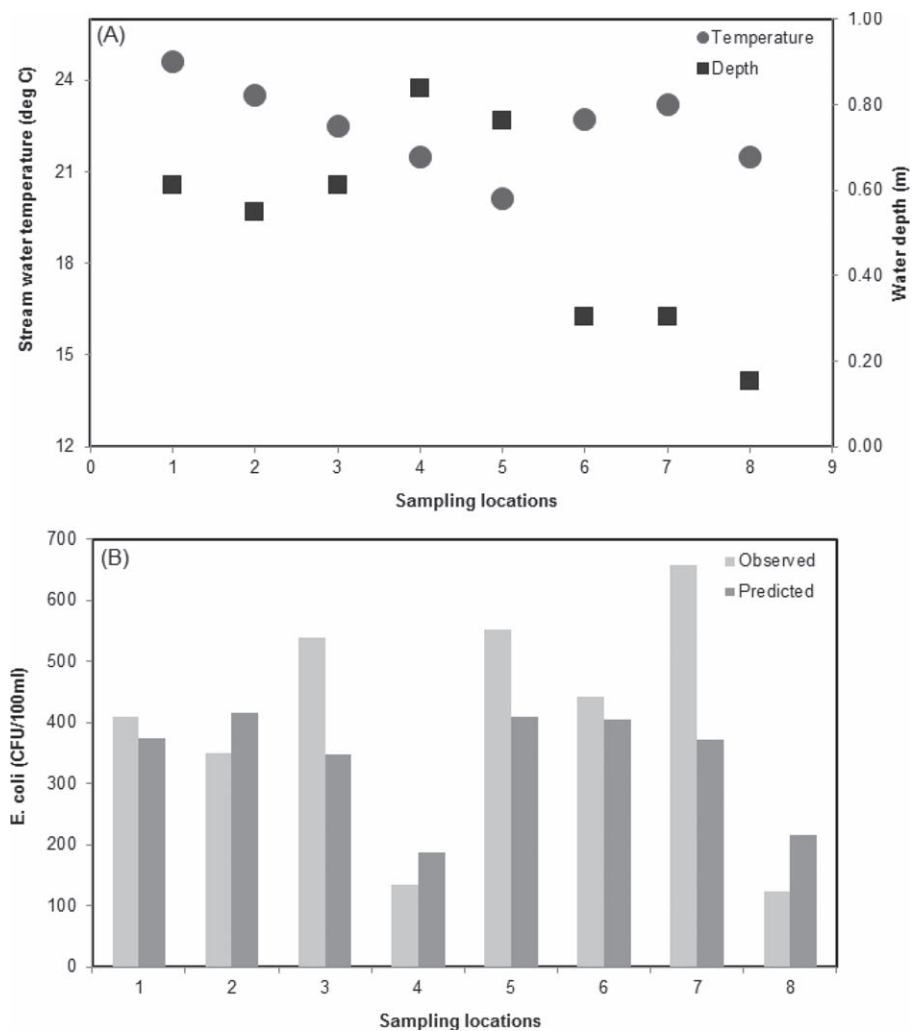


Figure 2 Stream water temperature, water depth, observed *E. coli* level (i.e., measured), and predicted *E. coli* levels. A) shows stream water temperature and water depth; B) shows observed and predicted *E. coli* levels.

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