

# Spatial and Temporal Modeling of Microbial Contaminants on Grazing Farmlands

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## ABSTRACT

This paper introduces an integrated spatial and temporal modeling system developed mathematically for assessing microbial contaminants on animal-grazed farmlands. The model uses fecal coliform, specifically *Escherichia coli*, as an indicator of fecal contamination and describes the sources, sinks, transport processes, and fate of *E. coli* contaminants in catchments and associated streams. Spatial features include grazing location, land topography, distance to a nearby stream, and distance through the stream network to the outlet. Temporal features are population dynamics on the land surface, in flow, and on streambeds. The model applies the principles of conservation of mass balance on two different types of pools: grid cells on land surfaces and networked stream segments. The model aims to improve the prediction of the effects of different land management strategies on the fecal contamination of waterways. This is achieved by characterizing the movement of fecal contaminants from land to streams and in-stream mobilization. Processes of attenuation, diffusion, and transport govern the movement. Our study site is a hill land catchment with an area of 140 ha and is used exclusively for animal grazing. The model was calibrated with previous research results, and then tested using the data collected at the outlet of the catchment. The sensitivity of the model predictions was analyzed for different scenarios: effect of stock rate, attenuation rate, and flow volumes. The similar pattern between monitored and predicted *E. coli* concentration proved that the model captures the key features that control the population dynamics of fecal contaminants. Further experiments are required to expand the model's functionality for covering more mitigation options.

OVER THE LAST THREE YEARS the fecal contamination of freshwaters, originating from animal-grazed farmlands, has been studied in New Zealand. This study revealed that fecal contamination (including several pathogenic microorganisms) of lakes and rivers is widespread, with concentrations of the fecal indicator *E. coli* often exceeding 1000 cfu/100 mL (Tian, unpublished data, 2000). As a consequence, concerns have been raised over the public health risk posed by these pathogens (including *Cryptosporidium*, *Giardia*, *Campylobacter*, *Salmonella*, and viruses) occurring in freshwaters.

Since farm animals can become infected by these pathogens, they act as reservoirs for potential human infection. Pastoral grazing practices, which create a diffuse source, and the disposal of animal waste (e.g., from meat processing plants and dairy sheds), significantly contribute to the fecal contamination of catchments. The public health risk from agricultural pollution has substantial implications for farming practice and international image, both for trade and tourism (Rose and Sobsey, 1993; Teunis et al., 1997). Pollution also restricts

the recreational use of freshwater (e.g., swimming, waterskiing, and windsurfing) and potential sources of water for potable treatment.

Stainer et al. (1979) demonstrated that the main pathway by which fecal material of agricultural origin reaches streams and lakes is through surface water runoff. Population distribution, transport process, and fate of fecal materials are difficult to explain using only monitored information due to the complexity of temporal and spatial variations. Such variations include animal grazing density, grazing distance to nearby stream, hydrologic and climatic conditions, land-surface topography, additional point sources, and vegetative cover. Some attempts to model fecal contaminants have been made in recent years. However, most of these models focus on individual processes at small scales such as streams (Wilkinson et al., 1995), wetlands (Chendorain et al., 1998), surface runoff (Iivanainen et al., 1999), or lakes and ponds (Auer and Niehaust, 1993; Canale et al., 1993; Jemmer et al., 1999).

The recent advances in geographic information systems (GIS) technology and hydrologic modeling have made it possible to construct models simulating microbial ecosystems at large scales (Fraser et al., 1998; Rousseau et al., 2000). However, existing GIS-based models of fecal contaminants were mostly developed for end delivery ratios of fecal material from land surface to streams or distribution in lakes. Few studies have considered using systems approaches for integrating and characterizing the interactions of the fecal contaminant evolution processes.

This paper presents an integrated and process-based system for describing spatial and temporal variation of the sources, transport processes, and fate of microbial contaminants in catchments. This GIS-based system uses fecal coliforms, specifically *E. coli*, as an indicator of fecal contamination (Bohn and Buckhouse, 1985). The system consists of six components: nonpoint-source dynamics and distribution, attenuation processes, diffuse runoff, point sources, transport via runoff to nearby streams, and in-stream mobilization (including deposition and resuspension). The hydrology in the system was processed using the Watershed Assessment Model (WAMView) (Bottcher and Hiscock, 2001). The WAMView model provides estimation of surface runoff from individual land units (raster grid cell) as well as the stream flow within watersheds. Our proposed system characterizes the movement of fecal materials from land to streams and in-stream mobilization through interactions among processes on fecal pools in land surfaces and stream segments. The conservation of mass is balanced for each pool at daily intervals. Spatial features of the system include grazing location, land topography,

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**Abbreviations:** FC, fecal coliform; SU, stock unit.

distance to a nearby stream, and distance of a position in stream networks to the outlet. Temporal features are population dynamics on land surface, in flow, and on streambeds.

The methods introduced can be used to identify livestock operations that contribute disproportionately to diffuse sources of pollution and improve the prediction of the effects of land management on the fecal contamination of waterways in large multi-use watersheds. Many mitigation methods have been considered as effective to reduce levels of microbial contamination entering surface waters from nonpoint-source and non-grazing perspectives (Chendorain et al., 1998; Hunt and Marinas, 1999). This paper discusses the potential of incorporating the effects of natural treatment methods, such as riparian zones, buffer strips, wetlands, and ponds, in the system.

## MODEL DEVELOPMENT

The concept of process interactions on fecal contamination pools is displayed in Fig. 1. The system characterizes a large-scale landscape as a regular grid of equal-area squares termed *cells*. Each cell is thereby a contamination pool influenced by three process interactions for the mass conservation balance: (i) inputs from grazing animals, (ii) removal by diffusion runoff, and (iii) reduction due to attenuation.

The in-stream mobilization characterizes the process of routing material from upstream to downstream and ultimately to a river or a lake. Each channel segment of the stream network is also a pool subject to conservation of mass balance. Input sources of fecal contaminants in a stream-type pool are a combination of surface diffusion, point-source discharges (i.e., meat processing plants and dairy sheds), and inflow from upstream. Three processes control the population dynamics in streams: (i) *E. coli* die-off (attenuation), (ii) stream deposition, and (iii) stream outflow.

### *E. coli* Source

The *E. coli* source in this model refers to nonpoint fecal contamination origins, mainly generated by grazing animals on pastoral farms. The factors that affect the generation of livestock fecal pollutants are (i) livestock density, (ii) length of grazing period, and (iii) livestock defecation rate. Since microbial contamination varies with the grazing animal type, the concept of stock unit (SU) is used to standardize the input units for all types of grazing animals. For example, a one-year-old cow is equivalent to six stock units, while a 45-kg ewe is equivalent to only one. The stock unit transform is similar to that used to compare feed intake among animal species (Anonymous, 1975).

Under the assumption of random manure distribution within a paddock, the rate of addition of *E. coli* to each cell from stock defecation is given as:

$$I(t,i,j) = \frac{R \times D(t,i,j) \times \rho}{A_p} \times C_s \quad [1]$$

where  $I(t,i,j)$  is the loading mass on day  $t$  over a cell with coordinates  $i,j$ ;  $C_s$  ( $m^2$ ) is the area of cell;  $D(t,i,j)$  is the stock units (SU) in a paddock on day  $t$ ;  $R$  is the mean *E. coli* mass per fecal pat;  $\rho$  is the number of fecal pats  $SU^{-1}$ ; and  $A_p$  is the paddock area ( $m^2$ ). The variables  $R$  and  $\rho$  were determined from the experiments conducted at the study site. Daily records of animal grazing for the farm were provided in a spatial

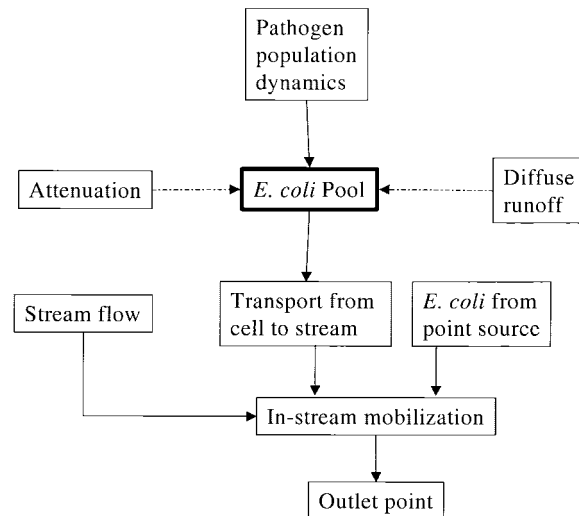


Fig. 1. Conceptual model of *E. coli* sources, transport processes, and sinks within catchments.

and temporal database. The database attributes include grazing paddock identity number, the stock rate, and type of animals. The grazing record database is the key data source for Eq. [1] for calculating *E. coli* spatial distribution and population dynamics.

### Attenuation Process

The attenuation process determines the inactivation rate of pathogenic microorganism indicators. There are differences in the factors that influence the inactivation rate in water and in soil. The ultraviolet light in solar radiation has the primary influence on inactivation of *E. coli* in water (Davies-Colley et al., 1999). However, microorganisms remain intact at a minimum 10-mm depth in soil or residual pastures. Inactivation on the land surface is often correlated to temperature more than to radiation (Howell et al., 1996; Niemi and Niemi, 1991). The attenuation rate of *E. coli* in this study is modeled as a function of daily mean temperature and solar radiation:

$$k = \left( \frac{TE}{a_1} + \frac{IR}{a_2} \right) \quad [2]$$

where  $k$  is the total attenuation rate per day,  $a_1$  is the inactivation rate by temperature,  $a_2$  is the inactivation rate by irradiation,  $IR$  is the daily irradiation ( $MJ m^{-2} d^{-1}$ ), and  $TE$  is the daily temperature.

Microbial populations on pastoral land vary not only with inactivation by solar radiation and land surface temperature but also with insect activity depending on surface conditions. Microbial activity within bovine fecal matter may remain on soil and plant surfaces for up to 1.5 years (Marsh and Campling, 1970). Coliform bacteria could survive for lengthy periods within fecal deposits over the summer despite exposure to high sunlight and temperatures (Buckhouse and Gifford, 1976; Thelin and Gifford, 1983). All these factors could affect mortality rate of the microorganisms. The model only tests those parameters for which we have monitoring data.

### Diffusion of Fecal Contamination

Diffusion in this study is defined as the movement of fecal indicators due to random water motion or mixing. This process causes *E. coli* contaminants to spread out of each pool in time with negligible net movement within it. Diffusion of *E. coli*

from a pool has been considered as a function of surface runoff volume, although it is three dimensional if infiltration were accounted for. The diffusion rate of *E. coli* mass from a cell on a day (*t*) is:

$$h(t) = K_0 * \frac{Q(t)}{Q_0} \dots \dots Q(t) > 0 \quad [3]$$

$$h(t) = 0 \dots \dots \dots Q(t) = 0 \quad [4]$$

where *h(t)* is the *E. coli* mass diffusion rate on day *t* from a cell, *K<sub>0</sub>* is the unit conversion constant (1 for liters, and 0.001 for milliliters), *Q* is the runoff volume (L d<sup>-1</sup>) from surface and subsurface flow, and *Q<sub>0</sub>* is a constant. The kinetics of the diffusion process of surface water runoff have been described in a hydrology model (Groundwater Loading Effects of Agricultural Management Systems [GLEAMS]).

The GLEAMS model (Knisel et al., 1991) is used to predict surface runoff hydrology. It is a well-known mathematical model developed to evaluate diffuse-source pollution from field-sized areas. This is a continuous simulation model for evaporation and soil water movement between storms, and a shorter time increment during storms dictated by available rainfall records.

Estimation of the runoff volume on each unit area (cell) is parameterized by available data such as: precipitation records, soil characteristics, surface roughness, land use, vegetative cover, and topography. Land areas are categorized according to their characteristics. The WAMView model was used to determine the surface runoff information for each of these categories. The predicted daily surface runoff volumes were then used as input for the *E. coli* diffusion process.

**Conservation of *E. coli* Mass Balance in a Cell**

The current model has the assumption that *E. coli* mass is randomly distributed over a cell. Three processes control the conservation of *E. coli* mass balance: fecal contaminant population dynamics, attenuation, and diffusion. The rate change of *E. coli* mass in a cell, on a day *t*, is:

$$\frac{dE}{dt} = I - kE - hE \quad [5]$$

where *E* is the number of *E. coli* in the cell, *t* is the time (d), *k* is the die-off rate (fraction per day), and *h* is the diffusion rate (fraction per day). The terms *E*, *I*, and *h* are functions of time (d). The incorporation of *E. coli* population dynamics in cells is a significant improvement over those models (Fraser et al., 1998) that implicitly have assumptions of constant *E. coli* concentration. From the daily change rate, the remaining *E. coli* population after attenuation and diffusion processes on day *n* is:

$$E^n = E^{n-1} + \Delta t \left( \frac{dE}{dt} \right) \quad [6]$$

where *E<sup>n-1</sup>* is the *E. coli* population persisting in a cell after day *n - 1* and  $\Delta t$  is the time interval (d).

**Point-Source Processes**

Fecal pollution from point sources is an important component of the model. There are several kinds of point-source discharges on grazing farmland including effluents from ponds, dairy sheds, urban wastewater treatment, and meat processing facilities. The model adds the microbial loading from each point source directly to the stream segment receiving water without considering physical processes in the transfer pipe. It

was recognized that in reality flow velocities and contaminant concentrations vary with time. However, in the model, only the mean daily flow volume and concentration is used to calculate the daily fecal input:

$$YP = K_p/Q_p \quad [7]$$

where *K<sub>p</sub>* is the point-source *E. coli* concentration, *Q<sub>p</sub>* is the point-source runoff volume per day, and *YP* is the *E. coli* mass produced from a point source per day.

**Transportation of Microbial Contaminants**

**Land to Stream**

The proportion of *E. coli* diffused from a cell that reaches a nearby stream is the delivery ratio. Several researchers (Thelin and Gifford, 1983) have shown that the delivery ratio of fecal pollution to a stream decreases with distance between the cell and the stream. The number of *E. coli* transported from the pasture (cells) to a nearby stream is a function of *E. coli* mass in the cell and its distance to the stream. Each reach has one and only one stream segment (pool), and an identity is assigned to each cell in the reach. The transport process of fecal indicator mass from a cell to the stream is described by using the delivery ratio (SDR):

$$SDR = \frac{a_3}{DTS} \quad [8]$$

where *DTS* is the distance from the center of the cell to the stream and *a<sub>3</sub>* is the parameter for the deliver ratio that may vary with land use, etc. The delivery ratios are used to calculate the effective delivery (ED) of *E. coli* mass from a cell to the stream:

$$ED = SDR * hE \quad [9]$$

where *hE* is the *E. coli* mass diffused out of the cell. The effective delivered *E. coli* from a cell to its nearby stream is proportional to the cell runoff volume and is inversely proportional to distance to the nearby stream. The model considers the *E. coli* lost on the delivery to a stream as mortality losses.

Total effective delivery of *E. coli* to the stream in a reach from point and nonpoint sources is integrated as follows:

$$X_j(t) = \iint_{\Omega_j} YP_j(t) + \iint_{\Omega_j} ED_j(t) \quad [10]$$

where *X<sub>j</sub>(t)* is the total *E. coli* mass input to stream (*j*) from its reach (*j*) on a day *t*, *YP<sub>j</sub>(t)* is the *E. coli* mass input to stream *j* from each individual point source in a reach (*j*) on a day *t*, *ED<sub>k</sub>(t)* is the *E. coli* mass from runoff in each individual cell within a subbasin (*j*) to stream (*j*) on day *t*, and  $\Omega_k$  is the domain of the reach (*j*).

The topography and vegetative cover of the land leading to the stream have also been reported to influence the delivery ratio (Fraser et al., 1998). Further field tests are needed for considering these two factors in the model in future.

**In-Stream Mobilization**

In-stream mobilization is the movement of *E. coli* mass from upstream to downstream. A unique identification number was assigned to each stream segment. All these stream segments connect to form a stream network. Flow is directed on a stream segment from the end point with higher elevation to lower. The flow sequence can further be described by stream order. A stream is assigned to a first order if there is no other stream flowing into it. A stream is assigned to the *i<sup>th</sup>* order if the highest order from the multiple inflowing stream is (*i - 1*)<sup>th</sup>.

The stream terminating at the catchment outlet always has the highest stream order.

The sediment of a stream can act as a transient reservoir for fecal pollution, absorbing microbial mass during periods of low flow and releasing mass during high-flow events (Geldreich, 1970). In-stream mobilization is controlled by a routing algorithm, which considers each stream segment as an *E. coli* pool. Conservation of *E. coli* mass balance in each stream segment pool is driven by flow volume in the stream. The daily changes of *E. coli* concentration  $c_k$  (*E. coli*/100 mL) on a stream segment  $k$  can be calculated differently by either deposition or scour (resuspension). Resuspension occurs in turbulent water when the flow volume is higher than a certain threshold. Otherwise, under low-flow conditions, deposition takes place. The deposition scenario is modeled as:

$$c_k = \frac{\left( \sum_{i=1}^l c_i v_i + X_k \right) (1 - D_k) (1 - S_k)}{v_k} \quad [11]$$

where  $v_k$  is the flow volume through stream  $k$ ,  $S_k$  is the deposition fraction,  $D_k$  is the death rate (fraction),

$$\sum_{i=1}^l c_i v_i$$

is the total *E. coli* inflow into segment  $k$ , and  $l$  is the total number contributed by upstream tributaries of segment  $k$  ( $l$  is always greater than one as each new stream is defined by a confluence). The variables  $c_k$ ,  $c_i$ ,  $v_i$ , and  $X_k$  are a function of time (d). The  $v_i$  is produced by WAMView, which is a physically based continuous hydrology model. The  $S_k$  is:

$$S_k = \exp \left( -\frac{v_k}{v_0 - 0.66v_k} \right) \dots \dots v_k < v_0 \quad [12]$$

where  $v_k$  is the flow volume on day  $n$  and reach  $k$ , and  $v_0$  is the threshold turning point of flow volume between deposition and resuspension.

The outflow of *E. coli* population (EO) on day  $n$  and stream  $k$  is:

$$EO_k = c_k v_k \quad [13]$$

The remaining *E. coli* population (EP) accumulated on the channel bed of stream  $k$  on day  $n$  is:

$$EP_k^n = \left( EP_k^{n-1} + \left( \sum_{i=1}^l c_i v_i + X_k \right) S_k \right) (1 - D_k) \quad [14]$$

In the scour situation:

$$c_k = \frac{\left( \sum_{i=1}^l c_i v_i + X_k + RS_k EP_k \right) (1 - D_k)}{v_k} \quad [15]$$

where  $RS_k$  is the daily resuspension rate:

$$RS_k = 1 - \exp \left( -\frac{v_k - v_0}{Q_0} \right) \dots \dots v_k \geq v_0 \quad [16]$$

The term  $Q_0$  is a parameter controlling the resuspension rate. The remaining *E. coli* count at the end of day  $n$  on the channel bed of stream  $k$  is:

$$EP_k^n = EP_k^{n-1} (1 - RS_k) (1 - D_k) \quad [17]$$

The daily flow volume ( $v_i$ ) for each stream segment was stored in a database. The daily hydrographs were the main factors that drive *E. coli* in-stream mobilization.

**Table 1. The calibrated model parameters.**

Parameter	Calibration
$R$	$108 \times 10^6 E. coli \text{ pat}^{-1}$
$P$	$2.1 \text{ pat SU}^{-1\dagger}$
$a_1$	250
$a_2$	4 000
$K_p$	point-source concentration
$a_3$	0.005
$K_0$	0.001
$Q_0$	100
$v_0$	250 000
$D$	0.1
$S$	function or 0.2
$RS$	function or 0.2

† SU, stock unit.

## MODEL CALIBRATION

The model parameters were calibrated using previous research results and data from climate stations. The calibrated parameters are listed in Table 1.

To estimate the *E. coli* multiplication rate from cattle, parameters  $R$  and  $P$  were derived using the experimental results provided by Wilcock et al. (1999). Wilcock's research showed that a cattle of live weight 450 kg produces 12.3 pats per day on average, and each pat contains  $1.3 \times 10^9 E. coli$ . The average *E. coli* attenuation rate  $k$  was between 0.06 and 0.182 (Gameson and Saxon, 1967; Hanes et al., 1966; Howell et al., 1996). Investigation from Howell et al. (1996) demonstrated that fecal coliform (FC) mortality rate is between 0.04 and 0.084 at temperatures ranging from 11 to 21°C. The mean daily irradiation received at the study site ranged from 117 to 491 MJ/m<sup>2</sup> and the temperature was usually between 11 and 21°C. Following previous research results, the mortality rate in this study should be between 0.025 and 0.098. We obtained these rates by setting parameters  $a_1$  and  $a_2$  in Eq. [2] as 4000 and 250, respectively.

According to the 1998–1999 data measured at the Whatawhata research center, 7% of the daily flow volumes,  $v_k$ , were greater than 250 000 L. Thus  $v_0$  was set to 250 000, which assumes that 7% of the flows in a year resuspend fecal coliform. With the above assumption plus setting  $Q_0$  to  $10^5$ , the deposition rate ranges between 0.05 and 1 when  $0 \leq v_k \leq 250 000$ . The resuspension rate is between 0.003 and 0.8 when  $250 000 < Q < 1 872 009$ .

In an extreme scenario, runoff volumes received by a stream from a cell would be about 6978 L d<sup>-1</sup> and *E. coli* pollution in the upstream reaches would be about  $1.4 \times 10^8$ . In such an extreme case with choice of 0.1 as mortality rate  $D_i$ , *E. coli* concentration in the downstream reaches resulted from the deposition function ranges from 0 to 930 per L while flow is between 0 and 250 000 L. The concentration resulting from resuspension ranged from 1430 to 2803 per L while the flow is between 250 000 and 1 872 009 L. The ratio of downstream over upstream is between 30 and 89% while flow volume ranges from 4944 to 307 648 L. The ratio rose to 139.74% when the flow volume was at 1 872 009. This result is consistent with that investigated by Crabill et al. (1999), who summarized three-year (1994–1996) field experiment results of spatial and temporal variation of measured sediment and water fecal coliform concentrations (Table 2). The dataset covered situations of upstream versus downstream areas and seasonal effects.

The mean factor of winter over summer on FC concentration ratio is 2% for FC in sediment, 23% for water-borne FC in the upstream and 6% for downstream. The mean ratio of upstream versus downstream is 23% in summer and 82% in winter.

In summary, the parameter settings in Table 1 are appro-

**Table 2. Fecal coliform concentration variations with seasons.**

Description	Summer		Winter		Year	
	Mean	Range	Mean	Range	Mean	Range
Sediment FC†	$1.9 \times 10^6$	$0-7.4 \times 10^7$	$3.5 \times 10^3$	$0-4.4 \times 10^4$	$1.3 \times 10^6$	$2.8 \times 10^7$
Water FC	67.5	0-910	Upstream		51	0-910
			Downstream			
Water FC	295	0-6400	18.5	0-270	207.7	0-6400

† FC, fecal coliform.

appropriate for the model by comparison with previous research results.

**STUDY SITE AND DATA FOR MODEL PRELIMINARY TESTING**

The study site used for model testing against the monitored data was at the Mangatoama basin of the Whatawhata Research Centre, Hamilton, New Zealand (37°48'S, 175°5'E; approximately 220 m above mean sea level). The site map is displayed in Fig. 2 and contains two subcatchments with outlets PW<sub>2</sub> and PW<sub>3</sub>. The contributing area is about 948 000 m<sup>2</sup> to PW<sub>2</sub> and 488 000 m<sup>2</sup> for PW<sub>3</sub>. The light gray lined polygons represent subbasins and shaded polygon areas are paddocks. Each subbasin has a unique identification number. The streamlines are classified by flow order. Grazing pasture is the predominant land use for the two subcatchments. The catchments have median slope of 20°. The *E. coli* and fecal coliform concentrations were monitored once each month at a pump intake below the outlet (PW<sub>2</sub>/PW<sub>3</sub> confluence). The concentration unit used was cfu/100 mL.

Daily temperature and solar radiation required by the model were obtained from monthly mean climate data. The model requires rainfall data indirectly via the WAMView hydrology model for surface runoff (both in cell and basin scales) and stream flow.

To simplify this preliminary model test, we produced daily mean surface runoff using monitored mean flow rate FI<sub>5</sub> (L/s) at the outlet PW<sub>5</sub>. Outlet PW<sub>5</sub> was located further downstream of our study site and receives runoff from an area of 2 590 000 m<sup>2</sup>. We assumed that the entire area contributed evenly to the flow and all contribution is from surface runoff. With such assumptions, we calculated the mean surface runoff (L/d) at the cell scale (400 m<sup>2</sup>) as:

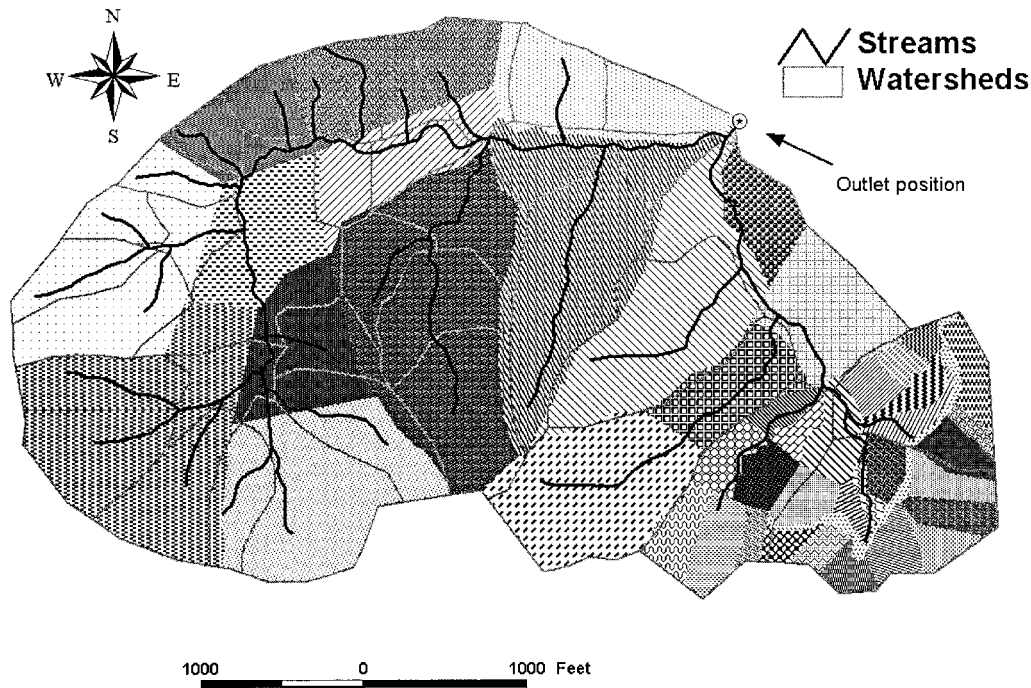
$$FI_5 \times 60 \times 60 \times 24 / (259 \times 10^4) \times 400 \quad [18]$$

The daily flow volume in each individual subbasin (stream segment) was calculated as runoff from the surface within the subbasin plus inflow from upstream. The surface runoff within a subbasin was the integration of surface runoff at each cell. The inflow volumes to each subbasin were the combinations of the outflows from upstream segments. The physical stream network structure provides the information for an additional routing program to assess the dynamics of flow volume of individual stream segments.

**RESULTS AND DISCUSSION**

**Model Validation**

We tested the model against the *E. coli* concentration monitored monthly at the Mangatoama study site. The



**Fig. 2. Map of watersheds, streams, and paddocks (shaded areas) at the study site.**

test was for the period beginning 1 Nov. 1998 and ending the same date in 1999. Figure 3 presents the model estimation and the monthly monitored *E. coli* concentration for the stream segment connecting to the outlet of the entire study catchment. The sampled data has a similar pattern of the model prediction in all instances. The model prediction explains about 50% of the variation of the field measurements (adjusted  $R^2 = 0.501$ ). However, the reliability of the result needs to be tested with more data. Both sampled and estimated concentrations ranged mostly between 200 and 1300 cfu/100 mL (*E. coli*/100 mL for prediction). In one instance, sampled data were three times higher than that of the model prediction. This might be due to some unusual events, such as dead animals and animal activities (i.e., direct deposition from livestock standing in water of streams). These unusual events are not normally recorded, and therefore they were not handled by the current version of the model. In spite of these limitations, the model results showed that the animal grazing intensity and grazing distance to the streams are the main factors controlling the total *E. coli* outflow mass.

The model estimation includes concentration, outflow mass, and population dynamics in the streambed. The results show that total outflow *E. coli* mass at the outlet is proportional to the catchment runoff volumes. This result is consistent with the reality that the higher flow volumes would have more resuspended *E. coli* from the streambed. Also, high stream flow volume is a consequence of high surface runoff transporting more *E. coli* from the land. The *E. coli* population dynamics on the

sediments of streambed have the same pattern as at the outlet. This phenomenon reflects that the high quantity of *E. coli* on the streambed is a rich source of suspended mass during higher stream flow. Likewise, deposition rate on the streambed demonstrated in model runs would be greater when the flow is lower.

In spite of the fact that hydrological data on surface runoff and stream flow, as well as climate data on temperature and radiation, have strong seasonal variations, there are no seasonal patterns in the monitored and predicted *E. coli* population dynamics as illustrated in Fig. 3. This outcome demonstrates that grazing intensities (number of grazing days and stock rate), frequency, and distance to a stream may have cancelled out an otherwise high attenuation rate. Specifically, there is higher generation of fecal contaminations from grazing animals in summer; however, summer has many advantages of reducing contaminants to streams. These advantages include severe attenuation, greater distance of grazing events from streams, and lower delivery rate from land surface to a stream because of dense vegetation. These advantages and higher contamination generation would have cancelling effects.

### Scenario Analysis

The model was further evaluated with five scenarios as listed in Table 3. The first three were to examine the effect of stocking rates (high, medium, and low). The ordinal values of low, medium, and high are used in this context simply for model sensitivity testing and are

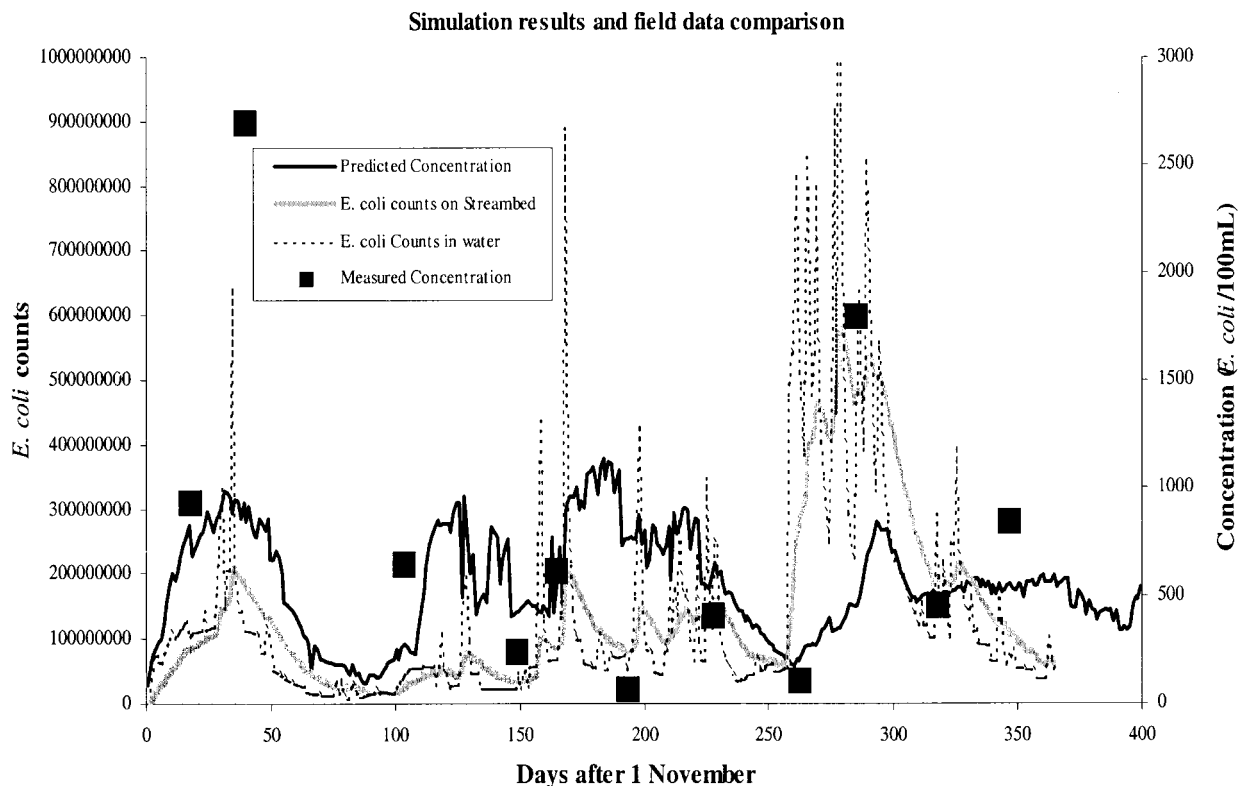


Fig. 3. Daily prediction of *E. coli* mass flow, concentration in water at catchment outlet, and *E. coli* mass on the streambed of the basin that the outlet resides on, and field measurement of *E. coli* concentration at the catchment outlet.

**Table 3. Input data settings for model sensitivity in three scenarios.**

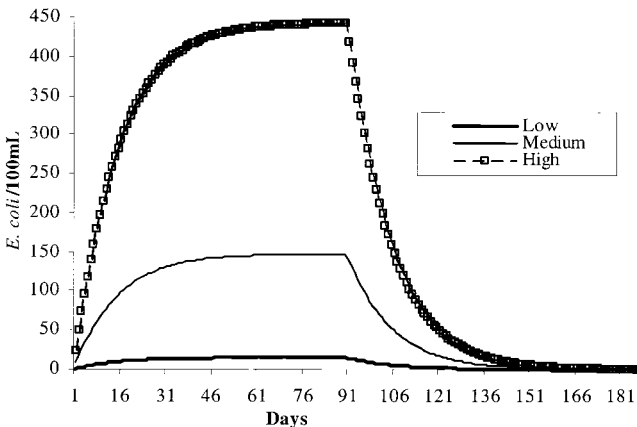
Scenarios	Mean stock rate per cell†	Days	Flow	Mean daily temperature	Radiation
			L cell <sup>-1</sup> d <sup>-1</sup>	°C	MJ m <sup>-2</sup> d <sup>-1</sup>
Stocking 1	low (0.1 SU‡)	first 90	860	16	25
	0	second 90	860	16	25
Stocking 2	medium (1 SU)	first 90	860	16	25
	0	second 90	860	16	25
Stocking 3	high (1.5 SU)	first 90	860	16	25
	0	second 90	860	16	25
Temperature and radiation	1 SU	first 90	860	10	20
	1 SU	second 90	860	21	34
Flow effect	1.5 SU	first 90	168	16	25
	0	second 90	14 388	16	25

† Cells are on the scale of 20 × 20 m.  
‡ Stock unit.

different from the reality. For example, the high stock rate is represented with 1.5 stock units (SU)/400 m<sup>2</sup> in the scenario analysis, but in New Zealand hill land grazing systems, stock rate is on average 10 SU/ha (4 SU/400 m<sup>2</sup>). A fourth scenario was to examine the effect of a changing attenuation rate controlled by temperature and radiation. The fifth and final scenario was to vary surface runoff flow volume. The scenarios assumed that no *E. coli* existed on the studied land before the simulation period. Analyses are for the stream segment connecting to the catchment outlet.

Except for the sensitivity testing variables, all parameters were set to constants as displayed in Table 3. Parameters such as bacterial die-off, deposition, and resuspension within the streambed were also assumed to be constant rates. Although the self-regulating functions for deposition ( $S_k$ ) and resuspension ( $RS_k$ ) are more appropriate to use, using constant values for  $S_k$  and  $RS_k$  simplified the evaluation process for the variables of interest.

Three different stocking activation levels were applied for the first 90 d, then no stock for the remaining 90 d. In the case of 1.5 SU/400 m<sup>2</sup>, average *E. coli* concentration was up to 450 per 100 mL. After stopping the stock application at 90 d, it required about 45 d to wash out the remaining *E. coli* with the constant runoff during the second 90 d. This cleanup period is slightly different among the three stocking rates. This result

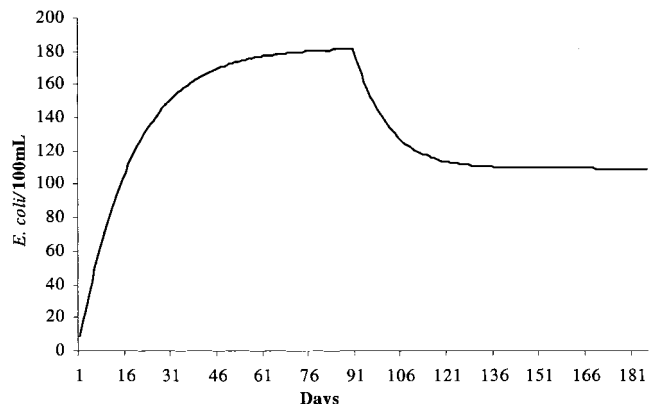


**Fig. 4. Effects of stocking rates on *E. coli* concentration: high (1.5 stock units [SU]/400 m<sup>2</sup>), medium (1 SU/400 m<sup>2</sup>), and low (0.1 SU/400 m<sup>2</sup>). The above rates were applied to the first 90 d, no stocks to the second 90 d.**

demonstrated that there is a potential source of organism to enter stream water long after the animals have left the watershed (Tiedemann et al., 1987). The sensitivities of *E. coli* concentration to stocking rate are displayed in Fig. 4.

The effect of attenuation simulated by the model is displayed in Fig. 5. A lower temperature and radiation were applied for the first 90 d, then raised for the second 90 d. The higher and lower temperature and radiation are representative of New Zealand climate conditions. The stocking rate was held constant through the entire 180 d. After the attenuation rate changed from low to high, *E. coli* population dropped sharply then reached a steady state. Due to the constant stocking rate throughout the entire 180 d, the simulated *E. coli* population at the steady state was not zero.

The model produced very encouraging results on evaluating the effect of flow volumes (Fig. 6). The result showed that the *E. coli* concentration at the outlet was boosted immediately after the flow volume changed from low volume to high. The model indicated that the period for catchment-wide cleanup was about one month. This is consistent with the results reported by Carvey et al. (1998) and Chendorian et al. (1998). The lengthy period of cleanup might be due to the land surface areas acting as persistent population sources. Thelin and Gifford (1983) discovered that bacteria, such as fecal coliforms, are able to survive for long periods under as little as 10 mm of soil surface. Based on these results, our model prediction of the cleanup period is reasonable.



**Fig. 5. Effect of temperature and solar radiation. A low treatment was applied to the first 90 d, then high for the remaining period.**

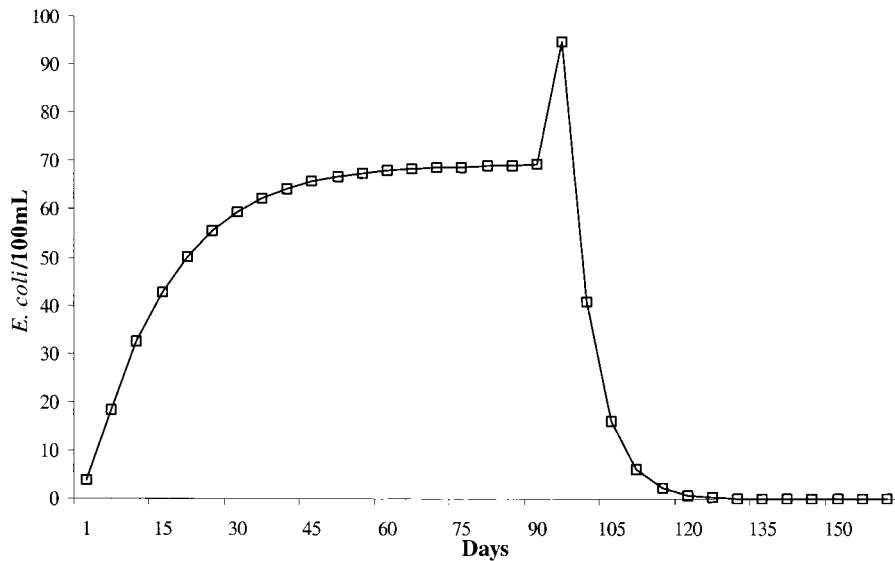


Fig. 6. Effect of flow volumes. Low volume was applied to the first 90 d, then high for the remaining period.

### Model Sensitivity

The purpose of the sensitivity analysis is to evaluate the amount of change in model output caused by changes in input. It is a measurement of how the output of a model is controlled by the input parameters and initial conditions. Our sensitivity analysis examined the model responses for the period specified in Fig. 3. The analysis was conducted by varying one parameter for  $\pm 50\%$  of the initial value at a time (while keeping all others constant) and by looking at the effect on some key summary statistics on average *E. coli* concentration at the catchment outlet. The analysis involved six parameters listed in Table 1:  $R$ ,  $a_1$ ,  $a_2$ ,  $a_3$ ,  $Q_0$ , and  $D$ .

The result of the sensitivity tests indicates that all of these parameters have significant influence on model prediction. The  $Q_0$  controlling diffusion rate and *E. coli* rate per pat are the most sensitive parameters. Changing either of these two parameters has up to  $\pm 63\%$  influence on the model outputs of average *E. coli* concentration for the study period. On the other hand, mortality rate has the least weight in the model output (23%). Varying 50% for each parameter alone relative to the initial parameter setting in Table 1 did not improve the prediction ( $R^2 < 0.5$ ). The sensitivity rank of these examined parameters is  $Q_0$ ,  $R$ ,  $a_1$ ,  $a_2$ ,  $a_3$ , and  $D$ . Further to this analysis, the model may be fine-tuned so that results fall within acceptable ranges of field study estimates by using some common tools such as Monte Carlo method.

### Other Possible Effects on *E. coli* Dynamics

#### Effects of Freezing on *E. coli* Survival

Little research has been published on *E. coli* viability at freezing and/or snowing temperatures. Without data on the effect of temperature intensity on *E. coli* survival rate, this cause of *E. coli* loss has not been quantified and was not included in the model.

### Insignificance of Fecal Coliform Regrowth

Hendricks and Morrison (1967) found that *E. coli* and other enteric bacterial, some of which are pathogens, continue to multiply after the bacteria are outside the host. Howell et al. (1996) demonstrated that pathogenic microorganisms regrow shortly after deposition. Once voided from the body, the fecal coliform population immediately goes into the retardation phase in which the population's specific growth rate declines until growth ceases (Lynch and Poole, 1979). Thelin and Gifford (1983) confirmed that the decline in growth rate was rapid, with growth ceasing not more than a day after the feces were voided. Their research also showed that the growth and leveling of periods of the first three days were not significant in animal-grazed agricultural lands. Because of the insignificance of fecal coliform regrowth, the model does not implement a fecal coliform regrowth factor.

### Other Fecal Contaminant Sources

The model focuses the fecal coliform pollutants associated with livestock production and included a component for estimating point sources of fecal contamination. Although Thelin and Gifford (1983) concluded that the discharge of pathogens into streams is most clearly associated with livestock production on grazing farmlands, including fecal contaminants from wildlife (such as opossums, rabbits, deer, and birds) could improve the model's prediction. The extension of the model to include wildlife requires additional field measurements and quantification of the fecal coliform sources received from wildlife. Adding a separate *stock unit* can incorporate the issue of fecal contaminants from wildlife.

### Direct Deposition from Livestock in Water

In a study of 13 forested watersheds subjected to four grazing treatments, Tiedemann et al. (1987) reported a clear relationship between presence of cattle and FC

concentrations. They suggest fecal coliform levels may be more related to animal access to streams than to stock densities. Grazing animals have been observed to stand right in the water on a summer day. Direct deposition from livestock in water might be a significant pathway of the extremely high concentration events of microorganisms at the outlet. An experiment is being conducted in New Zealand to obtain quantitative information on direct deposition of animal pollutant to stream water for future model improvement.

The model did not include ground water transport of fecal pathogens. This factor is generally negligible due to efficient filtering and adsorption from soil particles (Reddy et al., 1981; Hunter et al., 1992; Weiskel et al., 1996), except in the case of karst topography (Howell et al., 1996) or where extensive macrospores are present (Hunter et al., 1992).

## CONCLUSION

Despite the limitations of this modeling analysis, several clear conclusions emerge. The presented spatial and temporal system has promising potentials for analyzing the influence of animal grazing on microbial contaminants in streams and lakes at the catchment scale. The modeling result demonstrated that livestock waste is a primary source of bacteria and pathogens on agricultural land. This result is consistent with the conclusions of Khaleel et al. (1980). In this paper, dynamics of microorganisms in a catchment are characterized at two levels: (i) an animal grazing database that contains grazing location, intensity, animal types, and duration, and (ii) a description of fecal contamination movement from land to stream and in-stream mobilization. The result of comparing the model prediction and monitored *E. coli* concentration demonstrated that the model is capable of interpreting the complicated physical interaction processes among grazing management, surface runoff, and climate conditions.

The system is based on interactions among various processes in desired time intervals. Using *E. coli* as an indicator, the system links farming management with environmental quality. The sensitivity analysis results proved that the model's response to independent variables is reasonable. Although the system was evaluated in a condition lacking of distributed measurements of surface runoff at daily intervals, it nevertheless explained the complexity of monitored *E. coli* concentrations. Therefore, the system has potential to improve the prediction of the effects of grazing management on the fecal contamination of waterways in large catchments. The simulation process can inform decisions on practical management options for reducing fecal contamination of freshwaters.

The current model is limited by not accounting for the pollutant direct deposition to water from animals. The model could also be extended to cover more specific conditions including climatic conditions of frozen and/or snow-covered ground and to incorporate wildlife contaminants.

Further experiments are required to expand the mod-

el's functionality for covering more mitigation options to reduce fecal contaminants. For example, the rate of microbial attenuation or removal may be improved through vegetation buffer strips and wetland zones. This type of extension needs to incorporate more environmental chemistry, soil science, and microbial ecology. All the improvements under discussion would enable users of the model to produce even more realistic and accurate predictions for the purpose of farm management and water quality control.

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