

# Predicting Stream Pathogen Loading from Livestock using a Geographical Information System-Based Delivery Model

Robert H. Fraser, Paul K. Barten,\* and David A. K. Pinney

## ABSTRACT

Recent cases of drinking water contamination by pathogens have underscored the importance of preventing livestock waste from entering surface waters. To this end, analytical tools are needed that can identify subwatersheds or livestock operations that contribute disproportionately to contamination. This paper presents a geographical information system (GIS)-based transport model (SEDMOD) that provides an index of pathogen loading potential to streams by characterizing five key transport parameters: flow-path hydraulic roughness, gradient, and slope shape, stream proximity, and a normalized soil moisture index. We applied SEDMOD to 12 subwatersheds (10 agricultural, 2 forested controls) of the Saw Kill, a tributary of the Hudson River, New York, and compared model predictions with measured fecal coliform (FC) levels. The transport model, combined with a livestock density GIS layer, could explain 50% of the variation in average FC discharge among the subwatersheds ( $r = 0.71$ ,  $P = 0.01$ ,  $n = 12$ ). By contrast, neither total livestock FC output nor predicted FC transport were correlated with geometric mean FC concentration ( $P > 0.05$ ). In a multiple regression, predicted FC transport, mean water temperature, and mean turbidity could account for 80% of the observed variation in FC discharge ( $r = 0.90$ ,  $P = 0.001$ ,  $n = 12$ ). We conclude that, although more field work and algorithm development is needed to yield more accurate quantitative predictions, the model is useful for predicting the relative contribution of diverse livestock operations within a varied landscape. This provides watershed managers and regulators with a rating method to prioritize sites for nonpoint source pollution control.

**W**ATERSHED MANAGEMENT is the process of planning resource use within a watershed to provide multiple goods and services (e.g., potable water, agriculture,

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recreational uses) without adversely affecting the soil and water resource base (Brooks et al., 1991). When drinking water is one of the desired goods, watershed managers must contend with potentially serious problems of soil erosion, pollution by industrial and wastewater effluents, and contamination by pathogenic organisms. Recently, waterborne pathogens such as *Cryptosporidium*, *Giardia*, and viruses have emerged as a priority concern, especially after a massive cryptosporidiosis outbreak in Milwaukee in the spring of 1993. That contamination event infected an estimated 403 000 people and led to nearly 100 deaths, making it the largest documented outbreak of waterborne disease in U.S. history (MacKenzie et al., 1994). Indeed, the resistance of *Cryptosporidium* oocysts to chlorine disinfection could eventually compel New York City to construct a multibillion-dollar water filtration facility (Okun et al., 1993).

Many microbial pathogens such as *Cryptosporidium* are difficult and expensive to monitor routinely (Watanabe, 1996). Consequently, bacteria are normally measured to detect fecal contamination that may contain associated pathogenic organisms (Bohn and Buckhouse, 1985). Fecal coliform bacteria (primarily *Escherichia coli*) are widely used indicator organisms and are the statutory basis for many water quality regulations promulgated from the Safe Drinking Water Act (Berger and Regli, 1990). If the factors leading to high FC (and potential pathogen) transport to streams can be characterized, then it becomes possible to select and implement Best Management Practices (BMPs) to prevent or reduce pathogen loading.

Waterborne pathogens originate from wastewater treatment plant and septic tank effluents, and from urban and agricultural stormwater (Geldreich, 1990).

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**Abbreviations:** GIS, geographical information system; FC, fecal coliform; BMPs, best management practices; NPS, nonpoint source.

Livestock waste is a primary source of bacteria and pathogens on agricultural land (Khaleel et al., 1980). Fecal coliform levels in streams have been directly related to the presence of livestock (Stephenson and Street, 1978; Gary et al., 1983; Tiedemann et al., 1987; Howell et al., 1995) and to manure spreading on croplands (Khaleel et al., 1980). For example, Stephenson and Street (1978) measured bacterial pollution weekly over 3 yr in a stream draining a 233 km<sup>2</sup> rangeland watershed and found that FC counts increased significantly (e.g., from 0 to 2500 colonies 100 mL<sup>-1</sup>) when cattle were moved onto the range. Fecal coliforms remained elevated for several months after the cattle were removed. 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 FC levels may be more related to animal access to streams than to stocking densities. Background contamination by wildlife also has been observed in nonagricultural areas (Niemi and Niemi, 1991).

### MODELING BACTERIAL POLLUTION

Many studies have been performed to explain variability in stream FC and other indicator organisms. Some have taken an empirical approach, using regression techniques and variables such as livestock density, rainfall, stream discharge, and various water quality parameters (Kay and McDonald, 1983; Hunter and McDonald, 1991). McElroy et al. (1976) proposed a loading function for livestock operations in which pollutant (e.g., coliform) loading rate to a stream was determined using the equation:

$$Y(i) = a \times Q \times C(i) \times D \times A \quad [1]$$

where

- $Y$  = loading rate of pollutant  $i$  from a livestock facility (kg d<sup>-1</sup>),
- $a$  = unit conversion constant (0.1),
- $Q$  = direct runoff (cm d<sup>-1</sup>),
- $C(i)$  = concentration of pollutant  $i$  in runoff (mg L<sup>-1</sup> or colonies L<sup>-1</sup>),
- $D$  = delivery ratio (a simple function based on distance to stream), and
- $A$  = area of livestock facility (ha)

With additional terms, this equation is similar to the Rational Formula (Pilgrim and Cordery, 1993). The loading function does not account for animal stocking density and implicitly assumes that bacteria concentration in subsurface and overland flow is constant. Kay and McDonald (1980) used a distance-dependent decay function to simulate the reduction in bacteria within two reservoirs receiving agricultural drainage. Canale and others (1993) employed a more mechanistic modeling approach. They simulated spatial and temporal variation of FC in a lake using a two-layer, mass balance model coupled with a bacterial loading model.

Few studies have considered animal waste loading and factors influencing transport to a stream network on a spatially explicit basis. Geographic information systems are well suited to process the considerable spatial data required for high resolution, distributed modeling of nonpoint source (NPS) pollution (DeVantier and Feldman, 1992; American Water Resource Association, 1993). In one GIS application, Gilliland

and Baxter-Potter (1987) created a spatially distributed estimate of bacterial pollution in overland flow by assigning typical literature concentrations for feedlots, pastures, and cornfields. They did not, however, consider bacterial transport to the stream in the analysis. A model called MWASTE was developed by Moore and coworkers (1988) to track daily bacterial numbers in runoff from various manure management systems. Heatwole and Shanholz (1991) calculated a spatially distributed, animal waste pollution index that ranked livestock operations based upon waste load, slope, and distance to stream. The model was created as a large-scale screening tool; predicted nutrient loads were not compared with field measurements of water quality. Hamlett et al. (1992) developed a GIS-based screening tool to rank the agricultural pollution potential of 104 watersheds in Pennsylvania. The ranking, derived from commonly available data, was based on a runoff index, a sediment production index, an animal loading index, and a chemical use index. Within each watershed, all cells were weighted equally because a pollutant routing procedure was not included in the model. Despite some limitations, these studies demonstrate that a spatially explicit modeling approach using GIS can be effective for identifying critical livestock areas.

The purpose of this study is to investigate the utility of a GIS-based transport model for identifying livestock operations having high pollution (i.e., bacteria and pathogens) potential. We test the hypothesis that fecal coliform stream loading can be better predicted by using SEDMOD, a Spatially Explicit Delivery MODEL (Fraser et al., 1996), than by considering only aggregate watershed properties, such as total animal numbers and watershed size.

### The Model

SEDMOD was initially developed to estimate spatially distributed delivery ratios for eroded soil and associated nonpoint source (NPS) pollutants. The aim of the model is to provide an index of transport potential that is consistent with spatial data commonly available at larger scales (e.g., USGS digital elevation models, USDA soil surveys, land cover from satellite imagery or aerial photographs). SEDMOD is a menu-based application implemented entirely within the ARC/INFO GIS (Environmental Systems Research Institute, 1994) using ARC/INFO's programming language (AML) and raster modeling package (GRID). The model calculates a delivery ratio for each watershed cell to predict what proportion of eroded sediment (or other NPS pollutant) is transported from the cell to the stream channel. The ratios are estimated by characterizing the magnitude of five key parameters controlling NPS pollutant transport (Table 1). A raster layer is created for each parameter to represent, on a cell-by-cell basis, the influence of that characteristic on the transport process. Each variable is normalized to a common range of 0 to 100 using empirical relationships from the literature or a hypothesized relationship with delivery potential. The transport variables are combined using a linear weighting (Eq. [2]) that is specified by the analyst from an interactive menu. The final product is a GIS layer with delivery ratio values that can range from 0 to 100%.

$$\begin{aligned} \text{Delivery ratio} = & SG_r SG_w + SS_r SS_w + SR_r SR_w \\ & + SP_r SP_w + ST_r ST_w + SM_r SM_w \quad [2] \end{aligned}$$

where  $SG$  = flow-path slope gradient;  $SS$  = flow-path slope shape;  $SR$  = overland flow-path vegetation roughness;  $SP$  = stream proximity;  $ST$  = soil texture (represented by percentage of clay);  $SM$  = soil moisture index;  $VAR_r$  = rating of

**Table 1. Description of parameters used to calculate SEDMOD delivery ratios.**

Transport variable	Method of characterization	Effect on bacterial transport
Flow-path slope gradient	Power function of average slope gradient to stream	Momentum of overland flow
Flow-path slope shape	Averaged profile curvature to stream	Concave slope has greater deposition at its base than convex slope
Flow-path surface roughness	Hydraulic roughness coefficients based on cover type	Ground cover reduces momentum of flow and filters out soil and waste particles
Stream proximity	Negative exponential relationship with distance	Opportunities for deposition increase with distance
Soil moisture index at source	Topographically-based index = contributing area / (soil permeability × slope)	Represents the likelihood of overland flow and, therefore, bacterial transport

variable VAR from 0 to 100, and  $VAR_w$  = relative weight of variable VAR (normalized to sum to 1).

A more detailed description of SEDMOD is presented in Fraser et al. (1996).

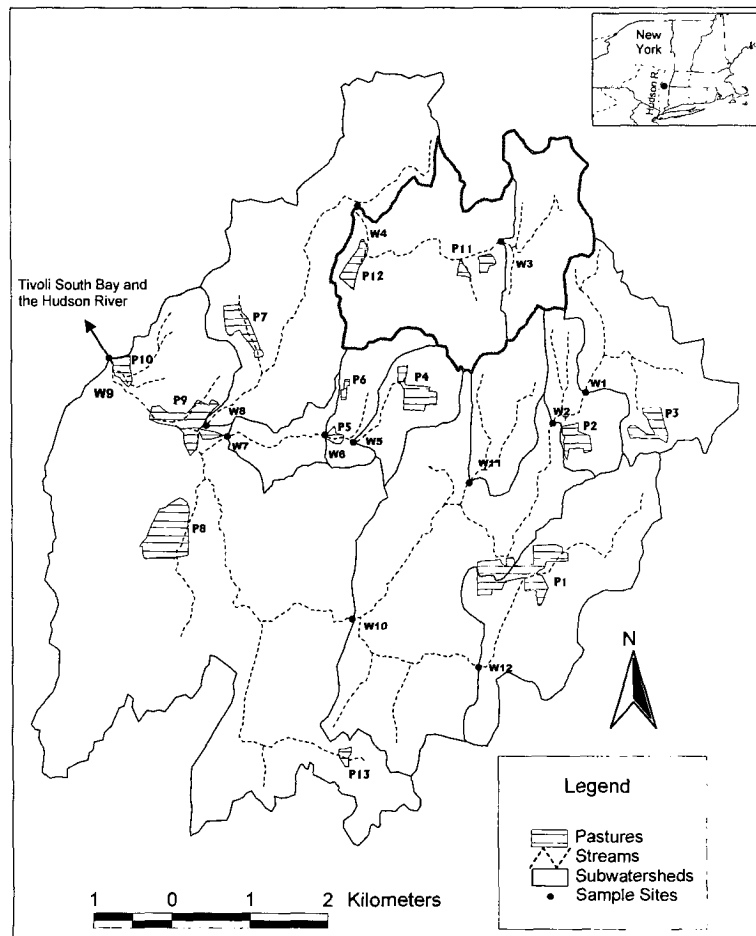
## METHODS

### Study Area

The research was conducted within the Saw Kill watershed, located on the east shore of the Hudson River in New York. The Saw Kill, located approximately 170 km north of New York City, is the principal tributary to Tivoli South Bay. The Tivoli Bays are one of four sites in the Hudson River National Estuarine Research Reserve, jointly administered for research and education by the New York State Department of Environmental Conservation and the National Oceanic and Atmospheric Administration.

The climate of the mid-Hudson River Valley is influenced by continental-polar and maritime air masses. Mean January air temperature is  $-4^{\circ}\text{C}$ ; mean July air temperature is  $23^{\circ}\text{C}$ . Annual precipitation ranges from 900 to 1100 mm and has a relatively uniform distribution through the year. The silty loam soils are derived from glacial till, outwash, and lake sediments. Undulating hills in the eastern portion join a broad outwash plain in the western portion of the study area. Mixed deciduous forest and agricultural land comprise most of the land cover.

Twelve subwatersheds were delineated within the easterly 50 km<sup>2</sup> portion of the Saw Kill watershed lying upstream of a wastewater treatment plant at the town of Red Hook (Fig. 1). The subwatersheds, ranging in size from 1.5 to 50 km<sup>2</sup>, encompass pasture and agricultural fields, mixed deciduous forest, and low density residential development. Livestock, including dairy cattle (*Bos taurus*), beef cattle, sheep (*Ovis aries*), and horses (*Equus caballus*) numbered from 0 to 1474



**Fig. 1.** Location map of the pastures (P) and subwatersheds (W) within the study area used to test SEDMOD. Subwatersheds W3 and W11 are controls. The flow sequences through the subwatersheds from the headwaters to the outlet are: W3→W4→W8→W9; W5→W6→W7→W9; W1→W2→W10→W9; W11→W10→W9; and W12→W10→W9. The shaded boundary for subwatershed W4 indicates the area shown in Fig. 7.

**Table 2. Summary data for pastures within study area (Pinney and Barten, 1997), Saw Kill Watershed, Hudson River Valley, New York.**

Pasture ID no.	Subwatershed ID no.	Pasture grazing area	Livestock type	Livestock density	Crops grown for livestock fodder
		ha		no. animals ha <sup>-1</sup>	
P1	W10 and W12	37	600 sheep	16	
P2	W2	9	65 sheep, 1 horse	7	Hay
P3	W1	11	25 beef cattle	2	Hay
P4	W5	13	90 dairy cattle	7	Hay, corn
P5	W6	3	20 sheep	7	
P6	W5	2	12 beef cattle	6	Hay
P7	W8	13	16 dairy cattle	1	
P8	W9	33	414 sheep	13	Hay
P9	W9	24	130 dairy cattle	5	Hay, corn
P10	W9	6	60 sheep	10	Hay
P11	W4	6	5 horses	1	Hay
P12	W4	9	33 beef cattle	6	Hay
P13	W9	3	3 beef cattle	1	Hay
<b>Totals</b>		<b>169</b>	<b>1474 animals</b>		

in the subwatersheds. Two of the subwatersheds selected (W3 and W11) contained no domestic animals. Table 2 presents the livestock data for each pasture and subwatershed.

### Water Quality Data Collection

Surface water samples (10 cm depth) were collected at the outlet of each subwatershed on eight dates at weekly intervals during the period 2 June to 15 July 1996. Streamflow conditions varied between sampling dates, yet in relative terms, revealed a consistent pattern across sampling sites. Since average FC discharge is used to test the model, eight sampling dates were sufficient to describe relative differences between subwatersheds. The samples were placed in 250 mL sterilized bottles, cooled on ice, and transported to the laboratory within 5 h of collection. A state certified laboratory analyzed the samples for fecal coliform concentration using the membrane filtration technique (American Public Health Association, 1992). Cultures were incubated with M-FC medium for 24 h at 44.5°C then counted. At the time samples were collected, we recorded water temperature using a mercury thermometer and turbidity using an optical turbidimeter. Stream discharge was calculated by multiplying velocity, measured using a Swofler digital flow meter, by stream cross-sectional area. Discharge was used to convert FC concentration (colonies 100 mL<sup>-1</sup>) to FC discharge (colonies passing the sampling site s<sup>-1</sup>).

### Geographical Information System Database Development

Spatial characteristics of the subwatersheds are stored as a series of raster GIS layers using ARC/INFO. We compiled a GIS database for the Saw Kill watershed by converting and updating soils and terrain layers constructed in an earlier study (Reichheld and Barten, 1992). In addition, a land cover layer was created by classifying a SPOT multispectral scene from 2 July 1992 using a hybrid supervised-unsupervised classification algorithm (Fraser et al., 1995). The resulting general classification has categories for water, coniferous forest, deciduous

forest, and agriculture and had an overall accuracy of 98% compared with 72 ground truth sites.

Animal numbers within the subwatersheds were established by interviewing local farmers in the summer of 1996 (Pinney and Barten, 1997). We also collected information about the use of pastures and site-specific, farm management practices. Livestock grazing areas were plotted on USGS 7.5 min quadrangles using GPS coordinates, 1:12 000 black and white aerial photographs, and the SPOT scene for reference, then digitized. An animal density layer was created by dividing the number of livestock by the area of each pasture and converting this to a raster layer. The GIS layers, described in Table 3, are registered to the Universal Transverse Mercator (UTM) coordinate system and stored at a 30 m cell resolution.

The livestock density GIS layer was used to derive a spatially distributed, FC loading function based on published values of expected daily FC output per animal (Reddy et al., 1981) multiplied by animal density. The FC loading function assumes that livestock waste is deposited uniformly over the pastures. Furthermore, it assumes that waste transported in overland and shallow subsurface flow is the predominant FC input to nearby streams. The influence of background contamination by wildlife [e.g., deer (*Odocoileus virginianus*) and waterfowl] and septic systems was assumed to be less significant within the study area. Units of (billion FC d<sup>-1</sup>) are used in the analysis.

### Application of Transport Model

SEDMOD was used to estimate what proportion of livestock waste (FC bacteria) is transported from each 30 by 30 m land cell to the stream channel. Since waste-associated bacteria are thought to be mainly transported while adsorbed to sediment and waste particles or suspended in overland flow (Reddy et al., 1981), we believe our sediment delivery model applies just as well to fecal pollution. Groundwater transport of bacteria is generally negligible due to efficient filtering and adsorption from soil particles (Reddy et al., 1981; Hunter et

**Table 3. Description of primary and derived GIS layers and data sources.**

Primary layers	Description	Derived layers	Data source
DEM	30 m digital elevation model	Slope, slope shape, flow distance, moisture index, flow-path directions	U.S. Geological Survey
Soils	Soil mapping units	Permeability, moisture index	Digitized USDA County Soil Survey
Stream	Stream network	Used to create DEM with corrected flow directions	Digitized (with field corrections) from USGS quadrangle
Land cover	General vegetation types	Manning's hydraulic roughness coefficients	Classification of SPOT multi-spectral scene
Livestock	Livestock grazing areas	Livestock density, FC loading function	Interviews, aerial photos, digitized from SPOT scene
Watersheds	Subwatershed boundaries		Delineated on 7.5 min USGS quads then digitized

al., 1992; Weiskel et al., 1996), except in the case of Karst topography (Howell et al., 1995) or where extensive macropores are present (Hunter et al., 1992).

Five of the model's six transport parameters were used to calculate delivery ratios: slope gradient, slope shape, proximity to stream, vegetation surface roughness, and a soil wetness index. Percentage of clay in the surface soil horizon was not used; it is included in the model for application to soil erosion-sediment transport (Fraser et al., 1996). The GIS layers and overlay steps performed for each subwatershed are shown in Fig. 2. Figure 3 shows six GIS layers used in the analysis, including the computed delivery ratios, for a sample area around pasture 12 (P12).

In addition to the spatially distributed delivery ratios, we used Eq. [3] to calculate sediment delivery ratios, as a lumped parameter, for each subwatershed (ASCE, 1975). The spatially lumped delivery ratios are based on the empirical observation that average watershed sediment delivery varies approximately with the  $-1/8$ th power of drainage area.

$$DR = C \times A^{-1/8} \quad [3]$$

where  $DR$  = average watershed delivery ratio (percentage);  $C = 39$  (calculated by assuming  $DR$  is 100% for a standard 22 m Universal Soil Loss Equation plot); and  $A$  = watershed area ( $\text{km}^2$ ).

To calculate what proportion of waste-associated FC are transported to the stream, SEDMOD delivery ratios were multiplied by the coliform loading function on a cell-by-cell basis, and the product was summed for all cells in each subwatershed. This resulted in a prediction of the number of FC bacteria transported daily to the stream sampling site in each

subwatershed. Using linear regression, predicted FC numbers were related to mean FC discharges and concentrations measured in the field. Log-transformed values were used in the regressions to normalize the variables and linearize the relationships.

## RESULTS AND DISCUSSION

### Fecal Coliform Discharge and Concentration

Average FC discharge ( $\text{colonies s}^{-1}$ ) and FC concentration ( $\text{colonies } 100 \text{ mL}^{-1}$ ) for the eight sampling dates are shown in Table 4. Since the data are log-normally distributed, geometric means are presented, calculated by taking the antilog of the arithmetic mean log concentration. Concentrations varied substantially between sampling dates at each site, as indicated by the high coefficients of variation ( $CV = \text{standard deviation mean}^{-1}$ ; Table 4). Mean FC concentration exceeded the U.S. Environmental Protection Agency standard for primary water contact of  $200 \text{ colonies } 100 \text{ mL}^{-1}$  in all but two subwatersheds (W10 and W11). Mean FC discharge ( $\text{colonies s}^{-1}$ ) at each site was calculated by multiplying concentration ( $\text{colonies } 100 \text{ mL}^{-1}$ ) by stream discharge ( $100 \text{ mL s}^{-1}$ ). Geometric mean discharge ranged from approximately  $44,000 \text{ colonies s}^{-1}$  for one of the control watersheds (W11) to  $16,000,000 \text{ colonies s}^{-1}$  for the outlet of all subwatersheds (W9).

Daily FC numbers transported to the stream, pre-

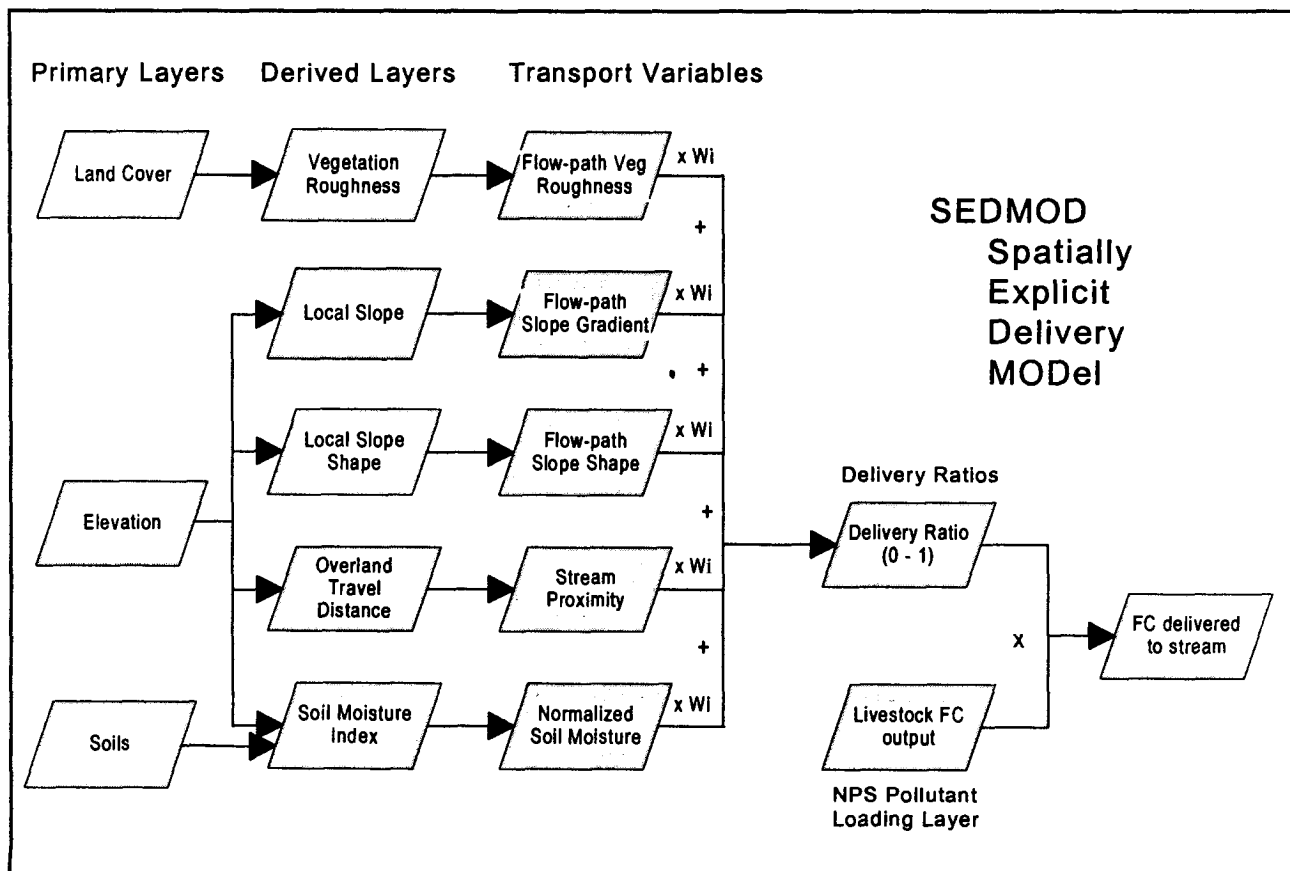
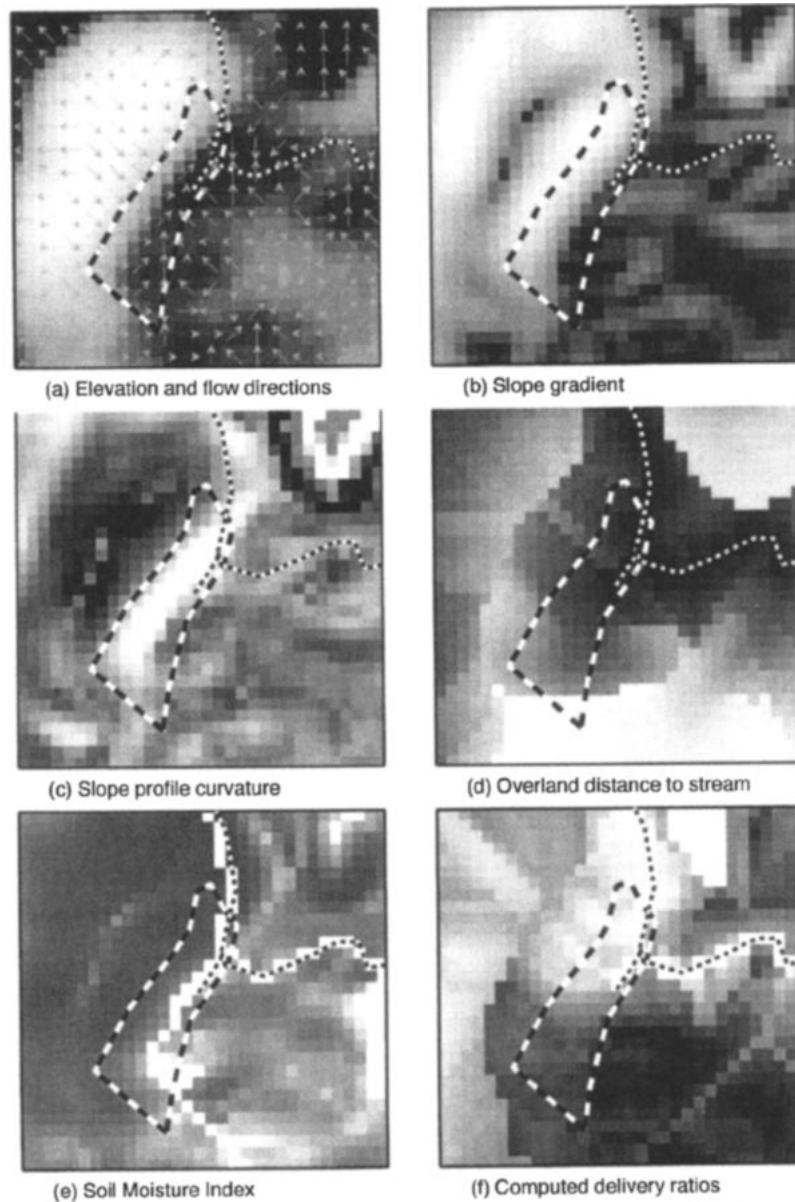


Fig. 2. Geographical Information System (GIS) overlay steps used to estimate fecal coliform delivery for each subwatershed.  $W_i$  represents the relative weighting applied to each variable (in this application all weights were equal).



**Fig. 3.** Various geographical information system (GIS) layers used in the analysis for the (960 by 930 m) area surrounding Pasture 12. The ranges of each layer have been normalized from 0 (black) to 100 (white). Image (a) shows elevation and arrows depicting flow-path directions; (b) slope gradient; (c) slope profile curvature (relatively concave to convex); (d) distance to stream; (e) soil moisture index; and (f) computed SEDMOD delivery ratios. The stream and pasture boundaries are superimposed on the GIS layers.

dicted by SEDMOD with all variables weighted equally, are shown in Table 4. To test the hypothesis that stream bacterial loading can be better predicted with a spatially explicit approach rather than spatially lumped delivery ratios, two regressions were performed. First, we found that FC delivery predicted by our model could explain 50% of the variation in measured FC discharge at the 12 watershed outlets (Fig. 4;  $r = 0.71$ ,  $P = 0.01$ ,  $n = 12$ ). A regression of FC delivery calculated using the lumped delivery ratios vs. FC discharge accounted for slightly less variation ( $r = 0.69$ ,  $P = 0.01$ ,  $n = 12$ ). The spatially distributed approach was more effective for quantifying relative livestock pollution potential within the subwatersheds.

Interestingly, a regression using published values for

total livestock FC output produced essentially the same correlation coefficient as did the regression using SEDMOD. There may be at least two reasons for this similarity. First, average subwatershed FC deliveries predicted by the model spanned a narrow range of 19 to 34% of livestock output (Table 4, Column 5). This small range is at least partly due to the similar juxtaposition of many pastures with respect to the stream channel (Fig. 1). If configurations were more varied, the model might perform better. Second, since the regression variables were log-transformed, relative differences between livestock FC output and FC delivery were reduced further. For example, after applying a log transformation, predicted transport of 1000 FC would be 2.3 assuming 19% delivery and 2.5 using 34% delivery. Nevertheless, in

**Table 4. Summary of results for each subwatershed.**

Subwatershed ID	Area km <sup>2</sup>	No. animals <sup>†</sup>	Livestock FC output	SEDMOD predicted FC delivery to stream	Predicted FC delivery using spatially lumped ratio	Measured mean FC discharge	Measured mean FC discharge	Mean FC conc.	CV for FC conc.	Mean water temp.	Mean turbidity (NTU)
				billion d <sup>-1</sup> ‡							
W1	3.0	25	135	28 (21%)	46 (34%)	38	437 000	626	2.61	15.8	2.55
W2	4.2	91	1 317	269 (20%)	425 (32%)	86	995 000	797	1.25	16.1	2.41
W3	1.9	0	0	0	0	13	144 000	594	2.19	17.6	3.07
W4	5.9	38	237	65 (27%)	73 (31%)	41	472 000	597	2.07	11.9	1.16
W5	1.2	90	486	120 (25%)	184 (38%)	21	241 000	389	1.55	14.8	1.91
W6	2.1	122	911	308 (34%)	320 (35%)	108	1 249 000	1657	1.81	14.9	3.52
W7	2.9	122	911	295 (32%)	307 (34%)	28	323 000	341	2.46	18.6	2.08
W8	12.1	54	323	98 (30%)	91 (28%)	187	2 161 000	450	0.96	13.8	2.45
W9	50.0	1 474	22 601	4 255 (19%)	5 334 (24%)	1 421	16 440 000	1118	1.19	15.5	4.86
W10	1.7	690	12 117	2 327 (19%)	3 284 (27%)	37	423 000	142	1.92	16.7	2.89
W11	1.5	0	0	0	0	4	43 800	167	1.12	17.5	2.17
W12	4.0	600	8 251	1 952 (24%)	2 682 (33%)	48	555 000	453	1.68	16.0	1.98
Mean	7.5	275	3 941	810 (21%)	1 062 (27%)	169	1 956 983	611	1.73	15.8	2.59

<sup>†</sup> See Table 2 for species and density data.

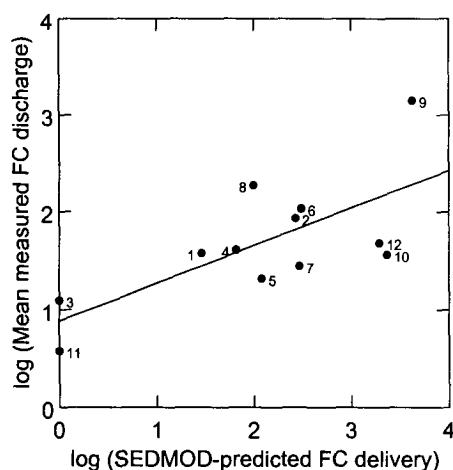
<sup>‡</sup> Percentage of estimated livestock fecal coliform (FC) output is shown in parentheses.

absolute terms, FC delivery predicted using the distributed approach was closer to measured FC discharge (except for W1) compared with predictions using the spatially lumped delivery ratios or total expected livestock FC output.

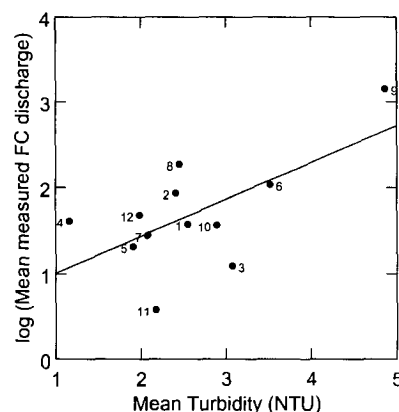
Regressions of both SEDMOD-predicted FC delivery and livestock FC output against mean, measured FC concentration are not statistically significant ( $P > 0.05$ ). Concentration is the most common unit in which biological water quality parameters are measured and reported. While bacterial concentration is important from a stream use perspective (e.g., swimming, shellfish harvesting), discharge is more appropriate for quantifying total loading and cumulative effects to drinking water reservoirs. In addition, measurements of FC discharge are better suited than concentration for testing our model, since it predicts total FC loading and transport to streams.

The numerical predictions from the GIS analysis appear to be useful for ranking bacterial pollution potential among several watersheds and/or livestock oper-

ations. Yet, since the technique considers only steady-state geographic factors, it is not able to estimate a FC mass balance reliably. Note that for 8 of the 10 treatment subwatersheds, predicted FC delivery exceeded measured FC discharge (Table 3). Environmental factors influencing bacterial mortality, including solar radiation, water temperature, pH, and microbial predation (Reddy et al., 1981), are not incorporated into the model. We also elected *not* to mathematically optimize or calibrate the model to reduce this discrepancy. We did, however, measure two water quality constituents (temperature and turbidity) that may be correlated with FC discharge or concentration. Temperature has been demonstrated to be inversely related to bacterial survival across a 4 to 35°C range (Howell et al., 1996). Over a more limited range (13.8–19.6°C) within the study area, mean temperature was correlated with neither FC discharge ( $P = 0.21$ ) nor FC concentration ( $P = 0.53$ ). Turbidity demonstrated a positive correlation with FC discharge (Fig. 5;  $r = 0.63$ ,  $P = 0.03$ ,  $n = 12$ ) and FC concentration ( $r = 0.58$ ,  $P = 0.05$ ,  $n = 12$ ). This relationship could result from several processes including: entrainment of bottom sediment and associated bacteria at higher flow velocities (Wilkinson et al., 1995); enhanced



**Fig. 4.** The relationship between the logarithm of mean measured fecal coliform (FC) discharge (billion colonies d<sup>-1</sup>) and the logarithm of FC delivery (billion colonies d<sup>-1</sup>) predicted using SEDMOD. Subwatershed identification numbers and the line of least squares fit also are shown.



**Fig. 5.** The relationship between the logarithm of mean measured fecal coliform (FC) discharge (billion colonies d<sup>-1</sup>) and mean water turbidity (nephelometric turbidity units). Subwatershed identification numbers and the line of least squares fit also are shown.



**Fig. 6. (a) Photograph of P4 (90 dairy cattle, within W5); (b) P12 (33 beef cattle, within W4); and (c) northerly portion of P4 where stream intersects. All were taken 8 May 1997.**



survival of bacteria adsorbed to suspended clay particles (Howell et al., 1996); and simultaneous transport of eroded soil and sediment-adsorbed bacteria to the stream.

We performed a forward, stepwise multiple regression to investigate possible combined effects among the stream and FC loading parameters. Of four candidate independent variables [temperature ( $^{\circ}\text{C}$ ), turbidity (NTU), SEDMOD-predicted FC delivery, and FC delivery using lumped delivery ratios (colonies  $\text{s}^{-1}$ )] three were selected in a regression against field measurements of FC discharge. Together, temperature, turbidity, and SEDMOD-predicted FC delivery could account for 80% of the variation in FC discharge between subwatersheds (adjusted  $r = 0.90$ ,  $P = 0.001$ ,  $n = 12$ ):

$$\log_{10}(\text{mean FC discharge}) = 2.5 + 0.25 \log_{10}(\text{SEDMOD-predicted loading}) + 0.40(\text{mean turbidity}) - 0.15(\text{mean temperature}) \quad [4]$$

### Sensitivity Analysis

In the above analysis, SEDMOD's transport variables were given equal weighting when combined to calculate the delivery ratios (Eq. [1]). A sensitivity analysis was conducted to assess how different combinations of weights might influence the performance of the model. Our sensitivity analysis examined the results of 30, separate weighting scenarios. The scenarios included every possible combination in which variables are given a weighting of 0 or 100% (i.e., considering each variable alone, every possible pair of variables, and each combination of three and four variables).

The results of the sensitivity tests indicate that, for the present application and study area, various weighting scenarios had little or no influence on model predictions. Regressions of SEDMOD-predicted FC delivery vs. measured FC discharge had coefficients of determination ( $r^2$ ) ranging from 0.48 to 0.51. The lowest correlation was obtained when only vegetation hydraulic roughness was considered; the highest correlation resulted from considering only flow-path slope gradient. As noted earlier, we believe the small range of correlations is related to the log-transformation applied to the regression variables.

### Example Application for Watershed Management

Subjective (aesthetic) appraisals may bias a watershed manager's perception of the relative impact of livestock operations and appropriate response. As an example, P4 (Fig. 6a) would *appear* to have a more substantial effect on water quality than the pastoral setting of P12 (Fig. 6b; Fig. 7, which shows orthographic view); however, both field data and model results demonstrate the opposite case. Notwithstanding obvious opportunities for improvements in management practices and on-site conditions, the location of P4 in a broad depression with inefficient connection to the Saw Kill limits its off-site

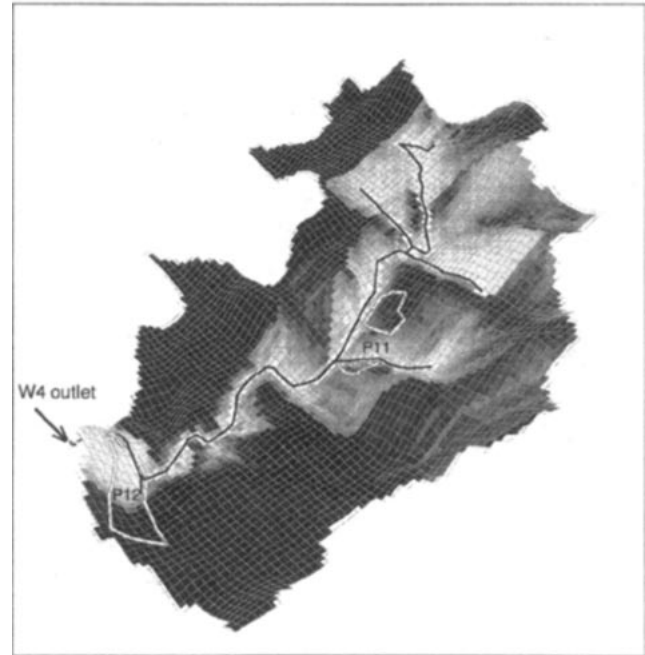


Fig. 7. Orthographic perspective of SEDMOD delivery ratios draped over elevation layer for W4. Pastures (P11 and P12) are shown using white lines and stream is shown using black line. The surface is viewed from a southwest azimuth and  $7^{\circ}$  vertical angle.

impact. Table 5 presents a ranking of pastures based on total and proportional FC delivery to the stream. The predicted FC delivery from P4 was 14% of total loading from 90 dairy cattle. By contrast, predicted FC delivery from P12 was 25% of total loading from 33 beef cattle at a lower stocking density. The northern portion of P12 slopes directly to the stream and allows direct access by the animals (Fig. 6c; Fig. 7). Together, field data and spatial modeling demonstrate that pasture and subwatershed characteristics have more influence on water quality than the appearance of a farm; looks can be deceiving.

Table 5. Ranking of pasture based on total predicted fecal coliform (FC) delivered to stream and proportion of expected livestock FC output delivered to stream.

Pasture ID no.	Subwatershed ID no.	Pasture absolute FC ranking <sup>†</sup>	Pasture proportional FC ranking <sup>‡</sup>	Mean percentage delivery <sup>§</sup>
P1	W10 and W12	1	7	19
P2	W2	6	1	12
P3	W1	10	8	18
P4	W5	7	10	14
P5	W6	5	1	41
P6	W5	12	13	9
P7	W8	9	4	31
P8	W9	2	9	16
P9	W9	4	5	29
P10	W9	3	3	31
P11	W4	12	12	10
P12	W4	6	6	25
P13	W9	2	2	33

<sup>†</sup> Pasture ranking based on the total predicted number of FC (billion/d) delivered to the stream.

<sup>‡</sup> Pasture ranking based on the proportion of livestock FC loading (billion/d) delivered to the stream (equivalent to average delivery ratio within pasture).

<sup>§</sup> Predicted FC delivered to stream/expected animal FC output.

### Model and Study Limitations

SEDMOD appears to be useful for ranking potential pollution impacts from livestock, but some limitations of the algorithm and in the methods used in applying the model should be noted:

1. As mentioned previously, the transport model assumes steady-state conditions and does not consider environmental factors, such as rainfall and temperature, that affect bacterial transport and survival. Therefore, the model cannot be used to reliably estimate a FC mass balance.
2. The five transport variables are linearly combined to estimate delivery potential. In the field, these variables can interact in complex ways; however, short of building and validating a physically based model with detailed, site-specific data these interactions are very difficult to quantify.
3. Stream processes that influence bacterial transport, including settling, mortality, and entrainment (Wilkinson et al., 1995), are not addressed. We plan to investigate the influence of these factors using a 2 km, longitudinal stream transect downstream of P12. If appropriate, a stream routing function will be incorporated into the model.
4. Possible background contamination by wildlife that frequent the stream and riparian zone (waterfowl, white-tailed deer, raccoons, opossums, and others) and septic effluent was not quantified. FC discharges observed at the control watersheds, especially W3, indicate that these sources are more important than we anticipated.
5. The spatially distributed, livestock loading layer assumed that all animal waste is deposited uniformly over the pastures. It is possible that livestock may spend a greater portion of the time near the stream (Gary et al., 1983); however, we observed relatively random distributions during numerous site visits. Furthermore, the survey by Pinney and Barten (1997) indicated that, at all farms, dry barn manure is collected and spread onto the pastures and supporting crops. In our study, we considered the pasture lands where livestock are confined and spend a large part of the day grazing. It was beyond the scope and central theme of the current study to quantify spatial and temporal distribution of manure spreading in other areas. In addition, we observed a maximum rate of FC loading in association with sheep herds, animals that are rarely confined to barns or sheds.

Despite these shortcomings and opportunities to expand our fieldwork and model development, our initial results extend the surprisingly small literature on the relation between livestock operations, landscape characteristics, and potential pathogen loading.

### SUMMARY AND CONCLUSIONS

This study illustrates the use of a GIS to design a water quality sampling strategy and subsequently support spatially explicit modeling. Once the model was

validated with limited field data, it could be used to predict the relative contribution of varied livestock operations in a heterogeneous landscape. Taking into account the recent admonitions of Lovejoy (1997), the model uses commonly available terrain, soils, and land cover–land use data and readily acquired data on livestock numbers. Therefore, watershed managers and regulators could apply it over relatively large management areas to prioritize sites for NPS pollution control.

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