

Development of a process-based model to predict pathogen budgets for the Sydney drinking water catchment

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ABSTRACT

In drinking water catchments, reduction of pathogen loads delivered to reservoirs is an important priority for the management of raw source water quality. To assist with the evaluation of management options, a process-based mathematical model (pathogen catchment budgets - PCB) is developed to predict *Cryptosporidium*, *Giardia* and *E. coli* loads generated within and exported from drinking water catchments. The model quantifies the key processes affecting the generation and transport of microorganisms from humans and animals using land use and flow data, and catchment specific information including point sources such as sewage treatment plants and on-site systems. The resultant pathogen catchment budgets (PCB) can be used to prioritize the implementation of control measures for the reduction of pathogen risks to drinking water. The model is applied in the Wingecarribee catchment and used to rank those sub-catchments that would contribute the highest pathogen loads in dry weather, and in intermediate and large wet weather events. A sensitivity analysis of the model identifies that pathogen excretion rates from animals and humans, and manure mobilization rates are significant factors determining the output of the model and thus warrant further investigation.

Key words | catchment, *Cryptosporidium*, model, pathogen, watershed

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NOMENCLATURE

$\delta_{j,i}$	fraction of microorganism (j) in material (i) (soil or water) surviving at the end of one day	$c_{j,l}$	post treatment concentration of microorganism (j) in effluent from STP in sub-catchment (l) (microorganisms.L ⁻¹)
λ	land use category	C_l	proportion of the population in sub-catchment (l) connected to an STP (%)
a	number of animals of species (s)	d_s	the amount of manure produced per day for animal species (s) (kg.day ⁻¹)
a_l	area of sub-catchment (l) (km ²)	D_s	probability of species (s) defecating directly into stream
$A_{s,l}$	number of animals of species (s) in sub-catchment (l)	e	event duration (days)
β_j	number of microorganisms (j) excreted per person (accounts for excretion rate from infected persons multiplied by the prevalence rate within the population) (microorganisms.d ⁻¹)	$E_{j,l}$	exported load of microorganism (j) for sub-catchment (l) (microorganisms.d ⁻¹)
b_l	buffer capacity for sewage treatment plant (STP) in sub-catchment (l) (ML)	f_l	relative mean annual rainfall for sub-catchment (l) (rainfall with respect to mean annual rainfall for total catchment area)

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F_j	probability of microorganism (j) (both bound and not bound to suspended sediment particles) being deposited or bound to bed sediment over a 1 km reach (0–1)	v	flow velocity ($\text{m}\cdot\text{s}^{-1}$)
G_l	identifies the downstream sub-catchment into which an upstream sub-catchment (l) drains	V	volume of effluent produced per person per day (160 L)
H_l	identifies the sub-catchment location of the STP to which an upstream sub-catchment (l) was connected	W	volume of effluent transported in a wet weather event overflow (ML)
$I_{j,k,l}$	input to stream of microorganism (j) from source (k) for sub-catchment (l) (microorganisms. d^{-1})	X_s	access to streams for species (s) (whether stream was fenced or animals are housed) (0–1)
L_j	land budget for microorganism (j) (microorganisms. d^{-1})		
m	catchment moisture deficit (mm)		
M_s	fraction of faeces on land that would be transported to stream in a large rainfall/runoff event for each animal species (s)		
n_l	proportion of population connected to a sewage treatment plant in sub-catchment (l) (%)		
O_d	proportion of on-site systems connected to streams in dry weather (%)		
O_w	proportion of on-site systems connected to streams in wet weather (%)		
$P_{j,s}$	the concentration of microorganism (j) in the manure of animal species (s) (microorganisms. kg^{-1})		
r	rainfall depth (mm)		
r_l	rainfall depth for sub-catchment (l) (mm)		
R_l^l	local reach length from node (l), assumed to be the square root of the sub-catchment area (km)		
R_l	reach length between node (l) and next node downstream (km)		
so	stream order		
S_l	population of sub-catchment (l)		
t	threshold of moisture deficit (m) for producing flow (mm)		
T_l	travel time from node (l) input to receiving node (days)		
U	effective rainfall (mm)		
U_l	effective rainfall for sub-catchment (l) (mm)		
U_o	scale factor for event size (event size for mobilization to equal $[1-\exp(-1)]$ of the maximum value) (mm)		

INTRODUCTION

The Sydney Catchment Authority (SCA) was formed in 1999 to manage the catchment providing the bulk water supply to Sydney, Australia, a city of four million people. Its formation was a direct result of the detection of *Cryptosporidium* and *Giardia* at levels of concern in Sydney's water supply in July – September 1998 (McClellan 1998). The incident was precipitated by a series of large rainfall-runoff events within the catchment following a prolonged period of drought. The pathogens *Cryptosporidium* and *Giardia* are parasitic protozoa that cause gastrointestinal illness. Illness is usually mild and of short duration, but infection in immunocompromised hosts can become persistent with cryptosporidiosis potentially causing mortality. Community disease surveillance data indicated that there was no detectable increase in the reported level of illness during the period of the incident, suggesting that the genotypes or viability status of both *Cryptosporidium* and *Giardia* present in the supply were non-infectious for humans. Neither the source nor the genotypes of the pathogens were identified. However, it was confirmed that poorer quality water arising from catchment runoff had short-circuited the main reservoir and reached the treatment plant in a much shorter time than previously predicted by the mean retention time for the storage (Hawkins *et al.* 2000).

The SCA developed a strategy to identify and prioritize the research and management needs within the catchment. An important component of this strategy was to reduce the risk of pathogen contamination by implementing a multi-barrier approach to the protection of raw drinking water quality. The development of a conceptual model and a review of existing information identified some significant knowledge gaps regarding the fate and origin of pathogens in drinking water catchments (Ferguson *et al.* 2003a).

Preliminary work focused on the identification of the key processes that govern pathogen fate and transport in surface waters (Ferguson *et al.* 2003b) enabling the SCA to prioritize its pathogen research program. The knowledge needs were identified as follows (i) characterisation of pathogen sources within the catchment, including domestic, native and feral animals, and septic seepage; (ii) quantifying the processes that determine pathogen fate and transport; (iii) development of tracing and tracking tools to identify the origin of faecal contamination; and (iv) development of a model for the estimation of catchment pathogen and faecal indicator loadings from various sources over time and space. The aim of this last objective was to integrate all of the research information into a single modelling tool that will assist catchment managers to prioritize pathogen control measures within catchments.

The development of a model requires detailed knowledge and understanding of the sources of microorganisms, the processes that influence their mobilization and transport, and the factors that cause their inactivation and/or loss. Numerous studies have quantified various individual parameters required for such a model (Crane & Moore 1986; Mawdsley *et al.* 1995; Olson *et al.* 1997; Freire-Santos *et al.* 2000; Atwill *et al.* 2002; Heitman *et al.* 2002; Characklis *et al.* 2005). However, relatively few attempts have been made to integrate this data into a microbial fate and transport model for catchments. Therefore, it is not surprising that a high priority for water utilities is to develop a methodology for quantifying pathogen hazards in catchments that enables them to spatially identify pathogen “hotspots” and target the implementation of effective barriers and control measures. One of the earliest models was developed by Jenkins *et al.* (1984) and was a process-based model to predict bacterial levels in upland catchments in the United Kingdom. It utilised a “mass balance” approach to describe bacterial sources and transport in catchments as a multiple storage and release system (Jenkins *et al.* 1984). Similarly, Walker *et al.* (1990) developed a probabilistic model that used Monte Carlo simulation to combine selected deterministic relationships with statistical information on rainfall and temperature. The model (COLI) predicted faecal coliform bacteria concentrations in surface runoff resulting from a storm presumed to occur immediately after animal manure was applied to

land surfaces. In a later study Fraser *et al.* (1998) used a geographical information system (GIS) based hydrologic model (SEDMOD) to estimate the load of faecal coliforms in streams for several sub-catchments of the Hudson River in the state of New York. However, all of these models were limited to predicting transport of faecal indicator bacteria.

This reliance on faecal indicator bacteria may lead to either an underestimation or overestimation of pathogen risks. The frequent lack of correlation between the presence of indicator bacteria and pathogens, and the differences in their fate and transport characteristics indicates that reliance on faecal indicators will result in improper assessment and management of pathogen risks. Walker & Stedinger (1999) developed a model that accounted for pathogen loading from diffuse pollution to predict *Cryptosporidium* concentrations in the raw water supplied to New York City from the Catskill-Delaware catchment. They based their model on a generalized watershed loading function (GWLf) model (Haith & Shoemaker 1987), utilising first-order decay functions to estimate oocyst decay in manure and in water. However, the model did not include estimates of surface washoff or the release of pathogens from the faecal matrix. A more recent study in the Netherlands modeled the discharge of *Cryptosporidium* and *Giardia* into surface water and the dispersion into rivers and streams using an emission model (PROMISE) and a dispersion model (WATNAT) (Medema & Schijven, 2001). The authors noted however that this model was unable to account for the impact of diffuse agricultural pollution and was thus primarily a point source and dispersion model. Several other faecal indicator models have also been developed recently (Tian *et al.* 2002; Crowther *et al.* 2003; Collins & Rutherford 2004) and at least one other pathogen model is currently under development (Dorner *et al.* 2004). None are yet commercially available.

This study describes the development of a process-based mathematical model or pathogen catchment budget (PCB) to quantify pathogen and faecal indicator loads within catchments. The model is based on a conceptual model that identified key processes for microbial sources and transport within drinking water catchments (Ferguson *et al.* 2003a). The model uses a mass-balance approach and will predict the total loads generated and the total loads exported from each sub-catchment for the pathogens *Cryptosporidium* and

Giardia and the faecal indicator bacteria *E. coli*. The model does not account for the potential infectivity of the pathogens and thus should be used as a “worst-case scenario” of the predicted pathogen loads.

MODEL DESCRIPTION

The model is based on the earlier conceptual model that represented the primary sources of microorganisms within catchments as animals (domestic and wildlife species) and human wastewater, including sewage treatment plants (STPs) and on-site septic systems (Ferguson *et al.* 2003a). The model was constructed to predict pathogen and faecal indicator outputs for the predominant conditions in the catchment, defined as “dry” (<5 mm in 24 h), “intermediate wet weather” (30 mm in 24 h) and “wet weather flood events” (100 mm in 24 h). It should be noted that these definitions are adjustable within the PCB model. The model consists of 5 components: a hydrologic module, a land budget module, an on-site systems module, a sewage treatment plant (STP) module and an in-stream transport module. The model is coded using the Interactive Component Modelling System (ICMS) software (Cuddy *et al.* 2002) freely available from the Commonwealth Scientific Information and Resource Organisation (CSIRO). The software can be requested from the website (www.clw.csiro.au/products/icms). Inputs to the model include GIS land use data and catchment specific information to predict pathogen loads, and parameters derived from a comprehensive review of the published literature (Ferguson *et al.* 2003b).

Hydrologic module

The hydrologic module uses the non-linear loss module of the IHACRES rainfall-runoff model described by Croke & Jakeman (2004). Briefly, this model assumes an initial catchment moisture deficit and using the distribution of surface rainfall (GIS layer), an amount of rainfall is converted into a depth of effective rainfall (rainfall that ends up as streamflow) for each sub-catchment. The effective rainfall is used to estimate the wet weather

mobilization of faeces that have been deposited on the land (as described in the land module).

The effective rainfall for sub-catchment l (U_l) is then given by:

$$\begin{aligned} U_l &= r_l + m(1 - e^{-r_l/t}) && \text{for } m < t \\ &= r_l + m - te^{-[r_l(m-t)]/t} && \text{for } t \leq m < t + r_l \\ &= 0 && \text{for } m > t + r_l \end{aligned} \quad (1)$$

where m is the initial catchment moisture deficit, t is the flow threshold and r_l is the event rainfall depth for sub-catchment (l), which is given by the mean event rainfall depth r , and the spatial variation in rainfall f_l (all measured in mm).

Assumptions

The catchment moisture deficit (m) describes the moisture deficit prior to a wet weather event (an input value).

All sub-catchments use the same initial moisture deficit and model parameters. However, the rainfall surface modifies the event rainfall for each sub-catchment by the factor (f_l).

The drainage threshold (t) is the moisture deficit (saturated water content – actual water content) of a sub-catchment before runoff and is generated for a wet weather flood event.

The depth of effective rainfall (U) depends only on the amount of rainfall and the soil moisture.

The antecedent dry period is adjustable (30 days used in this study).

The amount of rainfall is adjustable (30 mm and 100 mm for intermediate and large events respectively, in the current simulations).

Land module

The number of microorganisms leaving the sub-catchment is summed over all animal species present in the sub-catchment. Animal species are assigned as present or absent for a particular land use at a defined density. Animal density per sub-catchment is calculated from the GIS layers using the land use categories and animal density data shown in Table 1. The variables in Table 2 describe the buildup of

Table 1 | Animal Density by land use categories

s: Animal species	Type [†]	X _s : Access [‡]	D _s : Likelihood [§]	Density (km ⁻²)	λ: Land use category [§]
Cattle, grazing	0	0.1	0.01	500	2
Cattle, intensive	0	0.05	0.01	2000	5
Sheep	0	0.1	0.005	500	3
Pigs, domestic	0	0	0.025	5000	7
Pigs, feral	1	1	0.025	1	13
Kangaroos	1	1	0.001	200	9, 12, 13
Dogs, domestic	0	0.2	0.001	400	6, 10, 11
Dogs, feral	1	1	0.001	0.25	13
Cats, domestic	0	0.2	0.001	400	10, 11
Cats, feral	1	1	0.001	1	13
Horses	0	0.01	0.005	3	11
Goats	0	0.01	0.005	2	11
Deer	1	1	0.005	0.5	13
Other marsupials	1	1	0.01	20	1, 9, 12, 13
Rodents	1	1	0.005	50	4, 9, 10, 11, 12, 13
Rabbits	1	1	0.001	50	9, 13
Foxes	1	1	0.001	1	9, 13
Poultry	0	0	0.01	5000	8

[†] = wildlife species are represented as 1, domestic animals as 0.

[‡] = animal access to streams based on wildlife having full access and domestic livestock having more or less access dependent on farm management practices.

[§] = estimate of animal behaviour increasing or decreasing the likelihood of animal species entering and defecating in the stream assuming they have unlimited access.

[§] = land use categories for which this species is present (1 = water, 2 = improved pasture cattle, 3 = improved pasture sheep, 4 = commercial and industrial, 5 = intensive animals cattle, 6 = intensive animals dogs, 7 = intensive animals pigs, 8 = intensive animals poultry, 9 = intensive plants, 10 = urban residential, 11 = rural residential, 12 = forestry with native fauna, 13 = forestry with native and feral fauna).

microorganisms in faecal material deposited on the land surface. The rate of *Cryptosporidium*, *Giardia* and *E. coli* inactivation on land are shown in Table 3.

In dry weather, the only linkage between the land budget module and the in-stream transport module was through direct input into the stream i.e. animals defecating directly into the stream. This is calculated based on an estimate of the access to streams (X_s) (wild animals have unrestricted access, domesticated animals may be prevented

from accessing streams) and the estimated likelihood of a particular species defecating into the stream (D_s). The number of microorganisms entering the stream is given by:

$$I_{j,l,l} = \sum_{s=1}^a A_{s,l} P_{j,s} D_s d_s X_s \quad (2)$$

where $I_{j,l,l}$ is the input to stream of microorganism j from animal sources for sub-catchment l (microorganisms.d⁻¹),

Table 2 | Microbial concentrations in manure and manure characteristics

s: Animal species	d_s: Manure (kg.d⁻¹)	M_s: Fraction of manure mobilized	$P_{j,s}$: <i>Cryptosporidium</i> (log₁₀ oocysts.kg⁻¹.d⁻¹)	$P_{j,s}$: <i>Giardia</i> (log₁₀ cysts.kg⁻¹.d⁻¹)	$P_{j,s}$: <i>E. coli</i> (log₁₀ cfu.kg⁻¹.d⁻¹)
Cattle, grazing	27.25	0.02	3.71	5.23	9.32
Cattle, intensive	27.25	0.02	3.71	5.23	11.04
Sheep	1	0.03	4.91	5.64	10.40
Pigs, domestic	6.2	0.02	5.51	5.72	10.86
Pigs, feral	6.2	0.02	0	0	12.11
Kangaroos	0.2	0.03	6.48	0	11.20
Dogs, domestic	0.5	0.05	5.52	5.40	10.62
Dogs, feral	0.5	0.02	5.52	5.40	10.62
Cats, domestic	0.2	0.05	3.45	5.90	10.00
Cats, feral	0.2	0.02	3.45	5.90	9.84
Horses	23	0.005	2.99	3.38	8.68
Goats	1	0.03	0	0	11.90
Deer	1	0.03	3.30	0	9.34
Other marsupials	0.2	0.03	4.53	0	7.18
Rodents	0.01	0.05	5.45	0	7.46
Rabbits	0.2	0.03	3.78	0	8.70
Foxes	0.3	0.02	0	5.77	9.98
Poultry	0.12	0.005	6.32	2.88	11.40

Table 3 | Microorganism characteristics

j: Microorganism	$\delta_{j,i}$: Proportion of the initial population surviving.d^{-1s}		β_j: Microorganisms excreted. person⁻¹.d⁻¹ (log₁₀)	F_j: Fraction bound instream to sediment per km (%)
	Soil	Water	On-site effluent	Water
<i>Cryptosporidium</i>	0.95	0.98	3.9	5
<i>Giardia</i>	0.63	0.79	4.1	5
<i>E. coli</i>	0.71	0.43	10.0	50

^swhere $\delta = \exp(-k)$.

$A_{s,l}$ is the number of animals of species s in sub-catchment l , $P_{j,s}$ is the concentration (in microorganisms.kg⁻¹) of microorganism j in the faecal material of animal species s , D_s is the probability of species s defecating directly into a stream, d_s is the amount of manure produced (kg.day⁻¹.animal⁻¹) by animal species s , X_s is the access to streams for species s .

Assumptions – dry weather

Any faeces deposited directly into the stream become available for transport – i.e. the faeces disperse relatively quickly.

The concentrations of microorganisms in manure, and the manure production rates are based on total counts estimated from previous studies and fieldwork (Cox *et al.* 2005; Davies *et al.* 2005) and do not account for pathogen infectivity (Table 2).

Access to streams is assumed to be 100% for native and feral animals. Access of domestic animals is based on local knowledge and field observations, e.g. domestic pigs within the catchment must be housed in barns, thus access to streams is 0. However, cattle are free range, so access is set at 0.1 based on the observations of Gary *et al.* (1983).

The likelihood of direct faecal deposition to streams is estimated at 1% for cattle and 2.5% for wild pigs.

Material deposited to land is assumed to start to decay after one day and decay rates are based on microbial inactivation rates for soil (Table 3).

The model uses decay rates expressed as the proportion surviving per day ($\delta_{j,i}$) for microorganism j in material i . The instream decay module uses the decay rates for water ($\delta_{j,1}$), while the manure deposited to land decays according to the δ values for survival in soil ($\delta_{j,2}$). Inactivation rates can also be reported as the rate of inactivation per day (k values). Davies *et al.* (2005) reported inactivation rates for *Cryptosporidium* in soil ranged from 0.0135 to 0.0151 at 20°C while in manure they ranged from 0.0107 to 0.0234 (at 20°C). As these values were not substantially different and because manure deposited to land will often be trampled and mixed into the soil, we decided to use an averaged k value of 0.02 based on these and other studies. The k values for *E. coli* in water and soil are calculated using data from a number of previous studies (Crane *et al.* 1980; Crane & Moore 1986;

Sherer *et al.* 1992; Medema *et al.* 1997; Stoddard *et al.* 1998; Khatiwad & Polprasert 1999; Lau & Ingham 2001; Trevisan *et al.* 2002). The k values for *Giardia* in water and soil are also calculated using data from a previous study (Anderson *et al.* 1998).

The wet weather budget includes the daily build up of material on the land, and the likely fraction of material that will be mobilized to the stream. The build up of the store of microorganisms on the land depends on the length of the antecedent dry period, the assumed storage at the start of the antecedent dry period, and the decay rate for each microorganism in soil ($\delta_{j,2}$).

$$I_{j,1,l} = \sum_{s=1}^a M_s (1 - \exp(-[U_l/U_0]^2)) A_{s,l} P_{j,s} \frac{1 - M_s \delta_{j,2}}{1 - \delta_{j,2}} \quad (3)$$

where M_s is the fraction of faeces for animal species s on land that would be transported to stream in a large rainfall-runoff event, U_l is the effective rainfall (mm) generated in sub-catchment l , U_0 is the scale factor for event impact, $A_{s,l}$ are the number of animals in the sub-catchment, $P_{j,s}$ is the concentration of microorganisms in the manure of each animal species and $\delta_{j,2}$ is the rate of microbial survival (Table 3).

Assumptions – wet weather

The fraction of manure mobilized assigned to each species is a considered estimate based on the size, shape and consistency of faecal material (Table 2).

Mobilization varied with effective rainfall U_l as outlined in equation (3).

Microorganisms remaining after the preceding event correspond to a full mobilization ($U_l \geq U_0$) of a store initially at the equilibrium value.

U_0 is assumed to be 50 mm (adjustable within the model).

The maximum manure buildup is defined by the length of the antecedent dry period set at 30 days in this study (adjustable within the model).

Sewage treatment plant module

Selection of sub-catchments connected to STPs is based on proximity to a STP, and spatial connection of urban areas.

STP connectivity is calculated based on the proportion of the total population located in urban land use areas ($\lambda = 10$) compared to the total sub-catchment population. In urban areas 98% of the population is assumed to be connected to the STP. In dry and intermediate wet weather conditions the number of microorganisms entering the stream is given by:

$$I_{j,3,l} = n_l V c_{j,l} \quad (4)$$

where $I_{j,3,l}$ is the input to stream of microorganism j from the STP in sub-catchment l (microorganisms.d⁻¹), n_l is the population connected to a sewage treatment plant in sub-catchment l , V is the volume of water used per person per day (L) and $c_{j,l}$ is the post treatment concentration of microorganism j in the effluent from the STP in sub-catchment l (microorganisms.L⁻¹).

Assumptions - dry weather

The dry weather budget is simply the product of the population connected to the STP, the volume of water used per person per day and the post treatment microorganism concentration measured in the water released by the STP.

The volume of effluent produced per person per day is adjustable (160 L in this study).

In wet weather the volume of effluent that may be released during an event can be allocated based on the buffer capacity for each STP and available data on overflow volumes. The percent prevalence of microbial infection in the population is estimated at 1% for both *Giardia* and *Cryptosporidium*, which is within the ranges used by Anderson *et al.* (1998) and 100% for *E. coli*. The number of microorganisms entering the stream is given by:

$$I_{j,3,l} = (n_l \beta_j W e) / (W + b_l) \quad (5)$$

where β_j is the number of microorganisms j excreted per person per day (microorganisms.d⁻¹), W is the volume of effluent transported in a wet weather event (ML), e is the event duration (days) and b_l is the buffer capacity for the STP in sub-catchment l (ML).

Assumptions - wet weather

The wet weather budget is the load of microorganisms entering the STP (population connected · microorganisms.person⁻¹.day⁻¹) buffered by the available storage at the STP.

Any water entering in excess of the buffer is assumed to leave the STP without treatment.

On-site systems module

The input of microorganisms to the stream from on-site systems is assumed to depend on the population using on-site systems; an estimate of the number of microorganisms excreted per person per day; and the fraction of on-site systems connected to the stream. The only difference between wet and dry conditions for the on-site systems module is the level of connectivity to streams. Inputs from on-site systems are given by:

$$I_{j,2,l} = (S_l \beta_j (1 - C_l)) (O_d + (O_w - O_d) [1 - \exp\{- (U_l / U_0)^2\}]) \quad (6)$$

where $I_{j,2,l}$ is the input to stream of microorganism j from on-site systems in sub-catchment l (microorganisms.d⁻¹), S_l is the population of sub-catchment l , C_l is the proportion of the population in sub-catchment l connected to an STP, and O_d and O_w are the proportion of on-site systems connected to streams in dry and wet weather, respectively.

Assumptions

10% of on-site systems are connected to the stream under dry conditions (O_d). In wet conditions (O_w) this increases to 20%.

There is no decay of microorganisms between on-site systems and the stream network.

The variation of the fraction of on-site systems connected to streams with size of event is described by equation (6).

In-stream module

Faecal material, mobilized to the stream in wet weather or deposited in the stream, decays at the inactivation rate for each microorganism in water. Decay is calculated based on

the estimated travel time to reach the sub-catchment outlet. Until recently, little data was available regarding the rate of attachment of microorganisms to sediment and their subsequent rate of deposition in water courses. However, Characklis *et al.* (2005) determined that during wet weather events 30–55% of *E. coli* were likely to be attached to particles. Recent studies by Davies *et al.* (2005), Kaucner *et al.* (2005) and Brookes *et al.* (2006) suggest that *Cryptosporidium* and *Giardia* (oo)cysts remain largely unattached to particles and may remain suspended in the water column for considerable lengths of time. The in-stream export from the sub-catchments during dry weather is given by:

$$E_{j,l} = \left[\sum_{k=1}^2 I_{j,k,l} \delta_{j,1}^{(R_l^k/v_l)} (1 - F_j)^{R_l^k} + I_{j,3,l} \right] + \left[\sum_{i=1}^z E_{j,i} \delta_{j,1}^{(R_i/v_i)} (1 - F_j)^{R_i} \right] \quad (7)$$

where $E_{j,l}$ is the exported load of microorganism j from sub-catchment l (microorganisms.d⁻¹), R_l^k is the local reach length for node l (km – assumed to be $\sqrt{a_l}$ where a_l is the sub-catchment area in km²), v_l is the flow velocity over the reach (m.s⁻¹), F_j is the probability of microorganism j being deposited or bound to bed sediment over a 1 km reach and R_i is the reach length between node l and the next node downstream (km).

Assumptions – dry weather

During dry weather, all microorganisms that are bound to sediment settle out, and there is no resuspension of settled material in either dry or wet weather.

50% of *E. coli* are assumed to be bound to sediment and thus lost through settling. *Cryptosporidium* and *Giardia* primarily remain in the water column with only 5% becoming bound and lost through settling. The stream reach (km) was divided by the flow velocity to estimate the loss due to settling per km for each sub-catchment.

Inactivation is calculated using the microorganism-specific decay rate for water (Table 3) and an estimated travel time. The decay rate is expressed as a percentage of the initial population surviving per day ($\delta_{j,i}$).

There is no decay of microorganisms entering the river network from the STPs before reaching the outlet of each sub-catchment due to the STP being located near the sub-catchment outlet.

During dry weather (low flow conditions), the flow velocity is assumed to be 0.1 m.s⁻¹.

In wet weather the in-stream export from the sub-catchments is given by:

$$E_{j,l} = \left[\sum_{k=1}^2 I_{k,l,j} \delta_{j,1}^{(R_l^k/v_l)} + I_{3,l,j} \right] + \left[\sum_{i=1}^z E_{j,i} \delta_{j,1}^{(R_i/v_i)} \right] \quad (8)$$

Assumptions – wet weather

During intermediate wet weather events flow velocity is assumed to be 1 m.s⁻¹ and for the larger wet weather event, flow velocity is assumed to be 3 m.s⁻¹. All flow velocity values are adjustable for each sub-catchment.

CASE STUDY – WINGECARRIBEE CATCHMENT

The model was developed and tested using data for the Wingecarribee catchment located approximately 200 km south west of Sydney in the Sydney drinking water catchment. Wingecarribee is a mixed land use catchment comprised of unsewered and sewerred urban areas, rural residential, improved pastures, horticulture, native vegetation and grazing areas as well as a protected upland swamp. The catchment was divided into 52 sub-catchments (Figure 1) based on the digital elevation map and spot sampling of the water quality in the catchment carried out in 2002.

For each sub-catchment, data on the population, fraction of people using on-site systems and number of animals of each species present were extracted from the land use data. The human population densities were assumed to be 2 400 people.km⁻² for urban residential ($\lambda = 10$), 100 people.km⁻² for rural residential ($\lambda = 11$), and 10 people.km⁻² for agricultural land uses (sum of $\lambda = 2, 3$, and 5 to 9). Land uses allocated zero population included water ($\lambda = 1$), commercial and industrial ($\lambda = 4$) and forestry ($\lambda = 12$ and 13). Comparison with population statistics from Australian Bureau of Statistics (ABS) suggested these were acceptable estimates of densities for

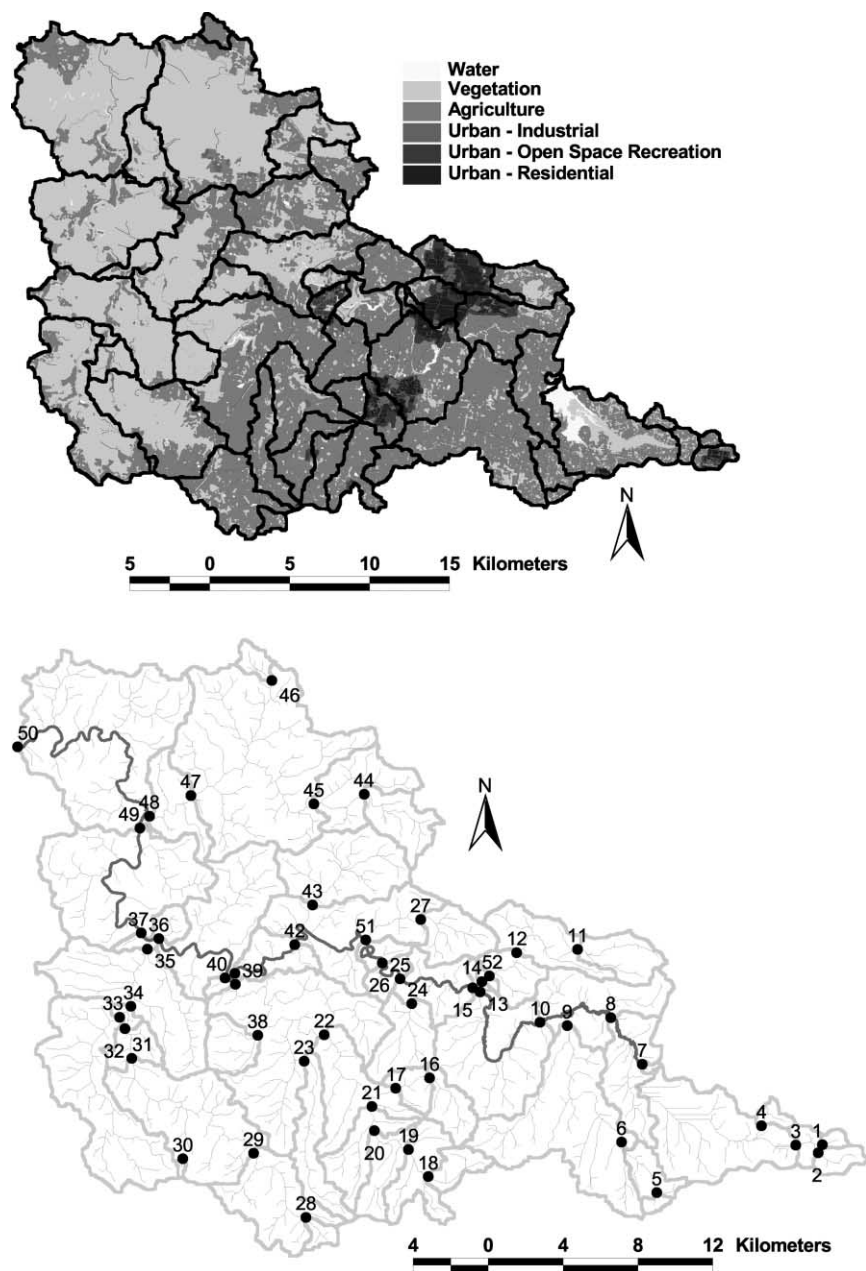


Figure 1 | Map of the Wingecarribee catchment showing the 52 sub-catchments used in this study. The top panel shows the distribution of land use across the catchment, while the bottom panel shows the stream network and the sample site for each sub-catchment. Site 1 is the most upstream, site 50 is located on the Wingecarribee River at the downstream catchment outlet.

the Wingecarribee catchment (www.abs.gov.au). The specific sub-catchment characteristics of the Wingecarribee catchment required to run the model are summarised in [Table 4](#). Many of these variables were derived from the GIS land use layer (such as the proportion of each land use category present in a specific sub-catchment and sub-

catchment area). However, other variables such as the location of the STP that an upstream sub-catchment is connected to (H_i) are identified and input manually. All but one of the sub-catchments containing urban land use were located upstream or near to an STP and effluent data for these STPs is shown in [Table 5](#).

Table 4 | Sub-catchment data file for the Wingecarribee catchment

<i>I</i>	<i>so</i>	<i>a_i</i>	<i>R_i</i>	<i>G_i</i>	<i>n_i</i>	<i>H_i</i>	<i>f_i</i>	λ: Land use category ⁸							
								1	2	3	4	9	10	11	13
1	1	1.13	1.71	3	0	0	1.75	0.0044	0.5279	0.3048	0.0482	0	0	0	0.1146
2	1	3.25	1.80	3	0	0	1.75	0.0028	0.2732	0.0829	0.255	0	0.264	0.0567	0.0653
3	2	2.63	10.24	7	0	0	1.75	0.003	0.5213	0.2011	0.0292	0	0	0	0.2454
4	1	1.80	8.74	7	0	0	1.59	0	0.391	0.3113	0.0356	0	0	0	0.2622
5	1	1.11	3.67	6	0	0	1.42	0.0092	0.4886	0.2619	0.0593	0	0	0	0.181
6	2	5.31	9.77	9	0	0	1.40	0.0043	0.4969	0.3276	0.0375	0	0	0	0.1338
7	3	30.59	3.66	8	0	0	1.47	0.1486	0.3286	0.1949	0.0329	0	0.008	0.0033	0.2836
8	4	14.77	5.12	10	0	0	1.29	0.0244	0.6245	0.2212	0.0417	0	0	0	0.0882
9	3	41.26	2.06	10	0	0	1.22	0.0023	0.7174	0.1448	0.0267	0	0	0	0.1088
10	5	18.75	8.78	13	0.98	52	1.16	0.0116	0.5406	0.1199	0.0594	0	0.0972	0.091	0.0803
11	1	8.53	5.14	12	0	0	1.20	0.0055	0.491	0.1362	0.0195	0	0	0.0001	0.3477
12	2	12.34	2.44	52	0.98	52	1.05	0.0005	0.1362	0.0381	0.1336	0	0.317	0.3147	0.0599
13	6	30.40	0.49	15	0.98	17	1.09	0.018	0.5621	0.044	0.0973	0.0035	0.1213	0.0738	0.0801
14	4	0.83	0.79	15	0.98	52	1.04	0	0.3215	0.1117	0.0657	0	0.2673	0.0511	0.1827
15	7	1.03	4.91	25	0.98	52	1.04	0.0064	0.5602	0.0404	0.1227	0	0.0362	0.0644	0.1697
16	1	6.67	2.23	17	0.98	17	1.14	0.0011	0.2414	0.0522	0.261	0	0.2699	0.166	0.0085
17	2	4.28	7.11	22	0.98	17	1.11	0.0167	0.7495	0.1368	0.0479	0	0.0065	0.013	0.0298
18	1	4.65	2.08	19	0	0	1.21	0.0005	0.6652	0.2917	0.0184	0	0	0	0.0241
19	2	10.73	2.74	20	0	0	1.18	0.0052	0.6655	0.2101	0.0451	0	0	0.015	0.0592
20	3	8.08	1.52	21	0	0	1.17	0.0026	0.6918	0.1647	0.0406	0	0.0005	0.02	0.0799
21	4	9.88	5.99	22	0	0	1.12	0.0006	0.7607	0.099	0.0615	0	0	0.0248	0.0535
22	5	16.40	10.10	39	0	0	1.04	0.0024	0.7108	0.0816	0.0382	0	0	0	0.1671
23	1	11.63	10.13	39	0	0	1.09	0.0011	0.7706	0.0849	0.02	0	0.0065	0.003	0.1138
24	1	10.96	1.95	25	0.98	26	1.02	0.0064	0.7275	0.0941	0.102	0	0.0114	0.0031	0.0555
25	8	10.24	2.47	26	0	0	1.01	0.0366	0.5919	0.0608	0.0254	0	0	6E-05	0.2852
26	9	3.50	3.42	51	0.98	26	0.99	0.0014	0.0855	0.0078	0.3793	0	0.0657	0.3278	0.1325

Table 4 | (continued)

<i>I</i>	<i>s₀</i>	<i>a_I</i>	<i>R_I</i>	<i>G_I</i>	<i>n_I</i>	<i>H_I</i>	<i>f_I</i>	λ: Land use category [§]							
								1	2	3	4	9	10	11	13
27	1	9.28	10.90	42	0	0	1.00	0.0018	0.8013	0.0892	0.0284	0	0	0	0.0792
28	1	2.01	6.10	29	0	0	1.16	0.0109	0.7699	0.0961	0.0346	0	0	0	0.0884
29	2	18.65	11.23	31	0	0	1.10	0.0041	0.6392	0.1861	0.032	0	0	0	0.1385
30	1	0.37	8.04	31	0	0	0.93	0.0197	0.7343	0.1734	0.0602	0	0	0	0.0123
31	3	32.30	1.84	32	0	0	0.96	0.0049	0.3253	0.0443	0.0203	0	0	0	0.6051
32	4	5.06	1.41	34	0	0	0.87	0.0003	0.0662	0	0.0248	0	0	0	0.9088
33	1	35.35	0.93	34	0	0	0.87	0.0018	0.2392	0.0068	0.0273	0	0	0	0.7248
34	5	1.38	4.10	35	0	0	0.87	0	0.1182	0.0018	0.0296	0	0	0	0.8504
35	6	30.07	1.16	37	0	0	0.87	0.0017	0.123	0.0021	0.0341	0	0	0	0.8391
36	14	28.20	1.24	37	0	0	0.87	0.0013	0.2777	0.0352	0.0166	0	0	0	0.6692
37	15	4.52	10.44	49	0	0	0.86	0.0003	0.1028	0	0.0349	0	0	0	0.862
38	1	6.95	6.05	39	0	0	0.90	0	0.0341	0	0.0672	0	0	0	0.8987
39	6	44.38	0.81	40	0	0	0.97	0.0102	0.5527	0.0636	0.0466	0	0.0002	0	0.3266
40	13	1.33	7.23	36	0	0	0.90	0	0	0	0.0114	0	0	0	0.9886
41	12	7.85	0.88	40	0	0	0.92	0.0054	0.2788	0.0358	0.0175	0	0	0	0.6625
42	11	26.40	5.34	41	0	0	0.96	0.0042	0.4133	0.0143	0.0366	0	0	2E-05	0.5315
43	1	22.03	3.55	42	0	0	0.97	0.0072	0.5793	0.0569	0.0224	0	0	0	0.3342
44	1	9.36	3.26	45	0	0	1.02	0.0091	0.5791	0.0543	0.0409	0	0	0	0.3167
45	2	13.76	10.16	47	0	0	1.01	0.0047	0.3389	0.002	0.0407	0	0	0	0.6137
46	1	2.55	9.18	47	0	0	0.95	0.0008	0.9371	0.0109	0.0189	0	0	0	0.0323
47	3	67.41	3.63	48	0	0	0.94	0.0007	0.2154	0.0129	0.0268	0	0	0	0.7442
48	4	10.62	17.35	50	0	0	0.84	0.0035	0.1353	0.0058	0.0318	0	0	0	0.8236
49	16	42.08	18.01	50	0	0	0.85	0.0022	0.1333	0.0017	0.0189	0	0	0	0.8438
50	17	59.52	0.00		0	0	0.82	0.0032	0.1779	0.0009	0.0208	0	0	0	0.7972
51	10	3.18	7.31	42	0.98	26	0.99	0.025	0.3541	0.004	0.0835	0	0.0161	0.0152	0.5022
52	3	6.90	0.57	14	0.98	52	1.05	0.0018	0.1407	0.0298	0.1276	0	0.48	0.1444	0.0756

[§]Land use categories not included in the table were not present in the Wingecarribee catchment.

Table 5 | STP and effluent quality data for the Wingecarribee catchment

STP (l)	<i>C_{J,K}</i> : Microorganism concentration (L ⁻¹)			<i>b_f</i> : Buffer capacity [§] (ML)	<i>W</i> : Overflow volume [§] (ML)
	<i>Cryptosporidium</i>	<i>Giardia</i>	<i>E. coli</i>		
Bowral (52)	9.6	23	56 000	0	24.5
Berrima (26)	0.03	1.2	28 000	11.1	0.5
Moss Vale (17)	0.66	3.9	87	19.7	1.6

[§]from (Paterson & Krogh, 2003).

Model outputs

The model predicts for each microorganism a local generated source budget (input) and the routed downstream (export) budget. Figures 2 to 4 show the input and export budgets for

Cryptosporidium, *Giardia* and *E. coli*, respectively. The predicted *Cryptosporidium* and *Giardia* input budgets both show dry weather peaks at sub-catchments 52, 17 (Bowral and Moss Vale STPs) and 2 (Robertson township) (Table 6). Dry weather input load predictions in the

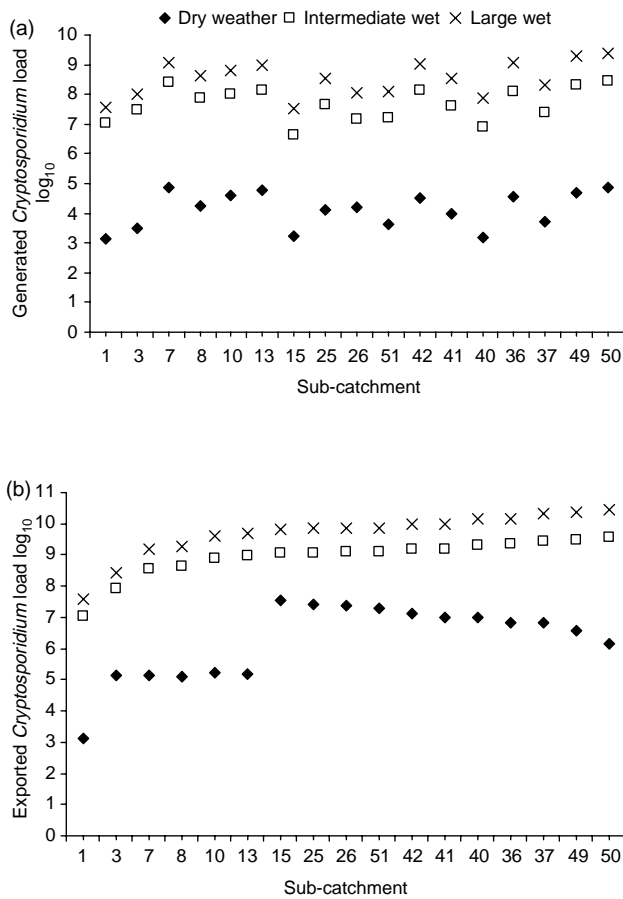


Figure 2 | *Cryptosporidium* loads, log₁₀ oocysts a) generated in each sub-catchment (input) per day and, b) routed downstream from each sub-catchment (export) per day. Only sub-catchments located on the Wingecarribee River are shown in sequential downstream order.

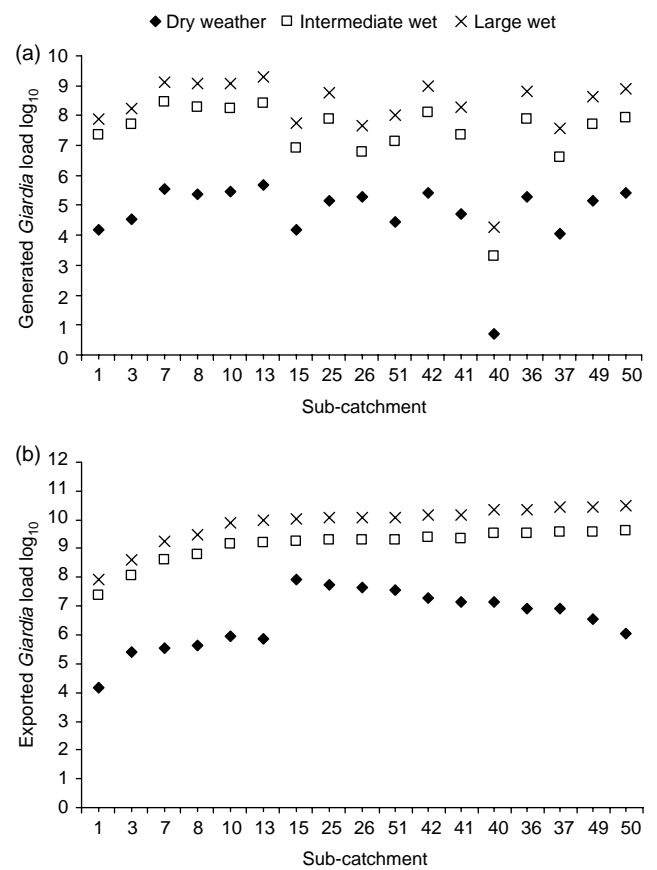


Figure 3 | *Giardia* loads, log₁₀ cysts a) generated in each sub-catchment (input) per day and, b) routed downstream from each sub-catchment (export) per day. Only sub-catchments located on the Wingecarribee River are shown in sequential downstream order.

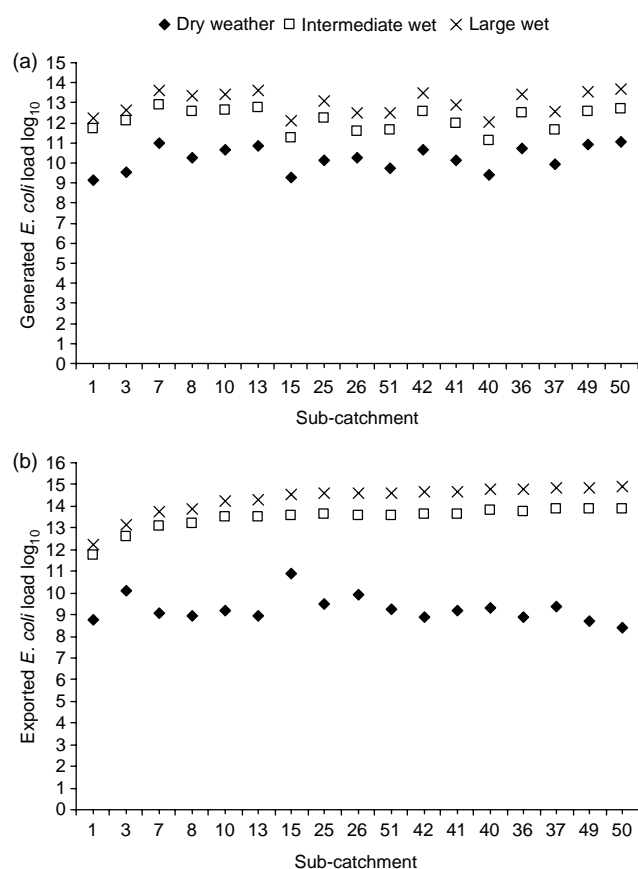


Figure 4 | *E. coli* loads, log₁₀ mpn a) generated in each sub-catchment (input) per day and, b) routed downstream from each sub-catchment (export) per day. Only sub-catchments located on the Wingecarribee River are shown in sequential downstream order.

remaining sub-catchments vary between 3 to 5 log₁₀.d⁻¹ for *Cryptosporidium* and 3 to 6 log₁₀.d⁻¹ for *Giardia*. The exceptions are the low predicted input loads of 2.7 log₁₀.d⁻¹ for *Cryptosporidium* in sub-catchment 30 and 0.69 log₁₀.d⁻¹ for *Giardia* in sub-catchment 40. Sub-catchment 30 is very small (only 0.3 km² and 73% improved pasture) while sub-catchment 40 is only 1.3 km² and is 99% native forest. Predicted wet weather inputs of *Cryptosporidium* are generally 3 to 4 log₁₀.d⁻¹ higher than the dry weather inputs whereas the wet weather input loads for *Giardia* are 2 to 3 log₁₀.d⁻¹ higher than the dry weather input loads. The *E. coli* dry weather input loads are several orders of magnitude higher than either *Cryptosporidium* or *Giardia*, ranging from 9 to 11 log₁₀.d⁻¹ with small peaks above 11 log₁₀.d⁻¹ for sub-catchments 2 and 52. The lowest predicted input load is again from sub-catchment 30, with low loads

also predicted for small sub-catchments where the predominant land use was either native forest or improved pasture, for example, 1, 5, 14, 37 and 51. In most sub-catchments wet weather events increased the predicted wet weather input loads by 2–3 log₁₀.d⁻¹ compared to dry weather.

The predicted export loads of *Cryptosporidium*, *Giardia* and *E. coli* highlight the cumulative effect of routing contaminants downstream, particularly during wet weather events when the transport time (3–30 minutes per sub-catchment) is too short for microbial inactivation or in-stream settling. However, in dry weather the rapid inactivation rate reduces the cumulative effect for *E. coli*. The predicted total export of *E. coli* from most sub-catchments were reasonably constant at approximately 9 log₁₀ per day in dry weather with the exception of those sub-catchments impacted by on-site sewage discharges (2, 3) or STP effluent (52, 14, 15, 26). During large wet weather events the predicted daily load of *Cryptosporidium* and *Giardia* exported from the Wingecarribee catchment (sub-catchment 50) is greater than 10 log₁₀ while the predicted *E. coli* load is almost 15 log₁₀.

Table 6 shows the ten sub-catchments generating the highest input loads of pathogens and *E. coli* in the Wingecarribee catchment. The sub-catchments are ranked according to the total load exported (raw ranking) and by the total load per unit area (area ranking). The dry weather rankings are dominated by sub-catchments receiving inputs from STPs (52, 17 and 26) and on-site sewage systems (2). The wet weather rankings are more varied than the dry weather rankings. The highest loads by unit area for intermediate wet weather events are predicted for small sub-catchments in the upper part of the Wingecarribee catchment. Sub-catchment 1 located upstream of Robertson township is the highest generator of *Giardia* per unit area for intermediate wet weather events. It consists of improved pasture with diffuse impacts from cattle and sheep. Bowral STP is still ranked third highest exporter of *Cryptosporidium* and *Giardia* per unit area for intermediate wet weather events, but in larger events STP overflow make this sub-catchment the highest ranking for both *Cryptosporidium* and *E. coli* loads. In the larger wet weather events *Giardia* and *Cryptosporidium* loads ranked by unit area are dominated by inputs from sub-catchments with agricultural land uses (46) and native forest land use (40, 47).

Table 6 | Ranking of sub-catchments generating the highest input loads of pathogens and faecal indicators in the Wingecarribee catchment (by total raw load and by sub-catchment area)

Raw ranking	Sub-catchment number (l)								
	<i>Cryptosporidium</i>			<i>Giardia</i>			<i>E. coli</i>		
	Dry	Int	Wet	Dry	Int	Wet	Dry	Int	Wet
1	52	47	47	52	9	9	52	9	52
2	17	50	50	17	7	39	2	7	47
3	2	7	49	9	39	13	47	47	9
4	47	49	33	39	13	7	50	39	39
5	7	9	39	13	8	47	7	13	50
6	50	39	31	47	29	29	49	50	13
7	13	31	35	7	10	43	13	31	7
8	39	33	9	43	22	22	39	10	49
9	9	35	36	29	47	10	33	8	31
10	49	13	7	2	43	8	12	49	33
Area ranking [§]									
1	52	3	52	52	1	28	2	2	52
2	17	2	40	17	3	46	52	3	2
3	2	52	38	2	52	9	26	1	17
4	26	4	32	26	8	21	12	4	3
5	12	1	47	46	9	17	16	6	1
6	16	7	37	23	4	23	7	5	9
7	23	5	34	27	17	18	23	7	18
8	7	6	45	21	6	20	14	8	28
9	14	11	35	28	5	27	10	9	8
10	10	40	49	30	28	19	13	18	20

Int = intermediate wet weather event (30 mm).

Wet = large wet weather event (100 mm).

[§] = Ranking based on total load divided by sub-catchment area in km².

Both the local source (input budgets) and the exported budgets can be reproduced as spatial (raster) graphs to highlight the areas generating and exporting the greatest loads of pathogens and *E. coli*. For example, Figure 5 shows

the predicted total load of *E. coli* exported from the Wingecarribee in dry, intermediate, and large wet weather events. In dry weather the water quality impacts are localised due to bacterial inactivation and settling.

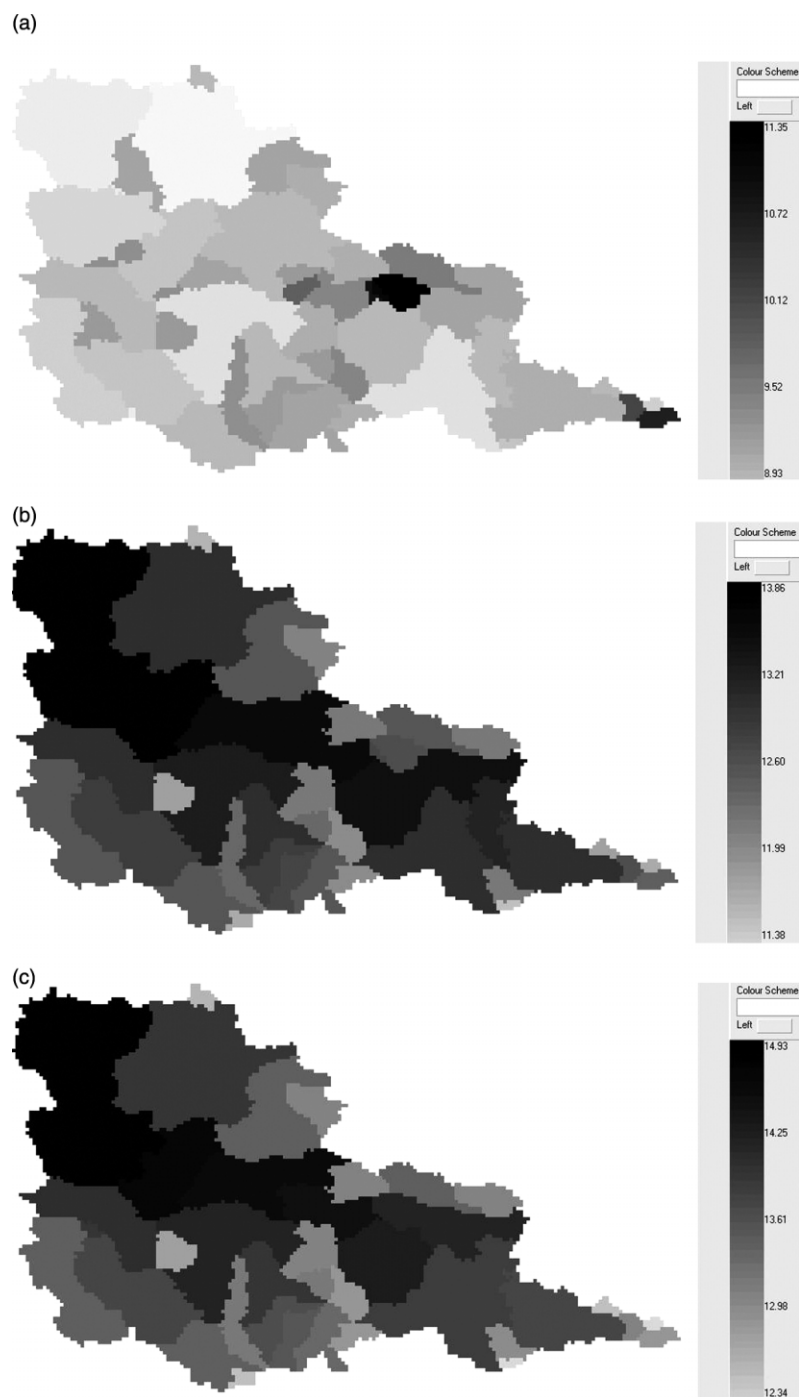


Figure 5 | *E. coli* loads exported from each sub-catchment in a) dry weather, b) an intermediate wet weather event and c) a large wet weather event (scale is shown as the daily load of *E. coli* expressed as \log_{10} mpn where mpn = most probable number).

However, in wet weather there is a cumulative effect in downstream sub-catchments as there is negligible inactivation or settling of the microorganisms during transit in these large events.

Sensitivity analysis

Analysis of model outputs of exported loads

A sensitivity analysis was performed to evaluate the effect of single perturbations of selected input parameters on the predicted loads exported from each sub-catchment. Thirteen key parameters were selected from the 27 model parameters and varied from the model default values by multiplying them by the factors shown in Table 7. Rather than selecting extreme perturbation values for the parameters, the sizes of the perturbations were selected based on plausible estimates of their likely uncertainty. For example, the model default values for animal

microorganism concentrations. kg^{-1} manure, which are likely to have a high degree of variability (Wade *et al.* 2000; Sturdee *et al.* 2003), were perturbed by an order of magnitude. But the volume of sewage effluent per person per day, which is likely to be less variable, was only perturbed by 5%.

Results of the sensitivity analysis were viewed in several categories as follows: for each of the three microorganisms; for dry and wet weather; for each of the 52 sub-catchments; and for each of the 13 parameters perturbed. This resulted in over 4,000 relative change outputs (Ferguson 2005). Take for example the results of sensitivity analyses for the *Cryptosporidium* loads delivered in wet weather from four representative sub-catchments (Figure 6). Loads are most influenced by plausible variations in the number of animals assumed to be in the sub-catchments, the extent of mobilization of microorganisms from manure and by the assumed concentration of microorganisms in the faeces. In synthesizing the results of the sensitivity analysis the following observations emerged.

Reducing the number of microorganisms excreted per person per day by 90% causes linear reduction in the estimated dry weather loads of *Cryptosporidium* and *Giardia* in those sub-catchments affected by on-site systems (2, 3, 7), and approximately a 70% reduction in the *E. coli* load downstream of Moss Vale STP (17). The wet weather effect is limited to reductions in the estimated *E. coli* loads, by approximately 30% downstream of STPs and on-site systems and by as much as 70% downstream of Bowral STP (52, 14).

In dry weather reducing the load of microorganisms excreted by animals each day by 90% decreases the predicted loads of *Giardia* by approximately 90% and *Cryptosporidium* and *E. coli* loads by between 20–80%. In wet weather the reduction in animal microorganism loads produces a 90% decrease in the predicted load of *Cryptosporidium* and *Giardia* in all sub-catchments. *E. coli* loads are also reduced by 90% in most sub-catchments, with the exception of those sub-catchments that are impacted by on-site systems and STPs. In dry weather the fraction of manure mobilized is set to zero. But in wet weather, reducing the fraction of manure mobilized by raising the M_s parameter in equation (3) to the power of 2 results in >90%

Table 7 | Perturbation factors for the sensitivity analysis

Parameter	Perturbation factor
Population (S_i)	0.9
Population connected (n_i)	0.8
Microorganisms per person per day (β_j)	0.1
Animal density ($A_{s,i}$)	0.1
Animal access to streams (X_s)	\wedge 1.5
Likelihood of direct defecation (D_s)	\wedge 1.5
Animal microorganism concentrations. kg^{-1} ($P_{j,s}$)	0.1
Microbial decay rates ($\delta_{j,i}$)	\wedge 1.5
Fraction of manure mobilized (M_s)	\wedge 2
Connectivity of on-site systems (%) (O)	0.5
Volume of sewage. $\text{person}^{-1}.\text{day}^{-1}$ (V)	0.95
Fraction bound (F_j)	\wedge 1.5
Flow velocity ($\text{m}.\text{s}^{-1}$) (v)	0.5

\wedge raised to the power of.

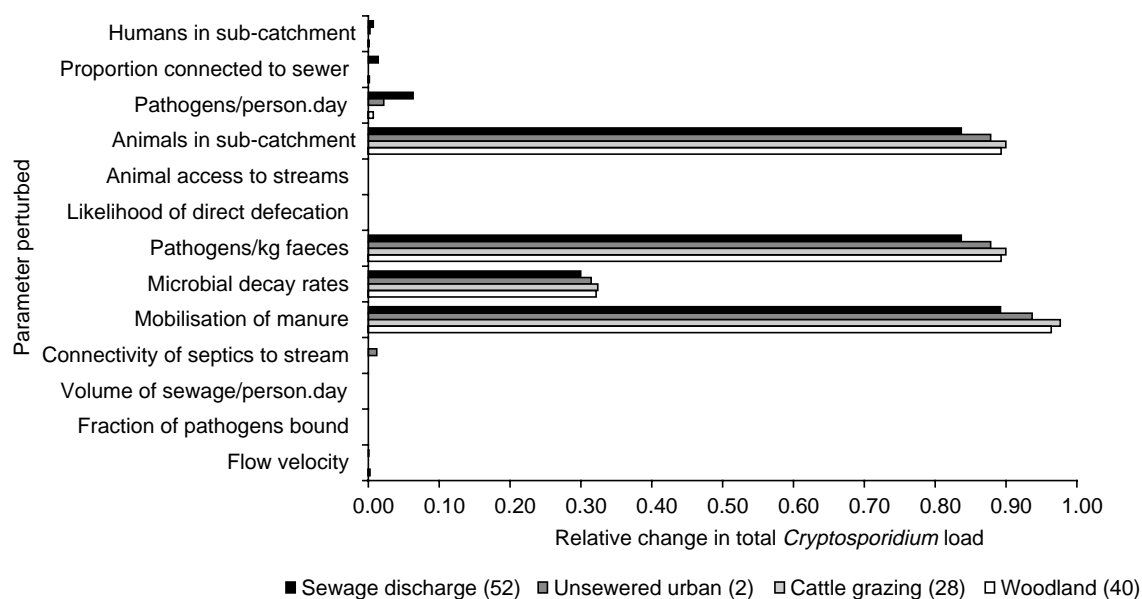


Figure 6 | Relative change in total *Cryptosporidium* loads exported during wet weather events from four representative sub-catchments (52, 2, 28, 40). The dominant pathogen source for each sub-catchment is indicated in the legend.

decreases in the predicted loads of *Cryptosporidium* and *Giardia* in all sub-catchments. *E. coli* loads are again reduced by more than 90% in most sub-catchments, excluding those impacted by on-site systems and STPs.

Reduction of the microbial decay rates ($\delta_{j,i}$) by raising them to the power of 1.5 had little impact on the predicted load of *Cryptosporidium* in dry weather, however predicted loads of *E. coli* and *Giardia* are increased by 30%, with the magnitude of the impact increasing in the downstream catchments dominated by improved pasture and native forest. Decay rates were not factored into wet weather predictions because of the short duration of these events and the rapid movement of water through the stream network. Reducing the connectivity of on-site systems, the volume of effluent produced per person per day, the proportion of microorganisms bound to particles and the flow velocity caused little change in the model predictions for either dry or wet weather conditions.

Analysis of sub-catchment input rankings per unit area

Ranking of sub-catchments by both input and export loads, and particularly ranking by scaling these loads by unit area is a useful mechanism for the identification and

prioritization of individual sub-catchments that require management interventions. The raw and unit area rankings of the export loads (Table 6) indicate which sub-catchments are delivering the greatest pathogen and *E. coli* loads from the Wingecarribee at an overall catchment scale. Input loads per unit area rankings can be used to identify the sub-catchments that are the highest individual sources of pathogen and *E. coli* loads. These sub-catchments may have a large impact on water quality at a local sub-catchment scale and may therefore be of interest to local stakeholders as well as to catchment managers responsible for drinking water quality. Sensitivity analysis was used to examine the effect of single parameter perturbations on the ranking of sub-catchments based on input loads per unit area. The analysis weighted the sub-catchments in the top (n) number of sub-catchments by summing the sub-catchment rankings that disappeared out of the top (n) with a value of n for the first, n-1 for the second and 1 for the nth ranking. The analysis was performed using the same perturbations that were applied in the previous analysis of the export loads (Table 7).

The greatest impact on sub-catchment rankings is observed in response to changes in manure mobilization rates, the number of microorganisms excreted per person per day (Table 8), and the concentration of microorganisms excreted by animals. Some impacts on the predicted dry

weather loads of *Giardia* and *E. coli* are also observed in response to changes in animal density and the likelihood of direct faecal deposition. Connectivity of on-site systems is also an important parameter for the prediction of dry weather loads of both *Cryptosporidium* and *Giardia*, while animal access to streams impacted all three microbial loads

but only in dry weather. Six of the parameters had negligible impact on the ranking of sub-catchment loads. They include population, population connected to the sewerage system, microbial decay rates, volume of effluent per person per day, flow velocity and the fraction of microorganisms settling out. This analysis indicates that future work to refine the

Table 8 | Sensitivity analysis of sub-catchment rankings for input per unit area budgets

		Sum of sub-catchment rankings that disappear from top (n) sub-catchments																			
n		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Microorganisms per person per day (β_j)																					
C	Dry	0	0	0	0	1	3	6	10	15	21	28	36	45	55	66	78	91	>100	>100	>100
G	Dry	0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	0	0	1	3
E	Dry	1	0	1	3	3	6	10	15	21	28	35	42	50	58	66	74	82	90	98	>100
C	Int	1	2	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
G	Int	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E	Int	0	1	3	5	4	5	6	7	8	9	11	11	12	13	14	15	16	17	18	19
C	Wet	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
G	Wet	0	0	0	0	0	0	0	0	0	0	0	1	2	3	0	0	0	0	0	0
E	Wet	1	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Fraction of manure mobilized (M_s)																					
C	Dry	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
G	Dry	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
E	Dry	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C	Int	0	1	3	3	6	10	10	15	15	15	14	13	13	13	10	10	15	16	15	15
G	Int	1	3	6	6	5	4	3	3	3	3	4	3	3	5	4	3	3	3	6	5
E	Int	0	0	0	1	3	6	10	15	21	28	35	40	48	47	47	52	56	57	49	42
C	Wet	1	2	3	1	3	3	3	6	6	10	9	10	14	13	18	19	14	11	9	7
G	Wet	1	3	5	4	3	5	3	4	1	1	2	0	0	0	0	0	1	3	3	4
E	Wet	0	1	3	6	10	11	15	13	18	17	23	30	38	38	35	34	34	32	32	26

C = *Cryptosporidium*, G = *Giardia*, E = *E. coli*, Dry = Dry weather, Int = Intermediate wet weather event, Wet = Large wet weather event.

model should focus on achieving improved estimates of manure mobilization rates for the entire range of animal species included in the model. Improved estimates of pathogen and *E. coli* excretion rates from both humans and animals in the local population would also significantly improve the accuracy of outputs from the model.

DISCUSSION

Few studies have attempted to model variations in pathogen concentrations or loads in drinking water catchments (Walker & Stedinger 1999; Medema & Schijven 2001; Dorner *et al.* 2004). This model incorporates a land budget of diffuse pollution as well as STP and on-site systems modules to calculate source generation of pathogens and *E. coli* based on geographic information system (GIS) land use layers. These sources are then routed through the sub-catchments using hydrologic and in-stream modules. In the Wingecarribee catchment in dry weather the only source of manure reaching streams is from the direct deposition of faeces, primarily from cattle, plus a small component from wildlife and certain sub-catchments also receiving inputs from on-site systems and STP effluents. Following rainfall, direct deposition will be supplemented by the mobilization of manure deposited on land into surface water runoff. Walker & Stedinger (1999) noted that if oocysts were easily freed from manure due to runoff processes, then their model would considerably underestimate oocyst concentrations in surface waters. A recent study by Davies *et al.* (2004) indicated that *Cryptosporidium* oocysts were easily freed from cow manure and that the oocysts were readily transported in the surface runoff, particularly in the absence of vegetation. The PCB model uses manure mobilization estimates to predict the transport of faeces from land to water during wet weather flood events. Sensitivity analysis indicates that the fraction of manure mobilized in events is an important parameter for determining pathogen and *E. coli* loads in sub-catchments with land uses that contain animals. But sub-catchments that contain on-site systems and STPs are more affected by the presence of these individual point sources. Improved estimates of manure mobilization for different species and for a range of rainfall-runoff event scenarios would enhance

the predictive capability of the model and reduce the level of uncertainty. Other important parameters in the model include animal access to streams and the rate of direct faecal deposition to the stream network. This highlights the need for quantitative data regarding these types of activities in water catchments. Animal access rates will be catchment specific. The likelihood of direct deposition, however, relates to animal behaviour and farm management practices and is thus a more generic research need.

Fraser *et al.* (1998) noted that the application of their model in the field was limited by a number of poorly understood factors, including the assumption of steady state conditions which did not allow for variation in environmental conditions, such as rainfall or the variation in the deposition of faecal material on pastures. Our model accounts for variations in rainfall-induced runoff by incorporating a surface rainfall layer from the GIS. We include a parameter that estimates microorganism attachment to sediment particles and use this along with stream velocity to estimate in-stream loss due to settling, although we have not been able to estimate re-suspension. We also incorporate inputs from native and feral animals in the land budget. Although wildlife excrete significant loads of *E. coli* to the land, they have lower prevalence and concentration of *Cryptosporidium* and *Giardia* (Cox *et al.* 2005) and it is unlikely that these pathogens are of genotypes that are infectious to humans.

Insufficient data was available to account for non-random deposition of manure on pastures. Further research to investigate the behaviour of animal species that have access to the riparian zone would improve estimates of the rate of direct deposition, and also quantify the location and distribution of manure on pastures. Future refinements to the model could include the development of additional point source modules for manure spreading and/or biosolid applications and improvement of the hydrologic component to account for time series flow data. If estimates of pathogen infectivity for *Cryptosporidium* oocyst isolates from these catchments were available, it would be possible to use the model for quantitative microbial risk assessment (QMRA) to predict the proportion of the total load that represents a potential risk for human infection.

The PCB model was developed to predict export loads of *Cryptosporidium*, *Giardia* and *E. coli* from drinking water

catchments for dry weather and for two wet weather event scenarios. The fate of these organisms within storages can subsequently be predicted by using the outputs of the PCB model as the input parameters for the hydrodynamic model developed by Hipsey *et al.* (2005). In addition to the load data, the raw and unit area rankings of sub-catchment inputs and exports (Table 6) can be used to prioritize catchment management activities at both catchment and sub-catchment scale. Scenario evaluation of various management activities can also be achieved by simply varying the input parameters to the model. For example land use changes can be modeled by altering the proportion of each land use category in the sub-catchment input file. The model could be augmented to include economic estimates of various management options, thus enabling catchment managers to perform cost-benefit analysis of catchment rectification scenarios.

CONCLUSIONS

The development of this model was prompted by the lack of any existing commercially available pathogen export models, and the need to quantify the sources and fate of pathogens in the Sydney drinking water catchment. Although application of the model is constrained by the availability of appropriate data and by a number of assumptions, the outputs represent the first attempt to quantify pathogen loads, and hence, risk in the Sydney drinking water catchment.

Future work will involve the application of the PCB model to predict pathogen budgets for all 27 of the catchments in the SCA area of operations. The outputs will be used to rank catchments and sub-catchments with both the highest net pathogen and *E. coli* inputs and also the greatest export potential to deliver pathogens to the reservoirs. The identification of these high-risk sub-catchments will enable catchment managers to prioritize the implementation of catchment control measures and to evaluate the potential benefits and improvements that may be attained, thereby achieving the greatest possible improvements to water quality.

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