

# Modelling the fate and transport of faecal bacteria in estuarine and coastal waters



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## ABSTRACT

This paper details a numerical model developed to predict the fate and transport of faecal bacteria in receiving surface waters. The model was first validated by comparing model predicted faecal bacteria concentrations with available field measurements. The model simulations agreed well with the observation data. After calibration, the model was applied to investigate the effects of different parameters, including: tidal processes, river discharges from the upstream boundaries and bacteria inputs from the upstream boundaries, wastewater treatment works (WwTWs), rivers and combined sewer overflows (CSO), on the concentrations of faecal bacteria in the Ribble Estuary. The results revealed that the tide and upstream boundary bacteria inputs were the primary factors controlling the distribution of faecal bacteria. The bacteria inputs from the WwTWs in the model domain were generally found not to have a significant impact on distribution of faecal bacteria in the estuary.

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## 1. Introduction

Pathogens are often responsible for the spread of waterborne diseases (Kashefipour et al., 2002). However, due to the difficulties of direct measurement of pathogens, indicator microorganisms have generally been used in water quality management (Chapra, 1997). Faecal indicator bacteria (FIB) groups, such as total coliform, faecal coliform, *E. coli* and enterococci, are used commonly around the world to measure the health hazards in bathing and shellfish harvesting waters (Thomann and Muller, 1987; Sanders et al., 2005). This is due principally to the fact that the faecal indicator bacteria can be easily quantified using laboratory tests and are generally not present in unpolluted waters, and the concentrations of these indicator bacteria tend to be correlated with the contamination level (Thomann and Muller, 1987). Various sources of faecal indicator bacteria exist in estuarine and coastal waters, which include: effluent outfalls, combined sewer overflows (CSO), diffuse source inputs etc. (Kashefipour et al., 2006). The importance of quantifying the effects of different bacteria sources has been emphasized in a recent work by Atwill et al. (2003), who suggest that nonpoint sources are important sources of faecal contamination. Sanders et al. (2005) assessed the effect of different faecal bacteria sources on surface water quality at an inter-tidal wetland, where sediment re-suspension was the dominant source of bacteria concentrations near the mouth and urban

runoff controlled bacteria concentrations at inland sites. Hydrodynamic and hydrological processes play very important roles on the distribution of faecal bacteria and pathogen concentrations in river, estuarine and coastal waters. de Brauwere et al. (2011) found that tidal processes play a very important role on the distribution of bacteria concentrations in the Scheldt river and estuary. Ge et al. (2012) investigated the effects of waves on *E. coli* concentration distribution at an embayment beach.

The Ribble Estuary is located to the south of the Fylde coast, Lancashire, in the north west of England, (Fig. 1). Upstream of the estuary, there are three main rivers; namely the River Darwen, the River Douglas and the River Ribble (Fig. 1). At the mouth of the estuary there are two well-known seaside resorts, namely Lytham St Annes and Southport, with both being designated EU (European Union) bathing water sites. The Fylde Coast, which is located between Fleetwood in the north and the Ribble Estuary in the south, includes Blackpool, one of the most famous beaches, in England for tourism, receiving on average more than 17 million visitors a year. This stretch of coast includes some of the UK's premier resorts and bathing beaches and has been subject to significant infrastructure investments to reduce point-source impacts in achieving the standards of the 1976 Bathing Water Directive (BWD) (Stapleton et al., 2008). A major civil engineering investment program has been undertaken to reduce bacterial input to the estuary and enhance bathing water quality along the Fylde Coast. About £600 million was invested over the past 20 years on building new sewerage treatment plants along the Fylde Coast and the Ribble Estuary. Although the reduction in input bacterial loads has resulted in a significant decrease in the concentrations of bacterial indicators in the receiving

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**Symbol list**

$f$	Coriolis parameter
$H$	total depth of water
$U, V$	depth-averaged velocities in $x, y$ directions respectively
$\bar{\varepsilon}$	depth-averaged eddy viscosity
$\xi$	water surface elevation above datum
$\rho$	fluid density
$\tau_{xw}, \tau_{yw}$	surface wind shear stress components in $x, y$ directions
$\tau_{xb}, \tau_{yb}$	bed shear stress components in $x, y$ directions
$T$	top width of the channel
$\zeta_R$	water elevation
$Q_R$	discharge
$\beta$	momentum correction factor due to the non uniform velocity over the cross section
$A$	wetted cross section area
$R = \frac{A}{P}$	hydraulic radius
$P$	wetted perimeter of the cross section
$U_R = Q_R/A$	cross-sectional averaged velocity
$C$	bacterial concentration (cfu/100 ml)
$C_0$	source or sink of bacteria
$D_x, D_y$	depth averaged dispersion coefficients in $x$ and $y$ directions, respectively
$K_x$	longitudinal dispersion coefficient
$I$	light irradiance ( $cal/cm^2/day$ )
$k$	decay rate for bacteria in the water column
$k_{20}$	decay rate at $T = 20^\circ C$
$\theta$	a dimensionless temperature correction constant, typical values for $\theta$ are about 1.07
$T$	water temperature ( $^\circ C$ )
$k_n$	darkness condition decay rate at $20^\circ C$
$S$	salinity (ppt)
$\alpha_i$	a light irradiance correction factor ( $0.00824 cm^2/cal$ )

waters, occasional higher bacterial counts have still been measured in recent years. As a result, the bathing waters still occasionally failed to comply with the EU mandatory water quality standards of the Bathing Framework Directive (Kashefipour, 2002). In addition, the Ribble catchment has been selected as a test area for the acquisition of environmental information, needed to underpin implementation of the revised Directive 2000/60/EC in the UK (Wither et al., 2005). The coastal system contains both bathing and shellfish harvesting waters and the Ribble river basin is the only UK research basin for studies linked to implementation of the Water Framework Directive (WFD) (Kay et al., 2005). The main objective of the current study is to better understand the effects of different factors, including tidal processes, upstream discharges and inputs of faecal bacteria from upstream rivers, combined sewer overflows (CSOs), diffuse sources and wastewater treatment works (WwTWS), on the distribution of faecal bacteria concentrations in the Ribble Estuary.

The Ribble river basin has a range of land uses from low intensity grazing systems in the upper catchments, to some heavily urbanised and industrialised areas in the lower catchments. These diverse variations in the river basin characteristics, provide a range of excellent land use variability for model development and parameterization, thus the Ribble Estuary and the marine receiving waters provide a typical sink for a range of solutes advected into the estuarine and coastal basin following storm conditions. The range of characteristics of the system therefore provides the potential for transferability to other sites across the UK and internationally. The estuarine system contains both bathing and shellfish harvesting waters with considerable regulatory data records for relevant parameters. The Ribble Estuary is complex with a tidal reciprocating estuarine system and the shallow near-

shore waters present a number of modelling challenges; these regulatory and modelling characteristics again, provide an environment ideal for transferring the modelling science advancements to other sites. The methods adopted in this study are generic and can readily be applied to other case study sites.

**2. Material and methods****2.1. Hydrodynamic model**

In modelling estuarine and riverine systems, the co-existence of one- and two-dimensional flow patterns is quite common. As suggested by Kashefipour et al. (2002) and Lin and Falconer (2005), in this study, an integrated one- and two-dimensional model, which was based on the DIVAST (Depth Integrated Velocities And Solute Transport) and FASTER (Flow And Solute Transport in Estuaries and Rivers) models were used. In the two-dimensional model, the depth-integrated equations are given below:

$$\frac{\partial \xi}{\partial t} + \frac{\partial UH}{\partial x} + \frac{\partial VH}{\partial y} = 0 \quad (1)$$

$$\frac{\partial UH}{\partial t} + \beta \left\{ \frac{\partial U^2 H}{\partial x} + \frac{\partial UVH}{\partial y} \right\} = fVH + gH \frac{\partial \xi}{\partial x} + \frac{\tau_{xw}}{\rho} - \frac{\tau_{xb}}{\rho} + 2 \frac{\partial}{\partial x} \left( \bar{\varepsilon} H \frac{\partial U}{\partial x} \right) + \frac{\partial}{\partial y} \left[ \bar{\varepsilon} H \left( \frac{\partial U}{\partial y} + \frac{\partial V}{\partial x} \right) \right] \quad (2)$$

$$\frac{\partial VH}{\partial t} + \beta \left\{ \frac{\partial UVH}{\partial x} + \frac{\partial V^2 H}{\partial y} \right\} = -fUH + gH \frac{\partial \xi}{\partial y} + \frac{\tau_{yw}}{\rho} - \frac{\tau_{yb}}{\rho} + \frac{\partial}{\partial x} \left[ \bar{\varepsilon} H \left( \frac{\partial U}{\partial y} + \frac{\partial V}{\partial x} \right) \right] + 2 \frac{\partial}{\partial y} \left( \bar{\varepsilon} H \frac{\partial V}{\partial y} \right) \quad (3)$$

where  $\xi$  = water elevation above (or below) datum;  $U, V$  = depth averaged velocity components in  $x, y$  directions;  $H = \xi + h$  = total water depth;  $h$  = water depth below datum;  $\beta$  = momentum correction factor;  $f$  = Coriolis parameter;  $\tau_{xw}, \tau_{yw}$  = surface wind shear stress components in  $x, y$  direction;  $\tau_{xb}, \tau_{yb}$  = bed shear stress component in  $x, y$  directions; and  $\bar{\varepsilon}$  = depth averaged eddy viscosity.

The one dimensional hydrodynamic equations can be expressed in the following form:

$$T \frac{\partial \zeta_R}{\partial t} + \frac{\partial Q_R}{\partial x} = 0 \quad (4)$$

$$\frac{\partial Q_R}{\partial t} + \frac{\partial}{\partial x} \left( \beta \frac{Q_R^2}{A} \right) + gA \frac{\partial \zeta_R}{\partial x} + g \frac{Q_R |Q_R|}{C^2 AR} = 0 \quad (5)$$

where  $T$  = top width of the channel;  $\zeta_R$  = water elevation; discharge;  $\beta$  = momentum correction factor due to the non uniform velocity over the cross section;  $A$  = wetted cross section area;  $R = \frac{A}{P}$  = hydraulic radius and  $P$  = wetted perimeter of the cross section.

**2.2. Bacteria fate and transport model**

In the faecal bacteria fate and transport model, the bacteria are normally modelled as a reactive tracer, wherein they will be transported by the flow processes once they enter the model domain and their concentrations are affected by faecal bacteria specific processes (de Brauwere et al., 2011). The bacteria transport model presented herein was developed by Gao et al. (2011a, b), which includes bacteria advection, mixing, dynamic growth/mortality, sedimentation and re-suspension processes.

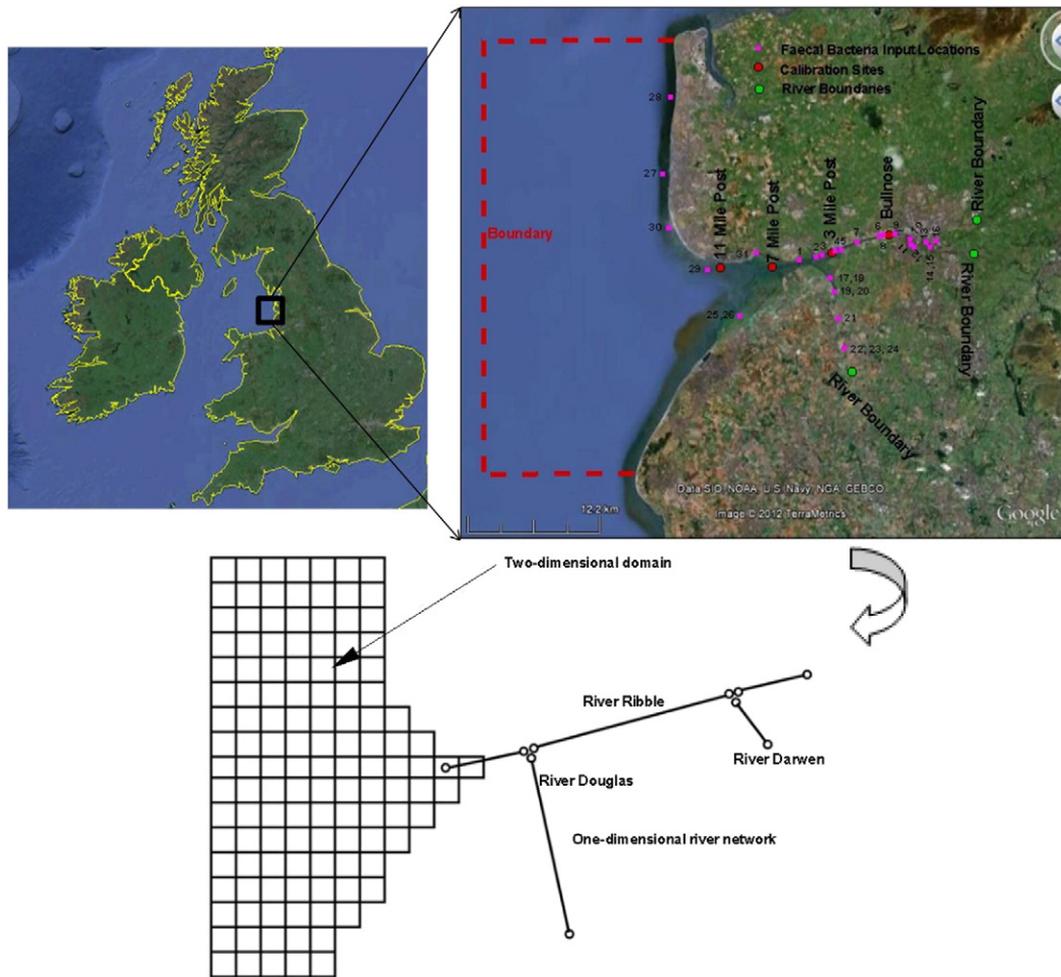


Fig. 1. Site and schematic illustration of linked one- and two-dimensional models.

The two-dimensional equation can be expressed as:

$$\frac{\partial HC}{\partial t} + \frac{\partial UHC}{\partial x} + \frac{\partial VHC}{\partial y} - \frac{\partial}{\partial x} \left( HD_x \frac{\partial C}{\partial x} \right) - \frac{\partial}{\partial y} \left( HD_y \frac{\partial C}{\partial y} \right) = C_o - kCH \quad (6)$$

where  $C$  = depth averaged total faecal bacteria concentration,  $C_o$  = source or sink of bacteria;  $k$  = the decay rate for bacteria in the water column;  $D_x, D_y$  = depth-averaged dispersion coefficients in  $x, y$  directions respectively.

Likewise, the 1-D cross-sectional averaged faecal bacteria transport equation can be written as:

$$\frac{\partial AC}{\partial t} + \frac{\partial Q_R C}{\partial x} - \frac{\partial}{\partial x} \left( AK_x \frac{\partial Q_R C}{\partial x} \right) = C_o - kCA. \quad (7)$$

Previous studies have shown that the faecal bacteria decay rate is highly dependent on the solar radiation and temperature. In coastal waters the decay rate of faecal bacteria is also affected by salinity (Chan et al., 2013). Therefore, in this study, effort has been made on integrating a dynamic decay rate in a linked two- and one-dimensional numerical water quality models, namely DIVAST and FASTER. These integrated models have been successfully used in previous hydrodynamic studies (Lin and Falconer, 1997; Kashefipour et al., 2002; Liang et al., 2006) and for water quality predictions (Kashefipour et al., 2002, 2006; Gao et al., 2011a,b, 2013). In this study the dynamic decay rate

for faecal coliform bacteria was expressed as a function of salinity, temperature and solar radiation, as follows:

$$k(I, S, T) = (k_n + 0.02S + \alpha_i I(t)) \theta^{(T-20)} \quad (8)$$

where  $I$  = Irradiance ( $cal/cm^2/day$ );  $k_{20}$  = the decay rate at  $T = 20^\circ C$ ;  $\theta$  = a dimensionless temperature correction constant, which describes the relationship between the decay rate and temperature; typical values for  $\theta$  are about 1.07 (Thomann and Mueller, 1987);  $T$  = water temperature ( $^\circ C$ );  $k_n$  = darkness condition decay rate at  $20^\circ C$ ;  $S$  = salinity;  $I$  = light intensity; and  $\alpha_i = 0.00824 cm^2/cal$ .

### 3. Results and discussion

#### 3.1. Model set up and calibration

The model covers the whole Ribble Estuary (Fig. 1). The downstream (or seaward) boundary was specified as a tidal water elevation boundary, whilst the upstream boundaries were specified in the form of open flow boundaries. The seaward boundary was selected far enough away from the estuary area to avoid reflection of the tide at the open boundary. The bathymetric data were digitized from the Admiralty Chart. Measured hydrodynamic and faecal bacteria concentration data were available for the summer period of 1999, for different tide conditions, with the data including: water elevations, current speed and direction, and faecal coliform concentrations.

Faecal bacteria enter the Ribble Estuary through different sources. In total, there were 31 input sources identified that contributed to the faecal pollution of the estuary, including direct discharges from WWTWs, inputs from CSOs and small rivers. The locations of these sources are shown in Fig. 1. It can be seen from Fig. 1 that the faecal bacteria enter the model domain through the upstream open boundaries of the Ribble, Douglas and Darwen rivers. The concentrations at these boundaries were measured and inserted as boundary data in the model. The concentrations at the seaward boundary were assumed to be zero. In this study the hydrodynamic model was calibrated against measured data at Bullnose, and 3, 7 and 11 mile posts. The time step was set to 9 s and the momentum correction factor was set to 1.016. The main hydrodynamic parameter used for model calibration was the bed roughness. In this study the two-dimensional model bed roughness was represented as an equivalent roughness length  $k_s$ , which could be related to the height of bed forms. For the one-dimensional part of the estuary, the Manning's  $n$  roughness coefficient was used. A number of simulations were carried out and the calibrated roughness length was found to be approximately 20 mm for the two-dimensional region of the model. For the one-dimensional model, the calibrated Manning's

roughness coefficient was optimised at 0.022. The measured velocities at four sites, including: Bullnose, and 3, 7 and 11 mile posts, were used for the hydrodynamic calibration of the model. Typical comparisons of field data and predicted current speeds, directions and water elevations at 11 mile post are shown in Fig. 2.

The main parameter to be calibrated for bacterial predictions is usually the decay rate, which depends on a number of environmental parameters, such as: sunlight intensity, temperature, salinity, sediment concentrations etc. Generally, increasing the light intensity, temperature and salinity will increase the mortality rate of coliform bacteria, with increasing turbidity levels having an adverse effect on the decay rate (Kashefipour et al., 2006). Burkhardt et al. (2000) examined the effects of different environmental factors on faecal coliform and *E. coli* and found that sunlight and/or temperature most significantly affected the decay rate, with sunlight being found to have the greatest impact, particularly on faecal coliform. Wilkinson et al. (1995) presented linear and power relationships between decay and light intensity. However, the decay processes of faecal bacteria were normally modelled as a first order process, using a constant decay rate. Kashefipour et al. (2002) used different day and night constant decay rates for the Ribble Estuary.

Lin and Falconer (2001) developed a three-dimensional hydrodynamic and faecal bacteria transport model for Swansea Bay and the Bristol Channel with a constant bacteria decay rate. Bedri et al. (2011) adopted a constant bacteria decay rate in their three-dimensional model to simulate *E. coli* concentrations in Dublin Bay. In recent years effort has been increasingly made in using various decay rates in numerical models. Liu et al. (2006) integrated a time-dependent inactivation rate, based on water temperature, solar radiation, and sedimentation in their numerical model to simulate faecal bacteria in Lake Michigan. Servais et al. (2007), de Brauwere et al. (2011) and Liu and Huang (2012) considered the effects of water temperature, mortality and sedimentation as the main factors affecting faecal bacteria concentrations in bacteria transport models and applied their models to different water columns. Hipsey et al. (2008) presented a generic microbial model for surface water systems, which included the effects of temperature, salinity, pH, dissolved oxygen, sunlight, nutrients and turbidity on the growth and mortality of enteric organisms. Ge et al. (2012) integrated site specific light effects into a decay function in their model. Chan et al. (2013) used a dynamic decay function, together with the effects of light and temperature, to forecast coastal water quality in Hong Kong, China. The decay rate can vary for different conditions and needs to be estimated for different weather and water conditions. In this study a dynamic decay rate was used to include the effects of light intensity, salinity and temperature on bacteria decay. The decay rate was calculated every time step during the simulations. This meant that the decay rate in this study did not need to be calibrated using a trial and error method. Since the exact light intensity data during the simulation time was not available; therefore the light intensity data of a typical summer day near the Ribble Estuary were used to represent light intensity of a typical day, as shown in Fig. 3. The salinity was

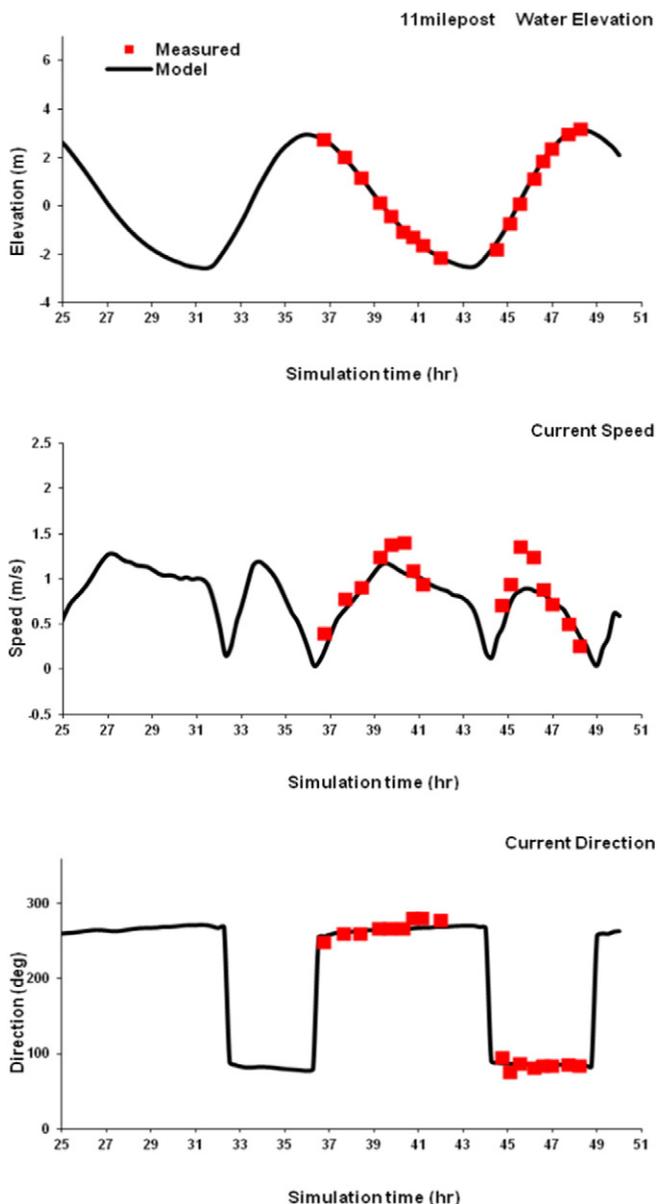


Fig. 2. Comparison of water elevations, current speed and directions at 11 mile post.

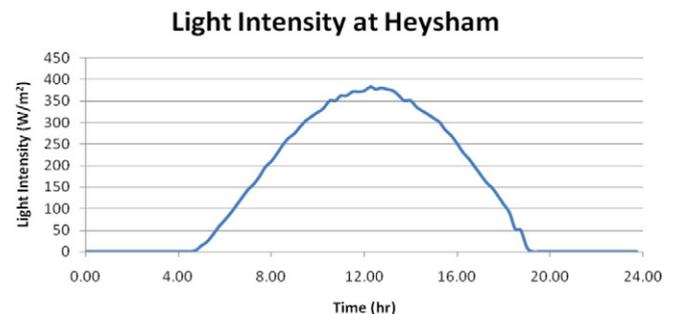


Fig. 3. Typical summer day light intensity variation near Ribble Estuary.

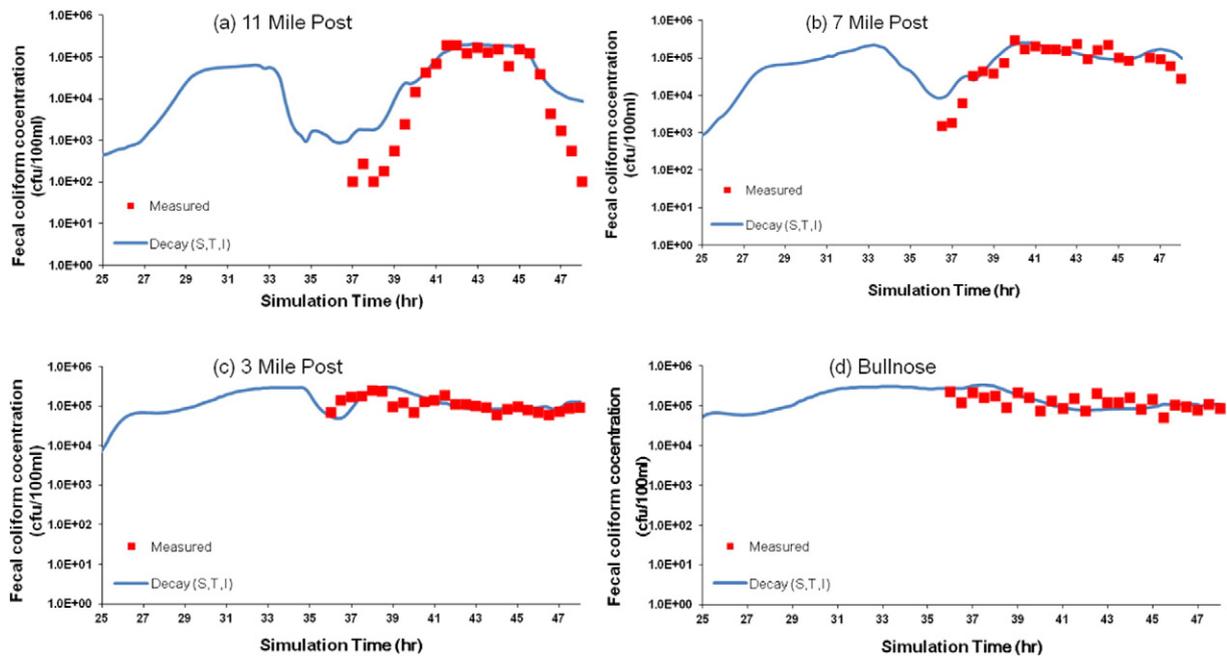


Fig. 4. Comparisons between predicted and measured bacteria concentrations at Bullnose, and 3, 7 and 11 mile posts.

predicted every time step during the simulation period by using the built-in salinity model for this study, which was based on the DIVAST model framework, and which had been verified and tested through a number of studies e.g. Wu et al. (2005). Measurements of the water temperature showed that during the simulation period, the temperature in the study area was fairly stable, and remained at about 14.3 °C, therefore the temperature was set as a constant. Simulated time series of faecal coliform concentrations at four sites, namely Bullnose, and 3, 7 and 11 mile posts, were compared with the field measurements. The comparisons are shown in Fig. 4. In general, the model captured the major features and variability of the faecal coliform concentrations reasonably well. A comparison between the model results and observations at the four sites are also presented in Table 1. The RMS (Root Mean Square) error and the RRE (Relative RMS Error) for faecal coliform concentrations at the four calibration sites were calculated. The RMS error is given as:

$$RMS\ Error = \sqrt{\frac{1}{N} \sum_{n=1}^N (O^n - P^n)^2}$$

where  $N$  = number of observation–prediction pairs,  $O^n$  = the value of the  $n$ th observed data, and  $P^n$  = the value of the  $n$ th predicted data. The relative error is given as:

$$RRE = \frac{RMS\ Error}{Observed\ Change} \times 100 = \frac{\sqrt{\frac{1}{N} \sum_{n=1}^N (O^n - P^n)^2}}{O_{max} - O_{min}} \times 100$$

Table 1  
Statistical analysis of measured and modelled bacteria concentrations.

Site	Measured mean (cfu/100 ml)	Modelled mean (cfu/100 ml)	Mean absolute error (cfu/100 ml)	RMS error (cfu/100 ml)	Measured change (cfu/100 ml)	Relative RMS error (%)
11 Mile post	60427	61286	15612	26488	189900	13.9
7 Mile post	100600	79444	35363	53486	288500	18.5
3 Mile post	113704	100941	40859	56554	193000	29.3
Bullnose	123222	125623	47442	63430	170000	37.3

where  $O_{max}$  = maximum value of observations and  $O_{min}$  = minimum value of observations. The mean absolute error is  $MAE = \frac{1}{N} \sum_{n=1}^N |O^n - P^n|$ .

The RRE varies from 13.9% at 11 mile post to 37.3% at Bullnose. The MRRE is defined as the mean value of the last column in Table 1. It is used as an indicator of the overall model performance. The MRRE of 24.8% indicates that the model results are reasonably good.

### 3.2. Model application

After the calibration the model was then applied to investigate the effects of different parameters on the fate and transport of faecal bacteria, including the tidal processes, the upstream boundary discharges, the upstream boundary bacteria concentrations, and other inputs from CSOs, rivers and WWTWs. Each of these processes was removed from the model one by one to investigate the effects of the individual parameter on the fate and transport of faecal bacteria in the estuary. Fig. 5 presents the box plot of the field measurements for the faecal coliform concentrations at different monitoring sites, with the location of the monitoring sites being shown in Fig. 1. The model predicted results for different scenarios at the sites of Bullnose and 3, 7 and 11 mile posts are shown in Figs. 6, 7, 8 and 9 respectively. For all of the box plots, the whiskers represent the minimum and maximum simulated concentrations. The measure of the central tendency was the median, and the upper and lower bars of the box represent the 75<sup>th</sup> and 25<sup>th</sup> percentiles, respectively. The highest faecal coliform concentrations observed were at the upstream site Bullnose. The observation results show that the overall tendency of the faecal coliform concentrations is that they

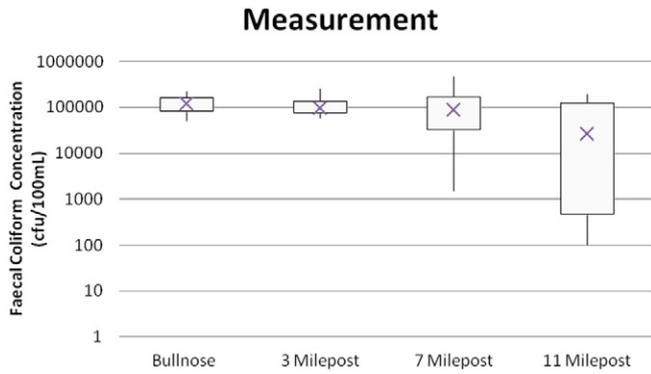


Fig. 5. Faecal coliform concentration measurements at monitoring sites.

decrease in the downstream direction. The reason for this reduction is not only related to the sources and their locations, but also due to the effects of the tide at the different sites. The effects of a tide on the variation in the faecal coliform concentration can also be seen in Fig. 4 at 7 and 11 mile posts. The measured concentrations show a clear rise and fall pattern during a tidal cycle. The pattern become less obvious at the upstream sites, i.e. Bullnose and 3 mile post, as shown in Fig. 4. The significant difference in the tidal effects on the faecal coliform concentrations, at the different observation sites, can be explained by the tidal processes being less dynamic at the upstream sites, where the tidal effects are much weaker.

In order to assess the role of the tides, a simulation was run with the tides removed from the hydrodynamics, whilst all other processes were kept identical. Figs. 6, 7, 8 and 9 present box plots of faecal coliform concentrations for the different scenarios. The modelling results were studied at four monitoring sites, namely Bullnose, and at 3, 7 and 11 mile posts. It can be seen that the median faecal coliform concentrations significantly increased at both 7 and 11 mile posts when the tidal processes were excluded as compared to the results for the reference run, as shown in Figs. 8 and 9. Figs. 8 and 9 showed dramatically decreased variations in the faecal coliform concentrations at sites 7 and 11 mile post without the tide effects. The concentrations at the Bullnose and 3 mile post sites were less influenced by the tide. The median and variation of faecal coliform concentrations at 3 mile post and Bullnose did not change much when the tidal processes were excluded, as shown in Figs. 6 and 7. The observations proved that the tidal processes have a greater effect on the faecal bacteria distribution in the lower estuary sites. The tide has a significant influence on the faecal coliform concentrations in the estuary, but the effects depend on the location of the individual site. Overall, not only do the tidal processes accelerate and increase the pollutant mixing processes significantly, but also the tide has the effect of enlarging the influence radius of a source by pushing water upstream and further downstream than when the tide effects are excluded. For any site located upstream of an important source,

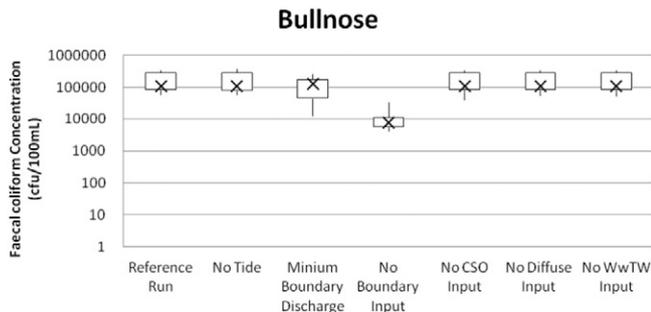


Fig. 6. Effect of different parameters on faecal coliform concentrations at Bullnose.

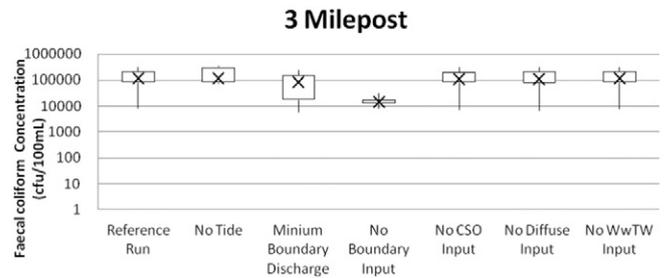


Fig. 7. Effect of different parameters on faecal coliform concentrations at 3 mile post.

the tide therefore cause an increase in the average concentrations, as found in de Brauwere et al. (2011), otherwise the average concentrations tend to decrease, as in this study.

The effects of the upstream boundary discharges were investigated by reducing the upstream boundary discharges to only 10% of the boundary discharges, the scenario was referenced as minimum boundary discharge condition, but the other processes were kept the same. The simulation results showed that the concentration at Bullnose, as shown in Fig. 6, increased the under minimum boundary discharge condition, which can be explained as the low flow condition has less capacity to carry the faecal bacteria from the upstream boundaries downstream. This leads to faecal bacteria accumulating more at the upstream sites. This can be supported by the observations from Figs. 7, 8 and 9, where the faecal coliform concentrations at 3, 7 and 11 mile posts reduced significantly for a low boundary discharge condition, which is due to less bacteria contributing from the upstream boundaries carried by the river flow.

Investigation of the effects of bacteria input from the upstream boundaries were carried out by removing faecal bacteria input from upstream boundaries, and then the result were compared to the reference run at the four monitoring sites. The results demonstrated in Figs. 6, 7, 8 and 9 showed that faecal bacteria inputs from the upstream boundaries play a dominant role on the bacteria concentrations at all sites along the river and estuary. Once the bacteria inputs from the upstream boundaries were removed, the faecal coliform concentrations at all monitoring sites showed an order of magnitude drop in concentration, with the largest concentration reduction being at Bullnose, followed by a decreasing trend in downstream direction. This indicated that the faecal coliform inputs from the upstream boundaries were a dominant source in contributing to the faecal bacteria concentrations in both the river and estuary.

The effects of bacteria inputs from combined sewer overflows (CSOs), diffuse source and wastewater treatment works (WwTWs) were carried out in the same way. Exclusion of each of these processes led to a relatively small drop in the median value of the faecal coliform concentrations, but the variation in the range of faecal coliform concentrations was almost identical to the reference run. Comparisons between Figs. 6, 7, 8 and 9 suggested that faecal bacteria inputs from

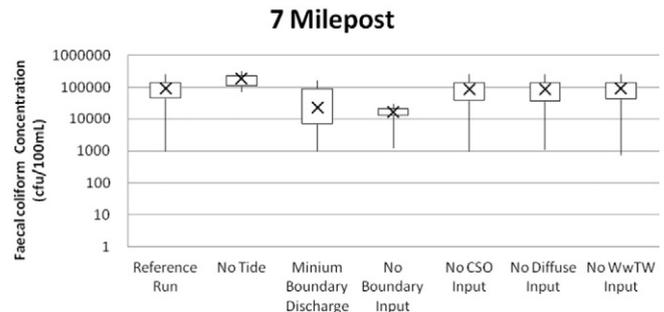


Fig. 8. Effect of different parameters on faecal coliform concentrations at 7 mile post.

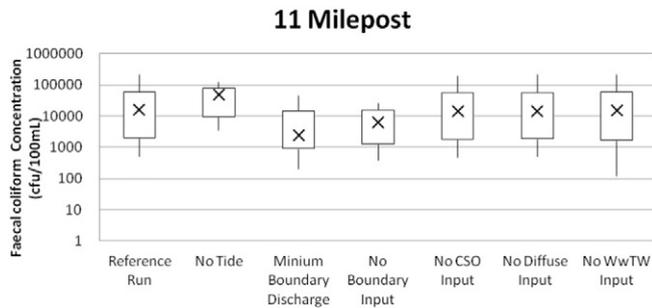


Fig. 9. Effect of different parameters on faecal coliform concentrations at 11 mile post.

the CSOs, WwTWs and the diffuse sources only play a limited role, compared to other processes, influencing the bacteria distribution in the Ribble estuary.

#### 4. Conclusions

A linked one- and two-dimensional faecal coliform transport model, based on the DIVAST and FASTER models was developed and applied to the Ribble estuary. The model was calibrated and validated against field measurements. The simulated distributions of faecal coliform concentrations at different monitoring sites were compared with field measured data. The predicted results generally agreed well with the measurements. The validated model was then applied to investigate the effects of tidal process, river discharges and different inputs of faecal coliform on the distribution of bacteria concentrations in the estuary.

The tidal processes play an important role in the faecal bacteria distribution along the estuary. The tidal processes were shown to reduce the median faecal bacteria concentrations significantly in the lower estuary area. However, sites in the upstream rivers the concentrations were affected less significantly by the tides. The variation in the faecal bacteria concentrations at a site was therefore shown to be strongly influenced by the tide.

The simulation results showed that the faecal bacteria inputs from upstream boundaries played a significant role in the distribution of bacteria concentrations in the river and estuary. Hence, accurate quantification of the faecal bacteria inputs from the upstream rivers is very important. In subsequent studies, the catchment model HSPF will be used to estimate the bacteria loads from upstream catchments.

The impacts of bacteria inputs from CSOs, diffuse sources and WwTWs inside the model domain were all found to be less significant. However, improving facilities, such WwTWs and CSOs in the upstream reaches of the domain for this study would help in improving the water quality in the estuary. It has been shown that the bacteria entering from the upstream rivers to the model domain plays a dominant role, therefore a more accurate representation of the upstream bacteria inputs could further improve the modelling capabilities and decision planning for improved water quality in the estuarine and coastal waters. This can be achieved either by extending the model further upstream in the rivers or by integrating the current model with a watershed scale model, such as HSPF, or other suitable watershed water quality models.

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