Particle tracking as modelling tool for coastal management in the Baltic Sea

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General introduction

1.1 Motivation of this dissertation

Baas Becking (1934) stated *"Everything is everywhere, but the environment selects"*, which also refers to microorganisms adapting to different marine environments as i.e. fresh water (Pernthaler (2013)), low temperate water (Grant (2004); Oren (2007)), high temperate water (Jaenicke and Sterner (2013)), saline water (Oren (2013)) or deep sea sediments (Teske (2013)). A considerable number of investigations have been made concerning the distribution of bacteria in sea water. Among the earliest of these were the studies of Russell (1892), who conducted systematic studies of the distribution of bacteria in the Gulf of Naples.

Bacteria are sensitive indicators of water mass (Kriss (1963)) and they have a strong spatial and temporal distribution, the latter of which is relatively unexplored (Fuhrman et al. (2006)). The transport of bacteria in sea water is dominated by hydrographic regime parameters and water currents (Rheinheimer (1977)). Parameters as temperature and salinity determine the survival and/ or growth (Mazur (1980)). Together with the water currents (including turbulent mixing) these factors control the transport ranges of bacteria. Marine bacteria are well adapted to their environment and can further benefit from anthropogenic influences. For example *Cyanobacteria*, well known prokaryotes of the Baltic Sea, profited from increasing eutrophication during the last decades (Bundesamt (2012)). The increased nutrient concentration, arriving via estuaries as i.e. the Oder Lagoon, led to a pronounced growth during summers of the last decade (HELCOM Helsinki Commission (2006)). Additionally, bacteria of the genus *Vibrio* seem to benefit from high sea surface temperature, which is believed to increase due to climate change (cf. Theede et al. (2008); Baker-Austin et al. (2013)), favouring an increased *Vibrio* growth. In contrast, bacteria arriving in the coastal ocean via run-off from land (by e.g. sewage treatment plants, agriculture), as faecal bacteria, cannot reproduce in the saline environment (Rhodes and Kator (1988); Kashefipour et al. (2002)), but their die-off rates vary according to e.g. temperature and salinity (Mallin et al. (2000)). Therefore, their concentration decreases with increasing distance to the coast (Weyland (1967)) and spatial gradient patterns are visible (Fuhrman et al. (2006)). An issue with high practical relevance in the field of bacterial transport in sea water is the distribution of human pathogenic bacteria in coastal waters since insufficient hygienic bathing water quality is often associated with bacterial contamination. This topic underlines the importance of a detailed analyses of bacterial transport and allows, furthermore, to test and apply new approaches. Therefore, the overall aim of this dissertation was to improve the understanding of bacterial transport in coastal waters and to identify the environmental key control parameters and their effect on the transport pattern.

There are many different types of water pollution, but the most common and wide-spread type is faecal pollution (European Environment Agency (2013a)). A contamination like this can present a risk for human health during swimming or bathing activities in water. Water pollution at bathing places can be caused by insufficient sewage treatment or sewage treatment plant overflow during strong rain events, or even by diffuse run-off from agriculture land. Alternatively, animals like sea birds or dogs can also be sources for faecal pollution close to or even at the beaches.

Since human pathogenic bacteria, as all microorganisms, are passive in the water, they cover small spatial areas and are temporally highly variable even at single beaches. Therefore water quality measurements are limited in how they are able to represent the condition of a single beach over time or the region as a whole and therefore can shed only partial light onto possible bacteria sources and spatial transport patterns. However, monitoring programs are time and cost intensive and there is often not enough money and staff to allow an expansion of the spatial and temporal sampling in order to provide a more complete picture of the bacterial distribution across the region. The monthly water quality monitoring, therefore, does not give insights in the bacterial distribution and neither provides support for a decision in favour of new tourism infrastructures, nor does it help deciding on better water quality management.

The application of circulation and particle tracking models presents a good and promising addition to the observations. They can add to the measurements by expanding the observations from single part measurements to a spatio-temporal picture. This is done by computing water currents with a circulation model, forced by e.g. measured wind and river run-off, and based on this, compute the pathways of hypothetical particles, representing microorganisms. A temporal and spatial picture of the particle distribution can be provided via forward-tracking simulations, while backward simulations can be used to find possible emission sources. Furthermore, the analyses of different wind and river run-off scenarios are possible. Particle tracking can be used as an off-line tool together with pre-simulated flow fields and also as an online tool. In the latter approach the tracking module is coupled or linked to the circulation model (cf. Navas et al. (2011)) whereas in the former case the circulation and tracking models are successively executed. In this dissertation we apply the off-line approach.

Although former studies on coastal management in the Baltic Sea area have used particle tracking together with circulation models, most of the studies were computed with two-

dimensional model systems (Schernewski and Jülich (2001); Schernewski et al. (2002)). These are not able to fully reproduce the three dimensional flow and transport patterns like with the model system applied here. Additionally, the advantages of the model approach used in this thesis, compared to the one recently used in Schernewski et al. (2012), are the much higher resolution and the large number of particles released. I was therewith able to assess the risk even at single beaches and could provide a better spatial distribution of the microorganisms than in previous studies. Therefore, the simulation results could be used to support authorities in beach management and to identify future monitoring sites. Applying the model system to different case studies within this dissertation demonstrates its potential for not only scientific analyses but also as a tool capable of answering questions of practical relevance. Moreover, the model system can act as a general tool for bathing water quality management. In the event that only short-term measurements are available, as in case of an accidental pollution event (e.g. with *Salmonella*), the model application can be used to derive concrete action recommendations.
Since there is not only a risk to human health from faecal pollutions in the Baltic Sea, but also from microorganisms which are a natural component of the water (e.g. potential human pathogenic *Vibrio spp.*), the application of the model system can be further used to analyse the impact of single parameters influencing the bacteria behaviour (i.e. water temperature) and therewith improve the understanding of the distribution of indigenous bacteria. Additionally, the system can help to support the authorities in identifying future monitoring parameters.

1.2 Bathing water quality of the Baltic Sea

The Baltic Sea is relatively small compared to world oceans, but is nonetheless one of the world's largest brackish water bodies. It is connected to the North Sea by only a small and narrow outlet: the Sound, which limits the water exchange and salt water inflow. The Baltic Sea area covers nearly 416.000 km^2 while its catchment area extends across a region about four times as large as the sea itself. In Germany, Denmark and Poland as much as 60-70% of the Baltic's catchment area consists of farmland. Forests, wetlands and lakes make up between 65% and 90% of the catchment area in Finland, Russia, Sweden and Estonia. (HELCOM Helsinki Commission (2013)) All in all over 85 million people live in the Baltic catchment area - 26% in large metropolitan, 45% in smaller urban, and 29% in rural areas. Population densities vary from over 500 inhabitants per km^2 in municipals of Poland, Germany and Denmark to less than 10 inhabitants per km^2 in the northern parts of Finland and Sweden. In the 10 km radius of the coastal zone alone live almost 15 million people.(HELCOM Helsinki Commission (2013))
For centuries the Baltic Sea has faced extensive pressure from different sources. These include pollution from cities and large industries. However, diffuse pollution from the densely populated catchment area, agriculture, tourism along the coasts and maritime transport also influence the Baltic Sea environment. (HELCOM Helsinki Commission,

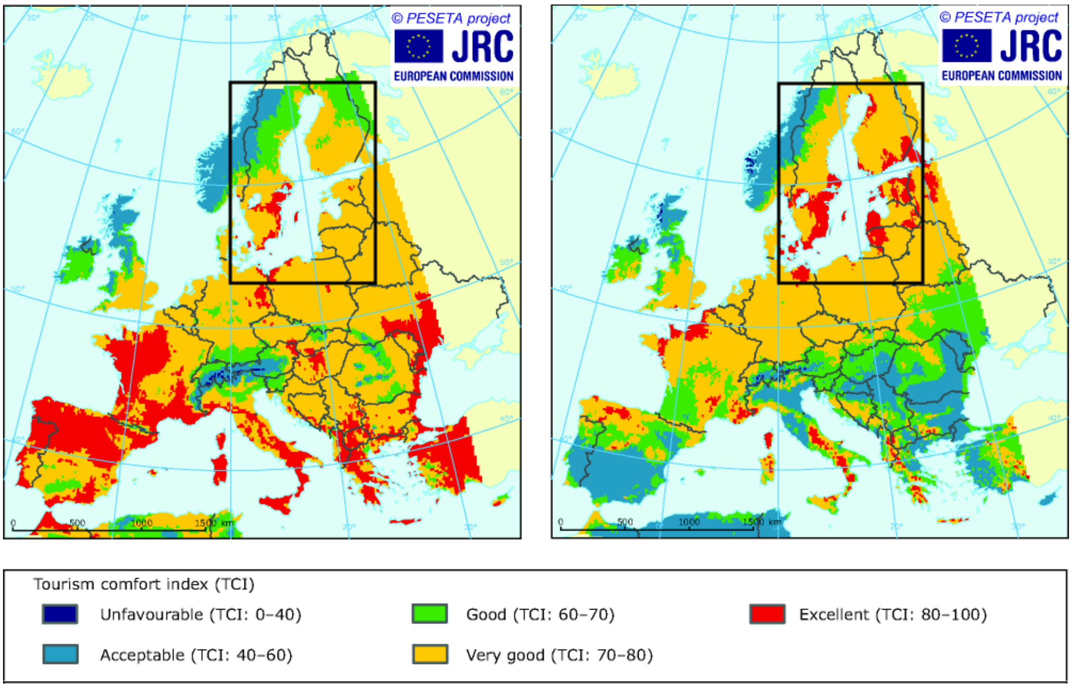

Figure 1.1: Simulated conditions for summer tourism in Europe for 1961–1990 (left) and 2071–2100 (right) according to high emissions scenario (modified after European Environment Agency (2012b)). The black frame marks the Baltic Sea.

Baltic Marine Environment Protection Commission (2010)) Tourism has become a major source of income in the southern Baltic Sea area due to the attraction of the long and sandy beaches, cliffs, island and lagoons are attractive for beach and bathing tourism. Millions of tourists visit these beaches every year (Schernewski and Sterr (2002)) and this industry is expected to grow continuously in the future (Figure 1.1, European Environment Agency (2012b)). For the Baltic coastal regions of Germany and Poland tourism has become the most crucial economic factor (e.g. more than 50% of the public income in Germany, Schernewski et al. (2002)). A large number of tourists visit these areas for bathing and water sport activities. For example, the coast of Mecklenburg-Western Pomerania has been coveted as beach and bathing destination for more than 200 years. The first German sea side resort Heiligendamm was founded in 1794 already while other important resorts (also at the island of Usedom) followed by the end of the 1890's (Schernewski and Sterr (2002)). Moreover, areas like the Bay of Greifswald (Pomeranian Bight) or the Oder Lagoon are frequently visited due to their shallow water bodies and comparative high water temperatures in summer. In order to develop sustainable bathing tourism high bathing water quality is of great importance. The deterioration of bathing water quality and the subsequent closing of beaches can have serious economic consequences for seaside resorts and may include a loss of reputation. However, despite the high pressure from different sources (mentioned above), the bathing water quality along most coasts of the Baltic Sea are regarded as good to very good (Figure 1.2) according to the EU Bathing

Figure 1.2: Bathing water quality of the Baltic Sea in July 2013. Places with excellent bathing water quality are marked in dark green, with good quality in green, sufficient in yellow and poor in red. (source: European Environment Agency (2013b))

Water Directive.

1.3 EU Bathing Water Quality Directive

To guarantee that European bathing waters are clean and without any health risk, the European Union passed the EU Bathing Water Directive 1976/7/EEC. The objective was to safeguard public health and protect the aquatic environment from pollutants in coastal and inland areas (European Environment Agency (2010)). It contained rules and standards for measurements of physical, chemical and microbiological parameters, for example pH-value, transparency, nitrate, coliform bacteria or *Salmonella*. Each EU member state was required to measure these parameters two weeks before the main bathing season started and biweekly afterwards. The Directive contained mandatory and guide threshold values for each parameter. Bathing places were closed if the recommended values were not met. Overall, the bathing water quality of the EU member states has improved throughout the recent years under the 1976 Bathing Water Directive. However, the EU has revised and updated it and adopted the new European legislation on water quality in 2006 (Directive 2006/7/EC). This new directive simplifies the management and surveillance methods. It allows faster and better information about the water quality to the public, and demands that bathing water profiles contain the potential impairment and risk. Its classification of bathing water quality is based on a three/four years trend instead of a single year result (European Environment Agency (2010)) whereas water samples were taken once a month at each bathing place. Furthermore, the new directive contains 4 threshold categories (excellent quality, good quality, sufficient and poor) instead of the two (mandatory, guide) in the Directive 1976/7/EEC. One of the main changes is the replacement of the parameters total and faecal coliform bacteria by *Escherichia coli* (*E. coli*) and intestinal *Enterococci*. According to Auchenthaler and Huggenberger (2003) faecal coliform bacteria are more reliable than *total coliform bacteria* at indicating faecal contamination, but since *E. coli* is the only bacterium originating from faeces (Roijackers and Lürling (2007)), the correlation between *E. coli* and faecal pollution is far better (World Health Organisation (2003)). The new directive is however not binding yet. It was

	guide /excellent	**mandatory / sufficient**
1976/7/EEC	100*	2000**
2006/7/EC	250*	500**
transition period	100	2000

Table 1.1: EU Bathing Water Directive threshold values for *E.coli* in cfu /100 ml (corresponds to faecal coliforms). (*) Based upon a 95-percentile; (**) Based upon a 90-percentile (European Environment Agency (2010); European Union (1976, 2006)).

transposed into the EU law in 2008 and should be implemented by the member states by 2014. All member states could choose to report under either the directive (1976/7/EEC) or (2006/7/EC) until 2012. For example Germany, Denmark and Cyprus started reporting their water quality according to the new directive European Environment Agency (2010) in 2008 while Poland started to report under this directive in 2011 (Institute for Meteorology and Water Management Poland (2010b)). As a result of this diversity, the assessment of the EU was undertaken with transition period values until 2012 (Table 1.1). 19 European states (18 member states + Croatia) were benchmarked according to the new Directive in 2012. The benchmark was conducted under the thresholds of the transition period for the other ten countries. The Baltic Sea neighbouring countries Germany (88.1%) and Finland (83.4%) belonged to the ten countries which reached compliance levels with excellent quality (or complying with the guide values) that were above the EU average in 2012. During this year up to 94% of European bathing waters complied with minimum quality standards of the Directive whereas 78.3% of all bathing places have excellent water quality. There is only a small number of places (1.9%) which did not conform with the EU standards. (European Environment Agency (2013a))

1.4 Microorganisms

Microorganisms mainly concerned about in this study are the bacteria *Escherichia coli (E. coli)*, *Salmonella* and potential human pathogenic *Vibrio spp.* The information given in this section about these bacteria are mainly taken from Dworkin et al. (2006) and the according chapters therein (Welch (2006); Ellermeier and Slauch (2006); J.J. Farmer III and F.W. Hickman-Brenner (2006)).

E. coli (Figure 1.3) is a Gram-negative, facultative anaerobic, rod-shaped bacterium that is nonsporeforming. It has a diameter of 0.5 μm and a length of 1-3 μm. *E.coli* is commonly motile in liquid by means of a peritrichous flagella and found in the lower intestine of birds and warm-blooded organisms (endotherms) including humans. It can be secondly found in soil and water as results of faecal contamination. It therefore provides a useful indicator for faecal pollution in bathing waters. The bacterium can grow at temperatures/ pH value ranging from 15 - 48° C/ 5.5 - 8, whereas its growth is optimal at temperatures/ pH value ranging from 37 - 42° C/ 7 (Ingraham and Marr (1987)). However, *E.coli* is known to be not able to replicate outside the intestine. *E. coli* can enter the water via effluents, the excretion of animals or after sewage treatment plants due to insufficient micro-biological treatment of effluents. Most of the *E. coli* strains are harmless, but some serotypes can cause intestinal illnesses (Brenner et al. (2005)). For example diarrhoea in human and animals by enterotoxigenic *E.coli* (ETEC) are estimated to cause 600 million cases of human diarrhoea and 800.000 deaths world wide.

Samonella (Figure 1.4) is a Gram-negative, rod-shaped, facultative anaerobic, non-sporeforming and predominantly motile enterobacteria. The bacterium is closely related to the *Escherichia* genus and is found worldwide in the intestinal tract of cold- and warm-blooded animals (including humans), and in the environment. The main difference to *E.coli* is their pathogenesis, since the serovars are capable of infecting a variety of different hosts, causing diseases ranging from mild self-limiting gastroenteritis to potentially lethal systemic infections.

There are two species recognised *Salmonella bongori* and *Salmonella enterica*, the latter of which is subdivided into seven subspecies on the basis of biochemical characteristics. Overall, there are more than 2.500 documented *Salmonella* serotypes (Popoff et al. (2001)). Members of the *S.enterica* subspecies I account for 99% of all human infections. Infections with *Salmonella* cause illnesses such as typhoid fever, paratyphoid fever, and food-born illness (Auchenthaler and Huggenberger (2003)), but most often lead to self-limiting gastroenteritis. However, 10% of untreated Typhi patients will shed bacteria for up to

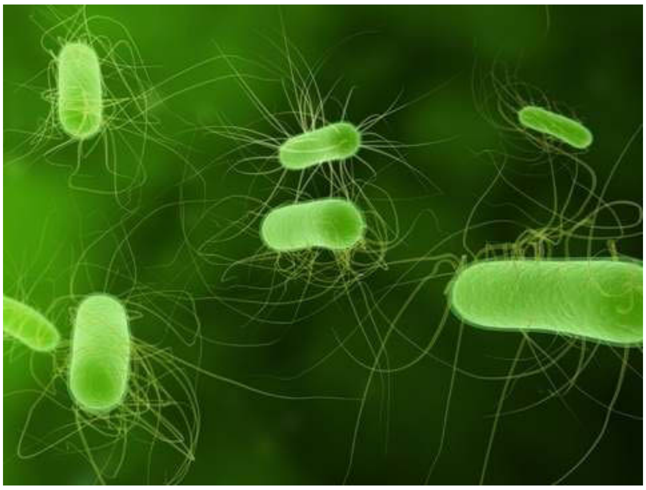

Figure 1.3: *E. coli* stock (source: Marler (2011)).

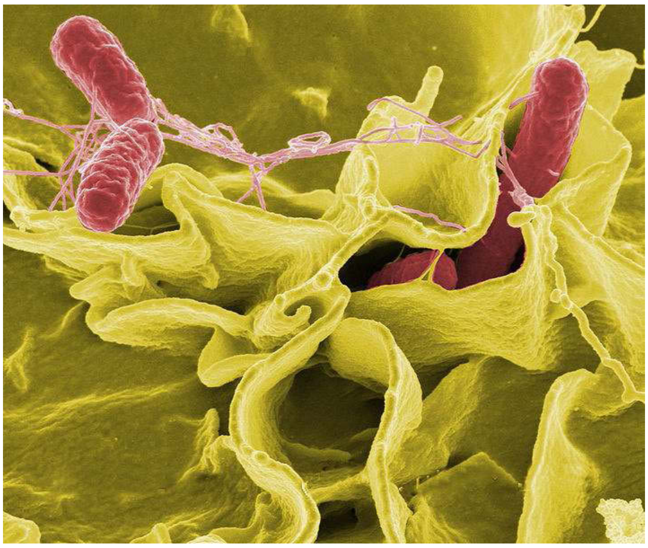

Figure 1.4: Color-enhanced scanning electron micrograph showing *Salmonella Typhimurium* (red) invading cultured human cells (source: Rocky Mountain Laboratories, U.S. Department of Health and Human Services, National Institutes of Health (2005)).

three month, whereas 1-4% become long term carriers producing infective bacteria in their stools over a year (Miller and Pegues (2000)). The bacterial dissemination requires the survival outside of the animals. *Salmonella* bacteria can enter the water via the faeces of infected animals or humans, where contaminated water is a significant source of serovar Typhi in endemic areas. Generally, the bacterium is able to replicate in contaminated food, which is rich in nutrients. However, it is not clear so far, whether the bacterium is able to survive or replicate in other environments. Several studies suggest that although the organisms can survive, they do not replicate significantly in other environments.

Potentially human pathogenic *Vibrio spp.* (Figure 1.5) are a natural component of

the bacterial flora in oceanic, coastal and estuarine saline waters (Böer et al. (2012)) and lakes (Kirschner et al. (2008)). They are Gram-negative, facultative anaerobes with comma shape and have a polar flagella. *Vibrio* belong to the family *Virbionaceae* and are halophile bacteria which prefer salt concentration larger than 5 PSU, but can also be found in less saline water (Hauk (2012)). There are 12 human pathogenic species, but the most important for European waters are e.g. *V.vulnificus*, *V.parahaemolyticus*, *V.cholerae* and *V.alginolyticus*. All of them are non-cholera *Vibrio* which do not carry the cholera causing antigen 01 and O139 (Robert Koch-Institut (2012); Landesamt für Gesundheit und Soziales Mecklenburg - Vorpommern (2010)). Most of the strains could be isolated from human and the environment.
The occurrence of *Vibrio* in sea waters presents a potential risk for humans with predisposing factors for *Vibrio* infections (e.g. pre-existing diseases like diabetes mellitus, liver diseases and heart diseases as well as a general low immunity, (Robert Koch-Institut (2012); Oliver (2013))). An infection with *Vibrio* taken up orally (via contaminated water or raw seafood) is generally marked by gastrointestinal symptoms (mainly caused by *V.parahaemolyticus* and *V.alginolyticus*) and represents one of the main causes of food-born diseases worldwide (cf. Su and Liu (2007); Jones and Oliver (2009)). An infection following contact with sea water (bathing, handling of raw fish and seafood (Dechet et al. (2008))) is associated with ear and wound infections which can lead to septicaemia and eventually even death. This is most often caused by *V.vulnificus* which is wide spread in the marine environment. Infections with *V.cholerae* cause cholera like diseases. It could be isolated from patients with mild diarrhoea, extraintestinal infections and the environment, which presents a very important reservoir.

Since all three presented bacterial groups can cause several illnesses (e.g. gastrointestinal infects, typhoid fever, septicaemia), they present a risk for human health if detectable in recreational waters. However, while *E. coli* is used as an indicator in the EU Bathing Water Directive 2006, there are no tests for *Salmonella* and *Vibrio* bacteria.

1.5 The model system

1.5.1 General Estuarine Transport Model

The numerical modelling tool applied for the present study is the General Estuarine Transport Model (GETM, see `www.getm.eu` and Burchard and Bolding (2002)). GETM is a primitive equation hydrostatic numerical model using the concept of bottom and surface following general vertical coordinates, such that even in shallow coastal waters a sufficient vertical resolution is obtained. Vertical turbulent mixing is calculated by a two-equation turbulence closure model with parameterised second moments (Umlauf and Burchard (2005)) provided by the turbulence module of the General Ocean Turbulence Model (GOTM, see `www.gotm.net` and Umlauf et al. (2005)). In the horizontal, the

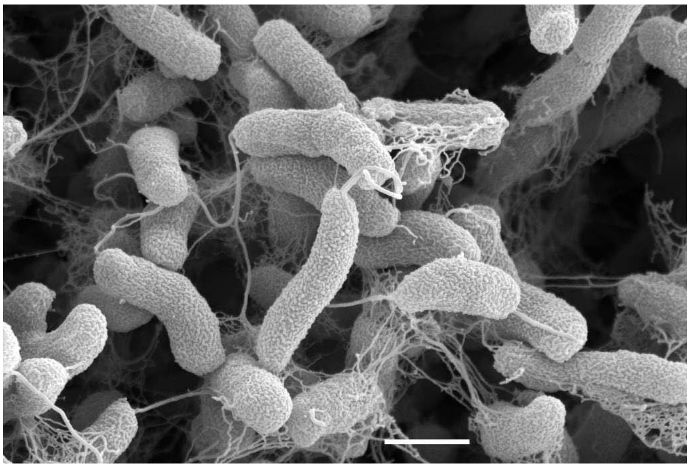

Figure 1.5: Electronic microscope picture of *V.cholerae* with scale = 1 μm (source: Muhsin Özel, G. (Holland/ Robert Koch Institute) (2012)).

discretisation can be carried out on Cartesian, spherical or curvilinear coordinates, the latter of which is applied for the present study to obtain variable horizontal resolution. For the advection of momentum and tracers, the high-accuracy positive-definite schemes according to Pietrzak (1998) are applied. For the vertical resolution the user can choose between bottom following and adaptive coordinates (Hofmeister et al. (2010)). Moreover, it is possible to attune the coastline variable with the help of the implemented wetting and drying algorithm. The transport model computes the physical state variables temperature, salt, currents (transport of momentum), bottom shear stress, turbulent kinetic energy and surface elevation with the help of state of the art advection/diffusion schemes of second and third order (Pietrzak (1998)). The computation of 2D and 3D variables are split within the circulation model. The fast barotropic part (2-D) is computed with the so-called micro timestep, while for the computation of the much slower baroclinic mode (3-D), where vertical velocity, diffusion, salt, etc. are calculated, a macro time step is used. GETM has already been successfully applied to a number of realistic high-resolution coastal and limnic areas such as for Willapa Bay (USA, Banas et al. (2007)), the Limfjord (Denmark, Hofmeister et al. (2009)), the Western Baltic Sea (Burchard et al. (2009)), the alpine Lake Alpnach (Switzerland, Lorrai et al. (2011)) and the Oder Lagoon (Poland/Germany, Schippmann et al. (2013a)). The GETM code is written in Fortran 90/95 with a modular code structure and prepared for parallel computing. This advantage has been used to compute both setups of this thesis. They have run on the *North-German Supercomputing Alliance* in Berlin and Hannover.

1.5.2 Stochastic differential equations and the General Individuals Transport Model

In various branches of natural sciences, like physics, chemistry or biology, processes can be described via differential equations. For example in marine biology these processes can be the transport of microorganisms in the water. The transport of bacteria in ocean waters is not linear, but random disturbances influence the natural phenomena Spivakovskaya (2007). These call for the use of stochastic differential equations (SDE) also known as Langevin equations to realistically model the natural process. Focussing on hypothetical particle concentration fields (C), which represent the bacteria, their dispersion is often described via the advection-diffusion equation

$$\begin{aligned} \partial_t C &= -\nabla \cdot (\underline{u}\, C - \underline{K} \cdot \nabla C) \\ \nabla \cdot \underline{u} &= 0 \end{aligned} \tag{1.1}$$

where $\underline{u}$ is the divergence free velocity field and $\underline{K}$ is the diffusivity, a symmetric and positive definite tensor. In the following only diagonal diffusivity tensors are considered with K_h as horizontal and K_z as vertical diffusivity.

This Eulerian approach focuses the fluid motion on specific locations in space (Batchelor (2000); Lamb (1994 [1932])). On the contrary, the Lagrangian approach describes the dispersion process and tracks the movement of individual particles in space and time Charles et al. (2009). Instead of solving equation (1.1), the whole solution process can be transformed into the solution of a stochastic differential equation. The concentration field $C(t, \underline{x})$ may be interpreted as a transition density field in that case (cf. Gräwe (2011)). Consequently, equation (1.1) can be interpreted as Fokker Planck equation whose solution can be written in the Îto sense (Arnold (1974)) as

$$d\underline{x}(t) = (\underline{u} + \nabla \cdot \underline{K})dt + \sqrt{2\underline{K}}d\underline{W}(t) \tag{1.2}$$

where $\underline{x}$ is the position vector. As an additional term, this equation contains a normally distributed random variable $\underline{W}(t)$, called Wiener noise increment. It is a Gaussian process with independent increments which possess a mean of $\langle d\underline{W}(t) \rangle = 0$ and a standard deviation of $Std(\underline{W}(t) - \underline{W}(s)) = \sqrt{|t-s|}\underline{I}$. This variable accounts for the random movement of particles due to horizontal turbulence. Equation (1.2) becomes an ordinary differential equation if no turbulence is available.
If computing particle distribution in a turbulent medium, turbulent diffusion needs to be included in the equation. This is achieved via random displacement of each particle due to eddies of an average size of $\sqrt{2\underline{K}}$ (Gräwe et al. (2010)). Adding up $\nabla \cdot \underline{K}$ prevents the artificial noise induced drift (Visser (1997); Hunter et al. (1993)) caused by the spatially variability of the turbulent diffusivity $\underline{K}$.

This approach was implemented in the General Individuals Tracking Model (GITM, Wolk (2003); Nagai et al. (2003); van der Molen et al. (2007)), a Lagrangian particle-tracking model, which was used to simulate the transport of the microorganisms. It was originally designed for GETM and has already been successfully applied (Wolk (2003); van der Molen et al. (2007); Schernewski et al. (2012); Schippmann et al. (2013a)). The transformation to a curvilinear grid was included by Schernewski et al. (2012).

These reflect the coastline and the bathymetry of an estuary with high accuracy. The off-line model, forced with pre-simulated flow fields of GETM, solves the equation of motion of individual particles and describes particle movement depending on advection and turbulence whereas advection dominates the tracking process. The reliability of this process is guaranteed via the GETM validation. However, wave dynamics are not taken into account in GETM and therefore cannot be reflected by the particle transport. The diffusion plays only a minor role since the advective length scale is much larger than the diffusive length scale.

The transport of particles is evaluated in the GITM within two steps. First, the advection step is calculated as analytically solution of the ordinary differential equation (Duwe (1988)) on a discrete grid and linearly interpolated to the curvilinear grid according to the velocity field. Second, the diffusion is computed by solving equation (1.2) with a random walk scheme according to Hunter et al. (1993). Finally, both terms are added together. This principle of superposition is possible because both processes, advection and diffusion, do not feedback on each other and hence are linearly independent. More detailed information about GITM can be found in Wolk (2003).

GITM assumes that the organisms are floating passively with the currents. The horizontal and vertical diffusion of every particle was simulated with the random walk method of Hunter et al. (1993). It uses a constant horizontal diffusion of K_h =1 m^{2}s^{-1} and temporally and spatially varying vertical diffusion coefficients calculated by the hydrodynamic model to compute the vertical motion. We used a first order accurate tracking scheme according to Gräwe et al. (2012). In the simulations conducted with constant wind the time step was 10 s whereas it was set to 100 s in the realistic simulations of chapter 4. The output was stored every 30 minutes. Flow field simulations were validated by comparison of drifter experiments (as described in Schernewski et al. (2012)) with similar particle tracking scenario.

The most important property of the microorganisms to be included is the mortality rate. It is described via the exponential die-off rate (Chick (1908)) in chapter 2 and 3

$$\ln C = \ln C_0 - \lambda t \tag{1.3}$$

where C and C_0 are the present and initial concentrations, respectively, λ is the inactivation rate and t is the time. The mortality process has been added in post processing to keep the particle tracking simulations as general as possible. A temperature dependent division rate of microorganisms was applied to compute the results in chapter 4 (details see chapter 4).

1.6 The thesis structure

In the present dissertation, the following two chapters represent my work published during the past two years[1]. Chapter 2 presents a first model application with the three-dimensional model system for the bathing water management in the Oder river mouth where the often insufficient bathing water quality led to several bathing prohibitions in the past. The analysis focus on scenario experiments to evaluate e.g. environmental key parameters and their effect on *E. coli* transport patterns as published in Schippmann et al. (2013a). In chapter 3 the model system was applied to an exemplary case study of *Salmonella* pollution in the Pomeranian Bight. The results were expanded with backtracking simulations to determine possible emission source areas. Moreover, supra-regional recommendations towards an improved management were derived in this study as published in Schippmann et al. (2013b). In contrast to the former chapters, where the bacteria obtained a constant mortality rate, in chapter 4 a temperature-dependent growth rate was implemented. The model system was applied to a case study in the Bay of Greifswald, where the recurrence of potential human pathogenic *Vibrio spp.* caused several infections (and deaths) in the past, in order to benchmark e.g. whether the seasonal cycle of *Vibrio* presence and the inter-annual differences in *Vibrio* occurrence in the bay and in the southern Pomeranian Bight can be attributed to water temperature and depth. In the last chapter 5, the simplified online version of the presented model system and its implementation into a web platform is presented. It was developed during this dissertation in the framework of the EU-project "GENeric European Sustainable Information Space for Environment (GENESIS)".

[1] also sections 1.3 and 1.5 in the thesis's introduction are based on the published work listed below the thesis

Chapter 2

Escherichia coli pollution in a Baltic Sea lagoon: A model-based source and spatial risk assessment

2.1 Introduction

More than 95% of the European beaches have been awarded the blue flag (Foundation for Environmental Education (2012)), an indicator for good water conditions including good hygienic water quality. Bathing places of the outer Oder Lagoon coast, located at the Pomeranian Bight, belong to them. This fact has promoted the tourism development of that region since decades. For the last 50 years, tourism and especially bathing tourism has also become an important economic factor around the Oder Lagoon. However, the main focus is still on the outer coast. Each year approximately ten million tourists book an overnight stay in this region, whereas there are only about 40.000 overnight stays for the inner coasts (Statistical Government Poland (2012)). There are several plans by the German and Polish governments to support the development of this region. For example, the extensions of beaches, marinas and various water sport activities (Institute for Meteorology and Water Management Poland (2010a)) are planned in order to reduce the existing strong social and economic gradients between outer coast and hinterland. However, two main problems counteract the improvement of the inner lagoon coasts. At first, the often insufficient hygienic water quality, particularly in the Oder mouth area (from Szczecin to Trzebiez), led to beach closings in the past. These damaged the reputation of the region. Secondly, monitoring data gives only an incomplete picture of *Escherichia coli* (*E. coli*) bacteria sources and spatial transport patterns. It neither provides support for a decision in favour of new tourism infrastructures, nor does it help deciding on a better water quality management.

Since the direct study of pathogen agents is often too laborious, indicator organisms are used as scale for the hygienic water quality. These organisms show a possible presence of pathogens with similar biological origin and hence a potential health risks (Kreikenbaum

(2004)). *E. coli* is the most reliable indicator for faecal contamination (World Health Organisation (2003)). Wheeler et al. (2003) and Whiteman and Nevers (2004) showed that *E. coli* bacteria concentrations are spatially small-scale and temporal highly variable even at single beaches. Thus, the water quality measurements can neither show a valid temporal course for one beach nor a full picture of a region.

The application of circulation and particle tracking models presents a good and promising addition to the observations. They can be used to compute water currents, forced by e.g. measured wind and river run-off, and according to this, compute the pathways of particles as for instance *E. coli* bacteria. A temporal and spatial picture of the particle distribution (forward-tracking) can be provided. Furthermore, the analyses of different wind and river run-off scenarios are possible.

Particle tracking can be used as an off-line tool together with pre-simulated flow fields and also as an online tool. In the latter approach the tracking module is coupled or linked to the hydro-dynamical model (cf. Navas et al. (2011)) whereas in the former case the circulation and tracking models are successively executed. This approach has already been applied as a coastal management tool in the Oder lagoon (Schernewski and Jülich (2001); Schernewski et al. (2002)), at the north-west coast of England (Kashefipour et al. (2002)) or in the Mediterranean Thau lagoon (Fiandrino et al. (2003)).

In previous work of Schernewski et al. (2012), the authors applied the same 3D model system as we do in this study (section 1.5.2). The authors figured out the sources of *E. coli* pollution at Ueckermünde beach in the Oder Lagoon with the help of realistic simulations and idealised scenario modelling. In the present study the focus is on the Oder mouth area. It is the most interesting area of *E. coli* contamination in the Oder lagoon. Scenario analyses help to find the key control parameters for *E. coli* transport ranges on the one hand. On the other hand, realistic simulations of the bathing period in summer 2006 show a spatial and temporal picture of the *E. coli* distribution. Together with the good data availability, the high model resolution allows to zoom in on single beaches.

The main objectives of this study are a) to identify the environmental key control parameters and their effect on *E. coli* transport patterns, b) to evaluate whether Szczecin and the Oder river have been the sources of pollution in the past and whether this is still the case today, c) to locate places where to establish new bathing places and d) to benchmark the effect of the new bathing water directive on the beach closings of the past.

2.2 Study site

The Oder (Szczecin) Lagoon is part of the Oder estuary located at the western Baltic Sea (Figure 2.1). It is shared between Germany (Small lagoon) and Poland (Wielki Zalew). The lagoon covers an area of 687 km^2 and has an average depth of 3.8 m. The highest natural depth is 8.5 m which can exceed 10.5 m in the artificial shipping channel (Radziejewska and Schernewski (2008)). Water exchange between the lagoon and the Baltic Sea happens via three outlets: the Peene Strom in the north-west (17% of water

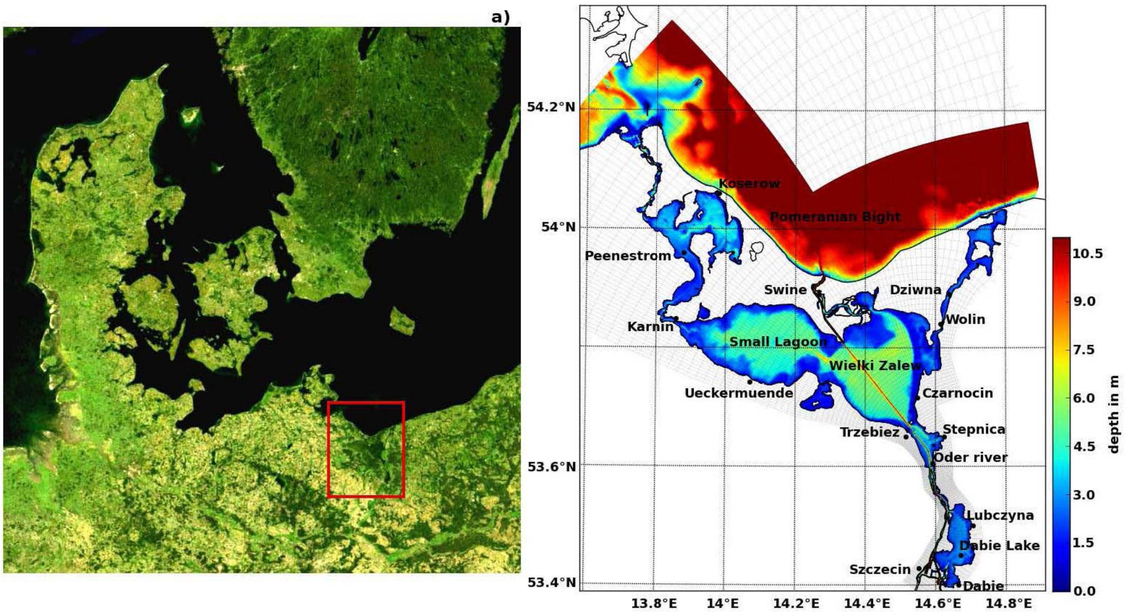

Figure 2.1: (a) Satellite picture of the Western Baltic (Flash Earth). Selected: area of Oder Lagoon. (b) Topography of entire model set-up area and grid outline showing every 20-th grid box.

exchange), the Swine river in the north (69% of water exchange) and the Dziwna river at the north-east side (14% of water exchange) (Mohrholz and Lass (1998)). At the same time the Oder river run-off transports about 17 km^3 water per year. The overall water transparency is often below 1 m in summer due to wind- and wave-induced resuspension of sediment and high primary production (Schernewski et al. (2012)). The main processes that govern the fluxes in the Oder Lagoon are Oder river run-off and wind. The Oder river water drains continuously into the lagoon. The strength of the river run-off depends on the river lever (low and high water) caused by rainfall and storm events. The Oder river water needs 20-40 days until Swine river and circa 100-140 days until Peenestrom (Schernewski and Jülich (2001)). On the contrary, water exchange between the Baltic and the lagoon occurs only pulse-like via Swine river (Mohrholz (1998)) and hence plays a minor role. Strong wind events and higher water level in Pomeranian Bay allow the penetration of saline Baltic water along the shipping channel into the lagoon (Bangel et al. (2004)). The salt water influxes reach, however, not farther than the area around the Swine channel (Radziejewska and Schernewski (2008)). No water is exchanged via the Peene and Dziwna since the channels are too long (40 km) and shallow (max 3m) (Mohrholz and Lass (1998)). Due to the sporadic inflows of sea water into the Oder lagoon, the salinity ranges from 0.5 – 2 in central parts. In the Oder mouth area the salinity concentration is seldom larger than 1 (Bangel et al. (2004)). Overall, the shallowness of the lagoon hinders a temporal vertical stratification (Bangel et al. (2004)). Mohrholz and Lass (1998) find the theoretical water exchange time of about 2 month.

Szczecin is located 21 km upstream the lagoon, has nearly 420.000 inhabitants and produces 77.000 m^3 waste water per day (European Comission (2000)). In 2003 only 16% of the city's population was connected to waste water treatment facilities and more than 60% of all waste water was discharged untreated into the Oder river (IKZM Oder (2007)). In 2006 65% of the sewage was treated biologically/chemically while 27% of Szczecin's effluents were still treated mechanically and 8% of the water even went untreated (Council of Ministers Republic of Poland (2008)). As a consequence of the EU project *Water quality improvement in Szczecin* (European Comission (2000)) more than the 80% of Szczecin's households were connected to waste water treatment plants in 2009 (World Health Organisation (2009)). In addition to Szczecin, diffusive or small local sources of *E. coli* contribute to the overall budget (cf. Schernewski et al. (2012)). These originate from agriculture fields, cattle ranching or even seagull faeces and tourists themselves. Although the general Lagoon bathing water quality has improved during the last ten years (European Environment Agency (2010)), the beaches at Dabie, Lubczyna, Stepnica, Trzebiez and Czarnocin needed to be closed in 2006 due to too high coliform bacteria concentrations (Depellegrin (2008),Schernewski et al. (2012)). Together with faecal Streptococci these are typical indicators for faecal pollution in the 1976 EU Bathing Water Directive (European Union (1976)).

2.3 Measurements and methods

2.3.1 Measurements

Within our study we apply several measurements to validate and force our models. Time series of water gauges and sea surface temperature are used to validate the circulation model. These are provided by the Federal Maritime and Hydrographic Agency for all German stations. All data, including water quality measurements, at the Polish stations have been provided by our GENESIS project partners from the Institute for Meteorology and Water Management Krakow. The wind measurements, used as forcing for the circulation model, are taken from the German Weather Service.

In 2006 the water quality measurements for the Oder mouth area started in May. Even at this time and again in June increased coliform concentrations have been observed. In contrast, the first increased *E. coli* concentrations have been measured at the end of June. *Coliform* bacteria concentrations reached their peak at the end of July and at the beginning of August. In mid July more than 10.000 cfu/100 ml total-coliforms have been measured at all beaches. The mandatory values of the 1976/7/EEC directive (2000 cfu/100 ml) are exceeded more than eightfold (Figure 2.2). Although *E. coli* have their highest concentration in the middle of June in Trzebiez, the measurements have seldom reached the thresholds of the new directive 2006/7/EC (Figures 2.2 (b)). The period of increased concentrations lasted until the end of September for both *coliform* and *E. coli* bacteria. However, the measurements are not continuous for all surveyed beaches. Comparing meteorological and *E.coli* measurements allows the same conclusion for all

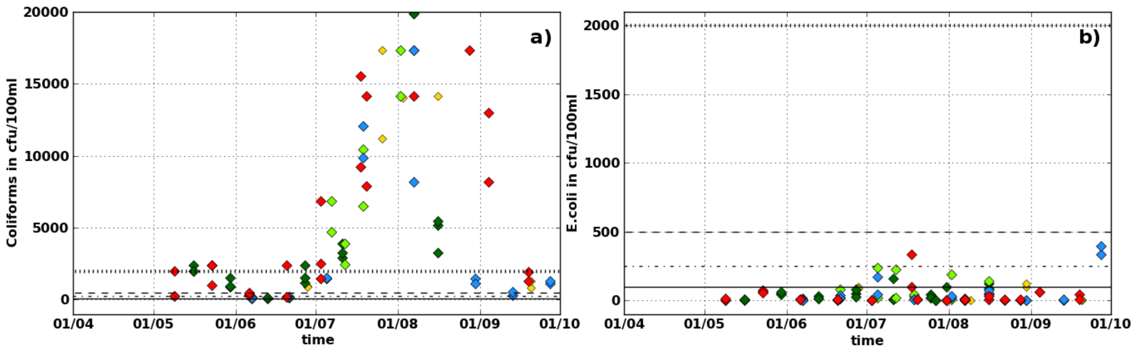

Figure 2.2: Coliform (a) and *E. coli* concentrations (b) in 2006 measured in Czarnocin (yellow), Trzebiez (red), Stepnica (blue), Lubczyna (light green), and Dabie (dark green) plotted against the thresholds of the EU Bathing Water Directives 1976/7/EEC (solid line: guide value, dotted line: mandatory value) and 2006/7/EC (dashed-dotted line: guide value, dashed line: mandatory value).

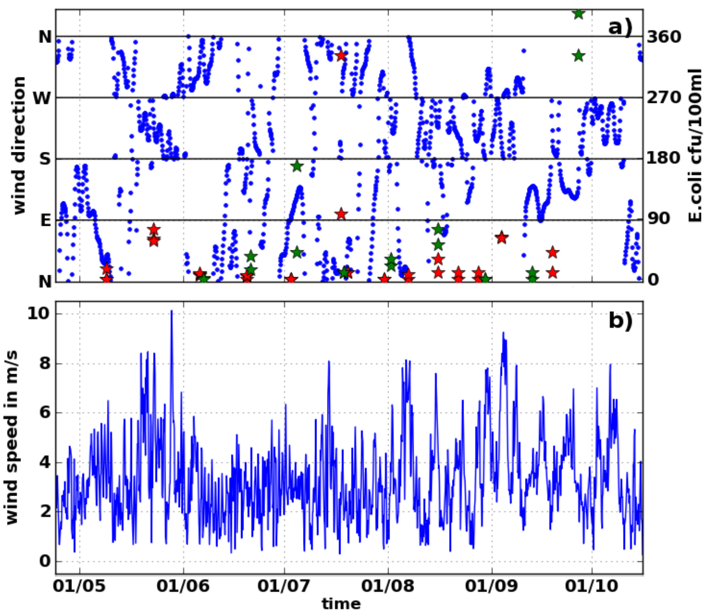

Figure 2.3: Filtered wind direction (a) together with *E. coli* measurements at two exemplary stations Trzebiez (red stars) and Stepnica (green stars) and wind speed (b) summer 2006.

beaches. Most of the bathing water samples have been taken at days with south winds (Figure 2.3). Particularly in August the wind direction was mainly south-west with speeds of 3-6 ms^{-1}.

2.3.2 Forcing the circulation model

The used topography is a combination of several data sets (Glockzin (2006), Bundesamt für Seeschifffahrt und Hydrographie (2010), pers. comment K. Buckmann). The raw bathymetry has an overall resolution of less than 50 m, which is interpolated to a curvilinear grid (Figure 2.1(a)). The model grid-spacing varies between 15 m in the southern Oder mouth and 200 m in the Pomeranian Bight. For the vertical resolution 10 sigma levels are used. The whole domain ($800 \times 1300 \times 10$ grid-points, 33.6% active water points) was decomposed into 294 active sub domains of $44 \times 44 \times 10$ grid-points to maintain the computational feasibility of the simulation. A micro time step of $t = 0.4$ s is used, while a macro time step of $t = 8$ min is chosen to compute the 3D variables. The output fields are stored on an hourly basis.

The realistic simulations start in April with a constant initial temperature of 5°C where the initial salt is given as 3D concentration field, interpolated from an older realistic Oder Lagoon simulation (Schernewski et al. (2012)) with lower resolution. The initial velocities are set to zero.

Realistic meteorological forcing with a resolution of 7 km, taken from the German weather service, is applied when computing the realistic flow fields. The steady state simulations are obtained by applying constant wind speeds from the 8 cardinal wind directions N, NE, ..., NW (45 degrees intervals) and the two 10 metre wind speeds 3 and 6 ms^{-1}, respectively.

The freshwater river run-offs of the Peene and Uecker have been chosen as constant values of 20.6 $\mathrm{m}^3\mathrm{s}^{-1}$ and 9.5 $\mathrm{m}^3\mathrm{s}^{-1}$ (summer median) for all simulations, respectively, since they are negligible. In contrast, the measured discharges of the Oder river are used for the realistic model simulations of 2006 and 2008. On the contrary, the climatology summer median, summer min and mean summer max discharge of 1912 – 2003 (414, 64, 1606 $\mathrm{m}^3\mathrm{s}^{-1}$), respectively, have been taken as Oder river run-off in different steady state simulations. Due to their relevance for tourism, we only considered the summer months April - October and the according Oder discharge.

GETM was forced with 2D and 3D fields along the open boundaries at the Pomeranian Bight (Figure 2.1). The 2D forcing includes sea surface elevation and depth averaged currents in combination with Flather boundary conditions (Flather (1976)). The 3D forcing includes salt and temperature. All boundary information is taken from a 600 m Baltic Sea simulation model. The 2D and 3D fields have a temporal resolution of 1 and 6 hours, respectively. This setup was also used to compute the results of chapter 3, but using a different area of interest (the Pomeranian Bight).

2.4 GETM validation

2.4.1 Elevation

The circulation model has only a few degrees of freedom and was fed with reliable boundary information from both meteorological forcing from the German Weather forecast Service and boundary conditions (sea level, velocities, salt and temperature). The latter of which were used to force the model from the open boundaries of our model domain (the area of interest). This "outer model", which has produced the boundary information, has been successfully validated against measurements. At the Oder Bank Buoy, located at the northern boundary of our model setup, modelled salinity has a Bias of -0.12 PSU and a root mean square error (RMSE) of 0.95 PSU. The temperature Bias was about 0.1 K and the RMSE was 0.7 K. In comparison with the standard deviation of the measurements (5.9 K) this is comparatively small. Consequently, our model setup was fed with reliable information and, moreover, validated itself. Since there is no defined river plume visible according to salt gradients, the ability of GETM to simulate the hydrodynamics of the Pomeranian Bight is proven with the water gauge time series. However, one of the most important tool so far to make Oder river plumes visible is the remote sensing of Chlorophyll-a and particulate matter (cf. Siegel and Gerth (2000)).

The 2006 and 2008 time series of the modelled sea surface elevation are compared to the corresponding water gauge measurements between April and October at Koserow (Pomeranian Bight), Karnin (Peene Strom) and Ueckermünde (Small Lagoon) in 2006 (not shown) and Koserow, Karnin (not shown), Ueckermünde, Wolin (Dziwna) and Trzebiez (Oder river mouth) in 2008.

GETM reproduces the general trend of the observations (Figure 2.4). Especially, the outer lagoon dynamics with their strong variability are very well captured (Figure 2.4 (a)). However, the forcing misses the strong peaks (caused by seiches) at the outer boundary (Koserow). This is due to the fact that the boundary information have too low variabilities which a high resolution model, that is nested, cannot produce by its own. Thus, the variabilities of the sea surface elevation are dominated by the open boundaries and hence GETM cannot reproduce the variability within the lagoon. Nevertheless, the overall water level coincides with the observations (Figure 2.4 (b)-(d)). This can also be found in the statistics. The mean root mean square error (RMSE) is approximately 7 cm (Table 2.1) in both years. In comparison with the standard deviation of the measurements (21.3 cm) this is comparatively small. The mean coefficient of determination (R^2) of 0.68 and 0. 67, respectively, shows that the modelled sea surface elevation is in good agreement with the observed one (Table 2.1).

2.4.2 Temperature

The 2008 time series of the modelled sea surface temperature are compared to the corresponding measurements between April and October at Swinoujscie (Swine) and Trzebiez (Oder river mouth). GETM reproduces the seasonal temperature at both stations (Figure 2.5). The temperature deviations (RMSE) of the simulation are approximately 1.5 °C and 1.63 °C. Furthermore, the mean R^2 of 0.93 and 0.96 shows overall high agreement of model results and observations (Table 2.2).

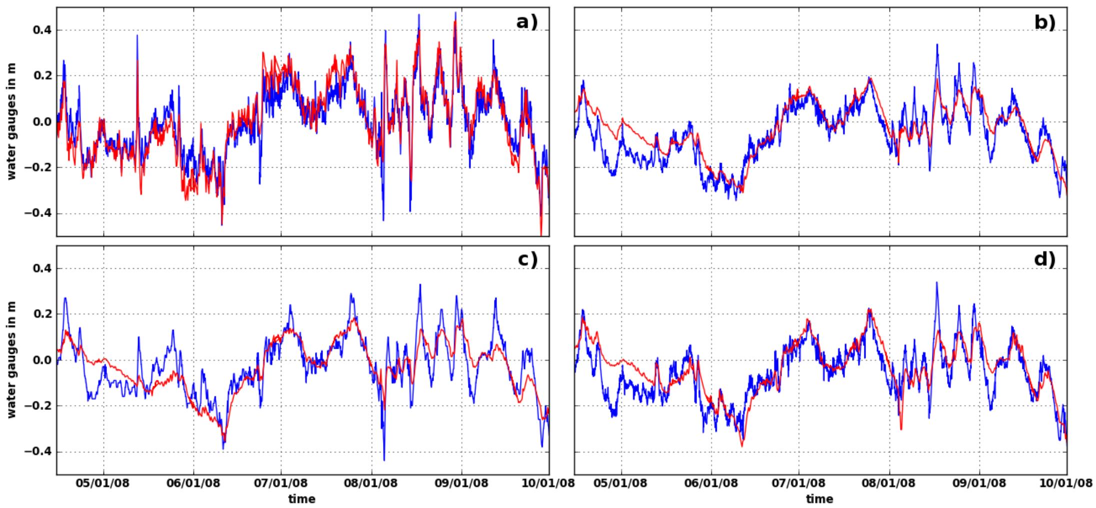

Figure 2.4: Time series of the measured water gauges (blue) against the model results (red) from April to October 2008 at stations: Koserow (a), Wolin (b), Ueckermünde (c) and Trzebiez (d).

2006	**mean**	**max**	**min**
RMSE	0.07	0.08	0.06
R^2	0.68	0.78	0.55
2008			
RMSE	0.07	0.09	0.06
R^2	0.67	0.79	0.45

Table 2.1: Mean, maximum and minimum root mean square error and coefficient of determination computed from the surface elevation model results of 2006 and 2008.

2008	**Trzebiez**	**Swinoujscie**
RMSE	1.63	1.51
R^2	0.96	0.93

Table 2.2: Root mean square error and coefficient of determination for surface temperature at Trzebiez and Swinoujscie.

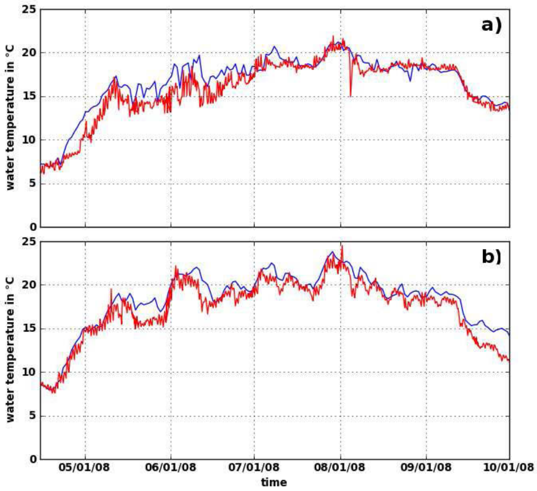

Figure 2.5: Time series of the measured water temperature (blue) against the model results (red) from April to October 2008 at Swinoujscie (a) and Trzebiez (b).

2.4.3 Scenarios

Scenario analyses help to find the key control parameters for *E.coli* transport. These are carried out under the assumption of a present state situation where all waste water is treated biologically/ chemically in Szczecin. As known from literature (Hagendorf et al. (2004); Umweltbundesamt (2011)) the total number of *E. coli* bacteria in treated effluent is 10^6 cfu/100 ml. Further we know that the sewage treatment plant *Zdroje* (close to emission location in the south) has a capacity of 18.000 m^3 per day. In case of our steady state simulations that means $2 \cdot 10^{14}$ *E. coli* bacteria enter the river off the treatment plant per day. Adding the mean bacterial concentration of the Oder river ($2 \cdot 10^{14}$ cfu/m^3 per day) at this position (personal Comment IMGW) we end with a bacterial load of $4 \cdot 10^{14}$ cfu/m^3 per day at the source in the south. Assuming the complete renovation of the sewers in Szczecin (according to European Comission (2000)), no diffuse loads are entered in the city and hence only the bacterial river load of 10^{14} cfu/m^3 per day at this position is taken into account. Since we emit 10.000 particles at each emission location every particle represents $4 \cdot 10^{10}$ *E. coli* bacteria in the south and 10^{10} *E. coli* bacteria off the city.

In order to validate the impact of wind on the *E. coli* transport, 16 tracking experiments have been done according to the 8 cardinal wind directions and two different wind speeds in the first scenario.

In the following scenarios a constant south-west wind with 3 ms^{-1} is used as forcing since this is the prevailing summer wind condition (Schernewski et al. (2012)).

The second steady state scenario comprises a mortality rate experiment because the inactivation rate of *E. coli* bacteria is not well-defined. The mortality rate strongly depends on the turbidity, salinity, temperature conditions of the environment and also on the measurement method. Kashefipour et al. (2002) reported about die-off rates/T_{90} times (the time needed to reduce the initial bacterial population by 90 %) in coastal and riverine waters between $\lambda = 0.097$ h^{-1} (T_{90}=10.3 h) and $\lambda = 0.0296$ h^{-1} (T_{90}=33.78 h) according to wet and dry weather conditions and also varying temperature. The very low salinity concentrations of 0.5 - 1.5 PSU in the Oder mouth area (Bangel et al. (2004)) together with the overall high water turbidity, due to nutrient loads, favour *E. coli* growth (Atwill et al. (2004); Anderson et al. (2005)). On the contrary, the high summer temperatures have a negative influence on the survival of these bacteria (Medema et al. (1997); Mallin et al. (2000)). However, *E. coli* survival experiments with brackish Lagoon water are seldom and no exact mortality rate has been established for such a special environment. Thus, we take three different mortality rates to present worst, mean and best case situations. Schernewski et al. (2012) empirically calculated the die-off rate of $\lambda = 0.0571$ h^{-1} (T_{90}=17.51 h) from laboratory survival experiments. One has to note, these experiments are idealised and contain a high uncertainty. Albeit, we assume this rate to describe the best case scenario in the Oder lagoon. In their microcosm study, Mezrioui et al. (1995) showed survival rates of *E. coli* in Brackish Thau Lagoon water of $\lambda = 0.009$ h^{-1} (T_{90}=111.1 h) during autumn 1985 and $\lambda = 0.0185$ h^{-1} (T_{90}=54.1 h) as mean of the measurements in summer 1985 and 1986. Both experiments are carried out at temperatures similar to the summer temperature of the Oder Lagoon (18-22 °C, Dueri et al. (2010); Schernewski and Janßen (2007)). As the autumn rate is fairly small compared to other known values from literature, we assume this to be the worst case mortality rate in the Oder lagoon. Considering a more general scenario, the Thau lagoon summer mortality rate of $\lambda = 0.0185$ h^{-1} (T_{90}=54.1 h) is applied to present the mean situation.

In the third scenario experiment flow fields computed with the climatological summer minimum, summer maximum and summer mean run-off, respectively, are used to force the particle tracking model in the third steady state scenario. In the fourth steady state experiment three different emission amounts of E. coli are used to evaluate the impact of waste water treatment. If we further consider a future scenario where the river water is additionally UV-disinfected as in the Isar river (Bavaria, Germany, Wasserwirtschaftsamt München (2012)) a 99% reduction of *E. coli* load would be possible ($2 \cdot 10^{12}$ cfu/m^3 per day). Due to vegetative filter strips along the Oder river coast, cattle treading and agriculture inflows into the river can also be reduced (Kistemann et al. (2009)). We assume again a 99% reduction of *E. coli* load (10^{12} cfu/m^3 per day). Hence, in this future scenario each of the 10.000 particles emitted would carry 10^8 *E. coli* bacteria.

GETM flow fields of the summer season in 2006, based on realistic meteorological and river forcing, serve as forcing for a realistic *E. coli* transport scenario, where 10^3 particles have been emitted daily and tracked for 7 days. In this scenario each m^3 water of the sewage treatment plant contains 10^{12} *E.coli* bacteria (10^8 cfu/100 ml in untreated sewage (Mehlhart and Klaus (2002))). Hence, $2 \cdot 10^{16}$ E. coli bacteria enter the river off the treatment plant per day. Measurements off Szczecin indicated E. coli concentrations of $2 \cdot 10^{16}$ per day (personal comment IMGW). The background river load concentration plays thus a minor role in both cases. That means $2 \cdot 10^{16}$ bacteria need to be emitted per day at both emission locations. As 500 particles have been emitted at each of both release points, every particle represents $4 \cdot 10^{13}$ bacteria.

An overview of all scenario parameters can be found in Table 2.3. Please note, all following concentration maps in this study show the mean concentration in the whole water column.

scenario	**mortality** $[h^{-1}]$	**wind** $[ms^{-1}]$	**river** $[m^3s^{-1}]$	***E. coli*** **amount [cfu/100 ml]**
wind (W)	0.0185	N, NO, ...,NW: 3, 6	414	10^6
mortality (M)	0.009 0.0185 0.0571	SW 3	414	10^6
river (R)	0.0185	SW 3	64 414 1606	10^6
emission (E)	0.0185	SW 3	414	10^8 10^6 10^4
real 2006	0.0185	measurements	measurements	10^8

Table 2.3: Parameter sets for the different particle tracking scenarios.

2.5 Results

2.5.1 Wind scenarios

The prevailing wind conditions and resulting flow fields mainly control the transport distance and concentrations of *E. coli* bacteria. According to the dominant wind conditions (Schernewski et al. (2012)), GETM simulations with constant 10 meter wind speeds of 3 ms^{-1} and 6 ms^{-1} were carried out for 8 different wind directions.

In terms of the particle tracking, the influence of the wind speed is mainly visible in the spatial distribution of high flow velocities (Figure 2.6). The typical wind situation in the Oder lagoon area is represented with a 10 meter south-west wind of 3 ms^{-1}. The surface flow (Figure 2.6) shows a complex flow pattern of the Oder mouth region with strongly varying surface velocities. At the Oder entry in Dabie and even in the deep channel-like area north of the Lake (shipping channel) these are higher than 0.15 ms^{-1} whereas the velocities are smaller in shallow waters close to the coast (Figure 2.6 (a)). Particularly in

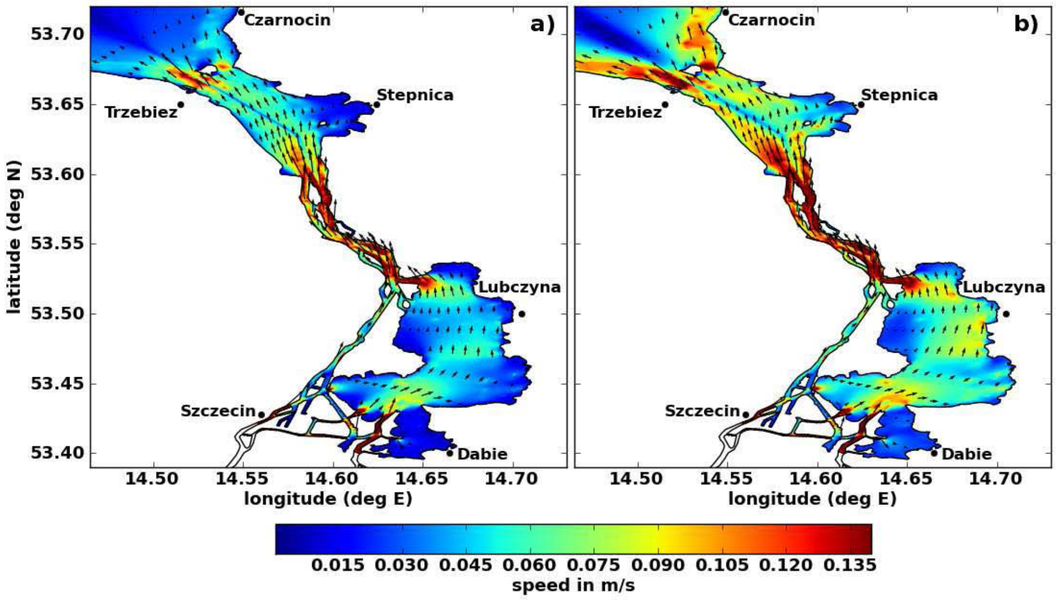

Figure 2.6: Surface flow fields in the Oder mouth area for a steady south-west wind at a speed of 3 ms^{-1} (a) and 6 ms^{-1} (b).

the small coves along the east cost of the river the velocities are less than 0.02 ms^{-1}. In contrast, at wind speeds of 6 ms^{-1} higher velocities occur even in the small, shallow coves along the east cost, in the Dabie lake and in the north Oder mouth (Figure 2.6 (b)).

The wind scenario shows that variabilities of the *E. coli* concentrations depend more on wind direction than on the wind speed (cp. Figure 2.7(a,c) and 2.7 (b,c,d)). Northern winds lead to the development of reduced concentrations at the eastern coast of Dabie lake (2.7 (b,d)), where the concentrations are equally distributed under south-west winds (2.7 (a,c)). These favour the bacterial upriver transport. However, all scenario simulations show equally high likelihoods for hazardous *E. coli* concentrations near the emission locations namely, in the central Dabie lake and in the west branch of the Oder river. The main plume of the *E. coli* bacteria is, in general, transported along the west coast of the Oder river, next to the shipping channel. Bacteria originating from Szczecin are pressed through a small straight into the lake. These flow downriver through central Dabie lake together with the bacteria originating from the Oder river entry. The EU threshold for sufficient bathing water quality of 500 cfu/100 ml is exceeded in whole Dabie lake and Trzebiez for all simulations. The north-east coast of the Oder mouth (Stepnica, Czarnocin) is not at risk in most of the wind situations.

2.5.2 Mortality scenarios

The very low salinity concentrations and overall high water turbidity of the Oder lagoon favour *E. coli* survival (Atwill et al. (2004); Anderson et al. (2005)). Given that, to our knowledge, there are no valid survival times for this special environment stated in the

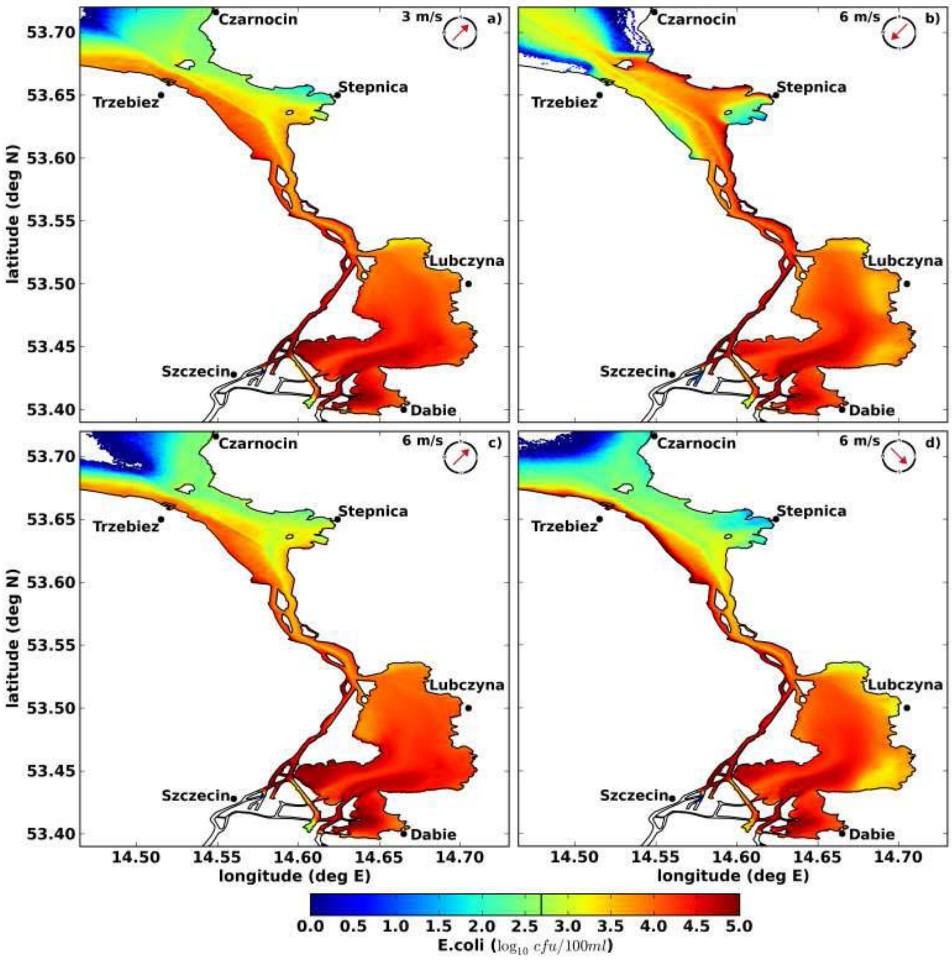

Figure 2.7: *E. coli* bacteria concentration pattern at: south-west wind at speed of 3 ms^{-1} (a), north-east wind at speed of 6 ms^{-1} (b), south-west wind at speed of 6 ms^{-1} (c) and north-west wind at speed of 6 ms^{-1} (d). The black line within the colour scale shows the EU threshold of 500 cfu/100 ml.

relevant literature, extreme and most probable values need to be taken into account to evaluate their impact on the *E. coli* concentration level. The general climatological summer situation without any extreme wind or discharge events is assumed for these experiments. It is computed with the parameters given in scenario M (Table 2.3).

Taking the worst case survival rate of λ =0.009 h^{-1} (Figure 2.8 (a)), hazardous *E. coli* concentrations of more than $10^{4.5}$ cfu/100 ml are possible at all coasts in Dabie lake and alongside the Oder river until Trzebiez. Even in the northern Oder mouth close to the Oder lagoon high concentrations of more than $10^{3.5}$ cfu/100 ml are possible. The most dangerous concentrations (more than 10^5 cfu/100 ml) occur close to the emission locations.

Applying the mortality rate of λ =0.0185 h^{-1} (Figure 2.8 (b)), the whole Oder river and Dabie lake are likely contaminated (more than $10^{3.5}$ cfu/100 ml). Although high concentrations (of more than $10^{3.5}$ cfu/100 ml) enter the Oder lagoon via the western

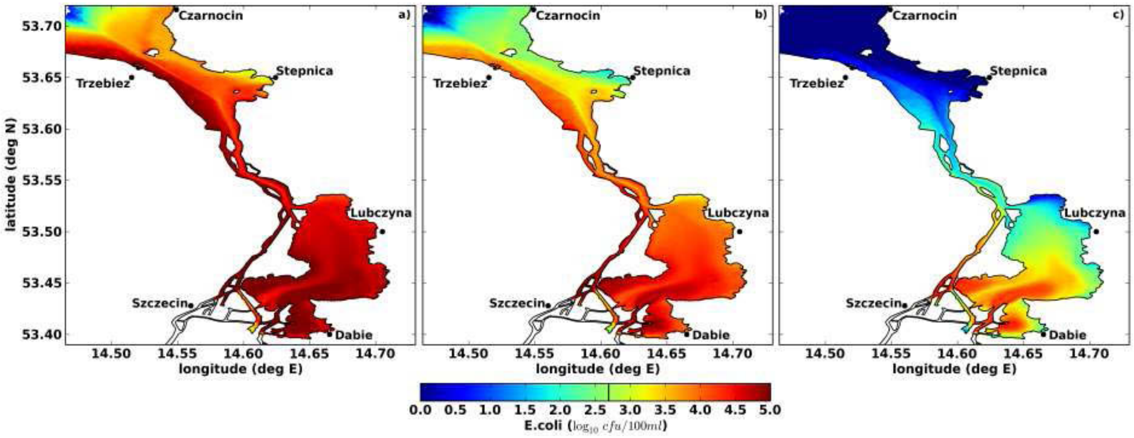

Figure 2.8: Risk map of maximal *E. coli* concentration computed with different mortality rates (scenario M). (a) λ =0.009 h^{-1}, (b) λ =0.0185 h^{-1} and (c) λ =0.0571 h^{-1}. The black line within the colour scale shows the EU threshold of 500 cfu/100 ml.

river flow (Trzebiez), these bacteria will die before they reach the next bathing place at the Oder lagoon coast. Concentrations of less than 500 cfu/100 ml occur in the small branches at the north-east of the Oder river (Stepnica) as well as in the north-eastern Oder mouth. Thus, these areas are not at risk.

With the best case die-off rate of λ =0.0571 h^{-1} (Figure 2.8 (c)) no risk can be found at the surveyed bathing areas. Contaminated areas are the south-west coast of Dabie Lake (island) and the complete eastern branch of the Oder river. Even at the beach in Dabie, close to the emission source, a sufficient bathing water quality is likely.

2.5.3 River discharge scenarios

In addition to the wind also the Oder river discharge influences the flow field pattern in the Oder mouth area and thereby the transport of *E. coli* (scenario R, Table 2.3). During minimum river run-off the currents are less than 0.04 ms^{-1} in the whole Oder mouth (Figure 2.9 (a)). Thus, nearly all of the released bacteria stay in Dabie lake until they become inactive (Figure 2.9 (d)). It takes approximately 6 days before the bacteria reach the beach of Lubczyna. The main *E. coli* plume stays close to the emission location. It scarcely reaches the northern part of the lake. The anti-clockwise flow pattern, established in the north-west Dabie lake, leads to north-eastward directed transport of the emitted bacteria. However, no hazardous concentrations are probable outside Lubczyna. Simulations with the summer mean river discharge (Figure 2.9 (b)) show mean velocities of 0.06 ms^{-1} which can exceed 0.1 ms^{-1} in the shipping channel. Hence, the bacteria reach Lubczyna after approximately two days and need additional four days to reach Trzebiez (20 km from Szczecin). The flow field transports *E. coli* bacteria into the Oder lagoon, but these get inactive until the next bathing place is reached due to their mortality rate. As described in detail in section 2.5.2, contaminations of the west coasts of the Oder river as well as Dabie lake are most likely (Figure 2.9 (e)). In contrast, the north-east coast of the river (Stepnica, Czarnocin) is not at risk. This is not the case for summer maximum river discharge (Figure 2.9 (f)). Due to the increased mean flow speed of 0.2 ms^{-1} the transport time of the bacteria has shorten and it takes only 2 days to reach for example Trzebiez. Active concentrations of more than $10^{3.5}$ cfu/100 ml are probable there. The increased flow speed leads generally to higher mixing in the Oder river which overlaps the influence of the wind. Hence, the *E. coli* concentrations are nearly equally distributed ($10^{3.5}$ - 10^4 cfu/100 ml) elsewhere in the area of interest (Figure 2.9 (c)). Hence, none of the surveyed bathing places is save for bathers under these conditions.

2.5.4 Emissions amount scenarios

Three different emission amounts of *E. coli* bacteria (scenario E, Table 2.3) have been used to show the impact of different sewage treatment on the concentration levels in the Oder mouth area. The waste water treatment and river water quality of the past, present and possible future provide the basis for these scenarios. If merely mechanically treated sewage or even pure effluents enter the Oder river, concentrations of 10^8 *E. coli* cfu/100 ml have been measured (Mehlhart and Klaus (2002)) (past scenario). Assuming a biological treatment of the effluent, 10^6 *E. coli* cfu/100 ml enter the water (Hagendorf et al. (2004); Umweltbundesamt (2011)) (present scenario). Considering the future scenario, where an additional UV-disinfection of the sewage is assumed and vegetative filter strips along the Oder river coast, 10^4 *E. coli* cfu/100 ml can be expected in the water.

In the past scenario hazardous *E. coli* concentrations are most likely to be found in the whole area of the Oder mouth (Figure 2.10 (a)). They exceed 10^6 cfu/100 ml close to the emission locations and still 10^5 cfu/100 ml in the north Oder river. At Czarnocin, the northernmost place examined in this study, concentrations of $10^{4.5}$ cfu/100 ml are likely. Moreover, *E. coli* bacteria reach the Oder lagoon most probable in high concentrations of more than $10^{4.2}$ cfu/100 ml. The situation is rectified by modern waste water treatment. As described in section 2.5.2, contaminations of the west coasts of the Oder river as well as Dabie lake are most likely. The north-east coast of the river is not at risk (Figure 2.10 (b)). The future scenario shows that a further enhancement of the bathing water quality is possible (Figure 2.10 (c)). The EU thresholds for a sufficient bathing water quality are exceeded only close to the emission source, in central Dabie lake and in the west branch of the Oder river. All surveyed bathing places can reach excellent water quality.

2.5.5 Realistic simulation in 2006

To present a temporal and spatial picture of *E. coli* bacteria concentrations, dynamic flow simulations have been carried out for the summer season 2006, forced by realistic wind fields, atmospheric and boundary data. Particles are released in two periods. First, every day from 13/07/06 till 18/07/06 at 12'clock tracked until 19/07/06 and second, every day from 10/08/06 till 16/08/06 at 12 o'clock and tracked until 17/08/06. The same emission

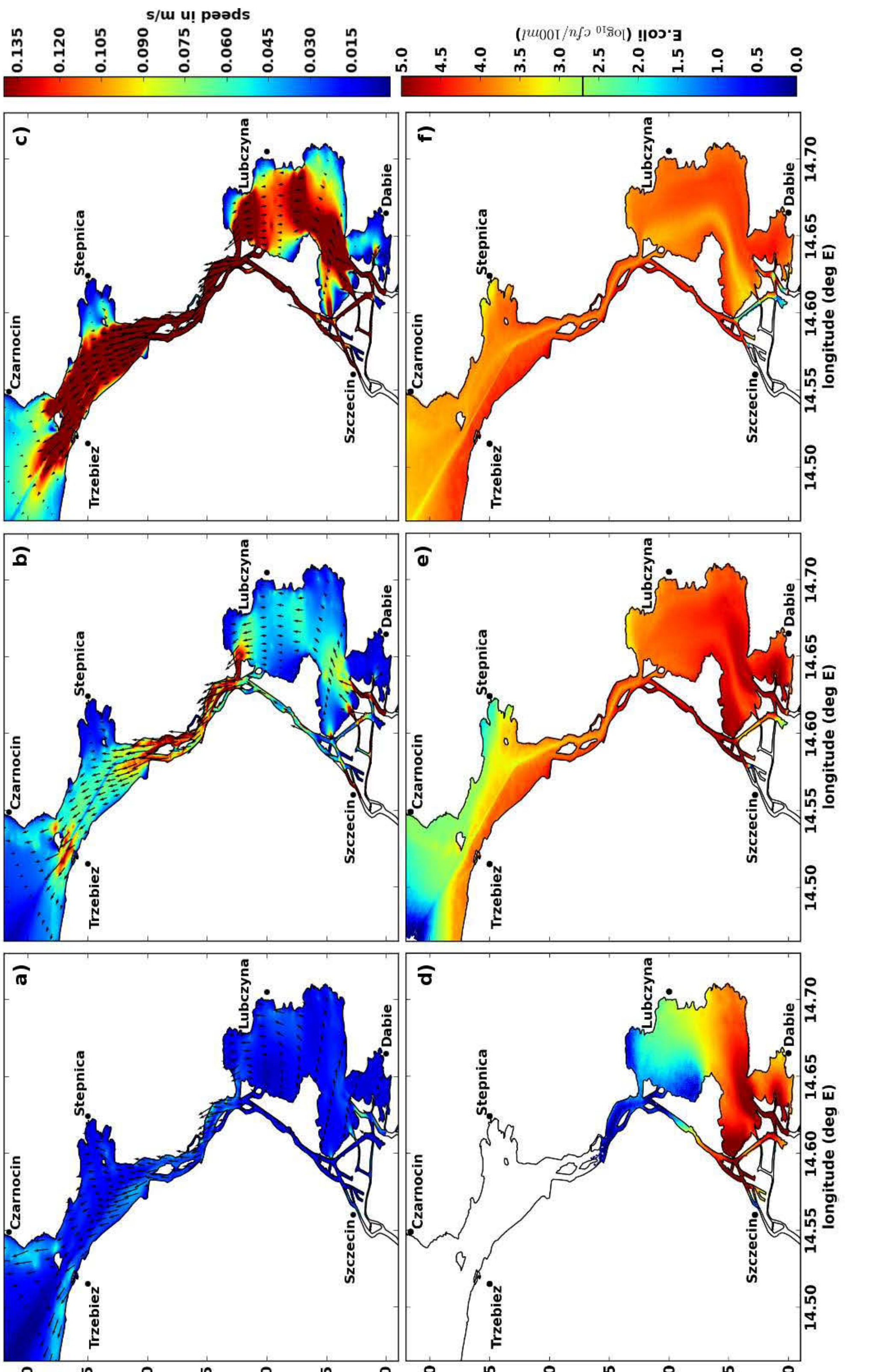

Figure 2.9: Water currents and speed, and *E. coli* concentration risk map (scenario R) at (a,d) summer minimum (64 m^3s^{-1}), (b,e) summer mean (414 m^3s^{-1}), and (c,f) summer maximum (1606 m^3s^{-1}) Oder river discharge. The black line within the colour scale shows the EU threshold of 500 cfu/100 ml.

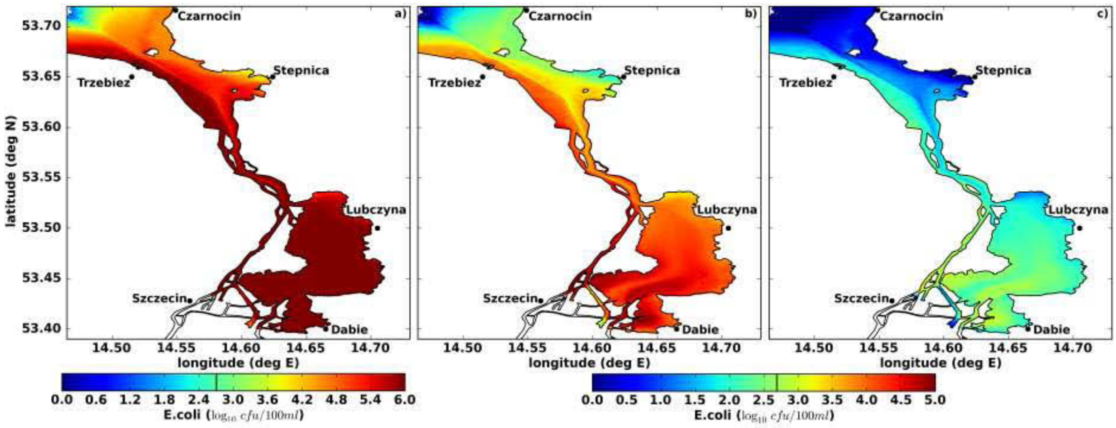

Figure 2.10: *E. coli* risk map computed with different *E. coli* emission amounts (scenario E). (a) 10^8 cfu/100 ml, (b) 10^6 cfu/100 ml and (c) 10^4 cfu/100 ml. The black line within the colour scale shows the EU threshold of 500 cfu/100 ml.

locations as in the former scenarios have been used.

The possible *E. coli* contamination in the Oder mouth area on 18/07/06 and 16/08/06 are presented in Figure 2.11 (a,c). The model results show a general contamination of the whole Oder mouth area for both dates. The bacteria concentration level ranges between 10^4 and 10^6 cfu/100 ml. The EU threshold for a sufficient beach is, thus, exceeded by factors of 20 - 2.000. The highest *E. coli* concentrations ($\approx 10^6$ cfu/100 ml) can be found in west Dabie lake and off the west coast of the Oder river on both dates. The central Oder mouth still hazardous concentrations of $10^{4.8}$ cfu/100 ml occur. In July 2006 the east coast of Dabie lake was polluted with concentrations of 10^4 - 10^6 cfu/100 ml. Figure 2.11 (b) indicates the onshore transport and accumulation of the bacteria off the coast. In contrast, the bacterial plume did not reach the east coast in August 2006 (Figure 2.11 (c,d)). The trajectory pattern shows, that the northward directed flow was more pronounced during this period than in July (Figure 2.11 (b,d)). Generally, the model results are in agreement to the samples which indicate a EU threshold exceedance at Lubczyna in July but not in August.

2.5.6 Scenario summary

All prerequisites and major outcomes of the scenario are collected in the following table 2.4.

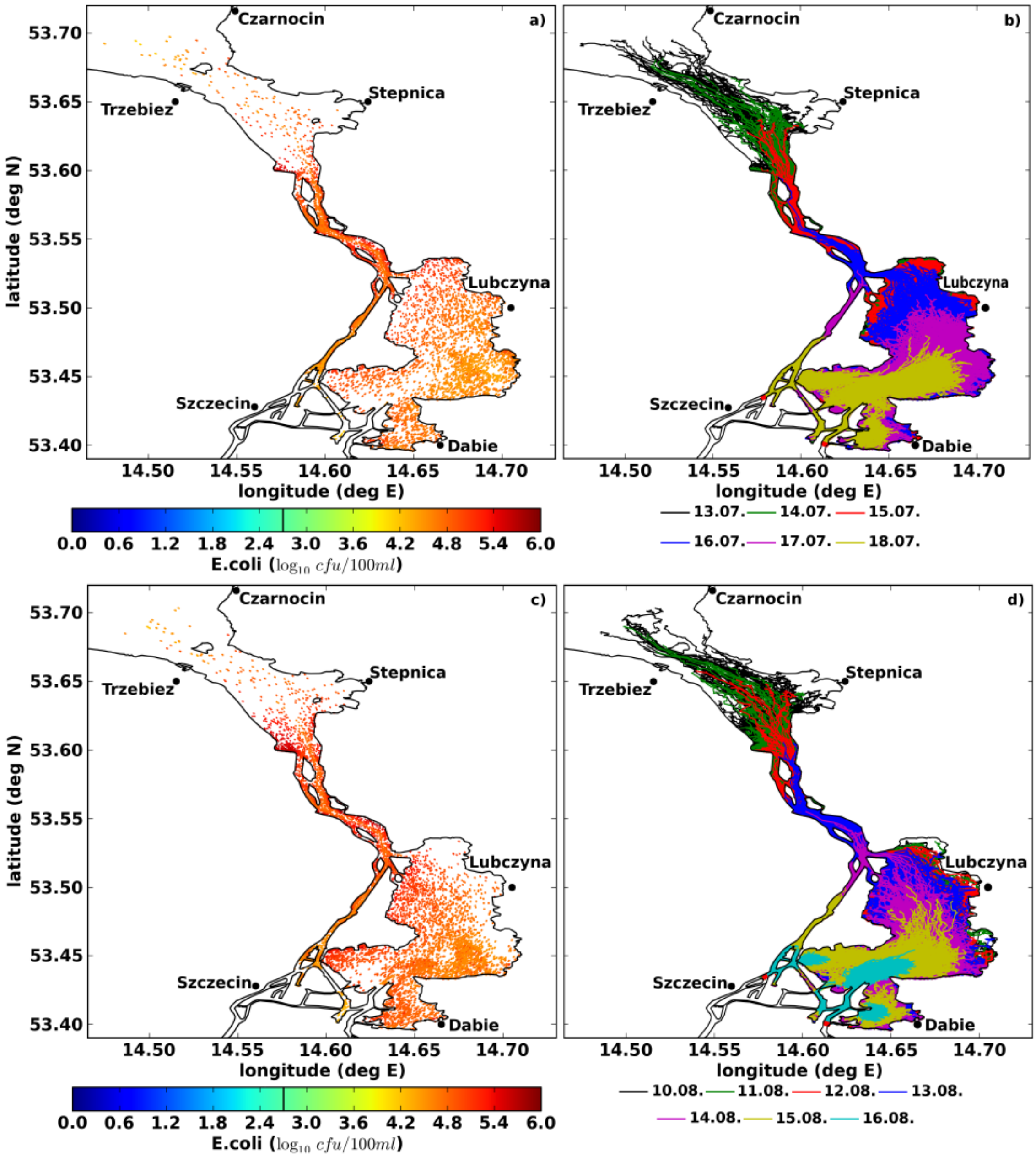

Figure 2.11: Possible *E. coli* contamination on 18/07/06 (upper) and 16/08/06 at 12 o'clock (lower). The concentration maps (a,c) are shown in the left column and trajectories of particles (b,d) representing *E. coli* emissions at different days are shown in the right column.

scenario	**mortality [h^{-1}]**	**wind [ms^{-1}]**	**river [m^{3}s^{-1}]**	***E. coli* amount [cfu/100 ml]**	**major outcomes**
wind (W)	0.0185	N, NO, ...,NW: 3, 6	414	10^6	wind direction influences east-west distribution of bacteria; wind speed less influence; SW favours upriver flow of bacteria
mortality (M)	0.009 0.0185 0.0571	SW 3	414	10^6	key parameter 1 for concentration level
river (R)	0.0185	SW 3	64 414 1606	10^6	influences bacteria distribution to the north; if increased overlap wind influence
emission (E)	0.0185	SW 3	414	10^8 10^6 10^4	key parameter 2 for concentration level
real 2006	0.0185	measure	measure	10^8	coastal pollution in Dabie lake in July, but not in August

Table 2.4: Prerequisites and major outcomes of the scenarios.

2.6 Conclusion and discussion

In the present study we have presented a 3D model system and its potential to serve as a tool for coastal water management. We used a 3D model system to simulate different scenarios with varying wind direction and speed as well as with different mortality rates, river run-off and emission accounts. Their analyses identify the wind direction to be the environmental key parameter controlling the east-west bacteria distribution. The variabilities of the *E. coli* concentrations depend less on the wind speed. The prevailing wind direction (south-west) favours the bacterial upriver transport. However, the north-east coast of the Oder mouth (Stepnica, Czarnocin) is not at risk. If the river run-off is additionally increased, the increased current velocities transport the microorganisms towards the north. Active bacteria can enter bathing areas 20 km downriver from the pollution sources (Trzebiez) in high concentrations as well as the Oder lagoon. Also the north-east Oder mouth area is affected by too high *E. coli* concentrations since the bacteria are equally distributed in the whole domain and even in shallow areas. Contrarily, there is only a risk for the south Dabie lake under low river discharge. Hence, we can conclude the river run-off controls the northward expansion of the bacteria transport. The steady state scenario results show moreover, that *E. coli* mortality rate and emission intensity are key parameters for concentration levels at downstream beaches. However, these factors are highly uncertain. On the one hand the concrete survival time of E. coli bacteria is unknown in such special environments as the Oder river mouth and Oder lagoon. The high turbidity and low salinity of the water are known to be survival favouring parameters where the high temperature counteracts. The insufficient information about the *E. coli* survival times in such a special environment could be compensated if additional mortality experiments with the microorganisms were carried out. On the other hand, not all households of Szczecin are connected to sewers so far (more than 80%) and hence the actual release of untreated water in the city is unknown. This could be changed if additional water quality measurements would be taken outside the city. These should also be carried out off the sewage treatment plant. The measurements could assess the existing emission situation and allow a successive elimination as required in Article 6 of the new bathing water quality directive (2006/7/EC). However, the EU project *Water quality improvement in Szczecin* (European Comission (2000)) was an important step to reduce pollution sources and improve the water quality. However, studies from Kistemann et al. (2009) and Kistemann et al. (2008) showed that the development of central sewage treatment plants lead to a reduction of the hygienic-micro-biological water quality. Besides these authors also Graw and Borchardt (1995); Hagendorf et al. (2004) and Riegler (2002) concluded, that further national and international methods are required to reduce the micro-biological load from sewage treatment and hence to ensure the EU threshold compliance. According to Kistemann et al. (2009) three different techniques are possible: to increase the sewer or sewage treatment plant volume, to use membrane- or retention-filtration (Gimbel (1998); Schilling and Kollbach (1998)) or to use disinfection techniques (chlorine, UV or ozone) as described by McNair-Scott and Lesher (1963); Chang et al. (1985); Hunt and Mariñas (1999); Papiri et al. (2003); Field et al. (2004). Although the latter method is laborious, its effect is promising. As reported by Wasserwirtschaftsamt München (2012) the ultraviolet radiation damages the genetic material such that the bacteria die quickly. In the Isar river (Bavaria, Germany) a 99% reduction of the bacterial load could be achieved with this method. However, we could show that the insufficient sewage treatment in Szczecin upstream is the major source for faecal pollution. Nevertheless, the Oder river is a pollution source itself. As especially meadows and grasslands dominate the landscape around the Oder river entry into Dabie lake. These are mainly used as pastures for cattle breeding (Schernewski et al. (2012)). Vinten et al. (2002) and Kistemann et al. (2009) have shown the importance of grazing animals and cattle slurry application as an E. coli pollution source for surface waters. Vegetative filter strips are a promising possibility to hinder the cattles from going into the river and further to reduce surface washes (Kistemann et al. (2008)). Particularly after heavy rainfalls, which are often described as major source for bacterial influxes (Rechenburg et al. (2006); Kistemann et al. (2009)), these surface washes provide a high amount of bacterial load (Kistemann et al. (2009)). In our future scenario experiment, we assumed both techniques, the vegetative filter strips and the UV-disinfection of the sewage water. The results indicate an increased water quality everywhere in the Oder mouth. With this full implementation of the sewage treatment in Szczecin new bathing places could be established close to the city in north Dabie lake and along the east coast of the Oder river mouth.

Total coliform bacteria have been the indicator organisms for faecal pollution in the directive 1976/7/EEC. These form a heterogeneous group of enterobacteria. They include *E. coli*, but also microorganisms that do not origin from faeces and, hence, do not present any health risk (Auchenthaler and Huggenberger (2003)). Thus, under the "old" directive a faecal pollution could only be conjectured. Consequently, the water quality benchmark was too strict in the past. Beaches have been closed although no hazard was existent for bathers e.g. in summer 2006. The reputation of the bathing area suffered and economic damages could be the consequence. In contrast, taking *E. coli* as an indicator only leads to beach closings if a justified possibility of faecal pollution (World Health Organisation (2003)) exists. Thus, the new EU-Bathing Water Quality Directive (2006/7/EC) reduces the risk of beach closings. A simulation covering July and August 2006, when several beaches had to be closed according to the old directive (1976/7/EEC), confirms that no beach closing would have been necessary according to the new directive (2006/7/EC).

Assuming a sewage treatment plant blackout or future contamination events, it is important to have an organised management, which can fast react and promptly notify the public. Our steady state simulations can support the authorities. The computed steady state simulations provide a management and risk assessment tool for future pollution events and can help to reduce the risk for bathers. For example, our analyses show that under prevailing summer conditions and increased Oder run-off the authorities need to close or at least warn the people on the beaches of Lubczyna and Trzebiez for approximately 16 hours and 2 days, respectively, to guarantee the safety of the bathers. This fast bacteria transport underlines the importance of article 12 of the bathing water quality directive (2006/7/EC) (European Union (2006)) which calls to "... use appropriate media and technology, including the Internet, to disseminate actively and promptly the information concerning bathing waters...". Besides this study, the authors have made their contribution to this task implementing the applied model system into the public information system "GENeric European Sustainable Information Space for Environment (GENESIS)". This is a web-based solution for monitoring air quality, fresh and coastal water quality, and the impact on health. GENESIS helped to developed an environmental management and health services in Europe and shall support public information according to Article 12 of the bathing water quality directive (2006/7/EC).

Although former studies about coastal management in the Oder lagoon area have used particle tracking together with circulation models, most of the studies are computed with 2D model systems (Schernewski and Jülich (2001); Schernewski et al. (2002)). These are not able to fully reproduce the three dimensional flow and transport patterns as it is now possible with our model system. Furthermore the advantages of our model set-up, compared to the recently used one in Schernewski et al. (2012), are the high resolution on the one hand and the increased number of particles on the other hand. We are therewith able to assess the risk even at single beaches and can give a better spatial distribution of the *E. coli* bacteria than in former studies. However, the high resolution means high computational coasts while producing. The possibility to run the circulation model on supercomputers of the HLRN (2007) reduces the effort immensely. Unfortunately, the tracking model cannot be scheduled in parallel, but Lévy et al. (2012) found out that a grid degradation of the circulation results does not decrease the particle tracking result quality. Nevertheless, this approach was not applicable in our study, since we wanted to follow the coastline in high resolution what makes it hardly feasible to degrade the grid.

Chapter 3

A model tool for bathing water quality management: A case study on *Salmonella* occurrence at the southern Baltic coast

3.1 Introduction

High bathing water quality is of outstanding importance for tourism all over the world. Deterioration of bathing water quality and the subsequent closing of beaches can have serious economic consequences for seaside resorts and may include a loss of reputation. *Salmonella* spp. is an important and wide-spread human pathogenic microorganism which can cause typhoid and paratyphoid fever (Baggesen et al. (2000); Polo et al. (1998); World Health Organisation (2003)). Its load in surface waters (by e.g. effluents) is very important for public health and environmental issues (Baudart et al. (2000)). Today, however, 92% of all bathing waters in Europe comply with the minimum water quality standards set by the bathing water directive (European Environment Agency (2012a)). The old Directive 1976/7/EEC (European Union (1976)) included physico-chemical and microbial indicators, such as total and faecal *coliform* bacteria, in the assessment of water quality. For cases where water quality showed deterioration, tests on faecal *Streptococci*, *Salmonella* and entero viruses were deemed necessary. It was a requirement that 80% of all samples taken during bathing season had to be free from *Salmonella* (Mansilha et al. (2010)). At present most European Union member states implement the new simplified Directive 2006/7/EC (European Union (2006)), which includes only two indicators, intestinal *Enterococci* and *Escherichia coli* (*E.coli*), with no additional tests.

Does this mean that *Salmonella* problems in European bathing waters do not exist anymore or that intestinal *Enterococci* and *E.coli* are sufficient indicators for *Salmonella* appearance? Can we be sure that bathing waters compliant with the quality standards are without any risk for human health? The recent publication by Mansilha et al. (2010) already suggests that there is no significant correlation between the presence of *Salmonella* and the guide values of indicators. Often, high concentrations of faecal indicators are correlated with *Salmonella* occurrence. However, many examples suggest that faecal indicators are insufficient in natural waters (Polo et al. (1998); Dionisio et al. (2000); Lemarchand and Lebaron (2003); Efstratiou and Tsirtis (2009); Mansilha et al. (2010)). *Salmonella* concentrations have also been found in the absence of classical indicator microorganisms (Moriñigo et al. (1990); Galeés and Baleux (1992); Mansilha et al. (2010)). In several cases *Salmonella* was found in a concentration of more than 10^3 per litre in samples although faecal *coliform* levels met the strictest bathing quality threshold of Directive 1976/7/EEC (Tobias and Heinemeyer (1994)). One important reason is the different behaviour and survival of different microorganisms in the natural aquatic environment (Mansilha et al. (2010)). We can conclude that problems with *Salmonella* have been and are still being reported and that, very likely, many other pollution events escaped and continue to escape our notice. The new European Directive 2006/7/EC will hardly change the situation.

The primary source of *Salmonella* is the gastrointestinal tract of humans and many animals (Bell and Kyriakides (2002)). It enters surface water through sewage, animal excreta (Clark et al. (1996)) and sediment (Ferguson et al. (1996)). It can survive several weeks in the natural environment while still maintaining its pathogenicity (Rhodes and Kator (1988)). However, salinity and low temperatures do not allow a reproduction in natural waters (Rhodes and Kator (1988)). Often *Salmonella* are attached to particles, where they can reach high concentrations and increase the infection risk for bathers, who swallow these particles. Resuspended near-shore sediments are of particular importance in this respect (Moore et al. (2003)) and the bathing zone remains a focus region for potential infections.

We present a model system which combines a three-dimensional hydrodynamic model with a Lagrangian particle tracking model. By applying this system to a precise, exemplary case study we will demonstrate its potential for not only scientific analyses but also as a tool capable of answering questions of practical relevance. Furthermore, we show that the model system can act as a general tool for bathing water quality management (assuming a point source at the beach). In our case study we present a *Salmonella* pollution event in coastal waters of the Polish seaside resort Miedzyzdroje (Island of Wolin at the German/Polish border in the southern Baltic Sea (Figure 2.1)) during the major bathing season in August 2008. The consequences include the closing of the beaches as well as extensive media coverage. The authorities faced a lot of pressure, but it became obvious that knowledge, experience and tools were lacking to manage the problem effectively. We analyse the pollution event with the objectives to: a) spatially locate possible *Salmonella* pollution sources, b) obtain a full impression of the spatial transport pattern and the temporal spreading of *Salmonella*, c) provide a management tool for future pollution events and d) give recommendations towards an improved monitoring and management. For this purpose, we carry out varied wind scenarios as well as forward and backtracking

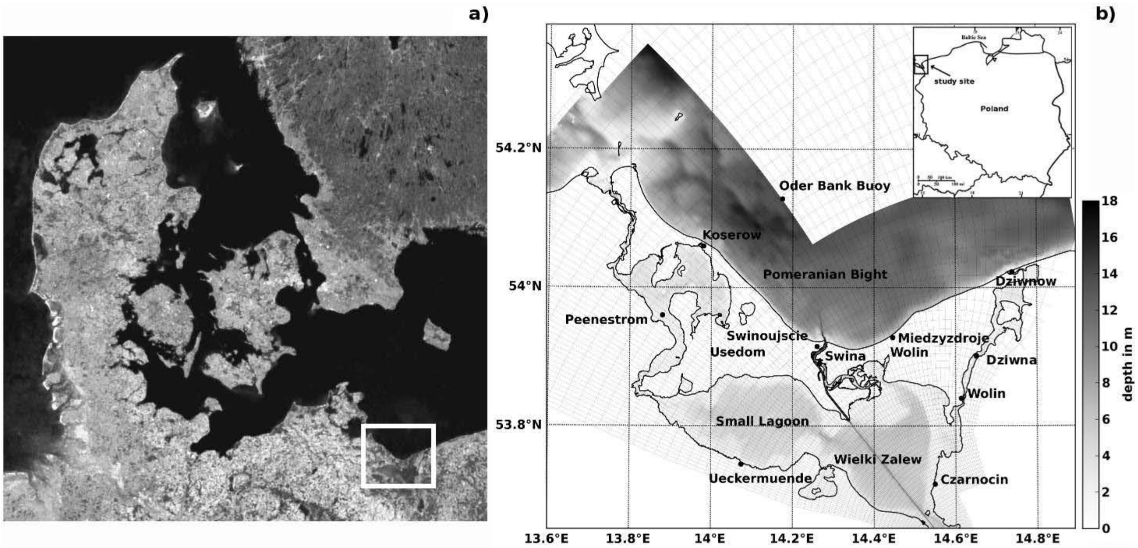

Figure 3.1: (a) Satellite picture of the Western Baltic (Flash Earth). Selected: area of Pomeranian Bight and Oder Lagoon. (b) Topography of entire model set-up area with grid outline showing every 20-th grid box, and a map of Poland indicating the study area location.

simulations for the pollution event.

3.2 Study site and measurements

Miedzyzdroje is a seaside resort located at the German/Polish border at the island of Wolin in the southern Baltic Sea (Figure 3.1). It comprises an area of 110 km^2 with 6.570 inhabitants. The city is coveted as holiday destination and the most important bathing place on Wolin ($\approx$ 473.000 overnight stays in 2010 (Statistical Government Poland (2012)). The beach is approximately 4 km long and is separated by a pier into a west and east beach. Close to the tourist bathing area, located at the eastern end of the beach, a fisher base had been developed (Figure 3.2). The related fishery activities provide a potential source of pollution.

Figure 3.2: The situation at Miedzyzdroje beach. Long sandy beach (left) with fisher boats docking close to the tourists bathing area (middle) and the shops at the beach (right).

The shallow Pomeranian Bight is characterised by water depths less than 20 m. Generally, the 20 m isobath separates the Pomeranian Bight from the large-scale circulation of the Baltic Sea. Water depths shallower than 10 m at the Oder Bank divide the bight into an eastern and a western part. The coastal area of the bight is well mixed and has a mean salinity concentration of less than 7 PSU (Siegel et al. (1999)). The dynamical processes in the Pomeranian Bight are driven by local winds and controlled by the earth's rotation, bathymetry and coastal alignment. The response patterns are characterised by horizontal scales down to a few hundred metres and time scales between a few hours and days (Siegel et al. (1999)). The system is dominated by an Ekman current in the surface layer and a compensating current in the deep layer. It is initiated by the constraint of the coastal boundary condition with respect to the offshore component of the barotropic flow (Lass et al. (2001)). The current is rectified within a coastal boundary layer (width of $\approx$ one baroclinic Rossby radius)(Lass et al. (2001)). Easterly winds, occurring frequently in spring, produce an offshore transport associated with upwelling at the Polish coast (Siegel et al. (1999)). Colder bottom water is upwelled to the surface and transported into the bight. Under westerly winds warm surface waters are driven onshore and sink down at the coast (downwelling). Vertical current shear, established by the surface Ekman current and the compensating bottom current (Lass et al. (2001)), causes vertical mixing by differential advection (Aken van (1986)) outside the coastal boundary layer. A relatively weak long-shore current establishes off the coast of Usedom, as well as near the Swina river mouth (Lass et al. (2001)).
The islands Usedom and Wolin separate the Baltic from the Oder lagoon. Water exchange happens pulse-like via the Swina channel (Mohrholz (1998)). It carries 300 - 500 m^3s^{-1} and hence plays only a minor role for the dynamics in the study area.

All bathing water quality measurements are provided by the Institute for Meteorology and Water Management Krakow. All measurements have been taken qualitatively (presence/absence) according to the old EU bathing water directive EU 1976/7/EEC (European Union (1976)). According to European Environment Agency (2010) Member States of the EU have until December 2014 to implement the new Directive 2006/7/EC, with the option to report either under the old or the new directive until 2012. During this transition period, samples are reported under the Directive 2006/7/EC but assessed according to the rules of Directive 1976/7/EEC (European Environment Agency (2010)). Since 2011 Poland has been reporting under Directive 2006/7/EC.

During the major bathing season in August 2008 insufficient bathing water quality, due to *Salmonella* occurrence, led to a bathing prohibition for more than 4 weeks. However, the measured *E.coli* concentrations did not exceed the threshold values of the EU Directive 2006/7/EC (Figure 3.3) at the entire period.

The first samples, wherein *Salmonella* were detected, were taken at the end of July at the pier, at rescue towers 7-12 (distance of 300 m; fixed station off Hotel Amber Baltic = tower 10), but no sampling was conducted at the fisher base (Figure 3.4). However, the beach closing started one week later on 2008/08/07 and was imposed to only the east

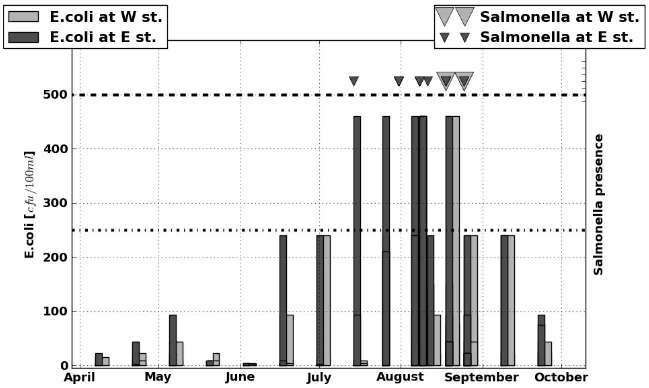

Figure 3.3: In-situ measurements of *E.coli* concentrations and *Salmonella* presence at all sampling stations divided in stations west (light grey) and east (dark grey) of the pier during the bathing season 2008. EU Bathing Water Directive threshold values for *E.coli* (cfu/100 ml) for sufficient (based upon a 90-percentile) and excellent (based upon a 95-percentile) quality are shown as dashed and dashed-dotted lines.

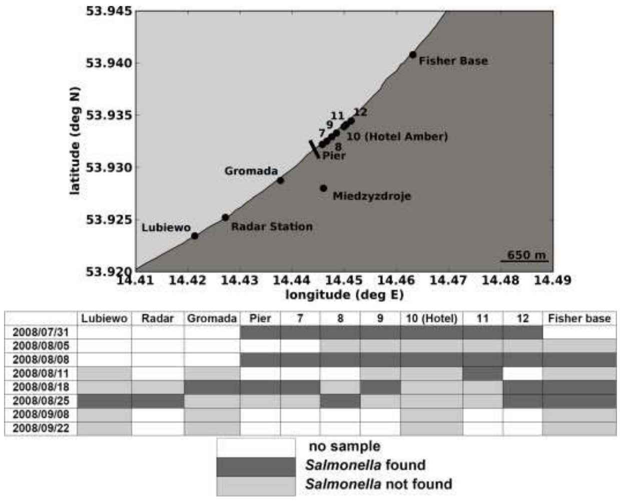

Figure 3.4: Measurement locations (a) and occurrence of *Salmonella* in summer 2008 (b).

beach (1.3 km long). The beach west of the pier (2 km) remained open to bathers and was frequently used. On 2008/08/05 no *Salmonella* was detected between rescue tower 8 to the fisher base, but no measures were taken west of tower 8. The observations from 2008/08/08 indicated a bacterial contamination from the pier towards the fisher base (distance 600 m), where again no measurements were carried out west off the pier. Since from mid July to mid August low/no *E.coli* concentrations were measured at the sampling stations west of the pier, a eastward directed flow might have been dominant during this period. In contrast from mid August to September, the water quality measurements indicated westward transport. *Salmonella* bacteria as well as increased *E.coli* concentrations were detected at westerly stations, whereas at easterly stations decreased *E.coli* concentrations were measured and no *Salmonella* was present (Figure 3.3). At the beginning of September no *Salmonella* had been detected off Miedzyzdroje, but the threat was determined in Swinoujscie. In October 2008 the sources had not been found. The media suggested several possible sources: septic tanks or leak in sewers at the fisher beach, dredging in the Swina river, deliberate release at the beach to hinder the establishment of new hotels and apartments (ANONYMOUS (a) (2008); ANONYMOUS (b) (2008); ANONYMOUS (c) (2008)). The closing of the beach had severe economic consequences for Miedzyzdroje including the drop of the total summer season income by 50% compared to previous years (pers. communication Institute for Meteorology and Water Management Krakow).

Since the water quality measurements have only a low temporal resolution (3-7 days during the bathing prohibition) the actual transport direction is not certain. The application of the model system allows the interpolation of the in-situ measurements and therewith provides a spatio-temporal picture of the *Salmonella* distribution.

3.3 Scenario application

In this chapter we applied the same model setup as in chapter 2, but the study area is in the Pomeranian Bight here.
The entire model system, with realistic forcing, was applied to the described case study to prove its suitability as well as its capability and practical relevance. Four different sets of experiments were performed. In the first set we reconstructed the situation at the second *Salmonella* measurement on 2008/08/08. Particles were released one week earlier on 2008/07/31 (the first day of contamination) to obtain a temporal and spatial picture of the distribution. In the second experiment different release locations were tested according to the assumed sources: east pier, fisher base, sampling station tower 12 and in northern Swina river (off the sewage treatment plant in Swinoujscie). The third experiment is a backtracking scenario which allows the evaluation of potential emission sources. For this purpose, particles were continuously released every day at the sampling station tower 12 from 2008/08/08 to 2008/08/15 and tracked backward in time. In the last experiment daily released particles were tracked forward in time to present a possible spatial-temporal distribution of *Salmonella* in August 2008. In these sets, $5 \cdot 10^3$ particles were released and realistic flow fields were used, based on realistic meteorological forcing. The last scenarios are idealised model application, where 16 steady state flow fields (according to the 8 cardinal wind directions and two different wind speeds) were taken to force the particle tracking model. Within these scenarios transport times and distances were derived. $5 \cdot 10^4$ particles were released at Miedzyzdroje beach. For all simulations particles were released in one surface grid cell to model a point source pollution.

In the first and and last experiment density maps were computed under the assumption of a sewer induced contamination (according to media reports (ANONYMOUS (a) (2008); ANONYMOUS (b) (2008); ANONYMOUS (c) (2008))). Hence, an emission of 10^8 *Salmonella* per day would have been possible (Baudart et al. (2000)). Releasing 10^8 bacteria into the surface layer at the source point leads to a *Salmonella* concentration of

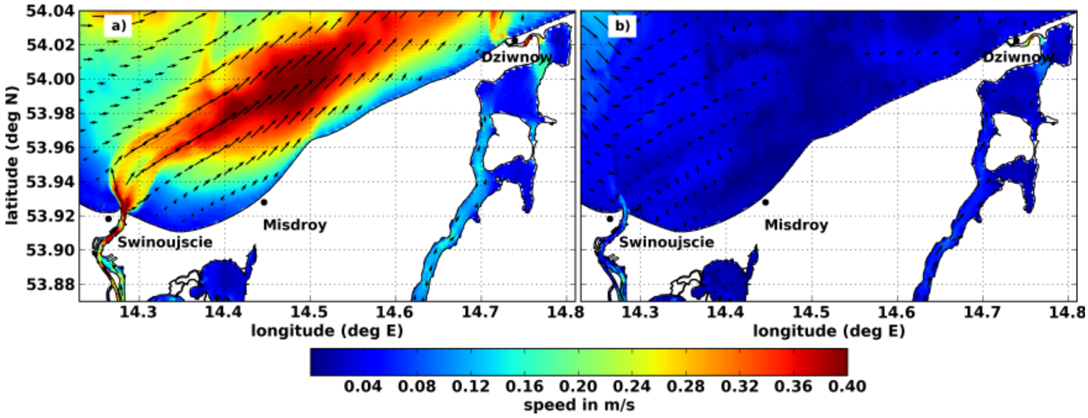

Figure 3.5: Daily mean surface (a) and above-bottom (b) flow field pattern of the southern Pomeranian Bight on 2008/08/08.

$4 \cdot 10^7$ bacteria per litre. Each particle represents 2.000 (real case) and 20.000 (steady state case) bacteria, respectively. The mortality rate of *Salmonella* spp. in seawater has been studied in numerous papers (e.g. Rhodes and Kator (1988); Mezrioui and Baleux (1992); Wait and Sobsey (2001); Moore et al. (2003)). All of them report a high correlation between survival rate and salinity and temperature. Low salinity concentrations as well as low temperatures increase the survival time, and hence reduce the mortality (Nabbut and Kurayiyyah (1972); Wait and Sobsey (2001)). The summer mean temperature and salinity, estimated from the Oder Bank Buoy is 18°C and less than 7 PSU. This is in accordance with Siegel et al. (1999). For our experiments we use a mortality rate of 0.0086 h^{-1} (T_{90}= 116 h, the time needed to reduce the initial bacterial population by 90 %) computed from the results of Mezrioui and Baleux (1992) via linear regression. It is applicable since the area of interest is well mixed. The used die-off rate corresponds with results of e.g. Wait and Sobsey (2001), who observed a mortality rate of 72 to 240 h at temperatures between 6 °C and 28 °C.

3.4 Results

3.4.1 Realistic model simulations

During the contamination at the beginning of August 2008 a north-eastward directed surface flow was dominant off the coast (Figure 3.5 (a)) while a weak onshore directed flow dominated close to the bottom (Figure 3.5 (b)). Strong winds (winds speeds > 12 m s^{-1} = 6 Bft) led to increased current speeds of more than 0.5 m s^{-1} in the vicinity of the beach. The model results indicate a strong water mass transport along the coast. Under the eastward directed current (mean speed of 0.12 m s^{-1}), transport from Miedzyzdroje to Swinoujscie (17 km) takes about 2 days (± 0.5 days), and 5 days (± 2 days) from Miedzyzdroje to Dziwnow (25 km).

Forward tracking (single release)

Four different emission locations were used in this set of experiments to study the fate of point releases (Miedzyzdroje pier, the fisher base, tower 12 and the northern Swine river). The simulation results indicate a transport time of three days from the source towards the eastern boundary of the domain if particles were emitted off Miedzyzdroje. In contrast, it takes only two days if particles were released in the Swina river. Particles were carried with the river water plume offshore into the Pomeranian Bight. The transport is faster with offshore water masses than with those close to the coast.
Particle emissions at the pier in Miedzyzdroje indicate a possible partial contamination of the west beach (Figure 3.6(a)) the like of which has not been measured. After four days particles remain close to the emission point. A pollution source at the fisher base did not indicate the observed beach contamination close to the pier (Figure 3.6(b)). The pollutants would have probably stayed at the beach for only one day before they were transported eastward. Releasing the particles at sampling station tower 12, only resulted in the east beach being contaminated with a high likelihood. The west part was likely not affected. This is in accordance with the measurements. Particles stayed at the beach for about three days (Figure 3.6(c)). Particles emitted in the Swina river were transported into the Pomeranian Bight with the Swina river outflow. Some particle were carried onshore towards the beach off Miedzyzdroje and farther east until Dziwnow (Figure 3.6(d)). All release scenario results show: particles were transported eastward along the coast. There was a high probability in the results that the entire beach up to Dziwnow was contaminated. Furthermore, a continuous emission seems highly probable in this scenario.

Backtracking

With the help of backtracking simulations source regions can be identified in the form of probability or likelihood maps (Batchelder (2006)). The particle distribution probability diagram (histogram, Figure 3.7) indicates the most likely pollution source points for the Miedzyzdroje case study. The highest probability ($> 10\%$) of the source location is close to the release point due to the continuous emission (Figure 3.7). Particles were drifting onshore towards the east beach of Miedzyzdroje after three days (Figure 3.7 (c)). The Pomeranian Bight can be neglected as a source due to the small distribution probabilities in that area ($< 0.4\%$). Similarly, the Swina river can be excluded as a source since there is no indication of particles being transported westward. A source at the west beach can also be excluded with high probability because our scenario results indicate a permanent eastward transport. Emission experiments with different start dates (2008/07/30, 2008/07/31, 2008/08/01) and end dates (2008/08/03 - 2008/08/08) show the distributions are similar and thus independent from the starting date (not shown).

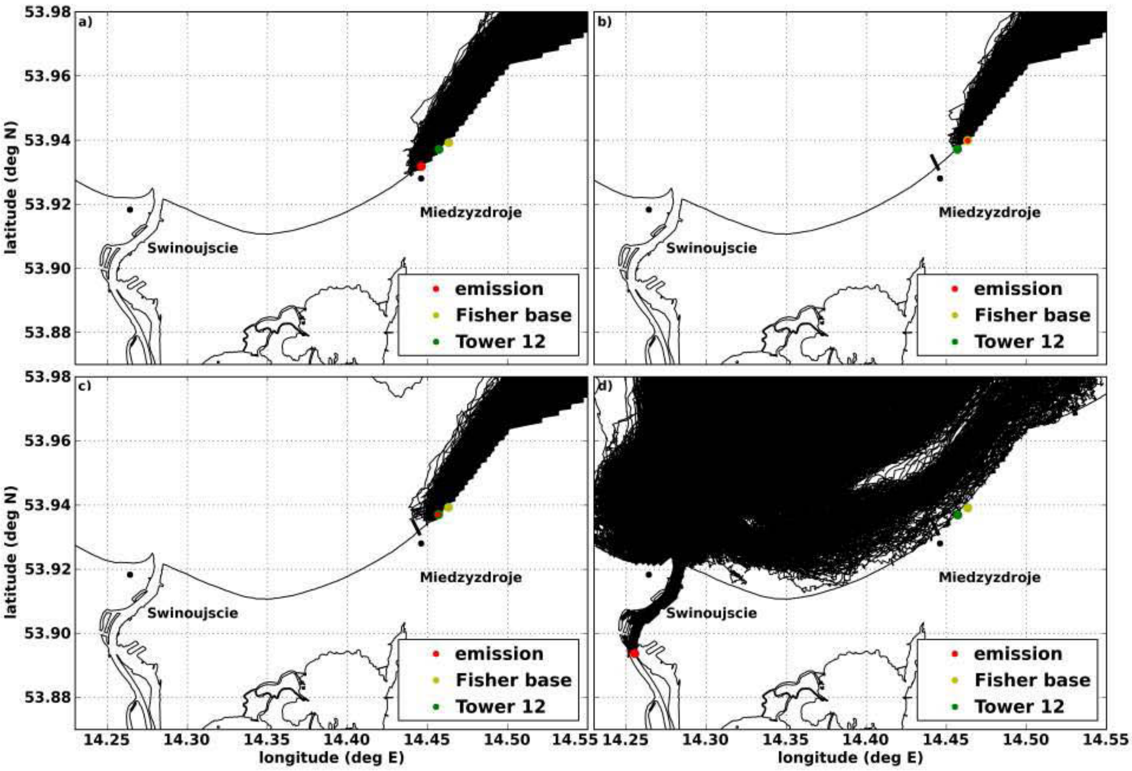

Figure 3.6: Trajectories of 5.000 particles emitted (a) east of the pier at Miedzyzdroje beach, (b) at the fisher base, (c) at tower 12 and (d) in front of sewage treatment plant in Swinoujscie (Swina river). For better visualisation the figure show only a limited region of the domain.

Forward tracking (continuous release)

A possible temporal and spatial picture of *Salmonella* bacteria concentrations during the bathing period in August 2008 is provided by a continuous release of particles every day at 12:00. They were emitted in two periods. First, from 2008/07/31 till 2008/08/08 (tracked until 2008/08/15), and second, from 2008/08/30 till 2008/09/07 (tracked until 2008/09/09). The assumption for calculating concentration maps (Figure 3.8) is a sewer induced pollution (10^8 *Salmonella* per day) at sampling station tower 12 in both experiments.

As within the single release experiment, all bacteria were transported onshore eastward with the flow (Figure 3.8 (a)). The western beach was most likely not affected. The bacteria accumulate at the release point and concentrations of 10.000 *Salmonella* per litre are possible. The density map indicates that concentrations of 100 - 1.000 *Salmonella* per litre could also be found 10 km east of Miedzyzdroje. During the second simulation period *Salmonella* were transported alongshore and westward (Figure 3.8 (b)). There is a high probability of them arriving at the east coast of Swinoujscie beach and the Swina channel after 3 days. The density map indicates that concentrations of 250 - 500 *Salmonella* per litre could partially occur at the beach of Swinoujscie, 17 km away from the source.

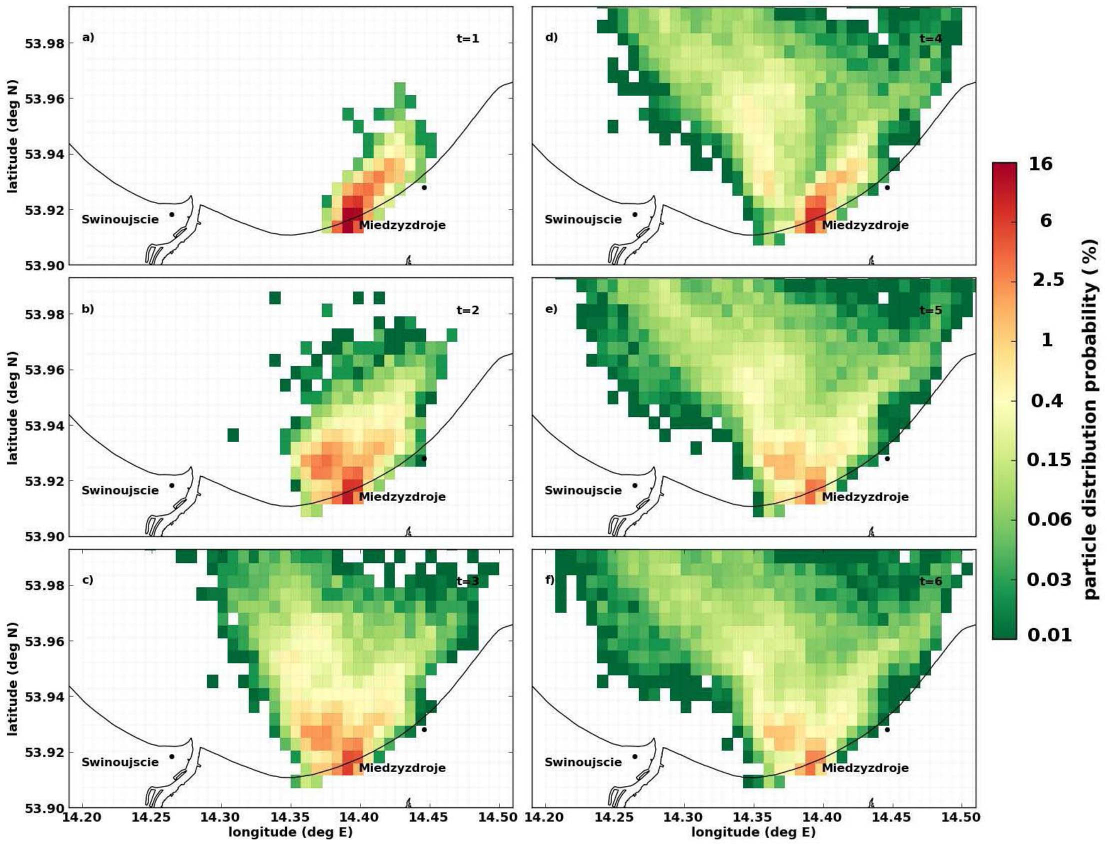

Figure 3.7: Percentage particle distribution after 1 (a), 2 (b), 3 (c), .. and 6 (f) days of backtracking. The values are clustered in boxes of size of 300 m x 300 m.

According to the infection dose of $2 \cdot 10^5$ (Briese and Heinemeyer (1989); Havemeister (1989)) and to the assumed emission amount, likely no risk for bathers occurred during August 2008. If the emission had been higher than that assumed one cannot exclude a possible risk for bathers.

3.4.2 Idealised simulations

Based on the prevailing wind conditions in the area of interest (Schernewski et al. (2012)), GETM simulations with constant 10 meter wind speeds of 3 m s^{-1} and 6 m s^{-1} were carried out for the 8 cardinal wind directions (N, NE, E,. . . , NW). During calm wind conditions mean flow velocities of 0.02 m s^{-1} is suggested. This leads to mean transport times of 10 days (± 2 days) between Miedzyzdroje and Swinoujscie, and 14 days (± 3 days) between Miedzyzdroje and Dziwnow. Increased wind speeds of 6 m s^{-1} reduce the transport time by a factor of two.

Independent from the wind condition, to the west of Miedzyzdroje surface flow velocities tends to increase whereas 5 km to the east they decrease (Figure 3.9 (a, b)). Eastern/western winds lead to offshore (onshore) directed surface flows caused by Coriolis force (Ekman transport). A clockwise (anti-clockwise) flow circulation develops in bottom

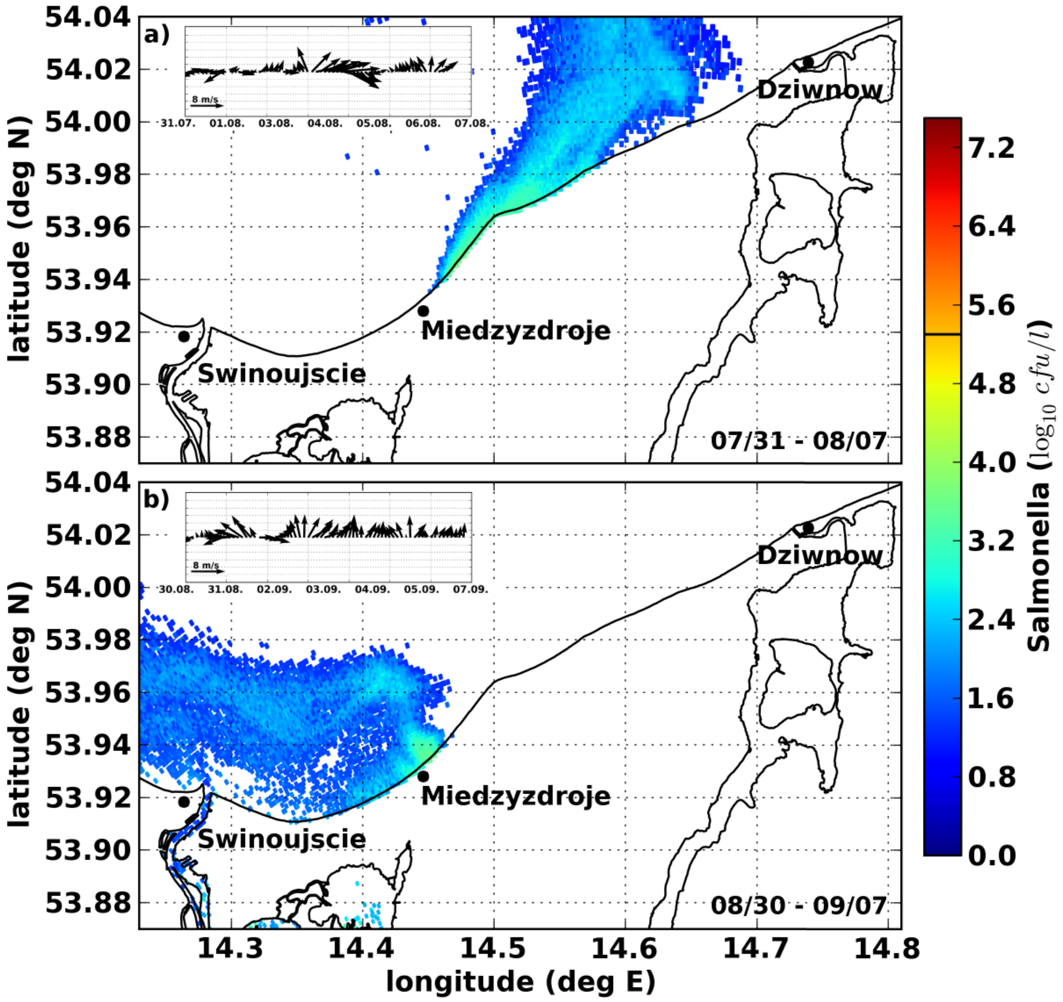

Figure 3.8: Possible *Salmonella* contamination on (a) 2008/08/08 and (b) on 2008/09/07 at 12 o'clock with an emission source in Miedzyzdroje. Shown are the concentrations integrated over the entire water column. The black line in the colorbar indicates the infection dose rate of an adult according to Briese and Heinemeyer (1989) and Havemeister (1989). The small panel in the upper left corners shows the wind direction and speed during the simulation periods.

water layers (Figure 3.9 (c, d)).

Tracking simulations, assuming a sewer induced emission, were carried out with a continuous release of $5 \cdot 10^4$ particles for two weeks. *Salmonella* density maps for different wind conditions are presented in Figure 3.10. Bacteria were transported westward/eastward and offshore (onshore) with the current flow under easterly/westerly winds, driven with the Ekman transport. Wind from north drove the flow offshore, while south winds lea to particle transport along the coast (Figure 3.10(d,e)). As assumed, forcing the setup with calm wind of 3 m s^{-1}, the bacterial plume has a smaller dispersion than under increased winds (not shown). Hazardous concentrations of more than 200.000 *Salmonella* per litre (Briese and Heinemeyer (1989); Havemeister (1989)) could be found

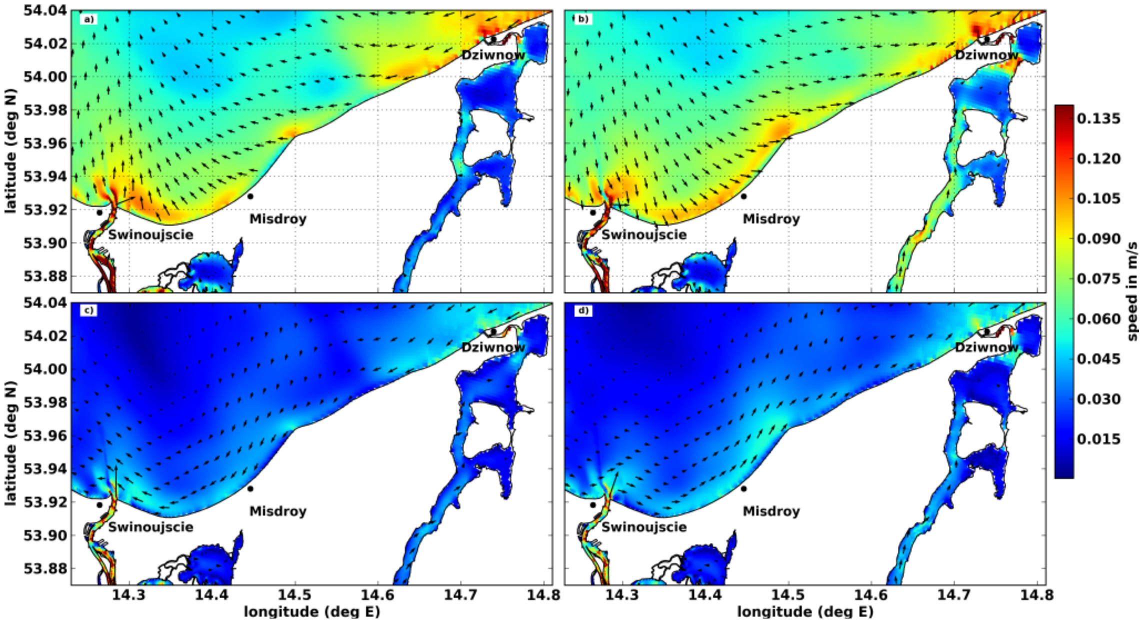

Figure 3.9: Modelled steady state surface flow fields (upper) and bottom flow fields (lower) forced with constant 10 m wind of 6 m s^{-1} from east (a,c) and west (b,d).

in a radius of at most 5 km around the source. During stronger winds of 6 m s^{-1} hazardous concentrations were dispersed about 10 km east/west under westerly/easterly winds (Figure 3.10(a-c, f-h)). Although particles were also transported into the Bight, the main plume stays onshore. Prevailing south-west winds led to a bacterial distribution along the entire coast of Wolin to Dziwnow (Figure 3.10(c)). For all wind scenarios the highest *Salmonella* concentrations of 1000.000 germs per litre appeared close to the release point due to continuous emission.

Often, *Salmonella* pollution results from single releases for example via accidental events. The measurement data are limited both spatially and temporally (single spot observations). Idealised simulations, in combination with the observation, can expand the measurement from a single position within the water column to a spatio-temporal picture of the bacterial distribution in the coastal zone. It acts as an addition to the measurements.

Simulations with single *Salmonella* release were carried out to show probable transport ranges. Again the 8 main wind directions with a speeds of 6 m s^{-1} were used as forcing. During the first day after emission, particles are transported to within 1 km around the source, independent of the wind direction. After 1 day the maximal transport distance of the pollutants was 5 km west/east under east/west winds. However, bacteria were transported about 20 km west/east after only four days and hence left the model domain (Figure 3.11 (a, b, c, f, g, h)). Under north and south winds, the dispersion is slower than under east and west winds (Figure 3.11 (d, e)). After 1 day the pollutants stay close to the source. Northern winds lead to an offshore particle transport with a 4 km radius around the source after 4 days where after it remains unchanged. Bacteria were equally

days	distance in [km] at wind speed of 3 m s^{-1}	distance in [km] at wind speed of 6 m s^{-1}
1	2.5	5
2	5	9
3	7	13
4	9	17.5
5	10	21
6	10.5	24
7	11.5	> 24
8	13.5	> 24
9	15.5	> 24
10	17.5	> 24

Table 3.1: Transport ranges in km towards east according to south west winds for two wind speeds 3 and 6 m s^{-1} after 1, 2, ... until after 10 days. The western dispersion is about 1 km for both wind speeds and all days.

dispersed 8 km (16 km) to east and west during south winds after 4 (9) days.

Table 3.1 contains transport ranges of bacteria according to the predominant wind direction (south west). In this experiment no specific emission amount was assumed and hence the number of particles emitted was not related to any concentration. Thus, we give here no risk radii, in terms of hazardous concentrations, as in Figure 3.8, but only transport distances.

Bacteria are dispersed two times farther under increased winds than under calmer winds. Within the first four days, released bacteria drifted more than 15 km at wind speeds of 6 m s^{-1}. The fast transport goes on for the following days and hence pollutants were dispersed wider than 24 km (out of the domain) already after seven days. In contrast, emitted bacteria drifted less than 2.5 km per day at wind speeds of 3 m s^{-1}. They reached Dziwnow (17 km away) after ten days.

3.4.3 Recommendations towards an improved management and monitoring

According to our knowledge the sources of the contamination in Miedzyzdroje in summer 2008 has not been identified. Our model results suggest that the source was most likely in town, but we were unable to identify the type of emission. For this reason future pollution events cannot be excluded since a similar emission may occur. Our study results give clear evidence of areas at risk and transport ranges in case of a future contamination with *Salmonella* in Miedzyzdroje. If *Salmonella* germs are again detected, information about wind conditions should be collected to use the right scenario map (see Table 3.1 and Figure 3.11) and derive the related transport ranges: 5 km to the west/east under easterly/westerly winds after the first day, and up to 20 km to the west/east after four days. The east-west dispersion is not wider than 4 km during north winds, where it is 8 km (16 km) during south winds after four (nine) days. The predominant south west wind (6 m s^{-1}) forces a fast, alongshore, eastward directed transport. Therefore, for each day elapsed after detection, the monitoring should be extended 5 km to the east. Independent from the wind direction, bathing areas 1 km away from the first detection location are affected by pollution, due to dispersion, and therefore sampling should be conducted there. Possible sources for a future contamination, e.g. sewers along the coast, the fisher base, the sewage treatment plant in Swinoujscie or local events at the beach should also be analysed. If the source is pinpointed and identified, the monitoring can be adapted to this location and further samples should be taken with respect to wind and flow field direction (see Table 3.1 and Figure 3.11). Moreover, selective measure should be carried out to close the source preventing a further contamination.

In general, we can derive supra-regional recommendations from the model application to the precise case study in Miedzyzdroje. The results indicate that pollutants are driven by the flow field, which is forced by the wind itself (assuming no higher, dominant flow). Hence, fast action is generally recommended. According to Figure 3.12 the following steps are recommended after the detection of a *Salmonella* contamination: The foremost step would be to repeat the analysis to make sure that no errors occurred during the initial analysis. Subsequently, the following steps should be carried out. A bathing prohibition should be imposed (1), if threshold values (e.g. infection dose according to Briese and Heinemeyer (1989); Havemeister (1989)) are exceeded. Since the main pollution has been found to drift with the flow direction, which is forced by wind direction and speed, the next step would be to get information about the wind condition (2). According to our results, the drifting speed of pollutants is at least 1% of the wind speed. That means even under calm winds transport ranges of 2 km per day are possible. Under increased winds transport ranges of more than five kilometre per day are common (cf. Table 3.1). A wind parallel to the coast favours an alongshore pollution transport. Independent of the wind direction, bathing areas 1 km from the initial detection location might be affected by the contamination due to dispersion. The next step should be to conduct sampling at these locations and impose a bathing prohibition if threshold values are exceeded (3). Simultaneously, the fourth action should be to locate possible *Salmonella* sources (4). These could be all locations where faecal matter occurs, such as sewage treatment plants, sewers, animal farms or meadows as well as cropland (fertilised with slurry). Following precise source identification, sampling should be adapted/shifted to this position. As discussed before, samples should be taken in a 1 km radius surrounding the source and in relation to the wind direction (same is valid as above). Finding the origin of the pollution allows action to be taken in consideration for the health of bathers (warning, bathing prohibition) or alternatively enables the closing off of the source. The latter could stop the pollution, reduce the bathing prohibition time and could prevent further pollution. In the event that the pollution source cannot be found or closed off and an emission is continuous, a model study, as shown in the presented case study, is helpful to derive concrete action recommendations for the local situation. However, it is important to run steady state simulations first, obtained with constant wind forcing. These provide rapid information regarding transport ranges and beaches at risk under different wind scenarios. The mortality rate of the microorganisms is therefore needed. Values from past research should be used as an approximation related to the underlying water conditions (salt, temperature). At the same time, it is important to collect the meteorological data. This is a necessary input for realistic simulations which can help find or at least localise the pollution source (backtracking).

3.5 Discussion and conclusion

In the present study we have applied a 3-D model system to an exemplary case study – a *Salmonella* pollution event in the coastal waters of the Polish seaside resort Miedzyzdroje. Our results showed that the pollution covered the entire beach 10 km east of the resort at the beginning of August 2008. Furthermore, there is a high probability that the city was the source for a *Salmonella* pollution at Swinoujscie beach at the beginning of September. The extensive transport distances due to the fast water mass transport and long survival times are in accordance with the results from Rhodes and Kator (1988) and Moore et al. (2003). Backtracking simulation results showed that a continuous emission in town was very likely in Miedzyzdroje during 2008. In addition, other possible sources, as for instance the sewage treatment plant in Swinoujscie, could be excluded. Although backward-in-time Lagrangian modelling is still a fledgling field to marine science (Breivik et al. (2012)), reverse-time models of passive tracers exist (see, e. g., Callies et al. (2011)) and have been used for tracking near-shore sources of hazardous materials to their origins (Havens et al. (2009)). Nevertheless, backtracking is an established scientific discipline in atmospheric research (e.g., Flesch et al. (1995); Stohl (1996, 2002); Rao (2007)), all related atmospheric and marine science have a similar goal: to identify the source of pollutants, when measurements are sparsely available. The benefit of backtracking simulations is that the resulting probability maps contain valuable information about source regions which may refer to a spatial distributions of organisms at an earlier time (Batchelder (2006)).

The detection of *Salmonella* bacteria in Miedzyzdroje during summer of 2008 was possible only because the Polish ministry analysed their bathing water quality according to the old Directive 1976/7/EEC (European Union (1976)). In the recent Directive 2006/7/EC only two indicator organism, intestinal *Enterococci* and *E.coli*, are used, the latter of which did not exceed the threshold values during the pollution event in Miedzyzdroje. A bathing prohibition would consequently not have been imposed according to the new Directive. Moreover, several studies showed that there is no sufficient correlation between *Salmonella* occurrence and the two indicator organisms (Moriñigo et al. (1990); Galeés and Baleux (1992); Mansilha et al. (2010)). One possibility for the reduction towards the two indicator organisms can be the low concentration of the organisms and the high cost and effort involved in the current detection technologies (Lemarchand and Lebaron (2003)). However, a faster, more cost effective method for the detection of *Salmonella* is available (Mansilha et al. (2010)). Since *Salmonella spp.* are wide spread human pathogens, which are known to cause problems in European waters, their detection is still necessary (Lemarchand and Lebaron (2003)). They can enter the water environment via effluent, sewers, infected animals through run-off, pet waste in storm-water run-off (Lemarchand and Lebaron (2003); Battenberg (2007)). Thus, waters compliant with the new Directive 2006/7/EC can still contain a risk to human health.

The sources of the contamination in Miedzyzdroje in summer 2008 had not been found through in-situ measurements. Further, the real emission amount had not been determined due to qualitative sampling analysis (presence/absence). Hence, our results could neither identify the type of emission. Hence, the sources could not be closed off and a future *Salmonella* contamination is possible. The results of our study can improve the management and response procedure in Miedzyzdroje in case of a future pollution event. The risk and scenario maps, produced within the steady state simulations with a constant wind forcing, provide clear evidence for places at risk during a contamination event under different wind conditions. These provide results comparable to realistic model results regarding transport ranges. Knowing these ranges, the total sampling amount can be reduced to locations in critical areas. For instance, the predominant south-west wind will favour an alongshore transport of pollutants towards the east. Under this wind condition the monitoring should be expanded to bathing areas 20 km away from the town and also to locations 1 km west of the town.

Salmonella pollution events will be detected by chance in the future, as has been the case in Miedzyzdroje in the past. Therefore, only short-term measurements will be available. This provides a challenge for the management of the region since short-term observations neither give information about the possible source nor about regions affected by the contamination. However, if the measurements are supported by model applications, concrete action recommendations can be derived. The results of this case study suggest that pollution events occur not only spot-like, but affect a wide area along the coast. Generally, pollutants are transported with the flow field, which is forced by the wind itself making the wind the most important factor during a contamination event. It is the main driver of transport ranges if no higher, dominant flow is present. Hence, fast progress of work is recommended as it is necessary to guarantee the health of bathers. The presented workflow, developed throughout our study, supports this task. It is a tool which provides clear recommendations for consecutive actions in case of a pollution event. For example a bathing prohibition is recommended if threshold values are exceeded. This is a difficult task since there is a) no threshold for *Salmonella* bacteria in the recent Directive 2006/7/EC and b) no correlation between the presence of *Salmonella* and the guide values of indicators (Mansilha et al. (2010)). Assuming a mean water swallow of an adult of 50 ml water per bath, it needs $10^3 - 10^6$ germs as infection dose (Poremba (1991)). Thus, it requires $2 \cdot 10^5 - 2 \cdot 10^7$ germs per litre water for enough pathogens to survive through the human intestinal tract (Briese and Heinemeyer (1989); Havemeister (1989)). This values could be used to derive thresholds instead of applying the presence/absence method of the old Directive 1976/7/EEC. Further, we suggest in our workflow the rapid acquirement of information about the wind condition as well as the rapid identification of the pollution source through in-situ measurements. However, during continual long-term pollution, if the source cannot be found or closed off, we recommend the computation of an entire model study similar to what is presented here. It expands the observations from single part measurements to a spatio-temporal picture of the bacterial distribution in the coastal zone. Concrete sampling locations are suggested, based on regions most affected by the pollution event. This reduces the effort and costs of the monitoring program. Since this is generally a task being performed by the public authority, money and time are often lacking and measuring water quality at bathing places with a high temporal resolution, as demanded by the EU directive 2006/7/EC during pollution events, is unattainable ("[...] timely and adequate management measures [...]", European Union (2006)). Notwithstanding, a model study is expensive in labour as well. Therefore, we recommend a collaboration of the public authorities with scientific institutes which could accomplish the model studies and use them for further studies. For example, there is an existing collaboration between the *Governmental Institute of Public Health and Social Affairs of Mecklenburg- Western Pomerania (LAGUS)* and the *Leibniz Institute for Baltic Sea Research Warnemünde* to study the increased occurrence of *Vibro spp.* in the Bay of Greifswald, southern Baltic Sea.

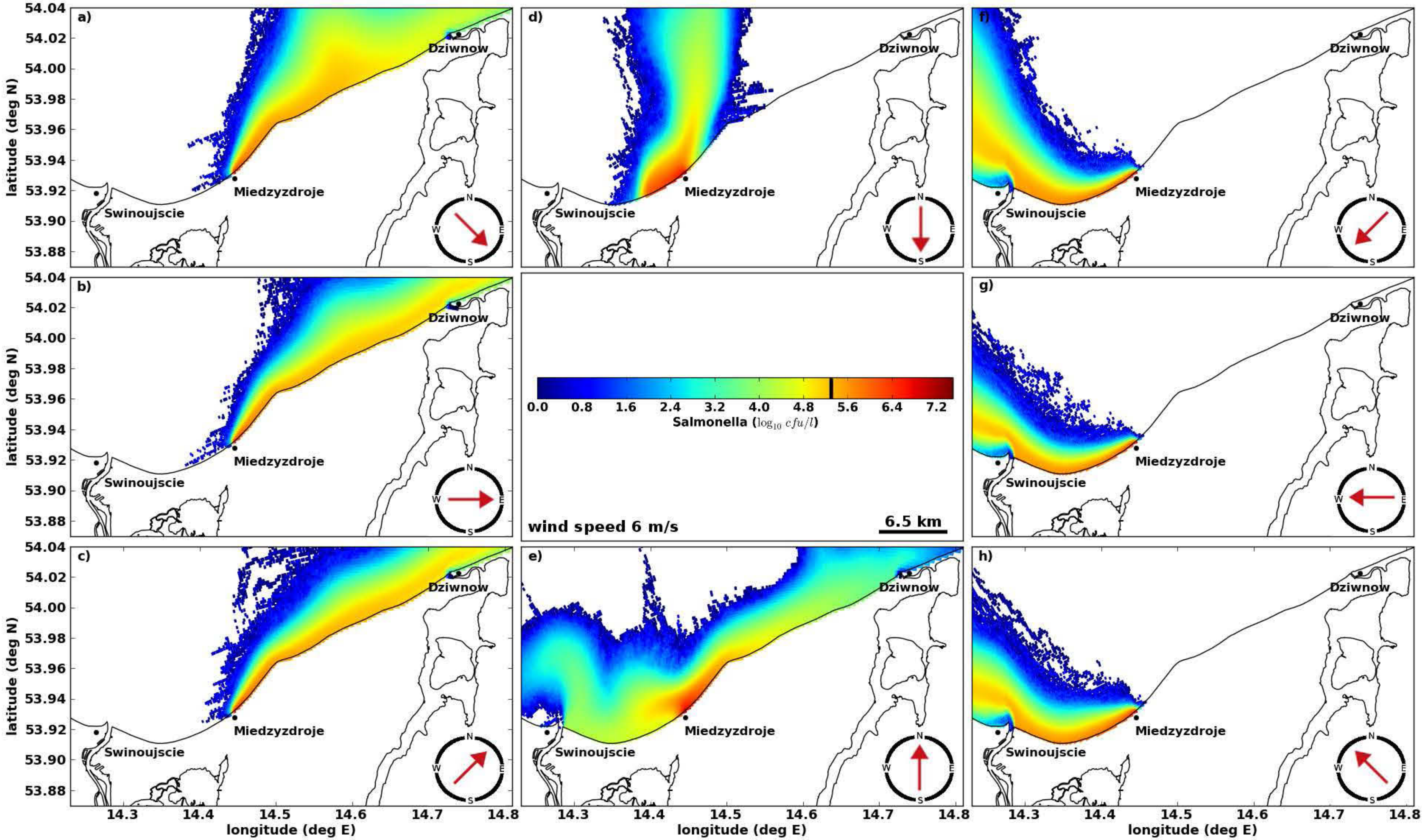

Figure 3.10: Scenario risk maps of maximal *Salmonella* density according to the forcing with steady state flow fields from the 8 cardinal wind directions with speed of 6 m s^{-1}. Shown are the concentrations integrated over the entire water column. The black line within the colorbar indicates the *Salmonella* threshold for an infection according to Briese and Heinemeyer (1989) and Havemeister (1989).

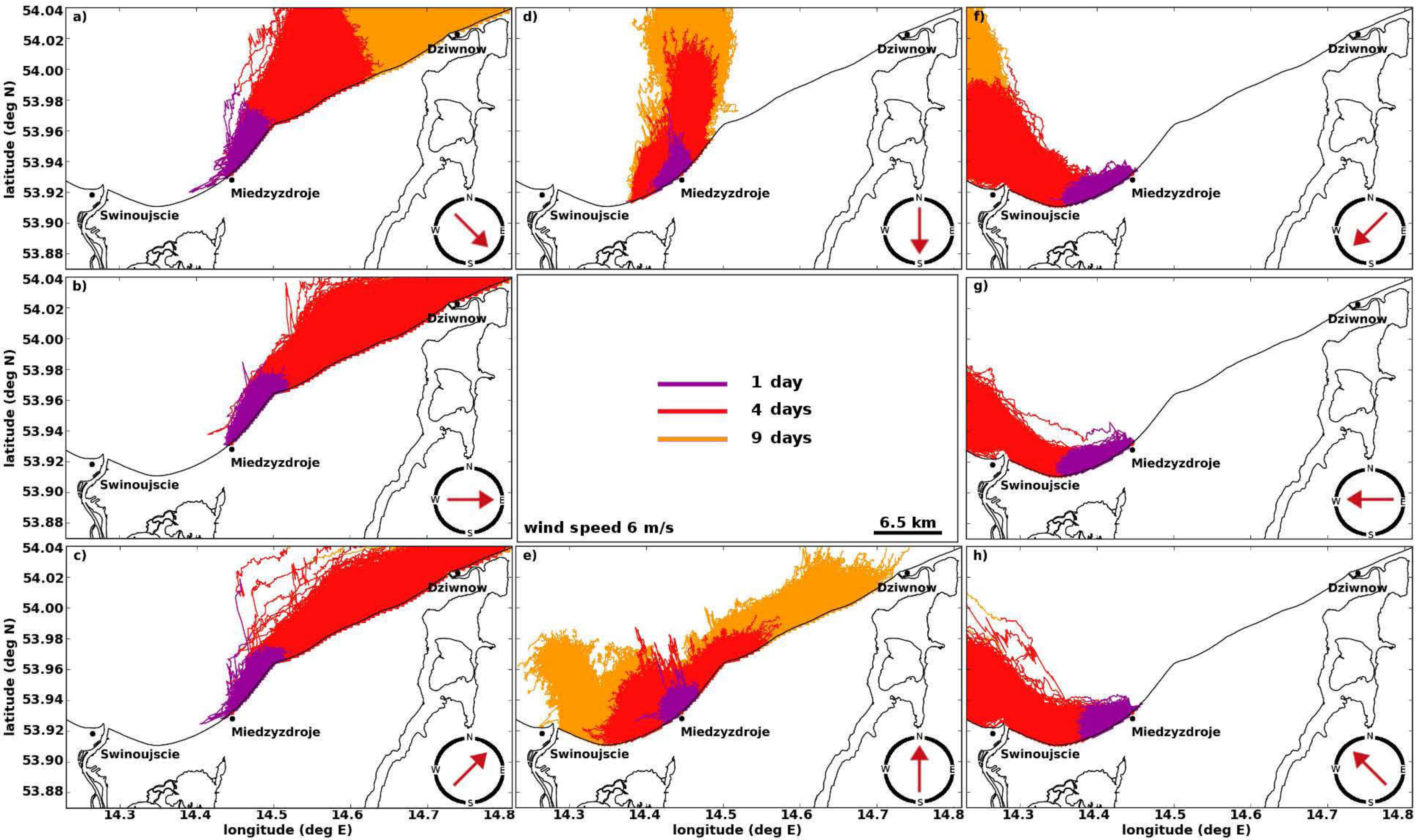

Figure 3.11: *Salmonella* tracks according to the forcing with steady state flow fields from the 8 cardinal wind directions with speed of 6 m s^{-1} after 1 (purple), 4 (red) and 9 days (orange).

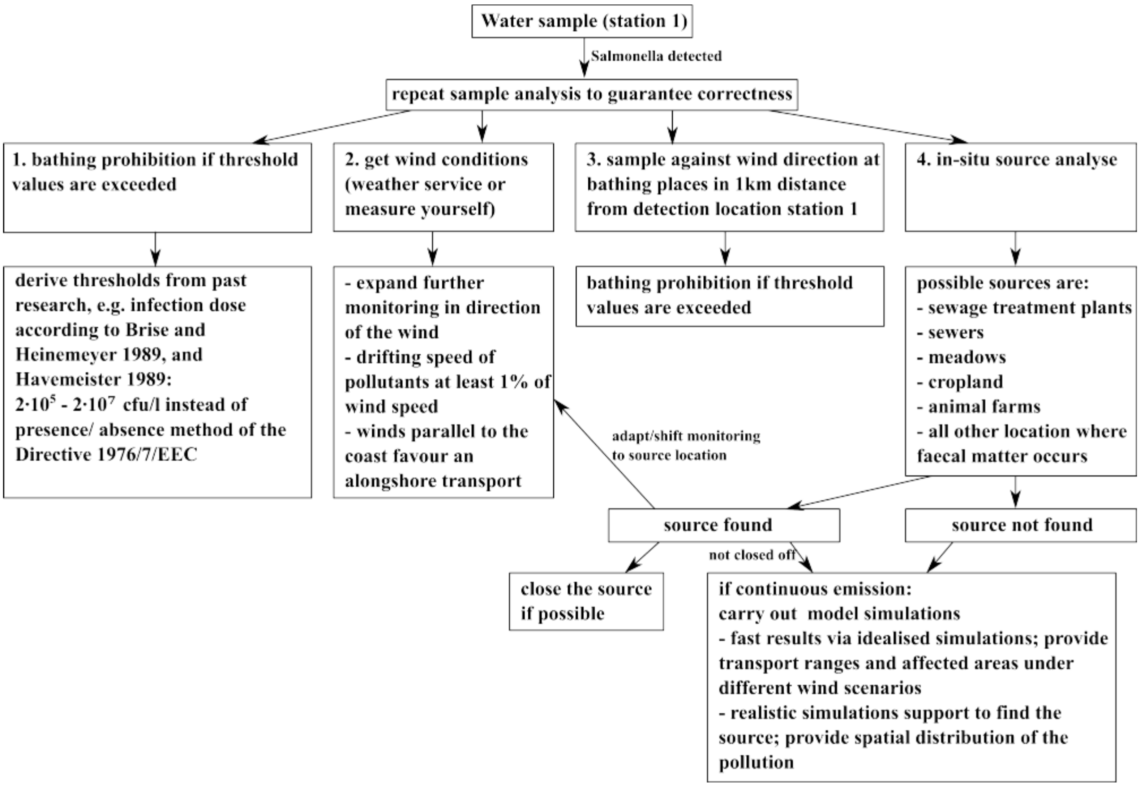

Figure 3.12: Schematic workflow for management and monitoring. A detailed description can be found in the text.

Chapter 4

Recurrence of potential human pathogenic *Vibrio* in a western Baltic Sea bay: analysis with a 3-D ocean model system

4.1 Introduction

Several *Vibrio* outbreaks were reported in Europe, including France, Spain, and the neighbouring countries of Baltic and North Sea (cf. Frank et al. (2006); Baker-Austin et al. (2010)), during the last two decades (Baker-Austin et al. (2012)). In the last decade twelve infections (four lethal) were reported in the German Baltic Sea region with the highest number of infections having occurred in the Bay of Greifswald in the western Baltic Sea, Germany (seven infections, at least one lethal) (Robert Koch-Institut (2012)). The area around the bay has been a tourist centre for decades with more than 15 million overnight stays in 2010 (Statistisches Amt Mecklenburg Vorpommern (2011)), and is also known for high quality rehab hospitals. Particularly, the long and sandy beaches at the 12 EU- registered bathing places with their shallow water body were famous for their very good bathing water quality in 2010-2011. However, the unpredictable but recurrent occurrence of potentially human pathogenic *Vibrio spp.* (e.g. *Vibrio cholerae*, *Vibrio parahaemolyticus*, and *Vibrio vulnificus*) presents a potential risk for tourists with predisposing factors for *Vibrio* infections (e.g. pre-existing diseases like diabetes mellitus, liver diseases and heart diseases as well as a general low immunity, (Robert Koch-Institut (2012); Oliver (2013))). An infection with *Vibrio* taken up orally (via contaminated water or raw seafood) is generally marked by gastrointestinal symptoms and represents one of the main causes of food-born diseases worldwide (cf. Su and Liu (2007); Jones and Oliver (2009)). An infection following contact with sea water (bathing, handling of raw fish and seafood (Dechet et al. (2008))) is associated with ear and wound infections which can lead to septicaemia and eventually even death, whereas food poisoning leads to death more often. However, the risk from *Vibrio* for human health is usually ignored in recreational waters. They are neither registered in the EU bathing water Directive 2006/7/EC nor in local directives of the federal states of Germany. One reason for this could be that the organisms are a natural component of the bacterial flora in the salty water of oceans, estuaries and lakes (e.g. Kirschner et al. (2008); Böer et al. (2012)) and thus there are no measures to hinder *Vibrio* occurrence. A second reason could be that bathing water related infections with *Vibrio* are relatively rare. Due to the lack of field data in the Baltic Sea, the research in this field is in its infancy and little is known about the effects of environmental parameters on the species' specific growth and mortality rates (Chase and Harwood (2011)) or potential reservoirs of *Vibrio* bacteria. For instance some studies indicate that the microorganisms occur not only in the water column, but also in sediments, on plankton, sea fish, crustaceans and shellfish (Hauk (2012); Rehnstam-Holm and Godhe (2012); Oberbeckmann et al. (2012)). Moreover, a strong correlation is suggested between the relative abundance of *Vibrio* and an increased annual-mean sea surface temperature (Baker-Austin et al. (2013); Vezzulli et al. (2012)). The highest concentrations of potential human pathogenic *Vibrio* in water were observed during months with increased temperatures of more than 20° C (cf. Pfeffer et al. (2003); Parvathi et al. (2004)). Besides this, in the recent study of Böer et al. (2013) the measurement of pathogenic *Vibrio* in the North Sea suggested a seasonal difference and inter-annual cycle in the presence of the bacteria. The results of an epidemiological study showed further that climate change and the expected increase in temperature are believed to favour *Vibrio* occurrence and infections in coastal areas of the mid and southern Baltic Sea (Baker-Austin et al. (2013)). However, standardised monitorings are lacking to understand the ecological connection and not much is known about the environmental factors influencing the *Vibrio* community.

Generally, monitoring programs are time and coast intensive and show only an incomplete picture of the bacterial distribution. Thus, a model study can add to the measurements by expanding the observations from single part measurements to a spatio-temporal picture. It allows the analysis of the impact of single parameters which can influence the bacterial behaviour and distribution. Therefore, we combine information about measured *Vibrio* concentrations with a model system, consisting of a three-dimensional circulation model and a three-dimensional Lagrangian particle tracking model which can act as a management tool for authorities (c.f. Schippmann et al. (2013b)). Within our study we focus on the Bay of Greifswald, an semi-enclosed embayment in the southern Baltic Sea, because seven infections with human pathogenic *Vibrio* occurred there during the last years and in addition, the bacteria were recurrently detected. Since this area gains increasing interest of tourism there is consequently a potential risk for further infections. The aim of this study is to find possible reasons behind the recurrent presence of human pathogenic *Vibrio* in the Bay of Greifswald and to help the authorities identifying future monitoring sites and parameters. Therefore the manuscript addresses the following questions: a) Are the seasonal cycle of *Vibrio* presence and the inter-annual differences in *Vibrio* occurrence in the bay and in the southern Pomeranian Bight attributed to water temperature and depth? b) Can the sediment of the Bay of Greifswald present a possible reservoir for pathogenic *Vibrio* and if so is the resuspension of sediments the cause of *Vibrio* recurrence? c) Is the seasonal large shoal of herrings a possible explanation for the *Vibrio* occurrence? d) Can external sources, as the Baltic Sea or the Peenestrom, and spatial transport patterns in the bay explain the recurrence of *Vibrio spp.*?

4.2 Area of interest and measurements

The Bay of Greifswald (GWB) is a semi-enclosed embayment located in the western Baltic Sea at the Pomeranian Bight (Figure 4.1). With an area of 510 km^2, it is the largest bay of the Baltic Sea. The main tourism attractions in the GWB are water sports and nature (Robakowski (2012)), but beach tourism is an increasing sector. In particular, the long, sandy beaches and the shallow water body are well suited for children and gain a still growing interest. Overall, there are 12 EU-registered bathing places at the bay (Figure 4.2 (a)) with very good bathing water quality according to the EU Bathing Water Directive 2006/7/EC (European Union (2006)). Moreover, there are many unrecorded bathing places, and thus not monitored, frequently used by tourists searching for untouched beaches.

The mean and maximum water depths of the GWB are 5.8 m and 13.5 m, respectively (Hupfer (2010); Statistisches Amt Mecklenburg Vorpommern (2011)). The western part of the bay is a shallow sag with depths of 6-8 m. The embayment has a small volume of approximately 3.000 million m^3 (Hupfer (2010); Statistisches Amt Mecklenburg Vorpommern (2011)). It has two connections to the Pomeranian Bight: one in the East and the other in the North-west via the Strelasund (Figure 4.2 (a)). Water exchange with the Baltic Sea occurs approximately eight to twelve times a year (cf. Schiewer (2007); Burchard and Schernewski (2008)). Water dynamics, flow and mixing conditions, inflow and outflow of Baltic Sea water mainly depend on wind conditions (Burchard and Schernewski (2008). The prevailing south west wind direction leads to water inflow into the bay via the Strelasund and an outflow via the eastern outlet (Schiewer (2007)). The flow direction changes frequently across time and leads to an oscillation of water masses at the outlets (Bauer et al. (2013)) resulting in a transition zone between the bay and the Baltic Sea (Lampe (1994)). Consequently, most of the same water mass is involved in the water exchange process (Bauer et al. (2013)). The temporal variations in wind stress suppress the formation of a constant flow regime within the bay (Miller et al. (1990); Smith (1994)).

The water body of the bay contains freshwater from precipitation, the river Ryck (1 m^{3}s^{-1}, 0.2%) off Greifswald and the Peenestrom (23 m^{3}s^{-1}), and salty water from Baltic Sea (87%, Burchard and Schernewski (2008); Landesamt für Umwelt, Naturschutz und Geologie Mecklenburg-Vorpommern (2008)). The bay has a mean salinity level of 6-8 PSU whereas in the Peenestrom mouth 3-8 PSU are common (cf. Bachor (2005); Landesamt für Umwelt, Naturschutz und Geologie Mecklenburg-Vorpommern (2008)). The mean pH-value lies between 7 and 8 (Ministerium für Arbeit, Gleichstellung und Soziales Mecklenburg-Vorpommern (2012)). High temperature variations, but weak temperature stratification, can be found in the GWB because of its shallowness and small volume. In contrast to the open Baltic Sea, increased sea surface temperatures can be measured in the GWB in comparison to the Baltic Sea (Figure 4.1) whereas inter-annual differences are common. Temperature increases strongly in summer and decreases in winter, often followed by ice coverage. Water temperature measurements taken by the *Federal Ministry of the Environment, Nature and Geology Mecklenburg West-Pomerania* from 1997 – 2010 show that temperatures above 10° C were rarely found before May and that summer temperatures higher than 20° C did occur not before the end of June.

Bathymetry and wind driven flow patterns strongly influence the sediment distribution

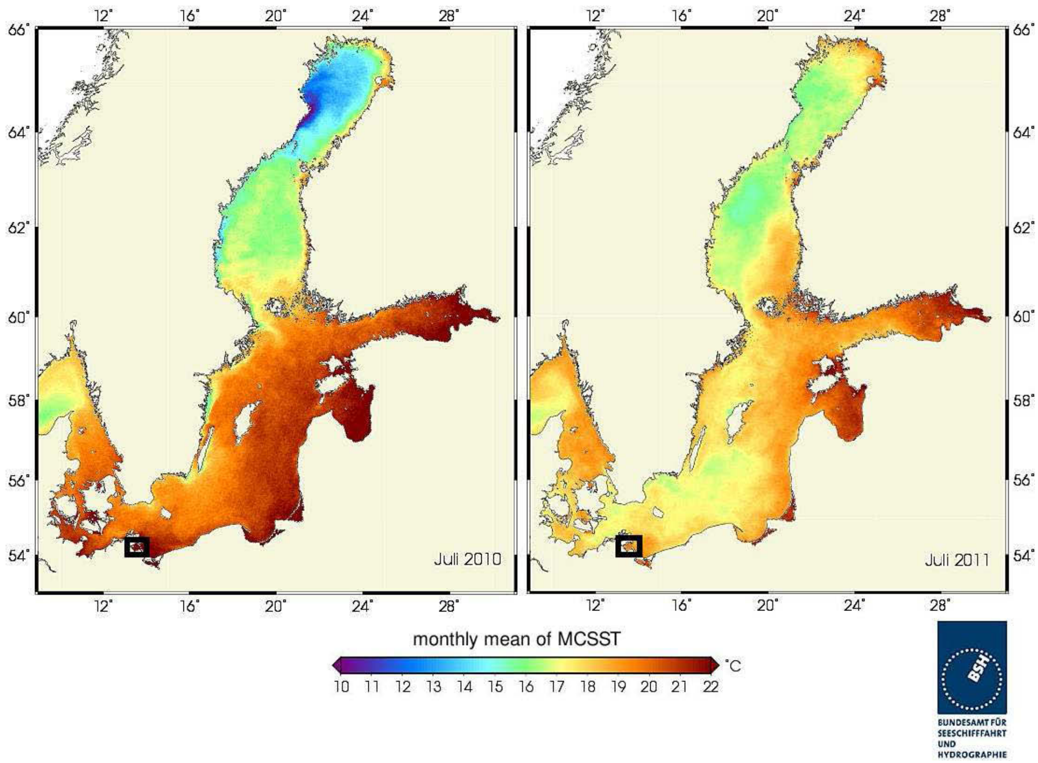

Figure 4.1: Satellite image of the July-mean sea surface temperature in 2010 (left) and 2011 (right) produced with the sensor NOAA-AVHRR with 1 km resolution (source: *Bundesamt für Seeschifffahrt und Hydrographie*). The black rectangle marks the location of the GWB.

in GWB. Generally, the sediment in the GWB is polymorphic. In the homogeneous west basin, in areas where the depth exceeds 6 m (Lampe and Meyer (1995)), silt is the dominant sediment (nearly 30% of the GWB area, Eidam et al. (1997)). The areas of the breaker zone and shallow waters are dominated by sandy sediment (Coastal Information System Oder Estuary (2004-2007)). A characteristic attribute of silt is its general high amount of organic carbon (up to 10 % of the dry matter) (cf. Schwarzer and Diesing (2003)). This is in accordance to the study of Leipe et al. (2011), who found up to 8% total organic carbon (TOC) in the GWB sediment. Additionally, the silt in the GWB is characterised by a high amount of silicate phases (silica, ternary feldspar and clay mineral) (Eidam et al. (1997)).

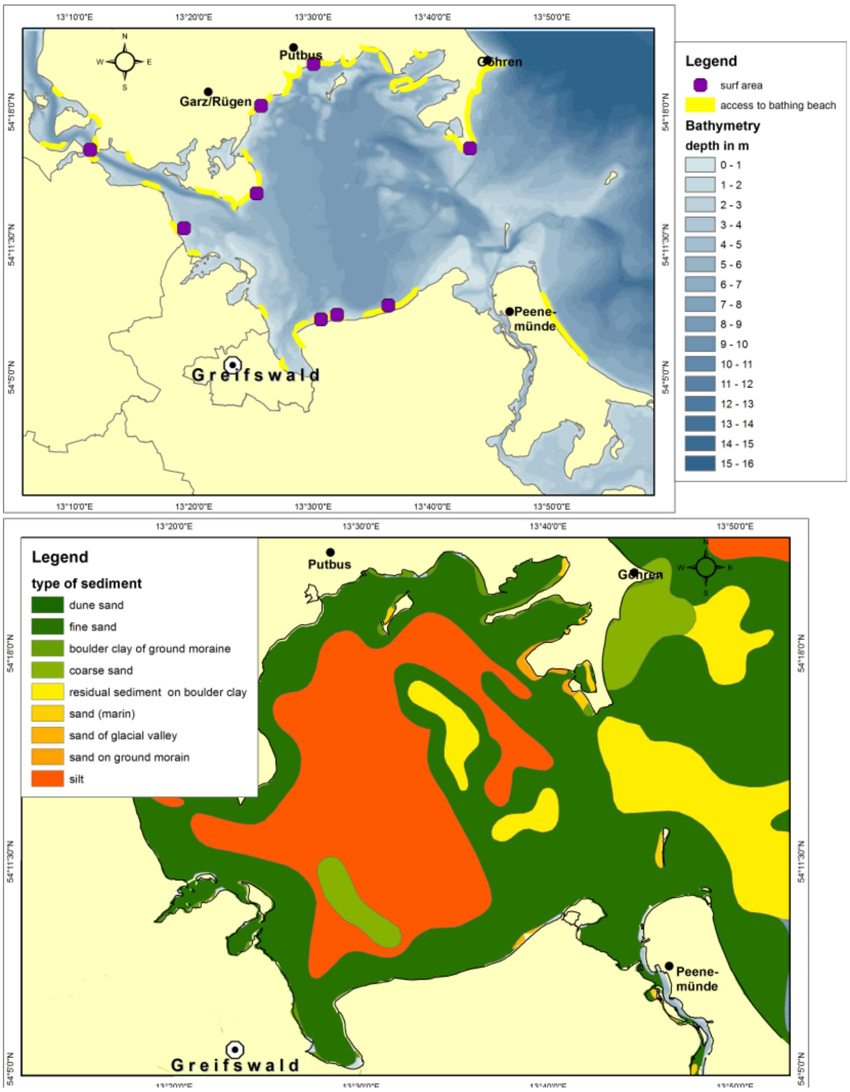

Figure 4.2: Maps of the GWB showing the bathymetry, beaches and surf areas (upper panel) as well as sediment distribution (lower panel).

Wind measurements

Since most infections with the human pathogen *Vibrio* occurred in the GWB in 2010 and 2011, these years were chosen for the model applications. In the following we will analyse the environmental parameters for the summer seasons of these periods. During both summers, 2010 and 2011, a south west wind was prevailing (763 and 1124 measurements of SW wind), where it was predominantly in 2011. In general, the wind direction varied mainly between south west and northerly winds in 2010, whereas during the first period of July easterly winds prevailed (Figure 4.3). In 2011, south west winds dominated the entire June, middle of July and the entire August. The mean wind speed accounted for 4.2 and 5.4 m s^{-1}, respectively. However, the maximum wind speed was reached only 14 days in 2010 whereas in 2011 wind speeds higher than 11 m s^{-1} were predominant for more than three weeks all over the summer.

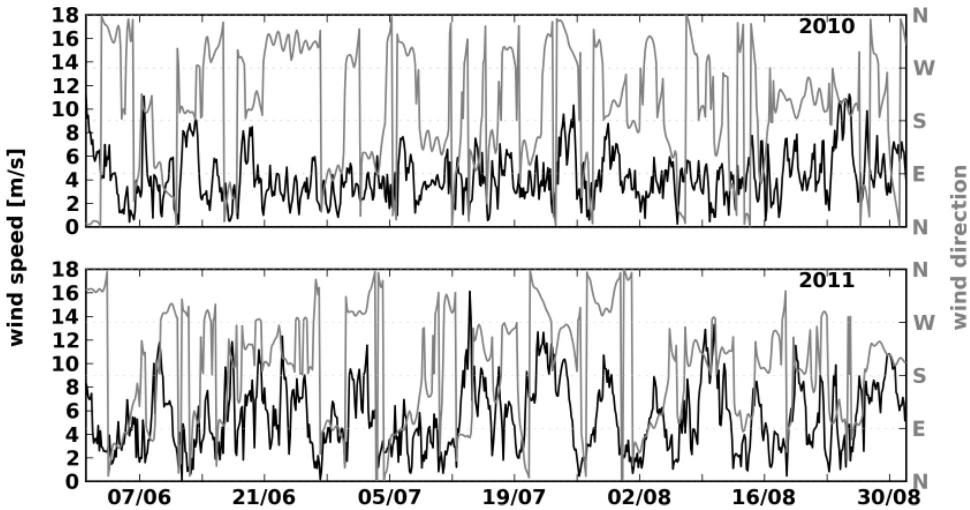

Figure 4.3: Wind speed and direction in summer 2010 and 2011.

Vibrio measurements

All data shown in this subsection are only parts of unpublished *Vibrio* measurements sampled by the *Governmental Institute of Public Health and Social Affairs of Mecklenburg-Western Pomerania (LAGUS)* and the *Federal Institute of Hydrology (BfG)* Koblenz.

Despite potential human pathogenic *Vibrio spp.* not being indicators of the EU hygienic Bathing Water Directive 2006/7/EC, the LAGUS established a biweekly *Vibrio* sampling campaign during the bathing seasons since 2004 (starting in July assuming the water temperature to be the most important factor driving *Vibrio* growth) based on the *Vibrio* infections in the past. Within this campaign samples were taken at several stations along the German Baltic Sea coast. The two stations, where human pathogenic *Vibrio* were measured recurrently are Lubmin (GWB) and Karlshagen (coast of Usedom, Pomeranian Bight, Figure 4.9). In 2010 and 2011 infections occurred after patience went bathing in the GWB and at the coast of Usedom. According to the measurements (Figure 4.4) both *V.vulnificus* and *V. cholerae* were found in Lubmin and in Karlshagen during both summer seasons. The number of positive samples changed between the years in Karlshagen whereas it stayed constant in Lubmin. In 2010, *Vibrio* were more dominant in Lubmin (75%) than in Karlshagen (50%) whereas the number of positive samples was equal in 2011 at both stations (50%). The number of *Vibrio* detections increased at both stations when the water temperature exceeded the 20° C threshold value, except in July 2010 and August 2011 in Karlshagen and August 2011 in Lubmin. However, at the end of the seasons the bacteria were detectable at temperatures below this threshold.

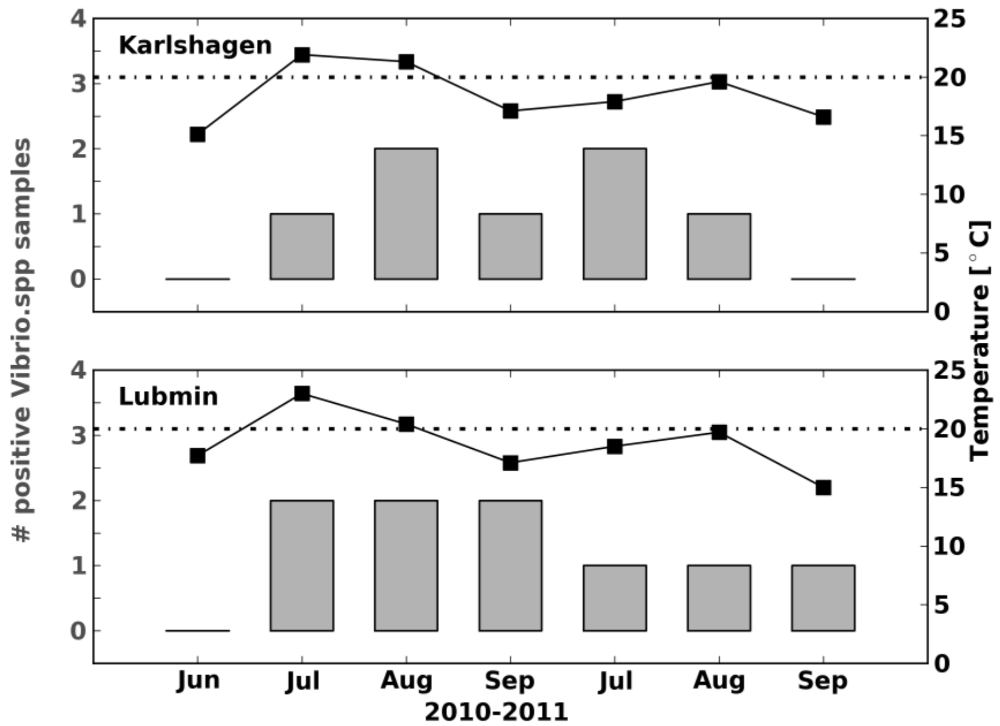

Figure 4.4: Positive *Vibrio* samples detected in Karlshagen and Lubmin and measured water temperature during the summer seasons 2010 and 2011.

Within the research programme KLIWAS further *Vibrio* measurements were carried out in the GWB. These include not only water samples but also sediment measurements. The samples were taken from October 2010 until April 2012 along a transect through the GWB (Figure 4.5). Due to ice coverage no samples were taken in winter 2010/2011. In October 2010 seven positive samples (water + sediment) were detected in the GWB whereas in April 2011 the total number was less than half as high (Figure 4.6). The closer the water temperature got to the threshold value of 20° C the more positive samples were detected in both water and sediment. Therefore, all together 9/ 7 positive *Vibrio* samples (water + sediment) were found in July/ August 2011. This number decreased again in October. Generally, *Vibrio* were detected in higher concentration in the sediment than in the water column (in October 2010 and August 2011 more than twice as high as in the water samples). In April 2011, when no *Vibrio* were detected in water samples, three sediment samples were positive. However, the concentrations of *Vibrio* per 100 ml water (data not shown) were in summary nearly five times higher than in the sediment. *Vibrio* were most frequently detected at the western stations (see Figure 4.5), which have

a mean TOC between 2.6 and 4.6% according to the measurements (not shown) and are covered by silt and clay. These sediment can be resuspended into the water column during mixing events (forced by i.e. heavy wind) and might hence present a reservoir for *Vibrio* (cf. Randa et al. (2004)). Therefore, we hypothesise that *Vibrio* mainly occur in the silty sediment of the GWB where they find good nutritional conditions due to the high TOC content. The eastern sampling stations were located in areas where sand dominates the sediment content structure. Although *V.parahaemolyticus* and *V.alginolyticus* were known to also occur in sandy sediments (c.f. Böer et al. (2013)), we neglect their presence here because these agents play only a minor role in the GWB.
During both sampling campaigns, LAGUS and KLIWAS monitoring, *V.vulnificus* and *V.cholerae* were the main agents found in the GWB.

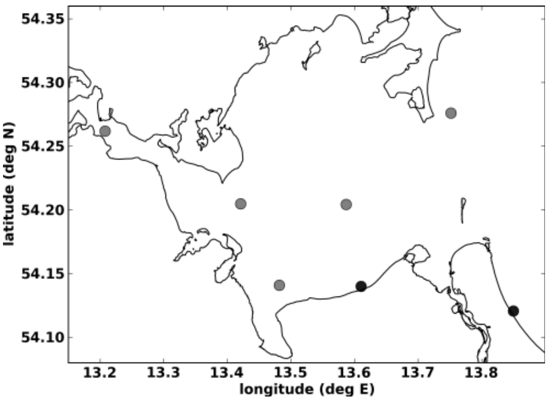

Figure 4.5: *Vibrio* sampling stations in the GWB of the research programme KLIWAS (light grey) and the two stations of the LAGUS monitoring (dark grey).

4.3 Methods and model scenarios

In order to simulate the transport of *Vibrio* bacteria they were assumed to act like passive drifters in the water column. These can be simulated as hypothetical particles in a particle tracking model forced by pre-simulated flow fields of a circulation model. With this model system the particle transport in the water can be reproduced and several hypothesis can be tested, as for example temperature dependence. The applied model system has already been successfully applied to model the transport of microorganisms in coastal waters (Schippmann et al. (2013a,b)).

4.3.1 Setup information and validation

The raw bathymetry is a combination of several data sets (Glockzin (2006), Bundesamt für Seeschifffahrt und Hydrographie (2010), pers. comment K. Buckmann) and has an overall resolution of less than 50 m. It was interpolated to the numerical grid with a spatial grid resolution of 100 m. The vertical water column was always subdivided into 10 layers with

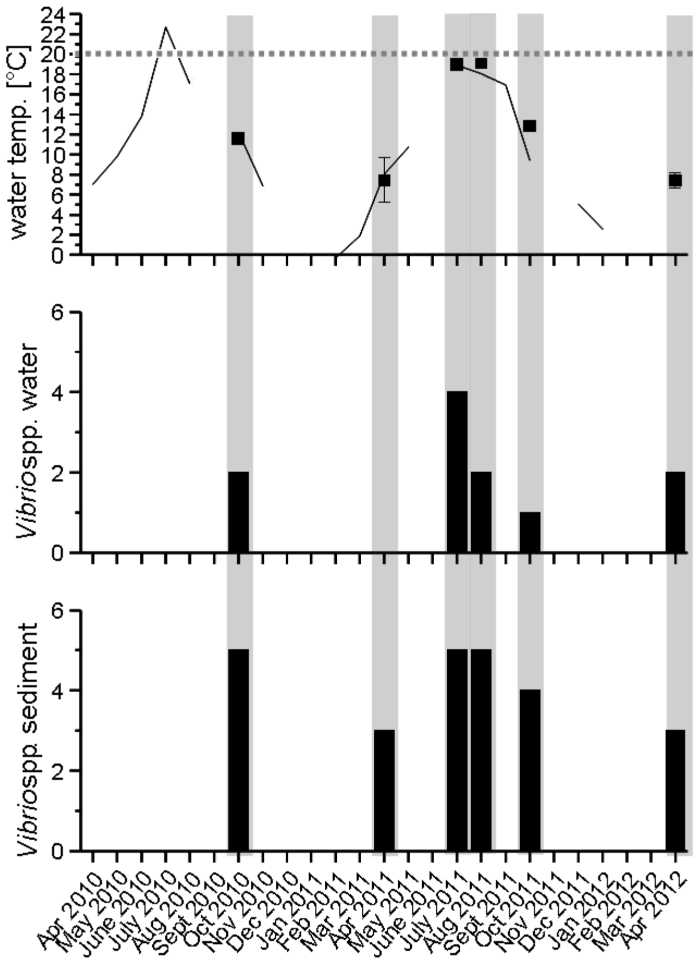

Figure 4.6: Water temperature and numbr of positive *Vibrio* samples (*V. vulnificus*, *V. cholerae*, *V. alginolyticus*, *V.parahaemolyticus*) in sediment and water summed up over the five GWB monitoring stations (Figure 4.5). The grey background marks the sampling time. Water temperature data, depicted as black line, were taken from the *Landesamt für Umwelt, Naturschutz und Geologie Mecklenburg Western Pomerania* sampling station in the central bay, empty spaces are times when no data were available. The black squares with the error bars show the temperature measurements taken during the KLIWAS monitoring averaged over the five sampling stations.

a similar thickness (sigma levels). Consequently, a high vertical resolution was obtained also in coastal waters. The whole area covered by the model-grid (domain) contains 793 $\times$ 630 $\times$ 10 (x, y, z) grid points (land inclusive) with 36.3% active water points on which the hydrological calculations were accomplished. The domain was decomposed into 115 active sub domains of 48 $\times$ 48 $\times$ 10 (x, y, z) grid-points and the setup ran in parallel on

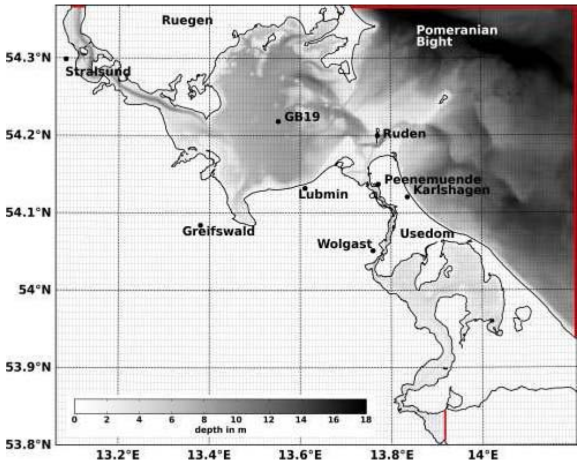

Figure 4.7: Model domain and bathymetry of the Bay of Greifswald model setup. The red lines depict the three open boundaries. The grid is outlined in grey showing every 5-th grid box.

a super computer at the North-German supercomputing Alliance (HLRN (2007)). The realistic simulations started in January with a constant initial temperature of 0° C and the initial salt was given as a 3-D concentration field constant in depth. The initial velocities were set to zero. Realistic meteorological forcing with a spatial resolution of 7 km and temporal resolution of 6 hours, taken from the operational model of the German National Meteorological Service, was applied when computing the realistic flow fields. Prescribed were the air temperature, humidity, cloud cover, air pressure, precipitation and wind fields taken at 10 meters above the mean sea level.

The riverine freshwater fluxes within the bay are generally weak with only the Peene River being of great importance. Its freshwater river discharge was given to the setup as constant value of 20.6 m^3s^{-1} (summer median) for all simulations. GETM was forced with two and three-dimensional fields along the open boundaries in the Strelasund, Oder lagoon and Pomeranian Bight (Figure 4.7). The two-dimensional forcing included sea surface elevation and depth averaged currents in combination with Flather boundary conditions (Flather (1976)). The three-dimensional forcing included salt and temperature. The two- and three-dimensional fields have a temporal resolution of 4.5 and 4 hours, respectively. All boundary information were taken from a 600 m Baltic Sea simulation model (Gräwe et al. (2013)). Calculated sea surface elevation, vertical and horizontal velocity fields as well as salt and temperature fields were stored on an hourly basis for further analyses. The steady state simulations were conducted with constant wind speeds from south west with 10 metre wind speed of 3 m s^{-1}.

Due to the correlation between water temperature and *Vibrio* growth, it is necessary to take this dependence into account when computing the bacterial concentrations. However, not much is known about mortality and growth rates of *Vibrio* (Chase and Harwood (2011)). The study of McFeters et al. (1974) showed that *Vibrio cholerae* is able to survive more than seven hours in fresh water, but nothing is known about its die-off in salty water. *Vibrio* growth experiments of Chase and Harwood (2011) indicated that the organisms were able to nearly duplicate per hour in water with pH value 5 and 25° C. Growth experiments at different water temperatures are rare and hence the results of Robert Potau Núñez (2011) for *V.vulnificus*, conducted with water sample isolates taken in the North Sea at the BfG Koblenz were used to calculate the temperature-dependent division rate λ, via linear regression (standard error of slope value< 0.021) (Equation 4.1).

$$\lambda(T) = 0.103T - 1.027 \tag{4.1}$$

This approach was applicable due the linear behaviour of the measurements and is in accordance with the results of McFeters et al. (1974) and Chase and Harwood (2011). It allowed the reproduction and die-off of the simulated particles per hour according to equation 4.2, where T presents the temperature, C_0 is the initial particle concentration and C the new particle concentration.

$$C(T) = C_0 \cdot 2^{\lambda(T)} \tag{4.2}$$

In general, particle concentration was calculated by dividing the particle numbers per grid cell by the volume of the cell and no *Vibrio spp.* concentrations, but the particle concentrations integrated over the entire water column are shown in the scenario maps. These shall indicate areas within the GWB in which an increased *Vibrio spp.* occurrence is highly probable.

4.3.2 Model validation

The tracking process in GITM is dominated by advection, whereas diffusion plays only a minor role. Therefore reliability of the advection process is guaranteed via the GETM validation. The circulation model has only a few degrees of freedom and was fed with reliable boundary information from both meteorological forcing from the German National Meteorological Service and boundary conditions (sea level, velocities, salt and temperature) the latter of which were used to force the model from the open boundaries of our model domain (the area of interest). This "outer model" which produced the boundary information was successfully validated against measurements. At the Oder Bank Buoy, located at the eastern boundary of our model setup, modelled salinity has a small Bias of -0.07 PSU and a root mean square error (RMSE) of 0.73 PSU. The temperature Bias was about -0.01 K and the RMSE was 0.56 K (correlation of 90%).
The validation of the applied model setup was accomplished by comparing the modelled results with measurements of water gauges and sea surface temperature. The former were kindly provided by the *Bundesamt für Schifffahrt und Hydrographie*, the *Wasser- and Schifffahrstverwaltung des Bundes* (WSV, www.pegel.online.de). The sea surface temperature data were kindly provided by the *Landesamt für Umwelt, Naturschutz und*

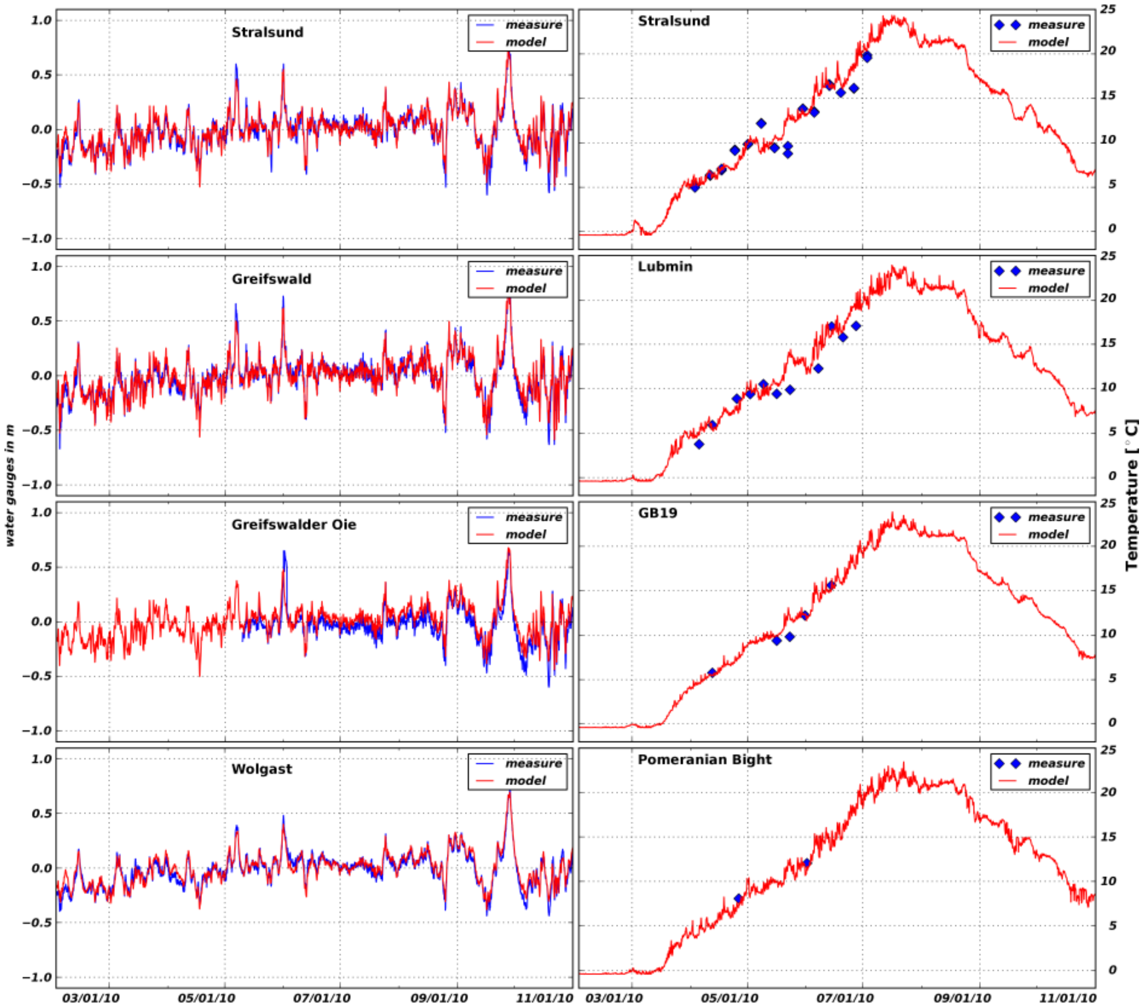

Figure 4.8: Left: Time series of measured sea surface elevation (blue lines) against the model results (red lines). Right: Time series of measured sea surface temperature (blue squares) against modelled sea surface temperature (red line) from January to November 2010.

Geologie Mecklenburg Western Pomerania, and the *Johann Heinrich von Thünen-Institut für Ostseefischerei, Bundesforschungsinstitut für Ländliche Räume, Wald und Fischerei.* The time series of the modelled sea surface elevation were compared to the corresponding water gauge measurements at Stralsund, Greifswald, Wolgast, Thiessow (not shown), Ruden (not shown) and Greifswalder Oie between January and November in 2010 and 2011 (not shown). GETM reproduced the observations with high accuracy (left column in Figure 4.8). Especially, the inner bay dynamics were very well captured. This can also be found in the statistics. The mean root mean square error (RMSE) is 8 to 9 cm (Table 4.1) in both years. In comparison with the mean standard deviation of the measurements (20.6 cm) this is comparatively small. The mean coefficient of determination (R^2) of 0.84 and 0.78, respectively, shows that the modelled sea surface elevation was in good agreement with the observations (Table 4.1). The time series of the modelled sea surface temperature

2010	**mean**	**max**	**min**
RMSE	0.09 (1.28)	0.09 (1.69)	0.07 (0.74)
R^2	0.84 (0.84)	0.89 (0.99)	0.55 (0.91)
2011			
RMSE	0.08 (0.98)	0.11 (1.56)	0.07 (0.54)
R^2	0.78 (0.96)	0.86 (0.99)	0.61 (0.91)

Table 4.1: Mean, maximum and minimum root mean square error and coefficient of determination computed from the modelled sea surface elevation and modelled sea surface temperature (in brackets) in 2010 and 2011.

were compared with the corresponding water temperature measurements (right column in Figure 4.8) in Lubmin, Stralsund, GB19, the western bay (not shown) and in the Pomeranian Bight between January and November 2010 and 2011 (not shown). GETM reproduced the seasonal temperature increase in summer with high accuracy. The mean temperature deviations (RMSE) of the simulation are 1.3°C which is small in comparison with the mean standard deviation of the measurements (5.3°C). The mean R^2 of 0.96 proves the high agreement of model results and observations (Table 4.1). Since there were no data available for the second half of the years, our model results could not be compared with observations during this period. The validation of the 600 m Baltic Sea model, in which our model was nested, showed high accuracy of the temperature (as mentioned before) for two consecutive annual cycles. Thus, we expect our results also to be in coincidence for the second half of the year.

Scenarios

The *Vibrio* measurements shown in section 4.2 have demonstrated parameters (temperature, sediment) which potentially influence the *Vibrio* abundance in the GWB. Based on this information we developed two model scenarios which allow the simulation of the correlation between the bacteria and these parameters in the GWB. Furthermore, a literature review (see 4.3.2) indicates the potential impact of sea fish on the *Vibrio* abundance. Although this has not been verified with measurements in the GWB we developed a hypothetical scenario 3 to test this hypothesis. The last scenario described in this section assumes the impact of long-distance transport dynamics on *Vibrio* presence in the GWB.

Scenario 1 water

Water temperature and *Vibrio* abundance are strongly correlated (c.f. Tamplin et al. (1982); Høi et al. (1998)). The highest *Vibrio* concentrations in environmental waters and the highest number of *Vibrio* infections were observed during warm months (cf. Parvathi et al. (2004); Baker-Austin et al. (2012); Böer et al. (2012); Vezzulli et al. (2012)). High temperatures lead to an increase in bacterial replication, e.g. *Vibrio vulnificus* abundance peaks at seawater temperatures > 19 °C (cf. Oliver (2005)). Therefore, it is proposed that water temperature is one of the main parameters correlated to *Vibrio* growth (Drake et al. (2007); Böer et al. (2013)). During colder months, when water temperatures are below 13°C, the bacteria change their status to the "viable-but-not-culturable"- state (cf. Oliver (2000)). However, once present, the bacteria were suggested to remain culturable for several months even at lower temperatures (Böer et al. (2013)).

Assuming that *Vibrio spp.* are a natural component of bacterial flora in oceanic, coastal and estuarine saline water (Böer et al. (2012)) and lakes (Kirschner et al. (2008)), hypothetical particles, representing *Vibrio* bacteria, were released at 300 m intervals into the surface layer (overall 8.563 particle) (Figure 4.9a), while the particle numbers were integrated over the entire water column to get an equal distribution in the GWB independent of the water depth (10^{-5} particles per 100 ml). Released particles were tracked from 19.06. to 19.07.2010 and from 06.06. to 06.07.2011, the periods during which sea surface temperatures of 20° C were reached for the first time and were shown to be favourable for the presence of *Vibrio* (Hauk (2012)).

Scenario 2 sediment

Previous studies from other regions showed that sediments can harbour high amounts of *Vibrio* (Blackwell and Oliver (2008); Vezzulli et al. (2009)) and it was further suggested that *Vibrio* are active members of the benthic bacterial community (Böer et al. (2013)). Moreover, their is evidence that if the bacteria are colonising in a thin floc zone just above the sediment-water interface during winter (Williams and LaRock (1985); Vanoy et al. (1992)), the resuspension, forced by e.g. storm events, and subsequent transport of *Vibrio* from the sediment presents a significant source of the bacteria to the water column (cf. Friesa et al. (2008)). In June 2010 and 2011 wind events (with wind speed larger than 5 Bft.) occurred in the GWB which might have caused a resuspension of sediment. In 2010, a strong wind event with speeds of 8 m s^{-1} (5 Bft) took place on the 18.06., whereas in 2011 the event took place earlier on the 06.06. and was stronger (12 m s^{-1} (6 Bft)). The wind direction was south-west in both cases and therefore a mean eastward flow field pattern developed (Figure 4.3).

The silty sediments in the GWB contain a high amount of TOC (pers. comment T. Leipe, (2013)) and therefore present a possible reservoir for *Vibrio*. Thus, particles were released in these areas (Figure 4.9b) at 300 m intervals into the layer above the bottom (1.624

particles; particle numbers are five times less than in scenario 1 according to measurements; initial concentration 10^{-4} - 10^{-5} particles per 100 ml (depth dependent)). The particles were tracked from 19.06. to 19.07.2010 and from 09.06.to 06.07.2011 when strong wind events occurred in the GWB at the starting dates which probably led to the resuspension of particles.

Scenario 3 herring

Beside their presence in the water column, potential human pathogenic *Vibrio* were also found e.g. in several coastal sea fish species with a prevalence of 17% when the concentrations in surrounding seawater and sediment were low (Brennholt et al. (2010); Alter et al. (2011); Rehnstam-Holm and Godhe (2012)). Fish stocks present a reservoir for *Vibrio* bacteria (Janssen (1996); Novotny et al. (2004)) especially during winter, when the water temperature is below 13°C and the bacteria change their status to the "viable-but-not-culturable"- state (Oliver et al. (1995); Oliver (2000)). *Vibrio* bacteria taken up by fishes might grow faster within the fish body and could be deposited in high concentrations (e.g. by faeces). This fact could be of importance for the *Vibrio* occurrence in the GWB, as it is one of the biggest bays along the German coast and therefore presents an important fishing area (Froelich and Sporbeck (Institut für Angewandete Ökologie) (2008)). The period from February to May is the main fishing season, with maximum fishing rates obtained in April. During this time the herrings seek the macrophyte covered areas for their spawning. Since the GWB is considered the main spawning area of the Western Baltic Spring-Spawning herring (WBSSH, Bauer et al. (2013)) immense amounts of herrings were fished there every year. In 2007 alone 30% of the fisheries of the Baltic Sea were achieved in the GWB (Froelich and Sporbeck (Institut für Angewandete Ökologie) (2008)), whereas in 2010 more than 42 kilo tons of the WBSSH (*Clupea harengus*) were fished in the GWB (ICES (2011)). Unfortunately, there are only few samples from the KLIWAS research programme indicating *Vibrio* occurrence in the sediment in April 2010 during the WBSSH spawning period, but no measurements were carried out from LAGUS before July. Therefore, no concrete correlation between *Vibrio* and WBSSH can be derived for the GWB from the measurements so far. However, according to literature the huge amount of herrings in the GWB presents a potential source of *Vibrio* transport into the GWB. The main pathways of herring stocks to the spawning areas, based on experience of the fisher men, are from the west via the Strelasund and from the east via the edges of Ruden. The fish remain in the central bay initially before they swim into the shallow spawning areas at the coasts (pers. comment Dr. Zimmermann *Johann Heinrich von Thünen-Institut für Ostseefischerei, Bundesforschungsinstitut für Ländliche Räume, Wald und Fischerei*). Therefore an equal distribution of the herrings in the GWB can be assumed which led to a comparable particle release as in scenario 1 (without the emission in the Pomeranian Bight). Again the number of particles was integrated over the water column due to the well mixed water column. Even though the herrings mainly occur in April, the low water temperature (< 10 °C) would not allow a bacterial reproduction but, a strong die-off. Therefore, particles were released one month later on 01.05.2010/2011, when the GWB has water temperatures between 10 and 15 °C and thus favour *Vibrio* reproduction. The simulation period ends at 31.05.2010/2011.

Scenario 4 external/internal sources

Although pathogenic *Vibrio* bacteria were known to be a natural component of salty water they could be transported in higher concentrations from external sources into the GWB leading to the positive detections. Flow field patterns mainly influence the transport direction and distance of microorganisms as they act like passive tracers. As shown in section "Study site" the prevailing south-west winds lead to water mass transports into the Baltic. However, the flow direction changes frequently leading to an oscillation of water masses at the outlets. Assuming that *Vibrio* can be transported from the Baltic Sea via the Strelasund, or from Karlshagen, or from the Oder Lagoon via the Peenestrom into the GWB, 1.000 particles were released at these stations (Figure 4.9c) in the surface layer. Additionally, the same number was emitted off Lubmin, where *V.vulnificus* were recurrently measured, to assume a source in this area. Particles were tracked during two periods, from 19.06. to 19.07.2010 and from 06.06. to 06.07.2011 and again particle numbers were integrated over the entire water column due to the well mixed water body.

4.4 Results

Modelled temperature variations in 2010 and 2011

In general, summer 2010 was warmer than summer 2011 (more than 20° C occurred in July 2010, but were seldom reached in 2011). This is reflected by the sea surface temperature statistics (Table 4.2). The mean daily-mean sea surface temperature/maximum temperature in summer 2010 was about 3° C/4° C higher than in 2011. In 2010 a constant warm water condition occurred, whereas this was not the case in 2011 due to recurrent high wind speeds (more than 8 m s^{-1}) and flow currents which transported colder Baltic Sea water into the bay and hindered a constant warming. However, the critical temperature for increased *Vibrio* reproduction occurred in June shortly before the initial *Vibrio* were detected in Lubmin. The daily-mean sea surface temperature alternated in July and August between 19 and 22° C. Besides the temperature differences between the two years, the areas where temperatures had the propensity to increase early *Vibrio* reproduction were similar (Figure 4.10). The model results suggest that in both years the first critical warming (> 20° C) took place in June in the southern Strelasund, the southern coasts of the bay and in the northern Peenestrom. In these areas water depths do not exceed 2 m up to 1 km off the coast which means they heat up very fast. The *Vibrio* detections coincide with the warm periods in both years and an increased *Vibrio* reproduction might therefore be favoured especially in these domains. The model results suggest further that

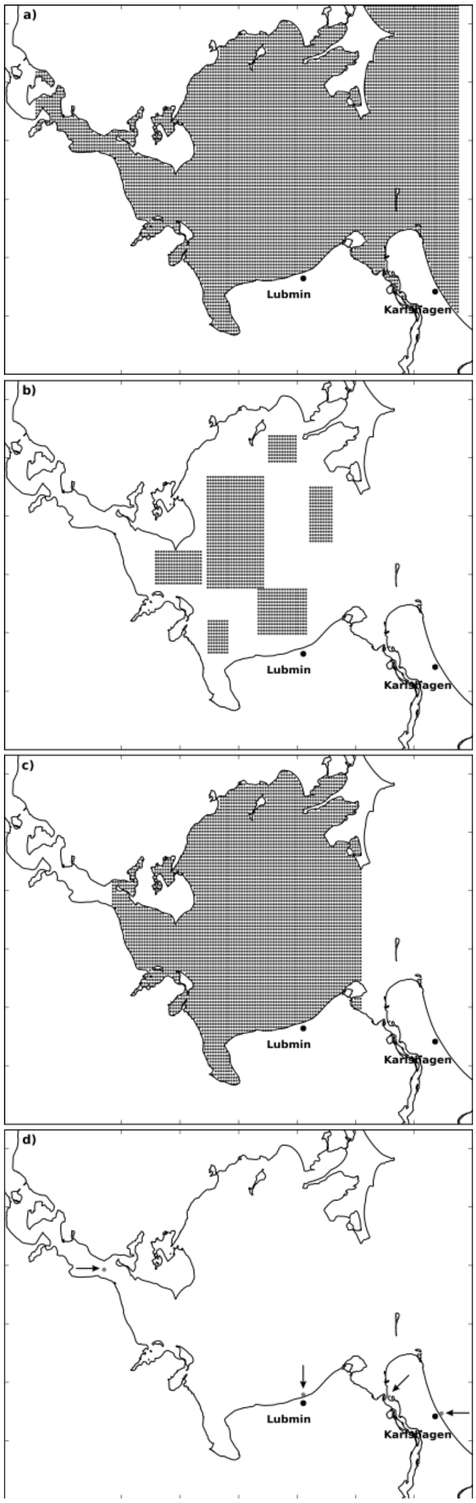

Figure 4.9: Particle release points for scenario 1 (a), 2 (b), 3(c) and 4 (d).

the warmed water was mainly transported along the shallow south coast within the bay. Water transport into the Pomeranian Bight happened rarely via the outlet north of Ruden and less southward along the coast of Usedom. The simulation results showed furthermore

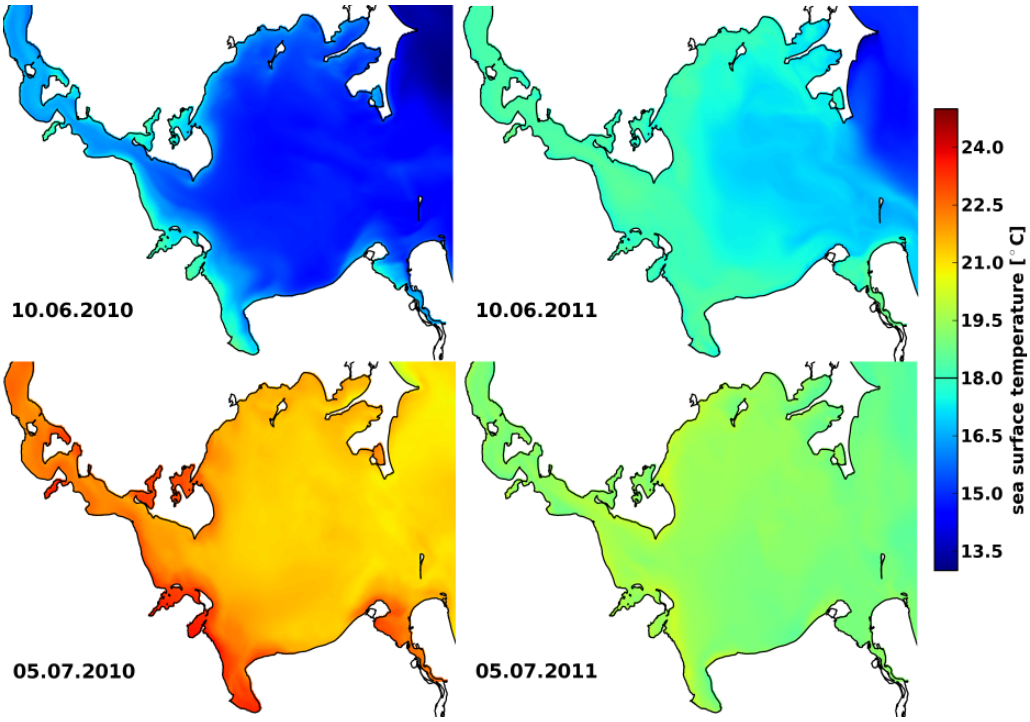

Figure 4.10: Modelled sea surface temperature in June and July of 2010 (left) and 2011 (right).

	2010	2011
Mean	20.17	17.51
Std	2.96	1.53
Min	10.67	11.87
Max	25.55	21.90
90-perc	21.42	19.33
95-perc	22.29	19.88

Table 4.2: Statistical evaluation of the daily-mean sea surface temperature in ° C from June to September in 2010 and 2011. Std: Standard deviation, Min: Minimum, Max: Maximum, 90-perc: 90 percentile, 95-perc: 95-percentile.

a frequently occurring cold water front off the coast of Usedom due to up-welling events at easterlies (Siegel et al. (1999)).

Modelled particle tracking simulations

Despite high water temperatures across the shallow coasts of the bay even in early summer the entire GWB has been identified as having a high *Vibrio* occurrence risk, with higher

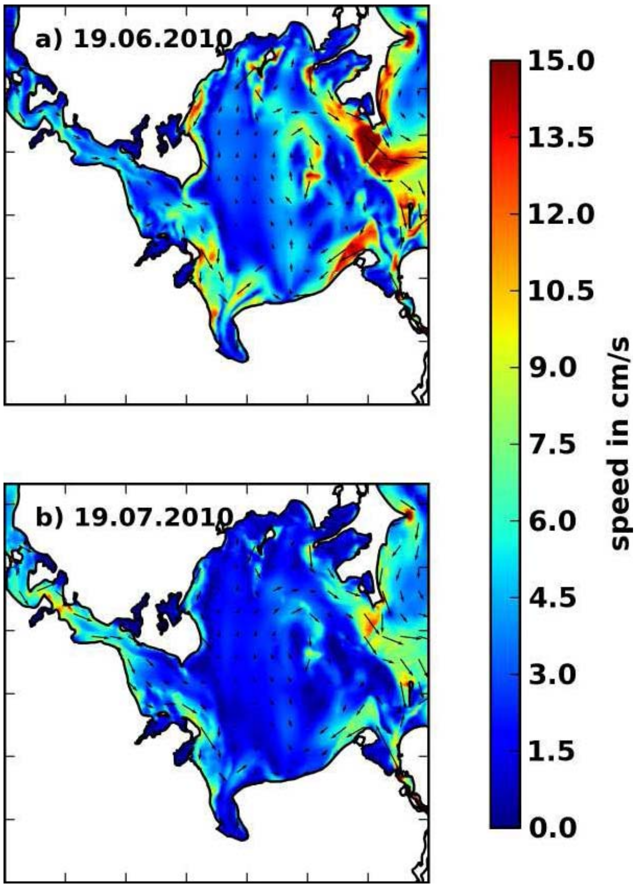

Figure 4.11: Exemplary daily-mean flow field patterns in the surface for different dates. (a) Currents on 2010/06/19 and (b) on 2010/07/19 12 forced with a variable, realistic wind.

concentrations in the western part decreasing to the east (Figure 4.12(a,b)). However, higher concentrations occurred in the western part, while the concentrations decrease to the east. The temperatures in 2010 favoured an increased *Vibrio* presence compared to 2011 (Figure 4.12(a,b). The second hypothesis to test was the transport of *Vibrio* bacteria resuspended from sediment (Figure 4.12(c,d)). Although the emission areas were mainly located in the central basin, particles were nearly equally distributed at the end of simulation. This was caused by the anti-clockwise circulation which developed in the central bay during the simulation periods (Figure 4.11). The particle distributions did not differ much between the years, but again in 2010 higher concentrations occurred in the western bay, as in scenario one, due to the higher water temperature. As in the first scenario, a general concentration decrease was visible from west to east, whereas no particles reach the Pomeranian Bight (or the coast of Usedom) after the simulation periods. Furthermore, particles entered the Peenestrom only in 2011. Assuming that *Vibrio* were carried by/ in herring into the GWB, the third scenario comprises the period of WBSSH spawning from May to June 2010 and 2011, when the water temperature exceeded 10° C which allowed *Vibrio* growth. The particle concentration within the bay was similar to scenario one, although the water temperatures were lower. However, only a few particles enter the Pomeranian Bight. Due to the lower water temperature these cannot reproduce properly and consequently lower concentrations occur there. Again higher concentrations could be found in the western part of the bay whereas the concentrations decreased to the east. No particles entered Usedom's coasts or farther south into the Peenestrom during either year, but high concentrations were transported towards the east coast of Rügen.

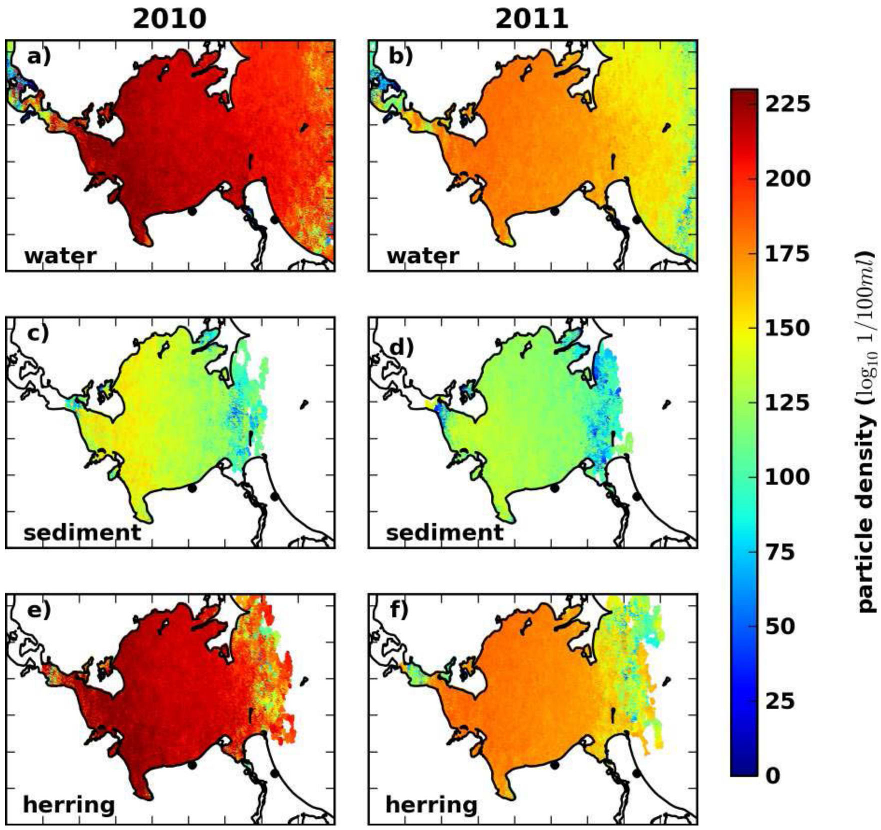

Figure 4.12: Transport and reproduction of particles with *V. vulnificus*-temperature-dependent division rate released in the water column (a,b) and above the sediment (c,d)in summer 2010 (left) and 2011 (right). (c,d) shows the transport and reproduction assuming the WBSSH to be the source of emission in May 2010 and 2011.

In order to figure out whether the recurrence of *Vibrio* in the GWB is caused by a long distance transport from external/internal sources simulations were conducted using different emission sources within and outside the bay during 2010 and 2011 (Figure 4.13). Based on the assumption that the Peenestrom with its low salinity and high water temperatures is the source and thus releasing the particles off Peenemuende (Figure 4.13(a,b)) a possible transport both into the bay towards Lubmin and Thiessow, but also along the coast of Usedom towards Karlshagen could be suggested. During the simulation period in 2010 the reproduction was faster, due to increased water temperatures, and hence higher concentrations were possible in the outlet of bay than during 2011. Directly at the coasts, however, the concentrations were reduced and no particles occurred in the west where measurements indicated *Vibrio* presence. Contrarily, no risk could be derived for the beaches of the GWB from the scenario results in which particles were released in the Strelasund (Figure 4.13(c,d)). The main numbers of particles stayed in the Strelasund and were transported east-and-westward in the back and forth flow (c.f. section 4.2). Therefore, it can be excluded that *Vibrio* germs were transported via the Strelasund into the GWB. Hypothesising that *Vibrio spp.* might be transported from the coast of Usedom into the GWB can also be excluded because particles emitted off Karlshagen (Figure 4.13(e,f)) were mainly driven with the flow into the Pomeranian Bight and rarely into the Bay. The high water temperatures at the shallow coasts favour the fast reproduction of the *Vibrio* germs which led to increased concentrations in these areas especially in 2010. Since *Vibrio* were recurrently detected in the coastal waters off Lubmin this area might present a potential source. The results of this scenario (Figure 4.13(g,h)) indicated that this assumption could be realistic. The released particles were transported from Lubmin through the entire lagoon and reached the northern coasts as well as the Peenestrom during both simulation periods, while no particle entered the Strelasund. The highest concentrations occurred close to the coast, due to the increased water temperature and in the central bay, where the currents are low. However, this potential source can be excluded as well since no concentration gradients were visible from West to East as it was measured.

Similar to other scenarios, the particle concentrations were higher in 2010 than in 2011 due to the generally higher water temperatures.

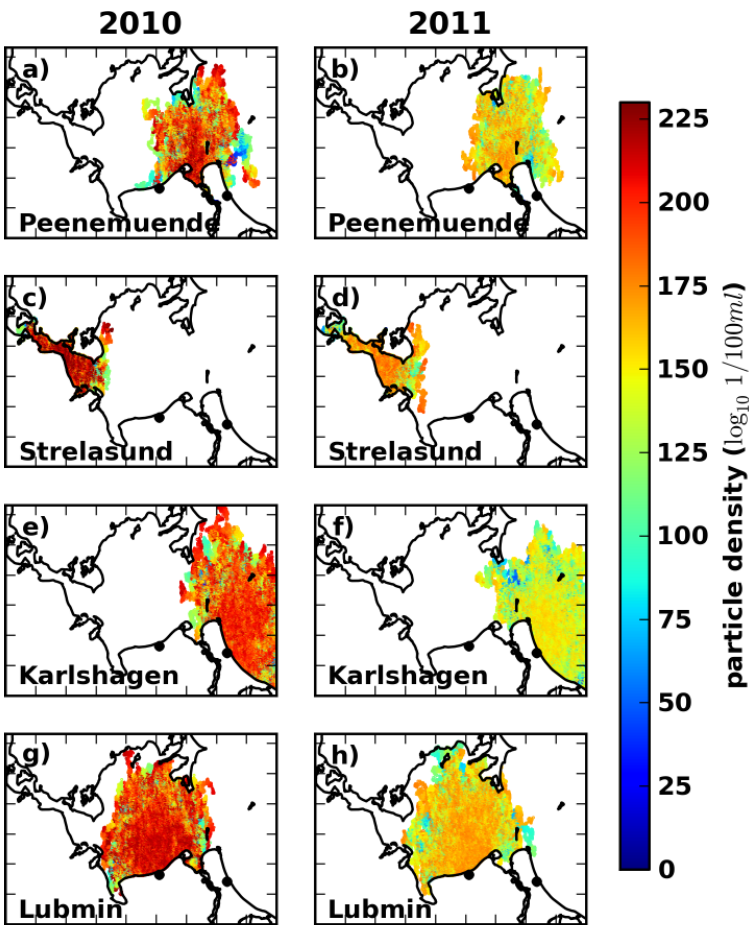

Figure 4.13: Transport and reproduction of particles with *V. vulnificus*-temperature-dependent division rate released at Peenemünde (a,b), Strelasund (c,d), Karlshagen (e,f) and Lubmin (g,h) in summer 2010 (left) and 2011 (right).

4.5 Discussion and conclusion

The potential human pathogenic *Vibrio*, an important bacteria within the GWB, has caused seven infections over the last years. That is why the LAGUS have been carried out a biweekly sampling campaign since 2004 where *Vibrio* were recurrently measured. High infection numbers were recorded in 2010 and 2011. Four infections (2 lethal) were counted in 2010 and one in 2011. Based upon results from several studies revealing correlations between human pathogenic *Vibrio* and temperature as well as between *Vibrio* and sediment (cf. Vezzulli et al. (2009); Böer et al. (2013)), a monitoring program was established within the research project KLIWAS in order to study these correlations in the GWB. Based on these measurements and literature reviews model scenarios were developed and simulated in this study using a three dimensional model system, consisting of a 3-D circulation model and a 3-D Lagrangian particle tracking model.

The results of the monitoring showed that *Vibrio* occurrence was strongly correlated to increased temperature (20° C) (cf. Oliver (2005); Baker-Austin et al. (2013)) which

commences in late June in the GWB. Assuming that water temperature is the most important factor driving *Vibrio* growth, the monitoring program of the LAGUS starts in July. In 2010 *Vibrio* were detected twice as often in Lubmin when a constant warming period developed until the end of August (water temperature up to 23° C). Contrarily, no such warming occurred in 2011 and hence less *Vibrio* were probably detected. This effect was also visible in the particle tracking results. In general, due to higher water temperatures in 2010 compared to 2011, higher concentrations were obtained in simulations of summer 2010. However, a more pronounced growth of the organisms was suggested by the model in the west bay whereas a concentration decrease was visible eastward until the Pomeranian Bight in both years due to lower water temperature in the bight. The simulation results are in accordance with the KLIWAS measurements which indicated higher concentrations at the west stations (data not shown). The analysis of the modelled sea surface temperature indicated that high water temperatures of more than 20 °C occurred at the shallow coasts especially in the south-west areas of the bay where the water depth does not exceed 2 m during early summers of 2010 and 2011. They heat up fast, early and continuously and hence present hotspot regions where an increased *Vibrio* growth can be assumed. Therefore, these areas could act as "regions of origin" from which the organisms might disperse into the bay starting in early summer. The alternating detection numbers of *Vibrio* in Karlshagen occurred due to upwelling events and therewith changing water masses off Usedom. These events happen frequently at the coasts of Usedom and Wolin under easterlies through the year (cf. Siegel et al. (1999)).
The results of the sediment samples suggested a high TOC content ($\geqslant 2.5\%$) in conjunction with *Vibrio* detection. This is in accordance with the results of Williams and LaRock (1985) and Vanoy et al. (1992) who found the colonising of bacteria in a thin floc zone just above the sediment. However, despite more positive samples being counted in the sediment, higher concentrations of *Vibrio* were found in the water column (data not shown). A possible reason could be an accelerated reproduction in the water column after the resuspension favoured by the warm water temperature. Moreover, the high TOC content in the GWB sediment might enhance *Vibrio* survival in winter (cf. Randa et al. (2004)) and could lead to increased initial bacterial concentrations in summer due to sediment resuspension during storm events. This hypothesis is supported by the particle simulation results of scenario 2, in which a particle density increase was visible in the entire bay after emitting the particles in the bottom layers with high TOC content. As in scenario 1 the highest concentrations were found in the western bay, which were not as pronounced as in scenario 1.
Several climate change studies did not show an increase of days with strong winds in the Baltic region (Nikulin et al. (2011); Lehmann et al. (2011)) and hence, an increased risk for *Vibrio* resuspension cannot be derived for the GWB in the future. Generally, climate change is believed to increase the sea surface temperature in the Baltic Sea (cf. Theede et al. (2008); Baker-Austin et al. (2013)) and therefore probably favours increased *Vibrio* reproduction also off-season in the GWB.

A further hypothesis of recent studies was that there is a correlation between *Vibrio* and sea-fish abundance (Brennholt et al. (2010); Alter et al. (2011)). As the GWB is one of the main fishing grounds of the WBSSH, large shoals of herring, originating e.g. from the Atlantic can be found there every year (ICES (2011)). The bacteria can be deposited here in higher concentrations into the water column by the large fish stocks where they can further reproduce. However, up to now no studies have been undertaken in the GWB which analyse WBSSH with respect to *Vibrio* bacteria. Nevertheless, Janssen (1996) found in his experiments that 25.5% of different seafood samples (e.g. fermented products from herrings) were tested positive for pathogenic *Vibrio* germs. Although the large shoals of herring could not be neglected as a potential source of *Vibrio* in the GWB, the scenario assumption could not be verified with the measurements which showed only small *Vibrio* concentrations in April 2010 and 2011. Thus, further analyses of the WBSSH are necessary to quantify their shares in the overall bacterial occurrence.

The scenario results from the simulations assuming long-distance transports from the Strelasund and Peenemuende suggested the exclusion of these source areas as an intake path for potential human pathogenic *Vibrio* into the GWB. No explanation was found for the high concentrations in the western bay, where measurements indicate *Vibrio* presence. Moreover, a *Vibrio* transport from Lubmin to Karlshagen and vice versa can be excluded from the simulation results. Particles entering the transition zone between the GWB and the Pomeranian Bight were driven back and forth with the flow but did only rarely drifted towards either Lubmin or the coast of Usedom. Therefore, we can exclude external sources in general and conclude that *Vibrio* are probably present in the water column of the GWB all year. According to other studies (Oliver (2005)), the bacteria are likely in a "viable-but-not-culturable"-state if they cannot be detected during the monitoring. We conclude further: there is only a small correlation between the *Vibrio* occurrence and the seasonal cycle of the water temperature, and the inter-annual difference of the *Vibrio* presence in the GWB. A certain temperature threshold of more than 20° C enables an increased growth of potential human pathogenic *Vibrio* (usually in mid to late June) (Oberbeckmann et al. (2012)), but organisms were detectable below this temperature afterwards (until October and later) (Böer et al. (2013)). Hence, in years with a strong varying water temperature (2011) *Vibrio* bacteria can be detected in similar concentrations as in years with a constant water warming period (2010).

The coupling of the particle growth with the water temperature was done via an equation which respects the temperature-dependent devision rate computed from the results of a *Vibrio* growth experiment (Robert Potau Núñez (2011)). The experiment was accomplished with North Sea isolates and hence might not represent the reproduction in the GWB correctly due to the lower salinity. Therefore, we recommend to verify our division function by a growth experiment with GWB isolates to develop a more appropriate temperature-dependent growth function. However, to our knowledge the described experiment has been the best attempt so far to implement this dependence into a model.

In general, potential human pathogenic *Vibrio* were suggested to be present particularly in the west of the GWB and not only there where the LAGUS monitoring takes place each year. Consequently, we recommend to expand the monitoring to the beaches in the west to verify our model results. Assuming the model results are correct, it would be necessary to continue elucidating the responsible on-the-spot physicians in the future about the *Vibrio* presence and its risks. Additionally, a short interview of patience (including for example questions like: *Are there any open wounds?/Did you went for bathing during the last days?/If so, where and when?*) could be helpful to narrow down the search for possible *Vibrio* infections. This would facilitate an appropriate medical care which is essential to safe human lives (Alter et al. (2011); Oliver (2013)). Informing patients at health resorts located along the coasts of the GWB as well as tourists visiting the affected beaches in the west about predisposing factors for infections with *Vibrio* could furthermore prevent infections.

Despite it being known that the GWB is a *Vibrio* hotspot and that recent studies in Europe have shown a correlation between the organisms and environmental parameters, no previous attempt has been made to fully understand the situation in the bay. This work contributes tremendously to the understanding of the dynamics of *Vibrio* communities harbouring potentially pathogenic species in the GWB. We can conclude that several factors favour the recurrent presence of *Vibrio* in the GWB all of which require more attention. In addition, recent studies showed a correlation between algae abundances and *Vibrio* occurrence (Stauder et al. (2010); Rehnstam-Holm and Godhe (2012)) and hence further analyses should be accomplished regarding this relation since cyanobacteria blooms occur regularly in the GWB . The KLIWAS monitoring measurements present a promising data base for this purpose.

Chapter 5

The bathing water quality information system

In the EU-project "GENeric European Sustainable Information Space for Environment (GENESIS)" 29 European partners worked together to develop a web-based solution for monitoring air quality, fresh and coastal water quality, and the impact on health. GENESIS helped to developed an environmental management and health services in Europe and shall support public information according to Article 12 of the bathing water quality directive (2006/7/EC). The information system used public open standards (W3C, CEN, ISO, OGC, OASIS, ...) which are in strong synergy to the major European initiatives (cf. GEOSS and INSPIRE). The project mainly addressed the health related impact of environmental issues conforming to the existing regulations and European Directives related to air and water quality. By providing generic services, portal components, information models, an application toolkit and related documentations, the system enabled users to develop their own regional and thematic information system all over Europe.
Within GENESIS the 3-D model system, described and applied in this study, was implemented for the Oder estuary as a new online bathing water quality information system to support regional authorities. It combines a model and simulation tool with an alerting and improved communication system. The work was carried out in co-operation with the Institute of Meteorology and Water Management Poland which provided the necessary background information.

5.1 The implementation

The project GENESIS provided web portal software and a set of distributed secured web services, including interfaces and adaptable web service clients that can be employed at the web portal. Typical services include data access services, catalogues services, viewing services, geo-information processing services, alert services as well as a workflow management component. To implement GETM and GITM in the GENESIS Internet portal, the toolbox, the viewing and geo-information services (Geoserver) had to be installed on the local IOW server. It allowed to run the model system online, link them to the GENESIS system and to visualise the results. Since space and calculation speed limitations do not allow in-situ flow simulations, pre-simulated steady state flow fields were stored and provided for online-users on the IOW server. The connection of the model to the GENESIS system worked via a workflow WPS service in the toolbox. It was defined as a bash shell script which called the necessary input files from the IOW server and ran GITM (a Fortran executable), ran a Python script to post-process the model results and converted this output via a Perl script into a gml output for visualising the particle movement. Both, input and output were defined by the service provider in the DescribeProcess.xml. It is imported into the toolbox when creating the WPS service. If end-users called the service on the portal, it was executed at the local toolbox. The graphical visualisation was done using the GeoServer on the local server by adding new layers from GIS shape files.

5.2 The application

The online simulation tool of the GENESIS service is only a simplified version of the 3-D model system which allows the fast and flexible computation of emission scenarios within the Oder estuary after e.g. high microorganism concentration at the beaches (Figure 5.1). The system used pre-simulated steady state flow fields computed according to the 8 cardinal wind directions. According to the prevailing wind condition one of these needs to be chosen for the successful service application as a first step. In the second step the user chooses the number, type and properties of particles (e.g. *E.coli* were defined by a specific die-off rate) and the simulation period. In the third step the emission locations were chosen by clicking at the positions in the GIS maps.

The service results could be displayed as a movie with a time line to start and stop at different steps. Further tools to control and display the results could be found in the toolbar of the platform.

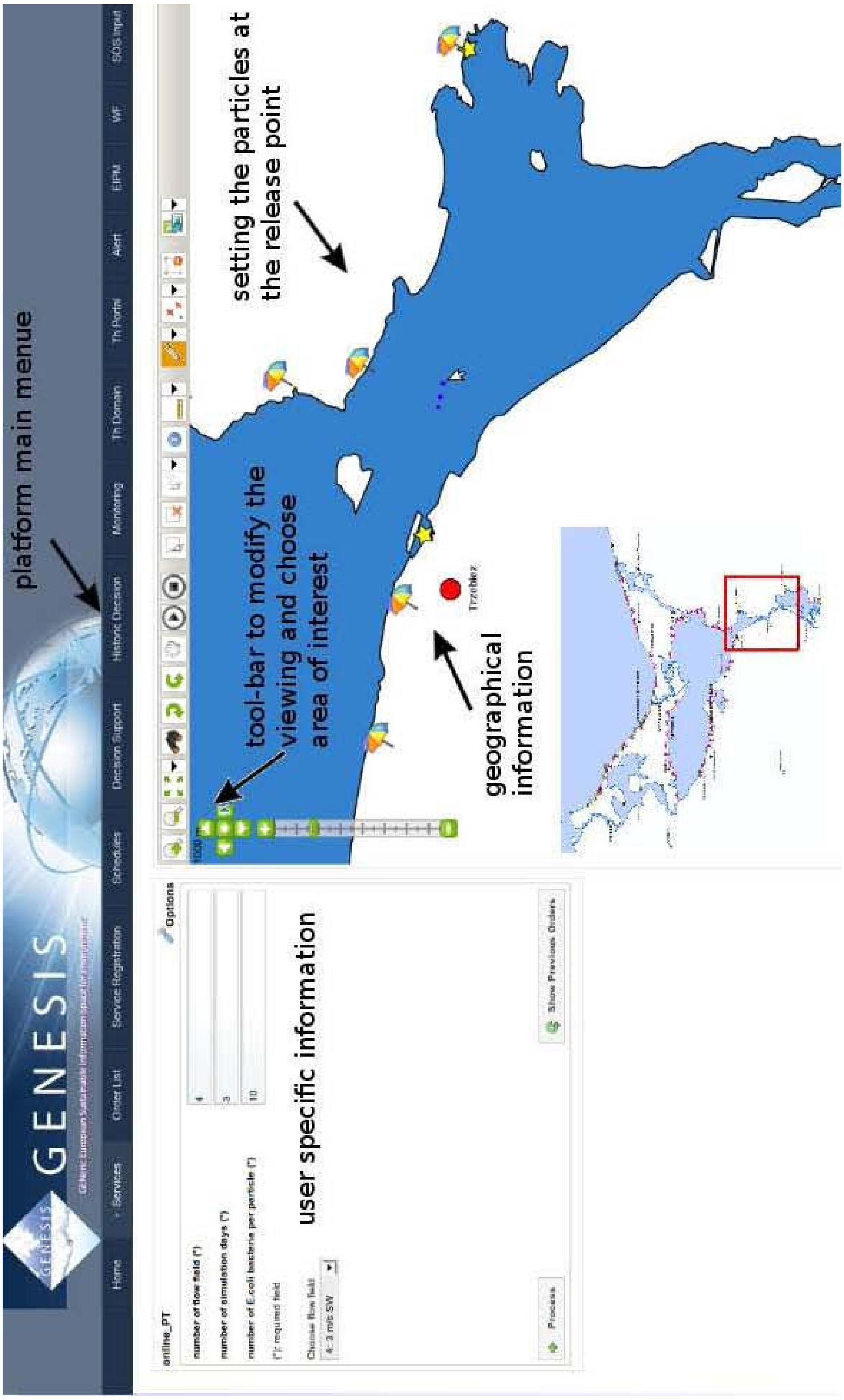

Figure 5.1: GENESIS bathing water quality information service of the Oder estuary.

Chapter 6

Summary and conclusion

This dissertation focused on the application of a three-dimensional model system to improve the understanding of bacterial transport in coastal waters and to identify the environmental key control parameters and their effect on the transport pattern. Additionally the system was shown to act as an addition to bathing water quality measurements enhancing the coastal management in the region of the southern Baltic Sea. The system was used to generate spatio-temporal pictures of *E. coli* bacteria, *Salmonella* and potential human pathogenic *Vibrio spp.* distributions (hygienic water pollution events) in recreational waters of the southern Baltic Sea. In order to obtain spatially, highly resolved model results in the shallow coastal areas, two model setups were generated in this project and constituted the main innovation of this study. The first one is a large setup comprising the area from the city of Szczecin to the Pomeranian Bight. The numerical grid was placed parallel to the coastline of the Oder river (curvilinear grid) to obtain a high horizontal resolution particularly in the region of the Oder river mouth (50 m). With this toll it was possible to zoom in on single beaches. This model setup was used to run the simulation for the first two chapters of this dissertation. The second model setup comprises the area of the Bay of Greifswald and has an equidistant horizontal resolution of 100 m.

The first chapter of this thesis dealt with the problematic of insufficient water quality and consequent bathing prohibitions in the Oder river estuary due to inadequate sewage treatment in the catchment area. It was evaluated during this chapter that *E. coli* mortality rate and emission intensity were key parameters for concentration levels downstream, while the wind and river discharge play a modifying role. The prevailing south-west wind conditions cause *E. coli* transport along the eastern coast and favour high concentration levels at the beaches. The simulations further indicated that beach closings in 2006 would not have been necessary according to the new EU-Bathing Water Quality Directive (2006/7/EC). The implementation of the new directive will, very likely, reduce the number of beach closings, but not the risk for summer tourists. The model results suggest, that a full sewage treatment in Szczecin would allow the establishment of new beaches closer to the city.

The second chapter, prepared during this doctoral research study, focused on the distribution of *Salmonella* bacteria in the well mixed coastal zone of the Pomeranian Bight and additionally on the development of supra-regional recommendations towards improved monitoring and management. The analyses were conducted at an exemplary case study analyse in the Pomeranian Bight where a *Salmonella* pollution event led to bathing prohibition for several weeks in summer 2008. The main innovation of this study was the application of the particle backtracking technique which allowed the location of possible sources. Together with forward scenario simulations a continuous pollution source in town was identified as the most likely origin of bacterial occurrence. Varied wind scenario results provide concrete *Salmonella* transport ranges and therefore the potential to improve the managerial response during a future *Salmonella* pollution event in that region. This cannot be excluded since the real source for the contamination has not yet been identified. Supra-regional recommendations were summarised in a generic workflow. It presents first action recommendations, aimed at safeguarding the health of bathers, in the event of a contamination event without implementing a model study.

In the third chapter, the recurrence of potential human pathogenic *Vibrio spp.* in the Bay of Greifswald was analysed with the help of the model system. Coupling the particle growth with the water temperature presented a further innovation within this study. It allowed to define areas within the Bay with a high potential of increased occurrence of potential human pathogenic *Vibrio spp.*. Particularly, the shallow western parts of the Bay of Greifswald present hotshot regions where an increased *Vibrio* growth can be assumed. Moreover, a *Vibrio* transport from the inner bay into the Pomeranian Bight and vice versa can be excluded from the simulation results. In general, there is only a small correlation between the *Vibrio* occurrence and the seasonal cycle of the water temperature, and the inter-annual difference of the *Vibrio* presence in the Bay of Greifswald. A certain temperature threshold of more than 20° C enables an increased growth of potential human pathogenic *Vibrio*, but organisms were detectable below this temperature afterwards (until October and later). These might stay in the nutrient rich sediments (high content of total organic carbon) which might enhance *Vibrio* survival. Hence, in years with a strong varying water temperature *Vibrio* bacteria can be detected in similar concentrations as in years with a constant warming period.

The last chapter of this dissertation demonstrated the way a simplified version of the applied model system was implemented into a web-platform of the EU-project "GENeric European Sustainable Information Space for Environment (GENESIS)" as a new online bathing water quality information system used to support regional authorities. It combines a model and simulation tool with an alerting and improved communication system.

To summarise, the overall impact of hygienic water pollution shows the necessity

of new management instruments. The results of my dissertation gave evidence that pollution events and the occurrence of microorganisms do not happen spot like, but affect a wide area along the coast. This makes it impossible to gain information about spatial transport patterns or possible bacterial sources from single point measurements. The application of a three-dimensional model system as an addition to the observations presents a good and promising tool to analyse the bacterial distribution and moreover to support coastal management. The simulation results showed that microorganisms are generally transported with the flow, which is forced by the wind itself making the wind the most important factor. It is the main driver of transport ranges if no higher, dominant flow is present as i.e. river run-off. Knowing the wind conditions during a pollution event and adapting the monitoring according to the water flow direction can, thus, reduce the effort and costs of the monitoring program. Using the model system as an addition to water quality measurements, management and risk assessment tools for future pollutions were derived for the different case studies presented in this thesis.
The results of my analyses, in particular those about different parameters influencing the bacterial transport and behaviour, improved the understanding of bacterial distribution in sea water. Furthermore, the results could be used to support authorities in expanding the monitoring programs in terms of sites and parameters. Generally, a microbial pollution of recreational waters can have a strong economic impact. For the Baltic coastal regions of Germany and Poland tourism has become the most crucial economic factor. The deterioration of bathing water quality and the subsequent closing of beaches can have serious economic consequences for seaside resorts and may include a loss of reputation. This is true, however, not only for the Baltic Sea coast, but also for other bathing destinations. For example, investigating in environmental improvements that increase the swimming period in the Great Lakes region by 20% would generate 2–3 billion dollars in direct economic effects (Kinzelman and McLellan (2009)).

This dissertation has proven the ability of numerical models to successfully reproduce bacterial transport patterns in sea water. They allow the detailed analyses of the bacteria distribution and can help to identify the environmental key control parameters and their effects on the transport patterns. This might be of further importance for different questions in microbiology, for example by answering the question where thermophilic bacteria in the Arctic have their origin since scientists assume these bacteria to originate from warm ocean areas (Max-Planck-Institute for Marine Microbiology (2009)). Another possible application of the model system would be to find areas in the oceans where marine litter accumulates. This topic gained heavy interest in several projects as e.g. MARLISCO Project Office (last visit 2013/07/29) or United Nationes Environment Programmes (last visit 2013/07/29) since marine debris becomes a major threat for the marine and coastal environment.
The application of particle tracking models in combination with ecology and microbiology can generally improve the research in the field of marine biogeography, which is the

investigation of patterns in the geographical distribution of organisms (Golikov et al. (1990)). The bacterial distribution does not only depend on the organisms ability to spread, but also on prevailing hydrographic conditions. These can nowadays be easily modelled, even for large areas, with the help of circulation models due to the still growing computational power (as presented in this thesis). The successive application of a particle tracking model can gain further insights in the distribution of marine organisms, as i.e. bacteria, if their properties and behaviour in changing environments are considered (by e.g. mortality or replication rates). This approach cannot replace the measurements and monitorings since these deliver necessary input variables. However, the model system application provides a time and cost effective addition and can shed new light on one of microbiology's great hypotheses: *"Everything is everywhere, but the environment selects"* (Baas Becking, 1934).

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Veröffentlichungen

Schippmann, B., Schernewski, G., Gerhard Hauk, Nicole Brennholt, Simone Böer and Schwarz, F., Recurrence of potential human pathogenic *Vibrio* in a western Baltic Sea bay: analysis with a 3-D ocean model system, in preparation

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Eidesstattliche Erklärung

Ich versichere hiermit an Eides statt, dass ich die vorliegende Arbeit selbstständig angefertigt und ohne fremde Hilfe verfasst habe. Dazu habe ich keine außer den von mir angegebenen Hilfsmitteln und Quellen verwendet und die den benutzten Werken inhaltlich und wörtlich entnommenen Stellen habe ich als solche kenntlich gemacht.

Rostock, 29.07.2013 Bianca Schippmann