

Modelling the seasonal occurrence and distribution of human-pathogenic bacteria within the German Bight, southern North Sea

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Abstract and motivation

In recent years, the occurrence of human-pathogenic bacteria of the genus *Vibrio* in the North Sea and the Baltic Sea has come into the focus of many marine research activities, as different *Vibrio* strains caused harmful infections, especially in summers 2003, 2006, 2010 and 2014 (Böer et al., 2013). Furthermore, it is anticipated that under global warming conditions, the risk of the occurrence of human-pathogenic bacteria in the summer season will very likely increase.

To present knowledge temperature and salinity are the most effective predictors of the occurrence of *Vibrio spp.* in coastal waters (Takemura et al, 2014). However, studies support the interaction of human-pathogenic *Vibrio spp.* with different host and vector organisms like chitinous zooplankton or with predator organisms such as *Vibrio*-specific bacteriophages.

The FVCOM modeling system (Chen et al., 2003) has been used to understand and predict the occurrence and distribution of harmful *Vibrio spp.* within the North Sea (Fig. 1) with a special focus on the German Bight including the shallower Wadden Sea areas and the estuaries of Ems, Weser and Elbe. Within this system, a biological module has been implemented, which considers specific *Vibrio* strains, and functional groups of phyto- and zooplankton and bacteriophages as potential host- and predator-organisms.

This modeling system has been applied to a hot summer season in 2006. It has been demonstrated that this system can reproduce the observed hydrodynamic conditions within the North Sea, and reasonable temporal and spatial patterns of *Vibrio* abundances have been obtained.

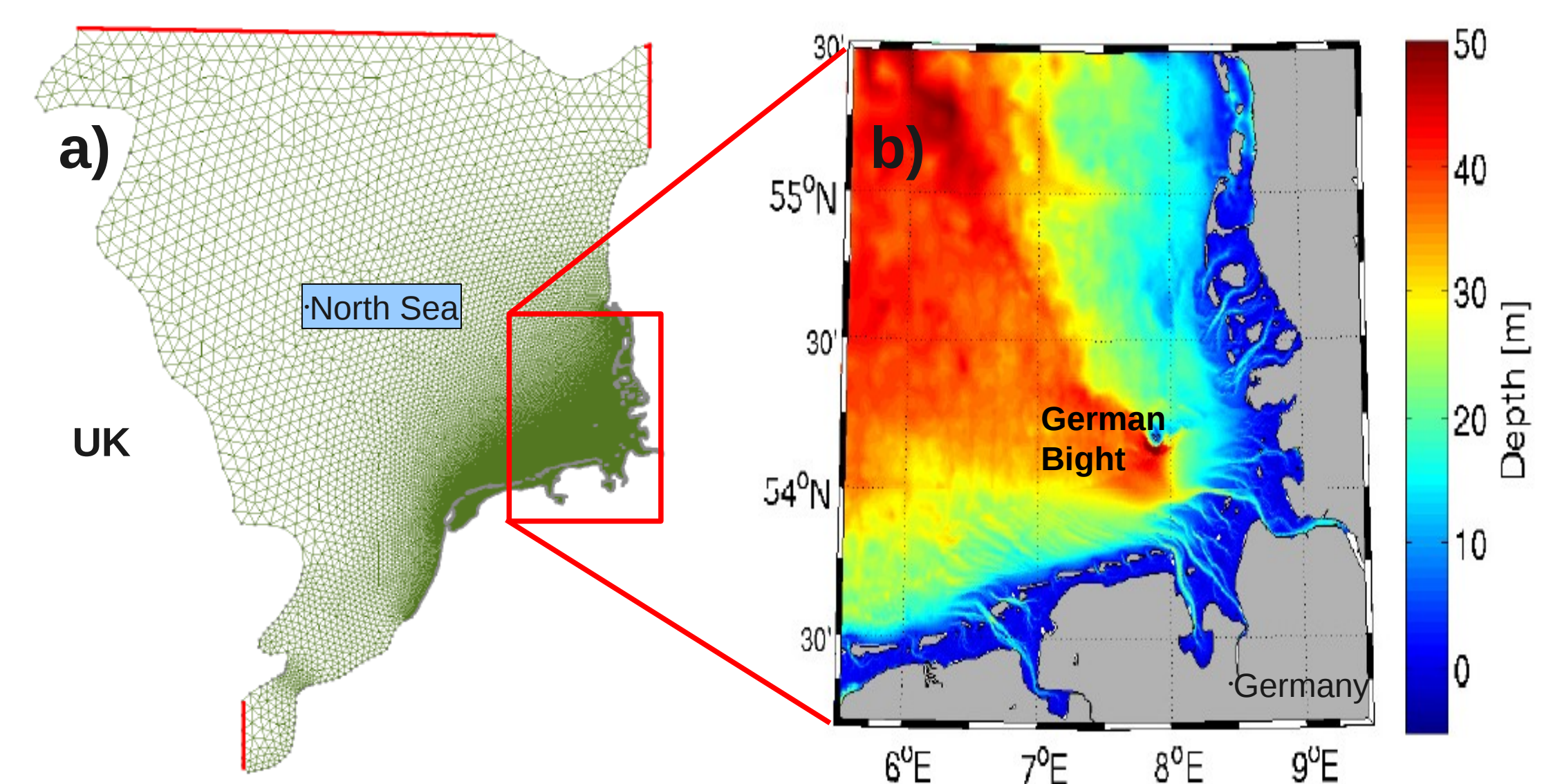
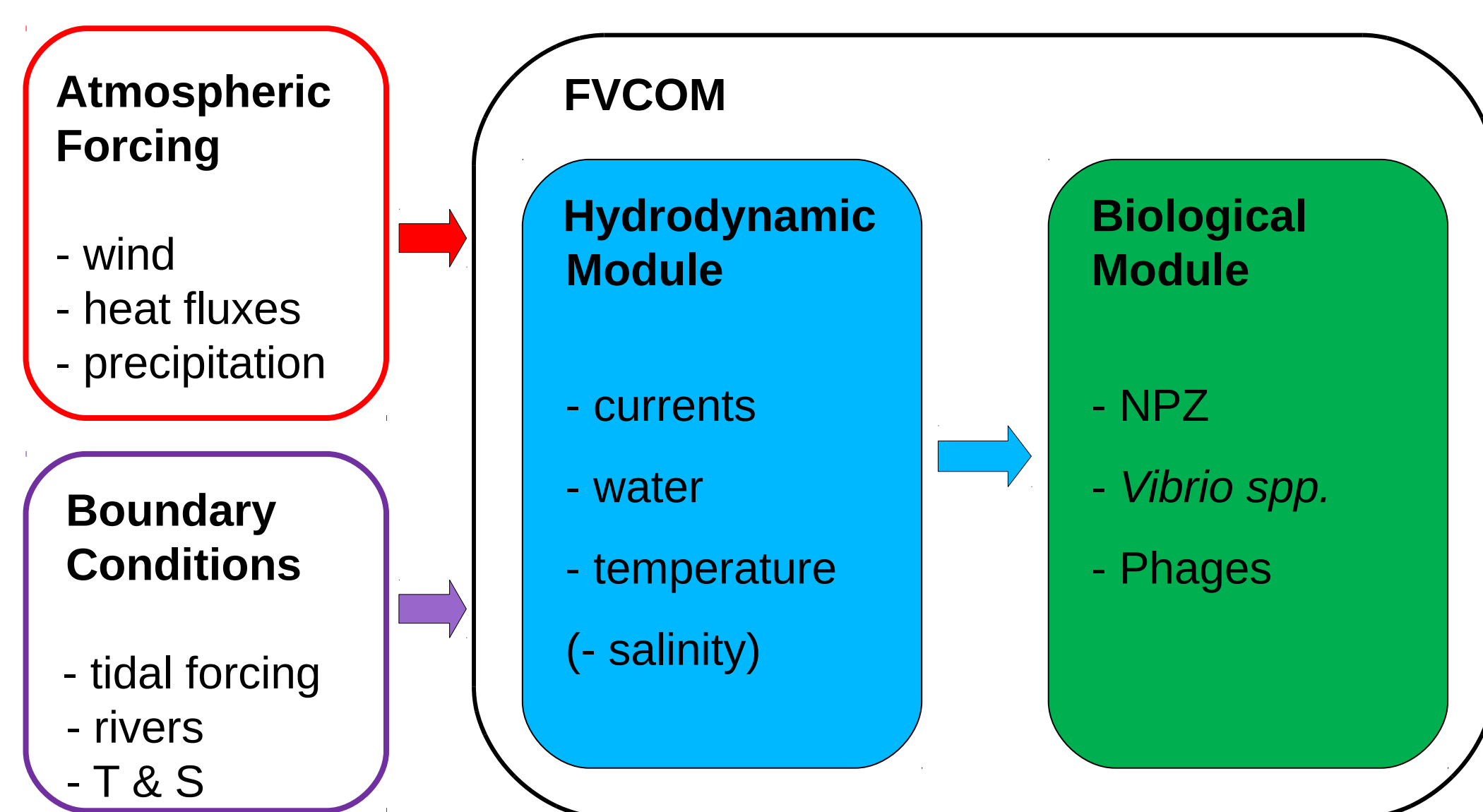


Figure 1: Location of the area of interest within the German Bight. On panel a), the unstructured model grid is depicted with a grid refinement within the German Bight. The thin red lines denote open model boundaries. Panel b) shows the model bathymetry within the German Bight.

The FVCOM Modeling System



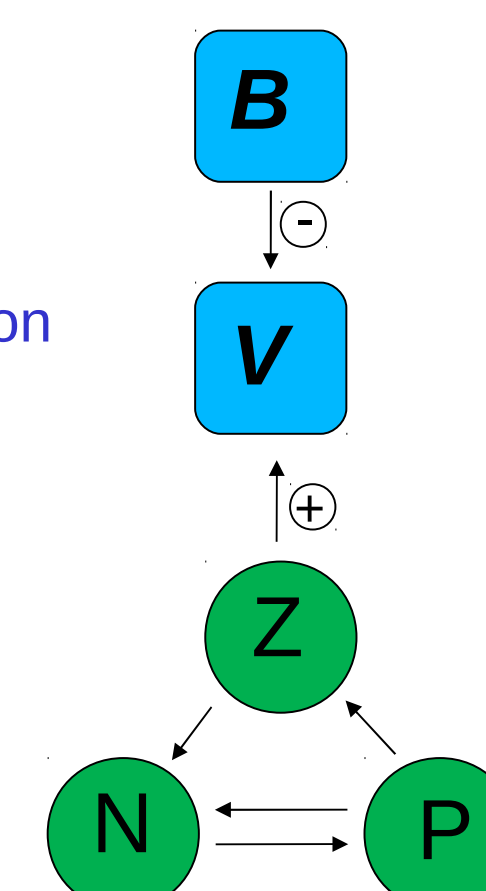
The Biological Module

Vibrio – Bacteriophages Submodule:

some *Vibrio species*
induced mortality by specific Bacteriophages
better growth of *Vibrio* in presence of Zooplankton

NPZ-Submodule:

Nutrients, Phytoplankton, Zooplankton
uses nitrogen units
parameters adapted to
North Sea region and taken from:
Cossins and Bowler (1987), Baretta-Bekker et al. (1997)
Collos and Berges (2002), Franks and Chen (1996)
Gutknecht et al. (2013)



$$\dot{V} = +r_{growth}(T) \left(1 - \frac{V}{K_V}\right) \cdot V + r_{growth}(T) \cdot f_Z \cdot Z \cdot V - r_{inf} \cdot B \cdot V$$

logistic free growth in water column growth due to zooplankton death due to phages

$$\dot{B} = +\beta \cdot r_{inf} \cdot B \cdot V - r_{lys} \cdot B$$

growth due to infection of vibrio death of phages

Jensen et al. (2006) model for *V. cholerae* and specific phages Núñez (2011) measured *Vibrio* growth rates "free" parameter: used for sensitivity studies

Model Validation and results

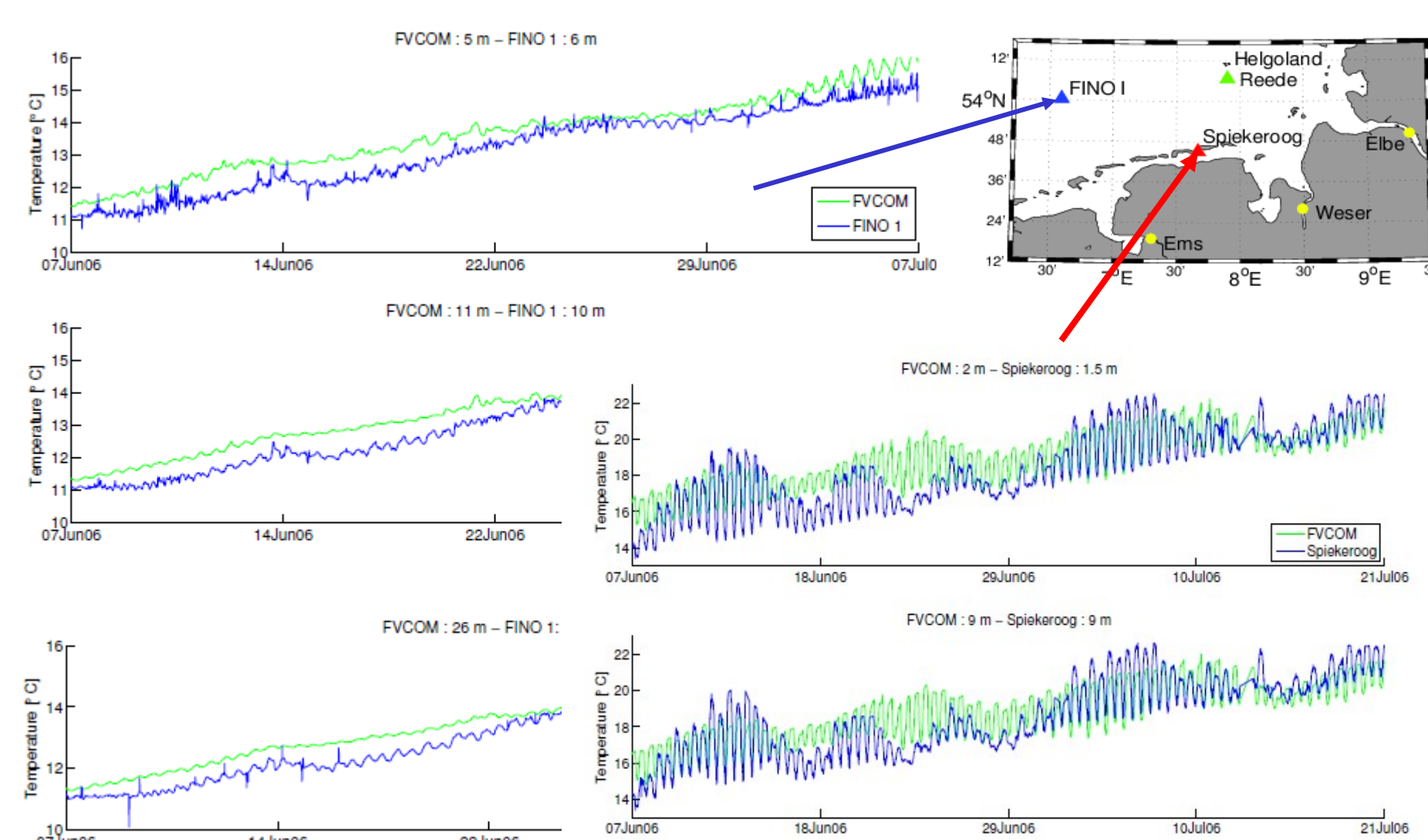


Figure 2: Validation of model temperature in June 2006 at two different time series stations and in different water depths (FVCOM: green line / data: blue line).

Time series of *Vibrio spp.* at Helgoland

Without much tuning, the correct order of *Vibrio* concentration is captured

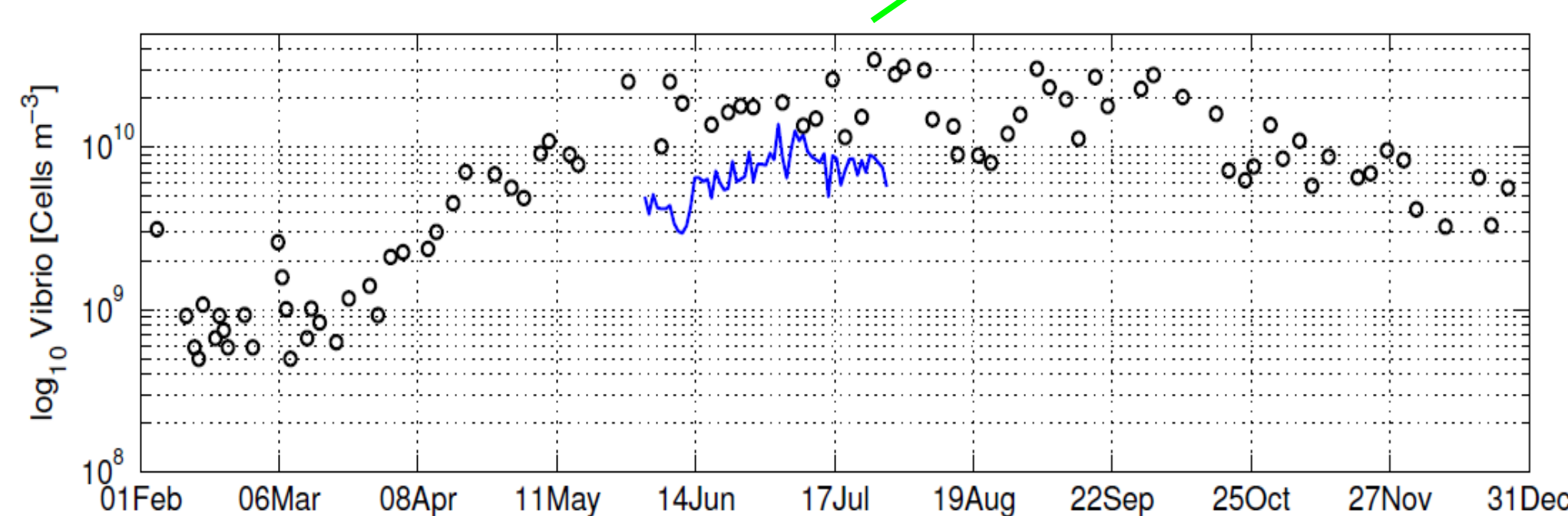


Figure 3: Comparison of total *Vibrio spp.* data from Oberbeckmann et al. (2012) (for year 2009) with *Vibrio spp.* model data (blue line).

Reports of *V. vulnificus* Map provided by Nicole Brennholt and Simone Böer, BfG, Germany

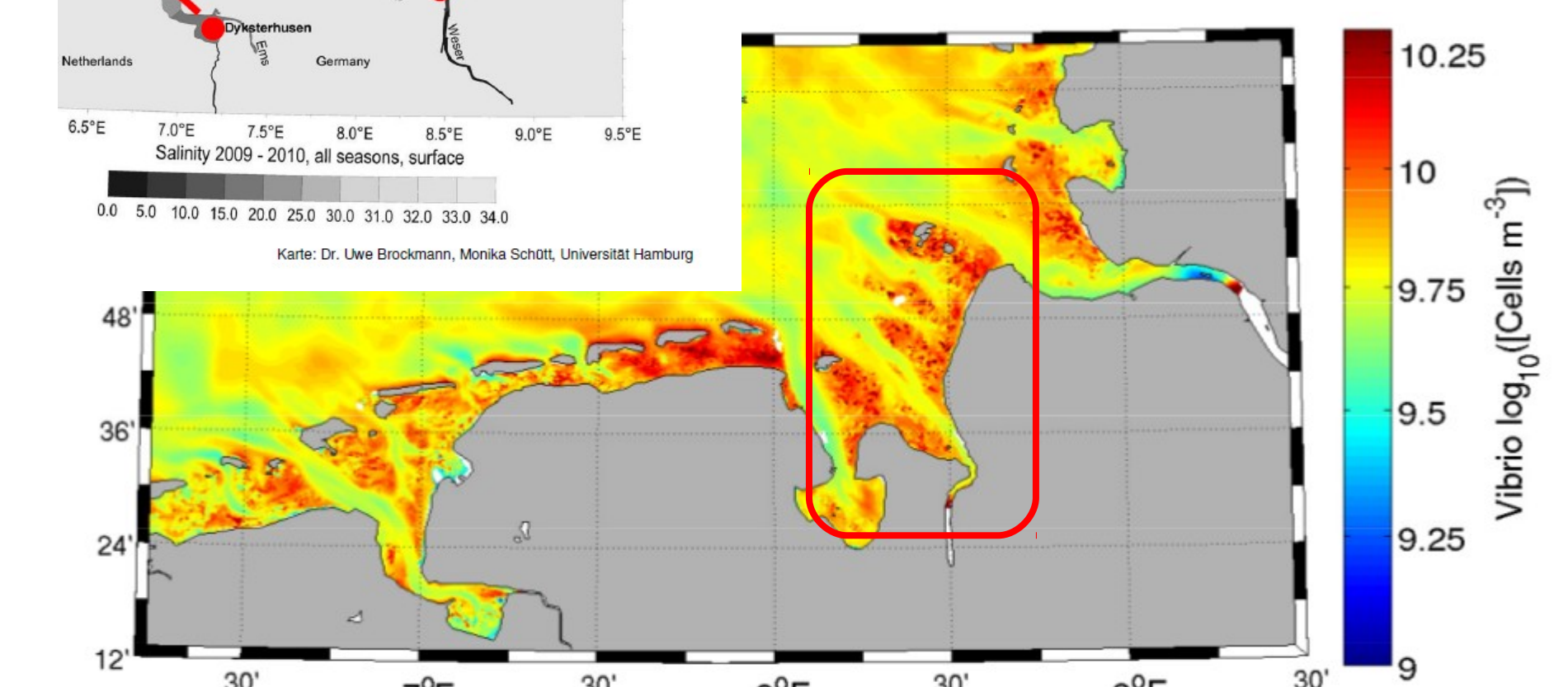


Figure 4: Model distribution of *Vibrio spp.* concentration in summer 2006 (larger panel) and reports of *V. vulnificus* detection within the German Bight (smaller panel, top left).

References

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