Geophysical Research Abstracts Vol. 18, EGU2016-18269, 2016 EGU General Assembly 2016 © Author(s) 2016. CC Attribution 3.0 License.



## Integrated network modelling for identifying microbial mechanisms of particulate organic carbon accumulation in coastal marine systems

Karlie McDonald (1), Valentina Turk (2), Patricija Mozetič (2), Tinkara Tinta (2), Francesca Malfatti (3), David Hannah (1), and Stefan Krause (1)

(1) School of Geography, Earth and Environmental Sciences, University of Birmingham, (2) Marine Biology Station Piran, National Institute of Biology, Piran, 6330, Slovenia, (3) OGS (Istituto Nazionale di Oceanografia e Geofisica Sperimentale - National Institute of Oceanography and Experimental Geophysics), Trieste, 34010, Italy

Accumulation of particulate organic carbon (POC) has the potential to change the structure and function of marine ecosystems. High abidance of POC can develop into aggregates, known as marine snow or mucus aggregates that can impair essential marine ecosystem functioning and services. Currently marine POC formation, accumulation and sedimentation processes are being explored as potential pathways to remove CO<sub>2</sub> from the atmosphere by CO<sub>2</sub> sequestration via fixation into biomass by phytoplankton. However, the current ability of scientists, environmental managers and regulators to analyse and predict high POC concentrations is restricted by the limited understanding of the dynamic nature of the microbial mechanisms regulating POC accumulation events in marine environments. We present a proof of concept study that applies a novel Bayesian Networks (BN) approach to integrate relevant biological and physical-chemical variables across spatial and temporal scales in order to identify the interactions of the main contributing microbial mechanisms regulating POC accumulation in the northern Adriatic Sea. Where previous models have characterised only the POC formed, the BN approach provides a probabilistic framework for predicting the occurrence of POC accumulation by linking biotic factors with prevailing environmental conditions.

In this paper the BN was used to test three scenarios (diatom, nanoflagellate, and dinoflagellate blooms). The scenarios predicted diatom blooms to produce high chlorophyll a at the water surface while nanoflagellate blooms were predicted to occur at lower depths (> 6m) in the water column and produce lower chlorophyll a concentrations. A sensitivity analysis identified the variables with the greatest influence on POC accumulation being the enzymes protease and alkaline phosphatase, which highlights the importance of microbial community interactions. The developed proof of concept BN model allows for the first time to quantify the impacts of biological, chemical and physical parameters influencing microbial community interactions mechanisms that regulate POC accumulation in marine environments. The dynamic modular nature of the developed BN will allow successive updating and improvement of the model structure as new data are emerging, thus, providing a powerful interactive framework for the investigation, prediction and mitigation of future POC accumulation events.