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Theoretical models to investigate microbial dynamics and interactions in the deep sea under present and future global changes

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Introduction

Over the last two decades, seawater warming has been documented for different marine regions (Levitus et al. 2005), increasing the concern about its potential consequences on a global scale. Climate change is progressively altering also deep-sea ecosystems, but the impacts of these changes are still largely unknown. In my PhD I investigate the effects of temperature increase and shift in C supply on the deep-sea ecosystem that is the largest and less known biome of the biosphere, in fact it covers about 65% of the Earth's surface and represents >90% of the global biosphere volume. In my analysis I focus on the microbial food-web interactions (e.g., viruses – prokaryotes) because they play a central role in global biogeochemical cycles (Danovaro, Dell'Anno, et al. 2016) and in the functioning of deep-sea ecosystem, with particular attention on viruses. Then, identifying the mechanistic explanation of the relationship between biodiversity and ecosystem functioning is crucial for a better understanding of the sustainability of deep-sea ecosystems in a period of increasing threats due to climate change and anthropogenic pressures.

Aims

- To identify patterns and drivers influencing viral and prokaryotic distribution in marine ecosystems.
- To develop models that describe viral and prokaryotic global distribution and simulate distribution changes under different environmental scenarios.
- To investigate the potential effects of temperature and C availability on prokaryotic metabolism.
- To investigate temporal changes of prokaryote-virus interactions in relation with changes of temperature and trophic availability.
- To develop theoretical/mechanistic models that describe microbial food-web dynamics and forecast their potential responses under future global change scenarios.
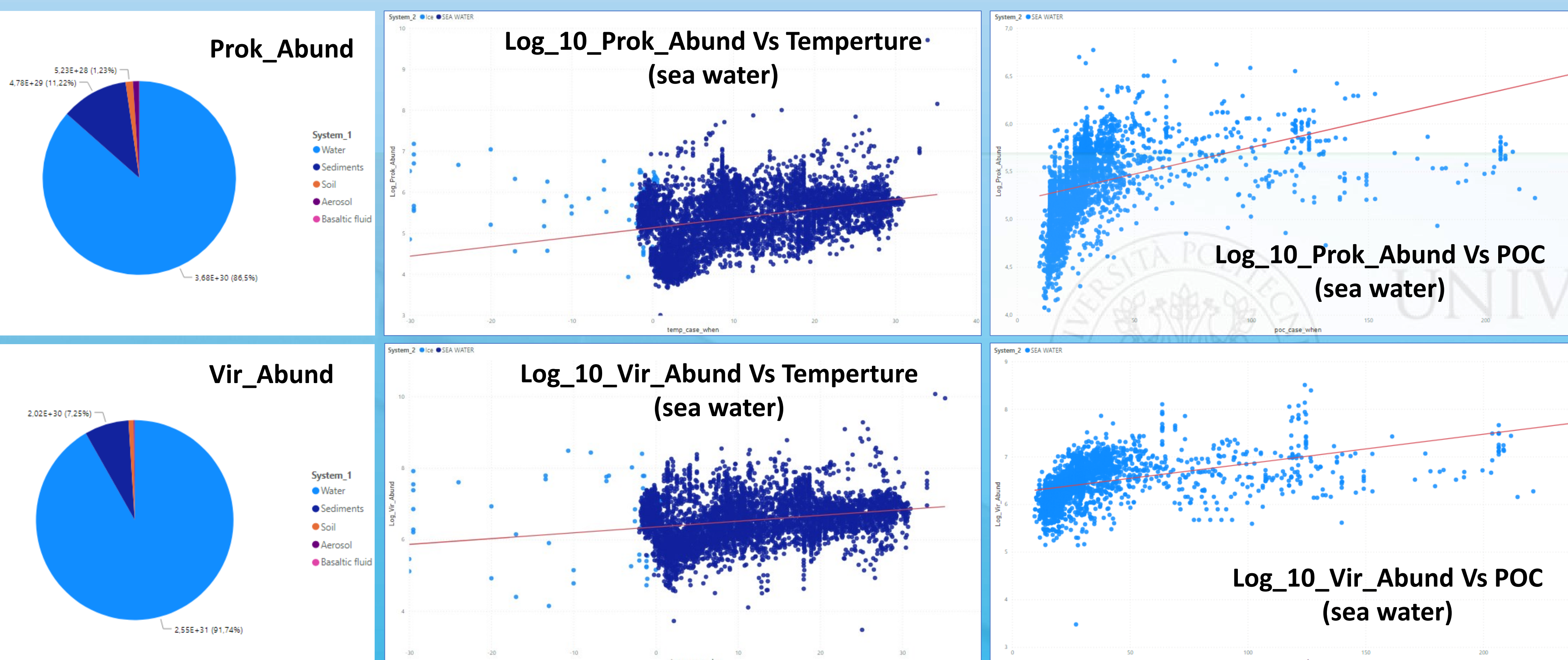
Material and methods

Data collection (> 10,000 records) from published papers and open source databases (Copernicus, Oregon). Multi-Collinearity Detection as prerequisite for the development of Generalized Linear Models used to investigate the relationship between microbial abundance and environmental drivers. Creation of mechanistic models using Ordinary Differential Equations to forecast the microbial dynamics in different climate change scenarios.

FIG. 1. Pie charts with global microbial abundances; scatterplots that show the relationships between microbial abundances and environmental drivers.

Results

- Marine ecosystems are the major reservoir of viruses and prokaryotes on Earth (FIG 1).
- Viral and prokaryotic abundances in the world oceans are significantly and positively related to temperature and trophic resources (POC; FIG 1).
- Bottom water warming in the deep sea may accelerate benthic microbial dynamics, leading to a decrease of prokaryote standing stocks and an increase of viruses (FIG. 2).
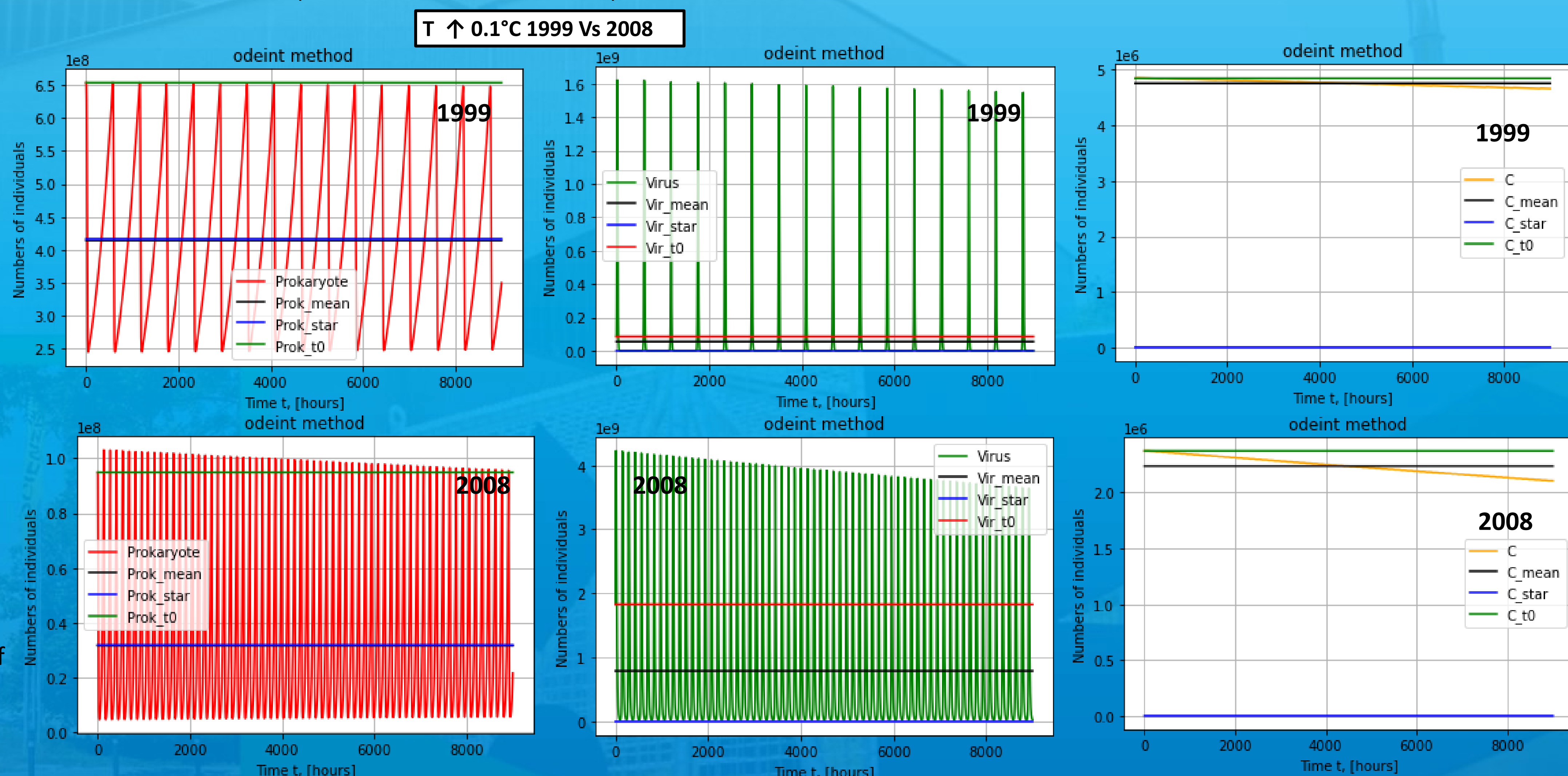

FIG 2. Theoretical solutions of the mechanistic models that simulate prokaryote-virus interactions (prey-predator) in relation to the availability of trophic resources.

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