Corso di Dottorato di Ricerca in Scienze della Vita e dell'Ambiente - Ciclo XXXVI

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

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Introduction

Viruses are by far the most abundant 'life forms' in the world's oceans and increasing evidence indicates that viral infection may be responsible for the high mortality of autotrophic and heterotrophic organisms in surface oceans, with cascading effects on carbon cycling and nutrient regeneration (Suttle 2007). Therefore, the integration of the viral component into trophodynamic and biogeochemical models is of primary importance for an improved understanding of the function of the world's oceans. The oceans are changing rapidly, and seawater warming has been documented for different marine regions and also for the deep seas (Levitus et al. 2005). Biogeochemical models predict a global decrease of the oceanic primary productivity (Steinacher et al. 2010), and hence a reduction of organic C inputs to the deep seafloor, although such an effect can be also opposite on a regional scale (Smith et al. 2013). As viral replication and life cycle are closely linked with host metabolism, increases in temperature and changes in organic C availability will likely influence the interactions between viruses and the organisms they infect. In my PhD I investigate the effect of these alterations in the host-virus interactions whose responses in altered temperature regimes are unknown.

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.
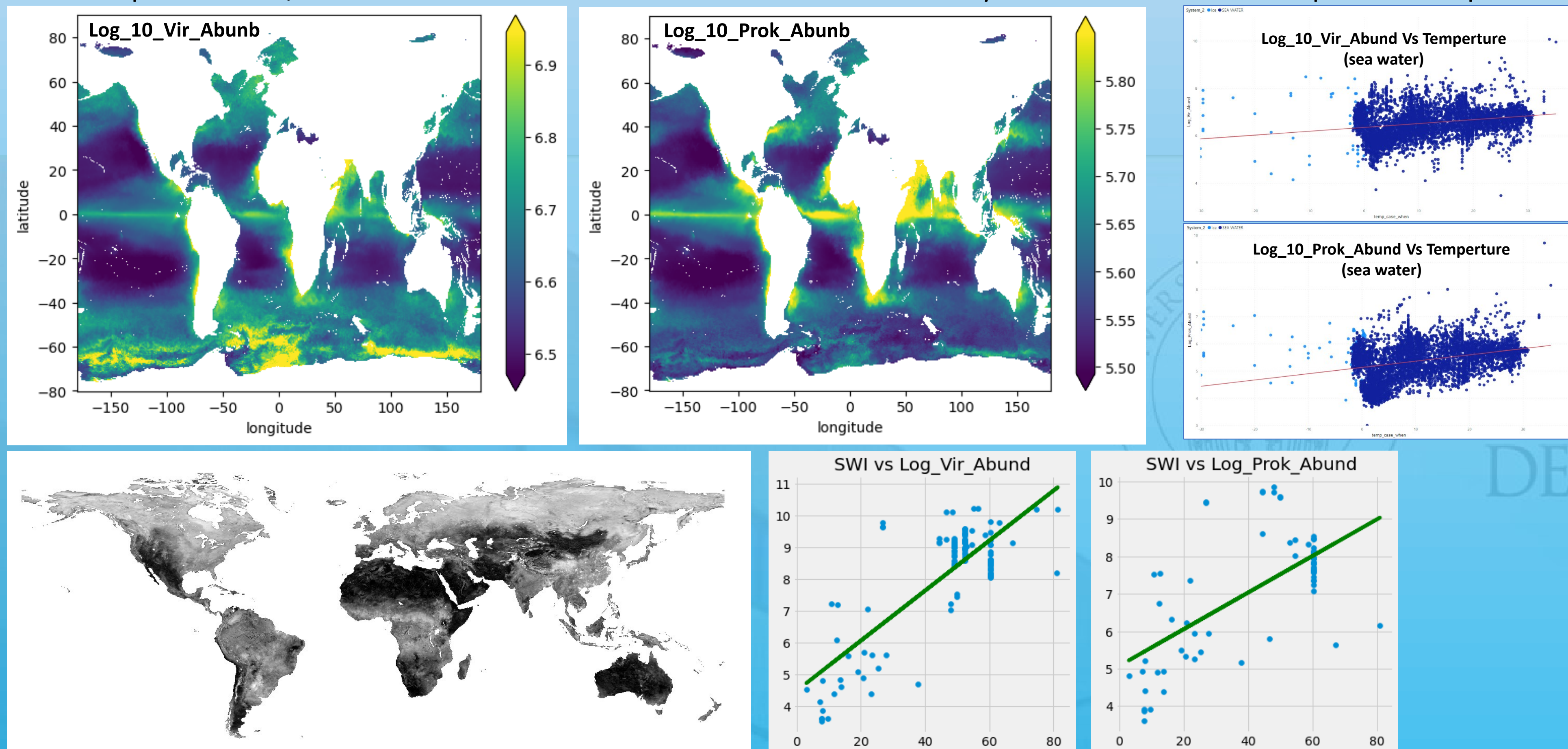
Materials and methods

Data collection (> 10,000 records) from published papers and open source databases (Copernicus, Oregon). Multivariate Regression Analysis using Generalized Linear Models used to investigate the relationship between microbial abundance and environmental drivers. Creation of parameterized mechanistic models using Generalized Lotka-Volterra models to simulate the microbial dynamics in different climate change scenarios.

FIG. 1. global maps obtained as prediction of the model for the spatial distributions of microbial abundances in the epipelagic zone; global map showing the distribution of the soil water index; scatterplots showing the relationships between microbial abundances and soil (soil water index) or water (temperature) drivers.

Results

- Viral and prokaryotic abundances, in the world oceans, are significantly and positively related to temperature and trophic resources, while, in soil, are positively related to trophic resources and water, and negatively to temperature (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).
- Temperature shift is not sufficient to explain the observed variations that depend from changes in the input of resources also (FIG. 2)

$$\cdot \; \frac{dV}{dt} = \delta * (\beta * V * B) - \Omega * V$$

$$\cdot \; \frac{dB}{dt} = \alpha * C * B - \beta * B * V$$

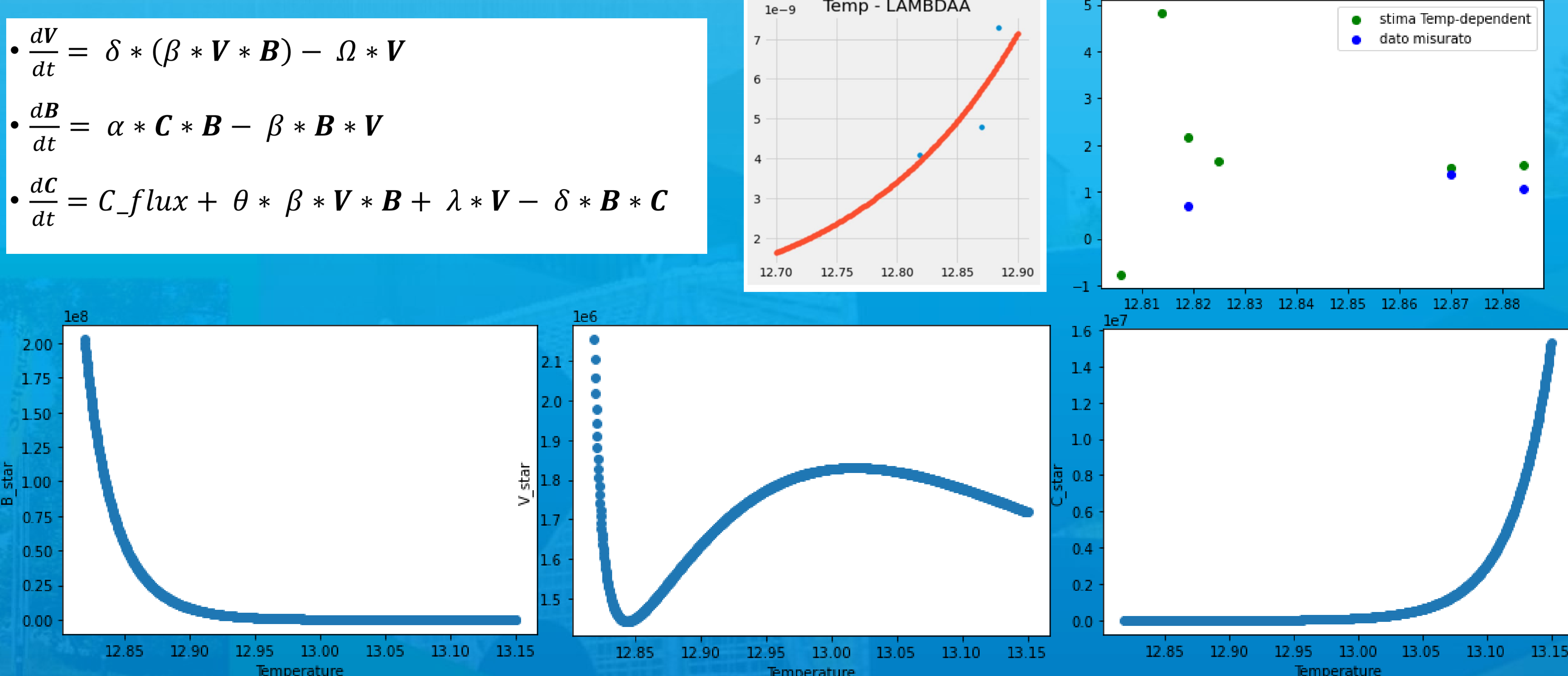$$\cdot \; \frac{dC}{dt} = C\_flux + \theta * \beta * V * B + \lambda * V - \delta * B * C$$

FIG 2. Mechanistic models that simulate prokaryote-virus interactions (prey-predator) in relation to the availability of trophic resources and temperature changes. Regression Analysis to integrate temperature as a model parameter; parameter analysis of steady states (param = temperature).

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