



Modeling the Biology of Phytoplankton in the Oceans

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The ocean is home to thousands of phytoplankton species, which constitute the base of the majority of oceanic food chains and are essential to sustaining life in the ocean. Moreover, the sinking of phytoplankton-derived organic matter from the surface into the deep ocean, i.e. the biological carbon pump, results in long-term storage of carbon in the ocean interior. Photosynthesis and the biological pump reduce ocean surface CO₂ concentration, which drives further influx of CO₂ from air into the ocean; if these biological processes did not exist, atmospheric CO₂ would be dangerously greater than the present 400 ppm level. The goal of my research was thus to understand how the behavior of phytoplankton has changed as a result of the Earth's shifting climate.

In order to do so, I investigated several novel frameworks for modeling the biological behavior of phytoplankton. These models are remarkable for their ability to quantify specifically the adjustment of phytoplankton growth in response to surrounding nutrients, light, and temperature. In order to understand these models, their limits, and their strengths, they needed to be tested at various locations in the Earth's oceans. To that end, I researched the characteristics of various oceanographic time-series for which there are decades of biogeochemical data available. After considering several such time-series, I have moved on to running the models using data from the ALOHA station on Oahu, Hawaii, which best matched our needs for input into the models.

Further, I investigated a promising "transport matrix" computation method that would permit the integration of these finely detailed biological models into larger-scale computational models. This matrix method is powerful because of its high efficiency; without it, the time required to run a 500-year simulation would be measured on the order of weeks rather than hours. The matrix method is a promising source for further investigation, as a successful implementation would allow for rapid and precise tuning of parameters in the novel biological models.

In all, I was exposed to many essential components of computational modeling. I was given experience in understanding, documenting, compiling, and running complex pieces of software provided by collaborators. Similarly, I learned how valuable academic collaboration can be towards reaching a common goal: through frequent correspondence with model authors, I was able to debug and improve their models while gathering data for my own research. It was a pleasure to work with the Marinov group this summer and I feel that the experiences, while challenging, were very instructive in the realities of collaborative and contemporary research in modeling.