



Leibniz Centre for Tropical Marine Research

Jacobs University Bremen

PhD Proposal

Modeling diverse phytoplankton communities in the eastern Cariaco basin, Venezuela

prop need broader title here for PhD Project

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Abstract

At an unprecedented rate our oceans are changing and so are the organisms within it.

- Global Change / Phytoplankton - it's important
- phytoplankton is a complex and diverse community, in a complex ecosystem, trait-based vs functional type
- CARIACO is a setting where both of these things are obviously happening/true and I have the data to back it up
- computational models are the way to synthesize and test hypotheses about these complex systems
- I have built a modeling framework to test functional type hypothesis, first study looking at bulk biomass changes
- the modelling framework itself is interesting and publishable
- now going to San Diego to work with Andrew Barton on expand upon first study and look at more detailed BDEF and other such stuff
- goal is to improve understanding of ocean ecosystem and how it might be affected by global changes

"Totally need to rewrite this:

We are struggling to find ways to characterize and quantify the organisms and their interactions in ways that can be effectively utilized in computational models to predict future scenarios. Phytoplankton are an integral part of modeling the biogeochemical interactions taking place in the ocean. One of the key questions is how to accurately describe the interactions and effects on the ecosystem of the remarkably diverse planktonic community. The field of marine biogeochemical modeling has seen great advances in the last 20 years, in particular the "trait-based" approach promises ecologically meaningful descriptions of biodiversity by moving away from treating species explicitly, but instead looking at the way organisms interact with the environment (i.e. their traits). Two such models form the basis for my doctoral studies: The PhytoSFDM model, developed by my supervisor Esteban Acevedo-Trejos, and the DARWIN model, a framework developed at MIT and used extensively by Andrew Barton.

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1. General Introduction

1.1 The ocean, phytoplankton and why it matters

The complexity of the ocean and its vast ecosystems has fascinated scientists to this day and most likely will continue to do so far into the future. Myriad life forms are embedded in a matrix so far removed from our mostly dry existence on top the earth's crust. In the ocean, life moves in dilution, and the equivalents of forests and grasslands are hard to spot unless the concentration of tiny phytoplankton is so large, that deep blue turns into a milky green.

The term phytoplankton refers to microscopic marine photosynthetic organisms. These microorganisms form the basis of the oceanic food web and are primary producers of planetary scale, contributing roughly half of the oxygen in our atmosphere through photosynthesis (Field et al. 1998). Phytoplankton consists of mostly single-celled organisms, prokaryotes and eukaryotes from a highly diverse evolutionary background (Falkowski et al. 2004). This large genetic diversity is accompanied by a remarkable range of survival strategies, biogeochemical roles, shapes and sizes within the polyphyletic phytoplankton (see Figure 1.1 for a size comparison). The emergence of such a large range of organisms and the mechanisms sustaining their persistence has been one of the key topics in phytoplankton ecology over the last 50 years. Hutchinson's paradox.X(REF here)X

_____ also explain MLD in the following paragraph _____

The distribution of phytoplankton is driven by the complex physical forces that govern ocean currents and the chemistry of the bodies of water the move. The key

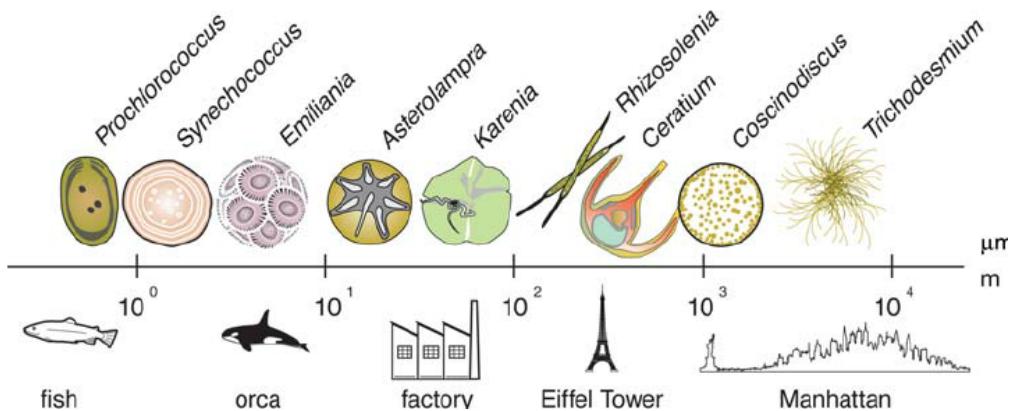


Figure 1.1: "A comparison of the size range (maximum linear dimension) of phytoplankton relative to macroscopic objects." from Finkel et al. (2010)

components are macronutrients (e.g. nitrogen & phosphorus) and micronutrients (e.g. iron & cobalt) welling up from the deeper ocean or flushed in from continental sources. Wherever there are sufficient nutrients available within the euphotic zone, the depth where photosynthetically available radiation (PAR) is 1% of the surface value, planktonic life begins to thrive. Ecosystems along continental margins provide a particularly productive habitat, with only 10% of total ocean surface area covered by continental margins, but 10-15% of marine primary production and more than 40% of carbon export to the seabed occurring along coastal lines (Yool & Fasham 2001; Muller-Karger et al. 2005).

Phytoplankton growth indirectly feeds a considerable part of earth's population through fisheries (Stock et al. 2017) and even shapes the elemental composition of oceanic water itself (Redfield 1958). The biomass produced is mostly consumed by higher trophic levels and either assimilated or excreted. Another large portion experiences natural mortality and viral lysis. Microbial degradation drives remineralization within the euphotic zone, which fuels regenerated production (Eppley & Peterson 1979) [Perhaps put quotation about Microbial Loop here!]. A small fraction sinks out of the photic layer as fecal or detrital matter to the deeper ocean and an even smaller fraction reaches the sea floor as sediment (roughly 1 %) and remains there over geological times (Honjo et al. 2008). This process has been termed the biological carbon pump. Carbon sequestered this way is removed from the ocean-atmosphere system for potentially millions of years. Given the projected rise of atmospheric CO₂ levels, it is of

grave importance to understand how changes in the phytoplankton community at the surface, driven by anthropogenic stressors and climate change, will affect the carbon burial potential of oceanic ecosystems. Studies have both reported a global declining trend in marine primary production (Boyce et al. 2012) and increasing trends in long-term ocean time series (Chavez et al. 2010). In order to answer questions of how phytoplankton will respond to a changing climate it is necessary to look the diverse phytoplankton community in greater detail.

1.2 Characterizing phytoplankton communities

From the early days of oceanographic research, scientists have been interested in the microscopic organisms that were floating in samples of sea water. These communities contain many species each and in total there are tens of thousands of species of phytoplankton that inhabit the surface ocean (De Vargas et al. 2015). All phytoplankton species use chlorophyll or bacteriochlorophyll to harvest light as the energy source to fix organic carbon, but there is wide variation in virtually all their other properties (Litchman & Klausmeier 2008). In addition to the complex community composition, there are many factors affecting measurements of their bulk properties in the ocean, such as the viral and bacterial community and the influence of diverse grazers, all within the complex three-dimensional physical environment that is the ocean. Where earlier phytoplankton ecologists focused on identifying individual species, decoding their phylogeny or growing them in controlled lab cultures, recent research is trying to integrate the insights gained from these approaches and quantify the diversity on higher levels of organization in relation to other properties of the ecosystem. The focus has shifted towards trait diversity both within and across species and within and across phytoplankton groups. In order to scientifically describe this perplexing diversity the concepts of trait-based ecology and functional types have been developed (Tilman 2001; McGill et al. 2006; Violle et al. 2007).

Functional types, traits and diversity

In the following I will try to clarify the complementary terms of phytoplankton traits, functional traits, and functional types.

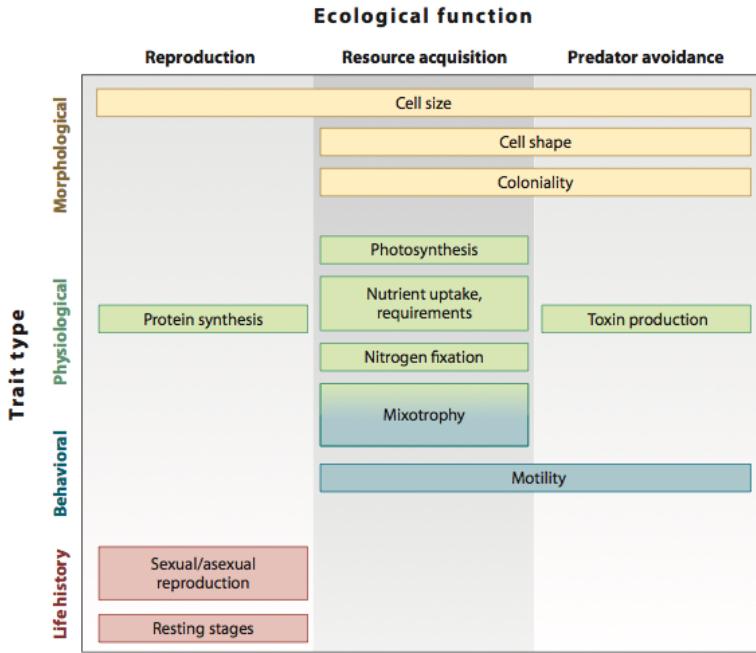


Figure 1.2: "A typology of phytoplankton functional traits" from Litchman & Klausmeier (2008)

The trait-based approach to phytoplankton ecology has been growing in popularity. Part of the fascination evoked by this term stems from its origin in evolutionarily theory. Over the last three decades, it has been adopted by ecologists trying to understand communities and ecosystems. In this new context, the concept of traits has been stretched far beyond its original meaning, which can lead to some confusion surrounding the scope of trait-based methods (Violle et al. 2007). In the simplest definition, a trait is a surrogate of organismal performance. In the ecological context this has been expanded to surrogates for the performance of populations, communities and entire ecosystems. This can include ecophysiological traits, life-history traits, demographic traits or response and effect traits of ecosystems (see Figure 1.2 for a selection of phytoplankton traits). Theoretically, any property of an organism or ecosystem could be defined as a trait, but ideally a trait should be functional. Functional traits are defined by Violle et al. (2007) as "morpho-, physio- or phenological traits which impact fitness indirectly via their effects on growth, reproduction and survival". An important facet of the trait-based approach is to describe organismal function via trade-offs between traits. For example when competing for multiple nutrients, phytoplankton species are thought to be constrained by trade-offs in their competitive ability

for one over another resource (Tilman 1990).

Phytoplankton are extremely diverse and the trait based approach lends itself to generalizations, as traits and ecological trade-offs can be defined and explored irrespective of species or taxa boundaries (McGill et al. 2006). However, depending on the study and hypotheses to be tested, it can be very helpful to structure the diversity of organisms into distinct groups. Major taxonomic groups of phytoplankton can be classified based on their ecological or biogeochemical roles within the ecosystem (Iglesias-Rodríguez et al. 2002; Flynn et al. 2015). The concept of functional groups is not in contrast to a trait-based ecology of phytoplankton, but can be complementary to it. By broadly sampling relevant traits across phytoplankton groups and species, functional types can be defined by functional traits and trade-offs and therefore extend the trait-based approach by another level of organization (Litchman et al. 2007). An early example is the work of Ramón Margalef. Margalef used observations of important traits, such as sinking rates and nutrient utilization to build the concept called "Margalef's mandala" to organize phytoplankton functional types (PFTs) on a spectrum of nutrient availability versus turbulence (Margalef 1978).

The terms functional group and functional type are used interchangeably, with functional groups more often referring to the grouping of species and the functional type describing the group as a whole, often as implemented in computational models. In fact, the simplification of the phytoplankton community into functional types has been widely used for the design and interpretation of computational models that try to recreate or make predictions about the biogeochemical cycling, biogeographic distribution, productivity and other ecosystem functions of phytoplankton (Gregg et al. 2003; Le Quéré et al. 2005). Biogeochemically defined functional types are most often used, as these functional traits can usually be well defined within an ecosystem model. Typical examples of such functional groups are silicifiers, which broadly correspond the phylogenetic group of diatoms, and calcifiers, which are usually represented by coccolithophores. Such functional types are always simplifications of the natural phytoplankton diversity. Silicoflagellates create silicified skeletons like diatoms, but are often not explicitly included because they rarely dominate modern phytoplankton assemblages. The choice of which functional groups to include in a model can also be driven by biogeography or analytical considerations concerning the measurement instrumentation used for a particular study (Irwin & Finkel 2017).

—————Perhaps small paragraph about functional diversity here?————— In biodiversity research, the trait-based approach has been readily adopted. It used to be that species diversity (i.e. the number of species) was the most important metric, but now it is functional

diversity, which can be described by the variance in the value of a functional trait of the community or ecosystem.

It is important to keep in mind that functional types are often composed of many species with a possibly large variance in trait values. Recent research is trying to understand the effects of diversity within functional types and within species (Violle et al. 2012, 2017; Des Roches et al. 2018).

1.3 Modeling phytoplankton communities

Given the complexity of the ocean ecosystem, it is necessary to aggregate our knowledge of the many smaller parts into comprehensive ecological models in order to test mechanistic hypotheses and investigate their full-scale implications.

Computational models of phytoplankton growth have been developed since the 1940s and have greatly increased in sophistication and complexity since then, co-evolving with the rise in computational resources (Gentleman 2002). Phytoplankton modelling started with formulations based on the Lotka-Volterra equations of predator-prey dynamics (Fleming 1939). From these relatively simple descriptions models evolved to describe the oceanic physical environment and the ecosystem it contains including multiple trophic levels. Originally developed by John Steele with a model ocean split in two layers, the nutrient-phytoplankton-zooplankton (NPZ) and nutrient-phytoplankton-zooplankton-detritus (NPZD) models succeeded in reproducing the typical annual bloom dynamics observed in the temperate ocean (Steele 1958; Evans 1988; Fasham et al. 1990). Further developments have been in more exact physiological descriptions of phytoplankton based in cellular metabolism and energy allocation (Geider et al. 1997) and both simple and more complicated ecosystem formulations driven by local and global 3D circulation models (Lacroix et al. 2007; Hirata et al. 2013).

However, in their simplified approach, these models unavoidably limit the characterization of a diverse phytoplankton community (Bruggeman 2009). These plankton ecosystem models are typically highly aggregated, such that a single variable determines the response of a diverse assemblage of phytoplankton species (Franks 2009). Implementing a meaningful treatment of biodiversity in ecological models is a key challenge in the field of phytoplankton modeling (Queirós et al. 2015). The most apparent way of implementing this within the framework of established NPZD models is to include multiple equations and state variables for different

phytoplankton functional types (Le Quéré et al. 2005). For every group that fulfills a distinct ecosystem function, a new set of parameters has to be added, which complicates the model structure and increases computational costs. This somewhat intuitive approach, however, does lead to problems. First and foremost, this is the lack and inherent uncertainty of data from field and culture experiments to constrain functional types. This again leads to the difficulty of validating the model output in light of insufficient information, leading multiple authors to criticize the PFT modeling approach as attempting to "run before we can walk" particularly when used for extrapolating into the future (Anderson 2005; Shimoda & Arhonditsis 2016).

The current scientific discussion can seem intimidating to an early career scientist, as both the most obvious future directions of ecosystem model design as exemplified by PFT models, as well as the very foundation of traditional NPZD models has come under scrutiny. Nowhere is this more apparent as with the formulation of nutrient uptake dynamics, which is traditionally defined by Monod kinetics that are based on the equations for Michealis-Menten enzyme kinetics. (Monod reference here)

ALSO: current modeling paradigms are discussed quite critically in the literature, in particular the Monod kinetics and also the lack of any adaptive mechanisms in these model (Smith et al. 2014) A bit earlier, but similar direction: (Flynn 2010) and more recent, but focused on Monod: (Hellweger 2017)

However, there are also examples of modeling approaches that show a way forward. To name an alternative to the modeling paradigm discussed so far, there is individual based modeling (IBM). In IBM the phytoplankton are explicitly represented as individual agents, allowing for a diverse and spatially interactive phytoplankton community (Hellweger & Bucci 2009). The computational cost and structural complexity of this approach however does not yet lend itself well to studies of large-scale or even global ecosystems.

Another approach which lends itself very well to just such studies is to extend traditional NPZD models via moment-based estimation of aggregate properties (Mericó et al. 2009). A specific implementation of this is the PhytoSFDM model developed by Acevedo-Trejos et al. (2016). Instead of modeling multiple size-classes of phytoplankton explicitly, the community is described not only by the biomass, but also by the mean size and size variance. Size is used as a master trait, with size variance being used as a proxy for functional diversity. Trade-offs related to nutrient uptake, grazing and sinking structure the phytoplankton community along the size spectrum as driven by the physical forcing. The model was used to

investigate latitudinal diversity gradients in the Atlantic Ocean (Acevedo-Trejos et al. 2018). One point of criticism for this approach is that due to the mathematical structure the size distribution is fixed to the shape of a skewed log-normal distribution, not allowing for the emergence of other (e.g. multi-modal) distributions that could arise in natural phytoplankton communities (Urusla Gercke, Tony Klaus, Francesco paper on size dist in lakes). This lends the PhytoSFDM model (in it's current formulation) more to studies of large scale processes and biogeographic patterns rather than to local ecosystem modeling studies.

looking at aggregate properties, how complex model has to be, how simple it has to be, aggregate model can not capture all of the variability, model capturing all of variability (Hellweger, Science article, biogeographic patterns emerging - GLOBAL FIX ERROR BEFORE)

1. very complex -*i* IBM 2. DARWIN 3. aggregate with adaptive dynamics and PhytoSFDM, similarly to optimality based model I am for interemdiate levels of optimality Tom Anderson "Running before we can walk"

ALSO: problem of looking at within FT diversity, look at the details of diversity -*i* including PFTs very complicated!

perhaps not cutting edge, but my method allows me to catpure variability wihtin functional groups!

don't rubbish other models/papers

A major advancement in the field of phytoplankton modeling was the DARWIN model developed at MIT (Follows et al. 2007). In the general framework of the DARWIN model, large numbers of phytoplankton types are initialized with equal biomass but with different parameters for the most important traits, namely those related to light harvesting, temperature dependence, and nutrient acquisition. These parameters are chosen stochastically from broad ranges of values, based on laboratory and field data, and constrained by simplified allometric functions describing ecological trade-offs. Different functional types are prescribed in the model via varying nutrient utilization traits (e.g. small phytoplankton that cannot assimilate nitrate as Prochlorococcus analogs). Over multi-annual runs this community self-assembles through ecological competition and physical changes produced by the simulated environment of a global circulation model (GCM). In the random initialization of phytoplankton types, the DARWIN model allows for the emergence and development of diverse phytoplankton communities. This approach of modeling biodiversity has been termed

"selection-based" (Follows & Dutkiewicz 2011). —more attention to this review—— The model framework is continually modified and expanded, for example for exploring the effect of grazing formulations (Prowe et al. 2012), the biogeography of phytoplankton traits (Barton et al. 2013) and the influence of ocean acidification at a global scale (Dutkiewicz et al. 2015). Size structured ecosystem models have been done before: (Baird & Suthers 2007) A study of particular interest is the size-structured food-web model component developed by Ward et al. (2012), because the modeling approach combines the trait-based approach of scaling parameters allometrically along cell size with a PFT modeling approach. Each functional type is assigned a different allometry based on the size ranges and relationships taken from data. Together with the selection-based biodiversity representation that the DARWIN framework provides, this seems to be a promising direction for future models. The model has however only been applied and compared to data at a global scale and the code of this specific implementation is not publicly available.

PhytoFLEX -*i* Systems of infinite Diversity -*i* structure paragraph along axis of complexity?

ALWAYS NEED A GOOD BASIS IN DATA TO VALIDATE MODELS AND HYPOTHESES

1.4 The Cariaco Basin and the CARIACO time-series

At the beginning of my PhD I was tasked with the mission to find publicly available ocean time-series data that could be used as the basis for my modeling work. Initially the plan was to choose multiple locations, to compare results from model applications in contrasting environments. Not surprisingly the search did quickly yield results, among the most prominent: the Bermuda Atlantic Time-series Study (BATS) and the Hawaii Ocean Time-Series (HOTS). Quickly the issues of public ocean time-series data became apparent. Links often lead to defunct sites and servers were sporadically maintained. In particular for my application the problem was that the basic physical parameters and bulk properties such as total chlorophyll were readily available, but more specific phytoplankton functional type or taxonomy data was harder to find, if not missing. In particular the type of phytoplankton data that was available differed widely between the stations and would have not allowed for a straightforward comparison. It was only later in my search that I came across the CARIACO time series, an acronym for "CArbon Retention In A Colored Ocean", located in the Cariaco

Basin off the coast of Venezuela. The data is available through the University of South Florida (USF) at <http://imars.marine.usf.edu/cariaco> and includes a wealth of data that was collected since 1995. Most importantly to my purposes, the data included both phytoplankton pigment measurements and taxonomic data of the phytoplankton community at monthly intervals. It was the first ocean time-series with such detailed public phytoplankton data and soon I decided to focus my work on this time-series.

In addition to the recent importance of the cariaco basin as the site of an important paleo-oceanographic time series, the Cariaco basin has served as a natural laboratory for biogeochemists for over 50 years. This basin has been key in constructing stoichiometric models of organic matter remineralization (Redfield et al 1963 and Richards 1975!), developing residence time and box models, and numerous other studies.

Cariaco basin is the worlds largest truly marine anoxic basin (Wakeham et al. 2012).

—————perhaps what is above is not entirely needed — maybe less colloquial, more why CARIACO is interesting! ——————

THE BASIN The CARIACO Ocean Time-Series program was established in 1995 off the coast of Venezuela ($10^{\circ} 30' N$, $64^{\circ} 40' W$, see Figure 1.5). Located in the south-eastern Caribbean Sea, the Cariaco Basin is a 160 km long and 70 km wide tectonic depression, reaching up to 1400 m in depth. The two deeper parts of the basin are separated by a saddle of 900 m depth, with the time-series mooring located in the eastern part. The entire basin is bound to the west and north by a shallow ridge at 100 m depth, restricting the exchange of deep water with the Caribbean Sea. The restricted circulation and high productivity at the surface resulted in anoxic conditions below 250 m depth within the basin (Richards & Vaccaro 1956). The hydrography at the surface is influenced by Guyana and North Equatorial currents that flow into the Caribbean Sea from a south-eastern direction, but this exchange is restricted to the two channels above the 100 m ridge. Observed and modeled horizontal surface water velocities within the basin are relatively weak, indicating a minimal influence of horizontal transport at the mooring site (Alvera-Azcárate et al. 2009).

SAMPLE COLLECTION The program was established as a joint-project of the Venezuelan Fondo Nacional de Ciencia, Tecnología e Investigación (FONACIT) and the US National Science Foundation (NSF), with the particular interest in creating a time-series of surface ocean biogeochemistry that could be linked to satellite observations and the sedimentation accumulating in the anoxic basin. Since 1995 there were over 200 core cruises at mostly monthly intervals, in addition to sediment trap and microbial-biogeochemistry process cruises.

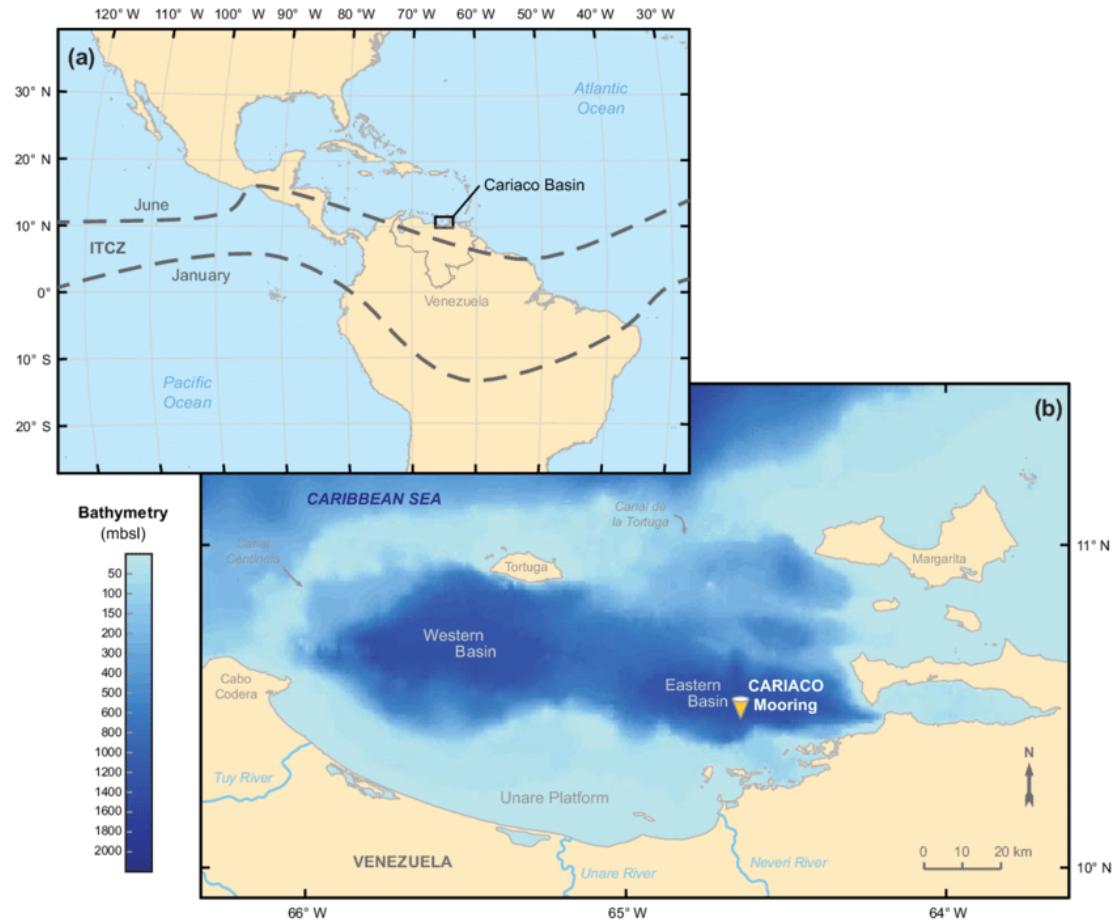


Figure 1.3: "Study area. A. Location of the Cariaco Basin off the Venezuelan coast in the southern Caribbean Sea, with January and June positions of the Intertropical Convergence Zone (ITCZ). B. Location of the CARIACO station in the eastern sub-basin, general bathymetry and local rivers emptying in the basin (bathymetric data from GEBCO_08 Grid)" from Bringué et al. (2019)

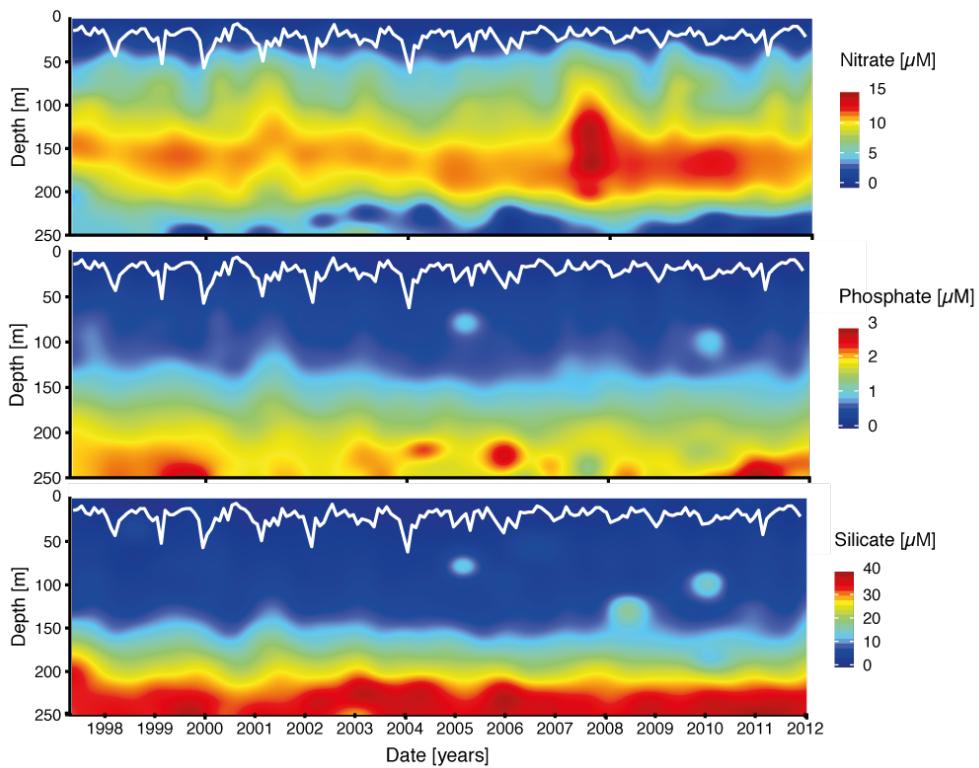


Figure 1.4: Contour plots of Nitrate, Phosphate and Silicate of the CARIACO time series down to 250 m. White line shows depth of MLD. Surface interpolation using R package MBA.surf.

MEASURED DYNAMICS Simply mention the major publications and rough findings, further discussion in section 2

perhaps here: inter-annual and subdecadal variability in nutrient geochemistry (Scranton et al. 2014)

LONG TERM TRENDS - not here, but discuss this in the 2nd section (MS 1)

SCIENTIFIC FINDINGS - RESULTS what has been found here?

- Interesting: Novel eukaryotes found at Oxic-Anoxic interface (Stoeck et al. 2003)

Say that JPincney loves me and how this is a promising data set, given the history, wealth of data, incl phytoplankton diversity data, and long term trends here.

ALSO: Time series has stopped, due to lack of funding, and cite review paper (scientific legacy of CARIACO) (Muller-Karger et al. 2019) Perhaps here go through the main points

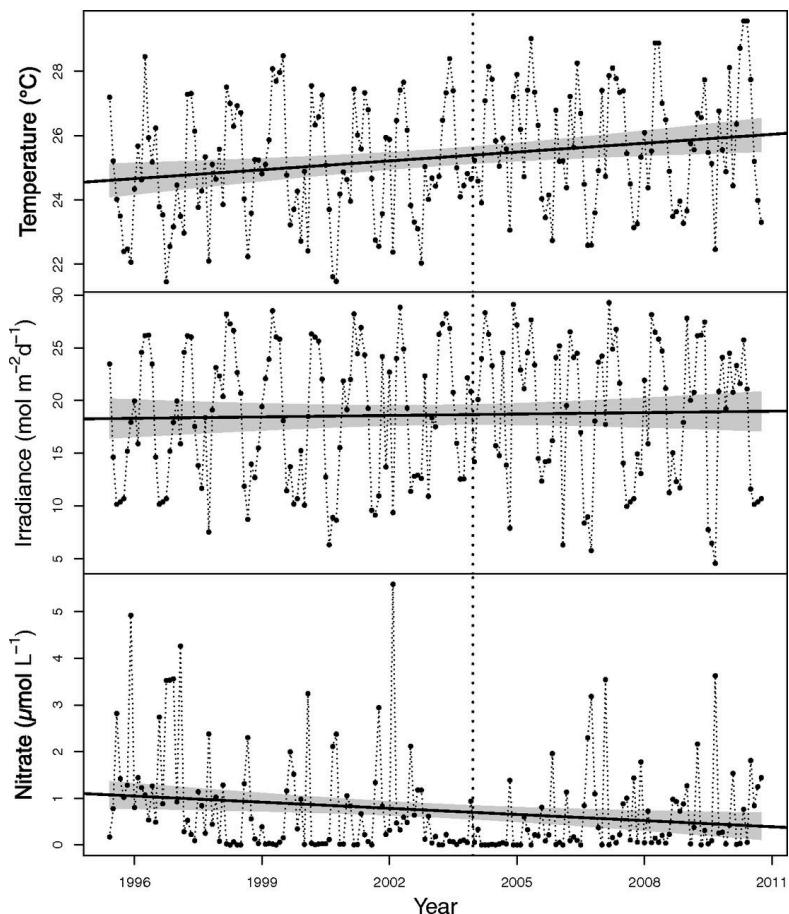


Figure 1.5: "Monthly environmental conditions averaged over the upper mixed layer (1, 7, 15, and 25 m depth) from the CARIACO Ocean Time-Series Program: temperature ($^{\circ}\text{C}$), irradiance ($\text{mol m}^{-2} \text{d}^{-1}$), and nitrate concentration ($\mu\text{mol L}^{-1}$). The vertical dotted line is drawn at the boundary (January 1, 2004) between the cool and warm periods. The straight lines are linear regressions: temperature = $(24.6 \pm 0.3) + (0.09 \pm 0.03)t$, $R^2 = 0.05$, $P < 0.005$; irradiance = $(18.1 \pm 0.9) + (0.05 \pm 0.11)t$, $R^2 = 0.001$, $P = 0.65$; nitrate = $(1.06 \pm 0.14) - (0.045 \pm 0.017)t$, $R^2 = 0.04$, $P = 0.03$, where t is time in years since January 1, 1996, errors are one SE, and the shaded region is the 95% confidence interval on the line. The R^2 is very low because of the tremendous interannual variation relative to the trend." from Irwin et al. (2015)

in the big review to give a nice overview

XX

SAMPLE COLLECTION

SEA SURFACE DYNAMICS

LONG TERM TRENDS

XXXX

XXXX

XXX

THEN TALK ABOUT THE COLLABOrDATASHARE WITH JPINCKNEY AND CBEN-ITEZNELSON, and how this allows an even deeper look at the biomass dynamics

1.5 Aims of the proposed PhD project

"The general goal of my Ph.D. project is to study the processes that structure the phytoplankton community in contrasting environmental regions of the Atlantic Ocean, using a trait-based modelling perspective. The specific aims during the course of the project are to:

- MANUSCRIPT 1 "Understanding Shifts in CARIACO"
- MANUSCRIPT 2 "technical paper" - Geoscientific Model development
- MANUSCRIPT 3 "BDEF in CARIACO"

2. Understanding phytoplankton community shifts in the eastern Cariaco basin

This is the current state of progress towards the first manuscript

2.1 Regime shift in the Cariaco Basin

The CARIACO time-series has been collecting detailed data on the phytoplankton community in the Cariaco Basin from 1995 to 2017 (see Section 1.4 for a full description). What has been a particular focus of the research based on this data set is the apparent changes in environmental conditions documented in both the physical boundary conditions as well as the biological data. As documented by Taylor et al. (2012)

and further investigated by Pinckney et al. (2015)

Interesting thing is that there was this shift in the PhytoplanktonCommunity but apparently no real reduction in Export! (This is in Taylor and Pinckney somewhere) this would be coherent with Pinckney, no real reduction in biomass, but shifts in the community and towards greater depth, talk about depth of the euphotic zone! also have that data thanks to JP and CBN

The term regime shift is actually not very well defined and has been used... (DeYoung et al. 2004) There are global trends and indications of a regime shift, but methods to identify regime shifts are not well established and have been critically discussed in the literature (Steele 2004; Mantua 2004; Litzow et al. 2016). To my knowledge no formal exploration of a potential regime shift has been performed with the CARIACO data,

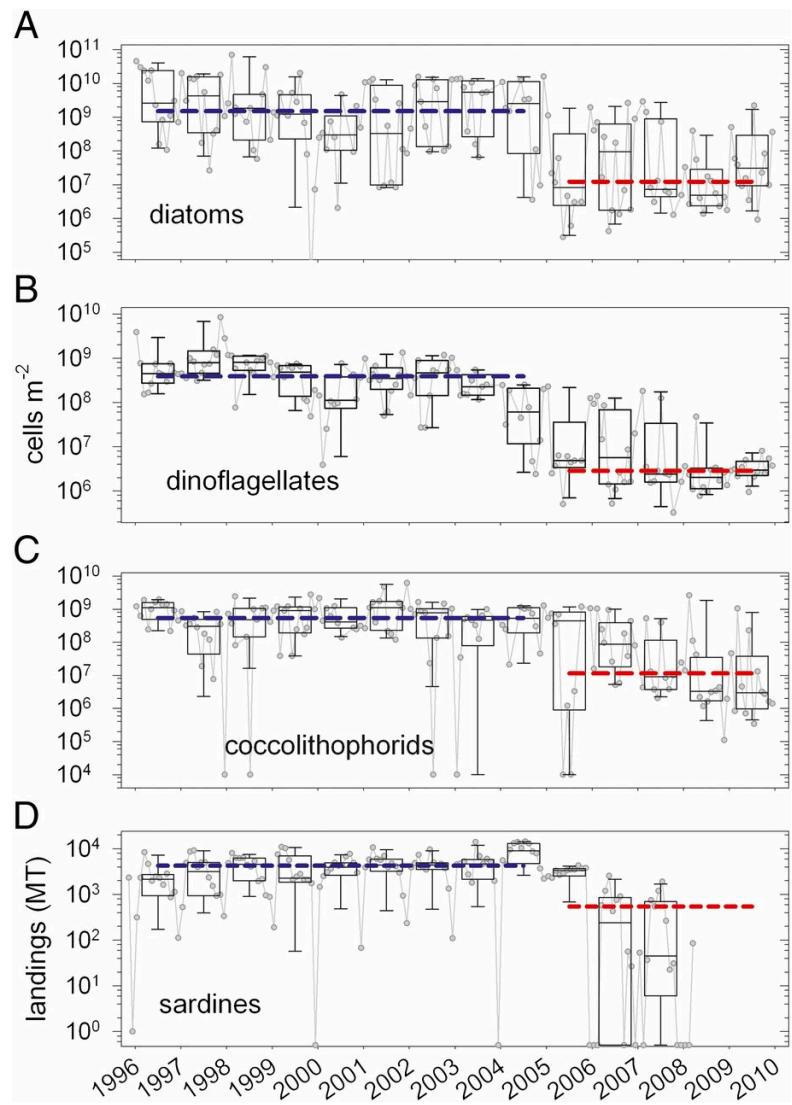


Figure 2.1: "Shifts in phytoplankton community composition and sardine landings from the southeastern Margarita Island fishery. Monthly observations presented as gray symbols. Box and whisker plots depict binned annual variations in diatom (A), dinoflagellate (B), coccolithophorid (C) inventories integrated over the upper 55 m and sardine fishery landings (D) in metric tons. Boxes represent the interquartile range of all observations (25th to 75th percentiles). Internal horizontal lines and whiskers are medians and 10th to 90th percentiles, respectively. Blue and red horizontal lines represent the grand medians of all observations between 1996 and 2004 and between 2005 and 2009, respectively. Data in early and late bins are significantly different in all cases (ANOVA; $P < 0.001$). [Fishery data are courtesy of L. W. González (Universidad de Oriente, Boca de Río, Isla de Margarita, Venezuela); zero values artificially set at 0.5 for plotting purposes.]" from Taylor et al. (2012)

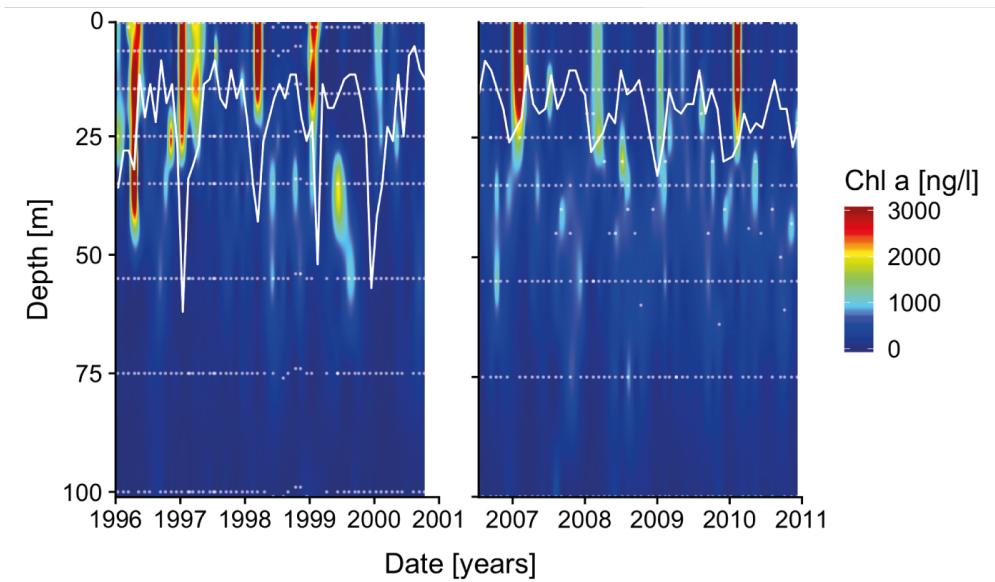


Figure 2.2: Contour plot of HPLC-measured *chl a* for the two time periods with full data coverage (January 1996 to October 2000 and July 2006 to December 2010). Light white dots indicate data points. White line shows the depth of the mixed layer. HPLC Data and MLD depth was received from James Pinckney and Claudia Benitez-Nelson.

therefore the term regime shift is used here to describe the observed changes in the phytoplankton community and physical environment without presupposing a formally defined state shift in the entire ecosystem.

Talk about the data again

Also talk about mutshinda et al studies! Mutshinda study one, bayesian approach:
Mutshinda et al. (2013a)

Mutshinda study, same year, environmental factors: Mutshinda et al. (2013b)

culminated in the study in PNAS: "Phytoplankton adapt to a changing environment"
Irwin et al. (2015)

detailed phytoplankton data has been used in the previous studies for statistical analysis, but surprisingly not yet for ecosystem or trait-based modeling This will be a first! first proper ecological model apart from this Export Flux model only including diatoms (Walsh et al. 2002)

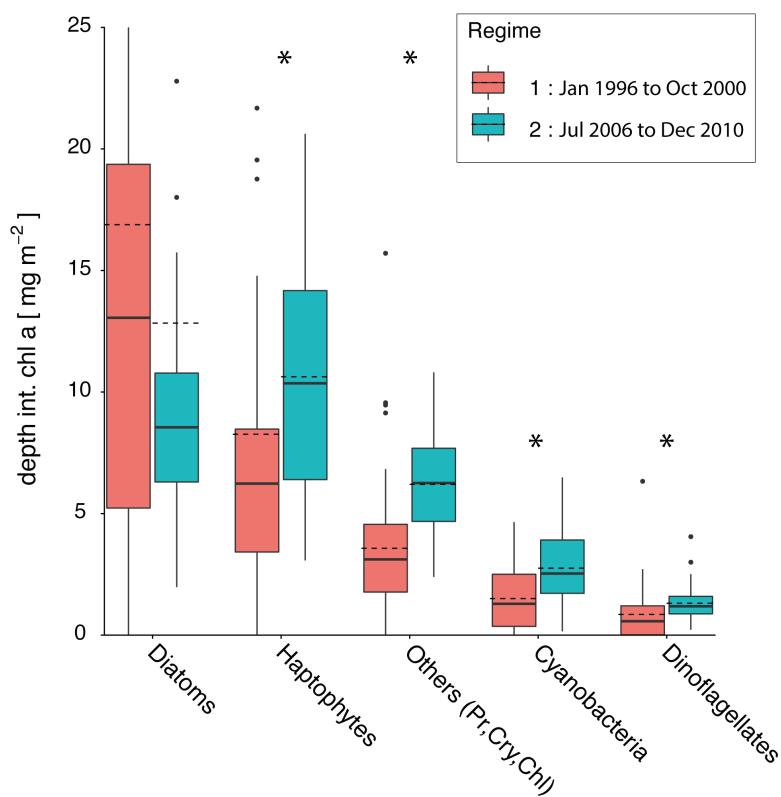


Figure 2.3: Boxplots of HPLC-measured *chl a* depth integrated to 100 m for the two time periods with full data coverage. Boxplots illustrate the 25th and 75th quartiles (the box), the whiskers show the 5th and 95th percentiles, full line shows the median, dotted line shows the mean value per regime. Asterisk * indicates a significant difference between Times 1 and 2 in a one-sided t-test ($p < 0.05$). Functional type *chl a* was separated using the software Chemtax as described in Pinckney et al. (2015). The analyzed data was received from James Pinckney and Claudia Benitez-Nelson.

FUNCTIONAL TYPES STRUCTURE – explain linkage between Pigment Data that I use and functional diversity measurements (XMoreno et al. 2012X) take this from Pinckney et al. 2015... Thus, photopigment-based measures offer an efficient way to quantify community or functional diversity (X Moreno et al., 2012 X). (From Pinckney et al 2015) .. this would also be good to discuss in part 4!

bb

LOOKING AT BIOMASS DYNAMICS, leading over from Intro where i mentioned JP CBN data at the end (ad-lib) XXX

EXPLAIN THE HYPOTHESES HERE; AND HOW THEY CAN BE TESTED

Main hypothesis, based on top down and bottom up processes: Top down grazing has great influence on ecosystem, not just from biomass, but also biodiversity aspects Prowe et al. (2012).

2.2 Methods

MODEL STRUCTURE:

- Cyanos as of yet not implemented as nitrogen fixers, given simplicity of model formulation, but actually are present and could be included: (Montes et al. 2013)

don't really go into depth here, just generally state how things are done, python, odeint, system of ODEs

COPY METHODS SECTION FROM PhytoSFDM in a way, but with the current model setup including the equations and all of that!

XXXX

FORCING DATA

Model physics in a tropical coastal setting

xXXXX

Most models built for temperate oceans, since that is where research (and funding) has been most well developed. Fasham NPZD type slab physics explain. Why won't this fit well in the Cariaco setting? - mostly due to shallow and comparatively invariable MLD, and nutrient fluxes don't correlate. Problem of nutrient forcing! If MLD driven, nutrients below MLD are highly variable, only below 100m do we get towards a relatively constant N₀ and Si₀ (can show plots here!)

Moved from slab physics of PhytoSFDM model (Acevedo-Trejos et al. 2016) which is based on Fasham (Evans & Parslow 2003; Fasham et al. 1990) to a box model formulation adapted from Tyrrell (Tyrrell 1999) The specific differences are (show equations):

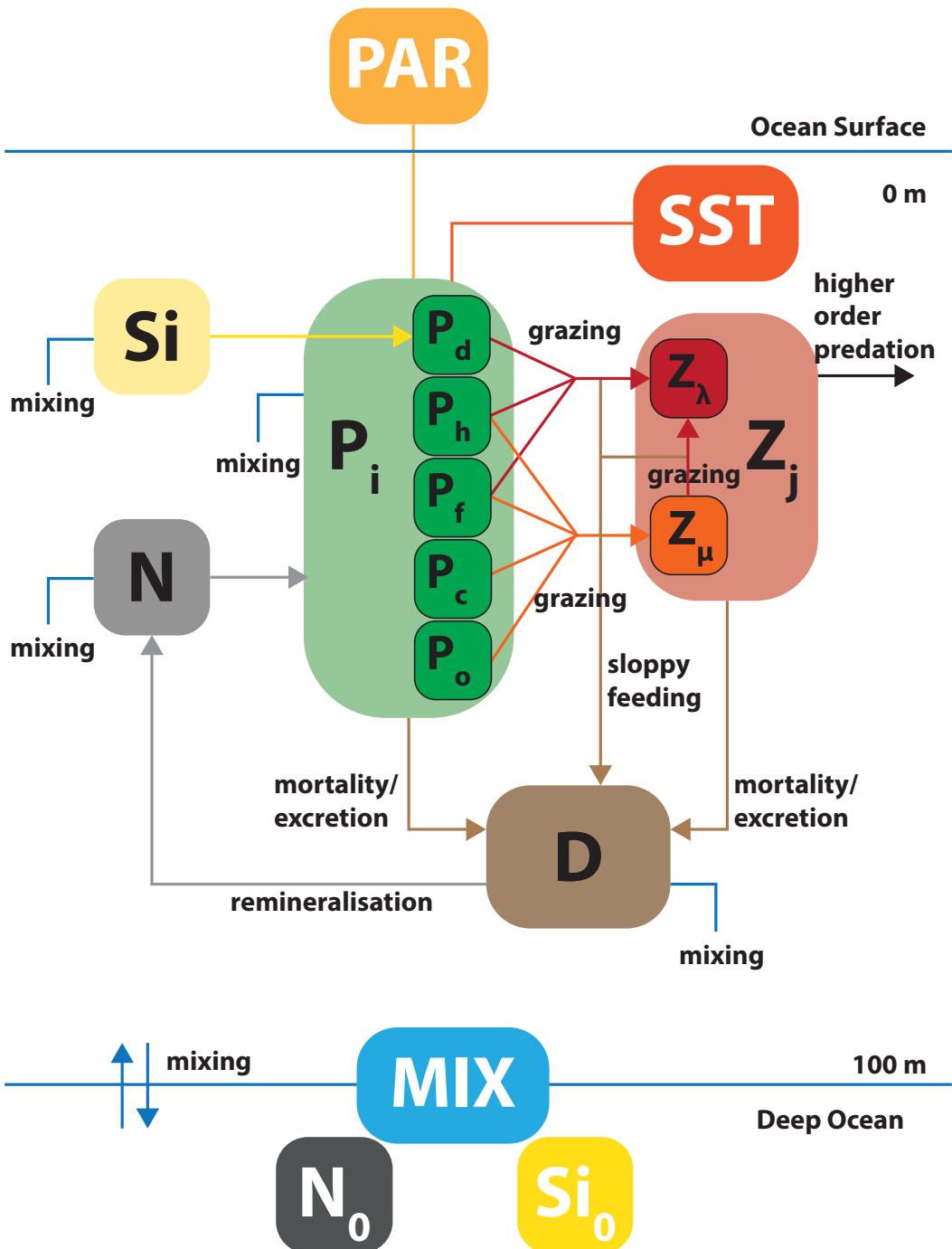


Figure 2.4: Model schematics of current iteration of the ecosystem model. The ecosystem is embedded in a box of fixed depth. Nutrients below are assumed to be constant, mixing is a function MLD to simulate seasonal upwelling. XXXX

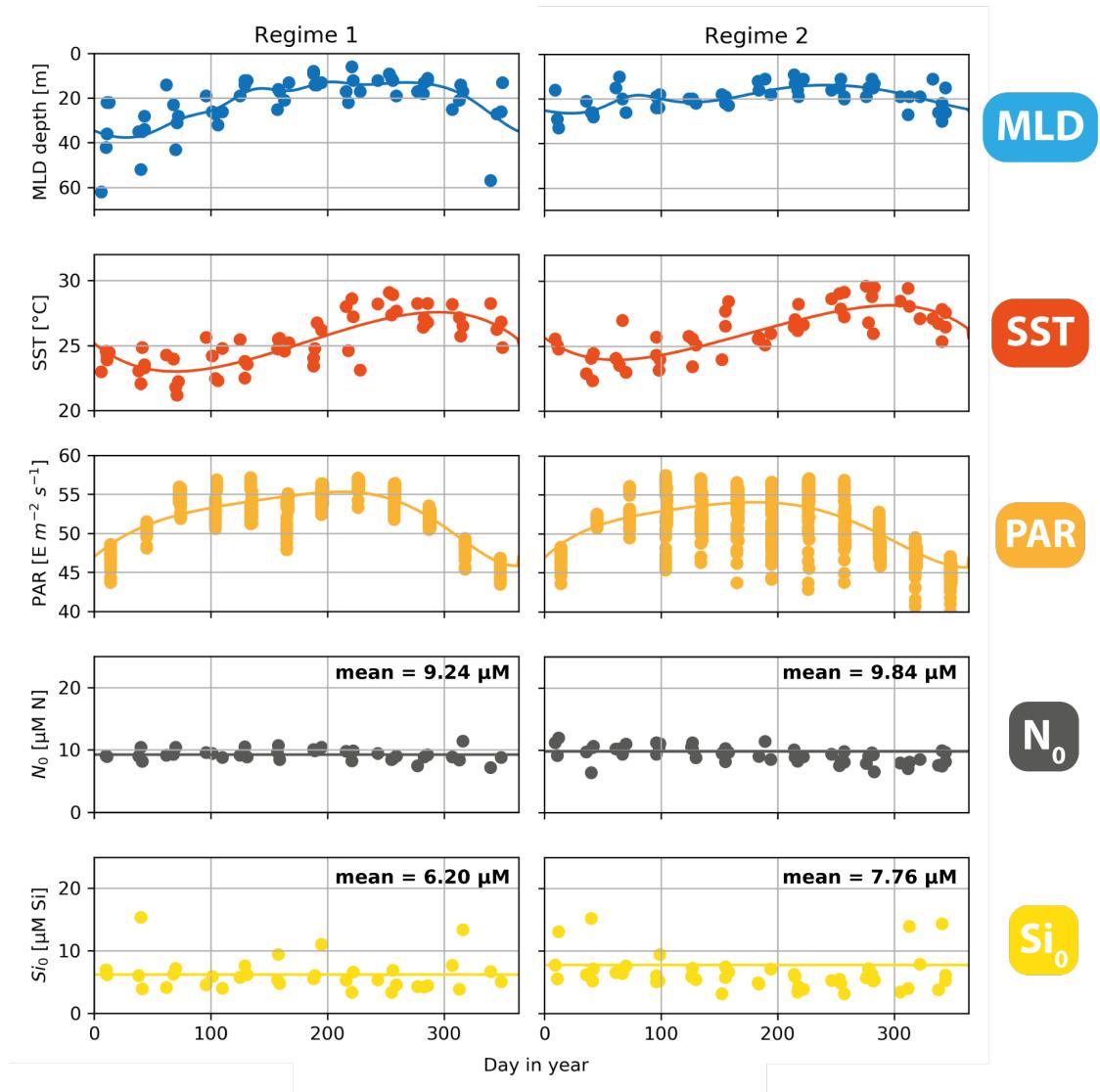


Figure 2.5: Aggregated forcing per the two regimes adapted from Pinckney et al. (2015). Regime 1 from January 1996 to October 2000, Regime 2 from July 2006 to December 2010, values are aggregated to a single year. Depth profiles of Nitrate and Silicate were interpolated to depth and averaged between 100 and 150 m. Continuous line shows interpolated values of MLD, PAR and SST used for model forcing and mean values for N and Si due to the assumption of a constant value at depth. SST and PAR data is taken from SeaWiFS satellite monthly climatological data.

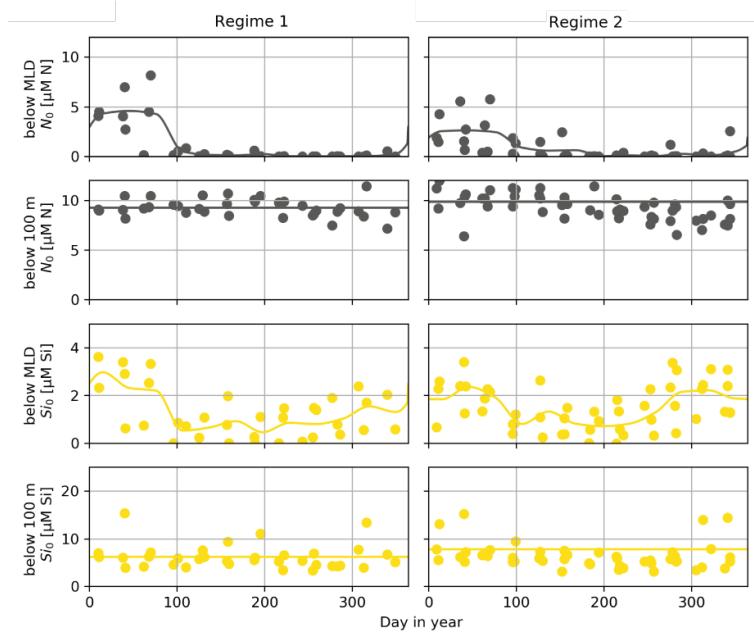


Figure 2.6: Nutrient concentrations below MLD and averaged between 100 and 150 m depth for both regimes aggregated to one year. For values below MLD the continuous line represents interpolated forcing, for values below 100 m the line shows the mean value.

HERE I CAN SHOW THE DIFFERENT MODEL RUNS, explain the difference for this box model needs to get running! This won't be so easy.. so plan ample time my friend!

XXXX

XXXX

XXX

A1. CARIACO model description

NPZD models are simplified marine ecosystem models that can be adapted to different physical settings and food web structures. For this model, the basic structure is inspired by the models of Fasham (1990) as it was adapted by Anderson et al. (2015). The physical setting of the model uses a zero-dimensional slab structure as originally presented in Evans and Parslow (1985) and adapted from Acevedo-Trejos et al. (2015) where the ecosystem is described within a seasonally varying surface mixed layer above a deep homogenous layer. The code structure is the PhytoMFTM model written in the open source programming language Python, which provides a flexible framework for NPZD-type models with multiple

functional types of phytoplankton and zooplankton. The model code and all statistical scripts are available publicly on Github (<https://github.com/ben1post/BennyPhD>).

The model framework was adapted to the setting of the CARIACO time-series in the Cariaco basin of the coast of Venezuela. The data includes phytoplankton species counts and two size-classes of zooplankton, which were included in the model as the 4 most prominent phytoplankton types, and 2 zooplankton types. The phytoplankton types include Nanoflagellates P_n , Diatoms P_{dt} , Coccolithophores, P_c and Dinoflagellates P_{dn} . There are two Zooplankton types split by size class, named Mikrozooplankton Z_μ and Mesozooplankton Z_λ .

Nitrogen N (and Silicate Si for Diatoms) is assimilated by the phytoplankton types P_i , which are grazed by the zooplankton types Z_j . Mortality of and excretion from phytoplankton and zooplankton, and sloppy feeding by zooplankton contribute to Detritus D . In addition to the linear mortality of P_i and Z_j , there is an additional quadratic mortality term acting on Z_j , which represents higher-order predation on zooplankton.

A1.1 Physical setting

The ecosystem component of the model is set within a zero-dimensional physical environment. The water column is divided into a 2-layer structure. A depth variable layer (e.g. the thermo- and/or pycnocline) separates a well-mixed surface layer containing the ecosystem component from a homogenous deep ocean. Concentrations of nutrients are averaged across the mixed layer, and remain constant below. There is no lateral advection, but vertical mixing is modeled as a function of mixed layer depth (MLD) over time $M(t)$. Temperature depth profiles have been used to reconstruct the MLD at the investigated location. The derivative of MLD over time is given as $h(t) = dM(t)$. Exchange between the two layers is described by the two processes of turbulent diffusion and entrainment or detrainment caused by a shallowing or deepening of MLD. Adapted from Fasham (1993), the effects of entrainment and detrainment on nutrients, phytoplankton and detritus are given by the term $h^+(t) = \max[h(t), 0]$. Zooplankton is assumed to be able to maintain themselves within the mixed layer depth, therefore entrainment and detrainment of Z_j are described by $h(t)$. Diffusive mixing between the layers has been parameterized with a constant factor k . The entire diffusion term is thus

$$\kappa = \frac{k + h^+(t)}{M(t)} \quad (2.1)$$

In addition to the MLD interpolated from time series data, the model is externally forced with sea surface temperature (SST) taken from in situ data and interpolated from monthly to daily values and photosynthetically active radiation (PAR) from 8-day averaged SeaWiFS

satellite data.

A1.2 Phytoplankton

Phytoplankton growth is a function of light (PAR), temperature (SST) and nutrients. These factors are assumed to independently limit growth, so that (exemplary for P_d , i.e. diatoms) the growth term is

$$\mu_d = \mu_d^{max} \cdot U_d(N, Si) \cdot L_d(PAR) \cdot T_d(SST) \quad (2.2)$$

where μ_d is the maximum growth rate per day and $T(PAR)$ is Eppleys formulation for temperature dependent growth (Eppley, 1972), given as $T(SST) = e^{0.063*SST}$ with temperature in $^{\circ}C$. The light-limiting term $L(PAR)$ represents the integrated photosynthesis within the mixed layer as a function of incident irradiance at the surface I_0 . Light attenuation is calculated using the Lambert-Beer law with irradiance at depth z equal to

$$I(z) = I_0 \cdot e^{-k_{PAR} \cdot z} \quad (2.3)$$

Here, k_{PAR} is calculated as the sum of the constant attenuation coefficient of water k_w and the self-shading of phytoplankton k_c with the unit μM^{-1} multiplied by total phytoplankton biomass P , i.e. $k_{PAR} = k_w + k_c P$. This model uses the Smith PI curve as a basis for the calculation, with V_p representing the photosynthetic rate, α , the initial slope of the PI curve and V_p^{Max} , the maximum photosynthetic rate

$$V_p = \frac{\alpha \cdot I \cdot V_p^{Max}}{\sqrt{(V_p^{Max})^2 + \alpha^2 \cdot I^2}} \quad (2.4)$$

Combining equation (2) and (3) as presented in Anderson et al. (2015), the integrated photosynthesis \bar{V}_p over depth z is calculated as

$$\bar{V}_p(z) = \frac{V_p^{Max}}{k_{PAR} \cdot z} \cdot \ln \left(\frac{\alpha \cdot I_0 + \sqrt{(V_p^{Max})^2 + (\alpha \cdot I_0)^2}}{\alpha \cdot I(z) + \sqrt{(V_p^{Max})^2 + (\alpha \cdot I(z))^2}} \right) \quad (2.5)$$

where \bar{V}_p equals the light-limiting term L in the growth equation (2).

Nutrient limited growth of the phytoplankton community is described via a Monod equa-

tion.

$$U(N) = \frac{N}{k_N + N} \quad (2.6)$$

For diatoms P_d the nutrient limiting term depends on both nitrogen and silicate concentration within the upper layer. According to Liebig's law of the minimum, always the lower nutrient availability limits Diatom growth:

$$U_d(N, Si) = \min\left(\frac{N}{k_d^N + N}, \frac{Si}{k_d^{Si} + Si}\right) \quad (2.7)$$

All other phytoplankton types are nutrient-limited only by available Nitrogen as in equation (6). Phytoplankton mortality and excretion are parameterized as a linear constant rate mo . With G_μ as grazing by Microzooplankton and G_λ as grazing by Mesozooplankton (defined below), the equations for all phytoplankton types P_i can now be written as

$$\frac{dP_i}{dt} = \mu_i \cdot P_i - mo_i \cdot P - G_\mu(P_i) - G_\lambda(P_i) - \kappa \cdot P_i \quad (2.8)$$

A1.3 Zooplankton

Two zooplankton types are resolved in the model according to size-class, Microzooplankton Z_μ and Mesozooplankton Z_λ . Following Anderson et al. (2015) the grazing of, for example, Z_λ on diatoms P_d is formulated as follows

$$G_\lambda(P_d) = \left(\frac{\mu_\lambda^Z \cdot \phi_d^\lambda \cdot P_d}{(k_\lambda^Z)^2 + \phi_d^\lambda \cdot P_d + \phi_c^\lambda \cdot P_c + \phi_{df}^\lambda \cdot P_{df} + \phi_n^\lambda \cdot P_n + \phi_\mu^\lambda \cdot Z_\mu} \right) \cdot Z_\lambda \quad (2.9)$$

$$\phi_d^\lambda = \rho_d^\lambda P_d, \phi_c^\lambda = \rho_c^\lambda P_c, \phi_{df}^\lambda = \rho_{df}^\lambda P_{df}, \phi_n^\lambda = \rho_n^\lambda P_n, \phi_\mu^\lambda = \rho_\mu^\lambda Z_\mu$$

with μ_λ^Z as the maximum grazing rate, k_λ^Z as the half saturation constant of grazing, ϕ_d^λ as the density dependent feeding preference of Z_λ feeding on P_d , defined as $\rho_d \cdot P_d$, with ρ_d^λ as the feeding preference coefficient.

A1.x Solving method

The system of differential equations was solved numerically using the fourth-order Runge-Kutta method in the `odeint` function of the `scipy` package in python 3.7.

Physical forcing is interpolated ... Taken from the regimes ... etc.

Full System of equations

$$\begin{aligned}
\frac{\partial N}{\partial t} &= \kappa \cdot (N_0 - N) + \delta_D^N \cdot D - \sum_{i=1}^{n_P} [\mu_i \cdot U_i(N_0, Si_0) \cdot L_i(PAR) \cdot T_i(SST) \cdot P_i] \\
\frac{\partial Si}{\partial t} &= \kappa \cdot (Si_0 - Si) - \mu_{dt} \cdot U_{dt}(N_0, Si_0) \cdot L_{dt}(PAR) \cdot T_{dt}(SST) \cdot P_{dt} \\
\frac{\partial P_i}{\partial t} &= \mu_i \cdot U_i(N_0, Si_0) \cdot L_i(PAR) \cdot T_i(SST) \cdot P_i - m_i \cdot P_i - \sum_{j=1}^{n_Z} [I_j^{tot} \frac{p_j^i \cdot P_i}{R_j} Z_j] - \frac{v}{M(t)} \cdot P_i - \kappa \cdot P_i \\
\frac{\partial Z_\mu}{\partial t} &= \delta_Z \cdot I_\mu^{tot} \cdot Z_\mu - \mu_\lambda \frac{Z_\mu}{Z_\mu + k_\lambda} Z_\lambda - \kappa_Z \cdot Z_\mu - m_\mu \cdot Z_\mu - g_\mu \cdot Z_\mu^2 \\
\frac{\partial Z_\lambda}{\partial t} &= \delta_Z \cdot I_\lambda^{tot} \cdot Z_\lambda + \delta_\lambda \cdot \mu_\lambda \frac{Z_\mu}{Z_\mu + k_\lambda} Z_\lambda - \kappa_Z \cdot Z_\lambda - m_\lambda \cdot Z_\lambda - g_\lambda \cdot Z_\lambda^2 \\
\frac{\partial D}{\partial t} &= \sum_{j=1}^{n_Z} [(1 - \delta_Z) I_j^{tot} \cdot Z_j] + (1 - \delta_\lambda) \cdot \mu_\lambda \frac{Z_\mu}{Z_\mu + k_\lambda} Z_\lambda - \sum_{j=1}^{n_Z} [m_j \cdot Z_j] + \sum_{i=1}^{n_P} [m_i \cdot P_i] - \kappa \cdot D - \delta_D^N \cdot D
\end{aligned}$$

where:

N_0 = Nitrogen concentration right below mixed layer [μM],

N = Nitrogen concentration above mixed layer [μM],

v = sinking rate of P_i [$m day^{-1}$],

$M(t)$ = mixed layer depth at time point t [m],

$\kappa = \frac{1}{M(t)} \cdot (h^+(t) + \kappa)$ Constant that parameterizes diffusive mixing across the thermocline,

$h^+(t) = \max(0, \frac{d}{dt} M(t))$ Function that describes entrainment and detrainment of material,

δ_D^N = Remineralization rate of nitrogen component of detritus D [$\mu M d^{-1}$],

μ_i = Growth rate of phytoplankton type i [d^{-1}],

$$U_i = \begin{cases} \min \left(\frac{N}{N+U_i^N}, \frac{Si}{Si+U_i^{Si}} \right), & \text{if P-type is Diatom} \\ \frac{N}{N+U_i^N}, & \text{otherwise} \end{cases} \quad \text{Nutrient uptake of phytoplankton } i,$$

$$L_i = \frac{1}{M(t) \cdot k_w} \cdot \left(e^{1 - \frac{PAR(t)}{Opt_i^L}} + e^{1 - \frac{PAR(t) \cdot e^{-M(t) \cdot k_w}}{Opt_i^L}} \right) \quad \text{Light dependence of phytoplankton } i,$$

$T_i = e^{0.063 \cdot SST}$ Temperature dependence of phytoplankton i ,

P_i = Biomass of phytoplankton type i [μMN],

m_i = Mortality/excretion rate for phytoplankton type i ,

$I_j^{tot} = \mu_j^Z \cdot \frac{R_j}{R_j + k_j^Z}$ Total intake of zooplankton type j ,

k_j^Z = Half saturation constant of zooplankton type j ,

$R_j = \sum_i (p_{ij} \cdot P_i)$ Total ressource density of zooplankton type j ,

p_j^i = Feeding preference of zooplankton type j feeding on phytoplankton type i ,

$R_\mu = p_\mu^n \cdot P_n + p_\mu^{dn} \cdot P_{dn} + p_\mu^c \cdot P_c$ Total ressource density of Mikrozooplankton Z_μ ,

$R_\lambda = p_\lambda^{dt} \cdot P_{dt} + p_\lambda^{dn} \cdot P_{dn} + p_\lambda^c \cdot P_c$ Total ressource density of Mesozooplankton Z_λ ,

Z_j = Biomass of zooplankton type j [μMN],

δ_Z = Grazing efficiency of zooplankton on phytoplankton (represents sloppy feeding),

$K_Z = \frac{1}{M(t)} \cdot \frac{d}{dt} M(t)$ Mixing term of zooplankton,

g_i = Higher order predation on zooplankton (quadratic),

m_j = Mortality/excretion rate for zooplankton type j ,

PhytoMFTM model parameters (preliminary)

symbol	variable	description	units	value	source
Physical parameters:					
κ	kappa	diffusive mixing constant	[m day ⁻¹]	0.1/0.01	[Fasham]
δ_D^N	deltaD_N	remineralization rate	[day ⁻¹]	0.05	[Fasham]
k_w	kw	light attenuation coefficient	[m ⁻¹]	0.2	[Edwards]
affecting phytoplankton:					
v	v	phytoplankton sinking constant	[m day ⁻¹]	0.04	[Edwards]
I_{opt}	OptI	optimum irradiance	[E m ⁻² day ⁻¹]	30	[Aevelard]
Phytoplankton parameters:					
m_{oP}	moP	mortality/excretion constant	[day ⁻¹]	0.09	[Fasham]
functional type specific:					
P_{dt}	pt1	Diatoms			
Δ_{Si}^{dt}	pt1_ratioSi	nitrogen to silicate ratio	[μMSi μMN ⁻¹]	1.12	[Brzezinski]
K_{Si}^{dt}	pt1_K_Si	half-saturation constant of Si uptake	[μMSi]	2	[Kristoffersson]
U_N^{dt}	pt1_U_N	half-saturation constant of N uptake	[μMN]	0.446	[Litchfield]
μ_P^{dt}	pt1_muP	growth rate	[day ⁻¹]	1.5	[Litchfield]
P_c	pt2	Coccolithophores			
U_N^c	pt2_U_N	half-saturation constant of N uptake	[μMN]	0.265	[Litchfield]
μ_P^c	pt2_muP	growth rate	[day ⁻¹]	1.1	[Litchfield]
P_{dn}	pt3	Dinoflagellates			
U_N^c	pt3_U_N	half-saturation constant of N uptake	[μMN]	0.009	[Litchfield]
μ_P^c	pt3_muP	growth rate	[day ⁻¹]	0.6	[Litchfield]
P_n	pt4	Nanoflagellates			
U_N^n	pt4_U_N	half-saturation constant of N uptake	[μMN]	0.045	[Litchfield]
μ_P^n	pt4_muP	growth rate	[day ⁻¹]	1.7	[Litchfield]
Zooplankton parameters:					
mo_Z	moZ	mortality/excretion constant	[day ⁻¹]	0.0125	[Prowe]
δ_Z	deltaZ	assimilation coefficient of grazing on P_i	[\cdot]	0.75	[Fasham]
δ_λ	deltaLambda	assimilation coefficient of Z_λ grazing on Z_μ	[\cdot]	0.75	[Fasham]
μ_λ	mulntGraze	maximum rate of Z_λ grazing on Z_μ	[day ⁻¹]	0.05	[?]
k_λ	kIntGraze	half-saturation constant of Z_λ grazing on Z_μ	[μMN]	0.5	[?]
Z_μ	zt1	Mikrozooplankton			
μ_Z^μ	zt1_muZ	maximum rate of grazing on P_i	[day ⁻¹]	0.1	[Prowe]
k_P^μ	zt1_Kp	half-saturation constant of grazing on P_i	[μMN]	0.5	[Prowe]

Feeding preferences:

	P_{dt}	P_c	P_{dn}	P_n
Z_μ	0	1	1	1
Z_λ	1	1	1	0

where number is p_j^i denoting feeding preference of Z_j grazing on P_i

End Methods here

2.3 Preliminary Results

SHOW PROPER RUN, With Biotic components fitting the base run comparatively well, try it!

XXXX (Figure 4.2).

kkkkkkkkkkkkkkkkkkkkkkkk here the results start, at least the text of it

°C°%°C°%°C°%°C°%

get it, get it

3. PhytoMFTM - a flexible object-oriented PFT model

This is the work towards the second manuscript, to be submitted to Geoscientific Model Development (GMD)

3.1 Python ecosystem model package development

General intro sentence"

Tao of open science for ecology: (Hampton et al. 2015) the concept of transparency at all stages of the scientific process

Important role of bioinformatics in ecology, as an ever evolving discipling: (Michener & Jones 2012)

A number of general-purpose simulation toolkits are in use today, in the form of specialized programming languages (Fritzson and Engelson, URL), software libraries (Fishwick, 1995, Minar et al., 1996, Lorek and Sonneschein, 1998) or pre-packaged models that a flexible parameter choice makes suitable to represent a large number of situations within a particular field (e.g. Klenner et al., 1997). Also, various simulation interoperability ‘blackboards’ have been developed over the last few years. Examples are FRAMES (PNNL, URL), DIAS (ANL, URL), HLA (DMSO, URL), MMS (Leavesley and Restepo, 1995). While many of these solutions have been successful in a restricted field, the lack of a strong and general declarative framework (along with platform dependency and often awkward installation and use) has made them unsuitable for

easy and general adoption by a wide modelling community. In comparison, a few highly successful and widely used simulation tools (Stella: HPS, 1995, Costanza et al., 1998; Powersim: Powersim Co., URL) have privileged the ease of use of well-developed graphical interfaces, at the cost of restricting their application to the limits imposed by the interface itself and the adoption of a single modelling paradigm. In most modern science, application of such tools is usually limited to prototyping, as they are unsuitable for large-scale simulation and model integration. (Villa 2001) - this is the quote above

why would this be interesting to anyone else

movement towards open source programming languages

As funding agencies embrace open science principles that encourage sharing data and computer code developed to produce research outputs, we must respond with new modes of publication.

Open Source, Open Access, Open Science! comparability

!!!!cite a nice pushing for this publication here!!!!

Necessity of standardisation of methods and open publishing of data and models: (Reichman et al. 2011) Focus on sharing data openly, but just as important is publishing of statistical scripts and actual model code

This only makes sense if model code is understandable to the average ecosystem modeler, need to use a widely available, standardized programming language: PYTHON programming language of the future for earth sciences (Lin 2012)

also well documented open source packages can play an important role in teaching computational literacy to university students (Farrell & Carey 2018)

teach PhD Students from the ground up to code their own models in Python, as of yet there is a lack of coherent ressources. Definitely cite the PhytoMFTM model and publication (?)

extensible framework bb

XXX

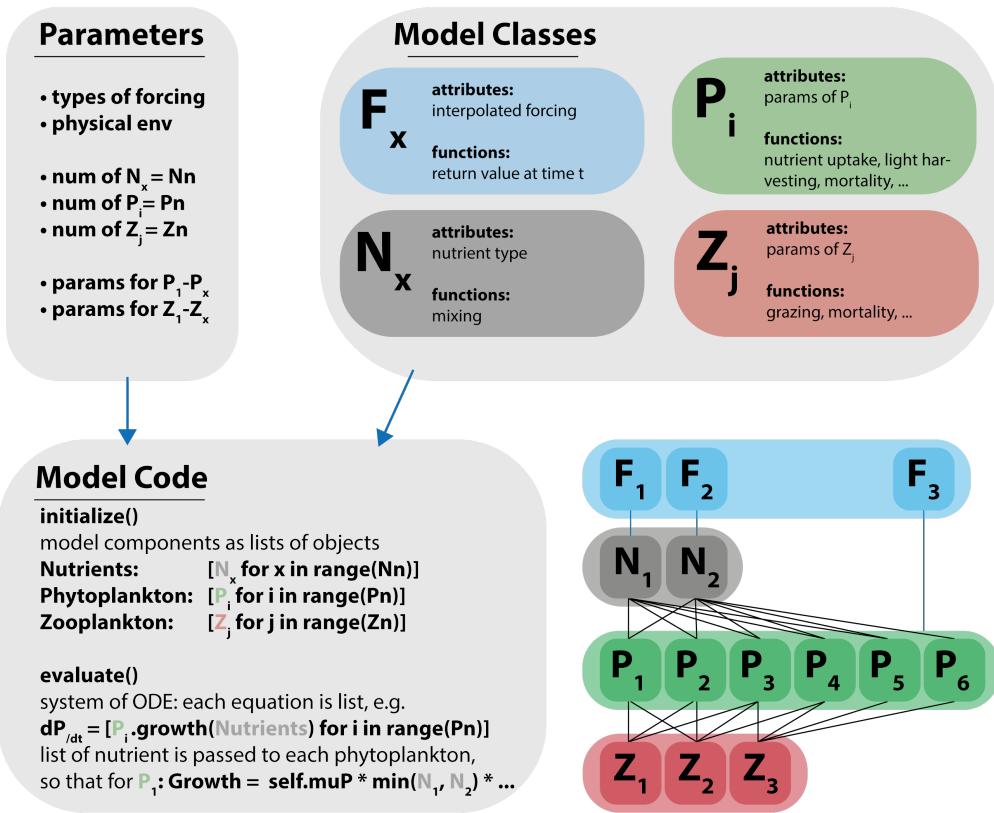


Figure 3.1: Schematic of code structure for PhytoMFTM model. Square brackets ("[]") denote a list object in Python, "for i in range(x)" within brackets creates list of length x of whatever comes before. Model classes are used to store both the parameters associated with each instance, e.g. different nutrient uptake parameters for PFTs and the functions that are used within the ODE. Each equation is also a list structure that calls every instance of the required objects using list comprehensions, so that all interactions are calculated according to the number of model components that were initialized in the parameters.

3.2 Methods

Object-oriented structure

Explain Code structure, with some nice graphicx XXX

```

XXXXXX xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx
xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx xxxxxxxx
xxxxxx xxxxxxxx xxxxxxxx xxxxxxxx xxxx xxxx x

```

Model formulation and usage

xXXX

explain how to run the model!

XXXX

XXXX

XXX

End Methods here

4. Further work

4.1 Where to go from here

4.1.1 How to complete project 1

XXXXXXX

essentially just check model physics again, and then create nice runs, and then go and test the hypotheses, like so and so and so.. XXXXXX

X

XXX

4.1.2 How to complete project 2

Just say that this model was the basis for the previous chapter work, and will be for the rest of my PhD, a toolkit for testing ideas with multiple functional types! go towards selection-based models, like DARWIN and how they allow to change the biodiversity explicitly, to test hypothesis

4.2 BDEF - Project No 3

HERE I should cite the Tilman and Ptacnik Papers that Esteban recommended, talk about how Biodiversity influences resource use efficiency

ALSO BDEF MODEL BY LOREAU: (Loreau 1998)

And then say how the model I am building is actually very well equipped to deal with this kind of

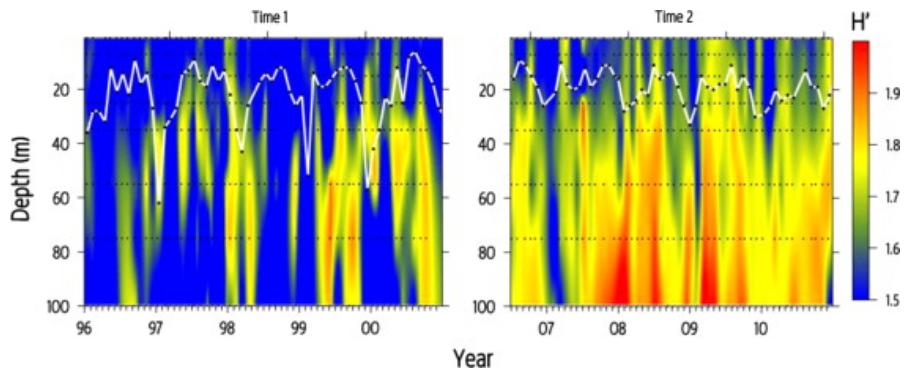
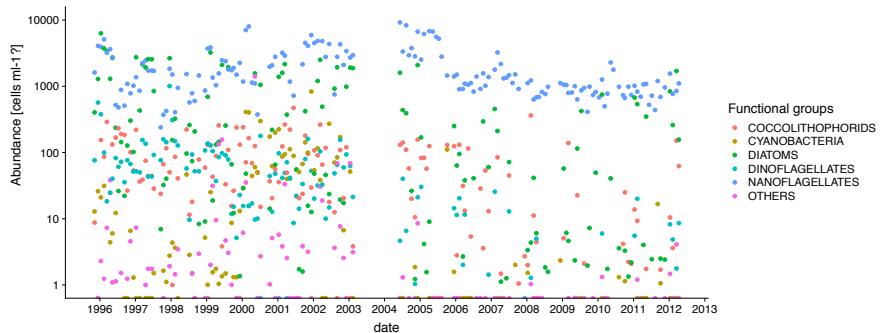


Fig. 5. "Time series contour plot of photopigment diversity index (H). Data points are indicated by dots on the plot and the white line shows the mixed layer depth." from Pinckney et al. (2015)



XXXXX

4.2.1 Method

XXXX

Again talk shortly about how biodiversity means ecosystem resilience (kinda) and how climate change and anthropogenic stressors will test, if not break the boundaries of the ecosystem resilience. We are still trying to understand the basic connections between the

main organisms and functional types in the ocean. Such that we can only guess at what steady state lies behind the boundary, but perhaps we should better never find out.

XXXXX

XXXX

XXXX

4.3 Time table

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
2011		Literature review		AMT data mining		Manuscript writing		Ph.D. proposal	Manuscript writing	Develop size-based model		
2012	Develop size-based model		Sensitivity analysis		Manuscript writing		Develop a coupled phytoplankton and zooplankton size-based model					
2013	Sensitivity analysis		Manuscript writing		Develop phytoplankton size-based evolutionary model		Sensitivity analysis	Manuscript writing				
2014	Manuscript writing	Ph.D. defense										

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Figure 4.1: The AMT subset of 410 samples used in this study. The dashed lines represent the simplified limits of the Longhurst (2006) ecological provinces.

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$$\frac{dP}{dt} = \left[r(\bar{s}) + \frac{1}{2}v \frac{\partial^2 r(\bar{s})}{\partial s^2} \right] P$$

$$\frac{d\bar{s}}{dt} = v \frac{\partial r(\bar{s})}{\partial s}$$

$$\frac{dv}{dt} = v^2 \frac{\partial^2 r(\bar{s})}{\partial s^2}$$

The approach of defining a trade-off that relates size to the competitive ability for nutrient

Figure 4.2: Phytoplankton community size structure of four ecological provinces in the Atlantic Ocean. The contours correspond to the convex hull of the size-fraction distribution of each province. The symbols indicate the corresponding mean values.

Figure 4.3: Relative mean abundances (\pm sd) of three phytoplankton size fractions of ten ecological provinces of the Atlantic Ocean. The symbols indicate the mean values of the normalized size fractions: picoplankton (●), nanoplankton(■) and microplankton (▲).

a) b)

Figure 4.4: Caption comes here my friend"////////".

Table 4.1: Mean values of environmental parameters for the different clusters: High temperature - Low nutrients (HTLN), Mid temperature - Low nutrients (MTLN), Mid temperature - High nutrients (MTHN) and Low temperature - High nutrients (LTHN).

cluster	$\text{NO}_2^- + \text{NO}_3^-$	PO_4^{3-}	SiO_4^{2-}	Temperature
HTLN	0.150 ± 0.575	0.064 ± 0.078	1.097 ± 0.575	25.299 ± 2.000
MTLN	0.556 ± 1.102	0.112 ± 0.141	0.816 ± 0.617	17.894 ± 2.191
MTHN	9.027 ± 3.593	0.799 ± 0.373	2.423 ± 1.375	11.925 ± 2.797
LTHN	30.324 ± 4.549	1.336 ± 0.208	4.590 ± 1.926	6.810 ± 3.435

acquisition and resistance to predation (Merico et al. 2009) leads to mechanistically capture bottom-up (nutrient availability and acquisition capabilities) versus top-down (avoid grazing) processes, major shaping forces of a phytoplankton community. The model will be tested against and constrained by the AMT observations on environmental data and community size structures in the Atlantic Ocean (chapter 2).

Smaller phytoplankton cell sizes have a competitive advantage over larger phytoplankton under low nutrient, low light and low grazing pressure (Litchman & Klausmeier 2008; ?). From our regression analyses (Figures 4.6 and 4.7) we inferred a strong control of $\text{NO}_3^- + \text{NO}_2^-$ and temperature on all three size fractions. Pico- and nanoplankton size fractions, however, appeared more sensitive to changes in PO_4^{3-} , SiO_4^{2-} and copepod abundance. We propose that these effects are caused by a trade-off between resource acquisition and predation pres-

Figure 4.5: Principal Component Analysis of environmental parameters and normalized phytoplankton size fractions.

Table 4.2: Summary statistics for linear fittings of the three size fractions to each environmental variable.

	Picoplankton			Nanoplankton			Microplankton		
	slope	p-value	r^2	slope	p-value	r^2	slope	p-value	r^2
$\text{NO}_2^- + \text{NO}_3^-$	-0.090	0.002	0.908	0.050	0.001	0.921	0.040	0.010	0.792
PO_4^{3-}	-0.0812	0.021	0.711	0.042	0.012	0.777	0.039	0.125	0.354
SiO_4^{2-}	-0.047	0.085	0.455	0.030	0.044	0.597	0.016	0.247	0.142
Temperature	0.082	0.001	0.914	-0.047	0.008	0.812	-0.035	0.003	0.885
Copepods	-0.063	0.064	0.520	0.068	0.051	0.567	-0.004	0.788	-0.222

a)

b)

c)

d)

Figure 4.6: Relative composition of picoplankton, nanoplankton and microplankton size fractions changing with concentrations of nitrate+nitrite (a), phosphate (b), and silicate (c) and with temperature (d). The bars represent mean values and the error bars indicate the standard deviation.

Figure 4.7: Relative composition of picoplankton, nanoplankton and microplankton size fractions changing with copepod abundance. The bars represent mean values and the error bars indicate the standard deviation.

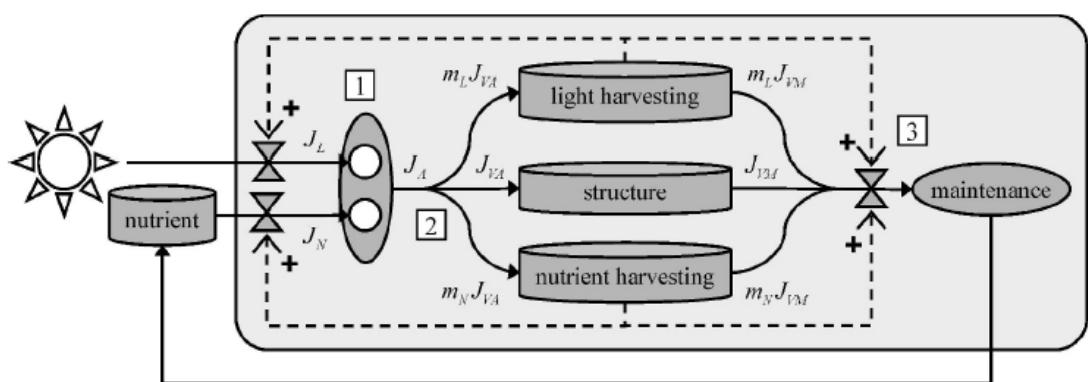


Figure 4.8: Bruggeman and Kooijman model scheme. Taken from ?

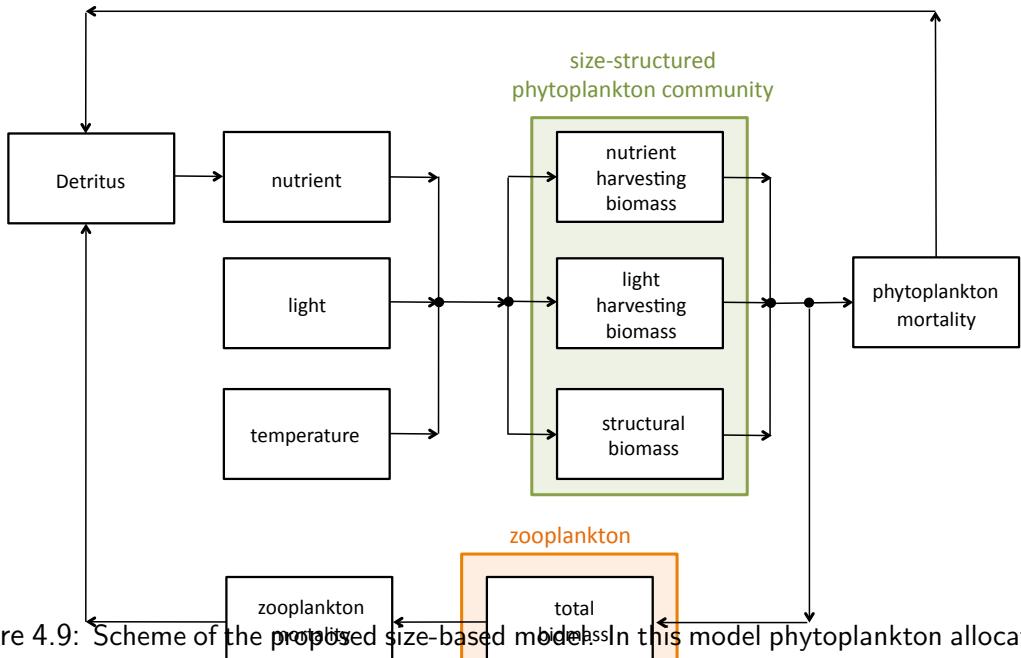


Figure 4.9: Scheme of the proposed size-based model. In this model phytoplankton allocates energy (or biomass) to different pools such as nutrient and light harvesting biomasses and generic structural biomass. A certain fraction of the phytoplankton biomass flows into the zooplankton biomass and a remaining fraction is remineralized into the nutrient pool

sure, although with the caveat represented by the paucity of the zooplankton data and by the qualitative value we attribute to zooplankton abundance as an indication of grazing pressure. There are a number of important physiological and ecological processes that strongly depend on phytoplankton cell size (??), including metabolic rates, maximum nutrient uptake rate, nutrient diffusion, light absorption, sinking velocity, trophic interactions and even diversity within taxa, which is often a log-normal distribution of body size. Our results are therefore consistent with this general "size rule" (?). To our knowledge it is the first time that this feature is observed in data extending across an entire ocean basin and irrespective of temporal changes.

The resulting, full size-based model will be approximated with a simpler model of aggregate macroscopic properties using the moment closure approximation proposed by ?? and further refined by ?Merico et al. (2009). The phytoplankton total biomass (P), the mean trait (\bar{s}), and the trait variance (v) will be formulated as follows:

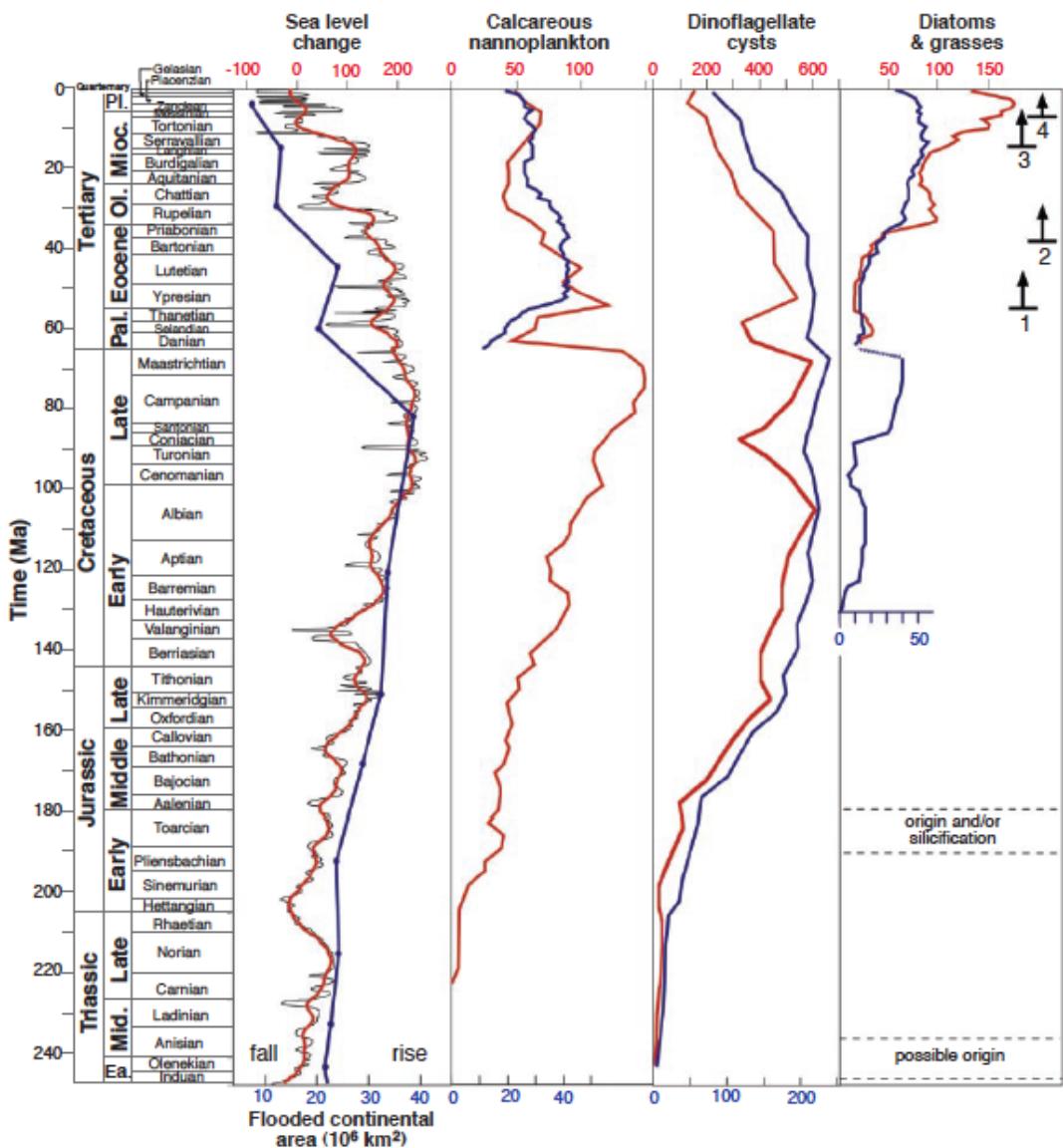


Figure 4.10: Comparison of major phytoplankton groups with sea-level change. The red line accounts for species diversities from published studies. The blue line accounts for the genus diversity compiled from public databases by the authors. Taken from Falkowski et al. (2004).