



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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August 10, 2019

## 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 backitup
- computational models are the way to synthesizze 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. (cite FALKOWSKI?) The distribution of phytoplankton is driven by the complex physical and chemical boundary conditions that govern ocean currents and upwelling systems, with the key component being macronutrients (e.g. nitrogen & phosphorus) and micronutrients (e.g. iron & cobalt) brought up from the deep ocean or flushed in through river estuaries.

Wherever there are plenty of nutrients and light, planktonic life begins to thrive. The biomass produced 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). This newly generated biomass is mostly consumed and either assimilated or regenerated within the euphotic zone, fueling regenerated produc-

tion (Eppley & Peterson 1979). 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 ( 1%) and remains there over geological times (Honjo et al. 2008). Carbon sequestered this way is removed from the ocean-atmosphere system for potentially millions of years. Given the projected rise of atmospheric CO<sub>2</sub> levels, it is of great importance to better understand this process, termed the biological carbon pump. In particular to grasp how changes in the planktonic community driven by anthropogenic stressors will affect it in the future.

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"Phytoplankton is important. Phytoplankton is diverse.

"it is amazing how little we actually know about phytoplankton globally and the effects that it has on biogeochemical cycles, and how it is affected by global change for example "quite a few publications using models go too far in their extrapolations, whilst the general discussion still strongly revolves around meaningful model structures.. but no consensus is anywhere to be seen! "need to identify the basic uncertainties and see if there is a way to discuss them scientifically "Michaelis Menten kinetics are really outdated.. and i suppose using them in a trait-based modelling approach is questionable just the same "plankton ecosystems are typically highly aggregated, a single variable gives the response of an incredibly diverse assemblage of phytoplankton species (P. Franks, 2009)

## 1.2 Characterizing phytoplankton

How did Researchers start dealing with Phytoplankton?

Two approaches to isolate strains, or take bulk properties

Obviously bulk properties also have to be taken from specific depth

so this adds the problem of the complexity of the physical environment that is the ocean, with enormous volume, turbulence/mixing, diffusion and absorbance

I want to look at phytoplankton diversity, particularly from a functional type point

of view. Quantify diversity as it relates to ecosystem function (as production for example).

XXX

"Phytoplankton can be characterised by many morphological, physiological, behavioural and life history traits and trade-offs (??).

"Studies on the phytoplankton community composition and their response to the environmental gradients are not novel. Ramón Margalef was probably one of the first ecologist to give an important momentum to the topic. (?) used observations of key traits, such as nutrient utilization and sinking rates, to support his well known concept called "Margalef's mandala". His classification of phytoplankton functional types (PFTs) at different nutrient and turbulent environmental conditions represents an excellent first example of how the trait-based notion can be applied to better understand phytoplankton community ecology, therefore setting up the stage for further developments in the field.

### 1.2.1 Functional types and traits

"Ecology has traditionally focused on species diversity as a way of characterizing the health of an ecosystem. In recent years, however, the focus has increasingly shifted towards trait diversity both within and across species" - from Functional Diversity Book

We have incredibly diverse Phytoplankton, and want to analyze traits and model - $j$  need to simplify somehow  $=j$  Functional Types

so I want to talk about: that phytoplankton can be divided in functional groups talk about the Work that Finkel and Irwin have done! question whether it makes sense to use functional types instead of species, ... 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)

XXXX

XXXX

XXXX

## 1.3 Modeling phytoplankton communities

Going into the details is necessary to understand the whole picture

One tool of integration are mathematical models

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 understand the full-scale implications.

Computational models of phytoplankton growth have been developed since the 1970s and have greatly increased in sophistication and complexity since then, co-evolving with the rise in computational resources. Ecosystem modelling started with simple box-model descriptions of a few trophic levels. These were the nutrient-phytoplankton-zooplankton (NPZ) and nutrient-phytoplankton-zooplankton-detritus (NPZD) models, which succeeded in reproducing the basic bloom dynamics observed in the temperate ocean (Evans 1988, Fasham et al. 1990). However, in their generalistic approach, these models unavoidably limit the characterization of a diverse phytoplankton community (Bruggeman 2009). To make up for this shortcoming, in the following two decades, these models were expanded to more complex plankton functional type (PFT) models (Le Quere et al. 2005).

For every group of species that fulfill a distinct ecosystem function, a new set of parameters was added, complicating the model structure and massively prolonging calculations. This somewhat intuitive approach of having every functional group represented in a model, however, did create 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 (Shimoda et al. 2016). Trait-based modeling, on the other side, tries to circumvent the problem of biodiversity (i.e. complexity) in natural systems with a radically different approach. The interactions of phytoplankton with their environment

are based on multiple traits which characterize generalized physiological properties like nutrient affinities or motility. Ideally, these traits can be directly measured and are independent of species and therefore they can be directly related to the properties of the organisms function within the ecosystem, such as nutrient affinity for example ideally, these traits can be directly measured and are independent of species and therefore they can be directly related to the properties of the organisms function within the ecosystem, such as nutrient affinity for example (Litchman and Klausmeier 2008).

A simple example of a trait-based description of phytoplankton succession is scaling the maximal nutrient acquisition rate and the respective affinity with cell size. A trade-off would emerge between different size classes, allowing for a modeled succession along gradients of nutrient depletion. One example of a very similar approach is the PhytoSFDM model developed by Acevedo-Trejos and colleagues (Acevedo-Trejos et al. 2013, Acevedo-Trejos et al. 2015). In their approach, the trait-based modelling of phytoplankton is even further simplified, by describing an entire community as a size-distribution with a mean value and a variance, instead of modeling all the different size classes explicitly. This moment-based structure further simplifies the mathematical basis of the model, and leads to much faster processing times and less uncertainty in parameter estimation.

"The study of phytoplankton community structure, also promoted by the work of ?, is therefore very relevant in marine ecology and is especially important for understanding how phytoplankton will respond to a changing climate and with which consequences.

XXX

XXX

XXX

XXX.

XXX

XXX

ALWAYS NEED A GOOD BASIS IN DATA TO VALIDATE MODELS AND HY-



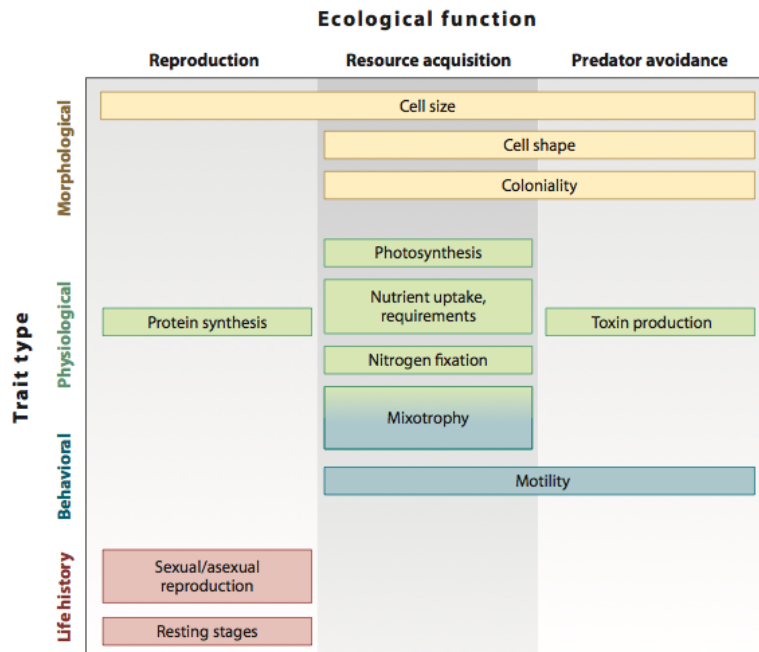


Figure 1.1: Phytoplankton functional traits. Taken from ?

POTHESES

## 1.4 The Cariaco basin & the CARIACO time series

"continental margins constitute only about 10% of the total ocean surface area, these regions are responsible for about 10–15% of the global marine primary production and greater than 40% of seabed carbon sequestration (Yool and Fasham, 2001; Muller-Karger et al., 2005). "The Cariaco Basin, located off the coast of Venezuela, has been the site of high frequency water column sampling for marine biogeochemical and ecological observations since 1995. The observations were collected as part of the Cariaco Ocean Time-Series Program (Muller-Karger et al., 2001; Thunell et al., 2007).

XXXX

XXXX

XXX

THEN TALK ABOUT THE COLLAB/DATASHARE 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**

### **2.1 Regime Shift in CARIACO data**

General intro sentence" For decades ecologists have been trying to understand how the structure of phytoplankton communities is associated to the environmental conditions, with a particular focus on the causes and consequences of natural variation.

Something about identifying and modeling regime shifts

Talk about the data again

This will be a first! first proper ecological model apart from this Export Flux model only including diatoms (Walsh et al., 2002)

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... 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

## 2.2 Methods

dont really go into depth here, just generally state how things are done, python, odeint, system of ODEs

XXXX

### 2.2.1 Model physics in a tropical coastal setting

xXXX

Most models built for temperate oceans, since that is where reasearch (and funding) has been most well developed. Fasham NPZD type slabe 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.

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

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

## 2.4 How to complete this project

XXXXXXXX

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

X

XXX

### **3. PhytoMFTM - a flexible object-oriented PFT model**

#### **3.1 Python ecosystem model package development**

General intro sentence"

why would this be interesting to anyone else

movement towards open source programming languages

Open Source, Open Access, Open Science! comparability

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

## **3.2 Methods**

### **3.2.1 Object-oriented structure**

Explain Code structure, with some nice graphicx XXX

XXXX

### **3.2.2 Model formulation and usage**

xXXX

explain how to run the model!

XXXX

XXXX

XXX

End Methods here

## **3.3 How to complete this project**

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 the allow to change the biodiversity explicitly, to test hypothesis

## **4. Further work**

### **4.1 Where to go from here**

#### **4.1.1 BDEF**

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

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

XXXXX

#### **4.1.2 Method**

XXXX

### **4.2 Relevance**

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										

## Bibliography

Walsh JJ, Dieterle DA, Müller-Karger FE, Bohrer R, Bissett WP, Varela RJ, Aparicio R, Díaz R, Thunell R, Taylor GT, Scranton MI, Fanning KA, Peltzer ET (2002) Simulation of carbon-nitrogen cycling during spring upwelling in the Cariaco Basin. *Journal of Geophysical Research: Oceans* 104(C4):7807–7825

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

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

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

The approach of defining a trade-off that relates size to the competitive ability for nutrient acquisition and resistance to predation (?) 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 (??). From our regression analyses (Figures 4.6 and 4.7) we inferred a strong control of  $\text{NO}_3^- + \text{NO}_2^-$  and

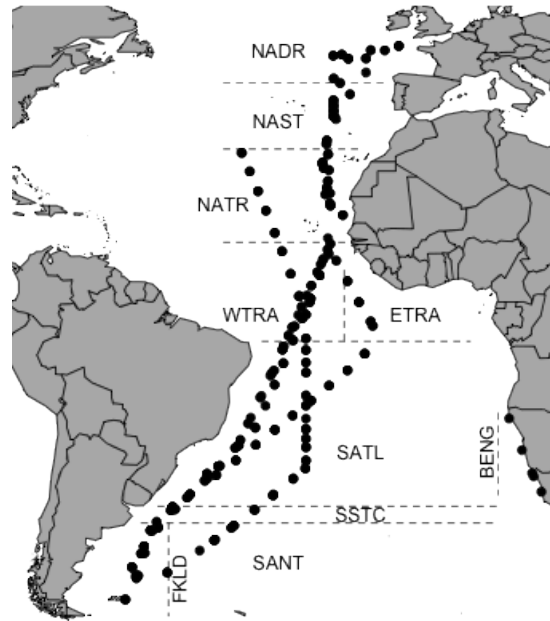


Figure 4.1: The AMT subset of 410 samples used in this study. The dashed lines represent the simplified limits of the Longhurst (2006) ecological provinces.

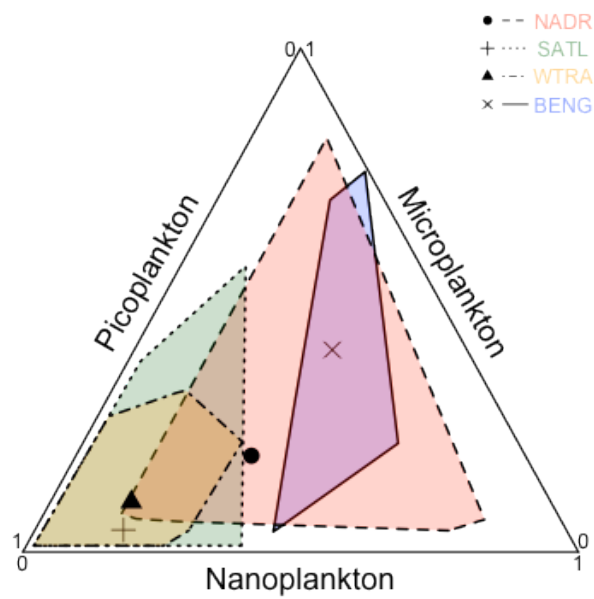


Figure 4.2: Phytoplankton community size structure of four ecological provinces in the Atlantic Ocean. The contours correspond to the convex hull of the size-fraction distribution of each province. The symbols indicate the corresponding mean values.

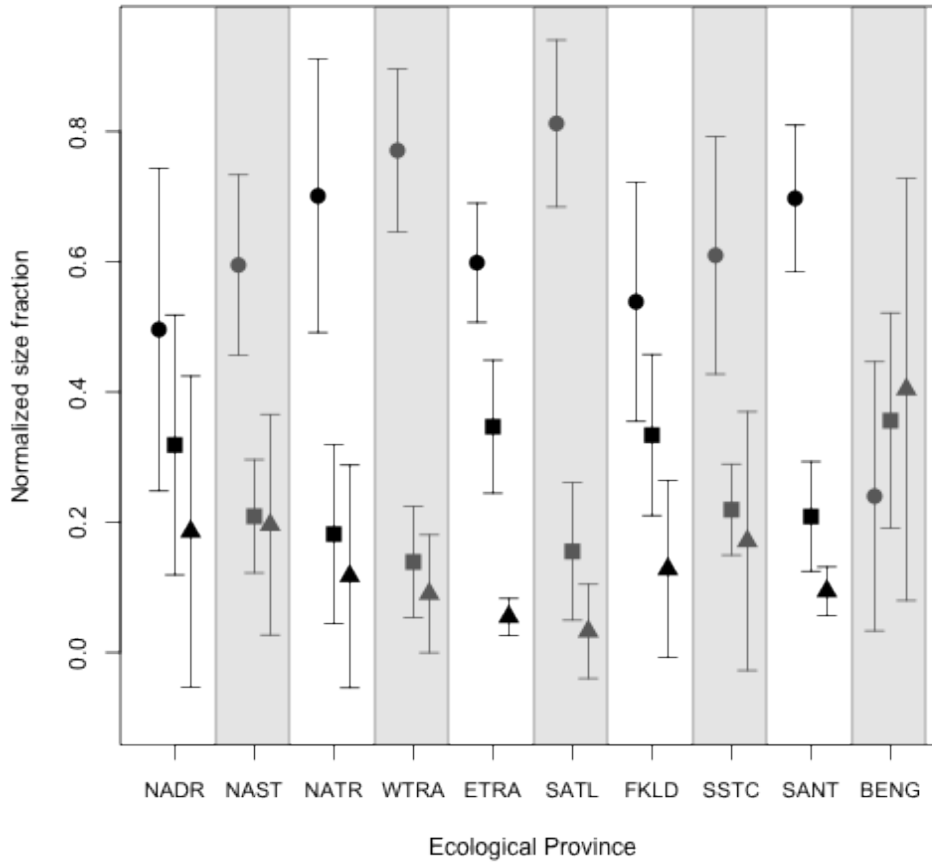


Figure 4.3: Relative mean abundances ( $\pm$ sd) of three phytoplankton size fractions of ten ecological provinces of the Atlantic Ocean. The symbols indicate the mean values of the normalized size fractions: picoplankton (●), nanoplankton(■) and microplankton (▲).

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	$\text{NO}_2^- + \text{NO}_3^-$	$\text{PO}_4^{3-}$	$\text{SiO}_4^{2-}$	Temperature
HTLN	$0.150 \pm 0.575$	$0.064 \pm 0.078$	$1.097 \pm 0.575$	$25.299 \pm 2.000$
MTLN	$0.556 \pm 1.102$	$0.112 \pm 0.141$	$0.816 \pm 0.617$	$17.894 \pm 2.191$
MTHN	$9.027 \pm 3.593$	$0.799 \pm 0.373$	$2.423 \pm 1.375$	$11.925 \pm 2.797$
LTHN	$30.324 \pm 4.549$	$1.336 \pm 0.208$	$4.590 \pm 1.926$	$6.810 \pm 3.435$

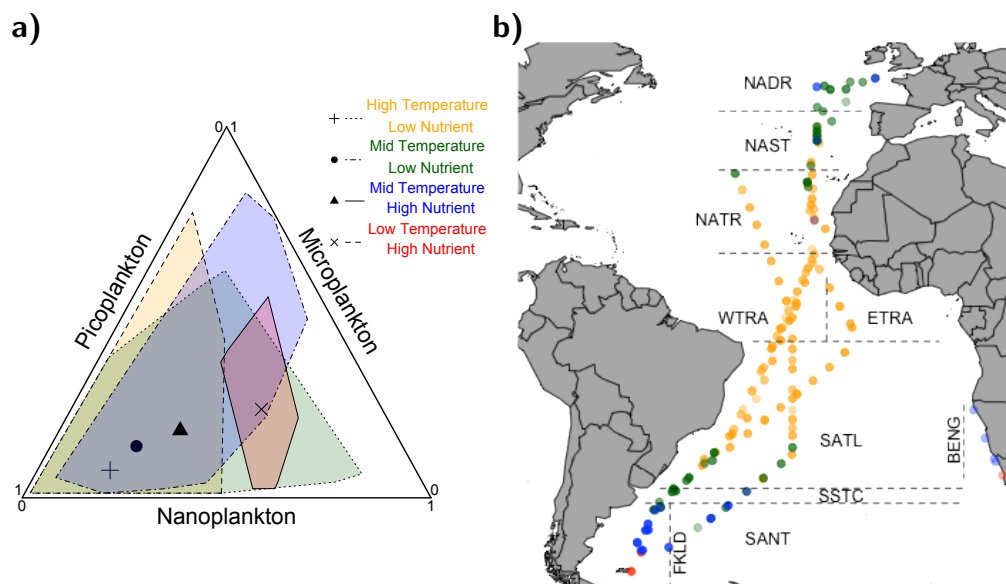


Table 4.2: Summary statistics for linear fittings of the three size fractions to each environmental variable.

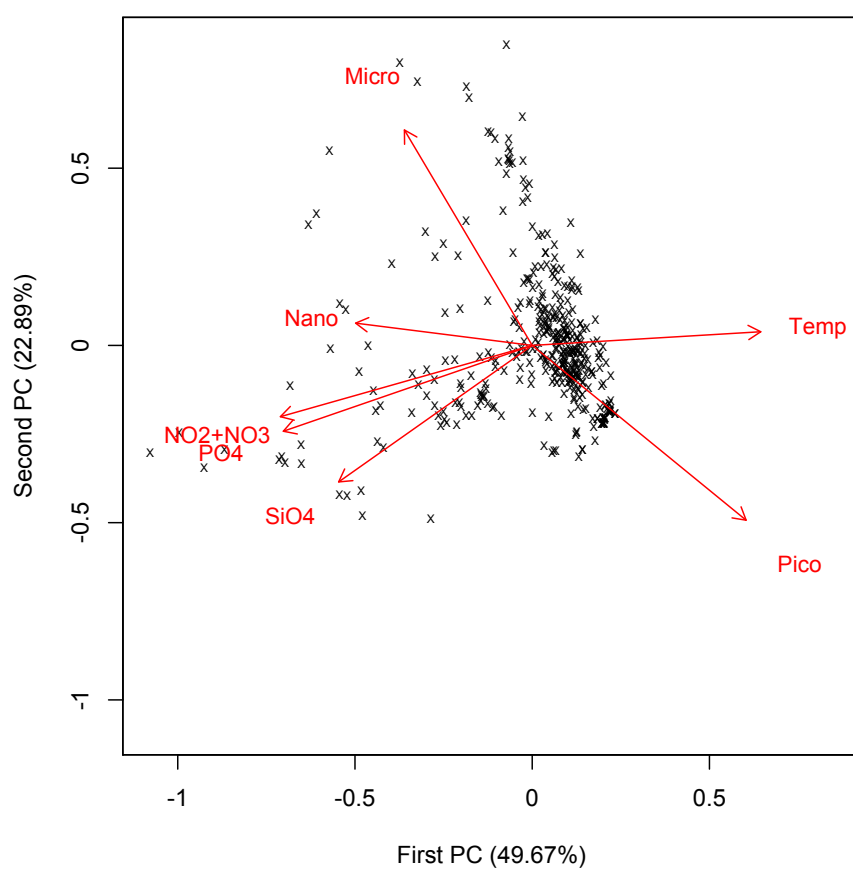


Figure 4.5: Principal Component Analysis of environmental parameters and normalized phytoplankton size fractions.

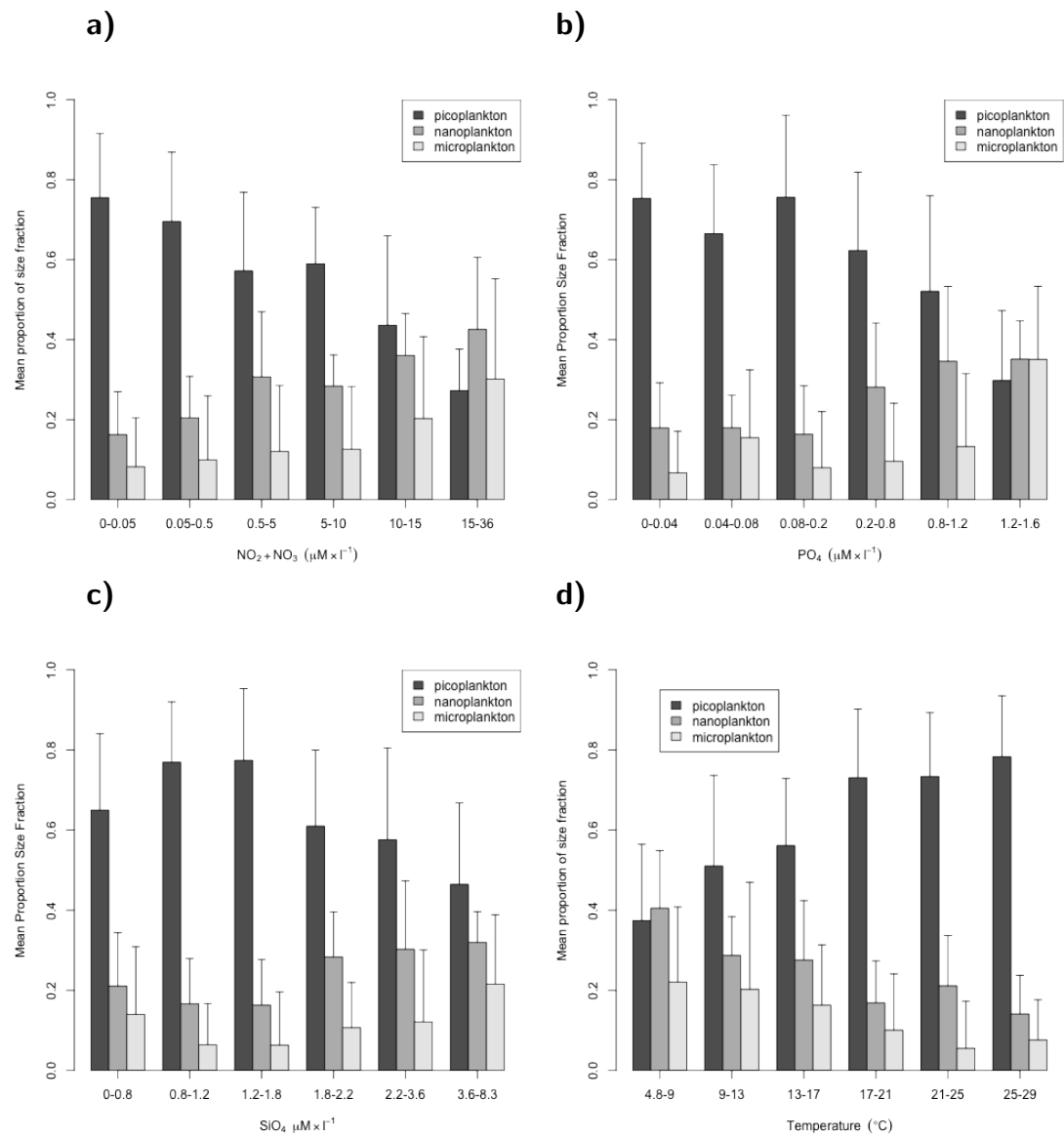


Figure 4.6: Relative composition of picoplankton, nanoplankton and microplankton size fractions changing with concentrations of nitrate+nitrite (a), phosphate (b), and silicate (c) and with temperature (d). The bars represent mean values and the error bars indicate the standard deviation.



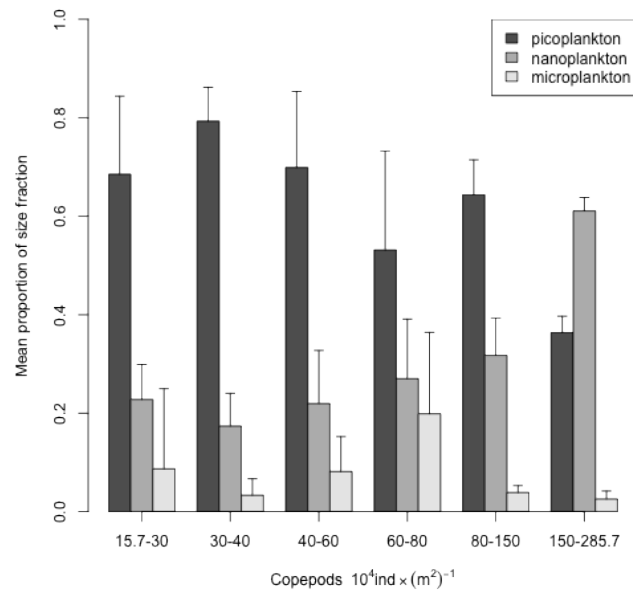


Figure 4.7: Relative composition of picoplankton, nanoplankton and microplankton size fractions changing with copepod abundance. The bars represent mean values and the error bars indicate the standard deviation.

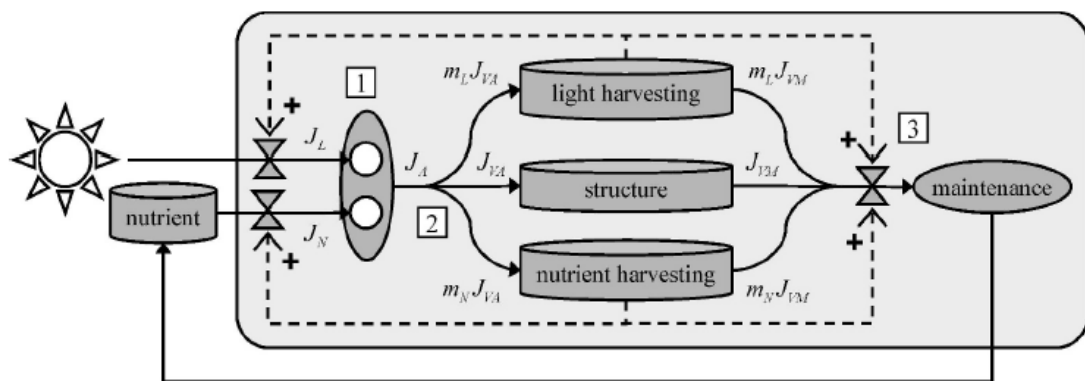


Figure 4.8: Bruggeman and Kooijman model scheme. Taken from ?

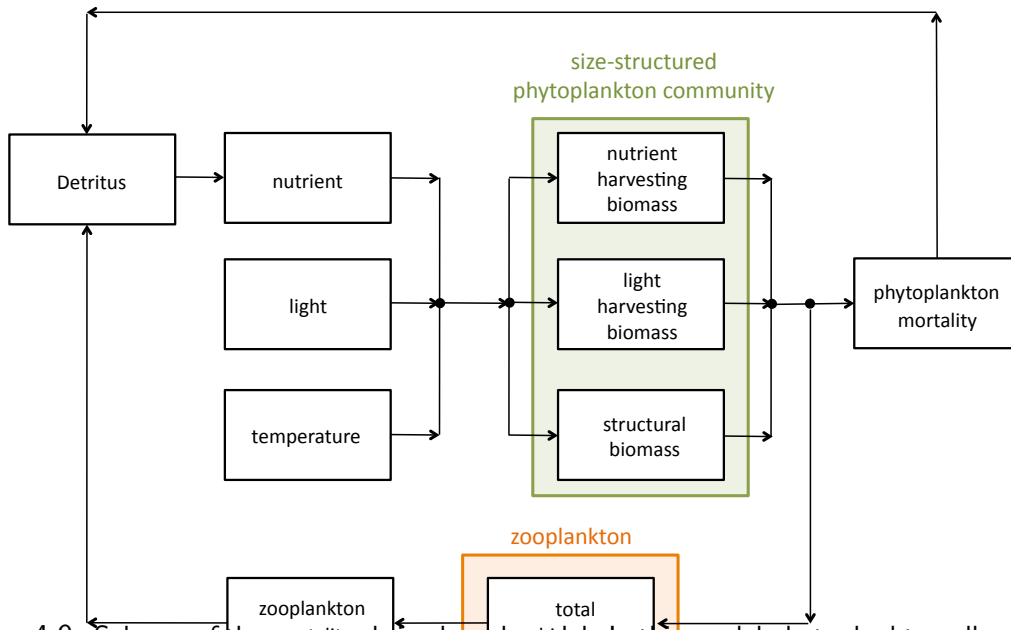


Figure 4.9: Scheme of the proposed size-based model. In this model phytoplankton allocates energy (or biomass) to different pools such as nutrient and light harvesting biomasses and generic structural biomass. A certain fraction of the phytoplankton biomass flows into the zooplankton biomass and a remaining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

temperature on all three size fractions. Pico- and nanoplankton size fractions, however, appeared more sensitive to changes in  $\text{PO}_4^{3-}$ ,  $\text{SiO}_4^{2-}$  and copepod abundance. We propose that these effects are caused by a trade-off between resource acquisition and predation pressure, 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 ?. The phytoplankton total biomass ( $P$ ), the mean trait



$(\bar{s})$ , and the trait variance ( $v$ ) will be formulated as follows: