Project Notes:

Project Title: Computational Modeling of Phytoplankton Dynamics with Climatic and Ecological Ramifications

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Note Well: There are NO SHORT-cuts to reading journal articles and taking notes from them. Comprehension is paramount. You will most likely need to read it several times, so set aside enough time in your schedule.

Knowledge Gaps:

This list provides a brief overview of the major knowledge gaps for this project, how they were resolved and where to find the information.

Literature Search Parameters:

These searches were performed between 7/10/2023 and 02/01/2024. List of keywords and databases used during this project.

Tags:

Template for Article Notes

Article notes should be on separate sheets

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NOTES

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Article #1 Notes: Scientists Say Ocean Circulation Is Slowing. Here's Why You Should Care.

Important Figures Thermohaline Circulation: The Great Ocean Conveyor Belt
Currents circulate water through the world's oceans like a giant conveyor belt, carrying heat from the tropics toward the poles and sending colder water back in deep ocean currents. Wind, temperature and salinity help drive them. This simplified map shows the pattern. SALINI
SALINI This figure depicts the thermohaline cycle in action, as well as ocean salinity. Arrows are used to indicate the direction of the current. Red lines represent the warm, fresh, less dense water at the surface of the ocean. Blue lines represent deeper, cooler, denser, and saltier ocean waters. Analysis of the color of the arrows throughout the globe reveals that the northeast Atlantic and western Antarctic are major sites for where water sinks, whereas the northwestern Indian Ocean and Pacfic are major sites for ocean water rising. Meanwhile, salinity is measured using the practical salinity scale, the ratio between the conductivity of a given seawater sample and that of a standard solution, where the standard solution has a salinity of about 35. Bluer shade indicate lower salinity, while the more orange ones indicate higher ones. Ocean waters at the poles and equator appear to be less saline, while salinity is higher for ocean waters at the intermediate latitudes. The bodies of water with the highest salinity seem to be the Meditteranean and Red Seas, as well as the Persian Gulf. **VOCAB: (w/definition) Thermohaline Cycling**- A major process by which ocean currents operate. Water at the surface of the ocean is warmer and more fresh, meaning it has fewer salts dissolved in it, and therefore less dense. However, this warm water evaporates, leaving behind ocean salts in the remaining water. The water therefore becomes cooler, denser, and more saline, and sinks. However, this water eventually returns to the surface as heat from the Earth's core increases its temperatures, and thus decreases its salinity and density. **Practical Salinity Scale**- Means by which salinity in ocean water is measured. Quantitatively, this is the ratio between the conductivity of the seawater sample and the conductivity of a standard solution that contains 1 kg of solution, and about 32.4 g of Potassium Chloride at 15 ℃. **Cited references to follow up on** Caesar, L., Rahmstorf, S., Robinson, A., Feulner, G., & Saba, V. (2018). Observed fingerprint of a weakening Atlantic Ocean Overturning Circulation. *Nature*, *556*(7700), 191–196. https://doi.org/10.1038/s41586-018-0006-5

NOTES:

- A prospective area of focus for the STEM research project that I have relates to climatology, specifically, how global warming is impacting various elements of the global climate system, and in turn, how that may impact the climate in the future.

- This scientific news article discusses how rising temperatures are slowing the rate of ocean currents and the impacts of that.
- Thermohaline circulation plays an important role in influencing climate and transferring heat and nutrients.
- Ocean currents have slowed to unprecedented rates, while ocean temperatures, due to carbon dioxide emissions, have reached historically high levels.
- Article places a heavy focus on the Gulf Stream, which flows Northeast along the North Atlantic from the Caribbean to Europe.
- Melting from the Greenland Ice Sheet due to rising temperatures has created more freshwater at a point in the Gulf Stream where warmer and less dense water usually begins to sink as freshwater evaporates and the water becomes more saline and thus more dense, sinking and cooling. With more freshwater present, the density of the warmer surface water is decreased, slowing the process of sinking and cooling, and in turn, the rate of the current.
- The exact consequences of warmer ocean temperatures and slower currents remains unclear, although in the past, they have been associated with extreme climate patterns.
	- For example, rapidly warming water off the New England coast has negatively impacted the cod industry and led to extreme weather such as Hurricanes Irene and Sandy.
- Similar trends of warming oceans and slowing currents have been observed in other regions of the ocean across the globe. Since many of these currents are much larger, the impact on the climate may be even more drastic.

- There is a need for further research into the effects of changing ocean conditions in order to paint a clearer picture of this situation and allow communities to make more informed choices with regards to preparation and mitigation efforts.

Article #2 Notes: Phytoplankton Responses to Marine Climate Change – An Introduction

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This figure is a flowchart of possible methods that can be use to study phytoplankton. Given that phytoplankton are microscopic in size, most methods performed are at a microscopic scale or smaller. Even so, methods vary from chromatography and pigment analysis to mass spectrometry, methods with electrons and light, and nucleotide analyses.

concentration and thus changes in the sea-oxygen flux. Excess anthropogenic carbon dioxide enhances its uptake by the ocean and leads to a gradual acidification of the ocean. A decreasing pH results in bicarbonate undersaturation, which causes dissolving of shells and other minerals. Regional input of reactive nitrogen can lead to fertilization and eutrophication. Another regional effect is the occurrence of high waves. Heating, reduced oxygen concentrations and eutrophication lead to higher stratification of water masses

This figure illustrates the various anthropogenic impacts on oceanic conditions. Higher sea levels, reduced nutrient concentrations, acidifcation, and other changes in ocean conditions, in addition to exerting their exclusive impacts, seem to result in further stratification in the ocean. Labels that are in italics indicate regional oceanic changes. For example, due to climate change, there is an increasing contrast between fresh and saline areas, as noted above. Visualizing these changes aids in understanding them, and in turn, what that may mean for phytoplankton populations.

VOCAB: (w/definition) Primary Production - The creation of energy for living organisms in the form of organic molecules. The main source of primary production on Earth is photosynthesis. **Spectrometry** - The means by which varying wavelengths of light (commonly spanning from UV to InfraRed light) is measured. There are varying types of spectrometry that focus on lights with different frequencies, electrical charge, and other elements of quantum mechanics. **Lysis** - In the context of biochemistry, the breaking apart of a larger molecule into smaller components.

NOTES:

- Aim was to combine two areas of interest for the STEM project, those being environmental science and climatology.
- This led to an idea for a potential project involving the investigation of how varying ocean conditions impact the concentration of various species of phytoplankton. Knowing what range of conditions different species can handle, coupled with the knowledge of how ocean conditions are changing due to global warming can reveal ecological and climatic insights.
- With that in mind, I chose to read this journal article, which provides an overview of the role phytoplankton play in climate and marine ecosystems and how climate change is impacting them.
- Phytoplankton refers to a broad range of photosynthetic species of viruses, bacteria, fungi, protists, animals, and archaea who are unable to move against ocean currents. As a

result, phytoplankton taxonomy is quite complex, and their structure, biochemical composition, habitat, and other features vary greatly.

- As photosynthetic organisms, phytoplankton are a significant source of carbon sequestration and oxygen production, accounting for 50% of global primary production. Carbon is cycled throughout the ocean through phytoplankton sinking, vertical migration of certain species, and other means (this carbon is known as oceanic dissolved organic carbon, or DOC).
- Phytoplankton also require nitrogen, phosphorus and trace metals for survival.
	- Iron in particular plays a role in increasing photosynthetic productivity.
- Phytoplankton are the base of marine food chains, serving as prey for fish, zooplankton, and various heterotrophs, and being decomposed by many bacteria and viral lysis.
- A wide range of methods exist to examine different properties of phytoplankton, including remote sensing, mass spectrometry, chromatography, and many others.
	- In particular, time series, that is, sampling of the ocean in intervals, is an important tool in studying phytoplankton in the long term. This technique has formed many other hypotheses about the ocean and revealed crucial insights about the long term trends in phytoplankton.
- - Higher greenhouse gas levels have led to warmer ocean temperatures, acidification, deoxygenation, increasing contrast between freshwater and saline conditions, eutrophication, stratification, and sea level rise.
- Even without the impact of climate change, phytoplankton already adapt to seasonal changes. The article highlights numerous examples of varying seasonal changes around the globe and how that informs trends among different phytoplankton species.
- The climate-induced changes in oceans will lead to less primary production in some regions, while it will lead to greater amounts in others.
- However, shifting bloom periods and stratification may decrease the availability of certain phytoplankton species, which in turn will limit food sources for predators, impacts which will spread to the rest of the food chain.
	- Predators may travel to new regions, becoming invasive species, in order to adapt to this lack of availability, causing further disruption.
- Changing ocean conditions may also limit the availability of essential elements and trace metals.
- Another impact is the increase in harmful algal blooms, which produce toxins.
	- These toxins, such as ones produced by harmful algal blooms (HABs), travel up the food chain, eventually reaching humans. Exposure of such sea toxins to humans has devastating socioeconomic consequences.
	- HABs drain ocean resources, creating an anoxic environment.
- Conversely, phytoplankton play a significant role in climate regulation, having been a major cause of ice ages, reflecting solar radiation, and sequestering $CO₂$.
- The impacts of climate change on the ocean and phytoplankton vary from region to region, and that making exact predictions is difficult. Hence, new and existing methods and models must be used to gain more insight.

Article #3 Notes: Oceans absorb 30% of emissions, driven by a huge carbon pump: Tiny marine animals are key to cycle, says study

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NOTES:

- This science news article takes a closer look at the marine carbon cycle.
- The ocean is a crucial component of the carbon cycle and climate, given that it contains 60 times more carbon than the atmosphere and absorbs about 30% of anthropogenic carbon emissions.
- In being a crucial carbon sink, the ocean acts as a thermostat for the climate. The amount of carbon stored in the ocean can vary, and even slight differences can result in drastic changes for the atmosphere and climate.
- Variation in carbon storage depends upon phytoplankton, as they sequester a high amount of carbon dioxide through photosynthesis, and form large carbon sinks in the deep sea following death.
- Developing proper models of the oceanic carbon cycle is crucial for having a full and accurate understanding of it and in turn its implications for the climate.
- As the climate changes, different models disagree on what will happen to primary production, the amount of carbon phytoplankton consume and consequently provide for other producers at the base of the food web, secondary production, the growth of zooplankton which impacts the fish populations who prey on them, and export production, the amount of carbon stored in the deep sea.
- The largest source of uncertainty in these models appears to be the rate at which zooplankton consume phytoplankton. Different models make different assumptions about the grazing pressures of zooplankton and the life cycles of both groups. This leads to fundamentally different predictions about carbon storage and other climate indicators when simulating various emission scenarios on different models. Until the true role of zooplankton can be properly simulated, the accuracy of these predictions cannot be guaranteed.
- Then, the article details a study where the growth rate of phytoplankton and grazing rates of zooplankton were both increased such that the carbon consumption of phytoplankton remained the same.
- Although this increase was only by a fraction of what current models assume, this resulted in an increase of 2 billion tons of annual oceanic carbon storage, and a 5 billion ton increase in the amount of carbon consumed by zooplankton. This would drastically increase the population of zooplankton for fish to feed on, which would be significant for fisheries and those who rely on fish for their diet.
- The idea is that even small variations in the role zooplankton play result in very different scenarios for the food chain and climate.
- Accurately understanding and modeling their role, therefore, is crucial for having a clearer picture of what is to actually happen with the carbon cycle, and in turn, the climate and food chain.

Article #4 Notes: Effects of oxytetracycline on the abundance and community structure of nitrogen-fixing bacteria during cattle manure composting

Fig. 1. Changes in temperature during cattle manure composting.

Figure 1 illustrates the temperatures for each of the piles over the course of the experiment (about 40 days). For about the first ten days, temperatures among all groups appear to oscillate rather heavily. From about days 12 to 16, the temperatures in groups CK and L are higher than those of M and H (approximately 20 \degree C versus about 15 \degree C). The temperature of the former groups only begin to converge with the latter ones at around day 20, with the temperature reaching around $10-12^{\circ}C$ for all groups. Therefore, this graph indicates that higher amounts of OTC hastens temperature decline. Cooler temperatures are less ideal for most bacteria in compost piles, as they inhibit their overall activity.

Fig. 2. Changes in nitrogenase activity during composting.

Figure 2 depicts the rates of bacterial nitrogenase activity among the four groups. These were measured on days 1, 8, 21, and 40 of the experiment. Examining these bar charts from multiple angles, it is clear that increasing OTC concentrations in compost piles inhibits nitrogen-fixing activity. On day 1, the control group has about quadruple the amount of activity in group L, and about eight times the activity of groups M and H. Even on day 8, when all groups have activity only ranging from about 0.1 to 0.2 nmol $C_2H_4^*g^{-1}*h^{-1}$, the amount in the control group is slightly higher than the rest. Then, on day 21, there is a

spike of activity in the control, while activity levels in the experimental groups continue to decline. Although rates of nitrogen-fixation in L and H are greater than the control on day 40, that does not change the fact that the control group, on average, had the most nitrogenase activity over the course of the experiment. Additionally, the degree to which H and L are greater than the control on day 40 is much less than when the control was higher than all of the experimental groups on days 1 and 21. Although there are fluctuations in the values across each of the days, there is an overall decline in nitrogen-fixing activity throughout the experiment.

Fig. 3. Changes in nifH gene abundance during composting.

Figure 3 displays the abundance of nitrogen-fixing bacteria through the varying measures of nifH genes observed on days 1, 8, 21 and 40. While there are considerable fluctuations in nifH levels among each of the groups, after 40 days, the groups with the highest quantity of the genes is the control. Although not the group with the highest amount of nifH genes initially, the decline in nifH genes was lowest for the control, while the degree of decline increased the more OTC each group had. This indicates that increasing amounts of OTC decreases the quantity of nitrogen-fixing bacteria in compost piles.

NOTES: Introduction:

- Oxytetracycline (OTC) is a commonly used antibiotic in the livestock industry to prevent infection. However, most livestock excrete large amounts of OTC. When these excretions, mainly manure, are used for composting, this poses a threat soil microbes, plant growth, and even human health.
- In the process of enhancing soil quality, compost that contains livestock manure is able to reduce the quantity and impact of harmful antibiotics.
- Nitrogen is an important element for life, especially when it comes to organism structure and proteins. Processes that occur along the nitrogen cycle, such as ammonification, nitrification, denitrification, and nitrogen fixation, are facilitated by nitrogen-fixing bacteria. The nitrogenase enzyme is used for nitrogen fixation specifically.
- Brief overview of methodology (see below)
- Goal of the study is identified: Determining the impact of OTC on nitrogen-fixing bacteria via examining the impact on the abundance of nifH genes (common marker gene for nitrogen-fixing bacteria) and the community structure of the bacteria.

Methods:

- Details how and where OTC, cattle manure and wheat straw were attained.
- Timeframe (26 Oct-5 Dec 2014) and composting parameters specified
	- Carbon/Nitrogen Ratio was 25:1, moisture content was around 55% (tap water used), dimensions and material of the composting box (foam, rectangular prism, holes for aeration, and so on), days of experiment when compost was turned, etc.
- Experimental groups: CK (No OTC), L (10 mg/kg), M (60 mg/kg), and H (200 mg/kg).
- Stratified random samples of the soil collected on days 1, 8, 21 and 40 of the experiment
- Temperature monitored via thermometer, moisture determined through drying, organic C content measured by organic carbon analyzer, and nitrogenase activity measured through incubating the sample in a flask containing acetylene (C_2H_2) and measuring the output of ethylene (C_2H_4) via gas chromatography
- Samples that had DNA extracted were freeze-dried, being stored at -20℃.
- qPCR (see definition above) was then used to determine the number of nifH genes.
- - Denaturing Gradient Gel Electrophoresis (DGGE) was then carried out. Specifies the amount of DNA template, various primers, water, and other pertinent fluids used (e.g. 1 μL of DNA template, 20 μL of water, etc.)
- For the above two processes, the sequences of nucleotides used to conduct the procedures is provided.
- The bands of the proteins from DGGE were then extracted from the electrophoresis, cloned via nucleotide sequencing, and then analyzed by computer software.
- The clusters of nitrogen-fixing bacteria were analyzed using non-weighted arithmetic means. To evaluate the diversity, specialized indices wee used, including the Shannon, Simpson and Evenness indices. Other methods of statistical analysis for this study includes the Student's t, and ANOVA.

Results and Discussion:

- (See figure 1 above) Temperatures fluctuate greatly among the four experimental groups. All groups started out in thermophilic conditions, indicative of microbial growth and activity, and ideal composting conditions. In general, the data of the temperatures of each

group seem to indicate that OTC lowered temperature faster (which may indicate that it inhibited microbial activity).

- (see figure 2 above) Data on the nitrogenase activity among the control and three treatments clearly indicate that higher OTC levels have an irreversible, inhibitory effect on nitrogenase activity. On day 1, the control has a much higher amount of nitrogenase activity whereas all treatments have far lower ones. Due to overheating in the soil on day 8, all groups had low nitrogenase activity. However, only the control was able to bounce back, as seen on day 21.
- (see figure 3 above) Data on nifH gene abundance among the four groups illustrates that OTC reduces nifH gene levels. The article speculates that this may be a cause of the degradation of OTC into products that nitrogen-fixing bacteria have less resistance to, which ultimately leads to less bacteria being able to survive, and hence, a decreased presence of nifH genes.
- Results from the DGGE and qPCR suggest that varying levels of OTC have significant impact on the composition of nitrogen-fixing bacteria in the soil, over the course of the experiment, when comparing the control to the treatment groups, the banding patterns varied greatly.
- Calculations done using the various indices mentioned above reflect that higher OTC levels lead to less microbial diversity. However, there may be other factors at play, including the degradation of OTC, which inhibits ribosomes and tRNA. Therefore, more study is required when it comes to evaluating the impact of OTC and other antibiotics on the diversity of these soil microbes.
- The gene sequences were used to identify the bacterial species in the soil. The study speculates about what role they may play in nitrogen-fixation, as well as any resistance they may have to OTC. This is another place for future study.

Conclusions:

- Overall, it seems more definite that OTC has an inhibitory impact on nitrogen-fixing bacteria, reducing nitrogenase activity and gradually reducing the abundance of nifH genes. However, the impact of OTC on the diversity and community structure is less clear and needs additional study.

Article #5 Notes: Phytoplankton response to a changing climate

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NOTES:

Section I: Introduction

- Phytoplankton comprise of 50% of primary production, are base of marine food chain, and play significant role in biogeochemical cycling and climate regulation.
	- The nature in which these processes are carried out is largely based upon the composition of phytoplankton
- Therefore, a major part of understanding how oceanic conditions shall change relies on knowing on how phytoplankton shall change due to global warming, which in turn relies upon knowledge of factors that impact the ocean.
- Climate oscillations, both seasonal and long-term, have a major impact on phytoplankton conditions, as they significantly modify the abiotic and biotic conditions that impact their populations.

Section II: Mechanistic links between climate and factors limiting primary production

- Some of the most influential variables that impact phytoplankton include ocean temperature, stratification, prevalence of light and nutrients, play a major role in impacting phytoplankton populations
- Climate change is modifying these factors, which is to have direct and indirect effect on phytoplankton populations.
- Metabolism in primary producers is mainly limited by photosynthesis.
- Cold temperatures typically do not inhibit phytoplankton growth.
- Light-limited rates of photosynthesis are not impacted by warmer temperatures, whereas light-saturated rates of photosynthesis increase with them (makes sense considering the definitions of these two types of rates of photosynthesis described above).
- This means that in areas of light-saturated photosynthesis, blooms could increase in abundance. However, this is would lead to greater grazing rates in certain areas, altering taxonomic composition of phytoplankton.
- Stratification and the mixing of ocean layers are two opposing forces; the former occurs under warm conditions, while the latter occurs under cooler ones. Layer mixing circulates nutrients, allowing different groups of phytoplankton be exposed to the nutrients and light of different levels. However, with more stratification, nutrients, abiotic conditions become more sporadically distributed, as opposed to being uniformly the same across a given area.
- Stratification leads to the preference of lighter, smaller, more buoyant species (makes sense considering basic principles of things a kin to density)
- Stratification will lead to less nutrients in certain areas, while leading to more in other areas, as well as inhibit their upward flux. This means that the best competitors for nutrients, in addition to groups that can maintain their vertical position will thrive in these conditions.
- On the other hand, for environments that have been subject to eutrophication, it seems that phytoplankton that lie at the intermediate layers of the ocean will have the best advantage.
- Stratification may also cause deoxygenation and accumulation of other nutrients such as sulphur that are traditionally associated with eutriphication.
- The impact of climate change on marine nutrient availability varies by region.
- Light availability under changing ocean conditions will also vary by region, as stratification, reduced mixing, and earlier melting are all factors that help increase it, whereas increased winds and run-off decrease it. However, winds and run-off are regional events, and so overall, light availability, and therefore, production in phytoplankton, is anticipated to increase.

Section III: Climate effects on phytoplankton processes

- While there are region-by-region impacts, there exist overall trends in the impacts climate change has had on phytoplankton, mainly relating to taxonomic composition, population size structure, and seasonal trends.
- Phenologically speaking, phytoplankton blooms are triggered by physiological responses to abiotic conditions, namely temperature and light. Nutrient access, predator-prey interactions, and population feedback all influence the degree at which these blooms grow. At deeper ocean layers, thermal stratification initiates blooms.
- Across multiple ecosystems, it has been observed that the time at which these blooms occur has gotten earlier, which is in agreement with the prediction of models of producer-grazer relationships.
	- This degree of advancement varies across different groups, likely due to different life strategies that different communities employ
- A possible explanation for this, based off some studies, is warmer temperatures and increased grazing pressure. These conditions are also associated with changes in taxonomic composition and population size structure.
- Changing climate conditions are also impacting the magnitude of phytoplankton blooms, but this is dependent upon light. For example, while higher intensity light increases the magnitude of blooms, when light intensity is lower, and blooms face higher temperatures and grazing pressure, the magnitude is lower.
- Impacts on photosyntehic output lack a consensus. Some regions have had higher chlorophyll outputs, while others have had lower ones.
- - Smaller, more buoyant phytoplankton, being able to resist sinking, are predicted to have a competitive advantage. This includes groups such as certain cyanobacteria and flagellates.
	- Fossils and other paleoclimatological evidence support these findings.
- Moreover, in eutrophic environments, groups that are able to move upward through oceanic layers are expected to have a competitive advantage.

Section IV: Conclusions

- These changes are to have significant ecological and climatic implications, especially when it comes to primary production, biogeochemical cycling, and predator-prey interactions.
- With the emergence and peaks of phytoplankton blooms becoming inconsistent across different regions, this may throw off feeding patterns of zooplankton. This means that there will definitely be changes in how energy is transferred up the trophic pyramid.
- Dominance of smaller, more buoyant phytoplankton populations means less export production.
- More research into the seasonal variabilites in phytoplankton and how those are changing due to global warming is needed. A particular area of focus should be on determining how energy shall be transferred up the trophic pyramid, given these changing norms in phytoplankton.

Article #6 Notes: Southern Ocean Phytoplankton in a Changing Climate

Important Figures

FIGURE 1. SCHEMATIC SHOWING THE CONNECTIONS AMONGST MEMBERS OF THE MICROBIAL FOOD WEB AND MICROBIAL LOOP AND THE PROCESSES DRIVING CARBON TRANSFER TO HIGHER TROPHIC LEVELS AND FLUX TO THE DEEP OCEAN.

This diagram illustrates marine carbon cycling. Much of the carbon sequestered in the ocean is due to photosynthesis in phytoplankton and similar organisms. This provides a source of organic matter for bacteria, viruses and protozoa. Carbon cycling between bacteria and viruses in what is known as the microbial loop. Phytoplankton and protozoa act as the base for the rest of the aquatic food chain. The sinking of dead phytoplankton as well as fecal deposits of organisms farther up the trophic pyramid sink to deeper levels of the ocean to form carbon sinks. Carbon dioxide is released back into the atmosphere via respiration.

This map models the concentrations of chlorophyll A across the Southern Ocean (milligrams per cubic meter). Warmer colors indicate higher concentrations, while cooler colors indicate lower ones. Given that warmer colors seem to be present

closer to coastlines of the various landmasses, and the cooler ones are farther away, there appears to be a negative association between oceanic chlorophyll concentration and distance from the coastline. This map also shows various details regarding the diminishing ice shelves and ocean currents.

This figure illustrates how ocean conditions in the SAZ are changing due to climate change. The pycnoclince, the area where water density in the ocean begins increasing rapidly is predicted to move farther up the surface. More dust and $CO₂$ exposure is expected, while the rate of circulation of nutrients, the depth of mixing, and carbon flux are expected to decrease. More storms are predicted, and sea surface temperature (SST) shall also rise.

FIGURE 6. SCHEMATIC SHOWING THE PRIMARY PHYSICAL CONSTRAINTS ON PHYTOPLANKTON IN THE PERMANENTLY OPEN OCEAN ZONE (POOZ) (A) before and (B) after climate change. Ovals represent the depth of mixing and arrow thickness reflects relative rates of flux. SST, sea surface temperature.

temperature

Another figure illustrating the impact of climate change on oceanic conditions, this time, for the POOZ region. It appears that $CO₂$ and Fe input will increase. The pycnocline is also expected to become deeper (there appears to be a relationship between circulation and the pyconoline line) Circulation is to occur at a deeper level, and the upward flux of nutrients is predicted to increase. However, carbon storage is expected to decrease. Warmer sea temperatures, melting icebergs, windier, cloudier, stormier conditions.

The article has figures like figures 4 and 6 for other oceanic regions. While there are some unique trends predicted region by region, all figures are of a similar calibre.

The presence of unique trends among these five regions of the Southern Ocean

NOTES:

Section I - Introduction:

- Article begins by explaining the importance phytoplankton play in cycling nutrients and acting as the base of food chains.
- Carbon cycling is mentioned (see explanation of figure 1 below), but so is the production of special sulfur compounds. Some species of phytoplankton create the compound dimethylsulfoniopropiothetin (DMSP), which when enzymatically broken down, forms dimethylsulfide (DMS). Atmospheric dimethylsulfide, when oxidized forms sulfate aerosols that reflect solar radiation. Therefore, this is another avenue through which phytoplankton play a role in climate.
- The southern ocean makes up 40% of the human-induced carbon dioxide that the ocean absorbs. If not for the southern ocean, atmospheric $CO₂$ levels would be 50% higher than they are currently.
- Changing ocean conditions due to climate (which shall impact conditions for phytoplankton) include acidification, stronger winds, greater solar radiation, rapid sea ice melthing, lower salinity, changes to the distribution of nutrients, and the southward movement of certain ocean fronts.
- The article then goes on to provide a geographic definition of the Southern Ocean (SO) used in this study (everything south of the Sub-Tropical Front, which encompasses 20% of the global ocean mass). Then, based off environmental factors that influence phytoplankton, the five regions that are to be focused on in this article are defined: Sub-Antarctic Zone (SAZ), Permanently Open Ocean Zone (POOZ), Seasonal Sea Ice Zone (SSIZ), Marginal Ice Zone (MIZ), and Antarctic Continental Shelf Zone (CZ).

Section II - Sub-Antarctic Zone:

- High nutrient, low chlorophyll region of the SO. $pCO₂$ in this region is lower than in the atmosphere, allowing for ease of $CO₂$ absorption. Significant contributor for the thermohaline cycle and convection currents (see definition above). Primary production in this region is limited due to various biological and physical factors, such as iron and light deficiencies, overdomination of certain species of phytoplankton that are good at absorbing silicon dioxide, among other factors. However, export of carbon to lower ocean levels is pretty high.
- Predicted changes for SAZ region include more frequent storms, increased radiation, acidity, temperatures, freshness and wind-blown dust.
- Warming ocean + more precipitation = stratification and more buoyancy needed, (as discussed in past articles)
- Less CO_2 absorption as pCO_2 increases
- Predicting *net results* for how phytoplankton will respond to global warming-induced ocean changes is too difficult. This is because there are multiple environmental factors that have to be considered, and they act in tandom, and modeling that with experiments is impossible. Moreover, this does not take into account interactions between phytoplankton species and with organisms farther up the food chain.

Section III - Permanently Open Ocean Zone (POOZ):

- Natural barrier between 5-10 °C SAZ and the cold Antarictic waters (< 2 °C)
- HNLC, but to an even more extreme degree than the SAZ, although pockets of Fe from sediments
- Dominated by pico- and nano- sized flagalletes.
- Antarctica Slope carries nutrients northward, however, these nutrients (e.g. nitrates, silicates, etc.) are consumed by phytoplankton, so their concentrations decreased farther northward
- Strong winter winds facilitate nutrient cycling which allows for the growth of phytoplankton in spring, although this growth is inhibited by feeding from various zooplankton species. Silicified diatoms, like in the SAZ, play the largest role in Carbon export.
- With climate change, the Westerly Winds (prevailing winds in this region) are expected to go faster, pH is decreasing, sea is becoming more fresher and warmer, cloudier conditions
- Increase in primary production from warmer temperatures are expected to be off-set by positive oscillation in SAM creating more cloud cover (i.e. less light), although, also b/c of SAM, the mixing layer is deepened, so primary production may increase
	- Deeper mixed layer = higher chlorophyll a concentration found
- Melting icebergs = more iron = more productivity and abundance for phytoplankton, more carbon exportation and carbon sequestration, higher grazing pressure,
- As climate warms, the POOZ has been moving farther and farther south, both from its northern and southern boundaries (in the north, the Polar Front has gone farther south, and in the south, more ice has melted).
- Overall, this means more area of the ocean is covered by the POOZ, which may be possible indication that primary production will increase. However, this may be complicated by changing ocean conditions
- The impacts on primary production come down to nutrients and light availability. A

deeper pycnoclince would reduce light availability, but more nutrients will be available from melting icebergs, so it seems that the effects may counteract each other. Overall, it seems that blooms will become a bit more subdued.

Section IV - Seasonal Sea Ice Zone:

- Given that ice melts and reforms annually in this region, and the area its covers, the SSIZ is one of the largest, most dynamic and ecosystems in the world.
- Snow-covered sea ice helps regulate heat exposure in the ocean, reflecting the solar radiation while also shielding the ocean from cold atmospheric conditions in winter.
- The largest source of primary production here, are the sea ice algae, who experience very \dim and cold conditions, as well as little $CO₂$ access, and high salinity, thriving best in harsh conditions.
- Primary production and biomass vary greatly even within small scales and timeframes.
- Like with all other ecosystems, the phytoplankton (in this cases embedded within the ice) is significant, being the base of the food chain in Antarctic ecosystems.
- The ice-water environment has optimal conditions (higher temp and nutrient concentrations, low salinity).
- Unoptimal conditions during the winter, with less light, but best source of food for zooplankton during this time.
- Thus any change in sea-ice conditions or phenology will have major impact for sea-ice ecosystems and phytoplankton dynamics, especially the timings of blooms.
- Interestingly, despite overall global warming trends, sea ice spread in Antarctice has slightly increased, with El Niño Southern Oscillation (ENSO) and SAM playing major part in this.
- However, ASL (see definition above) causes sea ice compression for the Amundsen and Bellinghausen Seas and expansion of the Ross Sea, so sea ice in the western Antarctic has been declining. Combined with increased impacts from global warming, ENSO and SAM will be outweighed and so sea ice will begin declining more universally.
- Sea ice expansion has reduced phytoplankton productivity. Observations of areas in SSIZ with less sea ice (later expansion, earlier retreats), have yielded little findings of increased productivity, due to light and nutrient limitations faced.
- As has been found in other articles, temporal asynchronies arise between the phytoplankton and their grazers, leading to significant changes to the distribution of energy up the trophic pyramid.
	- In particular, fatty acids significant in reproduction are being transferred up less, which can cause further constriction to population sizes up the trophic pyramid.
- Less sea ice in this region is predicted to reduce carbon exportation.
- Reduction in the contribution of phytoplankton to the biogenic sulfur budget is predicted, especially since much of the sulfur comes from the algae in the ice that is melting.
	- This includes production of Dimethylsulfoniopropionate (DMSP), which then is converted to emissions of Dimethyl sulfide (DMS) and the simpler sulfate compounds that it decomposes into which reflect solar radiation (via facilitating cloud formation).
		- Other possible uses include protecting biological tissue, controlling grazing pressure, metabolic product, antioxidant
	- Biogenic sulfur budget $=$ the amount of sulfur produced/emitted into the

atmosphere by living things (mainly autotrophs).

- There is a higher amount of phytoplankton in thicker ice, and with the ice thinning, there are fewer amounts of them. Being concentrated in the ice, they especially serve an important role in providing food source to zooplankton. Higher up the trophic pyramid, this may lead to longer, less energy and time efficient paths for energy to travel.
- Higher precipitation (i.e. snow) is predicted. This can form depressions in the ice, flooding the area, and allowing phytoplankton on the surface to grow in these pockets, while, via reflecting more light, inhibiting growth for groups under the ice.
- Sea ice plays a significant role in regulating the carbon cycle between air and ocean. This controls $pCO₂$ and the amount of $CO₂$ absorbed between the two.
- Ice algae, whose concentrations are predicted to decline due to the loss of their melting habitats play a significant role in regulating the transferral of energy up the food chain, and with their disappearance, will cause negative consequences ecologically.

Section V - Marginal Ice Zone (MIZ):

- MIZ is the location where the dense sea ice transitions into open ocean.
- Region of high productivity, accounts for majority of blooms in spring and summer, however, blooms tend to be sporadic both in location and time due to low level of the mixing layer.
- Phytoplankton are trapped into ice during the winter, however, the ice has concentrated iron. So, this leads to large blooms in the spring, with high-iron, low-salinity conditions.
- Home to diverse assortment of phytoplankton species
- These large blooms contribute to large amounts of marine snow (i.e. sinking phytoplankton, $CO₂$ sequestration). The melting sea ice provides a good source of grazing and reproduction for zooplankton
- For this region, the impacts of climate change on oceans are less sea ice, more icebergs, and a positive oscillation in the SAM. The SAM currents are expected to deepen and the mixing layer and as a result decrease productivity and lead to preferences in certain species.
- Overall, predicted impact for this region is uncertain.

Section VI - Antarctic Continental Shelf Zone (CZ):

- High concentrations of nutrients on the surface, iron from melting continental shelf and coastal sediments, and various currents that allow for proper nutrient mixing are major sources of productivity in this region
- Blooms here are critical for terrestrial ecosystems in Antarctica.
	- Release of DMS by grazers helps indicate mating season for penguins and other benchmarks.
- Big differences between the east and west within this region

West Antaractica:

- Includes area around Antarctica Peninsula (Wedell Sea, Amundsen Sea)
- Warm, nutrient-filled, saline water from the circumpolar deep water (CDW) contributes significantly to ice melt but increases phytoplankton productivity, at least, theoretically. Decreasing salinity and less abundant sea ice will likely overrule CDW and other trends that increase productivity.
- Changes in this region include acidification, rapid melting in glacier mass and ice loss, greater stratification, and fresher, warmer conditions
- A major impact of freshening waters (similar to what has been noticed for other changing conditions), smaller phytoplankton cell sizes are being preferred. This has had negative impacts up the food chain (krill population decrease, preference now on scalp and less efficient fish)
- Stratification renders certain species vulnerable to the damages of excessive sunlight, so this is yet another way the increased productivity in phytoplankton is halted.
- Melting means more icebergs (but these icebergs, although more numerous, are melting rapidly), so that means more iron, which means greater productivity, as well as greater $CO₂$ sinks.
- Not much research done on the impact of pH in this area (which, remember, is measured by $CO₂$ concentration as well as $pCO₂$)

East Antarctica:

- Major factors that influence productivity in this region is iron and light availability. Of the dominant phytoplankton groups, some prefer greater amounts of stratification, while others a deeper mixing layer. Phytoplankton (like everywhere else), support rest of the food chain, including the krill of this region that is a keystone species.
- Similar trends expected for this region as for what is expected in the west, although warming may be less severe here.
- With regards to acidification, polar waters are predicted to be the first to be impacted, as solubility of CO_2 in colder waters is increasing quickest. CO_2 is trapped in the water when it freezes, becoming dissolved in it, leading to acidification.
- Phytoplankton have maintained a surprising level of stability in lieu of acidification, but pH is now starting to become too low for that to continue, so taxonomic comp is changing
- Again with smaller cell sizes, there is to be less food source for grazers and less carbon export
- Multi-stressor experiments have not been performed in this region. Indeed, as we have seen throughout research hitherto, interactions between different oceanic parameters is complex to understand, but that's what's happening in the real world. This is the key area, the area not well understood currently.
	- E.g. Iron itself increases primary production, but when combined with warming, greater $pCO₂$, and light, this creates preference for certain species
- Freshening, ice melt, warming, and stratification seem to bolster phytoplankton activity, however, freshening and acidification seem to inhibit the transfer of energy up the trophic pyramid, which could have significant negative consequences for the Antarctice food web.

Section VII - Conclusion:

- Understand that phytoplankton are able to withstand very extreme conditions.
- Article asserts that no clear trend primary production (or phytoplankton in general) will be discovered until 30 years from now.
- For SAZ: Surface waters are to face lower nutrient levels due to stratification. It is possible that greater iron and warmer temperatures will increase productivity, however this hinges on storms and the amount of dust they provide oceans.
- POOZ: Increased nutrient supply, mixing between layers, and melting are expected to bolster productivity, whereas limited light due to deep mixing layer, as well as cloud

cover may limit it.

- SSIZ: With extensive melting occurring, ice algae abundance, and therefore, primary production and food availability for grazers and higher order consumers are decreasing.
- MIZ: Disruption of current phytoplankton phenology.
- CZ: Taxonomic shifts likely, especially towards smaller cell sizes; Melting, stratification are expected to generate more nutrients, thereby increasing productivity.
- Again, the key with the impacts that phytoplankton will face is the timing, interaction, magnitude, order of imposition, and other factors of the multiple stressors that phytoplankton face.
- Logistically hard to perform the multi-stressor experiments needed to generate understanding needed. Efforts in monitoring ought to be established.
- Many of the climate (and therefore oceanic) trends observed in the SO region specifically have been due depletion of the ozone layer, due to anthropogenic activity. However, many of these trends can be reversed if the ozone layer is replenished, which, currently, it seems that it is in the process of doing so.
- Another key thing to understand about phytoplankton is that many groups already face conditions that oscillate greatly, and, combined with high genetic diversity and short generation cycles, they are will fit to adapt to these conditions. However, it is unknown whether phytoplankton will be able to keep up
- Bottom line: There are to be significant changes for marine ecology, global climate, and biogeochemical cycling.

Article #7 Notes: Monitoring and modelling marine zooplankton in a changing climate

Important Figures

pro and NPP from 10 CMIP6 Earth system models for the historical period (1995-2014). future (2081-2100) and the change in SST and NPP by 2081-2100 relative to 1995-2014 based on SSP5-8.5. Publicly available datasets were analysed in this

ESM1.2HR, NorESM2-LM and UKESM1-0-LL. This data can be found at: http: lini.gov/

This figure depicts past (1995-2014) ocean temperatures and amounts of primary production, provides future forecasts for said metrics (2081-2100), showing the predicted changes between time periods below. Historical data for temperature indicates equatorial waters are warmer than polar ones, with temperature of either region being approximately 25[°]C and between 0[°]C and 10[°]C respectively. There is a clear gradient from the equator to the poles. This holds true for the future prediction. However, the temperatures are much warmer in the predicted model. Equatorial waters are over 30° C, and polar warmers have warmed up to. The mass of warm colors which graphically depict warmer temperatures has visibly expands between 1995-2014 and 2081-2100. Looking at the map of ocean temperature changes, with the exception of a few areas around Antarctica, Greenland, and Iceland, ocean temperatures increase, with the deepest shades of red, i.e. the greatest increased being concentrated in the North Pole. Meanwhile, looking at both the past and prediction models for primary production, it is difficult to easily discern any differences between the two. For both, it seems that coastal areas tend to be more productive than regions of open sea. However, the globe containing changes in production is a lot more revealing. Around the poles, the Bay of Bengal, Gulf of Mexico, Hudson Bay, and other patches of water, it is predicted that there will be light increase in primary production. However, in all other regions, primary production is expected to decline, in some places with a much faster rate than others.

This diagram is a very basic illustration of the carbon cycle, and the role zooplankton and phytoplankton play in it. What is notable about this diagram is that, with the exception of respiration, all variables have the chance of increasing or decreasing. This speaks to the overall nature of extreme variation and lack of overall trends in ocean conditions brought about by climate change.

Fig. 3 | Map of long-term n onitoring progra imes for zooplankton in the global ocean. Blue lines indicate Continuous Plankton Recorder (CPR) surveys and symbols indicate sites of specific long-term monitoring program nes (see Supplementary Data 1 for details of numbered sites). Stars indicate data is freely available to download, squares indicate data available on request, triangle indicates partially available, and circles indicate data either not available or unclear on data

sourced from the Marine Ecological Time Series Database, EuroSea survey and surveys undertaken as part of this review effort. More information and coordinates are provided in the Supplementary information. This figure was designed by Dr Stacey McCormack (Visual Knowledge).

This map depicts areas where zooplankton populations are studied and surveyed. There is a fairly clear Western bias here (South Africa and Japan are well-aligned with the West). The blue lines, which indicate oceanic areas where zooplantkon are monitored are concentrated around the Northeast Atlantic, Southern Australian Coast, and other areas where Western presence is highly dominant. A similar pattern can be observed with the location of facilities that investigate phytoplankton. This indicates that there is dearth in many regions on of the world

NOTES:

Introduction/Background Information

- Zooplankton, like phytoplankton, play a significant role in the carbon pump and in marine food webs.
- Focus: Establishing oceanic changes brought about by climate change that could impact zooplankton, how zooplankton are being affected, and how these dynamics are modeled.
- When it comes to global warming-induced changes in oceanic conditions, there are broad trends, but numerous regional variations
	- Sea Surface Temperature (SST) is increasing, but at different rates in dif. regions
	- Net Primary Production (NPP) is higher towards poles, lower towards equator. Here too there is much variation; uncertainty has increased with more accurate, realistic models (CMIP5, CMIP6)

Impact of Climate Change on Zooplankton:

- Ocean warming/acidification leads to certain groups being preferred, meaning taxonomic comp will be modified
- - Use of Long-term time series for easily delineating the three key trends observed:
	- Seasonal shifts in trends, mostly earlier occurrence of spring/summer groups, and later occurrence of autumn groups
	- Geographical shift towards the poles
	- Preference of smaller sizes under warming ocean conditions
- Possible impacts on the biological carbon pump; Ecologically, the decoupling of predator-prey interactions, which would harm marine ecosystem well-being (fisheries hurt in particular)

Seasonal Changes in Zooplankton:

- Seasonal changes vary significantly given temperature preferences and the rate of adaptations of different groups
- Highlights various examples of how zooplankton blooms and peaks are occurring much earlier
- More research has been done in the Northern Hemisphere, and there are other possible, more complex, findings in the Southern Hemisphere (i.e. no seasonal change in some regions)

Migration:

- Poleward migration has been brought about by the need for zooplankton to maintain their optimal temperature levels
- Movement rates vary among different species, with some species not migrating poleward in any capacity, withstanding the warmer conditions, while other species are actually migrating when warmer conditions are not present
- More mobile species may be able to regulate their location a bit better, and are less sensitive to environmental conditions
- In closed systems, like the Mediterranean, instead of poleward movement, movement is towards deeper layers of ocean
- Need for further research

Size:

- Temperature best indication of body size decline, based off the data.

- However, in southern ocean, the preference has shifted towards larger-sized species. Additionally, instances of more complex growth trends are noted.
- Other possible variables that may impact body size include species history and adaptive behaviour, competition, predation, etc.
- There are definitely connections to migration patterns and seasonal changes.

Climate Change & Biological Carbon Pump

- - Marine heatwaves (5 days of abnormally high water temperatures), as well as events such as El Niño also heavily impact zooplankton phenology and size
	- E.g. given w/ California waters: gelatonous species preferred, disrupted predator-prey interactions
- Positive and Negative Oscillations of SAM (see definition above in article #6), and the North Atlantic Oscillation (NAO) also affect different groups of zooplankton in varying ways
- Climate change can impact zooplankton directly physiologically, and indirectly through changing their diets.
- More research needed to determine impact of other variables on phenology, size and migration patterns and the various ecological ramifications
- Zooplankton contribute to carbon exportation and cycle essential nutrients for phytoplankton and other bacteria.
	- Although, the provision of these services varies among different groups, and that is not fully understood.
- Warmer temperature leads to stratification (i.e. nutrient limitation) and higher metabolic demands, which is why smaller body sizes are preferred
- Article considers three areas in tackling how warming oceans are to impact zooplankton's role in carbon sequestration: respiration, grazing and excretion
	- Respiration: Much carbon is lost from this process. Since more $CO₂$ is released from respiration when body mass is smaller, and smaller species are being preferred, that means more carbon is being lost and sequestration is working less well. Oxygen, pH, turbulence, pressure, and other variables impact respiration.
	- Grazing Pressure: Evidence existing to support notions that grazing pressure is decreasing and increasing. Biomass and varying nutrient conditions can limit it, while warmer temperatures can expand it.
	- Excretion: Analysis of C:N:P can be measured to see if excretion will +. If ratio between prey and predator are similar, there is less nutrient cycling but more assimilation (which is optimal). (therefore, dif ratios means more nutrient cycling, less assimilation). Ratios are based off environmental conditions
- 2 of 3 variables are uncertain, and when layered with uncertaintities about phenology, poleward shift, and size, there emerge many complexities
- In order to address this, multi-driver experiments with variables that match real-life conditions can help to develop models that can test these variables and discern trends.

Higher Trophic Levels:

- Zooplankton and Phytoplankton phenologies are peaking earlier at a more quicker rate than their peers up the trophic pyramid, meaning there could be negative consequences, mostly related to accessibility for fisheries (squid and crab, too)

- There exist clear links between zooplankton and fishery conditions, however, more concrete data collection is needed in this area.
- Harder to model impacts on other species higher up the food chain (e.g. whales, seabirds, seals, etc.)

Challenges of Modelling Zooplankton in a Changing Climate:

- Modelling is a very useful technique for modelling oceanic, phytoplankton and zooplankton dynamics. However, little confidence can be placed in some models as zooplankton are not represented or misrepresented. Three components needed (play biggest role in influencing biogeochem cycles– thus getting parameters for models):
	- Rates (things liked respiration, excretion, ingestion, etc.)
	- Traits (size, reproduction, stoich)
	- Stocks (biomass, abundance, area of coverage)
- Quantitative information on individual zooplankton species is needed. Use of DNA metabarcoding and other new, advanced technique to add to data deficit.
- Not enough empirical data to compare models to the real world conditions to carry out validation.
- Challenges can be overcome with image analysis and related advancements, especially when it comes to biomass estimation and assessing tax comp.
- Lack of data on zooplankton that live at lower depths of the ocean, which leads to information about nutrient cycling and other important processes being ignored.
- Integrating zooplankton into modelling systems can help address a myriad of experimental questions that were previously unanswerable. Progress has been made, but more needs to be made in order to get a fuller picture for impact of zooplankton.
	- This observation of inadequete data on zooplankton aligns a lot with how in Article #3, their role in carbon cycle was not well understood.

Sustained Observations Quantifying Impacts of Climate Change

- Article discusses the benefits of long-term ecological/climatic studies (provides insights over a longer period of time, allowing for more trends to be found, changes to be assessed, etc.) - important modeling crucial biological, biogeochemical, and physical phenomena
- The Longterm Ecological Research Network (LTER)
- Of 168 Long-Term Zooplankton monitoring programs, 81% is partially or completely unavailable. Severe lack of accessibility inhibits ability for scientific study to be carried out.
- Highlights the examples of past successes of experiments using LTER programmes to make a case for expanding accessibility.
- There also many opportunities for groups of zooplankton scientists worldwide to collaborate. With many gaps in data in certain regions of the ocean, article calls for these regions to be investigated more deeply.

The Future of Global Zooplankton Research

- So the main idea is that seasonality, pole-bound migration, and preferences for smaller body sizes are the 3 most definitive trends, which can have significant implications for biogeochem cycling and energy transferral up the trophic pyramid

- Shift from nets to sensors, methods involving nucleic acids, image tech, time series methods. Combining the best of old and new methods \rightarrow collect best data \rightarrow use that to create strong conclusions (use by policymakers and other members of society)
- Variety of sampling methods ought to be used. Best one for the given context.
	- Using satellites to connect zooplankton dynamics with oceanic/climate conditions
- Collaboration among different fields of scientists is necessary to attain data, offer methods of data collection, and attainment of necessary parameters.
	- This is what will lead to the multi-drive experimental models that can be used to test multiple experiments very easy through the use of computer modeling!

Linking Zooplankton Observations To Global Needs

- Modeling zooplankton dynamics will help humanity understand and protect them and the ocean better, helping environment in general
- Article identifies 4 goals going forward w/ regards to zooplankton
	- Create new time series programmes in addition to protecting existing ones
	- Improve integration of time series data
	- Better understand the impact of climate change on zooplankton
	- Make use of collaborative, interdisciplinary approaches in research
- That way, zooplankton can be better understood. Ramifications from the research can be developed, and society assisted.

Article #8 Notes: DNA methylation and gene transcription act cooperatively in driving the adaptation of a marine diatom to global change

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see the Materials and methods) after long-term high CO_2 , warming, and high CO_2 +warming adaptation compared with that under ambient condition, respectively. The red and blue colour in a certain symbol represent significantly up- and down-regulated genes, respectively. Grey indicates that genes were not significantly regulated. PAT, aspartate-prephenate aminotransferase; GOT2, aspartate aminotransferase: asnB, asparagine synthase: lysC, aspartate kinase: ASD, aspartatesemialdehyde dehydrogenase; thrA, homoserine dehydrogenase 1; thrB1, homoserine kinase; thrC, threonine synthase; SDS, L-threonine ammonia-lyase; ilvC, ketol-acid reductoisomerase; dapL, L, Ldiaminopimelate aminotransferase: lysA, diaminopimelate decarboxylase: glnA, glutamine synthetase; argAB, amino-acid N-acetyltransferase; argB, acetylglutamate kinase; argC, N-acetylgamma-glutamyl-phosphate reductase; P5CS, Delta-1-pyrroline-5-carboxylate synthetase; argD, acetylornithine aminotransferase; argG, argininosuccinate synthase; argH, argininosuccinate lyase; rocF, arginase; proC, pyrroline-5-carboxylate reductase; trpC, indole-3-glycerol phosphate synthase; PRPS, ribose-phosphate pyrophosphokinase; hisG, ATP phosphoribosyltransferase; hisB, imidazoleglycerol-phosphate dehydratase; hisC, histidinol-phosphate aminotransferase; PHGDH, D-3-phosphoglycerate dehydrogenase; serC, phosphoserine aminotransferase; cysE, serine Oacetyltransferase; MET17, O-acetylhomoserine; cysK, cysteine synthase; AGXT2, alanine-glyoxylate transaminase; GPT, alanine transaminase; leuA, 2-isopropylmalate synthase.

Figure 2 - This figure illustrates the various possible manners in which amino acid metabolism may be inhibited by the inhibition of carbon metabolism. Various pathways, processes, and reactions are included. Triangles, squares and circles represent the high $CO₂$, high temperature, and high $CO₂$ and temperature treatments, respectively. Among triangles, there are 9 that are blue, and 1 that is red. Among squares, there are 17 that are blue and 10 that are red. Among circles, there are 12 that are blue, and 10 that are red. This indicates that amino acid metabolism processes inhibited are most numerous for the phytoplankton exposed to high temperature conditions (the article does indeed discuss this

finding the subsequent section), However, along with the high $CO₂$ and temperature treatments, they have the highest amount of genes in the amino acid metabolism process that are being upregulated. This is unlike with high $CO₂$ treatment, which, despite having the lowest amount of downregulated genes, has the least upregulated ones. Although, this may be an indication that this treatment group has a weaker impact either way on amino acid metabolism.

This figure displays the rates of net photosynthesis and respiration among the four treatments given assay temperature. Evidently, for all treatments of both metrics, there is a parabolic relationship that concaves down. For respiration, the maximum points of the parabola are just above -2 pmol O_2 per cell per hour for the warming and combined treatment, whereas it is 0 for the other two treatments. This lines up with the finding that photosynthesis is inhibited most under warmer temperature conditions, and not so much under high $CO₂$ conditions. For respiration, the peaks for the warming and combined groups are lot farther up in temperature (along x-axis) than non-heated treatments, around 35[°]C, while non-heated treatments reach their optimum respiration rate at 20[°]C. The peak respiration of the latter is slightly higher, at around -1 pmol O_2 per cell per hour.

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NOTES:

Abstract:

- DNA Methylation is known for its largely regulatory functions, but an area that has yet to be investigated is the potential positive interactions it could have with gene transcription.
- Brief discussion of methodology: Various experimental groups of *Phaeodactylum tricornutum* (hereafter *P. tricornutum*) were exposed to high temperatures and $CO₂$ levels, with analysis of transcription and phenotypes and bisulfite sequencing being performed.
- Findings show that experimental groups with higher CO_2 , or groups with CO_2 and warm temperatures that had the DNA methylation expressed more genes.
	- Article refers to this as DEG, differentially expressed genes, and DMR, differentially methylated regions
- - These DEGS then acted in concert with DNA methylation to regulate processes including metabolism of carbon, amino acids, and lipids, production of ribosomes, recycling denatured proteins, among others.

- This illustrates the capabilities of phytoplankton to adapt to changing ocean conditions. Introduction:

- DNA Methylation (hereafter DNAM) is an epigenetic process, meaning it regulates the gene expression but not composition. Short-term modifications can lead to long-term adaptations across a species (via the means of evolution, natural selection, etc.)
- Area that has not been previously focused on is the impact of DNAM on long term adaptations in phytoplankton, especially given changing ocean conditions.
- DNAM theorized to play major role in phytoplankton evolution due to findings in previous research that DNAM regulated phenotypic traits under high $CO₂$ conditions
- Aim is to investigate possible positive relationship between DNAM and transcription.
- Model species *P. tricornutum*. Genes have been sequenced, mutations quantified, and methylation information has been obtained. There are many genetic and epigenetic factors at play that need to be investigated (namely, are changes observed due to environmental conditions or biochemical processes?)
- Four treatments: Control (400 μ atm of CO₂, 15 °C); High CO₂ (1000 μ atm of CO₂, 15 °C); High Temperatures (400 µatm of CO_2 , 20°C); Both High CO_2 and Temperature (1000 μ atm of CO₂, 20°C)
- *- P. tricornutum* grown under respective treatments for approximately two years.
- After this period of time, transcription analysis, bisulfite sequencing. DNAM and gene expression were correlated and then used to consider possible biological processes subject to regulation.
- Important insights for evolutionary biology of phytoplankton.

Methodology:

Conditions:

- Describes/justifies the use of the four treatments mentioned above. (1000 µatm $CO₂$ and 20° C temperature are the projected $CO₂$ and temperature levels by end of 21st century in high emissions scenario, while controls were chosen given ideal conditions for model organism)
- 100 umol flux of photons in a 12 hour light and dark cycle
- Cloning performed in order to create enough specimens for all four treatments
- For $CO₂$, margin of error of 30 μ atm for the control, 50 for the experimental groups.
- Study describes how various aeration and atmospheric regulation techniques were used to maintain desired $CO₂$ levels. Use of bottles to prevent undesirable air exchange.
- Cellular density was kept at constant $4*10^4$ and $5*10^5$ cells per ml, regulated as needed every 5-7 days
- About 1600 to 1700 generations were produced over the course of the two-year experiment.

Qualifying Phenotypic Traits:

- Main traits investigated include net photosynthesis and respiration.
- Samples of phytoplankton were placed in 5 mL Tris-buffered solutions that were adjusted to match $CO₂$ and pH conditions of their respective treatments. 10 minute acclimation period
- Oxygen evolution in the light and oxygen consumption in the dark were measured using oxygen electrodes in order to measure net photosynthesis and respiration. While this is standard methodology, rates may vary due to varying photosynthetic quotient in phytoplankton and macrmolecular composition. Either way, both of these metrics were normalized.
- Modeling net photosynthesis in relation to temperature was down using the Sharpe-Schoolfield equation (includes variables such as rates of metabolism, metabolic activation energy, temperature at which enzymes are inhibited, temperature in kelvin, extensive use of natural logarithms)
	- An equation relating the highest metabolic rates to their optimum temperature levels was also used.

Analysis of Transcription

- Specimen from all four treatments were removed from their respective environments at the same point in the cell cycle, during light exposure, for the purposes of RNA extraction, being stored in liquid nitrogen as -80℃

- Extracted via the use of Trizol reagent kit, following manufacturing instructions, quality assessed by using the software Agilent 2100 Bioanalyzer and performing electrophoresis.
- Enrichment of RNA (excising of extraneous sequences) was performed using oligosaccharides for eukaryotic cells, and prokaryotic cells using a magnetic kit
- mRNA was then reverse-transcribed into cDNA $(c = copied/complementary)$. The second strand of DNA was then created using DNA polymerase and other enzymes, with ligation process (i.e. connection of Okazaki fragments) also occurring
- 12 samples for each treatment (of sample size of about 40 million, that is reading of DNA sequences. Due to quality control to maximize data quality and accuracy, only about 94% of sequences were read)
- This DNA was then matched to *P. tricornutum* ribosome database to determine which of the reads were valid (about 90 to 95%).
- Gene expression quantified by calculating the fragment per kilobase of transcript per million mapped reads (FPKM)
- DNA was determined to be a DEG by analyzing the differential RNA expression between two different groups and finding genes with a false discovery rate (FDR) of less then 0.05, and that had absolute fold changes.

Gene Mapping

- All of these genes were then mapped on the Gene Ontology (GO) software, where the DNA was analyzed and assigned to one of three categories (this is known as annotation): molecular function, biological process, and cellular component
- Metabolic and signal transduction pathways were examined using Kyoto Encyclopedia of Genes and Genomes (KEGG)

Analysis of DNAM

- Similar to transcriptional analysis, specimens from all four treatments were removed from their respective environments at the same point in the cell cycle, during light exposure, to analyze the DNAM
- DNA was extracted, its efficacy verified through electrophoresis, and its concentration measured through a spectrophotometer.
- In order to perfom the bisulfite sequencing, DNA library was prepared. DNA was split up into multiple fragments, and adenine was added to the 3' prime end of the strand. All DNA was then ligated.
- During the bisulfite treatment, non-methylated DNA was converted into uracil. Meanwhile, methylated DNA was able to converted successfully by the bisulfite.
	- (Answers question of why use bisulfite good for differentiating between methylated and non-methylated DNA)
- For the DNA that was converted, the DNA was augmented using PCR, and then sequenced. However, raw reads were eliminated from analysis if over 10% of nucleotides were unknown and/or 40% of low quality nitrogenous bases had to be removed.
- BSMAP software was used to map the clean reads of DNA to *P. tricornutum* database. This software is able to detect methylation patterns. Using this, methylation rate (amount of methylation that occurred throughout entire genome

sample, each chromosome, and each region) was calculated. Average methylation rate helped detect patterns in methylation among different DNA regions

- DMRs were identified using chi-squared test and various criteria during sequencing (mainly pertaining to reading lengths)
- DMR genes were analyzed using using GO and KEGG to determine impact of DMR genes on function, and expression, and thus biological ramifications.

Correlating DNAM & Gene Expression; Correlating DEGs & DMRs

- Tested given the hypothesis that DNAM helps propagate gene expression, and how the regulation this brings about differs between $CO₂$ and temp levels.
- Spearmen correlation analysis performed. Rho value has to be either positive or negative, p-vale below 0.05 to have definitive positive or negative correlation between these two variables.
- Genes were divided based on the level of expression they underwent.
- Methylation rates were quantified separately among the four treatments
- The correlation between methylation of DMRs and gene expression of DEGs was also measured using Spearman correlation analysis and regression analysis.

Results:

-

Overall Regulation Among Treatments and Various Functions Impacted

- Among the three experimental treatments, the most overall regulation occurred in the high $CO₂$ and high temperature treatment, followed by high temperature, then high $CO₂$ groups
	- \sim ~1100 genes up-regulated and down-regulated in high CO₂ and high temperature
	- \sim \sim 700-900 genes up-regulated and down-regulated in high temperature
	- \sim 300-400 genes up-regulated and down-regulated in high CO₂
- Most genes regulated had to do with catalytic activity, metabolic process, and cells and cell parts.
- Analysis of DEGs reveals that the treatments conditions (in the regulation patterns described above) had heavily regulated metabolic processes.

Down-Regulation of Carbon Metabolism Following Long-term High $CO₂$

- Enzymes that play a role in glycolysis were significantly down-regulated. Same goes for genes encoding proteins that create the glycolysis pathway.
- Various enzymes and genes relating to pyruvate and its role in respiration were also inhibited under high $CO₂$ conditions
- Genes producing the enzymes involved in the tricarboxylic acid cycle (TCA) (Krebs Cycle) were also down-regulated.
- Genes involved in the enzymatic methods for concentration of $CO₂$ waste were likewise inhibited
- Overall, this indicates that the higher $CO₂$ levels in ocean (and thereby higher pH levels) reduces carbon metabolism due to lowered expression of the genes the produce enzymes and other substances that facilitate the steps of respiration.
- Since carbon metabolism plays a role in amino acid production and metabolism, certain amino acids have been observed to also have been downregulated. Lower amino acid metabolism would reinforce the findings of lower carbon metabolism.

Alterations to Amino Acid Metabolism Following Long-term High Temperatures

- As described in figure 2 above, the high temperature treatment experienced the most interference from DEGs, both up and downregulations.
- Comparison between high $CO₂$ and high temperature treatments: production of 5 amino acids prevented vs. 7
	- Gives examples of how genes involved in producing enzymes that synthesize alanine and histidine are being downregulated.
- However, recall again from figure 2, there was only one upregulated gene for the high- $CO₂$ treatment. Here, article notes the variations that the high temperature treatment experiences with regards to amino acid metabolism
	- Genes aiding in the synthesis of glycine were upregulated, while for ones metabolizing lysine and cysteine had both up and downregulation

Changes to Amino Acid Metabolism Under High Tempeatures and High $CO₂$

- As for the high $CO₂$ and high temperature treatments, there is evidence to suggest that these two conditions interact with each other to impact amino acid metabolism
	- One enzyme involved in producing lysine was more upregulated when exposed to high temperature alone than in this treatment, suggesting that the $CO₂$ inhibited the protein metabolism in this case.
	- Another enzyme that was downregulated with only $CO₂$ treatment was upregulated in this treatment.
- By contrast, many of the other upregulations and downregulations matched those of high CO₂ and high temperature treatments alone. (there were only four exceptions, and only the ones noted above were discussed)

Fatty Acid Metabolism Dynamics following High $CO₂$

- Many of the genes producing enzymes involved in fatty acid metabolism were significantly upregulated, which would therefore enhance fatty acid metabolism.
	- This includes a gene producing an enzyme that converts glycerol to glycerol 3-phosphate for making triglycerides, among many others
- However, there were two exceptions (i.e. downregulations)
	- A gene of an enzyme that helps in fatty acid anabolism by establishing double bonds among monounsaturated fatty acids.
	- Another gene which encodes an enzyme (a type of ligase) that helps create cellular lipids
- When carbohydrates cannot be metabolized, lipids and proteins are. Therefore, the increased ease of fatty acid metabolism observed through the overwhelming upregulation of the genes that produce the enzymes involved is an indication of the significant hinderance carbon metabolism faces under these conditions.

Down-Regulation of Photosynthesis Following Long-term High Temperatures

- Photosynthetic process, as a whole is inhibited. Genes encoding enzymes and other substances involved in the process of photosynthesis are inhibited.
- Down-regulation of genes that allow for chlorophyll a and b to absorb and use light energy via the creation of light harvesting complexes
- Down-regulation of genes that are involved in producing mechanisms for oxygen discharge during photosynthesis.
- Down-regulation of genes that produces enzymes and other substances that move electrons along the photosynthetic electron transport chain
	- (Unrelated but good to know for photosynthesis) Proton gradient of differing electrical charge is generated as the electrons are transferred to the transport chain. This allows for phosphorylation of ADP via ATP synthase.
- Down-regulation of genes that produces enzyme that helps transfer electrons from the transport chain to help convert NADP into NADPH.
- Production of Mitochondrial ATP Synthase was downregulated while chloroplast ATP synthase remained unaffected.
- Higher temperature seems to be the cause of the reduction in production of ATP synthase, as in high- $CO₂$ and control treatments, there is no reduction, only ones where temperature is greater.
- Since agents of the light-dependent reaction were inhibited, the Calvin cycle was too (although these two reactions are not always coupled)
- Indeed, most of the genes that produce enzymes and other substances directly involved in Calvin Cycle were inhibited.
- Most genes for the C_4 pathway are also being downregulated, although it is unknown whether *P. tricornutum*
- Overall inhibition of photosynthesis was even observed at the translational stage
- As photosynthetic process was inhibited, the genes producing pigments such as chlorophyll, caretenoids, porphyrins, and aiding in the metabolization of these various pigments were also downregulated.

The Impact of Simultaenously High $CO₂$ and High Temperature More In-Depth

- For the most part, downregulations and upregulations observed were consistent to what was observed for the separate high $CO₂$ and high temperature treatments.
	- For example, 29 out of 30 genes relating to proteasome, the regulation of the concentration of various proteins and the discardal of folded proteins, were consistently downregulated among all three treatment groups (only 1 was upregulated in the combined treatment)
- However, there were notable differences as well (beyond what has already been noted above):
	- Genes that experienced no impact under high $CO₂$ or temperature conditions experienced down regulation in the combined treatment, indicating that when these factors act in concert, gene regulation occurs.
	- One gene that was downregulated in the high $CO₂$ treatment was upregulated in the combined one, suggesting that high temperature prevented inhibition of the gene expression.
	- Conversely, a gene down-regulated in the high temperature treatment was less down-regulated in the combined one, meaning $CO₂$ helped reduce gene inhibition, with similar patterns being observed for various genes for photosynthesis (although up-regulation was also made less extreme)

Transcription and DNAM

- To evaluate the relationship between DNAM and gene transcription, methylation was measured among genomic samples collected.

- While methylation levels vary drastically across the genome, the methylation rates observed matched the well-established data of methylation for the model species.
	- This *should* be the case, however, possibly due to stress of environment and the bisulfite sequencing technique that was used.
- The proportion of various types of methylation, along with genomic rate of methylation was fairly similar among all groups.
	- There were 3 types of DNAM investigated, mCG, mCHG, and mCHH.
	- For mCG, there is a statistically significant negative correlation with gene expression.
	- For mCHG, all but one (assuming alpha $= 0.05$) have a statistically significant positive correlation with gene expression
	- For mCHH, there are few statistically significant regressions to observe any coherent correlation with gene expression.
- DMRs (standards of determining DMRs enumerated in methodology section) were also investigated.
- Many DEGs occurred in DMRs.
	- Meaning that for the genes were expressed or suppressed to a statistically significant degree, they occurred in regions where there was statistically significant amount of DNA methylation that occurred, indicating that DNA methylation plays major role in gene regulation
	- From least to greatest: High $CO₂$, High Temperature, and combined treatments
	- Numerous examples given of various genes that are DEGs that encode proteins for a myriad of processes that are in DMRs.
		- Metabolism of macromolecules, photosynthesis, ribosome biogenesis, among other processes (hey, matches abstract!)

Discussion:

- Previous study (done by this group?) showed how there was simultaneously significant genomic diversity losses and enhancements for *P. tricornutum* when exposed to high CO₂ and/or temperature conditions.
- Helped establish understanding of evolutionary biology needed for this study, from there, study is summarized:
	- Goal of showing DNA methylation is empirically connected to gene regulation (novel, as common understanding is DNAM is inhibitory)
	- Predominant finding that most genes were inhibited as a response to these treatment environments. Meaning DNAM causes downregulation of genes!
	- Area of future focus: molecular mechanics of DNAM and changes in gene expression
- Thus, the study argues that DNAM shall serve as an important tool for phytoplankton as they adapt to changing ocean conditions.
- However, some caution:
	- DNAM is not that common and frequent among other phytoplankton species.
	- DNAM might not really regulate gene expression unless in high quantities
	- E.g. larger DNAM was used used on same species only to do testing with nitrates.
- Only 18-24% of DEGs occurred in DMR, so DNA methylation may have nothing to do with the gene regulation observed.
- Possibly plays role in regulating sulfate pathways during chromium stress
- Although smaller part of genome for phytoplankton, its possible that DNAM helps metabolism, life cycle, and differentiation of tissue of certain species
- Still, conclusion is that DNAM, even in small rates, can be positively coupled with gene expression.
- Ambiguity persists over whether the traits observed (mainly metabolism) were due to DNA sequence itself changing or epigenetic processes like DNAM.
- Knowing this information is important for tracking biogeography and overall phytoplankton dynamics.
- Via all of those up and downregulations, it was found that phytoplankton can adapt to warmer, more acidic (i.e. water with more $CO₂$) conditions by establishing a new optimal metabolic rate, however, this may diminish primary production
- Of all articles so far, this has offered most concrete, realistic advice for helping understand phytoplankton: Long-term studies that examine the evolutionary biological response to stressors ought to occur.
- Establishing links across different levels of biological organization.

Article #9 Notes: Two-sided effects of the organic phosphorus phytate on a globally important marine coccolithophorid phytoplankton

Important Figures

course of the experiment. The cell concentration for the control group remained at a constant 0 cells for 1 million cells per milliliter. Meanwhile, the group exposed solely to DOP (that is, phytic acid, PA), has a linear increase in concentration. Both the groups that were exposed to both DOP and DIP and exclusively DIP followed the same track of concentration, however, at day 11, the former leveled off while the latter grew exponentially.

The right line graph shows the productivity of alkaline phosphatase. In the control environment, where there was no exposure to DOP or DIP, this enzyme became more and more productive (which make sense, as conditions without phosphorous would likely prevent inhibition of a dephosphorylating enzyme). The group exposed to exclusively DIP saw the least productivity, followed by the combined treatment and then the treatment involving exclusively DOP. Conversely to what was observed with cell concentration, it seems that DIP inhibits expression of alkaline phosphatase, whereas DOP allows for it.

lipid contents, and relative cell size were measured on the 5th day

Figure 2a illustrates the photosyntehtic efficiency of the four treatments over the course of the experiment. Although all of the non-control treatment have slightly declining efficiencies, they are all still above the non-phosphorous contaiining control. This indicates that while phosphorous boosts photosynthetic activity, the difference in quality between DIP and DOP is negligible.

Although more efficient, figure 2b clearly illustrates that the non-phosphrous treatment had a greater amount of chlorophll pigments produced than any of the treatments exposed to phosphorous. This is an interesting finding considering that this treatment had to lowest photosynthetic efficiency. Since the control is the least efficient, perhaps less photosynthesis is completed, leading to more chlorophyll pigments being leftover.

Figure 2c, which analyzes caretenoid pigments, might be indicative of a similar pattern. Here, the control and the treatment exposed only to DOPs had the highest caretenoid concentrations. This could indicate that treatments that were exposed to DIP were best able to metabolize, expending both chlorophyll and caretenoids. Figure 2d compares lipid fluorescence among the four treatments, clearly indicating that the control group exposed to no DOP or DIP had the greatest amount of lipids. While not having as much as the control, the treatment exposed exclusively to DOPs had a much greater amount of lipid fluorescence than the other two groups. The combined treatment has the third highest amount of lipid fluorescence, suggesting that DIPs inhibit the production of lipids. Figure 2e, which compares cell size among the four treatments, shows a similar pattern. However, while the control treatment had greater cell sizes on average, here, all three of the experimental treatments are a lot closer when it comes to cell size, although the DOP-exclusive group has considerably larger cell sizes. This once again suggests that DOP might help cell growth, whereas DIP might impede it.

Figures 3a and 3b show an interesting trends regarding particulate organic carbon and nitrogen (POC and PON) levels. In both cases, the control has a significantly greater amount of both particulates. This means that carbon and nitrogen absorption occurred to the least extent for the control group, implying that exposure to phosphorous assists phytoplankton in incorporating these compounds. However, following this logic, since the POC and PON levels are higher in the POC-exclusive treatment, followed by the combined treatment and then the PIC-exclsuive treatment, this suggests that PICs maximize carbon and nitrogen integreation.

Based of the scaling of each graph figures 3d through 3f, the ratio between carbon, nitrogen, and phosphorus is such that carbon is the most plentiful, followed by nitrogen, and then phosphorus. Otherwise, seeing as the control has little phosphorus to begin with, it make sense that it has the C:P and N:P highest ratios. However, from C:N, N:P and C:P, the ratios became more varied, likely due to the abundance levels of each substance.

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NOTES

Abstract:

- Phosphorous is a potential agent of eutriphication
- Inositol hexaphosphate, aka phytic acid (hereafter PA) is a major oceanic nutrient, but mechanisms and impact on phytoplankton not well understood
- PA, when the only source of P, plays a major role in enhancing metabolic processes, C $\&$ N fixation, and amount of lipids.
	- P also plays major role in various parts of homeostasis and community structure
- However, PA can also be toxic
- These findings are important in understanding the relationship between P and phytoplankton conditions
- The use of common DOP (dissolved organic phosphorous compound) was analyzed on a common species of phytoplankton.

- Both physiological and transcriptomic means of measurement and analysis.

Introduction:

Mentions different between DOP and DIP (dissolved inorganic phosphorus compound), risk of P causing eutriphication. DOP > DIP in concentration

- Two types of DOP: phosphoester (80% of DOP), and phosphonate (20% of it)
- PA, which is a phosphoester, cannot easily be absorbed by many land plants due to lack of enzymatic capabilities. This leads to run-off into the ocean as this is excreeted as aqueous waste, and thus, risks for eutrophication
- Eutrophication leads to different, disrupted community structure.
- *- Emiliania huxleyi* (*E. huxleyi*) is the most cosmopolitan and abundant coccolithophore
- Past work has shown that other phosphorus-containing molecules have been successful for this species, but PA and other compounds and species need to be investigated.
- PA is a good mechanism for growth and helps combat starvation of P
- Findings show large amounts of change in metabolic activity in order to adapt to varying P levels.

Means and Methods:

- Incubation: 14 hour light, 10 hours dark cycle in seawater.
- During the exponential growth phase of the algae (*E. huxleyi*), were extracted, deprived of all P, and the exposed to four following conditions in a media
	- No dissolved inorganic or organic phosphorus (sort-of a control) **(P-)**
	- 36 µM of Dissovled Inorganic Phosphorus **(P+)**
	- 12 µM Phytic Acid (the DOP used in the experiment) **(PA)**
	- 12 µM Phytic Acid and 12 µM Dissovled Inorganic Phosphorus **(P+PA)**
- Use of microscopes to track growth and cell size, along with flow cytometer.
	- Calculations used to track growth rate (original and final population, $ln()$)
- In order to measure photosynthetic output, all four groups had sample of 10m cells taken, put into a dark solution of methanol. Then, chlorophyll and carotenoid pigments were extracted and measured using spectrophotometer.
- DIP concentrations kept constant to the levels assigned through heating mechanisms and potassium persulfate.
- Alkaline phosphatase (see definition) activity was measured by taking samples, exposing them to 2 hours of darkness, followed by centrifuging process. Using nanowaves, absorbance rates were measured.
- In order to measure carbon fixation and nitrogen assimilation, all samples were cooked in oven, fumed in HCl, and placed in tinfoil sheets. From there, an element analyzer machine was used.
- Amount of Lipid quantified by taking sample of 1m cells, staining it, leaving it in the dark for 20 min, and then using flow cytometer, measuring fluorescence
- - For analyzing gene expression: 50m cells from each treatment were centrifigued. Then, RNA was extracted, subject to enrichment (see definition above), reverse transcription, the re-addition of the poly-A tails, Okazaki fragments were ligated, then PCR amplification, denaturation and cyclization were used to create a DNA sequence.
- Low quality nucleotides were eliminated, and the remaining ones where compared to the *E. huxleyi* genome to measure gene expression.
- Using KEGG and DEG analyses and a false discovery rate of $q \le 0.05$, differentially expressed genes were identified
- ANOVA, means, stdev, were used for statistical analyses.
- 17 day experiment

Results (see figures section, they're basically synonymous, given the article's structure):
- The cell concentration for the control group remained at a constant 0 cells for 1 million cells per milliliter. Meanwhile, the group exposed solely to DOP (that is, phytic acid, PA), has a linear increase in concentration. Both the groups that were exposed to both DOP and DIP and exclusively DIP followed the same track of concentration, however, at day 11, the former leveled off while the latter grew exponentially.
	- Barring the control (which I think is meant to be at 0 concentration), this suggests that DIP help increase cell growth and concentration, whereas DOP decreases it. This would explain why the concentration eventually leveled off for the combined treatment
- For Alkaline Phosphatase:
	- In the control environment, where there was no exposure to DOP or DIP, this enzyme became more and more productive (which make sense, as conditions without phosphorous would likely prevent inhibition of a dephosphorylating enzyme). The group exposed to exclusively DIP saw the least productivity, followed by the combined treatment and then the treatment involving exclusively DOP. Conversely to what was observed with cell concentration, it seems that DIP inhibits expression of alkaline phosphatase, whereas DOP allows for it.
- For photosyntehtic efficiency of the four treatments over the course of the experiment, although all of the non-control treatment have slightly declining efficiencies, they are all still above the non-phosphorous containing control. This indicates that while phosphorous boosts photosynthetic activity, the difference in quality between DIP and DOP is negligible.
- Although more efficient, the non-phosphrous treatment had a greater amount of chlorophll pigments produced than any of the treatments exposed to phosphorous. This is an interesting finding considering that this treatment had to lowest photosynthetic efficiency. Since the control is the least efficient, perhaps, since less photosynthesis is completed, more chlorophyll pigments are leftover.
- Data on the caretenoid pigments might be indicative of a similar pattern. Here, the control and the treatment exposed only to DOPs had the highest caretenoid concentrations. This could indicate that treatments that were exposed to DIP were best able to metabolize, expending both chlorophyll and caretenoids.
- As for lipid fluorescence among the four treatments, it is clear that the control group exposed had the greatest amount of lipids. While not having as much as the control, the treatment exposed exclusively to DOPs had a much greater amount of lipid fluorescence than the other two groups. The combined treatment has the third highest amount of lipid fluorescence, suggesting that DIPs inhibit the production of lipids.
- Figure 2e, which compares cell size among the four treatments, shows a similar pattern. However, while the control treatment had greater cell sizes on average, here, all three of the experimental treatments are a lot closer when it comes to cell size, although the DOP-exclusive group has considerably larger cell sizes. This once again suggests that DOP might help cell growth, whereas DIP might impede it.
- With regards to particulate organic carbon and nitrogen (POC and PON) levels, in both cases, the control has a significantly greater amount of both particulates. This means that carbon and nitrogen absorption occurred to the least extent for the control group, implying that exposure to phosphorous assists phytoplankton in incorporating these

compounds. However, following this logic, since the POC and PON levels are higher in the POC-exclusive treatment, followed by the combined treatment and then the PIC-exclsuive treatment, this suggests that PICs maximize carbon and nitrogen integreation.

- The ratio between carbon, nitrogen, and phosphorus is such that carbon is the most plentiful, followed by nitrogen, and then phosphorus. Otherwise, seeing as the control has little phosphorus to begin with, it make sense that it has the C:P and N:P highest ratios. However, from C:N, N:P and C:P, the ratios became more varied, likely due to the abundance levels of each substance.
- For the transcriptional analysis, of the 36,293 genes that were identified as expressed, 4,153 were considered DEGs, specifically when comparing the DOP-exlusive treatments with the DIP-exclusive treatment. This corresponded to 3 KEGG metabolic pathways related to amino acid metabolism and carbon fixation.
- However, when comparing the combined treatment to the DIP-exlusive treatment, there were 6,412 DEGs, mapped to 19 metabolic pathways, which, in addition to the ones above, included oxidative phosphorylation, photosynthesis, nitrogen and fatty acid metabolism, and so much more.
- Genes associated with carbon fixation and photosynthesis were significantly upregulated. This included genes related to electron transport chain, ATP synthase, light-harvesting complex, as well as numerous genes related to the Calvin cycle. Carbonic anhydrase, the main mechanism of carbon fixation, is upregulated.
- For amino acid metabolism, increased production and abundance of ribosomes, along with the upregulation of various enzymes responsible for the catabolizing and anabolizing various nitrogenous and other protein compounds was observed.
- Meanwhile, for carbohydrate metabolism, genes involved in Krebs cycle and glycolysis were also significantly upregulated.
	- These various upregulations were observed primarily in PA (DOP)-exlusive and combined treatments.

Discussion:

- Reiterates purposes of study, to understand specifically the impact of phytic acid (PA). References cosmopolition scope of both the compound and *E. huxleyi*.
	- Study with a previous diatom showed that phytic acid impeded iron availability.
	- Argues that *E. huxleyi* are versatile in adapting to different conditions, including the different DIP and DOP levels of this experiment.
	- PA use could play a major role in nutrient cycling done by phytoplankton
- In groups that contained the DOP-exlcusive (PA) treatment, there was no detection of DIPs, indicating that PA could be easily absorobed *E. huxleyi* by cells.
- However, observation of the DIP-containing treatments indicated that DIP had no impact of the ability for PA to be absorbed, which is surprising, b/c expectation is that DIP would be absorbed in favor of PA.
- Once absorbed, the PA serves as an important source of growth.
- Study investigates whether PA can be absorbed by *E. huxleyi* (it can indeed be absorbed by terrestrial plants), comparing it to *Phaeodactylum tricornutum*. Given the down regulation of certain genes, it is concluded the intracellular hydrolysis and utilization are

the main sinks for *E. huxleyi*, whereas for *P. tricornutum*, PA causes less growth due to greater extracellular hydrolysis and vaculoar storage.

- Different ways of using nutrients like PA have important ecological ramifications regarding phenology, bloom patterns, and succession that are caused by changing phosphorous levels.
- As we've seen, metabolism is impacted by the use of PA (the DOP). RNA is in fact an indicator of P nutrient quota and status, so the increased RNA points to how PA is being increasingly incorporated by *E. huxleyi*
- PA is used to enhance synthesis of Poly-P, an important molecule involved in cell signaling. In a similar vain, genes for the metabolism of phospholids were also upregulated, meaning PA plays an important in strengthened cell membranes, signaling, and communication.
- Additionally, the PA-grown treatments caused greater amount of phosphorylation, enhancing the production of ATP through facilitating production of ATP synthase.
- These trends represent intriguing allocation of PA on part of *E. huxleyi*
- The C:P, N:P, and C:N ratios have all increased due to improved ability to fix carbon and assimilate nitrogen. The higher ratios underscore the enhcaments to the metabolic processes for phytoplankton.
- To test for PA-induced toxicity (something observed in their previous study w/ *P. tricornutum*), stressors between the exclusively-PA and combined treatments were compared.
- Both PA-containing groups displayed same signs of metabolic stress, namely greater amounts of lipids and enhanced fatty acid metabolism. Genetic adaptations also included faster rates of metabolism, which is also associated with coping with environmental strains. Given that these stressors are the same despite the presence of DIP, this indicates that PA can potentially be toxic.
- PA is known for its attraction to various heavy metals (Fe, Mg, Ca, Zn), and restricting access to essential minerals and proteins.
- The lower growth rates observed in the PA-exclusive treatment could indicate toxicity
- More research needs to be done on heavy metals and proteins in relation to PA on phytoplankton.

Conclusion:

- PA is used to support growth (although it may be toxic and slow down growth in the process. This needs more research)
- DIP is not preferentially absorbed over PA by *E. huxleyi*, which challenges a long-held belief that they were. Moreover, DIP (which to clarify, was not in itself a variable, rather it was used in treatments to test the main variable, which was PA), does not impact the absorption of PA.
- Reiterates enhanced metabolic processes and other key findings

Article #10: Three-dimensional model for analysis of spatial and temporal patterns of phytoplankton in Tucuruí reservoir, Pará, Brazil

Important Figures

Fig. 2. Conceptual model of MOHID water quality module.

This diagram comprehensively illustrates biogeochemical cycling in a water body. Starting from the atmosphere, oxygen is absorbed via reaeration. Notice that the oxygen is DO, which, through various processes, is implemented into respective places in the cycle through the respective processes. Some DO becomes sedimentation, due to Sediment Oxygen Demand (SOD). Looking at another critical center point in the diagram, light allows for phytoplankton carry out photosynthesis. Through excretory processes and respiration, NH₄ is released. Nitrification occurs as NH₄ is converted into NO₂, and NO₂ into NO_3 . Through these processes, DO is implemented. Then, NO_3 is denitrified into N_2 . NH⁴ also contributes to the growth in the phytoplankton. Via grazing, nutrients are transferred to zooplankton (which is also able to grow via $NH₄$). Both zooplankton and phytoplankton, through both excretion and mortality, produced dissolved organic nitrogen and dissolved organic phosphorus. However, the formation of particulate organic nitrogen and phosphorus (particulate meaning concentrated into one entity, opposite of dissolved) occurs exclusively through mortality. Additionally, particulate organic carbon only forms from phytoplankton mortality, and only through mortality or excretion of phytoplankton is dissolved organic carbon formed. Particulate organic phosphorus, nitrogen and carbon all, through settling process, sink and contribute to sedimentation. Particulate organic nitrogen decomposes into dissolved organic nitrogen via the incorporation of DO (which occurs for processes for phosphorus and nitrogen). DON is then used to form $NH₄$ via mineralization. Similarly, particulate organic phosphorus becomes dissolved through decomposition, and all DOP is mineralized into PO_4 , which, like NH_4 , serves as nutrient of growth for phytoplankton. Lastly, through decay, all POC and DOC is converted into $CO₂$ and released into the atmosphere.

August and February. The slowest rate appears to be around October 2010, with a rate of around 3000 m $\frac{\gamma}{3}$ s. Meanwhile, all the nutrients oscillate at much faster rates and with much more unique patterns. For ammonium, the oscillation patterns seems to be that it reaches minimum concentrations between about 0.00 and 0.03 mg/L, reach one high of between about 0.10-0.13 mg/L, and another at around 0.16 mg/L, with these two peaks alternating between each other. For nitrates, there is also an oscillatory pattern, however, each peak is greater, reaching about 15, 25 and then 45 mg/L. Phosphate concentration starts off at low concentrations, around 0.002 to 0.004 mg/L. Then, between November and February, it increases gradually to about 0.015 mg/L, before declining (with another upward jump) back down to the lower levels. Lastly, DO tends to hover between 5.5 and 6.5 mg/L, with the exception of two oscillations downward to about 4.1 mg/L, and another two to about 4.7 to 5.0 mg/L.

This shows that each nutrient (in conjunction with flow rate), fluctuates at different rates, and that their concentrations vary greatly.

The various scatter graphs and accompanying table below display the comparisons of the model predictions and field data of temperature at the different vertical profiles. From these data and figures, it is very clear that the model has pretty accurate predictions. For all four instances of measurement (wet seasons and dry seasons $2010 \& 2011$), when comparing the raw data to the predicted values (i.e. the left graph in each quadrant), visually, the data plots of the actual field data do not stray that far away from the lines representing the predicted temperatures from the model. More quantitatively, looking at the scatterplots at each for each of the four instances (the ones on the right in each quadrant), we can observe more evidence of proper model calibration/good accuracy for predicting these trends. The gamma, i.e. the slopes, chronologically (high, then low rainfall 2010, and again for 2011), were 0.8285, 0.7934, 0.8218 and 0.834, meaning, overall, the model underestimated temperature at varying points along the vertical profile by about 20%. However, note that there are only a few data points. Thus, gamma (and thereby R^2 , and too an extent, entire linear model and NOF) is a weak indication of model efficacy. Gamma is the most "vulnerable" statistic to small sample size (because leverage points/outliers are going to be more drastic), other variables impacted too, but not as much. Either way, all R^2 values are above 0.93. These high R^2 metrics indicate that the variation in the predicted values are strongly based off the actual field data. Similarly, all NOF values are within 0.0300 of 0.0000, meaning the average of the difference between each individual predicted value from each field data value was nearly 0. Overall, there is considerable hegemony between the model predictions and the field data, indicating that in this respect, the model produces accurate results.

exception of a few outliers (for example, ammonium levels in Early March 2011 were severely overestimated, similar thing with phosphates and nitrates), all data points are very close, if not, visually on the line representing computer predictions. Quantitatively, going from the top left, the gamma slopes are 1.0864, 1.1957, 1.0425, 1.1268, and 0.9772. This suggests that, for predictions of this model in this area, nitrate and DO levels are most heavily overestimated for nitrates and ammonium (I don't know if it's ammonia or ammonium we're looking at in this study). However, among the four areas tested, while the slopes indicated the the model did overestimate a little bit, consider that small sample size, combined with outliers and leverage points created and accentuated these abnomalities. Of the four (station 1/3, surface/beneath), this one had the worst prediction rate when looking exclusively at slope. By contrast, the R^2 and NOF values were most ideal for the four tests of the model. From the top left, they are 0.9791, 0.9506, 0.9495, 0.964, and 0.9967. These high values suggest that all the computer modeling predictions are based almost entirely off (i.e. agrees with and properly simulates) the field conditions. It also demonstrates that some of these links are stronger for some nutrients and factors than others (and this itself would vary site to site). Lastly, from left to right, 0.0563, 0.3504, 0.2398, 0.0349 and 0.1667 represent the NOF for these parameters. All of these values are somewhat close to 0.0000, and although some are of a considerable numerical difference, all values are between 0.0000 and 0.10000 are considered signs that the data predicted from the model is in good match with the actual field data. Low NOF values indicate the difference between individually predicted and actual values, or at least the variation in said quantity (RMSE), is very little. Taken together, these data and findings clearly show that the model created is worthy of validation (which it did get).

Table 3

Statistical applied to verification model calculated phosphate, nitrate, ammonia, dissolved oxygen and chlorophyll a concentrations vs. surface and bottom field data in the Tucuruí reservoir (M1 and M3 Stations).

VOCAB:

(w/definition) Process-oriented Modeling - A technique that represents one or more variables, and how they are impacted by one or more processes as a means of characterizing an entire system and its dynamics. This technique operates on an input-output basis, and involves partial differential equations, the implementation of empirical data, and other advanced tools. **Advection** - The movement of nutrients and other material via fluid currents. **Water Mean Residence Time** - In the context of this study, this is equal to the total amount of water in the reservoir divided by either the inflow or outflow. More broadly, it is the measure of time a portion of a fluid stays in some controlled container. **Navier–Stokes Equations** - A set of four partial differential equations that model the

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Abstract:

- Study took place in the Tucuruí reservoir, Pará State, Brazil, which is a dam located in Northern Brazil, just south of where the Amazon empties out into the Atlantic.
- Knowing the variables and relationships that influence water quality is important for managing local aquatic systems (lakes, ponds, reservoirs, dams, etc.)
- Simulations for high and low rainfall periods were performed using a Hydrodynamic Model (hereafter MOHID), a type of process-oriented modeling system
- Field Data Collected: Weather conditions including air temperature, humidity, wind, could cover, solar radiation; Marine conditions including DO, temperature, micronutrients including nirtates, ammonia, and phosphorus.
	- Collection occurred 1 July 2010 to 1 July 2011
- Simulation based on data collected at the inlets and outlets of the reservoir.
- Findings include that the reservoir has a limited amount of phosphorus, growth in blooms is impacted by varying concentrations of nutrients between high and low rainfall periods. Additionally, chlorophyll a is a key indicator for modeling the ecology of the reservoir, in particular with regards to algal blooms.
- This study helped develop a better understanding of the reservoir as a whole, and helped developing mitigation policies for algal blooms

Introduction:

- As Brazil has developed and industrialized, it has made use of hydroelectric power for energy, but these systems have unknown and possibly irreversible consequences for marine ecosystems.
	- This is caused by the conflicting interactions of climate with the artificial currents generated by hydroelectric systems.
	- The Tucuruí reservoir (subject of the study) was one of the first hydroelectric power sources for the nation
- In particular, advective currents are modified by hydroelectric systems.
- Between light, temperature, and nutrients, nutrients are the only factor limiting phytoplankton growth that humans can (easily) control
	- This becomes important when considering the control of algal blooms, which is connected to nutrient concentrations
- However, in order for algal blooms to be regulated, it is important that the associated marine systems are well understood. Thus, this study aims to connect phytoplankton populations and nutrient concentrations to hydrodynamic forces.
- Most marine nutrients are lost due to uptake from algae. DO varies given the varying rates of photosynthesis (day) and respiration (night).
	- Greater loads of nutrient leading to greater uptake and oxygen production occurs during the day, transferring energy to higher-order organisms. Meanwhile, oxygen is depleted during the night, which can sometimes lead to anoxic conditions that harm higher-order organisms.
- Environmental processes can be better understood via mathematical modeling. Said models consider multiple factors including processes relating to water quality, sediment transport, and hydrodynamics. MOHID, a specific type of hydrodynamic model used in this field, which has these capabilities, is used in this study.
- Goal: Model the spatial and temporal trends of phytoplankton in the reservoir, connect phytoplankton populations and nutrient concentrations to hydrodynamic forces, as well as assess the impact on water quality (very multi-faceted).

Materials and Methods:

- Basic background information is provided about the reservoir,
	- Geographic coordinates (just south of the equator), surface area (2430 km^2) , water mean residence time (46 days), temperature range (27℃ - 34℃), average stream flow $(11k \text{ m}^3/\text{s})$.
	- Since 1984, properties (same as ones mentioned in abstract) have been monitored.
	- Inflows from Araguaia, Tocantins, and Itacaiunas river (45%, 40%, and 5% contributions, respectively)
	- NE prevailing winds, October to April is when reservoir is most full
	- Reservoir has been studied through a variety of lenses (chemical, environmental, social, floral, faunal, economics, etc.), however, this study was first one to focus on water quality and hydrodynamics
- Provides background info on the MOHID model, and various math equations:
	- Portuguese model programmed using object-oriented programming in FORTRAN (formula translation) 95,
	- Contains various modules that are able to analyze physical and biogeochemical factors, including the hydrodynamic and water quality modules.
	- Hydrodynamic module uses the Navier–Stokes equations (see definition above)
	- Mathematical modeling of nutrient and organic matter cycling is based on conservation equations that take into account DO and dissolved nutrients in the pelagic and benthic phases, phytoplankton, zooplankton.
	- Equation used to model the primary production of phytoplankton, which is based off exponential growth models which measure the variation in biomass given initial biomass.
- Biomass multiplied by net primary production (Gross primary production minus respiration, grazing, mortality, and excretion)
- Use of maximum growth rate equation is used.
	- Maximum growth rate at a given temperature, multiplied by the limiting factors of temperature, light availability (as measured through radiation intensity), and nitrogen, ammonia, and phosphorus conditions
- Lambert–Beer law is used to model reduction in light availability given greater depth in the water body (i.e. light attenuation), and another equation is used for finding the water column light extinction coefficient, which is based off the phytoplankton self-shading effect, chlorophyll concentrations, and suspended particulate material.
- Implementing the Model
	- Bathymetric measurements of the reservoir were attained. Generally, the further south, the shallower the reservoir becomes.
	- Using the field data collected from July 2010-2011, the hydrodynamic and water quality models were set up and verified.
		- The following variables were inputted into the model: Bathymetry, air temperature, solar radiation (i.e. light availability), wind speed and direction, inflow and outflow, water temperature, concentrations of the various nutrients, DO, and total suspended solids.
		- Various parameters were instituted for the model. Their values were derived from the literature, and then adjusted so that the model results and field data could be in agreement.
		- Parameters included the following:
			- Maximum gross growth rate at the reference temperature
			- Optimum light intensity for phytoplankton photosynthesis
			- Nitrogen and Phosphorus half-saturation constants
			- Endogenous respiration and Excretion constants
			- Maximum mortality rate (at reference temperature)
			- Phytoplankton mortality half-saturation rate
			- Phytoplankton assimilation efficiency
			- Phytoplankton nitrogen/carbon and phosphorus/carbon ratio (redfield ratio)
			- Particulate organic nitrogen and phosphorus decomposition rates (at reference temperature)
			- Dissolved organic nitrogen and phosphorus mineralization rates $($ ^{(('''})
			- Nitrification and Denitrification ("")
			- Oxygen/nitrogen ratio in nitrates, oxygen/phosphorus ratio in phosphates
	- Statistics
		- Uses R^2
		- Uses Root Mean Square Error (RMSE), which is like a population standard deviation, but for a time series. Essentially, instead of subtracting

the mean from each index, each predicted value is subtracted from the observed value.

- From there, the Normalized Objective Function (NOF), was used. This was equal to RMSE divided by the mean observed of the observed values. NOF values between 0.0 and 1.0 indicate ideal model calibration.
- Made use of special scatterplots, where the predicted values from the model were on the dependent axis, and the actual values observed were on the independent axis. The slope, gamma, indicates the error of the model, with 1 being perfect prediction. Thus, R^2 and gamma closer to 1 should indicate that the model is well-calibrated.
- Data collected included:
	- Comparisons between model predictions and actual field data, specifically comparing temperature and depth measurements between model predictions and actual field data, both in the high and low rainfall seasons.
	- Comparisons between model predictions and actual field data for all the data collected at surface level of the reservoir
		- One at station M1, another at station M3
	- Comparisons between model predictions and actual field data for all the data collected at bottom level of the reservoir
		- One at station M1, another at station M3

Results:

- For hydrodynamic module, there is an overall good agreement:
	- There was a good match between the model predictions and field data for surface elevation of the reservoir.
	- The comparisons of temperature along the vertical profile between the model and the field data during both the wet and dry seasons showed pretty good agreements (see analysis of Figure 7/Table 2 above)
	- Also found that the circulation in the reservoir is mainly driven by wind
- Results for water quality module are likewise in good agreement:
	- Most gamma and R^2 are within 0.2 or 0.3 of 1, which indicates that the models are fairly accurate, and that there is little straying of the actual field data from the predictions.
	- Similarly, most of the NOF values were within 0.5 of 0 (and 0.0 and 1.0 indicates porper calibration).
	- See analysis of figure 12 and table 3 above for more details.
- With the model validated, spatial and temporal variables for water quality, e.g. DO, chlorophyll and micronutrient concentrations, and their impact on phytoplankton were able to modeled (study provides multiple maps showing various color gradients to depict these trends. None of them are analyze here. Rather, the important findings derived from them are summarized in the notes below):
	- For phosphorus, during the dry season, upstream, there were lower concentrations (little inflow), but downstream, there were higher concentrations (urban dumping)
	- However, during wet season, the opposite is the case for each part of reservoir.
- All nitrate concentrations are found to be below 10 mg/L during the dry season, and during the wet season, there are more nitrates overall: <10 mg/L downstream, >30 mg/L upstream
- For ammonia, in both wet and dry seasons, downstream, concentrations were ≤ 0.04 mg/L, and upstream, ≥ 0.13 mg/L.
- DO in dry season, is 6-7.8 mg/L downstream, and 3-5.5 mg/L upstream. >7.8 mg/L and 3-5 mg/L respectively for the wet season
- For chlorophyll a concentration, model assumes that phytoplankton carbon concentration is directly proportional to concentration of the pigment in the water
	- Conversion factor of 60 mg C/mg chlorophyll was used. During both seasons, no concentrations exceeding 0.003 mg/L
- Article then proceeds to list out data from Tables 2 and 3, that we've already covered in figures section above.

Discussion:

- With model now validated, its results can be analyzed.
- Feb-Aug, the wet season provokes greater amount of mixing, less stratification (i.e. autumn/winter of the Southern hemisphere), and stratification is more in the hot, dry season (summer)
	- Trends we've observed time and time again.
- During thermal stratification, resources are released from the bottom layers.
- Analyzing wind velocities was prereq to analyzing impact of nutrients on phytoplankton
- In bottom layer, DO was higher during the dry season. Wind and rain lead to more mixing during wet season (plus more DO used by organisms), meaning DO is more uniform, less amount at the bottom.
- This possibly rings about anoxic conditions, harmful to the fish species of reservoir
- Station M3, which is shallower and hence always mixed, showed that at both bottom and top of water column, water properties were homogenous.
- Chlorophyll a concentrations were low b/c low water residence time inhibits algal growth
- Nutrients enter into the reservoir upstream being concentrated and saturated, and are then diluted downstream.
- Phosphorus conditions sometimes reach the legal limit. However, law does not account for trophic status of water, so other definitions were used for measuring this metric
- Nitrates are higher during wet season due to agricultural dumping. Upstream watershed transports nutrients. Law states that 10 mg/L means contamination, however, more scientific definitions considers 5-50 mg/L to be eutrophicated system.
- Upstream higher ammonia brought about by greater amounts of discharge in that area. No contamination on part of ammonia (ammonium?) observed, although its levels do indicate that the reservoir is mesotrophic.
- DO higher downstream b/c photosynthesis and reaeration, Lower DO upstream b/c decomposition, respiration, and reaeration. However, DO levels found indicate contamination for being below legal limit.
- By contrast, findings for chlorophyll a concentration don't show this to be the case, because it does not exceed 0.1 mg/L limit.
- N:P ratio of >10 indicates a phosphorus limited system. Seeing as here N:P = 100, the reservoir is undoubtedly phosphorus limited.
- This means management strategies must be focused on regulating P levels. However, P concentration might be independent of phytoplankton growth, meaning the system remains oligotrophic and has low chlorophyll a levels.
	- This indicates that reservoir water is quickly flushed out by the high incoming water flow. This means greater source of upward movement of nutrients came from cell lysis in the phytoplankton.
- We can safely assume the model is valid because gamma and R^2 values are close to 1, and NOF is close to 0.

Conclusion:

- Hydrodynamic module produced spatial and temporal distributions for the temperatures at varying points along the vertical profile, as well as the impacts of wind on the surface of the reservoir, during both wet and dry season
- Water quality module produced information about DO, chlorophyll a, various micronutrients.
- Although findings show that the reservoir is phosphorus-limited, there is a decreasing chlorophyll a gradient brought about by rapid inflow and outflow of reservoir, which inhibits phytoplankton growth and shows that hydrodynamics play a role in impact phytoplankton populations and eutrophication factors. (?)
	- So (i guess), even though, with phosphorus-limited environment, that is not what limits growth, rather the low amounts of chlorophyll a, which indicate lower primary production and productivity in the phytoplankton brought about the fast inflow and outflow, is what limits growth.
	- Nutrients are upwardly transported via cell lysis in the lower-level phytoplankton populations (?)
	- However, article suggest for future studies, analzying relationship between chlorophyll a and eutrophication.
- Overall, this study has helped develop a useful tool for modeling various factors that impact phytoplankton populations, and can serve as an important tool for managing environmental condtions in water bodies (such as the reservoir).

Article #11 Notes: Environmental Controls of phytoplankton in the river dominated sub-tropical coastal ecosystem of Bangladesh

data clearly indicate that the southeast region is the most saline, followed by the southwest and central regions. The median salinity for the central region is 5 PSU. The data is skewed towards higher salinity values, its upper tail of its distribution coinciding with the lower tail of the southwest region. The southwest's salinity distribution is skewed towards lower salinity, with a median of 19 PSU. Meanwhile, the entire distribution for salinity in the Southeast distribution is above those of the other two regions. It has a fairly symmetric distribution, with a median salinity at around 28 PSU, with range covering about 26 to 31 PSU.

This figure depicts the range of DO across the three regions (mg/L). The data suggest that the central has the most varied but greatest DO, with the Southwest region having the most after that but the least variation, and southeast region being second most varied but having least DO. All distributions are relatively symmetric. Median DO values are (all values are approximate) 6.5, 4.8 and 4.5 mg/L, with ranges between 5.5 to 7.3, 4.5 to 5.2 and 3.8 to 5.1 mg/L for central, southwest, and southeast regions respectively. Distribution of DO for central region is entirely above the other

This figure depicts the range of water temperature across the three regions (℃). Overall, the data indicate that the central region is the warmest, followed by the southeast and southwest regions. The central region has a severe skew towards cooler temperature, although the entire distribution is greater than the other two regions. Median temperature is (all stated values are approximate) 29.4, ranging between 26.25 and about 30.3. Meanwhile, for the southeast and southwest regions respectively, median temperatures are 24.9 and 22.5, with ranges between 23.75 to 26.1 and 21.3 to 24.1.

chlorophyll do not overlap with each other. This solidifies the assertion that the Southwest region, followed by the central and southeast, has the highest concentration of chlorophyll, meaning chlorophyll decreases west to east. The southwest distribution is extremely skewed towards lower concentrations, ranging from (all stated values are approximate) 1.63 to 2.20, with a median of 2.15. Meanwhile, the other two regions are fairly symmetric. Concentrations range between 0.77 to 1.13 with a median of 0.9 for the central region. In the southeast region, the range is between 0.55 and 0.75, with a median of 0.67.

The bar graph at the top displays silicate concentrations, while the bottom one shows nitrate concentrations (mg/L - same for phosphates). The black lines represent the interval of values for measurements across the three regions. It is apparent that the central region has the highest silicate concentration, followed by the southwest and southeast. Variation in concentration also increases in the same sequence. For the central, southwest, and southeast regions respectively, (all stated values are approximate), estimated concentrations were 675, 510, and 405, with ranges between 650 to 690, 440 to 560, and 315 to 475.

Meanwhile, nitrate concentrations were a lot lower, overall, given values for the concentrations among the three regions. From west to east, nitrate concentrations tend to decrease, while variability increases. From west to east, ranges in nitrate concentration are as follows (all values here are approximate): 18.5 to 20.3; 9.8 to 14.3; 5.3 to 11.3, with point estimates at 20.0, 12.4, and 9.1.

Similar west-east gradient can be observed for phosphates, although overall concentrations are higher than nitrates (but nowhere near silicates). From west to east, point estimates for phosphate concentrations are 86, 43, and 20, with ranges being between 80-87.5, 35-50, and 12-25.

This dotplot describes the relationship between depth and salinity among the three regions. The order of appearance for each region on the graph is based on the ascending value of a given variable (in this case salinity) across the regions (as found and described in the above figures). Also, (and this goes for figures below), the original figure has been rotated counter-clockwise 90° in order to better analyze the value of the given variable, given depth. That being said, here is analysis for salinity (source of bias from the varying depths collected for each region): For all regions, there seems to be a positive, somewhat logarithmic curve, that characterizes the relationship between depth and salinity. The salinity levels off quickest in the low-saline central

region almost immediately, at around 4.65 PSU. In the more saline southeast, the salinity increases rapidly within about the first 2 meters, going from 33.0 to 33.5 before leveling off. Lastly, for the southwest region, has the most gradual gradient for salinity, leveling off only after between 10 to 15 meters of depth at about 21 PSU.

On the left, the relationship between depth and temperature is shown. In the warmer southeast region, the temperature remains about the same throughout all depths (although there is a slight decrease) at around 24.9℃. Meanwhile, in the central region, temperature rapidly decreases within the first 2.5 meters of depth, going from 22.5℃ to 22℃ before leveling off. Lastly, the most dynamic relationship can be observed in the southwest region: within the first 5 meters, the temperature decreases from 22.2℃ to 22℃, before increasing back up to that value. Then, over the course of the next fifteen meters, the temperature increases, reaching about 22.6°C . On the right, the relationship between depth and DO is shown. The data indicate there is a curve of exponential decay encapsulating this relationship for all regions. The (comparatively) anoxic southeast has the sharpest decline, going from 4.625 to 4.25 mg/L within the 2.5 meters. The decline is greater but more gradual for the southeast region, going from 5.38 to 4.75 within the first five meters before leveling off. The decline is yet greater and more gradual for the (comparatively) oxygen-rich central region, which, over the first 7.5 meters, declines from 7.05 to 6.15, leveling off from there.

This scatterplot displays the relationship between depth and chlorophyll levels among the three regions. In the southeast, there is a small, gradual increase that levels off: concentration starts off at 0.5 mg/m^{\sim}3, reaching 0.75 mg/m \sim 3 by five meters of depth, and leveling off. In the central region, within the first 3 to 4 meters, there is a negative concavity, with chlorophyll levels increasing from 0.75, peaking at 1.25 around two meters deep, before decreasing and leveling off between 0.8 and 0.9. Meanwhile, the southwest region has a positive linear relationship between depth and chlorophyll levels for the first four meters of depth, then levels off at 2.2 mg/m^3.

This graph illustrates the PCA of the environmental variables among the coastal regions. Larger magnitude vectors indicate that a variable is a more significant driver of the phytoplankton heterogeneity. Notice that nitrate, phosphate and chlorophyll have incredibly small vertical components, albeit large horizontal ones. This means they have smaller magnitudes and hence are less impactful. Meanwhile, both the horizontal and vertical components of turbidity, silicate, and salinity are rather large. So, it is concluded that it is these factors that drive heterogeneity among coastal waters.

These are a set of AGAM functions depicting the impact of various biotic/abiotic factors on the 20 most abundant phytoplankton species among the three regions. The y-axis measures the abundance of the species in all cases. This has important ramifications on the habitable ranges of each species across the different variables.

Temperature:

Most species have a relatively high abundance, but at around 21.5° C, the abundance of the species begins to decline, reaching the lowest point around 24℃, before increasing once more, meanwhile other species continued to decrease in abundance. There are two notable species that have little abundance at lower temperatures, but greater amount at higher temperatures. Salinity:

Discounting the one or two species that have no impact on abundance due to salinity, and the on or two species that prefer hypersaline/fresher environments, the habitable range of salinity for most species is between 15 to 25 PSU.

Turbidity:

With the exception of three species that seem to prefer less turbid (and thus more light-intensive) environments, it seems that after 25 FTU, the abundance of most of the other species increases, indicating that most species prefer an aquatic environment that is at least somewhat cloudy, so as to allow for excessive light intensity to be curtailed.

Silicate graph is the same as turbidity, which is problematic. See [below](#page-102-0), that's the best possible analysis that can be offered.

Nitrates:

NOTES

Abstract:

- Data collection in species-rich coastal subtropical regions has been a challenge, hindering development of conservation strategies and overall understanding of these environments
- Focus was on getting the raw variability in environmental conditions, relationships between these variables and phytoplankton dynamics.
- Data was collected from the coastal regions of Bangladesh during the monsoon seasons between 2020 and 2022.
- Following variables were researched:
	- Temperature
	- Salinity
	- Dissolved Oxygen
	- Chlorophyll a (referred to as just chlorophyll for notes on this article)
	- Turbidity
	- Micronutrients:
		- Nitrates
		- Phosphates
		- Silicates
- Findings indicate that these metrics vary radically across the subtropical ecosystems of coastal Bangladesh, with micronutrients, salinity, chlorphyll, and turbidity being major drivers of this variability. All of the variables explained 44% - 73% variability in phytoplankton species abundance
	- Southwest: Moderate turbidity and salinity, higher levels of nitrate/phosphate
	- Central: Low salinity, high turbidity and silicate concentration
	- Southeast: High salinity, low nutrient concentration
- 121 Phytoplankton species id'd. 66 occur in all 3 of the regions. Genera by region:
	- Southwest: *Coscinodiscus*, *Odontella*, *Nitzchia*, *Proboscia*, *Ditylum* and *Thalassionema*
	- Central: *Coscinodiscus*, *Odontella* and *Nitzchia*
	- Southeast: *Skeletonema*, *Ditylum* and *Proboscia*

Introduction:

- Base of marine food webs (note specifically pelagic)
- Not just carbon cycle and climate regulation, also regulates nitrogen, silica, and phosphorus
- Various abiotic and bitcoin factors impact taxonomic composition, biomass, spatial distribution of species, and other fundamental phytoplanktonic dynamics.
- Background on Bangladeshi geography
	- Lots of rivers, major deltas (ganges, brahmaputra, etc.) emptying out into Indian Ocean, subtropical monsoon climate
	- 3.2E4 m^{\sim}3 of freshwater and \sim 10 \sim 3 of sediments discharged (4th and 1st largest globally, respectively), which plays major role in regulating coastal ecosystems, which is a major source of food and economic livelihood for the nation
		- Fisheries rely on phytoplankton, whose dynamics are changing
- Therefore, it is important to study phytoplankton on Bangladeshi coast, considering large geographic area and many explanatory variables, which hasn't been done previously.
	- This hinders understanding and thus conservation efforts of aquatic ecosystems. Therefore major goal is to minimize data gaps for this major geographic area.
	- Specifically, studying spatial variability of coastal Bangladesh, looking at the impact of the various physical/chemical variables (specified above) on phytoplankton

Materials and Methods:

Measurement:

- Data collection split into 3 zones: southwest, central, and southeast. (hereafter SW, C and SE) High sample size collected for each region, which spans 710 km coastline, and 21-23 °N/ 89-93 °E
- Samples collected during high tide, which occurred 2x (semi-diarnul), 3/4 m amplitude
- Data was collected during January and February of 2020-2022, as that is when the Northeast monsoon occurs.
	- Southeast monsoon season has waves that are too rough
- Given the large area the study was covering, rather than simultaneously collecting data from all stations, over cycle of 7 consecutive days, data from all stations was collected.
- Table I gives insight into measurement methodology:
	- CTD and mini-CTD were used to measure temperature and salinity. CTD alone was used to measure DO, and, in conjunction with spectroflurometer, chlorophyll. Spectroflurometer alone was used for turbidity, while Niskin bottle was used for the micronutrients. Plankton nets used to collect phytoplankton and zooplankton
	- Mini CTDs were located at 2500 sampling stations, CTDs and spectroflurometers at 210, 130 for Niskin bottles, and 120 for plankton nets.
	- SW had 76 sampling stations for temperature, salinity, DO, chlorophyll, and turbidity; 40 for the micronutrients, 45 for both planktons
	- Chad 70 sampling stations for temperature, salinity, DO, chlorophyll, and turbidity; 50 for the micronutrients, 43 for both planktons
	- SE had 64 sampling stations for temperature, salinity, DO, chlorophyll, and turbidity; 40 for the micronutrients, 32 for both planktons
- Salinity, temperature, DO, turbidity and chlorophyll were measured on-site, while micronutrient concentrations and phytoplankton and zooplankton abundance were measured in lab.
- Mentions CTD (use described above), along with chlorophyll and DO sensors, are common tools for understanding all aspects of a water column, monitoring algal growth and distribution, and outlining water masses.
- Mini-CTD attached to was attached to the boat, measuring pelagic temperature and salinity in 1 minute interval, operating for about 2500 times (thus 2500 sampling stations as described above)
	- Mini-CTDs are also used in studying migration patterns in fish and other aquatic organisms.
- Quality of data was checked \rightarrow made supplementary info., interesting...
- Flurometer measured its variables (inlcuding green-blue algae unmentioned above) along the vertical profile, performing rapid measurement without preparing the samples.
- Water samples collected were put through a 0.45 μm cellulose-ester filter in order to measure/analyze nutrients.
- An AutoAnalyzer (def'd above, as a the three methods below) was then used for the micronutrients:
	- Molybdosilicate method used for silicates
	- Semi-automated colorimetry used for phosphates
	- Automated hydrazine reduction used for nitrates

- Phytoplankton and zooplankton caught wet plankton net, preserved with 3% formalin solution and analzyed under microscope in order to identify species (based off phenotypic analysis, referencing guides).

Statistics:

- First, the spatial variability of the data collected was modeled, then, heterogeneity was calculated, and the factors driving these conditions were also determined.
- Spatial variability mapped on ArcMap software, discrete color scale used for displaying values for the variables analzyed.
- Mean and SD of the variables studied were calculated, being normally distributed.
- One-way ANOVA test used to confirm presence of spatial variability for these variables.
- Tukey's post-hoc test was then used to see which groups were significantly different.
- Temperature-salinity diagram used for understanding overarching characteristics of this water mass.
- Vertical profiles of salinity, temp, DO, turbidity, and chlorophyll established, averages calculated.
- Heterogeneity was measured using Non-metric multidimensional scaling (NMDS) ordination and Principle component analysis (PCA). NMDS was able to collate samples with similar values, identifying similarities and differences among the data. NMDS analysis was then used to produce a graph depicting the overlapping of ordination.
- Permutational Multivariate ANOVA was used to find the statistical significance of the differences observed from the NMDS process, while PCA helped identify drivers of homogeneity.
- Generalized Additive Model (GAM) used to observe the role that these biotic/abiotic factors play in driving phytoplankton dynamics. The dependent variable was phytoplankton abundance across different species, based off independent variables of each environmental factor (separately)
- With so many variables creating complex relationships, it is possible that there is collinearity among the different variables, meaning thet can just be disregarded as extraneous. In order to evaluate that, Variance Inflation Factor (VIF) was performed, eliminating any instances that resulted in $VIF > 2$.
	- (so goes the reasoning of the article, although personally I'm sure whether that's a wise decision)
- With that in mind, the following equation was established:

log (N_{i,j}) = δ + $f_k(X_{i,k})$ + γ

- N and X are matrices. Matrix N contains rows i, which represents the sampling stations, and columns j, which are the each of the species. Matrix X contains rows i and columns k, the value of the given environmental factor. Lowercase delta is the intercept, lowercase gamma is unaccounted variation, log transformation is performed on the N matrix, and f_k represents the smoothing function performed on matrix X, given the explanatory variable analyzed.
- Smoothing is determined by a restricted maximum likelihood approach, given that the function is transformed, both by the smoothing function and the logarithm.
- GAM outputs were analyzed in order to develop a better picture of the impact of explanatory variables on phytoplankton dynamics.

Results:

- (See extensive analysis of figures above) Key findings/things to note:
	- Silicate > Phosphate > Nitrate
	- Nitrate, Phosphate and Chlorophyll decrease west to east
	- East is most saline.
	- DO, temp, silicate highest in central region.
- Salinity: ANOVA: Significant; Turkey Post-Hoc: central < other regions
- Temperature: ANOVA: No significant difference
- From T-S Diagram: Central: low salinity & density (meaning freshwater environment); Southeast: high salinity & density, Southwest moderate for both metrics.
- DO: ANOVA: Significant; Turkey Post-Hoc: central > other regions
- Micronutrients: ANOVA: Significant; Turkey Post-Hoc: Silicate in central significantly greater; nitrate/phosphate greater in southeast.
- Turbidity: Significant difference. 140, 100 and 60 FTU for central, SW, SE respectively.
- With regards to depth and the various variables, no significant differences **within** each coastal region, but the differences of each variables among the profiles of the different regions were significant.
	- Suggests that there is good mixing in the water (variation suggests stratification)
- Phytoplankton dynamics observed through the lens of zooplankton, phytoplankton community comp, and chlorophyll concentrations
- Higher chlorophyll in SW suggests that it is likely to be productive (which seems to be true, given phytoplankton biomass and diversity measurements below):
- Chlorophyll was uniform within regions, but varied significantly between them; ANOVA significant, and Turkey Post-Hoc SW $>$ other regions to be significant.
- - 121 species ID'd: 81, 71, 56 in SW, SE and central respectively, although diversity was calculated to be 2.58, 2.21, and 2.01 for SW, SE and central coasts.
	- 66 species across all regions (indicating wider niches), 43 not present in central region (indicating they are not fit for high-silicate/turbidity and fresh conditions), 13 not present in SE (indicating they are not for high-saline $\&$ phosphate/nitrate, low-moderate silicate/ turbidity)
- Average biomass across all regions: 10.65×10^{3} cells/L, + 2.66 $\times 10^{3}$ cells/L. From SW to SE, biomass decreased. Similar observations for zooplankton
- In terms of heterogeneity, the NMDS performed indicated that the three regions were in fact distinct from each other.
- PERMANOVA tests further confirm this: SW different from Central w/o overlap, small overlap when compared to both central and SE.
- PCA shows that silicate, salinity & turbidity as major drivers of heterogeneity (see above)
- AGAM model used to assess impact of the 7 variables (micronutrients, zooplankton, turbidity, salinity, temperature) among the 121 phytoplankton species.
- Overall, these seven variables explain 44%-73% of the variation in phytoplankton biomass, taxon-comp (diversity), spatial variability (which gets into migration), etc.
	- Ofc, this is from looking at variation among the different species, which ofc varied (*Prorocentrum lima* best explained, *Actinelius* sp. worst)
- Phytoplankton spatial variability explained by variables in following proportions:
	- $-$ #1: Salinity (59.50% of species)
	- $-$ #2: Phosphate (10.74% of species)
- #3: Zooplankton (9.09% of species)
- #4: Silicate (8.26% of species)
- #5: Nitrate (7.43% of species)
- #6: Temperature (4.96% of species)
- #7: (turbidity not given)

Interesting that they did not consider DO… will add as a Q, therefore.

- Phytoplankton abundance explained by variables in following range of proportions (explaining factor of observed variation in abundance):
	- Salinity: 5%-28% *Tropidoneis* sp.
	- Phosphate: 8%-20% *Chaetoceros* spp.
	- Zooplankton: 5%-15% *Chaetoceros* spp.
	- Silicate: 7%-20% *Chaetoceros* spp.
	- Nitrate: 8%-24% *Pleurosigma* spp.
	- Temperature: 3%-5% *Thalassiosira* spp.
	- Turbidity: 2%-13% *Chaetoceros* spp.
- Additionally, each variable was the most impactful for given species/genera (listed \sim)
- See above analyzation of the AGAM model (very important).

Discussion:

- Spatial variability attributable to the variation in salinity brought about by variation in river discharge.
- Central region gets most river discharge $(1.5 \text{ m}^3)/\text{s}$ during SW monsoon, 61k during NE)
- SW: 30k m \textdegree 3/s during SW monsoon (\textdegree SE), and 100 m \textdegree 3/s during NE (\textdegree SE)
- SE: 5565.7 m^{γ}3/s during SW monsoon (<SW), and 419.80 m^{γ}3/s during NE (>SW)
- This explains the low-saline and high turbidity/silicate environment of central region. Exposure to coastal waters impacts SW and SE conditions.
- Conversely, the SE is high-saline and low nutrient due to less river outflow.
- SW: Nutrient cycling on part of mangrove plants + leaf litter, and moderate discharge (construction of barrage) makes it moderately saline/turbid, high nitrate/phosphates.
- DO, chlorophyll, salinity, density, and turbidity were uniform \rightarrow this indicates vertical mixing, which is based off tidal range, water current and river discharge.
- Strong winds during monsoon season and other subtropical climatic events drive tidal range and water currents
- Mangrove forest ecosystems and their contributions of organic matter is why SW was most predisposed to productive ecosystem (rich nutrients and phytoplankton abundance/diversity). Central has less (though gets nutrients from big discharge), and SE the least b/c of less discharge.
- Diatoms are dominant in Bangladeshi coastal waters, which is related to the micronutrients studied (silica, nitrates and phosphates). Having access to these resources, they are the most abundant species.
- By region, in the center, *Coscinodiscus*, *Odontella* and *Nitzchia* genera were most abundant. *C.* b/c adapted to lack of light, cytological significance of silica. The other two likewise rely on the high silicate levels.
- *- Skeletonema, Ditylum* and *Proboscia* genera most popular in the SE. This is due to the favorability of high salinity for these species, and their ability to tolerate lack of nutrients.
- Similarly, SW environment is ideal for following genera: *Oscinodiscus, Odontella, Nitzchia, Proboscia, Ditylum and Thalassionema*
- Salinity, micronutrients, zooplankton, water temperature, in that order, exerted a descending impact on phytoplankton dynamics.
	- Salinity/micronutrients has to do w/ varying river discharge/nutrient flux conditions. Along w/ turbidity, this is main driver of heterogeneity
	- Zooplankton control phytoplankton populations through feeding. They have a positive relationship with phytoplankton abundance.
	- Although temperature impacts metabolic rates, since temperature did not vary significantly for this study, it did not have that much of an impact on dynamics.
- Addresses how this varies globally!
	- Temperate: nutrients, light, zooplankton, temperature
	- Polar: Under-Ice light field, macronutrient concentrations
	- Tropical/Subtropical: pH, Salinity, nutrients from runoff, temperature, light (thus, findings are in line with what is regional norms)
- Heterogeneity means development of niches among phytoplankton species (adaptive radiation???), allowing for co-occurance and biodiversity

Conclusion:

- Implications: Climate change impact on fisheries, conservation actions, general info for fisheries, simulation data (!!!), marine spatial plan (i.e. modelling)
- Major limitations: only looked at data from NE monsoon.
- Areas of future foci: Collecting monthly data to understand phenological factors impacting phytoplankton, other aspects of phytoplankton dynamics (competition, carrying capacity, etc.), analyzing niches of phytoplankton and more broadly, trophic/ecological ramifications

Article #12 Notes: Incorporating carbon sequestration into lake management: A potential perspective on climate change

phytoplankton biomass and exportation allow for C seq. Additionally, pollutants as P and N to the system. This provides helpful information for understanding how to improve water quality and C seq. Table 2

*,** and *** indicate the significance at 10 %, 5 %, and 1 % levels, respectively.

This table illustrates relationship of various environmental parameters with chl a concentrations. The equations on the left represents the function used for the linear models for each of the relationships. Parentheses on the right indicate standard error. The parameter is plugged into the parentheses. γ_{00} is the intercept of each of the models. γ_{10} is the slope for each model. For example, the slope between temperature and chla is 1.21, meaning for every increase in temperature by one degree, 1.21 μg/L chla would occur. Using that for nitrogen and phosphorus, for every increase in mg/L of N and P, there was 5.05 μg/L and 47.55 μg/L chla increase respectively. Similar idea of biomass of zooplankton. All other ones increase/decrease by an amount that is close 0, meaning that factor isn't very impactful. For every increase by 1 mg/L in ratio of P:N, there is only a 0.12 μg/L chla decrease.

Table 3

The estimation of fixed effects and random effects in multivariate RCM.

*,** and *** indicate the significance at 10 %, 5 %, and 1 % levels, respectively.

From the results in table II, we now have a multivariate RCM that compares the magnitude of the impact of each variable on chl a concentrations. Phosphorus is at γ =
6.82, the highest amount of magnitude, but it is of the lowest significance, and note that its error is quite large. Following the decreasing γ values from there, nitrogen, then *Rotifera* biomass, then temperature have the next biggest impact on phytoplankton.

Table 4

The estimation of fixed effects and random effects in MEM.

Models	MEM^* with			
	Cultivated land	Forest land	Grassland	Artificial land
Fixed effects (with robust standard errors)				
γ_{00}	93.46***(7.33)	$93.22***(7.27)$	$93.30***$ (7.46)	93.27***(7.47)
γ^{10}	$1.35**$ (0.57)	$1.22**$ (0.56)	$1.16** (0.53)$	$1.28**$ (0.56)
γ^{20}	$4.90*(2.76)$	$6.34** (2.72)$	4.83(3.13)	5.11(3.19)
γ^{30}	3.45(26.22)	11.53(27.41)	10.26(31.47)	7.50(29.76)
γ^{40}	$1.87***(0.64)$	$2.15***(0.68)$	$1.90***(0.61)$	$1.78***(0.65)$
γ_{01}	54.24*(29.97)	$-452.75**$ (214.83)	$-82.49(324.96)$	13.69(32.53)
γ_{11}	1.46(2.49)	$-2.98(13.72)$	$-46.64**$ (19.97)	$-1.62(2.78)$
γ_{21}	-19.48	$-36.82(0.57)$	18.89(114.13)	10.21(11.63)
	(12.33)			
γ_{31}	107.39	772.85(0.31)	502.96(1127.71)	-57.62
	(123.24)			(115.60)
γ_{41}	$-1.99(2.21)$	20.67(22.22)	$-19.51(25.72)$	2.20(1.90)
Random effects (variance components)				
r_{ii}	74.34	74.59	74.23	74.54
(σ^2)	(5526.27)	(5562.97)	(5509.96)	(5556.87)
u_{oi}	55.85***	55.56***	57.15***	57.04***
(τ)	(3119.74)	(3086.70)	(3265.97)	(3253.39)

*,** and *** indicate the significance at 10 %, 5 %, and 1 % levels, respectively.

Adding on the level 2 parameters in order to establish the MEM, we see that only one combination has any significance: chl a is decreased because there is a negative relationship between the grassland and temperature. The grassland environment changes the temperature such that chl a concentrations decline. Otherwise, there is nothing significant.

Fig. 8. Maximum carbon value within 600 ticks under the point-source pollutant emission change scenario. In the initial water environment, the nitrogen and phosphorus concentrations were 1.5 mg/L and 1.0 mg/L, respectively, and the water temperature was 20 $^{\circ}$ C.

This bar graph indicates C seq given varying pollutant (N/P) phosphorus conditions). Given the description of the experimental groups, the data clearly indicate that higher amounts of phosphorus allow for the increase in C seq, and that nitrogen and C seq seem to be ambivalent to each other. Consider that NAPA and NBPA are nearly equivalent in C seq, 393,737 versus 396,712. Similarly, C seq in NAPB and NBPB is 670552 and

NOTES

Abstract:

- Understanding carbon sequestration capabilities of lakes is important in tackling climate change
- In order to understand the relationship between carbon sequestration and various environmental factors, specifically of a lake, an integrated method framework (see definition above, basically the bread and butter of your pro) was carried out.
- Important ramifications: offering additional lens on impact of climate change \rightarrow important for policy makers.
- Three series of models:
	- Vertically generalized production model: Used for assessing carbon sequestration capacities (via chlorophll a?), which was found to be prevalant in lakes
	- Hierarchical linear model: Used to identify the factors impacting phytoplankton dynamics
	- Multi-agents-based model: Used to identify possible mitigation and response strategies given changing carbon sequestration conditions
	- Findings indicate that lakes have stronger sequestration capabilities, especially compared to ocean and forest ecosystems.
	- Phosphorus, nitrogen, *Rotifer* biomass, water temperature, in that order, were driving factors impacted chlrophyll a (hereafter Chl-a) concentrations, which means it is the chemistry piece, going bottom-up, rather than the ecological piece (i.e. zooplankton, bottom-down) that appears to be impactful.
	- Negative syn relationships between chl a and grasslands due to temperature
	- Policy proposal based off the findings: Controlling the ratio of nitrogren to phosphorus and biomass of fish feeding on zooplankton in order to bolster C sequestration and maintain water quality.

Graphical Abstract:

Introduction:

- Oceanic carbon sequestration (hereafter C seq) is a major means through which mitigation of climate change can occur
- C seq depnds on (1) the solubility pump (i.e. $CO₂$ becoming more integrated into oceans due to increasing density in the air, and (2) the microbial pump, i.e. phytoplankton
- However, less research of lakes has been done than in oceans, so it is important to (1) understand their C seq capabilities, (2) understand facots influencing phytoplankton, and (3) suggesting action plans for policy makers.
- Moreover (similar to the findings that you have noticed for your own project, but a step even futher almost), there is dearth in focus on identifying the factors that influence phytoplankton dynamics acorss multiple scales (i.e. not just biochemistry or nutrient stoichiometry alone, rather, environmental, ecological in conjunction with chemical, biological and physical. Different scale in the breadth of the parameters).
	- Much work has been done using PCA, redundancy analysis, canonical correspondence analysis, mainly on micro-physical, chemical and biological factors
		- (lists a whole bunch of studies which can be very useful for data…) light, suspended solids, turbidity/transparency, micronutrients, DO, pH, salinity, chemical oxygen demand (COD).
	- Focus has only been on these micro-level factors, but what about macro-level factors, like land use, pollution, etc.
- Using hirearchcal linear model (HLM) is useful for separating impact of different IDVs of different scales on the DVs. It is good for analyzing the relationship phytoplankton has with any set of variables.
- Parameters establish the predictive model, which is important policymaking tool for enhancing C Seq.
- Need for complex adaptive systems to link different-scale parameters needed.
- Past device that have been used for policy reccomendation use techniques like stock, flow, time delay, state variables and feedback loops to perform simulation.
	- There are limitations posed for this. These computational techniques fail to connect microbiological and macrological factors b/c intervariable interaction can only be weakly understood.
	- We want to understand the micro-chemical aspects of phytoplankton, and then extend the ramifications of that to C seq
	- Hard to describe phenomena that cannont be modeled by equations, e.g. random reproduction/predation
- However, Multi-agents based modelling (MAB) is a good solution to these limitations, as all variables are autonomous and interact with each other. With these conditions of interactivity, the impact of mirco-scale conditions on marcological conditions can be observed
	- In this case, at the micro-level, for this study, phytoplankton, zooplankton, and other organisms, and macro-level, there was biomass, C seq, and water quality.
	- From this, a simulation was created, and it was able to model what would happened should recommended regulatory guidlines be followed.
- From this, >60 lakes in Wuhan, China were analyzed, as Wuhan, along w/ other Chinese cities have been making recommendations for lake management, so the ramifications of what they suggest ought to be evaluated.
	- Dealing w/ chronic eutriphication, biodiversity loss, water pollution
- Three-fold focus:
	- (1) Reveal C seq capabilities of lakes specifically
	- (2) Evaluate impact of environmental parameters impacting phytoplankton
	- (3) providing insights and policy reccs for decision makers on climate change
- Three-fold hypothesis:
- (1) Lakes are capable of C seq
- (2) There exists relationships that are cross-sectional among phytoplankton, zooplankton, macro-level land cover, environmental parameters,
- (3) By linking the microbiological with the macrological, policymakers can be informed in decisions on management of lakes given climate change
- Crucial ramifications!

Materials and Methods:

- Wuhan contains a myriad of, >100 lakes, having large water supply.
- Pollution is rampant; 63 lakes. Poses threats to inhabitants drinking water and Yangtze, into which these water bodies drain
- 2018 site-monitoring data collected for these 63 lakes. Following data collected: name of lake, month & time of year, water depth and temp, clarity, pH, Chl-a concentration, Permanganate index, micronutrients, abundance of phytoplankton and zooplankton biomass. *Rotifera*, *Cladocera* and *Copepoda* were the three groups of zooplankton.

Overview of the methodology:

- Vertically generalized production model (VPGM) calculated primary productivity and C seq
- Nest data structure: used to establish relationship between aquatic and terrestrial parameters (novel)
- HLM: Determined factors impacting phytoplankton dynamics
- Principles of Lake-ecological-social management system (LESMS) was then applied to the findings to make policy reccs.
- Multi-agent based modelling of the scenarios derived from this were performed on NetLogo.

VPGM:

- VPGM a type of vertical integrated model of clarity levels and common model of primary production. VPGM is initially used to calculate primary production in clear water. Following equation below was then used to account for the inland lake environments:
	-
	- $PP_{eu} = 0.66125P_{opt}^{B} \cdot \frac{E_0}{E_0 + 4.1} Z_{eu} \cdot C_{opt} \cdot D_{irr}$ variables include productivity in eutrophic zones, available light, light cycle (i.e. sunrise/sunset), Chl-a
- Other functions were used for calculating temperature: euttrophic depth, maximum photosynthesis rate, and another formula is used for water transparency.
- C seq = Avg net primary production $*$ lake surface area

HLM:

- C seq is dependent upon chl a. Here, we assume three levels of hierarchy impacting chl-a; one: micronutrients and water temperature from bottom-up, two: top-down impacts of the 3 zooplankton species, and land use, which accounts for pollution levels and water temp
- These factors impact C seq b/c they impact phytoplankton primary production and/or biomass
- Nested Structure Data was used to understand the impact of Chl a on marine ecosystems and organisms, and the change brought about by land use surrounding the lake, i.e. micro-marco variable relationship.
- HLM was what was used to analyze relationship between and within the mirco-macro variables.
- Three steps to developing the HLM. unconditional means model (UMM), single variable random coefficient model (RCM) and the multivariate variables RCM and mixed effect model (MEM)
- UMM:
	- Tests for significance between the micro-marco variables. Level_1 : Chl – $a_{ij} = \beta_{0i} + r_{ij}$

Level_2 : $\beta_{0i} = \gamma_{00} + u_{0i}$

General Model : Chl – $a_{ij} = \gamma_{00} + u_{0j} + r_{ij}$ -

- From left to right: chlorophyll, beta (simplified out) is the mean level of individual chla concentration, the r_{ij} is the variation among individual data points among portion of a lake. Gamma is the average chla concentration of the entire lake, u is the variation between different lakes.
- By analyzing if variances here are proportional (equal?), we get the following:
- Variance $(Chl a_{ii}) = Variance (r_{ii} + u_{0i}) = \sigma^2 + \tau$ -
- Sigma looks at the partial lake level, "t" looks at the whole lake level. Then, they get:

$$
\rho_1=ICC_1=\frac{\sigma^2}{\sigma^2+\tau}
$$

$$
\rho_2 = ICC_2 = \frac{\tau}{\sigma^2 + \tau}
$$

- Bottom line: if $ICC_2 < 0.059$, Chla is independent from the lake level, and the groups have no difference, in which case there is no significance and only multi-regression is done, not HLM
- Single Variable RCM
	- RCMs used to assess how much impact level 1 variables impact the dependent variables, and if the level 1 coefficient and intercept of the linear model causes significant variation at level 2.
	- Level 1 variables of the study = water temp, micronutrients, 3 zooplankton species
- Mixed effect Model (MEM)
	- (see def above for the significance of it)
	- Relationships between water enviroment, aquatic organisms, and land use, and their impact of chl a are able to be understood now.

- $L2 =$ "contextual variable"; $L1 =$ "Invidual variable" in the equations Multi-agent Based Modelling:

- MAB was used to simulate policy reccs from the LESMS (which is above in the figure section, and about to be described below)
- Broadly, when doing the MAB simulation, we set up a conceptual model, define relevant parameters impacting the agents, build agents' behavioural function, run and debug simulation, then experiment and predict scenarios, then analyze results
- Concept Model:
- From the LESMS, we have the five systems (see figure above): physicochemical factor environment subsystem (PES), zooplankton, phytoplankton and fish behaviour subsystems (ZBS, PBS, FBS), Policymaker Subsystems (PMS).
- Modelled the intra-inter relationship between all of these variables, minus PMS
- Biomass and debris of the behavioral systems comprises the C seq. N and P were used for PES.
- Transferred this info to the PMS.
- Biological manipulation and pollutant emission management were set up as parameters in order to help polciymakers be able to meet goals of better water quality and C seq
- Used NetLogo. Each model of the cycle was counted as a tick, and within each of these cycles, the agents would interact and update their values given the rules set, in turn impacting all other individuals and overall environmental conditions

Results:

- (remember, all the computer model results are derived from the input of the 2018 data)
- VGPM used for calculating C seq (primary productivity and lake size as intermediaries of that process, ofc)
- For 2018, Average C seq was $0.87 \text{ kg C/m}^{\text{2*}}a^{\text{-1}}$; $0.56 * 10^{\text{-6}}$ tC·a^{-1} was the total C seq. April-June, Aug-Sep, Jan-Feb, and Nov-Dev, in that order, had the most C seq. To my knowledge, a reference chla.
- Larger surface area was positively related to C seq (make sense)
- Clearly, there is spatial and temporal heterogeneity in patterns of C seq, so it is important to identify those factors impacting this (surface area, what else…)
- It was first determined that it was appropriate to use HLM, given the process described above in the methodology, as the equations showed that the $\text{ICC}_2 > 0.059$ was true.
	- This is the interclass correlation, meaning basically, that the threshold of some value has to be passed in order for there to be a significant noticeable relationship between the two levels of the hierarchy to do a HLM as opposed to only multi-regression analysis.
- First, single RCMs for the specific parameters were created for seeing which variables impacted the chl a levels the most significantly.
- (See analysis of table II above)
- Nitrogen, temperature, Phosphorus and *Rotifera* biomass were significant. N:P ratio and other two species were not. Indeed, *Rotifera* is known for its faster life cycles, small size, large population and big distribution, making it a big feeder on phytoplankton than the other 2 groups
- Isolating down from there, we get table 3 (see above). Using the gamma values, we know in this order: P, N, *Rotifera*, Temp; meaning the bottom-up chemical dynamics are more impactful than the top-down dynamics from predation.
- ICC_1 , the intra-class correlation, was significantly lower in the multivariate RCM, meaning these factors could be introduced into the MEM.
	- Why?
- Now, by implementing the level 2 parameters, the MEM was developed (impact of level 2 on chl a, plus the relationship with the significant level 1 parameters)

- Cultivated land being near the lakes with the phytoplankton had a positive correlation with the chl a, whereas there was a negative one for with the forest, mean chl a around cultivated lands was high, but low in forests. There was a negative correlation between grasslands and chla by decreasing the water temperature ($b/c \gamma_{11}$). Otherwise, no other results were significant. Land cover change did not impact N or P, nor the zooplankton

- So little connection between the upper scale impacts and the lower scale impacts. - Now the MAB:

- - Parameter values are entered, and then the program begins running, collecting and displaying the data.
	- Two scenarios of suggested management strategies were tested: changing point source pollution, and changing the fish culture dynamics.
	- C seq given point-source pollution:
		- Four experimental groups:
			- NAPA = 15 mg/L N, 0.5 mg/L P (of discharge)
			- $NAPB = 15$ mg/L N, 1.0 mg/L P
			- NBPA = 20 mg/L N, 0.5 mg/L P
			- NBPB = 20 mg/L N, 1.0 mg/L P
			- Temp was constant
			- These values of discharge come from the Chinese govt
			- (see analysis of results above)
			- Although pollution increased by a worrying degree b/c of more nitrogen and phosphorus, the phytoplankton and zooplankton were actually able to absorb it, without forming any blooms
	- C seq given changing fish cultures:
		- Four experiment groups:
			- $-$ P0Z0 = no fish (control)
			- $-$ P0Z1 = zooplankton-feeding fish (excl.)
			- $-$ P1Z0 = phytoplankton-feeding fish (excl.)
			- $-$ P1Z1 = omnivorous fish (excl.)
		- $N & P$ (initial and discharge rates), and temp were constant
	- Not only was the P0Z1 best for C seq, but it was also good for absorption of N and P pollutants, therefore best for water quality.
		- $-$ P1Z0 = no reduction in pollution
		- $-$ P1Z1 = P pollution significantly reduced only
	- Meaning, a good recommendation would be to use more exclusively zooplankton-feeding fish

Discussion:

- Lakes have better C seq capabilities than oceans and forest ecosystems.
	- Data found here was greater than found at various points along China's coast. Previous studies show that ocean was 10x more efficient than forest
- Restates their findings on P, N, *Rotfier*, and water temp (ok lol)
	- But this does align with previous findings.
	- In "longstanding debate" about whether top-down ecology or bottom-up chemistry influences phytoplankton more, the data here indicate the former.
- With regards to cross-scale factors impacting each other, all they really found was that grasslands led to lower temperatures, which led to lower chl a at the partial-lake level.
	- Pretty disappointing, given what they purported. Or i guess, the fact of the matter is that smaller and larger scale parameters, under certain contexts, like this one, can be independent of each other.
- These parameters could become important metric by which policymakers choose to manage lake ecosystems.
- Given the results of our finding (and all of their significance/ramifications as discussed above), it is imperative that a better understanding between C seq and water quality is established.
- Policy proposal: Input N and P, as well as overall control over proportion, increasing biodiversity, purifying water (b/c pollution absorbed by phytoplankton), increasing biodiversity
- P0Z1 highest \rightarrow Policy proposal: Input more zooplankton-feeding fish. With more phytoplankton there, there will be more primary production, absorption of nutrients, reducing pollution.
- However, caution should be present so as not to allow for blooms of phytoplankton to grow due to high biomass.
- Other suggests: Choose economically valuable zooplankton-feeding fish, and fix carbon, convert into biochar to meet carbon demands for the food supply.

Conclusion:

- Summarizes article
- Point source pollution is positively.corrleated/matches correlation w/ c seq (essentially, the findings from NANB simulation and such)

Article #13 Notes: Marine phytoplankton functional types exhibit diverse responses to thermal change

This figures (3a) provides a template model for the growth rate curve given temperature among the different groups. μ_{max} is the peak growth rate, which occurs at the optimal temperature T_{opt} . However, there exists some range of temperatures in the habitat under which a given minimum μ can exist (for example, μ has minimum value of 1 between 30 and 33 degrees, with minimum value being lower for larger range of temperatures), ranging from the habitat temperature, T_{hab} , and the temperature on the other end of the thermal-growth curve with the same μ , T_{equiv} . More broadly, there exists a T_{max} and T_{min} within which a functional group is viable. TSM, the thermal safety margin, is $|T_{\text{hab}} - T_{\text{opt}}|$, the temperature range within which the phytoplankton can viably grow without strain. The warming tolerance, by contrast, is $|T_{max} - T_{opt}|$, which represents functional group growth in any capacity. The DGE, the distance to the growth equivalent, is the range between T_{hab} and T_{equiv} .

This is figure 2 of the study. The left diagram contains a series of boxplots that measure the change in growth rate, given the temperature. Unshaded boxplots are for when the temperature ascended towards optimal temperature, and the shaded boxplots for when the temperature was past it (but still within the warming tolerance/viability range). Change appears to be most restricted for the dinoflagellates, followed by the cyanobacteria, coccolithophores, and diatoms.

The median change in performance is about 0.03 $|\mu|$ °C, with a tight, symmetric range between about 0.02 and 0.05 approaching T_{opt} . Cyan., Cocco., and Diat. have medians of about 0.04, 0.05 and 0.05 respectively at this thermal stage, and all of their distributions are more variable, being skewed to higher changes in performance. These three groups have at least 50 to 75% of the distribution in performance changes above the entire distribution for dinoflagellates. Meanwhile, a similar pattern is discernable when approaching T_{max} , past T_{opt} , the only difference is that all distributions are more varied (but with fewer outliers), and the median performance change is higher.

Meanwhile, the figure on the right illustrates the various diversions of each functional group's growth rate curve (given temperature) from the standard Eppley Curve. Immediately, a few key characteristics can be discerned. First, there is the viable temperature ranges. Cocco group has the most restricted temperature range, with a lower bound of about 6-8℃, and upper bound of just under 30℃. Cyanobacteria cannot survive under 9℃ (as discussed below). As discussed below, the Cyans have a higher exponent than the Eppley Curve, whereas the other three groups are smaller. That is, as temperature increases, this group's growth rate increases at a faster rate. This is not to be confused the growth rate itself. In that arena, Diats are the winner, having the highest μ_{max} at all temperatures. They also have the smallest standard errors, as indicated by the shaded regions (which reperesent 95% confidence intervals, the Markov Chain bootstrapping), which is likely attributable to its large sample size. The amount of spread increases, with Diats being the most finely distributed, followed by Cocco, Dino, and Cyan groups. This is because the variability in thermal growth rates among individual strains gradually increases, causing this higher variation.

From left to right, figures 3b depict the thermal safety margin (TSM) of the phytoplankton groups. This is measured by T_{hab} - T_{opt} , and represents the ability for performance to be maintained without strain incurrance. The gray line indicates expected increase in SST for 2100, with the shaded region indicating longitudinal variation. Figure 3c depicts DGE, which represents the entire thermal range under which μ_{max} (or greater) is maintained, which accounts for temperatures both above and below the optimum. Finally, figure 3d measure warming tolerance, the enitre thermal range under which the given group can even survive. For all three figures, individual strain results are plotted against latitude.

Starting with 3b, the datapoints seem to indicate that cyanobacteria are only found in the northern hemisphere (or, at the very least, the ones sampled were all from this range only). At the equator, the tempueratures presently appear too be below the optimal level, given that TSM is negative,

and for T_{hab} - T_{max} , T_{hab} < T_{max} would have to be true. Using a similar logic, at the middle latitudes, the T_{hab} is above the T_{opt} . Measuring corrleation between latitude and thermal safety margin, while stratifying for each of the four functional groups, there seems to be a trend of upward concavity between these two factors. In context, that means the mid-latitude areas are warmer than the optimal temperature, whereas equitoorial ones are cooler, conforming with the above observations. Once more, this is not the case for the cyanobacteria, which were not sampled from southern hemipshere.

For figure 3c and 3d, the same geographical patterns apply. Looking closer at 3c, there are no values below 0, which, numerically, makes sense, as the distance between habitat temperature and the equivalent growth rate achieved at the other end of the thermal spectrum, is an exclusively positive measurement. This may be due to sampling (which has been a trend throughout all studies– the dearth of data from the Southern hemisphere), but it would seem as though the thermal equivalent allows for a much broader range of temperatures for a given growth rate in the northern latitudes. However, a similar parabolic pattern follows from figure 3b. This suggests that for equitorial regions, the thermal allowance is more restricted, as a small distance between the t_{han} and the t_{equive} would be much more condensed. This could be in part due to the more cooler (relative to t_{oot}) temperatures, thermal homogeneity, or some other factor.

For figure 3d, the same patterns in spatial abundance of the functional groups, as well as the parabolic relationship, still hold true. The more equitorial a latitude, the lower the warming tolerance, which, given that this area of the ocean is already the warmest, make sense.

Both figures 4a and 4b come together to form a narrative of the geographical trends predicted by the modeling carried out in this study. On the left, figure 4a illustrates a relationship Similar to figure 3. Whereas the equitorial phytoplankton are expected to decline in terms of abundance, phytoplankton populations are projected to increase in the middle latitudes. The lines represent the mean proportional change prediction, with the shading representing deviation. Analyzing the troughs and peaks of each group, it seems that the coccolithophores are poised to experienced the greatest lost, while cyanobacteria the greatest growth. Figure 4b is a visualization of 4a, providing a global map that is shaded, with cool colors indicating decline and warmer ones growth. In all four cases, with the warm colors in the polar/midlatitude regions, and the cool colors in the equator, the findings from figure 4a are reinforced. This is supportive of the overall trend of

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Abstract:

- Phytoplankton are phylogenetically diverse, and have different attributes when it comes to thermal conditions
- Diatoms, Coccolithophores, dinoflagellates, and cyanobacteria, four major components of primary productivity and ecological biomass/organic matter.
- Each of their thermal growth properties are different, and their equations derived
- Impact on growth rate and geographic distribution of these four major groups were tested using models of temperatures from 1950-1970 (past/given data), and the 2080-2100 (future/projected data).
- It is found that growth maxima thermal dependencies, thermal ranges and temperature coefficients all vary for each of the four groups, indicating diverse responses, and therby changes in taxanomic composition and distribution (which in turn has major ecological/climatic impacts).
	- Contrasts with previous findings from the Eppley formula.
- Therefore, it is predicted that there will be significant changes to phytoplanton tax comp
- Specific findings include fewer lower-latitude coccolithophores and greater amounts of cyanobacteria.

Introduction:

- Phytoplankton sequestert 45 gigatons of $CO₂$, vulnerable to climate change.
- However, understanding the impacts different groups face has hitherto been challenging due to diverse phylogenic/evolutionary background.
- Whether primary production increases or decreases in phytoplankton depends on temp, and the biodiversity of the habital ranges of this paramter that lie therein
- Presently, the same thermal capacities are applied to all groups of phytoplankton, making estimations too broad.
- The ramifications of different thermal capabilities in different species has yet to be explored.
- These varying capabilities shall result in different migratory responses and abundance changes among different phytoplankton species, modifying tax comp
- One major ramification of changing geographic ranges is that nutrient cycling, and other biogeochemical cycles are to be highly altered.
- Hence, this study defines the different thermal capabiilities found among species, determining the impact on growth, distribution, and other dynamics.
- Dinoflagellates, coccolithophores, cyanobacteria and diatoms, 4 major functional groups, assessed. Distribution and abundance measured by using past data and future projections of temperature from Earth System Models.
- While there are other parameters that impact phytoplankton dynamics, temperature is a stronger indicator compared to pH, nutirent concentrations, light, etc. b/c they depend on complex biological processes, and have less confidence in terms of model accuracy/ prediction. Temperature is a strong indicator of phytoplankton growth and abundance.
- Findings validate the hypothesis (different temp coefficients, growth maxima thermal dependencies, and thermal ranges causing different trends in phytoplankton)

Methodology:

- Growth Data Compiliation:
	- Thermal growth rates of the four functional groups assessed (w/ sample sizes given. Unfortunately, they are not equal (but maybe the next best step would be to be proportional? Idk…)
		- 200 coccos, 500 cyans, 1800 diats, 750 dinos.
	- Built off pre-2012 data for thermal growth rates from previous author, Thomas et al., using his same selection criteria (something that ought to be enumerated), though with modifications:
		- Lowered minimum rate to 80 μmol of photons meters squared per second. (from 100) \rightarrow allowing for more representation of cyanobacteria (so there is a disparity in data availability here… major factor to consider?)
		- No data attained from experiments where nutrient cocentrations were studied (possible sources of confounding)
		- Diazotrophic species of cyanobacteria were not considered due to their physiological differences, resulting that may add confunding variable to the changing dynamics.
			- Separate analysis was performed. However, the data size was too small, and so no data was reported- future area of focus!
		- Dinos only worked with in the lab, possibly could have ingested bacteria
		- Data analysis using GraphClick
		- 243 strains, >3k thermal growth rates measured.
		- Thermal reaction norms were instrumental in producing predictions on how the phytoplankton would react. (Equations used from Thomas et. al)
		- For the new post-2012 strains that were added in, the thermal attributes were estimated using the "maximum likelihood approach" from Thomas et al. 2018, and R (the programming language \rightarrow reactive programming)
- Climate Data:
	- Focus here was on the temperature increasing, so it easily follows that temp data had to be extracted from climate databases \rightarrow sea surface temp (SST) specifically
	- Coupled Model Intercomparison Project phase 5 (CMIP5) model projections
	- <http://climexp.knmi.nl>
	- SST warming was estimated based on the existing 1950-1970 data as a basline, and, under the worst-case greenhouse has scenario, produced results for 2080-2100.
	- Done on a latitudinal basis (each had their own sd and x-bar)
	- T_{hab} = habitate temperature for the phytoplankton strain. Attained via comparison w/ mean data from '50-'70.
- Thermal Dependencies:
	- μ_{max} = maximum growth rate with temperature; expressed w/ exponential function
	- Key citations here (I wish they would not do this): Eppley was to 1st to describe this function. Bissinger et al. later standardized methodlogy through which curve-fitting occurs
	- Bissinger followed via fitting a 99th quantile regression model to logarithmically transformed data on growth rates for each of the groups (under warming conditions, using quantreg package from R)
- 99th quantile was used, although it requires a lot of data and the results are vulnerable to many sensitivities, however, this method is superior:
	- Compared to a plain LSRL and the metabolic theory of ecology, the quantile regression is more comprehensive; LSRL only includes data below thermal optima, and the metabolic theory only focuses on μ_{max} w/o regard between the direct relationship with temperature.
	- LSRL fits to the 50th percentile data, which is undesireable in this context: the focus is on the *maximum* growth rates, hence we want the 99%ile, or, to be more general, the 99th quantile of the data.
	- Quantile regression also does a better job of illustrating the dispersal of growth rates and the variable responses to temperature than LSRL
	- Another reason quantile regression is superiror to metabolic theory as there are no assumptions needed regarding cell size, which varies wildely among different species.
- Phytoplankton growth rates and μ_{max} are statistically signfiicant among the different functional groups. Thus, each quantile regression (applied to the 4 func groups), was applied to these parameters separately.
- AICc (defined above) was used to make the model even stronger.
- Hence we have the following equation:
- $\mu_{\text{max}}(T) = a \cdot e^{b \cdot T}$ -
- Where $\mu_{\text{max}} = \text{maximum growth rate, given temperature (the function of T,})$ temperature) - defintion offered above, but to reiterate (only difference is that the base is e, rather than a):
- a is the parameter representing the maximum growth rate at $0^{\circ}C$, while b is the rate at which the maximum growth rate increases as the temperature does (meaning there is a positively linear, or at least positive form of relationship between the two)
- 95% confidence interval was created for the curves of each of the functional groups via the use 10k iterations of a Markov chain marginal bootstrap. This is ideal as this produces a computational algorithm that calculates only a one-dimensional equation given multiple parameters, that is, multiple dimensions.
- From these exponential functions, the temperature coefficient Q_{10} , a measure of the rate at which μ_{max} increases for every increase in temperature by 10[°]C, was attained, allowing for the assessment on metabolism.
- This departs from previous studies, where the functional groups had the same b value, and thus the same μ_{max} .
- Activation energy was then calculated based off the exponential model/ Q_{10}
- Static Thermal Capacity and Statistical Analyses
	- Thermal safety margin (TSM) and warming tolerance (WT) were used as metrics to calculate thermal capacity (see above definition).
	- These metrics account for the thermal attributes of the organism, given habitat temperature, and are used to calculate the temperature at which performance begins to decline (TSM) and then when viability is lost (WT). The habitat is assumed to be the temperature at one point, hence the label "static".
- To measure these metrics, each strain's thermal optimum and maxima was calculated: TSM = T_{opt} - T_{hab} ; WT = T_{max} - T_{hab}
- T_{max} : Dino = 38, Dia = 115, Cyan = 31, and Cocco = 24 °C
- However, it has been found that phytoplankton do not operate at their maxium growth rate, even at temperatures below the optimal one. Therefore, (and I judge this to be a decision to be a bit dubious), the authors presume that the same holds true for temperatures above the optimal level (I suppose this does imply the presence of some gradient, so maybe this assumption is not totally fallacious).
- As a mathemtical consequence, a temperature between T_{max} and T_{opt} was assigned as T_{μ equiv, this temperature being the maximum temperature at which the growth rate of the phytoplankton remains the same as the habitat. The spread of temperature covered between the T_{hab} and T_{uequiv} was coined distance to the growth equivalent (DGE), that is, T_{μ equiv - T_{hab} .
- Variation in these thermal attributes were then measured using Kruskal–Wallis tests, followed by the Dunn's multiple comparison tests at alpha = 0.05
- Future Metabolic Projections
	- The proportional growth change $(\mu_{\text{future}} \mu_{\text{past}})/\mu_{\text{past}}$ for each strain among the four functional groups was calcuted as a first step to understanding what impact the change in temperature had on phytoplankton growth rates and those ramifications.
	- This relationship was modeled for each global grid cell (at 1.25° resolution)
	- Viability was defined as $\mu_{20\%\text{max}}$, which, as the name suggests, is 20% of the maximum growth rate. 20% was determined as the percentage, given that authors noted that species presence declined when starting off at lower percentages. However, 80% is typically used. (Clear reason for choosing 20% rather than 80% does not really make sense)
	- The growth change was then collected among all strains, and for each genus, the median value was used. Since the distribution is not normal (see figure 3a and other functions above), this is a better summary statistic (hence the quantile regression as well).
	- The viability criteria was applied at all latitudes to also assess whether there would be cyanobacteria, as this group is expected to grow greatly in range.
	- Spatial trends were enumerated via the average population growth rate change across different latitudes.

Results and Discussion:

- Disparities in Thermal Response
	- (Again, a broad range of temperatures from a wide area was used)
	- Through the data processing methods employed, authors claim that the data is 72% different from "typical data" (interesting, possibly controversial claim…)
	- Growth rate vs. time function fitted to a Norberg curve. Norberg curve was also utilized to find the growth rate maxima among individual strains.
	- Again, cutoff of 20% of the μ_{max} was used, eliminating bias (skew) in the data brought about due to ambiguous thermal minimum.
	- The absolute value of the difference of the thermal reaction norm slope from μ_{max} to 20% of μ_{max} was taken, and placed over the temperature in Celsius. Meaning, the slope was $|\mu|$ ^oC. Intuitively this makes sense, as the growth rate is being

altered by the changing temperature, so the performance change would be some measure of growth rate changing, given the temperature (independent variable).

- This slope was also used in understanding the skew of the data (the slopes of the growth rates given the tmeperature changes)- the greater degree of positive difference from T_{opt} indicated that these data were skewed to lower values (which makes sense, b/c if the difference exceeds T_{opt} , the values would have to be really low)
- The article first cites numerous data and evidence to suggest that the thermal attributes and responses among the four groups are not homogenous.
	- Cyanobacteria and Cocclithophores have notably limited temperature range: <9℃ and >30℃ respectively, neither can survive. Meanwhile, diatoms have a wider thermal niche.
	- (Somewhat obviously), the geographic distribution depended upon the thermal gradient
	- No significant correlation with the sample size, or the absolute isolation latitude, according the Pearson's Correlation test.
	- (see analysis of Figure 2 above)... the small changes observed in the Dino. group resulted in flatter curves. These trends (which match previous results, as this case with most results, unless otherwise stated), may be attributable to the daily vertical migration that this group engages in. This would have led to a lower amount/variability in growth rate, in exchange for greater thermal breadth.
- The article then provides data/discussion for Q_{10} , the growth rate change experienced for every increase in temperature by 10℃, and Eppley curve:
	- Temperature vs. growth rate maxima modeled via exponential function, in conformity with most models of Earth systems, primary production and growth rates.
	- Again, the main purpose of this article is to highlight the different thermal norms in the functional groups. Hence, the Q_{10} is proven to be statistically significantly different among the functional groups, diverging from methodologies of the previous studies (Kruskal-Wallis Test used).
	- 99th Quantile Regression Utilized (advantages of this choice described above in the methodology section), but main thing to note here is that this method allowed for the exponent to numerically characterize the relationship betwen group growth rate and temperature, allowing for Q_{10} to be calculated.
	- Epply curve characterizes the impact of temperature on growth rates as 1.88 (this is the b constant- measures the degree of increase the maximum growth rate experiences due to temperature- sorta basically just Q_{10}).
	- However, the functional groups differ from this greatly (even when evaluted as one collective entity), illustrating the sheer thermal variability observable among different phytoplankton groups. Collectively, $Q_{10} = 1.46$
		- Indeed, literature has been reaching a consensus that Epply Curve (1972) is an overestimate
	- Exponent values are as follows for each of the groups:
- Coccos (1.42), Diats (1.55), Dinos (1.67), and Cyan (2.13)
- Y-ints (i.e. growth rate at 0° C), were significantly lower for Cyan and Dinos (however, note that Cyan can't survive under 9℃, anyway)
- Cyan > other groups \rightarrow significant
	- Contrary to the finding explained in the previous bullet at this level, authors argue that Eppley is not merely an overestimate, rather, its error depends upon the Q_{10} of the given group
- However, there is another lens of analysis to consider: comparing the μ_{max} of the functional groups at a given temperature.
- Despite having the smallest exponents, at 20℃, Diatoms and Coccos had the greatest growth rate (based off model predictions) \rightarrow could indicate a superiror ability to compete, as, despite a low temperature-sensitive growth rate change, they still have a higher growth rate at this given temperature, b/c they can, well, compete better, thus allowing for γ growth
- Diatom trends are particularly notable, as they have the highest predicted growth rate at all temperatures compared to the other groups (see analysis of figure two above).
	- Indicative of them being r-strategists, groups that maxmimize the growth rate when under favorable conditions. Also indicates that this group would survive well under nutrient-sparse conditions, consistent with the findings of studies that analyze cocco-diat competition in oligotrophic systems.
	- Indicative of Diat's strong ability to adapt to unideal thermal conditions (excessively warm conditions, specifically).
- All of these dissimilar thermal-sensitive growth rate trends among the four groups speaks to their unique evolutionary history $($ > 1b years), which included 2 instances of endosymbiosis
- Thermal Capacity Across Latitudes
	- The article re-explains how it defined DGE, Thermal Safety, and Warming tolerance. However, key thing to note is that DGE is special for taking into account the growth rate staying equivalent at temperatures exceeding T_{opt} , is useful, given that temperatures are warming. Overall, a more full picture is offerred.
	- (see figure 3 analysis)
	- As indiciated by figure 3, even though many of the mid-latitudes had temperature levels above T_{opt} , death was prevented through the large warming tolerances, something seen across all functional groups. However, this indicates that there was a significant amount of strain placed on performance.
	- (see above, but good to retiterate) Overall finding in mid-latitudes: there are temperatures that are above optimal moreso in this region, inhbiting performance though not causing death, with the warming tolerance of the functional groups still buffered from that. Also, the DGE is able to indicate that growth rate itself is not too strongly impacted either.
	- Explanation offered for the parabolic trends noted in figures 3b-3d:
- Although the equitorial phytoplankton have higher optimal and maximum temperatures, the ocean habitat temperature here does not increase. (meaning homogenous temperature across the ocean (?))
- This may indicate that the equatorial phytoplankton may struggle to adapt to the warmer temperatures. (Well, this could also just be math; the same thermal norms remain, but since the t_{hab} is already warm, the difference will start off lower. However, maybe a relationship analogus to the mid-latitudes will emerge, only that the t_{bab} , t_{opt} , and all of those other parameters are all higher.
- Parabolic trend has been observed in other species as well.
- There was no significant difference between the PFTs with regards to warming tolerance and DGE, but cyanobacteria were significantly different w/ TSM compated to dino and diats, specifically inidicating that they are more likely to inhabit abormally cooler temperatures. (Makes sense — they prefer higher temps)
- Changing Rates and Shifting Ranges
	- Model for the ends of "simulating" changing geographic dist *does* take into account temperature gradients, migratory capabilities, and phenotypic variation w/n groups
	- Rather than actually simulate the movement of the phytoplankton, it was assumed that any region containing the proper temperature for phytoplankton to thrive could contain them (sort of a spatial probability approach).
		- Use of 20% of the maximum growth rate (methodology)
		- Use of CMIP5 models for SST + comparison between 1950-1970 and 2080-2100, calculating the median proportion of growth rate at each latitude
	- Differing changes in phytoplankton abundance = different composition, possible changes in competitive attributes
	- Cyanobacteria can now inhabit regions in that were once too cold for them due to ocean warming (e.g., Gulf of Alaska, Norwegian Sea)
		- Imposition of competition in new areas $+$ similar patterns in the cocco
	- Coccolithophore decline in equator leads to less calcium production and chemical interaction, altering alkalinity.
	- DGE exceeded the thermal capacities of most strains at the equator, so equitorial decline does makes sense.
	- Opposite trend in mid/polar latitudes: especially in Southern ocean, where iron concentration due to ice melt is expected to increase.
	- But this increase might be inhibited by nutrient availability, particularly the nitrogen deficiencies expected to arise in the ocean.
	- Model accounts for temperature alone, not considering other factors that impact growth rate and migration.
	- Overall, there multifarious impacts that warming ocean temperatures are expected to have on phytoplankton. This lack of homogeneity is in line with other studies' findings.
	- Specific focus on temperature, though narrow, allowed for ensured diversity to be determined among the functional groups for this specific trait
- Predicted losses in metabolism.
- Future applications using a time series.
- Standardizing thermal rates among different groups, analysis of primary production, and overall, further work on temperature and other parameters is required.

Article #14 Notes: Fatty Acid Profiles and Production in Marine Phytoplankton

Important Figures

Figure providing background on production of fatty acids in phytoplankton. First, from photosynthesis, glucose is attained, and pyruvate is fromed from glycolysis. This pyruvate becomes Acetyl-CoA and travels down various pathways, including Krebs Cycle, and another cycle, where A-CoA gets turned into Malonyl CoA. These two molecules provide the initial carbon for forming fatty acid chain. Subsequently, a series of complex enzymatic reaction occur in the ER whereby chains are elongated and doubly-bonded (i.e., desaturated). Various acids are formed from these processes, and when synthesized, the major fatty acid products are formed. This occurs in the smooth ER.

Illustration of proportion of mass of each macromolecule with respect to each phyla of phytoplankton. Proteins make up the plurality of organic matter in all phyla. About 40% -60% of the cells contain protein, with another 20-30%

NOTES

Abstract:

- Phytoplankton sequester carbon, use it to produce macromolecules
- In particular, main source of omega 3 polyunsaturated fatty acids (PUFA), critical nutrient in marine food webs.
- Meta-analysis performed on 160 fatty acid profiles across 7 phyla indicate significant inter-phyla and inter-class differences in the types of fatty acids produced.
- Goes on to list certain acids as being most abundantly produced by given class/phyla
- There are also highly unsaturated fatty acids (HUFA), of which some phyla are better at producing than others
- Important nutritional and environmental impacts on the transfer of these molecules
- Environmental stressors projected to decrease fatty acid movement

Introduction:

- Carbon integrated from common metabolic pathways, combined w/ phosphorus and nitrogen to create phytoplankton cell
	- Provides the macromolecular nutrients for upper trophic pyramid (crucial in growth, reproduction, health, stability, etc.)
- Zooplankton transfer these molecules \rightarrow important vectors
- Macromolecular analysis of the different phytoplankton genera to see quality of nutrition of zooplankton, given their role as vectors (holistic ecosystem analysis)
- Some essential nutrients aren't/can't be created by the upper-energy level organisms, which is where phytoplankton become important
	- PUFA omega3s specifically, hence focus on fatty acids.

Biochemistry Behind these dynamics

- C is the main element of all compounds and cell structure, binded to different types of molecules in different macromolecular nutrients (quality varies)
- $-C = \text{indicator of biomass}$
- N is main building block of the proteins which C is connected to- C/N ratio indicator of nutritional quality + protein structures info.
- See figure 2 analysis above on protein/macromolecular content
- Essential Amino Acid concentrations used to measure protein quality.
- Protein quality found to be homogenous, with significant differences only emerging when considering groups once they have received other nutrient, namely fatty acids.
- W/ regards to carbs, although providing energy, there is little nutriontial value for the zooplankton vectors (no trace/nitrogen in molecules)
- With const 5:3:2 ratio among marcomolecules, why does nutrional quality success in predators vary?
	- As such, lipids are the focus here
- Background on Glucose \rightarrow Lipid Metabolism.
	- Crucial for understanding fatty acid comp in phytoplankton
	- Aerobic production methods for fatty acids in ER and chloroplast
	- Pyruvate from glycolysis \rightarrow pyr becomes Acetyl-CoA (Coenzyme A) \rightarrow Krebs Cycle, bonding with carboxylase \rightarrow Malonyl A
	- A-CoA & M-CoA provide C for the fatty acid chain
	- A series of complex enzymatic reactions occur, elongating and desaturating (double bonding) the C chains in the ER.
	- Finally, various acids from the previous steps are synthesized to form the larger-scale macromolecules (e.g. trigcylerides, phospholipids, etc.) in smooth ER
- Key here is that phytoplankton have the enzymes that higher-trophic organisms lack to directly produce these essential fatty acids (namely omgea3s and 6s as stated by article), hence, phytoplankton are a crucial food source for their predators so they can get these essential but not self-prodcued molecules.

- Note: omega is the location of the first double-bond

Methodology:

- Meta-analysis performed
- Freshwater species omitted, and the species observed were sorted by Linneaus classification
- Data collated and sorted into categories of "protein", "carbs", and "lipids"
- Fatty acid data presented is a pecentage of total fatty acids. Homogeneity among the genera and species was analyzed, and the class means taken for each phyla.
- There are discrepancies in the fatty acid data, so to accomodate, any acids with concentrations below 0.1% were not counted or analyzed in the meta-analysis

Results:

- Lipid composition varies extremely among phytoplankton (figure 4 analysis above)
- Study attempts to determine the amount of fatty acids found per carbon as a means of understanding how much food value of fatty acids is contained when predation occurs,
- However, there is little data on this subject, hence the mean estimates produced for the phyla in the meta-analysis vary greatly. Nonetheless, it is still clear that the fatty acid content and the amount of nutritional value offered varies greatly.
- Chlorophyta, with regards to fatty acid nutrition, has the worst performance
- Higher temperature results in greater production of fatty acids but reduction in nutritional quality.
- Light is also a crucial component of fatty acid synthesis: elongation and desaturation enzymes rely on light
- Nitrogen and phosphate are also necessary components.
- However, more information is needed on the impact of trace metals on fatty acids.
- All of these parameters play a role somewhere along the chain of reactions that occur for fatty acid metabolism.
- These controls on metabolism can lead to changes in their chemical composition, which important to both (a) understand and (b) manipulate empirically.
- Fatty acids can be used as biomarkers given this heterogeneity.
- The main idea is that varying fatty acid concentrations provides different levels of nutrition to predators.

Discussion:

- Omega3-lipids are crucial to health, and it is through phytoplankton that it is transferred to the rest of the food chain.
- Major economic demand in fish industry
- Global warming \rightarrow ocean stratification, warmer temperature, nutrient deficiencies all limit phytoplankton growth.
- Emphasis on the need to understand (model!) the situation as changing dynamics are causing this increasing quantity but decreasing nutritional quality in fatty acids.

Article #15 Notes: Planktonic ecological networks support quantifcation of changes in ecosystem health and functioning

Important Figures

Principal components analysis of the consumption flows, along with the ranks of the most influential nodes is provided by magnitude in the above figure. The white plots represent the resulting datapoints from 2005, and the black ones represent 2007. Each vector represents the impact each node exerts on the model. In conjunction with the supporting bar graphs, it has been found that the nodes containing Strombididae, *Evadne* spp., and *Podon* spp. were the most impactful.

2007. In line with the findings of this study, there was not a significant

change in this ecological attribute between 2005 and 2007. The centers and spreads are mostly the same across both years, as seen visually above. There are some differences, however, they are not enough to be considered significant. Detritivory Relative internal ascendency Herbivory 200 150 200 100 100 50 Frequency 0.375 0.400 0.425 0.450 $\overline{20}$ $\overline{30}$ July 2005 **Primary production** Finn's cycling index Community respiration 2007 600 200 400 150 100 200 50 $\overline{0}$ 0.025 0.075 0.09 0.050 0.100 0.12 These histograms are of the frequency among the multiple samples collected of the various ecological characteristics measured as outputs of the food web. It performs a similar function as the above figure, only using a histogram as opposed to a violin plot. Here, there seems to be a few more differences between '05 and '07, indicating that there are *some* changes between the two years, even if they are not completely significant. It seems that 2007 saw less resiliency (internal ascendancy) but more cycling, whereas the opposite is true for 2005. From 2005 to 2007, it seems that community respiration increased, as did feeding on producers. **VOCAB: (w/definition) Turnover Rate** - Speed with which an enzyme is able to operate. **Monte Carlo Random Sampling** - A method involving repeated random sampling whereby numerical values are attained. The context is often to find some deterministic factor or trend. **Functional Nodes (FNs)** - A "point" on a neural network **Violin Plot** - Compares probability distributions of given factor or factors. It acts a broader form of a boxplot. Instead of just plainly having the median and quartiles, it also contains the distribution of the numbers themselves. It's basically just a histogram layed on top of a boxplot. **Mixotrophic** - An organism whose means of energy attainment lie on a spectrum in between autrophs and heterotrophs. **Detritivores** - Organisms that mainly feed on detritus, dead organic matter. **Cited references to follow up on** Kauhala, K., Korpinen, S., Lehtiniemi, M. & Raitaniemi, J. Reproductive rate of a top predator, the grey seal, as an indicator of the changes in the Baltic food web. Ecol. Indic. 102, 693–703 (2019)

NOTES

Abstract:

- Changes in aquatic changes impact metabolic rates and energy transfer of phytoplankton
- Good indicator of ecosystem health
- Water body in Venice Lagoon had food web data between July 2005 and July 2007 compared.
- Monte Carlo random sampling of parameters used to derive 1000 food webs
- Certain species of phytoplankton were found to be important in the splitting and controlling food web (controlling energy transfer and all that)
- Slight variations in functional nodes (FNs), but overall same results between the 2 years
- Consumer use leads to greater sediment resuspension, increasing turbidity,
- Main source of primary production = benthic FNs/organisms
- Food web maintained equilibrium, although environmental stress caused efficiency to be sacrificed in favor of resiliency.

Introduction:

- Dif. parameter values impact productivity and tax comp
- Particularly, the turnover rate, i.e., rate at which enzyme operates is impacted, making phytoplankton communities good indicators of ecosystem health
- Dif. phytoplankton dynamics = dif. Trophic structure
- Various processes, including mixotrophy, heterotrophy, and detritivory are used to facilitate rapid adaptation to environmental change
- Helps maintain resilience and basic processes of equilibrium state
- Transitional coastal lagoon is a good case study: area has a lot of variation.
- E.g. freshwater/seawater, hydrodyanmics, anthropogenic incluences, etc.
- These factors impact energy transfer among food web, changing ecological comp
- In observing how phytoplankton are changing can indicate ecosystem resilience, and importantly, the mechanisms behind that.
- Herein lies the utility of ecological network models. Due to their holistic nature that captures the line-by-line complexities, analysis can reveal impact of changes on ecosystem operation.
- The reason to focus on phytoplankton is due to their role in critical microbial and energy transfer mechanisms.
- Coastal area study is particularly useful: more data availability + looking at a situation where multiple parameters change.
- Venice July '05 vs. July '07 comparison of trophic conditions performed. July was chosen b/c it is when the biomass peaks, and as a corollary, when more data on wider variety of zooplankton is present, the occurrence of important ecological processes.
- Goal in this analysis is to identify specific roles among groups of phytoplankton, as well as compare trophic state to assess factors and their impact and implications at two dif. Timeframes.
- Innovative iterative random samplings of parameters approach was taken to construct the food webs.

Methodology:

- Venice Lagoon is part of the Italian Long-Term Ecological Research Network. Large water body, transitional, well-studied.Majorly important in socio-ecology,
- Northern area, Palude della Rosa, was studied, notable for salt (sewater, and this is the highly saline Mediterranean) and freshwater (river discharge) inflow.
- All sampling collected during specific tide times to avoid biasing data; July 2005 and Jul 2007 used (tax com., biomass in mg C m^{\sim}-3).
- Various types of phytoplankton and other related species (bacteria, zooplankton) were sampled/had specific laboratory procedure for testing
- FNs generated for each species at lowest tax classif possible: grouping together to form nodes and such based off similar ecological function, each FN contains size and role.
- Inter-species pref vary \Rightarrow only two params (benthic/pelagic preference)
- Parameters:

-

- $\mu \rightarrow$ production rate per biomass unit (d^-1)
- $\alpha \rightarrow$ consumption rate per biomass unit (d^-1)
- $-\epsilon \rightarrow$ unassimilated fraction of biomass consumed
- ph \rightarrow phototrophy proportion in individual metabolism (0 = heterotroph, 1 = autotrophs, and in between for mixotrophs)
- $\gamma \rightarrow$ Proportion of flows to non-living nodes (e.g. feces death etc)
- Properties range given the organism of the FN
- Ordinal variables describing strength of interaction 0 (none) to 3 (strong)
- Assumption: Balance between production, mortality and predation:

$$
\mu_k \cdot B_k - \sum\nolimits_{j=1}^n (\alpha_j \cdot B_j \cdot DC_{k,j}) - m_k = 0
$$

- μ_k = production rate per biomass unit; B_k = biomass; m_k = mortality; j is the index of the properties of the predator (consumption, biomass, and $DC_{k,i}$ is proportion of the prey in diet of the predator)
- Balanced model used for the non-living nodes:
	- $\sum\nolimits_{i=1}^n \big[\gamma_{i,d}\cdot(\epsilon_i\cdot\alpha_i\cdot B_i+m_i)\big] \sum\nolimits_{i=1}^n \big(\alpha_j\cdot B_j\cdot DC_{d,j}\big) \mathrm{ex}_d + \mathrm{im}_d = 0$ -
	- ε_i = unassimilated fraction of biomass consumed. The first summation is flow of energy of living node to nonliving one. Subtract from that the consumptions of the detritivores, as well as the export (ex_d) . Add the im_d, the import.
- Estimation of respiration

-

$$
R_i = Q_i - P_i \cdot (1 - p h_i) - U N_i
$$

- $Q =$ consumption, P = production, ph = phototrophy proportion for node i, UN = unassimilated material
- The above parameters for each FN was generated from taking random sample for the possible range.
	- Use of the ordinal variable strength 0-3 here; between 0 and 1 (minmax) normalization), two bounds for each parameter 0 to 1 were set.
		- 1: 0 to first; 2: 1st to 2nd; 3: 2nd to 1
- All FNs had a system of linear equation containing the range of the parameters. Other parameters not incorporated in model calculated by those that were.
- No specific values/solutions to the equation; rather, random values for the parameters were used by taking repeated random sample from the possible range
- Another assumptions made:

 $R_i \geq 0$

- $0.15 \leq G E_i \leq 0.5$ -
- Where R_i is the respiration flow and GE is the gross food conversion efficiency, ratio between heterotrophic production/consumption
- Various ecological attributes of the food web calculated for both '05 and '07 and statistical comparison was performed (formulae can be found in the article)
	- Relative Ascendency: The ability of an ecosystem to be resilient given disturbances due to sheer size and organization. Measure between efficiency and resilience $(0 = \text{min efficiency}/\text{max}$ resilience, 1 the opp)
	- Relative internal ascendency: The same measure described above, based on the internal transfer of energy (same scale)
	- Finn's cycling index: The proportion of flows attributable to cycling $(0 = no$ cycling, $1 =$ all material cycled)
	- Ratio of detritivory to herbivory: Comparison between consumption of producers vs. nonliving nodes; $>1 \rightarrow$ more nonliving nodes; $<1 \rightarrow$ more producers; $1 \rightarrow$ about equal
- Ratio of primary production to community respiration: During ecological succession, $=/- 1$; during equilibrium, $=1$
- Omnivory index: Variation of trophic levels of a consumer's prey (closer to 0 the more specialized in feeding)
- PCA used on only the non-constant flows of different sizes from '05 to '07
	- Two largers vectors == nodes most significant to the split of the food web
- Mood's Median Test and other nonparametric approaches taken (parametric conditions not met)
- R used as a programming language

Results:

- See figure analysis above

Conclusions

- Lack of significant ecological differnce betwen '05 and '07
- Valid computational food web with intruiging and accurate results successfully produced.

Article #16 Notes: A Link Between CMIP5 Phytoplankton Phenology and Sea Ice in the Atlantic Southern Ocean

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NOTES

Abstract:

- Bias/data problem in Coupled Model Intercomparison Project Phase 5 (CMIP5).
- Inaccurate depiction of late winter primary production
- Benthic/Sub-pelagic light availability is correlated with early growth, as winter mixing and ice cover prevent growth, dynamics which go unmodeled.
- Correlation between stratification and the extent of sea ice. Increased stratification (particularly in late winter) = ice extent \wedge (b/c closer to the equator)
- Given the correlation stated above, and how well models control for it (including each internal factor), models were sorted into groups.
- Models with less bias had better predictions (even when having proper control of one factor only)

Introduction:

- CMIP5 models on Antarctic sea ice trends have been known to be inaccurate, the implications of which have yet to be fully investigated
- Specific focus is on impact of the inaccuracy on phenological phytoplankton modeling in the Atlantic Southern Ocean (Atlantic b/c largest Chlorophyll concentrations and large spatial variability)
- Focus on the marginal ice zone, where ice exists in some degree but atmosphere-oceanic exchange is still possible. This area is known for greater pimary production
- As ice melts, the water column stabilizes, with a pelagic layer of freshwater forming that allows for the biomass of phytoplankton to increase. But there is also iron and other factors that CMIP5 doesnt account for.
- Many past studies have indicated that the CMIP5 predicts the location of the mixing layer to be shallower than what is actually the case, indicating that there was too much freshwater being input into the model

- Leads to a lack of mixing \rightarrow impacts the light/nutrient conditions, changing results (so let's see how those change, based off the inaccurate vs. accurate estimate of mixing layer) Methodology:

- 11 CMIP5 models on historical simulations were collected (1976-2005 data timeframe)
- Variables considered: pelagic chlorophyll mass concentration, sea ice area fraction, salinity, and potential temperature
- Various satellite models were tested and compared
- Data spreads from 20॰W to 20॰E
- Marginal Ice Zone (MIZ) defined as area of 15-80% ice concentration contours; 15% is the northern edge; to account for different definitions among models, a common region of analysis was used in all models: 58॰S to 62॰S
- Allows for meaningful comparisons to be performed
- Main measure here is the temporal prediction of bloom initiation and peak, defined when the chlorophyll concentration passes 5% greater than the median; bloom peak = chlorophyll peak

Results:

- See figure analysis above
- Poor modeling of chl a concentrations has been supported by evidence
- There is a bias towards shallower depths.

Concluson:

- All models are assorted into groups and analysis of them is performed. The findings show clear biases in chl a concentration, poleward bias of the MIZ line, shallower mixing layer, and earlier bloom periods.
- In the real ocean, ice cover, deep winter mixing, and associated light limitation prevent biomass accumulation until the late spring. This is not present in the CMIP5

Article #17 Notes: Disentangling physical and biological drivers of phytoplankton dynamics in a coastal system

Sharma 152

abundant. This is for spring and autumn,

NOTES:

Abstract:

- Surface current and time series data both analyzed to help identify driving parameters of dynamics
- Species succession was controlled by biological factors (inter-species interaction, physiology, etc.)
- Physical factors were also important (e.g. coastal movement, mixing), as offshore species are integrated into the ecosystem, regulating competition and dominant species
- Findings show that coatsal communities are resilient
- A proof-of-conept design to apply to other coastal ecosystems (unifying the heterogeneity among coastal areas)

Introduction:

- Allogenic (physical) and autogenic (processes) both regulate changes in phytoplankton
- Physical = mixing, movement, etc.; Biological = Ecological interactions, cytological and other itenral processes, etc. + shallower areas have more complex gradient \rightarrow difficult to understand.
- Important to consider for phytoplankton blooms, which can sometimes be toxic (algae).
- Particular problem with oversimplified analysis (as well known for this project)
- Tools exist to model these two major groups of factors: ecological information and surface circulation, modeled by ever-more-robust high frequency coastal radars (HFRs)
- Lagrangian models have yet to be applied well to marine environments
- This study combines this novel observation of the water currents with ecological site data collected.
- A proof-of-concept study focused on establishing a methodology for future investigations to follow.
- The HFRs produced high resolution observation of the biological and physical parameters, allowing easier connection to phytoplankton dynamics.

Methodology:

- Complex description of the HFR calibration is provided
- 2009 was used as year to study as it had the most radar and biological data.
- On Lagrangian Modeling:
	- Surface velocity used as input
	- 10 minute interval tracking movement retrospectively (backtracking sims)
	- 15% error used
	- Particles released in the simulation, with the initial location being determined by result of backtracking sim (accurate up to 4 days)
	- Probability model used to define spatial variability of the origin zones
	- Entry time (shift focus to temporal, not spatial scale), center of mass and the variability of that (this is spatial) was measured.
	- The origins points were designated into sectors, 1-4 and 8 being coastal, 5-7 offshore
- Positions had their corresponding salinity, chlorophyll a measured. There was element of phenologic comparison to this.
- Z-standardization used among these different timeframes to compare the measures in this area (so there was time the particle was located at a given position which had these parameter values which are now being compared)
- Chlorophyll a values determined from direct extraction
- Salinity/chlorophyll a cluster analysis to see the ecological characteristic of the lake studied (Gulf of Naples) (R was used)
	- Bray-Curtis similarity, logarithmic abundance data, alpha index of diversity - Independent of n
- Gulf of Naples $=$ area of study
- Complex benthic properties \rightarrow complex hydronamic properties; seasonal shift between moderately eutrophic and oligotrophic
- Data has been collected very regularly on this body of water (weekly since '84)
- Ratio between alpha diversity and biomass was also considered.
- All of these processes were to help disentangle biological and physical parameters

Results:

- Phenological variation in the speed of the water currents.
- Patches of phytoplankton concentrated closer to the coast, sporadic as distance increases
- Various complex interactions between the hydrodynamic and ecological parameters were observed.
	- Phenological variation in what is a driving factor, what is not. Location,
		- chlorophyll a and salinity driving factors in various cases, not in others, etc.
- See analysis of trends in the biomass in figures above

Conclusion:

- The computational system was able to successfully allow for the physical vs. ecological parameters in different situations to be determined.

- The farther the origin zone of ofshore waters, the larger the modifcation induced in the phytoplankton community.
- Successful displays of the interaction between biological and physical parameters, and the connection with those dynamics to the dual-impact of the coast and offshore currents.
- Proof-of-concept study applicable to other areas.
- Helpful for management decisions.

Article #18 Notes: Ecological stoichiometry influences phytoplankton alpha and beta diversity rather than the community stability in subtropical bay

This figure depicts the phenological trends of the alpha diversity indices in the Beibu gulf. These include the shannon, chao1, simpson indices, as well as the raw abundance. Interestingly, it seems that the indices, as well as the abundance, is highest in the winter, followed by the autumn, summer, and spring. Though, some indices have skewed distributions, for example, especially for chao1.

From left to right and top and down, the topmost graph on the left is the relationship between the shannon index and the AVD. To the right, is the relationship between the AVD and the Bray-Curtis dissimilarity. Given that higher AVD would suggest greater diversity, it makes sense that significant ($p<0.05$) positive relationship w/ Shannon and Bray-Curtis. Finally, various nutrient ratios and their relationship with the Shannon diversity index are depicted in the four graphs below, including C:N, C:P, N:P, and the redfield ratio. With the exception of N:P, all ecological stooichiometric relationships had significant postive

NOTES:

Abstract:

- Aim is to understand the exact relationship between nutrient stoichiometry and the tax. diversity of phytoplankton, specifically in sub-tropical bays
- Phenology observed and community comp in Beibu gulf of South China Sea observed.
- Various families/groups varied phenologically, use of the alpha diveristy index.
- Higher diversity = stabler community (Bray-Curtis Dissimilarities, Shannon Index)

- Redfield Ratio did not impact community structure or diversity, rather, nitrates, phosphorus and temperature did (providing new/unique insight/perspective)

Introduction:

- Diversity in phytoplankton helps maintain ecosystem stability, with multiple species present to perform cycling and other necessary functions.
	- Biodiversity = stability
- Many parameters impact their community structure
- Specifically highlights water temp and nutrients
- Ecological change \rightarrow 2 types of deterministic and stochastic processes in aquatic ecosystems.
- Stability is measured using average variation degree (AVD) (lower value = stability \uparrow)
- Although measured by diversity, article identifies importance in measuring correlation of stability with diversity.
- There is also lack of knowledge on ecological stoich on phytoplankton community structure and diversity
- To analyze these factors surrounding ecological stoich and stability/structure at the spatio-temporally, water samples during four seasons from the Beibu Gulf were analyzed with the ends of:
	- Phenological trends in community structure
	- Identify significant parameters impacting community structure + relationships

Methodology:

- Specific latitudes/longitudes where sampling of the Beibu gulf occurred
- Surface seawater data collected 0.5 meter below surface on specific dates from summer 2017 to spring 2018
- $n = 100$
- Temp, salinity and pH were measured, and filtration systems for DNA were used.
- Various spectrophotometric and colorimetric methods were employed to get data on nitrites, nitrates, phosphates, chl a, total organic C, COD, DO, total dissolved N and P, ammonium, kjedahl N, nutrient stoich ratios
- Specific laboratory procedures and tools used to extract, amplify, and sequence DNA. the sequences of all of the samples collected, were, at the end stored in a database
- 1 (n/N) (n= specific species size, N = total sample size) was performed (Good's coverage)
- Various R packages
- ANOSIM (analysis of similarity), PERMANOVA and ANOVA all used.
- Spearman's rank method used to to perform correlation analysis
- Alpha diversity calculated using various indices
- Principal *coordinate* analysis (PCoA), AVD, and Bray-Curtis all used as well
- Alpha < 0.05 or < 0.01

Results:

- See detailed figure analysis above; article material does not offer anything beyond what has been discussed.

Conclusions:

- Low temps arise in the spring waters, hence the drop in diversity observed
- Novelty of the spatio-temporal scale
- These nutrients are significant for the growth and thriving of phytoplankton populations and eocsystem; knowing their values are important
- Bacillariophyceae in winter/spring; Coscinodiscophyceae in summer/autumn;
- Nutrient stoich impacts taxonomic diversity, however more investigation into the underlying factors of these relationships is needed to develop a fuller understanding of what is going on.

Article #19 Notes: Mechanistic theory and modelling of complex food-web dynamics in Lake Constance

Sharma 164

NOTES:

Abstract:

- Having models helps understand the highly important dynamics of consumer resources.
- However, this is inhibited by model inabilities to produce comprehensive food webs.
- Use of neural nets to model pelagic food web of large, well-known lake (good case study)
- Using initial spring biomass and individual body masses, a neural net representing the food web was constructed and parameterized.
- Various measures of energy transfer were incorporated into this network, increasing accuracy of the representation of ecological dynamics.
- Potential new way to model food webs using network theory.

Introduction:

- Observing ecological dynamics is important for understanding energy transfer and other critical aspects of ecosystems.
- W/ regards to ecological modeling, computational models of organisms feeding on one another has been limited due to lack of data.
- This is where network theory analysis of food webs bceomes key: ecological energy transfer can be better modeled.
- Allometric Trophic Network uses bodily, metabolic properties, biomass fluctuations given resource availability, consumption, and other factors as inputs; fundamental to structure of the neural net model
- Other models have focused on local hydrodynamics and biogeochemical cycling, but given the scope, are not applicable to ecosystems at a broade level — goal is to est. generality.
- Aim was to produce a time series of a neural network food web, something that has not been too heavily evaluated.
- Phytoplankton are used here more as like a case study.
- Lake Constance in Germany/Switzerland/Liech/Austria was used to model the food web, given that it is well-known
- The dataset used contains phenological trends of the phytoplankton: In early spring, a few fast-growing phytoplankton develop during the clear water phase, being highly edible; then the late spring bloom occurs and the diversity increases at the expense of edibility.
- 5 ATNs were used to model this situation, each time with parameter requirements increasing

- This helps better fit the model to accurately capture phenological and ecological trends Methodology:

- Major seasonal trends Lake Constence: in later winter/early spring, irradiance, vertical
- mixing and temperature control abundance, whereas in the later spring, flowing stratification, nutrient depletion and food quantity and quality are the controls.
- Plenty of data on relevant parameters has been collected for this region
- 24 guilds and 107 feeding relationships were compressed into 20 guilds with 8 groups.
	- Phytoplankton (Phy), autotrophic picoplankton (APP), heterotrophic bacteria (Bac), heterotrophic nanoflagellates (HNF), ciliates (Cil), rotifers (Rot), herbivorous crustaceans (Herb. Cru), and carnivorous crustaceans (Carn. Cru)
		- Species therein are specified
- Time series based on phenological trends was constructed. Temporal phases employed for each season of the year
- Noramalization of the data therein was performed to account for differences in the temporal boundaries of these phases.
- Averages attained through the use of a spline function among all the data from the 10 years (1987-1996 (?)) \rightarrow allows for the weather events to be ignored thereby not confounding anything, and instead focus on the ecological dynamics
- ATN model is based on differential equations related that can be applied to be n species. However, this study adds in metabolism, phytoplankton exudate, and dead particulate and dissolved organic carbon as detritus
- - Equations for the foodweb model (takes into account abundance, biomass, metabolism, etc.): $\frac{1}{2}$

$$
\frac{dB_i}{dt'} = r_i \mathbf{B}_i G_i(\mathbf{B}) (1 - s_i) - \sum_j \frac{x_j y_j \mathbf{B}_j F_{ji}(\mathbf{B})}{e_{ji}} G_i(\mathbf{B}) = 1 - \frac{\sum_{j = produces} c_{ij} \mathbf{B}_j}{K_s}
$$

- Producers \wedge (the biomass makes use of logistic growth)

$$
\frac{dB_i}{dt'} = -\int_{m}^{maintename loss} f_a x_i \mathbf{B}_i \sum_j^{gain from resources j} y_{ij} F_{ij}(\mathbf{B}) - \sum_j \frac{x_j y_{ji} \mathbf{B}_j F_{ji}(\mathbf{B})}{e_{ji}} - M(\mathbf{B})
$$

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$$
F_{ij}(\mathbf{B}) = \frac{\omega_{ij} \mathbf{B}_{j}^{q_{ij}}}{\mathbf{B} \mathbf{0}_{ij}^{q_{ij}} + \sum_{k=consumes} d_{kj} p_{ik} \mathbf{B}_{k} \mathbf{B} \mathbf{0}_{kj}^{q_{kj}} + \sum_{l=resources} \omega_{il} \mathbf{B}_{l}^{q_{il}}
$$

- Consumers $\wedge\wedge\wedge$ (the bottom equation is also used to make fish guilds conform with the rest of the nodes, as they nonzero mortality values in the model).

$$
\frac{dD}{dt'} = \sum_{i} \sum_{j} \frac{x_{i}y_{ij}B_{i}F_{ij}(B)}{e_{ij}} \left(1 - e_{ij}\right) + \sum_{i} \frac{exudation by produces i}{r_{i}B_{i}G_{i}(B)s_{i}}
$$

$$
- \sum_{j} \frac{x_{i}y_{ji}B_{j}F_{ji}(B)}{e_{ji}},
$$

- Detritus matter $\wedge^{\wedge\wedge}$

- M0-M4, 5 iterations of increasing specificity and decreasing generalizability. Models progressively incorporate more and more parameters specific to Lake Constence
- The modelled time series were recorded over 240 time steps translating to 8 months from March to October
- Bray-Curtis similarity to measure the accuracy of the model with regards to parameters - Statisitcal variability in the time series was assessed.

Results:

- No extinctions occur
- Elaborations upon the overarching trends observed in the above analyzed figure
	- Since M4 does not account for clear water phase characteristics, the model is inaccurate

Discussion (Conclusion):

-

- Computational modeling of food webs has steadily increased in accuracy and scope
- The congruity between the computational model and the field data is novel, especially given the complexity of the model.
- Various adjustments between M0 and M4 needed to be made to perfect model
- Integrating biogeochemistry and ecological stoichiometry, as well as other parameters. Global scale of this model could be developed.
	- Other parameters/eco. factors to consider: prey-predator dynamics, detritus loop, topology, metabolism, abiotic factors, etc.

Article #20 Notes: Mix and match: how climate selects phytoplankton

NOTES:

Abstract:

- Aim is to understand poorly understand impact of climate on microorganisms, specifically phytoplankton
- Climate-phytoplankton relationship determined using competition theory, fossil record.
- - Thermal influences of climate influence mixing, which determines nutrient fluxes that influence tax comp and cell size
- Understanding the connections between the above stated processes shall allow for better basis of predictions on how phytoplankton will change due to global warming.

Introduction:

- Historically, metabolic activity has been able to adapt to sudden changes, though abundance has varied a lot.
- Using prognostic models on phytoplankton dynamics is difficult with a lack of historical data. Hence, historical models would be useful.
- Eukaryotic phytoplankton have a comparatively voluminous fossil record for these ends. Although accuracy cannot be ensured, a good frame of reference is offered.
- Climate \rightarrow ocean mixing \rightarrow phytoplankton population dynamics
- Being able to characterize this will not be fully complete until the prokaryotic phytoplankton too are incorporated have enough evidence to base this theory off of.
- Focus is on dinos, diats, and coccos.

Methodology:

- The article provides background the basics of ocean layer mixing and ocean structure
	- Pelagic/Benthic ocean varies in terms of nutrient concentration
	- There are two types of nutrient cyclings that result: isopycnal, which is the mixing coming in from the top with the bottom layer, and diapycnal mixing, which is mixing that comes from the ocean floor
- Differential equation for vertical denisty gradient established.
- Article discusses the connection between nutrient kinetics, uptakes, and mixing, providing key relationships in the form of certain equations:

$$
\text{growth} = \mu_{\infty} \left(1 - \frac{Q_{\text{min}}}{Q} \right) \quad \text{-}
$$
\n
$$
\text{update} = V_{\text{max}} \frac{R}{K + R} \qquad R^* = \frac{K\mu_{\infty} Q_{\text{min}} m}{V_{\text{max}} (\mu_{\infty} - m) - \mu_{\infty} Q_{\text{min}} m}
$$

- Focus is placed on the various biochemical and hydrodynamical parameters that inhibit diffusion of nutrients into the cell membrane
- With these premises established, the fossil record of phytoplankton is now investigated
	- Through historical analysis, it is determined that there is a direct impact that the climate exerts on ocean conditions
- In turn, the article hypothesizes that the climate impact the phytoplankton by controlling their habitat location (i.e. selecting it for them) on the basis of the exertions on nutrient availability.

Results:

-

- See Analysis of Figure 5 above; provides significant correlations for the findings of the study.
- Article asserts that it is possible to use the principles of nutrient circulation established as well as the historical data to make predictions about future phytoplankton habitat location and thereby the tax comp.
- Makes some preliminary predictions on this basis, such as that coccolithophorids will come to dominate, as they are well-adapted to low nutrient environments which stratification increasing the presence of.
- Limitations: This model can only be applied to eukaryotic phytoplankton; no fossil evidence of prokaryotes has been provided \rightarrow calls for the use of DNA evidence

Article #21 Notes: Causal networks of phytoplankton diversity and biomass are modulated by environmental context

right, we see that the linkage strength of parameters to EF is around 0.7, with the exception of temperatur, whichhas a weaker strength, standing at about 0.4. This is complement by corresponding distribution of the boxplot and histogram. This means that micronutrients and biodiversity are key to determining biomass. Similar means of analysis reveal that nitrate by has the greatest influence over biodiversity, followed by biomass, and far behind phosphate and temperature. The pairwise loop weight (as this is now multi-directional), between biodiversity and nitrates as well as biodiversity and biomass are much greater than any other interactions. All triangular relationships appear to have similar levels of loop weight, between 0.6-0.7.

This diagram (figure 3) compares linkage strength of pairwise, looking specifically at which direction holds a stronger link. A certain direction between pairs is chosen, and the number on top represents the number of ecosystems (of the 19) where that linkage was stronger than its opposite. Based off analysis on the range and distribution of the violin plots, and the numbers denoting the amount of ecosystems where the specific pair is stronger than its opposite, it is clear that biodiversity is more impactful towards other parameters than the other way around. Meanwhile, phosphate and nitrate seem to have a stronger link with biomass than the other way around. Meaning, the nutrients more strongly influence biomass than biomass does the nutrients.

Figure 4 illustrates redundancy analysis plots (RDA). Using the principles of RDA (similar to PCA), we can arrive at conclusions for environmental context. The blue vectors represent the raw parametric values, and the brown ones represent the directional networks being observed. Antiparallel vectors are negatively correlated, whereas adjacent ones are positively correlated.

For 4a, biodiversity most strongly impacts biomass in low-phosphate environments, and in moderate depths, temperature, and $NO₃$ values. Meanwhile, $PO₄$ has the strongest causal links with biomass in lower depths (meaning shallower), temperatures, diversity and $NO₃$. $NO₃$ is most strongly linked w/ EF in higher amounts of these parameters. Temperature and phosphate have a near synergistic impact on phytoplankton biomass. (insight below)

For 4b, biomass most strongly impacts biomass in shallow, cooler, oligotrophic conditions. The opposite is true for the causal link between temperature and biodiversity. Higher temperatures allow for stronger nitrate→ diversity links (reinforcing conclusion from 4a). Meanwhile, $PO_4 \rightarrow$ diversity is strongest when temperature and biomass are lower.

For 4c, $BD \rightleftharpoons NO_3$ is strongest under warmer temperatures. $BD \rightleftharpoons EF$ is strongest when depth, PO_4 and temperature are lower. For $BD \rightleftharpoons PO_4$ and $EF \rightleftharpoons PO_4$, higher phosphate levels (unsurprisingly) facilitate strength between these causal relationships, combined with low biomass. By contrast, $NO_3 \rightleftharpoons PO_4$ rely on lower phosphate and greater biomass for stronger causal relationships.

Finally, for 4d, greater depth NO₃, biomass and biodiversity facilitate BD \rightarrow EF \rightarrow $N \rightarrow \dots$ strength, whereas the opposite is true for the EF \rightarrow BD \rightarrow P $\rightarrow \dots$ cycle.

NOTES

Abstract:

- It is difficult to assess driving factors of ecological biodiversity and other crucial factors among different ecosystems due to the numerous circumstances surrounding them
- Meaning, unifactor experiments have highly inapplicable results
- 19 ecosystems within the midlatitudes of the Northern Hemisphere were investigated.
- As diversity and oligotrophic conditions increase, biodiversity factors supplant environmental ones as driving factors of biomass (make sense)
- Warmer, more productive ecosystems: Nitrate-mediation; Colder, less productive ecosystems: Phosphate-mediation
- Analyzing ecosystems through the lens of networks and network theory is crucial for future management of ecosystems

Introduction:

- The idea of **feedback** has been important for global-scale analysis of ecosystems. See definition above, but in network theory, this basically involves nodes and the causal interactions that come from it
- Looking at feedbacks has been suggested as a way of understanding the interaction between biodiversity/ecosystem function (BDEF) regulate nature
- However, there are also environmental parameters to consider.
- Herein lies conceptual networks of the causal interactions between these various ecological metrics (figure 1 analysis above)
- There exists a need to quantify these networks
- Once again, experiments fail to provide a full, applicable picture due to unidirectionality omitting the analysis of the impact of all other factors
- Regression approaches assume consistency among factor relationships, failing to be fluid in accounting for different time periods and environmental conditions, which are dynamic (exactly what I found as a limitation in my current project progress)
- Experimentally constructed ecosystems have diversity as the main driver, whereas natural systems are more complex in determining these factors
- Quantification helps make the picture clearer in this regard; it can also predict potential outside stressors on ecosystem dynamics
- The article asserts that it is helpful to analyze the lack of unidirecitonality of the triangular networks in addition to that of the pairwise functions. That way, systems as a whole are analyzed rather than just individual relationships
- This study focuses on the importance of BDEF for marine ecosystems. This is novel as most knowledge of these broad ecological qualifiers is based on results from terrestrial ecosystems
- This is specifically problematic considering the role of phytoplankton as >50% of primary production source; phytoplankton have only received marginal attention.
- Using nonlinear time series models and convergent cross-mapping (CCM, see definition above), an analysis of the networks within and between 19 sites among 16 globally distributed systems was performed.
- - Biodiversity characterized using species richness indices; ecosystem function \rightarrow biomass, given from approximation from chlorophyll a ; $NO₃$, $PO₄$, water temperature were also used.
- Following four questions were analyzed:
	- 1. When does phytoplankton diversity outweigh the environmental parameters as a driver of ecosystem functioning?
	- 2. What is the strongest causal determinant for species diversity?
	- 3. What ramifications for broad ecological qualifiers does a change in phytoplankton diversity pose?
	- 4. Do there exist macroecological factors in assessing the nature of networks between these broad ecological qualifiers
- The following four things were evaluated:
	- 1. Drivers of phytoplankton biomass
	- 2. Drivers of phytoplankton diversity
	- 3. Analysis of links between drivers of biodiversity
	- 4. How the strengths of the networks studied in 1-3 vary given environmental conditions
- Results indicate that in more diverse, oligotrophic systems, diversity plays a bigger role in biomass. In most systems, diversity is driven by nutrient concentrations.
	- Warmer, more productive ecosystems: network between nitrate-diversity-biomass
	- Colder, less productive ecosystems: network btwn phosphate-diveristy-biomass

Methodology:

- 16 Systems, 19 monitoring sites across the northern hemisphere (japan, europe, usa mainly)
- 5 Variables
	- Species richness (# of dif. species)
	- Chl a, common proxy for BDEF
	- Phopshate
	- Nitrate
	- Water Temp
- As well as: water column stability, irradiance, and zooplankton abundance, which also impact phytoplankton populations
- Impact of herbavorous zooplankton species, including cladocerans, copepods and crusteceans was taken
- Data had to be clean to fit the equal time-series intervals of monthly data, but CCM data was still validly carried out
- 5554 datapoints for each variable for each of the 19 sights.
- Long-term linear trend removed to maintain proper trend characterization of function. Seasonality accounted for using mean and standard deviation values.
- Biomass, diversity, and other indicators and networks had their relationships evaluated with CCM
- - See def above + can determine the degree to which time "causes", or rather, predicts, the level of the causal variable, as well as inter-time series causality (not just at variable level)
- Various means taken to minimize the pitfalls of CCM strategy, such as deseasonalization to account for false positive identification
- Interaction among environmental parameters tends to be weak to moderate, if at all ([here](https://www.nature.com/articles/27427))
- The multiscale-anlaysis' validity is limited, due to data dearth and poor structure (too many leading/lagging 0's, inconsistent data implementation into time series for CCM)
- Using lagged embedding, which looks at the retrospective variable and network measurements as the time series forms, confounding variables and their effects may be identified.
- Various time series operations involving the functions of various variable pairs are performed to allow for this investigation of confounding variables
- Though this dampens the strength of quantitative analysis, it allows for causality to easily be inferred. Correlations and relationships are able to dynamically shift on the temporal scale.
- Kendall's τ test and Fisher's $\Delta \rho$ Z test used to validate CCM use
- CCMs measure the strength of causality between two variables, as well as the impact of external factors.
- The correlation calculated were all standardized among one another.
	- Linkage strength (calculated using CCM) \rightarrow Standardized linkage strength
	- Minmax
- Neutel's loop weight taken by using geometric mean of linkage strengths. Bootstrapped intervals from 500 total sampling instances.
- Redundancy Analysis (similar to PCA) was performed for: drivers of biomass and diversity, as well as for the triangular neural nets
	- Not for causation, but rather for driver indentification
	- 10,000 samples pseudo-bootstrapping method

- R

Results and Discussion

- Phytoplankton diversity is a major controlling factor biomass, despite the 19 very different ecosystems (makes sense, intuitively)
- Nitrate concentration had a similar level of significance for this factor as well.
- See figure 2 analysis.
- On the other side of the coin, while biomass drives biodiversity, nitrate is the stronger driver.
- Nitrogen is a significant determinant of both biomass and biodiversity
- Using Shannon Diveristy index as an alternative measurement, same results were found, although biomass was shown to be more important.
- Therefore, as global warming modifies nutrient conditions, it will be important to watch how phytoplankton diversity and biomass change as a result.
- However, phosphate is also another significant nutrient to consider, as its interactions with nitrogen are not fully clear, and require further investigation
- When also looking at irradiance, column stability, and zooplankton, really the only significant parameter identified was the feeding of crustecean zooplankton.
- Figure 3 analysis
- Strengths of the BD \rightleftharpoons NO₃ were highly variable, though having the highest median linkage strength, whereas $BD \rightleftharpoons EF$ was less variable and had greater significance among the 19 ecosystems studied (15 vs. 11).
- We see that (1) environmental context and conditions formulate whether nutrients, ecological factors, or other parameters influence phytoplankton dynamics, and (2) that BD is a common factor here. Thus, bidirectional relationship networks also ought to be considered. (i.e. $EF \leftarrow BD \rightarrow NO_3$).
- Looking at the triangular feedbacks between nutrient to biodiversity to biomass to... when comparing phosphates and nitrates, and inputting them as "nutrients," within the described feedback loop (as seen below), nitrate tended to have stronger links to these ecological characteristics moreso than P, though not to a statistically significant degree.
	- Type I-N: $BD \rightarrow EF \rightarrow N \rightarrow$
	- Type II-N: $EF \rightarrow BD \rightarrow N \rightarrow$
	- Type I-P: $BD \rightarrow EF \rightarrow P \rightarrow$
	- Type II-P: $EF \rightarrow BD \rightarrow P \rightarrow$
- More of the lakes studied were eutrophic, and therefore less nitrogen heavy, thus making nitrogen concentrations a stronger focal point for ecosystem structure (of phytoplankton)
- Between Type I and Type II, there were no significant differences in linkage strength. Meaning, BD could impact biomass directly as well as indirectly through nutrient concentrations, and a similar idea for EF and N. (makes sense – think about a triangle)
- How environmental context impacts which variables have stronger links and greater influence over phytoplankton can be discerned using RDA chart and analyzing vectors. Below notes provide ramifications, and figure 4 analysis above specifies environmental contexts.
- Synergystic impact on biomass and temperature and eutrophic conditions matches findings in past literature. However, based off RDA chart, diversity is negatively correlated with these two variables, as is the case when $BD \rightarrow$ biomass is greater. Meaning, warming and eutrophic conditions, which are becoming increasing problems for biodiversity, however, biodiversity is the key to combating these problems (potential pursuit for policy)
- Shallower systems are comparatively homogenous, which allow for species interactions to be more influential (given lower temp and PO_4 and shallow \rightarrow stronger EF>BD). Additionally, when temperatures were warmer, $NO₃ > BD$ was stronger, indicating that drivers of biodiversity were determinants resulting from a temperature gradient.
- Based off the inter-parameter relationships depicting in 4c, we can say that the colder water temperatures allow for stronger $PO₄$ mediated feedbacks, whereas warmer temperatures allow for stronger $NO_3 \leftarrow \rightarrow BD$ impacts, which matches overall literature findings that N is more influential when temperature is warmer. Thus, as oceans warm, NO₃ is projected to become very important in determining biodiversity.
- From 4d, the stronger the biodiversity, the stronger the causal cycle is between biomass, biodiversity, and environmental conditions, meaning there is higher response, change, and therefore, stability, when diversity is higher. This contradicts the consensus that biodiversity encourages insensitivity and stability in face of environmental change, thus illustrating the need to clarify the impacts of biodiversity on ecological dynamics
- Causal links of the same parameters but order differently can respond different given inputs of environmental parameters, creating another layer of complexity to consider
- Highlights the needs for holistic computational approach
- Robust to different values sensitivity analysis
- Possible extension: looking at the impacts on taxonomic composition.
- Limitations the feedback networks could have their sign values accessed, meaning whether there is $a \pm i s$ unknown.
- Data availability and number of systems studied could be enlarged, i.e. iteration needed
- Overall, study effectively bridges various elements of ecological analysis and characterization and conditions of ecosystems. Causal networks ought to be analyzed, as they offer an effective approach. Improved understanding and considerable ramifications were achieved.
- HUGE ramifications for project methodology— using RDA to identify *when* parameters are significant, and not just the driving factors, allows for a sort of $PCA²$, wherein the driving parameters *of* the driving parameters can be understood— very powerful tool to potentially integrate into computational model.

Patent #1 Notes:

APA Citation:

Hiroharu, M. K., Masahiro , Y., & Okamura, O. I. (2022). *Calculation method and calculation device for the abundance of phytoplankton of a specific species, and sign detection method and sign detection device for red tide occurrence by phytoplankton of a specific species*. https://patents.google.com/patent/JP7007225B2/en?q=(phytoplankton)&oq=phytoplankto

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Title:

Calculation method and calculation device for the abundance of phytoplankton of a specific species, and sign detection method and sign detection device for red tide occurrence by phytoplankton of a specific species.

URL: [https://patents.google.com/patent/JP7007225B2/en?q=\(phytoplankton\)&oq=phytoplankton](https://patents.google.com/patent/JP7007225B2/en?q=(phytoplankton)&oq=phytoplankton) Summary/Notes:

The device is aimed at using varying phytoplankton fluorescence properties to identify specific species, and thereby abudance, composition and other properties. It is also designed to check if there is a red tide. A red tide is indicative of certain species of phytoplankton that have been found to be detrimental to economic and environmental well being (harming both fishing industry output and the stability of marine food webs). Hence, red tide identification has been a major priority.

Major question: What advantages and disadvantages does this device pose, relative to the use of genomic methods?

- Light calculations: As described, light properties are exploited to identify phytoplankton. More boradly, many of the optical properties of the water are used including absorption and scattering.
- Measurements are then analyzed by the tool. Beforehand, a desired phytoplankton species is chosen, and the light calculations calculate the presence of that species taking into account the species that may be present in the sample
- These properties can also be used to help identify red tides
	- This process involves temporal analysis of light properties in the water.
- Part of the apparatus contains a calculation device that takes into account the red tide measurements and the light properties, providing the gross calculations for the phytoplankton species identification and abundance measurements
- Compared to traditional methods (i.e. typical testing tool kits), this tool is advantageous:
	- Live coverage of water quality
	- Early warning system for red tides
	- Test results are overall faster, more reliable, and accurate.
- Very useful for management purposes, fisheries, health monitoring of the ecosystem, and the like

Patent #2 Notes:

APA Citation:

Terada, M. (2020). *Phytoplankton growing apparatus and phytoplankton growing method*.

https://patents.google.com/patent/WO2020070733A1/en?q=(phytoplankton)&oq=phytop lankton

Title:

Phytoplankton growing apparatus and phytoplankton growing method URL:

[https://patents.google.com/patent/WO2020070733A1/en?q=\(phytoplankton\)&oq=phytoplankton](https://patents.google.com/patent/WO2020070733A1/en?q=(phytoplankton)&oq=phytoplankton) Summary/Notes:

The patent proposes a circular device acting as a medium for phytoplankton growth. It involves a circulation mechanism so as to stimulate and equilibriate conditions within the contraption. The phytoplankton are pushed upwards via a pumping mechanism where they are subsequently exposed to light. If and when more abundance of phytoplankton is needed, methods such as these are crucial.

Deeper analysis of the structure of the device:

- The circulation apparatus is in fact helpful in allowing the phytoplankton to remain in an environment where they have sufficient light and nutrient exposure, thereby maximizing growth
- This is especially powerful when considering the fact that there is a vertical pump mechanism that sends the phytoplankton upward. At this destination lies the upper cover of the circular contraption, allowing for light exposure.
- Stacked structures, known as flangs are located within the structure, allowing for downward circulation. This completes the cycling of nutrients, allowing for optimal conditions.

Consequently, this device is more efficient than most of its peer horizontal tanks.

- Space efficient, with an internal equilibrium maintained
- The light-circulation mechanism is both novel and increase efficiency of the growth
- Although the model is made to be space efficient, what is more is that it is also able to be scaled up or down, allowing for an additional dimension of flexibility and optimization

There are many areas in which this patent can be applied. Namely, it would be useful for researchers, as they would have any easy way to grow phytoplankton for experimentation. There would be other uses with regards to R&D. The increased harvests could also serve as biofuel, feeding, and other useful ecological and economic purposes.

Patent #3 Notes:

APA Citation:

Zhao, Y. G., Lishi, N. H., Xiaoya, C. Y., Jingbo, F. L. D., Gan, X. X., Xinxin, T. D., Liu, Z. Y., & Wenqing, J. L. (2016). *Based on phytoplankton identification assay method and the device of discrete three-dimensional fluorescence spectrum*.

https://patents.google.com/patent/CN103868901B/en?q=(phytoplankton)&oq=phytoplan kton+

Title:

Based on phytoplankton identification assay method and the device of discrete three-dimensional fluorescence spectrum

URL:

[https://patents.google.com/patent/CN103868901B/en?q=\(phytoplankton\)&oq=phytoplankton+](https://patents.google.com/patent/CN103868901B/en?q=(phytoplankton)&oq=phytoplankton+) Summary/Notes:

This patent, similar to the first one, is aimed at identifying phytoplankton by taking advantage of different species' fluorescence properties. What is novel about this approach its use of a discrete three-dimensional fluorescence spectrum. This provides a convenient gradient by which known phytoplankton irradiance patterns can be compared to. This provides a clean sort of assay process in determining the phytoplankton species. The device, compared to Patent #1, is smaller and easier to operate. Hence, having methods to determine these characteristics quickly and well is very important. That way, not only can the crucial characteristics be measured, but this can be done efficiently.

More details on methodology:

- A device is used to take pictures of and observe the 3D fluorescence patterns of individual cells
- The specification and accuracy in identifications is more accurate than pigment and morphological methods, which have been used hitherto. Relies on less convoluted methods too, with the omission of pigmentation, chromatography and other complex apparatuses.
	- What is more is that it can operate very rapidly.
- Spectrometric methods and laser technology are utilized to gain data from the cytological fluorescence
- From the data attained, identification is performed via database comparison

Additional advantages:

- Its rapid testing is preferable to pigment and morphological methods, which are known to be convoluted and time-consuming
- By being able to identify species, even those that are similar, this model breaches a limitation that previous methods failed to
- The cells are analyzed without being harmed \rightarrow allows for empirical evidence w/o environmental harm (a win-win situation)
- Versatility applicable to many species and ecosystems

Applications are wide ranging as stated above, but notable areas of application include management of aquatic ecosystems, broad study of phytoplankton dynamics (*very topical for this project*), tracking, predicting, and addressing algal blooms, environmental monitoring, and biofuel and other economic ventures.

Overall, these patents offer practical solutions to the computational problem being assessed for the project.