"Trait-based Approaches to Ocean Life"
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Waterville Valley, NH, U.S.A

Presentation Abstracts

Acevedo-Trejos, Esteban (POSTER 1, SESSION 4)
Gunnar Brandt, S. Lan Smith, Agostino Merico

A comparative modelling analysis of phytoplankton size diversity

Models of marine phytoplankton assemblages that consider the whole community as a single adaptive entity represent an interesting alternative to those that discretely resolves species or functional groups. However, the treatment of functional diversity still poses some limitations to these models. Recently, a new mathematical method was developed to tackle the problem of maintaining functional diversity in plankton communities. This method, called trait diffusion, has been tested so far only in the idealised setting of a chemostat. Here we present experiments in which we compare different ways of describing functional size diversity in marine phytoplankton communities of the tropical and temperate Atlantic Ocean. Specifically, we contrasted the results obtained with 1) fixed size variance, 2) immigration, and 3) trait-diffusion against a “control” model treatment that does not sustain diversity. The results of the different methods are compared and discussed against observations of size variance.

Albert, Aurélie (POSTER 2, SESSION 7)
Coralie Perruche, Marion Gehlen, Yann Drillet

Global physical/biogeochemical coupling for the 20th century

The ERA-CLIM2 project aims at producing an extended climate reanalysis of the 20th century, with consistent descriptions of the global atmosphere, ocean, land-surface, cryosphere, and the carbon cycle. We, at Mercator Océan and in collaboration with the Laboratoire des Sciences du Climat et de l'Environnement, have therefore developed a low resolution (1°) configuration of the ecosystem PISCES model that is coupled either in an online or offline mode to the physical model OPA. A description and validation of primary production and air-sea flux of carbon at seasonal and interannual scales will be presented. We also study the impact of the two different coupling methods on the ecosystem representation in order to have a better understanding of the interactions between oceanic dynamics and biogeochemistry. Ultimately, the extended climate reanalysis will allow to evaluate impacts of global warming and ocean acidification on ocean biogeochemistry and discriminate between anthropogenic trend and natural variability.

Alexander, Harriet (TALK, SESSION 1)
Mónica Rouco, Sheean T. Haley, Samuel T. Wilson, David M. Karl, and Sonya T. Dyhrman

Functional group specific traits drive ecosystem state shift in the oligotrophic ocean

Aperiodic blooms of eukaryotic phytoplankton called diatoms can shift the ecosystem state of the low nutrient oligotrophic oceans from heterotrophy to autotrophy, sequestering carbon and driving carbon export to the deep sea. Little is known about the traits that govern the timing and magnitude of these bloom events, or why diatoms bloom as opposed to other functional groups of phytoplankton. We developed a metatranscriptomic approach to statistically parse, and experimentally assess, functional group specific metabolic shifts during simulated blooms in the North Pacific Subtropical Gyre. The results indicate blooms form when the phytoplankton population is released from limitation by resources such as nutrients, vitamins, and trace metals, and that the success of diatoms is driven by efficient reallocation of their transcript pool, a trait not present in the other functional groups. Predicted changes in resource inputs to the oligotrophic gyres may result in fewer blooms with concomitant impacts on carbon cycling.

Allen, James (POSTER 3, SESSION 1,4)

David Siegel

Retrieval of Phytoplankton Size Distribution from Satellite Imagery

Knowledge about the size, composition, and distribution of particles in the global ocean has led to breakthroughs in understanding surface ecosystem dynamics as well as the ocean's role in the Earth's carbon cycle. Remote sensing has recently become a powerful tool for characterizing the global particle size distribution and phytoplankton size composition on relevant spatio-temporal scales through the use of two distinct optical modeling approaches. Spectral backscattering models perform well in oligotrophic marine regions due to the lack of terrestrially derived particles, while spectral absorption models work well in productive regions due to their ability to key into the flattening of spectral absorption features in larger particles due to the package effect. However, these models often fail because they do not address the bio-optical complexity of the ocean. This project improves on current studies with a novel algorithm that merges PSD information from both particle backscattering and absorption spectra. These new models, as well as existing techniques, are applied to remotely sensed imagery from NASA's NOMAD dataset and are validated with available PSD field data. This allows for a detailed analysis of model sensitivities to changes in input variables while providing the ability to reconcile phytoplankton vs. particle size distributions.

Andersen, Ken (POSTER 4, SESSION 4)

T. Berge, R. J. Gonçalves, M. Hartvig, J. Heuschele, S. Hylander, N.S. Jacobsen, C. Lindemann, E.A. Martens, A.B. Neuheimer, K. Olsson, A. Palacz, F. Prowe, J. Sainmont, S.J.

Characteristic sizes of life in the oceans, from bacteria to whales

The size of an individual organism is a key trait to characterize its physiology and feeding ecology. Size-based scaling laws may have a limited size range of validity or undergo a transition from one scaling exponent to another at some characteristic size. We collate and review data on size-based scaling laws for resource acquisition, mobility, sensory range and progeny size for all pelagic marine life, from bacteria to whales. Further, we review and develop simple theoretical arguments for observed scaling laws and the characteristic sizes of a change or breakdown of power laws. We divide life in the ocean into seven major realms based on their trophic strategy, physiology and life history strategy. Such a categorization represents a move away from a taxonomically oriented description towards a trait-based description of life in the oceans. Finally, we discuss life forms that transgress the simple size-based rules and identify unanswered questions.

Barry, Cael (POSTER 5, SESSION 3)

Ocean color inversion & information content for phytoplankton functional type classification

What is a reasonable number of phytoplankton functional types (PFTs) we can split plankton amongst, if we detect them using a hyperspectral signal with a given uncertainty?" Sets of PFTs are often defined by their ecological/biogeochemical role, while inversion of remote sensing reflectance (Rrs) or other optical properties such as absorption spectra offers a powerful, direct approach to detecting PFT distributions. However, because the contributions of different PFTs overlap in the inverted measurement, and the measurements have some uncertainty, defining too many PFTs can result in an unstable inversion. Here we explore the above question using information content analysis, which quantifies whether inverting a signal on a set of kernels, or 'signatures' for each PFT, provides independent information about the PFT concentrations given the covariance of their signatures and the uncertainty of the measurement. This procedure is applicable for distributions of PFTs as well as ecotypes of a single species, and for Rrs as well as inherent optical properties. If optical methods are employed, quantitatively approaching the relationship between how PFTs are defined and detected is essential to a robust understanding of how PFTs are distributed. Additionally, we ask: "can we improve this detection threshold using additional data (e.g. temperature, mixed layer depth, scalar irradiance) by constraining the variability in PFT signatures?

Barton, Andrew D. (POSTER 6, SESSION 7)

Fernando González Taboada, Charles A. Stock

Tipping points in plankton community models

Changes in marine ecosystems can be dramatic, non-linear, and potentially irreversible. However, the climatic drivers and ecological underpinnings of these "tipping points" are poorly understood. Here, we identify and map tipping point-like events in a plankton community model of intermediate complexity that is embedded in a global-scale Earth system model forced with historical greenhouse gas emissions from 1901-2000. The frequency of model tipping points increases with plankton body size and trophic level, and these events occur more often in subtropical gyres than elsewhere. We discuss here how these patterns are related to plankton body size, generation lengths, and the timescales of characteristic physical forcing in contrasting regions of the ocean.

Bisson, Kelsey (POSTER 7, SESSION 3,4,7)

David Siegel

Linking shifts in remotely sensed planktonic community structure to changes in carbon export flux from the surface ocean to the mesopelagic

Understanding the drivers behind planktonic composition shifts is important for biogeochemical cycling, global climate predictions, and particle transformation processes in the ocean's interior, but these fundamental processes remain elusive. Here, we aim to mechanistically link shifts in remotely sensed parameters to the packaging and export of carbon into the mesopelagic using integrated methods of satellite data and ecological modeling. A simple food web model is presented to improve the characterization of surface ocean ecosystems on global scales throughout time. The food web model uses chlorophyll and the particle size distribution in conjunction with satellite-based proxies for diatom and coccolithophore abundances to determine planktonic functional groups. From this, the export flux composition is predicted at the base of the euphotic zone, and is validated using available sediment trap data. The fraction of CaCO3 and Si within a settling particle that exits the euphotic zone is quantified, enabling subsequent modeling on transformation processes to determine the biological pump's efficiency. Depending on the trophic transfer efficiencies and grazing levels set in the surface ocean, the export flux varies considerably (3-11 Pg C yr-1), offering insights into the ocean's current and future role in carbon cycling.

Bowman, Jeff (POSTER 8, SESSION 2,9)

Hugh Ducklow

Inferring microbial ecosystem function from community structure

The composition of marine microbial communities is easily and frequently explored through the analysis of taxonomic marker genes, such as the 16S rRNA gene. While these studies are useful for describing how microbial communities are structured within the environment, they provide little information on microbial ecosystem function and functional diversity – essential determinants of the overarching phenotypic trait. This information can be more directly developed from 'omics technologies, such as metagenomics and metatranscriptomics, however, these methods are expensive and low throughput, making them suboptimal for long term monitoring projects or very high resolution surveys. We've developed a novel framework to infer the metabolic structure of a microbial community – analogous to its ecosystem functions – from its taxonomic structure. In an initial analysis we applied our framework to 16S rRNA gene libraries collected along the coastal West Antarctic Peninsula. We propose that using a metabolic inference technique in combination with metagenomics is an effective and economical way to explore and monitor microbial community function at a high spatial and temporal resolution. Our framework has the additional advantage that it organizes inferred function in a manner that is amenable to both gene expression analysis and metabolic modeling, which we are pursuing in ongoing work.

Bruggeman, Jorn (TALK, SESSION 6)

Nick Stephens, Ana Queiros, possibly others

Traits of benthic fauna: from observations to community models

Marine benthic fauna include numerous taxa living on and within sediments, such as polychaetes, echinoderms, crustaceans, bivalves and gastropods. They exert control on the whole marine ecosystem by regulating pelagic-benthic fluxes of matter, and several are important commercially. However, members of the benthic fauna differ in many traits, including size, feeding mode, reproductive strategy and vertical distribution. Due to such diversity, the abundance and functioning of benthic fauna is notoriously difficult to capture in models. Here we describe the first steps towards a framework that links recent initiatives to compile benthic trait datasets with modelling approaches that explicitly describe species diversity. Stepwise, it addresses the collection and exploitation of discrete and continuous trait data, the identification of principal traits and trade-offs in the presence of taxonomic structure, and their implementation in population-level models based on stochastic method for community assembly and simulation. Looking forward, we discuss the potential application of adaptive dynamics type methods for efficient community descriptions, and the extensions that consider intraspecific size diversity.

Brun, Philipp (POSTER 9, SESSION 2,3)

Thomas Kiørboe and Mark R. Payne

Understanding observed copepod distributions with a trait data base

Copepods differ in body size, diapause strategy, spawning strategy, feeding behaviour and many other traits. A large body of literature on the traits of these comparably well-studied organisms exists but is scattered in a diverse literature. We compiled quantitative trait information into in a well-structured and user-friendly database. We collected thousands of records from hundreds of species and about 20 different traits. We combined this collection with species distribution data to investigate how traits affect the biogeography of copepods in the North Atlantic. Using almost 50'000 observations for more than 60 taxa from the Continuous Plankton Recorder, we gain insight into how copepod traits are distributed in space, what traits are the main drivers of biogeography, and which make the species vulnerable to climate change. We finally examine to what extent copepod distributions can be described with a trait-based model.

Bumbeer-Couto, Janaina (POSTER 10, SESSION 8)

Laura Pioli Kremer; Rosana Moreira da Rocha

Invasion Risk assessment of marine invertebrates: A unified approach linking species traits and social-environmental settings

Biological invasions are increasingly important in marine environments worldwide. Risk assessment (RA) can be used to prioritize which species and methods of prevention and control should be used to mitigate ecological and economical impacts of bioinvasion. Biological characteristics of species are good predictors of successful introduction. Also, geographic and social environments can influence the invasive potential of introduced species. In this context, we propose a RA based on species traits with environmental and socioeconomic characteristics of the location that may be invaded. Species traits and environmental conditions that most strongly predict invasion were defined by a review of the literature and summarized in 44 questions which are applied for each species. Responses are yes, no and unknown, and each question is weighted based on its relative importance. The resultant scores are summed, providing a final score that is positively associated with the likelihood of invasion. Twenty-four questions are about species traits (i.e., reproduction, ecological interactions, physiological tolerance), while the remainder are about local conditions. While these biological traits are associated with the likelihood of invasion worldwide, the model worked best when used at a local scale, because of the differences due to the social environment and context of each place.

Burd, Adrian (POSTER 11, SESSION 7)

Uta Passow and Deborah Steinberg

Trait-based models, community structure, and biogeochemical function

The trait-based and agent-based modeling approaches allow for models that can be used to investigate the interactions between community structure and biogeochemical function. Such models can be used to develop insight into how different communities affect biogeochemistry as well as to develop mechanistic- and behavioral-based parameterizations that can be incorporated into Earth System Models. Here we describe two possible applications of this modeling approach. The first uses organism traits and an agent-based approach to examine the effects of zooplankton community structure and behavior on attenuation of particle flux in the mesopelagic ocean. The second incorporates genomic and trait-based information to examine the interactions between community structure and nutrient recycling in the surface ocean.

Burns, Wilton (POSTER 12, SESSION 5, 7)

Marchetti, A., Ziervogel, K.

Primary production in future oceans: An analysis of how increased water mixing caused by global climate change will affect nutrient uptake by marine phytoplankton

Recent models have shown that with increasing atmospheric temperatures, some areas of the world's oceans will experience more mixing via higher wave heights and surface wind. This increase in water mixing could cause increased turbulence, meaning secondary motion caused by moving fluids, in marine photic zones –affecting environmental conditions for the majority of phytoplankton (Barton et al 2014, Karp-Boss et al 1996). There is some experimental evidence for the effects of turbulence on nutrient uptake by a monoculture of phytoplankton (Pasciak and Gavis 1975) but here is little experimental evidence for the effects of turbulence on nutrient uptake for a range of phytoplankton cell sizes and with mixed cultures. This project will investigate the physiological response of marine laboratory phytoplankton cultures with a size range of 2-40µm and natural assemblages obtained from the Gulf of Maine and the North Atlantic to increased turbulence levels under nutrient replete and deplete conditions. Nitrate uptake kinetics will be monitored because nitrate often limits marine phytoplankton growth in oceans. This project will examine the real-life implications of our changing planet, gaining a realistic understanding of how abiotic factors interact with phytoplankton and change carbon sequestration and oxygen production rates over large time scales.

Chakraborty, Subhendu (TALK, SESSION 4)

Ken H. Anderson

Correlation between organism size and trophic strategies

In aquatic systems, an organism's trophic strategy is to a large degree determined by the resource acquisition mechanisms which are greatly influenced by the size of the individual organisms. Size-based descriptions of feeding strategies are generally formulated as scaling laws. However, these scaling laws often have a limited size range of validity and change scaling exponent around some particular size or break down altogether beyond a range of validity. Here we move beyond the idea of characterizing the resource acquisition of all life in the ocean by a single scaling law and develop a model that automatically adjusts organisms resource acquisition strategy with its size. Specifically, the trophic strategy at a particular size is not prescribed a priori but is an emergent property. We have taken care of the investments of cells into different resource acquisition strategies and their trade-offs. We parametrize our model with data and search for optimal strategies at different size ranges.

Clayton, Sophie (POSTER 13, SESSION 2,5)

Dan Halperin, Francois Ribalet, Jarred Swalwell, Bill Howe, E. Virginia Armbrust

Phytoplankton Biogeography of the North Pacific from Continuous Flow Cytometry

We examine an extensive set of continuously collected flow cytometry data collected over 5 years in the North Pacific, to determine biogeographical patterns in the picoplankton size range (<10um). The dataset consists of <50,000 individual data points, representing measurements of the Cytometric properties of almost 2 Billion individual cells. Our analysis is based on the distribution of ataxonomic traits measured by the flow cytometer: forward scatter (proportional to cell size), chlorophyll and phycoerythrin fluorescence. Using a range of statistical analyses, we find that distinct community assemblages can be distinguished along the ship tracks. Their characteristic length scales coincide largely with those of mesoscale eddies, but this varies across the basin in concert with changes in the dominant physical dynamics.

Coles, Victoria (TALK, SESSION 9)

Raleigh Hood, Mike Stukel, Mary Ann Moran, John Paul, Brandon Satinsky, Patricia Yager

Emergent patterns of genes, transcripts and community structure in the GENOME model

To incorporate emerging genomic understanding of marine microbes, we developed an ecosystem model whose community is determined by randomly assigning functional genes to build each organism's gene repertoire. Microbes are assigned a size that sets their baseline environmental responses using allometry. These responses are modified by the costs and benefits conferred by each gene in an organism's genome. The microbes are embedded in a general circulation model where environmental conditions shape the emergent population. New organisms replace unsuccessful ones to generate communities that closely match observed particle size distributions. The distribution of genes, transcripts, organisms and biogeochemical transformations are determined by physical mixing and advection and by the biochemical transformations and sinking rates of the community. Vertical distributions of nitrogen species and transcripts for genes involved in nitrification match observations well, indicating that the resulting patterns are realistically constrained by physical processes. Modeled gene transcript abundance for nitrogen cycling processes matches patterns observed recently along the extreme gradients in the Amazon River plume, and helps to explain the factors controlling observed variability. This and other efforts to increase community and genetic plasticity of ocean ecosystem models are needed for evaluating the ecosystem impacts of changing climate in the Anthropocene.

Cornelissen, J. Hans C. (INVITED SPEAKER)

Plant traits and biochemical cycling on land: parallels with marine ecosystems?

Using variation in functional traits among and within species in order to find generalities of community assembly and ecosystem functions, has been a hot topic in terrestrial ecology for a few decades already. Here I will explore whether some of the trait approaches on land may be of interest to marine ecology, and discuss how fundamental differences and similarities between marine and terrestrial ecosystems may bear on the usefulness of these approaches and on adjustments needed. My main focus will be on the ‘Response-Effect Framework’, in which we investigate whether and how patterns of interspecific variation in ‘response traits’ (traits that help organisms to make a living in their natural environment) correspond to variation in ‘effect traits’ (traits indicative of the per capita or per mass effect of organisms on their environment) of the same species set. This concept is used to predict effects of environmental drivers on ecosystem functions such as biogeochemical cycling but may also inform about trophic cascades. I will also discuss the possible application of phylogenetic relations within this concept.

Davies, Kim (POSTER 14, SESSION 6,7)

Marc Sourisseau, Pieter Vandromme, Martin Huret, Franck Dumas

Simulating planktonic ecosystem dynamics in the Bay of Biscay, France, using a trait-based, auto-emergent zooplankton model coupled to a 3-D biogeochemical model (MARS3D)

Zooplankton is a diverse group of organisms comprising many taxonomic groups, several orders of body size, and a variety of behaviours. Ecosystem models typically represent the role of zooplankton with only one or two variables, micro- and meso-zooplankton (traditional Z2 model). Such models can only address questions in zooplankton community ecology through progressive approaches for characterizing zooplankton diversity. Recently, diversity has been represented in the phytoplankton and zooplankton compartments of ecosystem models by generating species with randomly drawn traits and allowing properties of the system to emerge. With this approach, selecting traits that represent ecologically significant indicators of diversity is a key issue. Other shared traits, such as diet, can explain variation in diversity and can interact with body size. We approach modelling zooplankton communities through a random draw of their size and diet traits, where processes such as ingestion, mortality and prey selectivity are allometric functions of size. This trait-based model is coupled with the 3-D physical-biogeochemical model MARS3D configured for the continental shelf in the Bay of Biscay to simulate the interactions among trait-selected zooplankton, their food, and environmental conditions that affect their growth and transport. We focus on emergence of zooplankton size-structure (slope of biomass spectrum) over the Bay during the spring bloom.

Dutkiewicz, Stephanie (TALK, SESSION 6)

Oliver Jahn, Ben Ward, Anna Hickman, Mick Follows, Chris Follett, Darcy Taniguchi

Combining phytoplankton size and functional traits in a global ocean ecosystem model

Phytoplankton diversity can be characterized along several trait axes: for instance biogeochemical function and cell size. Most marine ecosystem models, including those used in the latest round of the IPCC projections, include only a few phytoplankton functional types (e.g. diatoms, picophytoplankton). However, in reality, such functional groups are composed of diverse organisms, spanning orders of magnitude in cell size. Though a few global scale models have started to include size spectrum of plankton, these have not included functional differences. Here we present results from a global ecosystem model that explicitly includes a diversity of cell sizes within biogeochemical functional groups. We construct this model by providing phytoplankton cells with an array of traits – some of which are set by their size (e.g.

nutrient half saturation, sinking), some are set by biochemical function (e.g. silica use, nitrogen fixation, pigment composition) and some are set by both size and functional group (e.g. maximum growth rate). We find that bottom-up traits are important in setting the distribution of functional groups, and that top-down processes are essential for maintaining a size spectrum within functional groups. The new model shows significantly more local diversity than found in models that only include function or only include size. As such including several axes of trait space has important ramifications for the stability of the ecosystem, particularly to climate change.

Dyhrman, Sonya (INVITED SPEAKER)

Linking 'omic approaches to a trait-based view of ocean life: using transcripts to define microbial traits

Advances in sequencing and mass spectrometry have dramatically increased the development and application of genomics, transcriptomics, proteomics –so-called 'omics approaches – to studies of microbes in the sea. How can we link these 'omic approaches to a trait-based view of ocean microbes? Here we will highlight several cases studies illustrating how we are using 'omic information to define and track microbial functional traits, with examples from studies with phytoplankton in different ocean ecosystems. Information about the expression patterns of single genes can be used to track functional traits like nitrogen fixation, and validate model predictions about limitation scenarios in key groups. Moving beyond target genes, global patterns in gene expression can also be linked to microbial traits. For example, we are using metatranscriptome signals to identify microbial responses to shifting resource ratios, and nutrient pulses. In this context, examining how metatranscriptomes vary over time, or in response to a change in the environment, can be used to characterize the functional traits that govern how individual species or groups of phytoplankton interact with each other and their chemical environment.

Edwards, Kyle (POSTER 15, SESSION 3)

Mridul Thomas, Elena Litchman, Chris Klausmeier

How temperature changes light-use traits of phytoplankton, and how this scales up to ecosystem temperature sensitivity

The effect of temperature on phytoplankton communities and ecosystem processes is debated. Because phytoplankton are typically limited by either light or nutrients, temperature should change community structure by altering the traits that determine competition for these resources. Furthermore, the aggregate response of phytoplankton to temperature will depend on how community structure scales up to bulk rates. Here we synthesize experiments on 57 phytoplankton species to analyze how the growth-irradiance relationship changes with temperature. We find that light-limited growth, light-saturated growth, and the optimal irradiance for growth are all highly sensitive to temperature. These traits are co-adapted to similar temperature optima, but light-limitation reduces a species' temperature optimum by ~5 degrees Celcius, which may be an adaptation to how light and temperature covary with depth. Importantly, species with higher temperature optima have faster growth under light saturation (ala the Eppley curve), but these species do not have faster growth under light limitation. This implies that light limation erases the temperature sensitivity of bulk phytoplankton growth, even though community structure will be temperature-sensitive. Using a database of primary production incubations, we show that this prediction is consistent with estimates of bulk phytoplankton growth across gradients of temperature and irradiance in the ocean.

Fiksen, Øyvind (POSTER 16, SESSION 2,8)

Anders F. Opdal and Christian Jørgensen

Trait-changes in fish populations as evolutionary response to fisheries

During the last centuries the intensity of fish harvesting has increased substantially. Fisheries are now the most important source of mortality for many fish species around the world, and acts as an evolutionary selective driving force on important life-history and behavioural traits. We have modelled the adaptive response to harvesting in energy allocation, size- and age at maturation and spawning ground usage for cod, and explored how these traits are formed by patterns and methods of fishing. Predictions from these models are in line with long term observational data on the traits showing more northerly spawning ground distribution and smaller size at maturation. Other more behavioural traits may also be influenced by harvesting and the related benefits of higher growth rate, such as risk-taking, schooling behaviour and consequently predation rate. Here, we summarize some key trait changes predicted from evolutionary models along with available data on changes that has occurred in North-East Arctic cod.

Fragoso, Glaucia (POSTER 17, SESSION 2)

Glaucia Fragoso, Alex Poulton, Duncan Purdie

Using phytoplankton functional traits to describe species distribution in the sub-Arctic North Atlantic

The sub-Arctic North Atlantic is an ideal region to study how environmental factors shape the phytoplankton community structure due to the Atlantic and Arctic waters that divides the region into distinct hydrographic zones. Hydrographic zones create distinct ecological niches, where phytoplankton species are largely structured by functional traits. In this study, we identified several target phytoplankton species from the sub-Arctic North Atlantic and modelled their spatial niche distribution. Presence and absence data of key phytoplankton species were obtained from a database of North Atlantic observations. Cluster analyses of the predictions were applied to identify the biogeography of major species, which was reflected by the distinct hydrographic zones of the sub-Arctic North Atlantic. Functional traits (e.g. cell size, cold versus warm water, low versus high light species, etc.) of major phytoplankton species were analysed and compared to the species database. These results revealed that phytoplankton functional traits drive species biogeography in the North Atlantic. Future analysis including additional information based on phytoplankton physiology should be included to predict potential changes in species/traits distribution as a consequence of climate change.

Hagstrom, George (POSTER 18, SESSION 6,7)

Allison Moreno, Steve Allison, Simon Levin, Adam Martiny

Non-Redfield Stoichiometry and the Carbon Cycle

Evidence increasingly suggests that marine phytoplankton deviate substantially from the canonical Redfield ratio. These deviations strongly correlate with environmental and ecological variables such as nutrient levels, temperature, and community composition. We a model based on allocations to sub-cellular compartments in order to predict phytoplankton stoichiometry as a function of environmental conditions. As an application of this modeling approach, we study how phytoplankton stoichiometry interacts with environmental changes by coupling our biological model to a simple model of the carbon and phosphorus cycles. Since most models of the Earth's carbon cycle rely on an assumed Redfield ratio for organic matter, we investigate the effect of non-Redfield stoichiometry on the distribution of carbon within the oceans and atmospheres. Focusing on two important scenarios, anthropogenic CO2 release and glacial/interglacial transitions, we find environmental perturbations can have a large impact on stoichiometry and consequently the export of carbon. One potential consequence, predicted by our model, is an increased role for regions other than the Southern Ocean in effecting atmospheric CO2.

Hammock, Jen (POSTER 19, SESSION 1)

Katja Schulz, Jorrit Poelen, Anne Thessen

Making Trait Data Flow

TraitBank is the structured data service of the Encyclopedia of Life. Launched in 2014, it currently hosts 9 million data records for 1.7 million taxa, including trait records (eg: cell size, life history traits) and other attributes (eg: IUCN status, type specimen repository). Marine data is provided by WoRMS, AlgaeBase, OBIS, PolyTraits, and literature derived datasets, including cell masses of phytoplankton, life history and behavior of zooplankton, and tissue mineralization types. Hosted records include all available metadata, including detailed attribution; organism information including sex and life stage; date, locality and method information for field studies; etc. TraitBank is not a repository. Most hosted records are deposited with a scholarly publication, or an institutional or aggregator database. Presence in TraitBank makes individual records findable by EOL search (http://eol.org/data_search) or web search engine. Records are available by CSV download and via a JSON-LD web service, including all metadata. We are trying to prioritize traits that may be useful for big global questions (complementing organized efforts like EMODnet). We are also experimenting with deriving “estimated” traits in novel ways from occurrences and other aggregate data as well as the sea of literature. We are eager for feedback.

Harvey, Elizabeth (TALK, SESSION 9)

Susanne Menden-Deuer, Tatiana Rynearson

Linking individual movement to population-level dynamics: strain-specific behaviors of Heterosigma akashiwo

Functional traits have been increasingly employed in phytoplankton ecology to characterize and predict phytoplankton species abundance, distribution, and production in response to biotic and abiotic conditions. Frequently, these functional traits are used to distinguish between species; less recognized and understood is the role that intra-specific variability plays in determining functional diversity. Motility is a key functional trait that phytoplankton utilize to navigate the complex and heterogeneous marine environment. To examine intra-specific variability in motility within a single species, the swimming behavior and genetic identity of seven strains of the raphidophyte, Heterosigma akashiwo were measured using three-dimensional movement behavior and microsatellite analysis. Microsatellite analysis revealed all strains examined were genetically distinct individuals. Observed behaviors were significantly different among all strains examined, with swimming speed and turning rate ranging from 33–115 ?m s-1 and 41-110 deg s-1 respectively. Behaviors were sustained over the course of the 12 hour experiment (hourly %CV: 2-25%), and sample size analysis revealed that the exhibited behaviors were inherent to the strain. Exhibited behaviors showed no relationship to size or cell carbon content. These strain-specific behaviors resulted in genetically distinct vertical population distributions of the alga, linking individual movement to population-level dynamics. This study demonstrates that the traits of genetic identity and motility can provide high-resolution understanding intra-specific variability in order to better understand and predict phytoplankton population dynamics.

Hepner, Megan (POSTER 20, SESSION 8)

Frank Muller-Karger, Francisco Chavez, Steve Gittings

Building Demonstration Marine Biodiversity Observation Networks in the Florida Keys and Monterey Bay National Marine Sanctuaries

In late 2014 the National Ocean Partnership Program (NOPP) funded a proposal to utilize the Florida Keys and Monterey Bay National Marine Sanctuaries as sentinel sites for demonstration Marine Biodiversity Observation Networks (MBONs). The primary goals are to: 1) Implement a demonstration MBON; 2) Integrate, synthesize and augment information from ongoing programs; 3) Relate MBON information to social-economic context and provide MBON information rapidly to stakeholder; and 4) Develop a plan to transition the demonstration MBON into an operational system. The early objectives are to: 1) Provide geographically-integrated time-series metrics of biodiversity and ecosystem health; 2) Define a minimum set of observations required for implementing a practical MBON; 3) Develop environmental DNA technology and autonomous sample collection methods for conducting biodiversity assessments; and 4) Bring biodiversity measurements together in a relational database with links to national and international databases.

Hernandez, Christina (POSTER 21, SESSION 5,8)

Joel Llopiz, Claire Paris, Julie Kellner, Ana Vaz, Benjamin Jones

The influence of ontogenetic vertical distribution of coral reef fish larvae on dispersal and connectivity

The successful dispersal and settlement of pelagic larvae is crucial for sustaining populations of reef-associated organisms and allowing recovery after disturbances. A strong understanding of the processes controlling dispersal is needed to inform conservation efforts such as the establishment of marine protected areas. There is strong evidence that various taxa of reef fish have specific depth preferences during their pelagic larval phase, and that some taxa experience ontogenetic vertical migrations whereby preferred depths change with age and developmental stages. The Connectivity Modeling System (CMS) is a coupled biophysical model designed for tracking individual particles (e.g. fish larvae) in ocean currents with specified probability distributions of traits and behaviors. For this study, simulated fish larvae with a larval duration of 45 to 55 days were released from coral reef locations along the Yucatan Peninsula and the Florida Keys. Ontogenetic shifts in their vertical distributions were guided by empirical observations for wrasses, goatfishes, and parrotfishes. The results show a highly significant effect of vertical distribution on dispersal, with more limited levels of population connectivity in the case of surface-dwelling taxa.

Hickman, Anna (POSTER 22, SESSION 2)

Stephanie Dutkiewicz, Oliver Jahn, Mick Follows

The role of bio-optical traits for phytoplankton biogeography

Bio-optical characteristics vary considerably between different phytoplankton functional groups but the extent to which light availability shapes phytoplankton distributions remains unclear. Here, we use an ecosystem model coupled to a physical-biogeochemical model to test the hypothesis that bio-optical traits are important for setting global phytoplankton distributions. A series of model sensitivity experiments revealed that bio-optical traits, including intracellular pigments, were important in determining the competiveness of different phytoplankton in the (spectral) light gradient. However, shading by particular pigment types did not play a major role in shaping the distributions. Instead, the total phytoplankton biomass and concentrations of non-algal optical constituents, including detritus and coloured dissolved organic matter, were important controls on the available light spectrum and consequently the biogeography.

Hirst, Andrew (TALK, SESSION 4)

DS Glazier, MKS Lilley, D Atkinson

New insights from body surface: a major trait in determining life sustaining rates in metazoans

Metabolism underpins the vital rates of all organisms and is critical to understanding the organisation and evolution of life on earth. Metabolic rates have long been recognised as closely correlating with the ‘master trait’ of body size, while body surface area has been understudied. Although surface-related exchange of life sustaining molecules has at times been included in mechanistic explanations of metabolic processes, rarely has such analysis extended to multicellular pelagic invertebrate life forms. Such open-water species represent a huge diversity of phyla and occupy a pivotal role in fresh and marine ecosystems. These taxa commonly exchange respiratory gases and small molecules through much of their body surface, and they also show impressive shape changes during ontogeny. We use these properties to test a surface-area dependent theory of metabolism, and thereby demonstrate significant links between body surface enlargement and the scaling of a wide range of metabolic processes including respiration, nitrogen excretion and growth rates within species. We develop a next generation metabolic scaling theory that considers transport of resources and wastes across various body surfaces in addition to transport within internal delivery networks.

Hunt, Dana (POSTER 23, SESSION 7)

CS Ward, CM Yung and ZI Johnson

Evidence for temperature-related trade-offs in bacterial community and population dynamics

Microbial communities display repeated annual dynamics, driven by seasonal patterns in environmental variables of which temperature is often the most important. Here, we investigated the influence of temperature on the bacterioplankton at a temperate coastal site (Beaufort NC USA) using 16S rRNA gene library sequencing and bacterial isolates. Weekly bacterial community samples display an annual pattern linked to both light and temperature. However bacterioplankton changes were not continuous, at an apparent threshold of 19-24 °C the community transitioned between winter and summer composition. To test thermal specialization and trade-offs in greater detail, we isolated bacteria of the genus vibrio over an annual cycle. Isolate temporal niches and laboratory thermal performance curves suggest that it is not possible to be a thermal generalist, but that thermal specialization can occur at a very fine phylogenetic scale. Together, these results imply that temperature is one of the key organizing environmental variables for microbes and that seasonal or climatic temperature shifts can select for distinct microbial communities and populations.

Hunter-Cevera, Kristen (POSTER 24, SESSION 4,9)

H.M. Sosik, M.G. Neubert, A.R. Solow, R.J. Olson, A. Shalapyonok

Seasonal shifts in division rate determine Synechococcus population dynamics

Synechococcus is a significant primary producer in coastal and open ocean systems. A key trait for understanding changes in its population abundance over time is the rate of cell division. For phytoplankton, the diel change in cell size distribution can be related to division rate. We use a matrix population model, fit to hourly cell size distributions, to estimate daily division rates of the Synechococcus population at the Martha’s Vineyard Coastal Observatory for an 11-

year time series. This method effectively links an individual trait (cell size) to a population level trait (cell division), both of which have implications for the ecology of this organism. We find that division rate follows a striking seasonal pattern, driven primarily by temperature limitation during the winter and spring, but by light limitation during the fall. With this information and net change in abundance, we also calculate population loss rate. Division and loss processes are tightly coupled throughout the year. The annual cycle of Synechococcus cell abundance results from periods of time when there are small systematic differences that favor either net growth or loss. This approach opens a path to quantify the role of Synechococcus in ecological and biogeochemical processes in natural systems.

Jenkins, Bethany (POSTER 25, SESSION 1,9)

Dreux Chappell, Joselynn Wallace, LeAnn Whitney, Kristofer Gomes and Laura Filliger

Gene Expression as a Biological Reporter of Trace Metal Biogeochemistry

Rapid methodological advances in both analytical measurements of ocean chemistry and for detecting cellular readout in terms of genes and proteins expressed in response to in situ concentrations of biologically available trace metals are revolutionizing our understanding of trace metal biogeochemistry. This presentation will highlight how recent gene expression studies of natural diatom communities are beginning to reveal the similarities and differences in strategies different taxonomic groups use to adapt to iron limitation. Gene expression measures can also reveal when sources of iron may not be available to a biological community that might be missed by concentration measurements. These gene expression measures of iron limitation can be applied across ocean systems, and likely multiple functional groups and therefore could be readily incorporated into trait based modeling approaches.

Jennings, Simon (INVITED SPEAKER)

Size- and trait-based structures and processes in marine ecosystems

Size- and trait-based approaches provide insights into community interactions and food web processes that complement those from more complex species-based analyses. The approaches enable equitable analysis and comparison of diverse food webs and ecosystems because they have relatively low parameter demands and are based on established ecological principles that apply in diverse environments. This talk describes the development and application of size- and trait-based analysis to address fundamental and applied questions about the structure of marine ecosystems, the roles of marine fauna and the effects of human impacts. Examples of applications include prediction of community and food web responses to fishing, global patterns of fish biomass, biodiversity and production, assessing fish contributions to biogeochemical cycles and assessing the effects of fishing and climate change. The talk concludes by reviewing the strengths and weaknesses of size- and trait- based models, ongoing efforts to meld size- and species-based perspectives and emerging priorities for future research.

Jonsson, Bror (TALK, SESSION 5)

James Watson

The effect of advection on temperature adaptation by phytoplankton communities in the global ocean

Living conditions for oceanic phytoplankton and other marine lifeforms are expected to be drastically altered due to climate change. Increase in sea surface temperature will force planktonic communities to respond to new environments by local evolutionary adaptation or by ecological succession from migration. The relative contribution by each of these processes are still largely unresolved. To address this challenge, it is necessary to identify the timescales over which phytoplankton can evolve to warmer conditions and to quantify how fast heat adapted organisms can be transported into regions that experiences warming. In this study we focus on the latter question. We use Lagrangian particle tracking and network theory to quantify the timescale over which surface currents connect different regions of the global ocean. Our results show that fastest path between two patches, each randomly located anywhere in the surface ocean, is on average less than a decade. We use our results to calculate the shortest time it takes for organisms to travel to a patch from regions with at least 1°C higher temperatures, and find these times to be less than 5 years in most locations of the global ocean. Two significant exceptions are the Caribbean and the western tropical Pacific, where it can take several decades. These results are then combined with model simulations of future climate change to evaluate if marine communities can keep in pace with climate change through the advection of resilient types. Our results suggests that physical connectivity can act as a powerful aid for phytoplankton communities to adapt to climate change.

Kenitz, Katarzyna (POSTER 26, SESSION 6)
K.H. Andersen, P. Mariani, A.W. Visser
Optimal zooplankton feeding mode in a seasonally-stratified shelf sea
One of the fundamental traits characterising zooplankton populations is their feeding mode. The diverse modes can be distinguished into two types: ambush feeding that captures motile prey, and feeding current feeding that targets mostly non-motile prey. Distribution and abundance of motile and non-motile phytoplankton varies on temporal and spatial scales, reflecting the variability in the physical environment. Likewise, the strength of turbulence affects the ability of zooplankton to detect and capture prey, and their susceptibility to predation from higher trophic levels. A 1D model framework is implemented to capture the distribution of motile and non-motile phytoplankton in a seasonally stratified shelf sea. The model simulates the competition of two phytoplankton types (motile and non-motile) for a single resource, and incorporates adaptive feeding where zooplankton can switch their optimal feeding mode. The model predicts that, for an idealized shelf sea environment, zooplankton community shifts from ambush-dominated during the spring bloom to feeding-current feeders taking over in the summer. We combine location-specific model simulations and observational, time-series data analysis to investigate whether the seasonal succession of different copepod species can be explained by the modification of the optimal feeding traits driven by seasonal variability in prey abundance and turbulence.

Kerimoglu, Onur (POSTER 27, SESSION 6)
Richard Hofmeister, Joeran Maerz, Kai Wirtz
Role of phytoplankton adaptation in functioning of a coastal ecosystem
Adaptation processes are generally thought to play a significant role in ecosystem functioning. In this study, we employ a trait-based adaptive model framework for a quantitative assessment of the relevance of phtoplankton adaptation to functioning of a coastal ecosystem, the German Bight. With a relatively low number of free parameters and state variables, the model addresses the optimal allocation problem faced by the primary producers to regulate internal stores of carbon, nitrogen, phosphorus and chlorophyll. The model is first validated against chemostat experiments where phytoplankton were forced with marginal resource supply ratios. The plankton model is then embedded in a coupled biogeochemical-physical model configured for the southern north sea, with which, seasonal dynamics of organic and inorganic constituents of the system are realistically reproduced. First results of a scenario analysis indicate that key features of the system, such as off-shore deep-chlorophyll maxima, primary production and nutrient uptake rates critically depend on adaptive potential of the phytoplankton assemblage.

Kiørboe, Thomas (INVITED SPEAKER)
How traits are interrelated through tradeoffs in zooplankton
The key traits of an organism relate to its main Darwinian missions of feeding, surviving, and reproducing. No organism, however, can simultaneously perform optimally with respect to all of these missions because they are conflicting through behavioral interactions and competition for acquired resources. For example, feeding may compromise survival, and acquired energy must be shared between growth, reproduction, and maintenance and defense. Thus, traits are interrelated through tradeoffs. Tradeoffs may be inferred from correlations between traits or, better, quantified through a mechanistic understanding of the underlying processes. Here, I attempt the latter for marine zooplankton. Through an understanding of the mechanisms and fluid dynamics of feeding I make prediction of the efficiency and predations risk of the three different feeding modes of zooplankton, on implications of feeding mode for mate finding, and on how the different feeding modes lead to differences in energy allocation and senescence. I will show experimental tests of these predictions. The mechanistic understanding of key traits and associated tradeoffs is now utilized in the construction of trait-based models of plankton systems.

Kostadinov, Tihomir (POSTER 28, SESSION 2)

Anna Cabré, Harish Vedantham, Irina Marinov, Astrid Bracher, Robert Brewin, Annick Bricaud, Nick Hardman-Mountford, Takafumi Hirata, Amane Fujiwara, Colleen Mouw, Shovonlal Roy, Julia Uitz

Intercomparison of Phytoplankton Phenology from Phytoplankton Functional Types Satellite Algorithms and Earth System Models

Numerous satellite ocean color algorithms are now available for the retrieval of phytoplankton functional types (PFTs). These algorithms define the PFTs differently and retrieve variables on different scales. This makes inter-comparison of emergent properties such as phenology more meaningful. Here we inter-compare the phenological characteristics of the fraction of microplankton (or the most closely related variable) retrieved by a suite of ten PFT ocean color algorithms, as well as diatom carbon biomass from seven CMIP5 Earth System models. The Discrete Fourier Transform was first used to model the seasonal cycle as a sum of sinusoidal harmonics. Peak analysis was then applied and the following phenological parameters were quantified: seasonal amplitude, month of maximum blooming, bloom duration, and fraction of variance explained by the modeled signal. The DFT technique also permits the quantification of secondary blooms, which tend to occur in zonal bands. Since the analysis focuses only on large phytoplankton, it poses the question of to what extent phytoplankton size can be a predictor of traits, in other words to what extent various traits covary with size. This is very important to address since the particle size distribution affects optical properties and thus our ability to detect given traits from space.

Kremer, Colin (POSTER 29, SESSION 3,7)

Mridul K Thomas, Elena Litchman

Temperature and phytoplankton growth rates: disentangling empirical patterns and competing paradigms

Phytoplankton maximum growth rates are constrained by temperature and cell size. These compelling relationships have been documented repeatedly, and linked to multiple quantitative hypotheses. We use an extensive database of phytoplankton traits (growth rate, cell size, functional group) to evaluate the competing predictions of Eppley from 1972 and metabolic theory. Our results show that the scaling of maximum growth rate with temperature is consistent with metabolic theory, and shallower than predicted by Eppley. Additionally, we find that major functional groups (diatoms, dinoflagellates, cyanobacteria, greens) have inherently different growth capacities, but their growth rates scale similarly with temperature. Both the Eppley and metabolic theory paradigms focus on temperature-driven, monotonic increases in growth rate across species. However, in reality, finite standing variation in phytoplankton thermal traits means that there are limits to growth at high temperatures, even for communities from the contemporary tropical environments. We calculate conservative estimates of this constraint, again drawing on our thermal trait data. Accurate estimates of the thermal constraints of phytoplankton growth are critical for constructing reliable marine ecosystem models. Collectively, these insights into the regulation of phytoplankton growth by temperature advance our understanding of the responses of marine communities and ecosystems to climate change.

Krishna, Shubham (POSTER 30, SESSION 3)

Explaining variability observed in calcification during the PeECE-I experiment

During the past two decades a series of studies were conducted with large tanks or bags of enclosed volumes of water that comprised a plankton community called mesocosms. Some mesocosm experiments focused on ocean acidification (OA) effects on marine calcifying algae (coccolithophores) captured in enclosed water volumes and exposed to different CO2 concentrations, e.g. Pelagic Ecosystem CO2-Enrichment Studies PeECE-I, II, III (Riebesell et al., 2008, Biogeosciences). In these studies, for example during PeECE-I large differences were found with respect to calcification, the observed accumulation of particulate inorganic carbon (PIC) between mesocosms of similar CO2 treatments (Engel et al., 2004 L&O; Delille et al., 2005, GBC). In our study we apply a optimality based plankton ecosystem model (Pahlow et al., 2013) to understand and explain most of the variability observed in PIC during PeECE-I. Model is constructed by maximizing growth in the system and optimally allocating nutrients among cellular functions (light harvesting complex, structural protein and nutrient acquisition). According to the results of our data-model synthesis study we conclude that the variability observed in total alkalinity and calcification during the PeECE-1 experiment could be well explained by small differences in the initial plankton composition while mesocosms were filled.

Lanbehn, Tom (POSTER 31, SESSION 5)

Øystein Varpe

Visual search as a trait: consequences of sea ice change in high latitude oceans

Light is a multi-dimensional structuring variable for ocean life as it governs bottom-up control through primary productivity and exerts top-down control by determining visual foraging efficiency. High latitude oceans are dark during the winter, and even during the midnight sun the offset in seasonality between sea ice and light regime restricts light penetration into the pelagic realm. Prey encounter of visually searching predators such as seabirds, fish and large zooplankton is tightly bound to the light regime. Consequently, how are visual constraints on feeding in an extreme-light environment affecting predator-prey interaction and subsequently community composition and distribution patterns of arctic vs. boreal species? Reductions in sea ice extent and thickness will result in elevated light levels prompting an altered sensory environment in the future Arctic Ocean. Mechanistic modelling of light transmittance and foraging efficiency of visual predation in seasonally ice-covered waters yield new insights into ecological interactions, behavioural strategies, potential distribution shifts and trait-evolution. Here we focus on investigating the performance of visually searching predators over the annual cycle and along gradients of latitude and sea ice condition, allowing for the unique opportunity to study the complexity of sensory based traits in ocean life.

Le Bris, Arnault (POSTER 32, SESSION 4)

Andrew Pershing

Temperature induced variation in life-history trade-offs

In most ectotherms, elevated temperature increases growth rate, leading to earlier maturity and maturity at a smaller size. Assuming a von Bertalanffy growth function, this relationship between temperature and maturity implies a negative correlation between the growth coefficient (k) and the asymptotic length (Linf) such that Linf = a*k^(-h) Using a meta-analysis, we first demonstrate that the trade-off between Linf and k occurs in crustaceans with 0.25<h<0.75. Using metabolic theory, we explore the thermal constraints on asymptotic length and thermal sensitivities of growth rate. Furthermore, because Lmat/Linf = 1 - e^(-k*Tmat), we propose a general model to parametrize Lmat, Linf, k, based solely on temperature. This general model will facilitate the development of more complex life-history models to predict species responses to global change.

Leach, Clinton (POSTER 33, SESSION 4,8)

Ken T. Frank, Colleen T. Webb

Exploring the lack of recovery of Scotian Shelf cod through the development of a statistical framework for size-structured predator-prey models

The collapse of the cod fishery on the Scotian Shelf in the early 1990s led to a dramatic and persistent decline in the abundance and body size of predator fish over the last two decades. Hypotheses for the inability of these large predators to recover include predator-prey role reversal, wherein numerically dominant fish at lower trophic levels (forage fish) prey upon the early life stages of large predator fish, and intensified competition between these forage fish and small-bodied predators. Though there is correlative evidence for these hypotheses, here we explore their role more explicitly through the use of mechanistic, size-structured partial differential equation models. These models account for intraspecific variability in body size and diet by using species traits and individual physiology to track the flow of biomass through time and along a size spectrum (i.e. from small prey to larger predators). In order to explore the role of the above mechanisms in preventing the recovery of large predators, we develop a statistical framework around the mechanistic model that allows us to fit the model to a time series of abundance-at-length estimates from the Scotian Shelf.

Levy, Marina (TALK, SESSION 5)

Oliver Jahn, Stephanie Dutkiewicz, Michael J. Follows and Francesco d'Ovidio

The dynamical landscape of marine phytoplankton diversity

How phytoplankton diversity and composition varies on small spatial scales is not well documented, due to the difficult task of acquiring synoptic taxonomic data. Here we examine how the turbulent ocean shapes diversity. More specifically we analyse how small photo-autotrophs and fast-growing phytoplankton are preferentially distributed in eddies and at thermal fronts. We use a multi-phytoplankton mathematical model embedded in a turbulent flow representative of the North Atlantic. In agreement with observations, we show that there are no systematic rules for how differing phytoplankton types are organized in eddies and fronts. Nevertheless, on a statistical basis, our model reveals a tendency for larger diversity and more fast-growing types at fronts, where populations of adjacent water masses are constantly brought into contact, and lower diversity in the core of mesoscale eddies, where water masses are kept isolated long enough to enable competitive exclusion. Moreover, our model results show that phytoplankton assemblage varies between adjacent water masses that are segregated by rapidly evolving submesoscale fronts forming dispersal barriers. This modeling study suggests that in-situ observations in individual cases of eddies and fronts can only give a very partial view of the complex distribution of marine phytoplankton.

Litchman, Elena (INVITED SPEAKER)

Christopher Klausmeier

Trait-based approaches to microbial ecology and evolution

Phytoplankton account for about half of global primary productivity, form the base of the most aquatic food webs and play important roles in major biogeochemical cycles. Changing environmental conditions shift community composition with consequences for higher trophic levels and biogeochemistry. Trait-based approaches provide a mechanistic foundation for understanding how phytoplankton communities respond to interacting abiotic and biotic drivers. I discuss examples of how functional traits can provide insights into community assembly and dynamics. The new frontiers in trait-based research include looking at intraspecific trait variation due to genotypic differences and phenotypic plasticity and comparing it to interspecific variation to predict patterns in community responses. Investigating trait evolution due to interacting environmental pressures and incorporating it into predictive models of plankton communities and biogeochemistry is another experimental and theoretical challenge facing aquatic ecologists. Trait-based approaches can also be useful for applied issues such as ecological assessment and ecosystem restoration.

Maps, Frederic (TALK, SESSION 9)

Geneviève Parent, Stéphane Plourde, Nicholas R Record

Blurred lines between species in trait-based numerical approaches. A case study of Calanus hybrids

Trait-based approaches in marine planktonic ecology appear as an efficient trade-off between complexity and tractability in the pursuit of the elusive goal of a comprehensive model of pelagic ecosystems. It allows the grouping of species according to their prominent functional characteristics (traits). However, some ecological issues involve species that share almost all the same traits, and the very definition of a “trait” appears challenging. For example, the size (a usual trait) of closely related copepods species can actually overlap significantly depending on the environmental conditions. This may appear as a limitation of the approach and it can be further complicated by the recent discovery of hybrids between congeners. Here we present a numerical approach based on a genetic algorithm applied to the modeling of the dominant Calanus congeners from the sub-Arctic area, and we extend it to hybrids of C. finmarchicus and C. glacialis. The principal objective is to explore how to efficiently represent the phenotypes of hybrids that can borrow from either species for some traits, or become a combination (average) of each other for other traits. We used observations made on monospecific and hybrid individuals collected in the North-West Atlantic to parameterize and validate our numerical approach.

Mariani, Patrizio (POSTER 34, SESSION 6,8)

De Luca Giancarlo, Marsilli Matteo

Group formation and efficiency of migratory species

Individual preferences and social behavior are central traits of group formation in humans and other social animals. Being in a group is often a big advantage for those individuals performing complex tasks that are usually difficult, or impossible, to be carried alone. Schooling is an example of such complex collective dynamics and it is a common feature in several fish species performing seasonal migrations from the spawning to feeding areas. Combining an evolutionary individual based models and a novel framework based on network theory we demonstrate that three factors can control school formation and migration behavior of social fish: the strength of the social group, the relative number of informed individuals and the preference each individual has on the particular feeding area. While sociality and information ability are associated to the long-term evolutionary process that have selected them, the preference is a short-term property of single individuals and is related to the experience and memory of certain places. Intensive fishing and habitat degradation can reduce the frequency of those traits in the population up to a point at which migrations to feeding and spawning grounds are suddenly stopped.

Marki, Alexandra (POSTER 35, SESSION 6)

M. Pahlow, H. Hauss

Optimality-trait-based plankton ecosystem modelling of phosphorus uptake in microbes

Nutrient-phytoplankton-zooplankton-detritus-bacteria (NPZDB) model simulations highlight the importance of plankton and dissolved organic matter (DOM) dynamics and follow pathways of inorganic nutrients and organic food sources throughout the food web. Our optimality-trait-based plankton ecosystem model (OPEM) simulates DOM dynamics by applying biological and physiochemical forces to investigate DOM production, transformation and respiration. Since DOM uptake is mainly due to microbes, such as bacteria and Archea, which represent the major groups of osmotrophic heterotrophs in the ocean, we simulate possible molecular interactions between DOM and microbes. For example, inorganic phosphorus (DIP), which is assimilated by microbes and remineralised and excreted as inorganic phosphorus (DIP) or egested as dissolved organic particles (DOP) in vicinity of the microbes. Since the uptake of DOP is thought to be more expensive than DIP uptake, we introduce an inhibition function, based on the availability of ambient DIP. Thus, we simulate preferential DIP uptake, when DIP is abundant and allows DOP uptake when ambient DIP concentrations are too low to cover the basic phosphorus needs of microbes.

Martiny, Adam (TALK, SESSION 1)

Jennifer Martiny, Jay Lennon, Stuart Jones

Microbiomes in light of traits: a phylogenetic perspective

Microbial communities are intricately linked to ocean functioning. Despite their recognized importance, however, we still lack a systematic understanding of what determines microbiome diversity and composition and their implications for system functioning. New genetic technologies quickly characterize thousands of microbiome samples. Although these data provide a sweeping perspective on microbiome patterns, an emerging challenge is the interpretation. Here, we consider how a focus on microbial traits could address this challenge. We find that a phylogenetic framework of microbial traits can advance our interpretation of the rapidly accumulating amount of microbiome data. Despite high levels of horizontal gene transfer, our work indicates that many microbial traits are phylogenetically conserved. Further, the degree of phylogenetic conservation depends on the particular trait, leading to a hierarchical distribution of trait variability across the microbial tree-of-life. Not only does a phylogenetic trait-based framework allow comparing across systems and taxa, it can be applied across different levels of genetic resolution, from studies examining strain- or population-level differences to those considering the entire microbial community. Such a flexible framework is sorely needed for microorganisms, where the times scales of evolutionary and ecological processes overlap.

Menden-Deuer, Susanne (TALK, SESSION 6)

Julie Rowlett

The role of intra-specific trait variability in plankton biodiversity: a gametheoretic and model examination

The Paradox of the Plankton, coined by Hutchinson 1961, describes the discrepancy between theoretically explicable and actually observed numbers of co-existing planktonic species. We introduce a game-theoretic model for competing micro-organisms that incorporates vast populations sizes and high degrees of intra-specific variability to evaluate the role of intra-specific variability for the survival and ultimately biodiversity of plankton. Intra-specific variability was treated as a trait of strains by formulating an average competitive ability (identical for all strains). This competitive ability could either be invariant (reflect only the mean) or follow different distributions (e.g. uniform, bimodal, Gaussian). Intra-specific variability was the key characteristic that allowed co-existence of dozens of species because the outcome of competitions between individuals with variable competitive abilities was unpredictable. Simulations based on the theoretical model showed that 100 species can coexist for 10000 generations. High intra-specific variability in genetics, physiology, morphology or behavior is frequently observed in diverse plankton. We suggest this intra-specific trait variability has adaptive value and characterization of intra-specific variability will be important in assessing species ability to withstand changing environmental conditions and understand diverse planktonic communities in a seemingly uniform ocean.

Mills, Katherine (TALK, SESSION 4)

Andrew J. Pershing, Arnault Le Bris

Using size structure and metabolic theory to forecast fish community characteristics in a changing climate

Body size is an important trait that can be used to understand ecosystem functioning across multiple scales, and the ability to relate body size to ecological principles provides an avenue for forecasting community and ecosystem properties under future climate conditions. Macroecological theory suggests that community size structure and diversity are directly related to temperature and primary production. Relationships between temperature, metabolic rate, and body size have been well characterized by metabolic theories, and these relationships provide an avenue for predicting community properties such as size, abundance, and diversity under future climate scenarios. These properties then influence the resilience of communities to changes in physical conditions and to other perturbations such as fishing. In this presentation, we will (1) describe shifts in the size spectrum of the fish community on the Northeast Shelf over time and space, (2) evaluate relationships between size structure of the fish community and properties of the marine ecosystem, and (3) assess how these relationships can be used with metabolic theories to forecast future community characteristics.

Moeller, Holly (POSTER 36, SESSION 3,6)

Michael G. Neubert and Matthew D. Johnson

Acquired phototrophs as mediators of planktonic community dynamics

Acquired phototrophs—organisms that obtain their photosynthetic ability by hosting endosymbionts or stealing plastids from their prey—are widespread in marine planktonic ecosystems. These organisms vary in their dependence on this acquired metabolism: For example, the bloom-forming coastal ciliate Mesodinium rubrum obtains >90% of its carbon from photosynthesis, compared to oligotrich ciliates that acquire <30% of their carbon photosynthetically. We use a mathematical model to understand how this trait mediates an acquired phototroph's effect on community dynamics. Specifically, we show that strict acquired phototrophs (e.g., M. rubrum) may drive boom-bust population cycles, and validate this observation with laboratory experiments. In contrast, predominantly heterotrophic acquired phototrophs produce stable equilibria. These results, which match field observations of bloom-former identity, suggest that acquired phototrophs may be key modulators of bloom dynamics in coastal ecosystems.

Moisan, John (POSTER 37, SESSION 6,9)

Weiyuan Jiang and John McCarthy

Genetic Programming for Ocean Microbial Ecology and Biodiversity

Present day modeling efforts to resolve upper ocean microbial ecosystem processes use coupled sets of ordinary or partial differential equations. These sets of equations, or models, which represent both ecosystem function and diversity, are subjectively developed, more or less independently, using in situ observations and conclusions derived from scientific literature. Presently data assimilation (DA) is commonly used for optimizing model parameters. Because the equations are not 'optimized' to represent the actual ocean system under study, DA can only improve the model solutions, not the modeled dynamics. No objective methods existed that allowed for improving the model's equations. This presentation demonstrates the application of a programming technique called "Genetic Programming" (GP) to optimize not only the set of free parameters within an ecosystem model but also the coupled set of model equations. A new GP application, termed GP COupled Differential Equations (GPCODE) is verified using a set of "twin experiments" using previously developed simple ecosystem models. The GPCODE is presently being applied to real world ecosystem observations to evolve a microbial ecosystem model for the ocean. Presently, our group is attempting to merge this application to model ocean ecosystem traits rather than simply solving for biogeochemical processes. The presentation will focus on what we have learned in our journey to develop this dynamic trait-focused evolving ecosystem architecture.

Montalbano, Amanda (POSTER 38, SESSION 1,9)

Susanne Menden-Deuer

Intra-specific variability in growth rates and behavior of a harmful dinoflagellate species: trait variation broadens ecological niche

Growth rates and swimming behaviors of 6 strains of the dinoflagellate Akashiwo sanguinea were measured to quantify trait variability in growth and motility and its contribution to bloom formation potential. Measurements were made at 2 temperatures (10°C, 20°C), benchtop and on a shaker table, to emulate mild turbulence. Contrary to prior reports, turbulence had neutral or positive effects on growth rates and were higher than in still conditions. Intra-strain variability in traits was a distinguishing characteristic among strains, with significant differences (>50% coefficient of variation), within the same species isolated from a single water sample. All strains had both up and down swimming fractions, leading to predictions of vertically patchy distributions, rather than surface aggregations. Estimates of in-situ loss rates are a critical missing component for identifying bloom formation mechanisms of this species. Slow growth rates and dispersive swimming behaviors suggest in-situ mortality must be low and tolerance of seasonally varying water temperatures, enhanced by intra-specific trait variability, lead to accumulation and persistence of cells over months and kilometers. Assessment of species' traits based on single strains may not reveal the physiological, morphological, behavioral and genetic diversity to accurately characterize planktonic species and distinguish among groups.

Montes, Enrique (POSTER 39, SESSION 8)

Frank Muller-Karger, Francisco Chavez, Maria Kavanaugh, Steve Gittings, Megan Hepner, Mya Breitbart, Jennifer Brown, David Anderson, Scott Donahue

National Marine Sanctuaries as Sentinel Sites for a Demonstration Marine Biodiversity Observation Network (MBON)

We seek to develop a demonstration of a Marine Biodiversity Observation Network (MBON) using three iconic National Marine Sanctuaries as nodes: The Florida Keys, Monterey Bay, and Flower Garden Banks. The goals are to: 1) Integrate and synthesize information from ongoing monitoring programs collecting biological and environmental measurements at these sites; 2) Define the minimum set of observations required for implementing a practical, useful MBON; 3) Develop technology for biodiversity assessments through emerging environmental DNA (eDNA) molecular methods and autonomous sample collection; and 4) Integrate biodiversity measurements in a relational database linked to national and international biodiversity databases that informs NOAA's emergency response system and that dynamically updates Sanctuary status and trends reports. The program will test the deployment of autonomous platforms for in situ eDNA assessments that will allow to track changes in habitat diversity and diversity across trophic levels (from microbes to whales) in response to multiple stressors over time. Multidisciplinary remote sensing will be used to evaluate dynamic 'seascapes' to extend the spatial footprint of the in situ data. Time series of biodiversity and environmental observations will help construct conceptual and forecast models of the inter-relations between humans, climate and environmental variability, and ecosystem structure and health.

Moore, Tim (TALK, SESSION 2 – with Colleen Mouw)

Chris Brown

Projecting the environmental niche space for summertime coccolithophore blooms in the North Atlantic from satellite data

Coccolithophores are ubiquitous in the ocean, yet bloom only under certain conditions. Coccolithophore blooms can produce detectable signals in ocean color imagery, which reveals unique identification for the time and place of a bloom. It has been observed in ocean color data that coccolithophore blooms re-occur annually in certain places and times, and are constrained by environmental properties which defines a niche space for bloom promotion. Using satellite bloom patterns in ocean color imagery, the ecological factors favorable to bloom development are co-extracted from satellite data in the North Atlantic from 1998-2010. A statistical model is developed from environmental factors to represent the ecological niche for coccolithophore blooms. Patterns in generated probability maps are compared with in situ CPR data and ocean color data over time and space, and assessment of the model forecasting and sensitivity to environmental parameters is explored.

Mouw, Colleen (TALK, SESSION 2 – with Tim Moore)

Satellite Remote Sensing of Phytoplankton Groups

Phytoplankton are extremely diverse in terms of taxonomy, morphology and size. These characteristics impact their light absorption, scattering and pigment composition allowing them to be detected with ocean color satellite radiometry. There is a growing volume of literature of satellite algorithms to retrieve information on phytoplankton composition in the ocean. A synthesis review of types of algorithms available and simplified comparison of assumptions, strengths and limitations will be provided. The aim is to provide an overview of current remote sensing capability of phytoplankton composition, raising the level of awareness and use of these products by reducing the boundary of expert knowledge needed to make a sound selection with confidence.

Mouw Colleen (POSTER 40, SESSION 7)

Audrey Barnett, Galen McKinley

Utilizing satellite estimates of phytoplankton size to understand global export flux variability

The efficiency of the biological pump of carbon to the deep ocean depends largely on the biologically mediated export of carbon from the surface ocean and its remineralization with depth. Global satellite studies thus far have focused on the use of chlorophyll concentration and primary production to understand the role of phytoplankton in these processes. Recent satellite retrievals of phytoplankton composition now allow for the size of phytoplankton cells to be considered in the biological pump at large scales. The goal of this study is to improve understanding of how phytoplankton size structure controls particle export and remineralization. Particulate organic carbon (POC) flux observations from sediment traps and 234-Thorium were compiled across the global ocean and the distribution of the data is presented. Annual climatologies of primary production, percent microplankton, and POC flux at key time series locations and within biogeochemical provinces were compiled. Sinking velocity was calculated to align surface production with POC flux. Parameters that characterize POC flux vs. depth (export flux ratio, labile fraction and remineralization length scale) were fit to the aligned dataset. Times of the year dominated by different size compositions were identified and fit separately in regions of the ocean where phytoplankton cell size varied enough over the annual cycle. Cell size impacts were observed in export flux and remineralization length scales. Generally, periods dominated by small cells had lower transfer efficiency and greater export flux than periods when microplankton comprised a greater proportion of the phytoplankton community.

Pershing, Andrew (POSTER 41, SESSION 8)

Lisa A. Kerr, Arnault Le Bris, Katherine E. Mills

Trait-based strategies for estimating population abundance

The starting point of most conservation or management strategies is the estimation of the abundance of the target species. The precision of the estimate depends on the interaction between the sampling scheme, the species' spatial distribution, and of course, its abundance. Spatial distribution is an emergent property driven by a combination of factors, including aspects of the ecosystem (distribution of habitat, predators, and prey) and the species' behavioral traits. Here, we explore how two simple behavioral traits--preference for habitat and tendency to school or flock--alters spatial patterns, thereby impacting the ability of different sampling schemes to detect changes in abundance. These differences can have practical consequences for management, especially when abundance is low, and can contribute to tensions among stakeholders. For example, fishermen who sample repeatedly in high quality habitat will perceive the abundance of strongly habitat-dependent species to be high, even when the population is declining. At the same time, scientific surveys are more likely to detect the trend but precision will decline in concert with the population, requiring more precautionary management and lower quotas.

Prowe, Fi (TALK, SESSION 2)

K. H. Andersen, T. Kiørboe, A. W. Visser, M. Pahlow, A. Oschlies

Effects of trade-off based zooplankton feeding in a global ocean ecosystem model

Global marine ecosystem models link plankton community structure and biogeography to predicting ecosystem functioning and global change. In these models, typically a diverse assemblage of phytoplankton functional types interacts with an oversimplified zooplankton community governed by rigid trophic interactions. Zooplankton feeding, however, may drive simulated plankton community structure and biogeography, and thereby affect ecosystem dynamics and functions like the biogenic carbon export. In order to assess potential effects of an improved representation of plankton communities, we present a new trade-off based model of plankton trophic interactions. Using the traits size and motility, the model predicts for the first time the biogeography of zooplankton feeding strategies on the global scale. Combined with community structure, these predictions are compared to observations in order to assess the model's sensitivity to parameters and trade-offs. Contrasting our model to established, simpler formulations reveals the potential of trade-off based formulations for simulating ocean ecosystem dynamics and functioning. While the model advances the representation of trophic complexity within the plankton, it is based on prescribed rigid interactions. In addition, we therefore present new ideas for using optimality-based modelling techniques, which allow flexible feeding interactions, to predict plankton community structure in an emergent way.

Rao, Deepa (POSTER 42, SESSION 2)

Mick Follows

The paradox of the Prochlorococcus: A trait-based approach to modeling ecotype niche differentiation via light and nutrient resource competition

The habitat of *Prochlorococcus,* the most abundant photosynthetic organism on Earth, extends throughout the heterogeneous conditions of the euphotic zone of the tropical and subtropical oligotrophic ocean. Observations reveal that *Prochlorococcus* ecotypes are organized by vertical niche-partitioning in a seasonally dynamic, but annually stable, pattern. To mechanistically understand how ecotypes are structured, we employ a modified resource-ratio theory (Huisman & Weissing, 1994) to explore inter-ecotype competition for the essential resources of nutrients and light. We predict resource supply regimes related to the exclusion and co-existence of multiple *Prochlorococcus* ecotype-analogs defined using traits determined in the laboratory and ask if these predictions are consistent with the observed patterns in the North Atlantic and North Pacific subtropical gyres.

Ravn-Jonsen, Lars (POSTER 43, SESSION 8)

How to share fish resources?

Management of the marine ecosystem is based on social institutions. These institutions implicit assume a structure of the ecosystem, and often consider the structure fixed in time. As an example, international agreements on sharing straddling fish stock are often based on a principle of fixed share of harvest between nations. Therefore implicit assuming the migration pattern to be invariant over time. When the migration change the agreement break down, as for example the North Atlantic mackerel in 2010. Break down of a fishery agreement is often followed by excessive fishery activity of at least one party, leading to over exploitation of the resource. A solution may be to base international agreement on sharing fish resources on more stable ecosystem properties. Here understanding the ecosystem based on functional groups may be offer an alternative to the species view on the marine resource.

Record, Nick (POSTER 44, SESSION 2)

Mapping the jelly and fat of the world's oceans

Ocean ecosystems are often viewed in terms of the abundance of and interactions among species. An alternative view is to examine the movement in space and time of important materials. These materials can be properties or traits of ecological communities. To test this approach, we mapped the global climatologies of gelatinous material (measured as low carbon-mass-to-wet-mass ratio of the zooplankton community) and planktonic lipids (using community diapause as a proxy). Highly gelatinous areas/times corresponded to lower oxygen and higher temperature, suggesting an advantage to high-gelatinous communities under multiple types of anthropogenic forcing. The regions where lipids were stored in diapausing communities corresponded to regions of high seasonality in conditions and of productive fish and mammal communities. This study shows the potential of this approach to help understand ecosystems in terms of community properties. For biogeochemical and resource management objectives, the distributions of these community properties can be more important than the distributions of individual species.

Rivero-Calle, Sara (POSTER 45, SESSION 2)

C. Del Castillo, A. Gnanadesikan, A. Dezfuli, B. Zaitchik

Trichodesmium is not limited to tropical and subtropical latitudes

Distribution of the marine diazotroph Trichodesmium sp. is assumed to be restricted to warm tropical and subtropical oligotrophic waters. Laboratory experiments concluded that Trichodesmium is unable to grow or fix Nitrogen under low temperature regimes (Breitbarth et al. 2007, Breitbarth et al. 2008) but growth rates, N2 and Carbon fixation rates in the laboratory and in situ vary by several orders of magnitude (LaRoche 2005). Using over 200,000 in situ observations from the Continuous Plankton Recorder between 1960-2010, we show evidence that Trichodesmium is widely distributed in the North Atlantic and that their abundance in the Bay of Biscay increased 10-fold during1983-1997, predominantly in the fall. Based on NCEP/NCAR reanalysis wind and pressure anomalies, we show that the timing of increased abundances of Trichodesmium coincided with an intense drought in the Sahel region, anomalous pressure systems and strong near surface northward winds (>4m/s). Our results show an episodic conduit for meridional winds transporting iron-rich African dust to higher latitudes. In order to reconcile predicted patterns of nitrogen fixation with direct observations we need to move away from the temperature limitation assumption. Biased sampling towards warm oligotrophic waters may be underestimating Trichodesmium's role in the Nitrogen and Carbon budget.

Roelke, Daniel (POSTER 46, SESSION 5,8)

Sophia Spatharis

Phytoplankton Assemblage Characteristics in Recurrently Fluctuating Environments

In many coastal systems river inflow and water exchange with the ocean varies seasonally, and alternating periods can arise when the phytoplankton growth-limiting nutrient switches. Transitions between these alternating periods can be sudden or gradual and this depends on human activities, such as reservoir construction and interbasin water transfers. How such activities might influence phytoplankton assemblages is largely unknown. Here, we employed a multispecies, multi-nutrient numerical model to explore how nutrient loading switching mode might affect phytoplankton. We found that the effect of shift from a sudden resource supply transition to a gradual one, as observed in systems impacted by watershed development, was dependent on the level of complementarity in species life-history traits. In the extremes, phytoplankton species richness and overyielding increased when complementarity was lowest, and phytoplankton biomass increased greatly when complementarity was highest. For low-complementarity simulations, the persistence of poorer-performing phytoplankton species of intermediate R*s led to higher richness and overyielding. For high-complementarity simulations, the formation of phytoplankton species clusters and niche compression enabled higher biomass accumulation. Our findings suggest that an understanding of factors influencing the emergence of life history traits important to complementarity is necessary to predict the impact of watershed development on phytoplankton assemblages.

Rynearson, Tatiana (POSTER 47, SESSION 2,5,9)

Whittaker, KW

Global-scale gene flow in a marine plankton: implications for tracking and interpreting key traits in key organisms

Functional traits may be acted upon by evolutionary forces, changing their distribution, magnitude, and ultimately, influencing their importance in driving ecosystem function. Individual species are often subdivided into genetically distinct populations, each responding to different selection pressures, which can lead to the divergence of trait characteristics even within a single species. In planktonic organisms, it is challenging to examine how traits segregate with populations because these organisms are constantly drifting with tides and currents, making it difficult to track individuals and populations over time and space. By collecting samples from across the globe, at approximately the same time, we found that gene flow in a cosmopolitan marine diatom is not limited by global-scale geographic distance. Instead, environmental and ecological selection likely play a more significant role than dispersal in generating and maintaining genetic diversity over space and time. These types of selection pressures likely have a profound influence on the magnitude and distribution of key traits in the ecologically and biogeochemically important diatoms.

Schedler-Meyer, Nicolas (POSTER 48, SESSION 6)

Patrizio Mariani

A mechanistic model of jellyfish-fish competition

Jellyfish are increasingly recognized as an important factor in marine food webs, and there is some concern that the frequency and magnitude of jellyfish blooms are also increasing. This could in turn have an impact on the small pelagic fish stocks competing for the same resources. It has been hypothesized that such changes are linked to anthropogenic impacts such as eutrophication and overfishing, which, in combination with climate change and the differences in key traits of jellyfish and fish could favor gelatinous species. This link between individual traits and ecosystem effects has not been included in ecosystem models of fish-jellyfish systems, both due to a lack of good data on jellyfish, but also because of the lack of a mechanistic description of the feeding interactions. Here I present a simple mechanistic food-web model that includes two zooplankton size classes, a jellyfish, a small forage fish and a large predator. The results show how the combined effects of eutrophication and fishing pressure can cause drastic changes in community structure, similarly to those occurred in the Black Sea during the last 5 decades.

Smeti, Evangelia (POSTER 49, SESSION 3)

George Tsirtsis, Daniel L. Roelke, Sofie Spatharis

Important traits for phytoplankton species coexistence along a disturbance gradient

The importance of life history traits in species coexistence is being increasingly revisited in studies over the past years. In phytoplankton assemblages, knowledge of environmental conditions and species' life history traits could help predict population dynamics and assemblage composition. Starting from a common species pool, we explore the traits that can shape assemblages along a disturbance gradient. Our approach couples experimental microcosms originating from the Aegean Sea, Greece, with a widely applied resource competition model, partially parameterized with the experimental findings. Phytoplankton was self-organized under different nutrient pulsing frequencies (every 1, 3, and 6 days), resulting in assemblages of different structure and composition. To explore the underlying mechanisms of these emerging properties, different assumptions regarding species' trait trade-offs were considered in the model. Emerging assemblage structure and composition was successfully reproduced by numerical modeling, revealing that growth rate is the most important life history trait in shaping phytoplankton assemblages under our disturbance regimes, followed by the ability to compete for phosphorus.

Smith, S. Lan (TALK, SESSION 5)

Kai Wirtz, Sandip Mandal, Hidekatsu Yamazaki

Trait-based modeling of phytoplankton under realistic sub-scale variability

Improved models have recently been developed of flexible physiology and adaptive changes in eco-physiological traits and trait diversity. Like nearly all theoretical descriptions and models of plankton dynamics, these trait-based models are still formulated at the macroscopic level, assuming uniform micro-scale distributions of organisms and their traits. However, recent observations have revealed that particles and plankton are in general distributed intermittently in aquatic environments, as aggregates at the ?m- to cm-scale, which are often further organized into layers at the meter-scale and thinner. This micro-scale variability and structure of the aquatic environment, by controlling the availability of resources for plankton as well as their predator-prey interactions, must have shaped the trait distributions of plankton species. It must therefore also play roles in determining the response of plankton to changing environmental conditions. We apply a moment-closure representation of sub-scale variability to explore how sub-scale variability in the spatio-temporal distribution of plankton impacts the success of plankton having different trait values. Preliminary results with a simple phytoplankton functional type model show that sub-scale variability can impact model results at the macro-scale. We plan to extend this work to explore how sub-scale variability impacts the results of size-scaled models of phytoplankton communities.

Sosik, Heidi (TALK, SESSION 1)

Plankton traits from flow cytometry and imaging-in-flow cytometry

Flow cytometry is a powerful approach for rapidly and quantitatively characterizing large numbers of diverse plankton cells. Especially when combined with cell imaging approaches and when implemented in continuous automated sampling modes, these techniques can provide unprecedented information about phytoplankton traits ranging from cell size, pigmentation, and morphology to population division rates and community composition indices. I will provide a brief summary of these advantages, identify some on-going interpretation challenges, and showcase examples where these types of observations have been used to reveal patterns of short-term (days to event-scales) change in physiology and long term (seasonal to interannual) change in community structure. The examples will highlight observations from multi-year deployments of autonomous submersible flow cytometers (FlowCytobot and Imaging FlowCytobot) at the Martha's Vineyard Coastal Observatory, a cabled facility in northeast US continental shelf waters. The results document strong seasonality in community structure, important event-to-seasonal scale changes in physiology and ecological interactions, and multi-scale variability linked with climate-related environmental properties.

Stamieszkin, Karen (TALK, SESSION 4)

Andrew Pershing

Changes in North Atlantic copepod community size structure and fecal pellet carbon flux over 55 years

The diminutive copepod can play an important role in the vertical export of oceanic carbon due to its ubiquitous distribution and great abundance. Copepods feed on relatively small prey, and produce larger, sinking fecal pellets, the sizes of which are proportionate to the copepods' bodies. Pellet size in part determines whether they will be sequestered at depth, or be remineralized before reaching the "sequestration depth." A copepod's relative size is a result of its species and the temperature at which it grew. Warmer ocean regions support higher ratios of small to large copepod species and warmer temperatures increase individual growth rates, resulting in smaller-sized copepods at age. Therefore, size is a measureable trait that can be used to track the biological and biogeographical consequences of changing ocean temperatures. We use 55 years of Continuous Plankton Recorder copepod abundances, from the North Atlantic Ocean, to examine change in copepod community size composition over time. We use this size information in a fecal pellet carbon model, to reveal the impact of changing ocean conditions on fecal pellet carbon flux, a variable component of the biological carbon pump. This model addresses part of a climate-biogeochemical feedback loop, using size as a master trait.

Talmy, David (TALK, SESSION 2)

Follows, MJ

The influence of viral reproduction strategies on marine microbial community dynamics

Published observations of bacterial communities in the Mediterranean and Baltic seas reveal a shift from lysogenic, to predominately lytic infection from oligotrophic to eutrophic environments. We explore the underlying dynamics using an ecosystem model in which viruses with a range of traits compete for host resources. Competition is determined by one of three infection strategies: lysogenic infection, in which prophage is reproduced over multiple cell cycles; lytic infection, in which the host is lysed before cell division; and temperate infection, in which the host is able to switch between lytic and lysogenic strategies according to a prescribed environmental trigger. Consistent with the observations, the model predicts that in steady state, oligotrophic environments where resource competition determines survival, lysogenic strains are selected. In contrast, virulent strains are found to be optimal in permanently productive, eutrophic environments. Temperate strains dominate when resource supply is characterized with 'boom and bust' dynamics. In boom and bust regimes, the ability to switch back and forth between different strategies enables temperate phage to enhance average virus mediated host mortality, which may enhance viral mediated nutrient recycling by several orders of magnitude.

Taniguchi, Darcy (POSTER 50, SESSION 4)

Michael J. Follows, Susanne Menden-Deuer

How top-down effects influence preadator:prey ratios and planktonic community diversity in a size-structured model of phyto- and microzooplankton

In this trait-based modeling study, we examine how incorporating fundamental characteristics involving energy expenditure and energy gain among microzooplankton affect the planktonic trophic dynamics and community structure. In particular, microzooplankton are differentiated by their grazing rate, size, motility, and respiration rate. Among these traits, microzooplankton trade an ability to swim faster and encounter more food with an increased respiratory and mortality loss. While current models generally assume that planktonic predators typically consume prey 1/10 their size, our analyses suggest prey choice may be more variable and can depend on indirect interactions with other grazers. Interactions leading to a wider prey selection lead to increased prey size diversity. We will discuss the implications of this trait-based model for planktonic community structure and biogeochemical cycling in the context of an ocean model.

Thomas, Mridul (POSTER 51, SESSION 2)

Colin T. Kremer, Elena Litchman

Tropical convergence, temperate divergence: evolutionary inferences from the biogeography of phytoplankton temperature traits

Forecasting how phytoplankton communities will re-organize as a result of changing temperatures is a major challenge for ocean science. A primary obstacle is our lack of knowledge about the evolutionary constraints and trade-offs associated with adapting to a new temperature regime. Using the largest assembled dataset of phytoplankton temperature traits, we identify biogeographical patterns that shed light on these evolutionary questions. We show that species are adapted to their local temperatures, but that functional groups exhibit important differences in their trait-latitude relationships, reflecting differing evolutionary constraints. Optimum temperature, critical maximum and critical minimum temperature of all functional groups are very similar in tropical waters (where temperature variation is minimal), but are highly divergent at temperate and polar latitudes. Crucially, this suggests that diatoms are capable of adapting to higher temperatures than previously believed. We believe that this divergence in traits at temperate latitudes reflects temporal niche partitioning ultimately caused by differences in nutrient or light response between functional groups.

Törnroos, Anna (POSTER 52, SESSION 6)

Describing key traits and trade-offs of marine benthos: towards a mechanistic trait-based approach

Marine benthic organisms (> 0.3 mm in size) constitute an abundant life form occupying one of the largest habitats on earth, the soft sediments covering roughly 70 % of the seafloor. They live in or on the sediment and exhibit an overwhelming diversity in ecological strategies. They have major effects on the function and services of marine ecosystem by occupying a key link between primary producers at the bottom of marine food-webs, and commercially exploited fish populations at the top. Despite a long history of empirical studies and recent attempts to prescribe structure and function by functional group classifications, a mechanistic understanding of how benthic organisms behave and interact with their immediate environment, described in mathematical models, does not exist. Here we take the first step towards developing such a framework for marine benthos and describe key traits in feeding, growth, reproduction and survival and formulate the main trade-offs. Our study encompasses the major taxonomic groups of soft-bottom dwelling fauna: bivalves, gastropods, crustaceans and polychaetes. Extending the trait-based framework, accepted and well developed for terrestrial plants and plankton, to marine benthos will advance the transformation of this descriptive ecological field into a predictive one.

Våge, Selina (TALK, SESSION 6)

Bernadette Pree, T. Frede Thingstad

Combining internal and external pelagic prokaryote community control links biodiversity to ecosystem function

Studies of pelagic heterotrophic prokaryotes typically use either a “black box” approach with focus on how this community interacts with its trophic neighbors in the microbial food web; or they try to resolve the internal structure of this community. Understanding how phenomena at these two levels of description interact, remains, however, a major challenge. We here combine a recently published model for host-virus interactions with a previously published "minimum" model for trophic interactions between plankton functional types in the photic zone food web. This allows us to link controls external to the community, such as nutrient competition from phytoplankton and grazing from microzooplankton, to internal controls such as the balance between competition and viral defense and associated trade-offs in species and strains. The result is a unified mechanistic description, which links biodiversity to ecosystem function and molecular mechanisms to trophodynamics. We illustrate this by analyzing how ciliate abundance and supply of organic substrates interact with cost of resistance to viral lysis in regulating structure, both within the community of heterotrophic prokaryotes and in the microzooplankton grazing chain.

van der Linden, Pieter (POSTER 53, SESSION 2)

A. Marchini, M. Dolbeth, J. Patrício, H. Veríssimo and J.C. Marques

The performance of trait-based indices in an estuarine environment

The performance of several indices of benthic functioning based on biological traits of estuarine macro-invertebrates was tested in the lower Mondego estuary (Portugal), whose two arms exhibit different levels of environmental disturbance related to hydromorphology. The results showed that not all of the tested indices responded to disturbance, providing complementary information about the functioning of benthic communities in relation to the prevailing environmental conditions. Nonetheless, some indices were more informative than others. We argue that the Community weighted mean trait (CWM) in combination with the newly developed SR-FRED index provided the best overall picture of how the benthic communities might have been affected by a different level of disturbance. This study also showed that some indices should be used with caution when dealing with communities with few and dominant species, as in estuarine environments.

Van Oostende, Nicolas (POSTER 54, SESSION 7)

J. P. Dunne, S. E. Fawcett, and B. B. Ward

Phytoplankton succession explains size partitioning of new production during upwelling blooms

Large and chain-forming diatoms typically dominate the phytoplankton biomass after initiation of coastal upwelling. Their ability to accelerate and maintain elevated nitrate uptake rates has been proposed to explain the dominance of diatoms over all other phytoplankton groups. Moreover, the observed delay in biomass accumulation following nitrate supply after initiation of upwelling events has been hypothesized to result from changes in the diatom community structure or physiological acclimation. To investigate these mechanisms, we used both numerical modelling and experimental incubations that reproduced the characteristic succession in phytoplankton community composition and size structure from small to large species. The TOPAZ model best reproduced the bloom development and nutrient consumption in the mesocosm when i) using group-specific maximum growth rates that were lower than the original theoretical growth rates, and secondarily, when ii) nutrient acclimation ability was included. These factors reflect the differences in taxonomic composition of each size group, the averaging effect of amalgamating closely related species, and the sub-optimal growth of the phytoplankton community as a whole during transient environmental change. These aspects of phytoplankton physiology seem to be critical in determining differential success of small and large phytoplankton community in response to nitrate supply during upwelling.

Weigel, Benjamin (POSTER 55, SESSION 2,7)

Thorsten Blenckner, Erik Bonsdorff

Maintained functional complexity despite long-term contrasting community developments within a low diverse coastal system

Changing environmental conditions, largely forced by climatic drivers, influence community structures of ecosystems on a global scale. Ecological studies based on time series often investigate community changes based on species abundance or biomass but rarely expose the consequential functional aspects of such changes. Benthic fauna is a key actor in a multitude of marine ecosystem processes and a paramount food resource for coastal fish. The broad spectrum of phenotypic variation among zoobenthos species can thus influence the quality of its ecosystem service. Here we study a coastal system in the Baltic Sea, where long-term changes in zoobenthic communities (composition and biomass) have been observed over 40 years, with contrasting developments in sheltered and exposed areas, forced by system specific environmental drivers. Although contrasting spatiotemporal developments, the functional diversity (abundance weighted functional dispersion) of zoobenthic communities followed similar trends towards high and relatively stable values in both sheltered and exposed habitats. This pattern seemed to be promoted through the establishment of an invasive polychaete to existing species complex. Shifts in species identity and biomass may therefore not necessarily imply changes in the system's functional complexity, ensuring a certain resilience to environmental change, but may still lead to altered functionality of communities.

Wilken, Susanne (POSTER 56, SESSION 6)

Margarida PM Soares, Pablo Urrutia-Cordero, Jens Ratcovich, Ellen Van Donk, Mattias Ekvall, Suzanne Naus-Wiezer, Jef Huisman, Lars-Anders Hansson

Maintained functional complexity despite long-term contrasting community developments within a low diverse coastal system

Phytoplankton are well recognized for their role as primary producers in the global carbon cycle, but more recently, pigmented flagellates have also been identified as dominant bacterivores in aquatic ecosystems. While the acquisition of inorganic resources by phytoplankton has been studied for decades, the heterotrophic component of their nutrition is much less understood. The relative importance of autotrophy versus heterotrophy varies among strains and furthermore depends on environmental factors as some mixotrophs exhibit high phenotypic plasticity with respect to their nutrition. Physiological experiments with a mixotrophic chrysophyte showed a shift in the nutritional strategy towards heterotrophy with increasing temperatures. A similar shift could be observed in a natural phytoplankton community from a temperate lake subjected to a climate change scenario. Pigmented flagellates showed increasing rates of prey ingestion resulting in a substantial contribution of bacterivory to overall phytoplankton carbon acquisition under future climate conditions. Such shifts in phytoplankton nutrition will impact biogeochemical cycles and highlight the need to characterize the driving factors and trade-offs involved in controlling the nutritional strategies of mixotrophs.

Zakem, Emily (POSTER 57, SESSION 6,7)

M.J. Follows

Exploring a microbial ecosystem approach to modeling deep ocean biogeochemical cycles Though microbial respiration of organic matter in the deep ocean governs ocean and atmosphere biogeochemistry, it is not represented mechanistically in current global biogeochemical models. We seek approaches that are feasible for a global resolution, yet still reflect the enormous biodiversity of the deep microbial community and its associated metabolic pathways. We present a modeling framework grounded in thermodynamics and redox reaction stoichiometry that represents diverse microbial metabolisms explicitly. We describe a prokaryotic functional type with two parameters: a growth efficiency representing the chemistry underlying a bacterial metabolism, and a rate limitation given by the rate of uptake of each of the necessary substrates for that metabolism. We then apply this approach to answer questions about microbial ecology. Here, we resolve two dominant heterotrophic respiratory pathways- reduction of oxygen and nitrate- and associated microbial functional types. We combine these into an ecological model and a two-dimensional ocean circulation model to explore the organization, biogeochemistry, and ecology of oxygen minimum zones (OMZs). Intensified upwelling and lateral transport conspire to produce an oxygen minimum at mid-depth, populated by anaerobic denitrifiers. This modeling approach allows for the emergence of prokaryotic biogeography from competition of metabolisms.

Zhang, Lai (POSTER 58, SESSION 7)

Ken Haste Andersen, Martin Hartvig

Food web dynamics of climate change

In this ongoing project we aim to simulate the effects of climate change on both the demographic and the evolutionary properties of marine communities that are obtained by community assembly. Species in communities are characterized by three traits: body size, habitat trait, and optimal temperature trait. The body size governs species physiological rates, which are corrected by an environment temperature that increases extremely slowly. The habitat trait describes the interaction probability in the spatial direction, which together with the body size determines the interactions among different species. We assume each species has an optimal temperature that affects species reproductive efficiency.

When environment temperature is greater than a fixed range beyond the optimal temperature, efficiency is supposed to drop dramatically. We are interested in the climate change induced the frequency of extinctions and invasions, the resistance of closed communities to temperature increase, the role of system openness and species diversity in the responses of communities to climate change, and how warm-adapted species react to global warming.