

## **Greenocean workshop, 18-19 May 2022**

### **Building models fit to explore marine ecosystem stability under multiple stressors**

Ecole Normale Supérieure (ENS), 24 rue Lhomond, 75005 Paris  
Room E324, 'Salle Claude Froidevaux'

This workshop aims to exchange knowledge on the building blocks necessary to study marine ecosystem stability under multiple stressors. The workshop brings together theoretical ecologists, modelers and observationalists with knowledge on global marine ecosystem models, new observations and new computing methods including machine learning. The workshop aims to stimulate ideas and collaborations to better capture possible changes in ecosystems this century and beyond and their implications for climate. The workshop will focus on the following themes:

1. Linkages between surface ecosystems and sinking of organic carbon
2. Observing and modelling marine viruses
3. Understanding and modelling critical ecosystem pathways
4. Stability of marine ecosystems under multiple stressors

**Steering committee:** Corinne Le Quéré (UEA), Laurent Bopp (ENS), Lionel Guidi (LOV), Fabien Lombard (LOV), Marie-Fanny Racault (UEA).

## **Programme**

### **Wednesday 18 May**

9.00 Arrival, refreshments

9.15 Welcome – Laurent Bopp  
Goals of the workshop – Corinne Le Quéré

### **9.30 - 11.00 Linkages between surface ecosystems and sinking of organic carbon**

Co-chairs: Corinne Le Quéré, Nicolas Mayot

- Lionel Guidi (LOV) - *Key players of the gravitational carbon pump (8")*
- Hiroyuki Ogata (Kyoto University, remote) – *Viruses associated with the carbon export efficiency (8")*
- Stephanie Henson (NOC) – *Ecosystem controls on export efficiency (8")*
- Erik Buitenhuis (UEA, remote) – *Sinking flux as a function of latitude (8")*
- Louis Legendre (LOV) – *Ocean Biological Carbon Pumps: Continuous Vertical Sequestration (CONVERSE) Approach (8")*
- Discussion (50")

11.00 - 11.30 Break

### **11.30 - 13.00 Linkages between surface ecosystems and sinking of organic carbon**

- Christine Klaas (AWI, remote) - *Southern Ocean export processes (8")*
- Rainer Kiko (LOV, remote) - *Zooplankton diel vertical migrations and carbon flux (8")*
- Fabien Lombard (LOV) – *The missing piece of the different flavours of gelatinous plankton : are they important, where they are and are they connected to carbon fluxes? (8")*

- Corentin Clerc (ENS) - *Contribution of filter-feeding gelatinous macrozooplankton to global marine biogeochemistry: a model study (8")*
- Alban Planchat (ENS) - *From organic to inorganic matter export to understand improvements from CMIP5 to CMIP6 (8")*
- Discussion (50")

13.00 - 14.30 Lunch

14.30 - 15.45 **Observing and modelling marine viruses**

Co-chairs: Lionel Guidi, Marie-Fanny Racault

**Part I observations**

- Anne-Claire Baudoux (CNRS Roscoff) - *Overlooked viral reactions in DOM cycling (8")*
- Lorna Richardson (EMBL-EBI) - *Microbiome data: MGnify application tool (8")*
- Matthew Sullivan (Ohio University) - *Viromics, Virocells, and Eco-Systems Biology approaches to understand (and tune?) the ocean biological carbon pump (8")*
- Sakina-Dorothee Ayata (ENS, remote) – *Linking plankton diversity to marine ecosystem functioning through a trait-based approach: from observations to models (8")*
- Discussion (40")

15.45-16.15 Break

16.15-17.30 **Observing and modelling marine viruses**

**Part II modelling**

- Marie-Fanny Racault (UEA) - *Viruses in a global ocean ecosystem model (8")*
- David Demory (Georgia Tech) - *Modeling the impact of environmental stressors on virus-phytoplankton dynamics at different scales: A case study on temperature (8")*
- David Talmy (Tennessee University) - *A model of host-virus population dynamics reveals underlying controls on material transfer (8")*
- Discussion (50")

19.00 Conference dinner: Le Petit Bar, 57 bd Saint Marcel 75013 Paris

**Thursday 19 May**

9.00 - 10.30 **Understanding and modelling critical ecosystem pathways**

Co-chairs: Fabien Lombard, Rebecca Wright

- Damien Eveillard (University of Nantes) - *Modelling framework that simulates plankton behaviours from genome-scale metabolic model (8")*
- Rebecca Wright (UEA) – *Towards modelling the complexity of zooplankton life cycles and marine snow (8")*
- Olivier Aumont (IRD) – *Multi-lability of DOC and role for carbon cycle (8")*
- Anna Sommer (UEA) – *POC and GOC reconstruction using Machine Learning (8")*
- Discussion (50")

10.30 - 11.00 Break

11.00 - 12.30 **Understanding and modelling critical ecosystem pathways** (cntd)

- Joanna Guest (UEA) – *Recent trends in phenology and implications for carbon export* (8")
- Lester Kwiatkowski (ENS) – *Augmented variability of the ocean CO<sub>2</sub> system under climate change in a model that resolves diurnal cycles of net primary production* (8")
- Chris Bowler (ENS) - *linking remote sensing data with genomic data for photosynthesis related measurements* (8")
- Samuel Chaffron (Nantes) – *Community network models to reveal global-scale plankton systems ecology* (8")
- Discussion (50")

12.30 - 13.30 Lunch

13.30 - 15.30 **Stability of marine ecosystems under multiple stressors**

Co-chairs: Corinne Le Quéré, Stephanie Henson

- Laurent Bopp (ENS) – *Diazotrophy and projected export and NPP* (8")
- Boris Sauterey (ENS) – *Modelling the adaptive response of phytoplankton communities to environmental stressors, why and how? The specific case of temperature* (8")
- Meike Vogt (ETH) – *Modelling the impact of compound extreme events on marine organisms* (8")
- B.B. Cael (NOC) - *Abrupt shifts in plankton communities* (8")
- Discussion (40")

15.30-16.00 Discussion & next steps

**Participants:**

Steering committee

1. Corinne Le Quéré (UEA, in person)
2. Laurent Bopp (ENS, in person)
3. Lionel Guidi (LOV, in person)
4. Fabien Lombard (LOV, in person)
5. Marie-Fanny Racault (UEA, in person)

Linkages between surface ecosystems and sinking of organic carbon

6. Erik Buitenhuis (UEA, remote)
7. B.B. Cael (NOC, in person)
8. Christine Klaas (AWI, remote)
9. Anna Sommer (UEA, in person)
10. Hiroyuki Ogata (Kyoto University, remote)
11. Dieter Wolf-Gladrow (AWI, remote)
12. Rainer Kiko (LOV, remote)
13. Louis Legendre (LOV, in person)
14. Corentin Clerc (ENS, in person)
15. Alban Planchat (ENS, in person)
16. Florian Ricour (LOV)

Observing and modelling marine viruses

17. David Demory (Georgia Tech, in person)
18. Anne-Claire Baudoux (CNRS – Roscoff, in person)
19. Lorna Richardson (EMBL-EBI, in person)
20. David Talmy (Tennessee University, in person)
21. Damien Eveillard (University of Nantes, in person from Wed mid-day)
22. Matthew Sullivan (Ohio University, in person)

Understanding and modelling critical ecosystem pathways

23. Olivier Aumont (IRD, in person)
24. Rebecca Wright (UEA, in person)
25. Lester Kwiatkowski (ENS, in person)
26. Samuel Chaffron (Nantes, in person)
27. Joanna Guest (UEA, in person)
28. Nicolas Mayot (UEA, in person)
29. David Willis (UEA, in person)
30. Chris Bowler (ENS, in person)
31. Sakina-Dorothee Ayata (ENS, remote)

Stability of marine ecosystems under multiple stressors

32. Meike Vogt (ETH, in person)
33. Stephanie Henson (NOC, in person)
34. Tereza Jarníková (UEA, remote)
35. Boris Sauterey (ENS)
36. Jessica Luo (NOAA, remote)
37. Mathilde Dugenne (LOV, remote)
38. Margaux Perhirin (LOCEAN, in person)
39. Julie Lemoine (LOCEAN, in person)

## Minutes from the Greenocean workshop, for participants

18-19 May 2022

by M-F Racault, BB Cael, L Kwiatkowski, N Mayot, M Vogt and R Wright

### Wednesday 18 May

#### 9.30 - 11.00 Linkages between surface ecosystems and sinking of organic carbon

**Lionel Guidi: Key players of the gravitational carbon pump:** New advances using omics to investigate complexities at the surface and from video images for what happens at depth (Boyd 2019, Henson 2022, Benoitson 2017); further new evidence on the influence of viruses and sinking carbon (Kaneko et al. 2021); links between the euphotic layer to the deep ocean through predicting POC fluxes from knowledge on the community assemblages found in the bottom of the ocean (Cordier et al., Sci Adv 2022). *Moving from who to how:* e.g., Dunkin et al., 2021, Trudnowska et al Nat Com. 2021 looked at the shape of particles in the water column and with the Eco Taxa Eco Parts webtools for images database. Next step is to improve the links between surface and deep ocean carbon fluxes by looking at the individual particles. Importance of sampling timescale: e.g., deploying sediment traps that look simultaneously at genomic data and quantity of particles caught in traps, especially in regions where there are successions in phytoplankton populations. Discussion/ challenges: getting out of correlation to causal effects; make use of vertical time-series from BGC Argo; investigate minimum number of groups/ PFTs/ classes that are needed using genomic data and consider information from metabolic network of the communities; links emerging between diversity and carbon export and DOC, so useful to get to the complexities but with functional diversity the link was not direct.

**Hiroyuki Ogata: Viruses associated with the Carbon export efficiency:** Overview of marine viruses and their ecological & biogeochemical roles: e.g. Sullivan et al 2017, Guidi et al 2016, Yamada et al 2018, Laber et al 2018, Sheyn et al 2018. Key examples with Eukaryotic viruses: e.g., Nuclocyotoviricota, e.g., Blanc-Mathieu et al 2021, Ayleward et al Plos 2021, Endo et al 2020. Positive correlation between viral composition and carbon export efficiency. Discussion/ challenges: viruses associated with large sinking particles may be different to those of smaller particles; ongoing measurements of microbial communities in marine snow (large particles) and analyses of potential changes in viral activity between surface and mesopelagic?

**Stephanie Henson: Ecosystem controls on export efficiency:** very large uncertainty in modelled export flux and its response and feedback to climate change: Henson et al. 2022 synthesis of processes driving +, - or uncertain climate feedbacks in models, and need for obs on large spatial and temporal scales, computationally tractable, relevant on centennial, global scale. Main drivers in models for modern-export flux: particle fragmentation and zooplankton vertical, and for future projection: phyto size spectra. New research Henson et al GBC 2019 on when/where/under what conditions extreme occurs: high exp ratio and low production mostly in SO, high productivity but low export ratio in Eq Pacific. E-ratio highest associated with more plankton and changes in bacteria, but when more decoupling then possibly associated with more remineralisation. Discussion/ challenges: possibly fragmentation of material to be better included; changes in bio carbon pump in relation to oxygen; further investigation of role of microzooplankton: few obs are available, UVPs start

at 100µm; not much has been looked at in terms of trophic amplification; Action: potential MAREDAT 2 project.

**Erik Buitenhuis: Sinking flux as a function of latitude:** estimate sinking speed from sediment trap fluxes and UVP data. sinking speed decreases with latitude for the different size classes (which increase with latitude); CaCO<sub>3</sub> dominates export in carbon vs opal SiO<sub>2</sub>. Discussion/ challenges: when sinking speed converted to total export, the relationship remain negative despite latitudinal increase in size classes.

**Louis Legendre: CONVERSE:** Overview of DIC<sub>bio</sub> distribution in the ocean depending on depth, location and under six sequestration carbon pump mechanisms of Boyd et al., 2019: gravitational sequestration of DIC takes place over the whole water column and sequestration at 2000m is much smaller in Nowicki et al., 2022. Discussion/ challenges: Some DIC findings opposite to existing literature in the SO; very large range in export values 2-10PgC, and from inverse calculations (or from nutrients gradients: updates on this?) quite far; still large step for model intercomparison, requiring integrated / international piece of work.

#### 11.30 - 13.00 **Linkages between surface ecosystems and sinking of organic carbon**

**Christine Klaas: Southern Ocean export processes:** Deep sea sediment traps show a relationship between POC and CaCO<sub>3</sub> flux and lithogenic flux. Two relationships are apparent for opal flux; one relationship for iron deficient (low POC fluxes), one for iron saturated (high POC saturated). Discussion: around why deep sea relationships for POC are apparent despite the complexity of the system. Work is focussed on carbon sink south of 44S, where most of the carbon flux is found to come from faecal pellets. A South Georgia cruise is planned to look at diatoms - iron impact on diatom life cycles dominate flux in high iron areas, while in the iron deficient areas zooplankton faecal pellets dominate flux.

**Fabien Lombard: The missing piece of the different flavours of gelatinous plankton : are they important, where they are and are they connected to carbon fluxes?** Tara Oceans results show gelatinous dominate mega-zooplankton class (>2cm), much more than krill, both for body wet weight and carbon biomass. Question of whether higher plankton diversity results in less carbon export because of more recycling? Three ecosystem states are apparent, based on who dominates the bloom (specifically diatom, protozooplankton, jellyfish) and the effect on the export. New papers with models showing gelatinous zooplankton contribute heavily to carbon flux: Ramondenc et al., 2020 showing some indications that associated carbon flux could be high - due to only one species of gelatinous); Negrete-Garcia et al., 2022; Luo et al., 2022; Everett et al., 2022; Heneghan et al., 2022.

**Corentin Clerc: Contribution of filter-feeding gelatinous macrozooplankton to global marine biogeochemistry: a model study:** Study focuses on large pelagic tunicates (doliids, pyrosoma, salpida). A NEMO-PISCES model with added gelatinous zooplankton, including explicit carcasses & faecal pellets. Findings include; filter feeding gel (FFG) dominate macrozop in low productive oligotrophic regions playing a key role in POC export; with high export ratio there is a high transfer efficiency due to fast sinking speed; the model doesn't represent FFG distribution shown in other studies (i.e. Heneghan et al., 2022) where

salps are negatively correlated with chlorophyll/nutrients. Preliminary model results show increasing FFG dominating in low oligotrophic zones with climate change.

**Alban Planchat: From organic to inorganic matter export to understand improvements from CMIP5 to CMIP6:** From CMIP5 to CMIP6 particulate inorganic carbon export increases as POC export decreases. None of the BGC models represent explicit calcite vs aragonite producers. There is high inter-ESM variability in PIC export patterns. The alkalinity vertical profile in CMIP6 is closer to observations, driving the PIC export improvement. This relationship overpasses the influence of the modelling scheme for  $\text{CaCO}_3$  - different pathways & representation in models, but relationship holds. Carbonate pump enhancement drives reduction in vertical alkalinity & DIC bias. Improved representation of carbonate pump in CMIP6 has reduced both surface and vertical biases. Discussion: What improvements in the modelling of the carbonate pump is unclear - better sediment processes? Higher resolution? Tuning?

#### 14.30 - 15.45 **Observing and modelling marine viruses**

**Matt Sullivan: Viromics, virocells and ecosystems biology with links to the carbon pump** - 200'000 virus species catalogued from Tara according to genome-based taxonomy, with unexpected genes and an important role in carbon fluxes (explain >80% of export fluxes in correlative analysis). Biogeographic patterns and drivers mapped, ready to be used in model evaluation. About  $\frac{1}{3}$  of all phyto/bacterioplankton cells infected with viruses (virocells), with completely different metabolic footprint. Metagenomic genes also mapped (Tian et al., in prep.). 1.3rd of hosts of DNA viruses can be identified, more difficult with RNA viruses. Discussion: role of viruses in models as (a) source of mortality and (b) modifier of the phenotype of their hosts.

**Lorna Richardson: Marine metagenomic data in MGnify** - MGnify is a free to use resource for analysis, visualisation and discovery of metagenomic, metatranscriptomic, amplicon and assembly datasets. MGnify accesses data stored at ENA, assembles data and offers multiple pathways of data analysis. It has a bioinformatic pipeline for the determination of MAGs from genomes, and now contains data from AtlantECO, OSD, Malaspina, Tara and GEOTRACES, among others, thus harboring huge potential for 'omics data across cruises and efforts. Within the MGNify framework, VIRify will be released later in 2022, which is a resource for the detection, annotation and classification of viral content and genomes. Discussion/ challenges: relative abundances across samples but not absolute values. Ongoing efforts for inter-calibration and inter-comparison of MAGs et al across methods and institutions to assess uncertainty associated with chosen bioinformatic pipeline.

**Anne-Claire Baudoux: Viral reactions in marine DOM cycling** Viruses are an underexplored source of DOM since they use EPS depolymerases to infect hosts. DOM produced by phyto/zooplankton is usually degraded by bacteria, but new data shows that viruses can also take part in its degradation. Viral mediated DOM degradation affects the host cells and can lead to reduced bacterial growth due to changes in the chemical composition of DOM and a reduced bioavailability of the products.  $\frac{2}{3}$  of viruses studied have been documented to possess unique genes coding for these depolymerases. These

viruses and their genes are catalogued in the Ocean Gene Atlas. Discussion: possibly study substrate diversity.

**Sakina-Dorothee Ayata: Link between plankton functional diversity and marine ecosystem functioning using a trait-based approach** - Traits characterising zooplankton functional diversity and fitness (related to survival, growth and reproduction) were analysed in e.g. Arctic copepods based on imaging information (opacity, size, shape, elongation, redness,..). Traits were shown to vary with environmental conditions and distance from the coast. Machine learning methods have successfully been used to extract traits from imaging data. Master traits to be included in models should include vertical migration, size diversity and activity, as well as life stage characteristics. Traits identified in imaging can be matched against specific information from metagenomics where both have been assessed. Traits and trait distributions are particularly suitable for inclusion in marine ecosystem models, since they are associated with natural variability in the communities and populations under study.

#### 16.15-17.30 **Observing and modelling marine viruses**

**Marie-Fanny Racault:** Introducing a virus component in a global multi-plankton functional types (PFTs) ecosystem mode PlankTOM. The model currently has 12 PFTs, 4 nutrients, and Calcite, DOC, POC and very large particles GOC. First step: model interaction between the picophytoplankton group and viruses. Processes included: viral adsorption, burst size, probability of infection, and viral shunt/shuttle. So far only include lytic viruses, not lysogeny (have dormant stage). Presented some initial runs of the PlankTOM13-with virus model for the global oceans. Key parameters for which observations are needed: virus Carbon content, burst size, abs./inf. probability, decay rates. Potential observations from omics data: presence/absence, relative abundance, activity/expression, networks, environment. Further data are needed for model validation, some data on abundance from the literature at stations, e.g. HOT, BATS..., in cruises in the Southern Ocean: E-SAZ/Weddell/N. Pac. & others. In omics RNA viruses are tricky but necessary parameters are available from DNA viruses. Discussion/ Challenges/ Action: strong interest to work with experimentalists and observationalists to build a global database on key parameters and abundance of viruses in the global oceans. Exchanged MAREDAT spreadsheet template with Meike Vogt.

**David Talmy:** Viral influence on ecosystem Carbon/nutrient pathways. Model host-virus population dynamics. Approach is to fit to lab data and look for patterns. Discuss about challenges to avoid time delay with infection timescale. Found a nice feature showing that each parameter has a unique influence on data, including the number of infection states. No especially clear patterns emerge of trade-offs or relationships with covariates. Relationships occur when scaling in Carbon units. Cost of being large, but higher transfer efficiency

**David Demory:** temperature influence on virus-phytoplankton interactions: cellular interactions to communities. Can estimate life history traits and viral fitness as a function of temperature: production vs degradation. Show that temperature affects absorption, latent period, burst size. Other influencing factors include light. Temperature shown as an important driver of viral biogeography in global observations. But so far they did not find a strong link between host and virus biogeography.



**Thursday 19 May**

9.00 - 10.30 **Understanding and modelling critical ecosystem pathways**

**Becci Wright: Modelling the complexity of zooplankton life cycles and marine snow.**

We should first focus on targeted species/groups for which lots of information are available, eg. Krill in the Southern Ocean, including the influence of environmental variables on their life cycles. However, we should be careful because it will increase the computational time.

**Olivier Aumont: Introducing a continuum of lability of DOC in global ocean**

**biogeochemistry models** improves the oceanic DOC distribution. It has a major influence at river mouths, which can help to adjust the river inputs of DOC into the ocean. It could also help to improve the bacteria distribution by changing their interaction with the DOC pool.

**Anna Sommers: Reconstruction of small and large particles based on machine learning.** Improve the parametrisation of sinking particles in global ecosystem models.

Discussion: 1) how much the relationships between the drivers used to reconstructed particle distributions are model specific. And 2) how the distribution of particles at depth in plankTOM could be improved by introducing new ecosystem feedbacks.

**Damien Eveillard: Use of metabolic networks**, with the opportunity that they could be associated with global ocean biogeochemistry models to get parameters which are changing based on the simulated environment. This could increase the complexity in models without increasing the computational time, because it is like using “look up tables” for parameters. The downside, not enough metabolic networks are available. We need more of them, and they need to be more generic (e.g. at the scale of a community).

11.00 - 12.30 **Understanding and modelling critical ecosystem pathways (cntd)**

**Joe Guest: Trends in phytoplankton phenology and implications for C exp:** Estimated satellite trends in phytoplankton phenology metrics (timing of initiation, peak, termination, duration, max bloom amplitude) in the global oceans based on 2-yr climatologies over the last 2 decades and using the Sen Slope estimator to calculate trends (Salgado et al., 2019). Significant changes are found across most basin scales with some variations in the direction of the changes. Further investigations are ongoing to identify the main drivers (both physical e.g., changes in SST, and biological, e.g. top-down vs bottom-up control). Discussion: look at the possibility to use UVP data to investigate the relationship between phenology and export – taking into account the quantitative and qualitative information of the material that is exported.

**Lester Kwiatkowski: Augmented variability in the ocean CO<sub>2</sub> system under a Climate Change in a model that resolves diurnal cycles of NPP:**

For temperature, the diurnal variations are very small compared to changes in the seasonal cycles, however for CO<sub>2</sub>, there is very large variability in the diurnal cycle. Estimated the influence of changes in diurnal cycle on pCO<sub>2</sub> variability to ~3% increase under high emission scenarios by 2100 (with sensitivity in pCO<sub>2</sub> variability associated to temperature). In contrast, increase in the diurnal amplitude of pCO<sub>2</sub> and H<sup>+</sup> estimated to change to +226 and +170% respectively. Further analyses on extremes: 1 in 100 day extreme pCO<sub>2</sub> change becomes 1 in a 2 day

event by 2100. Discussion: what matters for organisms: absolute CO<sub>2</sub> system thresholds (diurnal cycle insignificant) vs rate of changes of the CO<sub>2</sub> system (diurnal cycle is a major driver). What about the coastal ocean?

**Chris Bowler: Linking remote sensing data with genomic data for photosynthesis related measurements**: bridging the gap between satellite data and in situ data (genomic and HPLC). In genomic data use psbO marker gene to quantify phototrophic organisms which allows to put all Eukaryotes and Prokaryotes on the same map, and then go to taxon and size fraction and get psbO-derived phyto diversity and biogeography (Hourany et al., 2020, Puissant et al., 2021). Further improved the algorithms using psbO and HPLC data to correct in terms of organisms that are present the biodiversity of phytoplankton and their photosynthetic activity/ ecosystem function (with biodiversity estimated using Shannon index BEF). Estimated relationship between PP and biodiversity and found emergent property showing for some regions more diversity associated with more PP. Also explored iron limitation depending on presence/absence of certain iron-genes and estimated biogeography of phyto-iron nutritional status up to the taxonomic level (e.g., diatoms / dinoflagellates). Discussion: potential to use emergent properties to improve PP models, and the estimations of vertical distribution variability.

**Samuel Chaffron: Community network models to reveal global-scale plankton systems ecology** and investigate influence of anthropogenic Climate Change: what are the mechanisms; co-presence and mutual exclusion (based on presence/absence of OTUs or genomes / species). Results in Chaffron et al. 2021 Sci Adv show distinct vulnerabilities of plankton communities to environmental changes, and use topological metrics to assess the robustness in the responses to the stress in communities (polar, tropical...), as well as assess sensibility to nutrients availability. New database of marine bacterial and archeal genomes; Giordano et al., in prep use global ocean genome abundance and activity profiling to infer co-activity networks and identify which genomes are partnering. No apparent overlap between co-activity and co-abundance of co-active environmental genomes to be functionally closer than just random. Next, they reconstructed metabolic maps between these genomes, which showed that co-active genomes display higher metabolic interaction potential and identified the potentially exchanged metabolites. Discussion/challenges: to integrate omics-based ecology with climate models and construct maps of association between genomes. Also use these data to infer biological traits (e.g., growth rates) to better constraints / parametrise models.

### 13.30 - 15.30 **Stability of marine ecosystems under multiple stressors**

**Laurent Bopp: Diazotrophy and projected export and NPP**: NPP projection uncertainties have increased in CMIP6. PISCES model partly responsible. Offline PISCES simulations show that NPP projections in Redfieldian models can be highly sensitive to the parameterization of implicit diazotrophy and specifically assumptions about the unresolved DOP (which is accessible to diazotrophs). More complex PISCES quota model (which resolve the DOP pool) suggest that IPSL-CM5 projections of NPP decline are more likely than IPSL-CM6 projections of NPP increase. Despite NPP uncertainty, projections of phyto biomass are consistent across model versions.

**Boris Sauterey: Modelling the adaptive response of phytoplankton communities to environmental stressors, why and how? The specific case of temperature:**

The potential role of adaptive/evolutionary thermal responses of max phytoplankton growth rates are explored in preliminary work using a 1D Bermuda version of MITGCM. The role of genetic mutation (& evolution) in response to temperature variability is explored with results compared to 2 end member simulations- a darwinian dummy population where there is no adaptation and an “Eppley” population where there is effectively perfect adaptation. The divergence between the Eppley simulation and the mutation/evolution simulations is minimal for annual mean temperature changes but is enhanced as the seasonality of T variability increases.

**Meike Vogt: Modelling compound extreme events.** An IBM of pteropod damage functions in the California Current was presented. The model allows separation of the influence of DVM/extremes and mean state change on pteropod impacts. Open questions: What is extreme? Should we use absolute extremes? How do we choose reference periods? Should we deseasonalize? How do we combine variables? Should we use derived variables e.g. habitability indices? Can we use OMICs data to inform organism stress indicators?

**B.B. Cael: Abrupt shifts in phyto communities in the Darwin model under RCP8.5.**

Abrupt shifts defined using trends and step functions. Showed simulations in the subtropics. Abrupt shifts in temp and nutrients do not predict abrupt phyto shifts. Instead in regions of low Si, small changes in the Si supply rate result in large shifts in diatom abundance which act to restructure the phyto community. No “critical slowing down” as might be associated with classical tipping points are observed in the system prior to abrupt phyto shifts.

15.30-16.00 **Discussion & next steps**

In the early 2010s, global ocean biogeochemistry models (GOBMs) switched from simple NPZD approaches to more sophisticated PFT configurations. Today, what are the next steps? During the GreenOcean workshop 2022, three main topics were discussed:

- Improving or going beyond PFT configurations: using metabolic network models, evolutionary models, new statistical approaches based on the upcoming MAREDAT2 atlas...
- Improving the vertical export of carbon in GOBMs: The vertical export process has a relatively simple parameterization in models. There are large and newly available datasets to improve its representation (e.g., in situ images, genetic approaches...), as well as components not included in models with potential significant influences on its magnitude and variability (e.g., biological life cycles, several DOM lability levels...)
- Modelling viruses: We are going from omics datasets to 0D models and to GOBMs.

Instead of adding PFTs and new tracers in models, we could add “ecological traits” that represent the required complexity, for example: the size spectrum in phytoplankton, zooplankton, and particle pools. A certain level of stochasticity could also be added into GOBMs, which will increase model complexity without adding computational time. However, the associated “model tuning” process is complex due to the number of unknowns and

already existing interactions in models. By adding new variables or PFTs, it could also mean less flexibility in models and the requirement of more computational power. In addition, do we have enough data to further validate these added variables and complexity in models?

Another way to work on model development will be to identify the new and promising datasets available and build new models that can take advantage of them. This implies a removal of the difficulties in the use of these observational datasets, as well as the identification of key processes that models need to simulate and the required observations for validation. A first step will be to assess what models are already doing well, or not, and which information modellers need from observational research groups. For this, essential metrics for model evaluation or emergent constraints are needed. For example, can we use simulated versus observed seasonal cycles and phenological indices? As a reminder, in the past, observations used to validate PFTs were patchy and the range of possible values for a given parameter was large.

Finally, if we want to develop a vast and new family of models, who will do that and how to manage it? A lot of AI approaches are available and used in ocean physics to represent complex processes (e.g. turbulence). Should the same be done with complex oceanic biogeochemistry processes? It might be the time for hybrid models for improving model parametrization. However, do we want black boxes in GOBMs? Instead, we could use AI to hasten the computational time of known processes that take long computational time. Moreover, we need to take advantage of the existing new computational methods and resources (e.g., newer, and faster computing languages).

All these methodological aspects were discussed during GreenOcean 2022. Scientific efforts are now also needed in the discussion of essential questions that GOBMs could respond to. For example:

- Do we need more complex GOBMs to evaluate the ocean carbon uptake over the next decades? Did the inclusion of PFTs and other biological aspects decrease uncertainties in oceanic carbon uptake? Looking at the variability between GOBMs (and GOBMs vs data-products) in the oceanic carbon uptake estimate: Are differences between GOBMs in their spatial resolutions, physical ocean models and/or atmospheric forcings more important than their differences in biological-chemical complexity?
- What is happening to the oceanic carbon exported into the ocean, in terms of carbon sequestration?
- Can GOBMs be used to evaluate marine ecosystem diversity, upper trophic levels, and deep habitats?
- Can GOBMs be used to evaluate proposed controversial methods, associated with the ocean, to reduce the projected global temperature change (following the Paris agreement)?
- On the topic of viruses: it appears important to introduce them in GOBMs and see if some new patterns are emerging. It could help in the identification of new ecological processes associated with viruses and trigger the need for new lab experiments. For this, we should use the available and growing global genomic datasets.