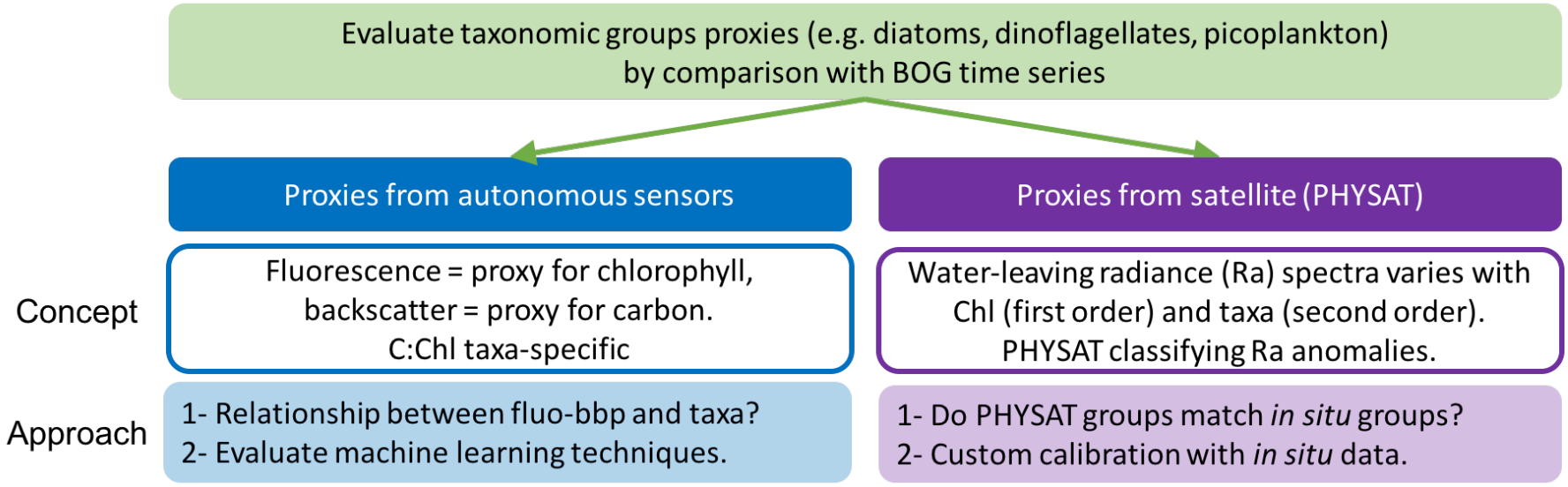
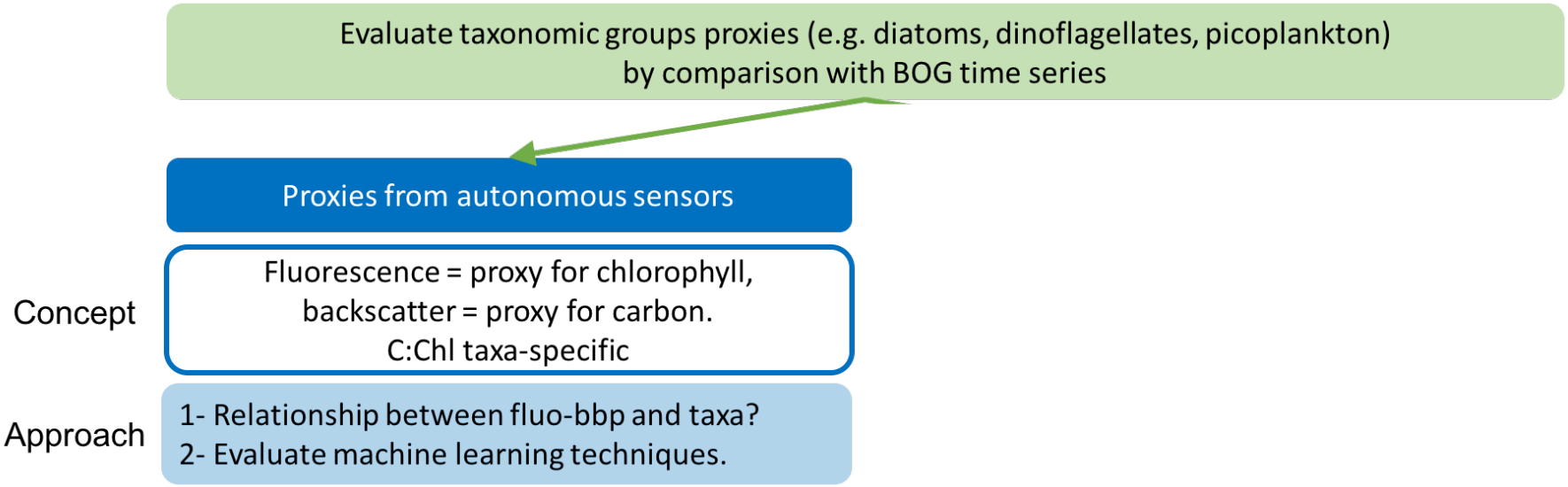
Plankton Proxies project



Proxies from autonomous sensors



Proxies from autonomous sensors

Goal: investigate the presence/absence and robustness of a relationship between phytoplankton taxa and fluo-bbp, based on:

(a) BOG phyto counts (carbon biomass per cell)
(b) concurrent fluo / beam-c datasets from the CTD (n ~ 1300)
(c) concurrent fluo / bbp datasets from the M1 mooring (n ~ 100)

Main conclusions:

- about 50% of BOG samples are mixed (no clear dominance by one group)
- when focusing on samples clearly dominated by one group, there is a relationship between taxa and Chl/POC (in situ)
- this relationship does not carry to fluo/beamc mostly because the POC/beamc relationship fails for dinos
- the mooring dataset (fluo/bbp) is more encouraging; however, the number of samples is too small to conclusively build a prediction model.

Proxies from autonomous sensors

Questions:

1) Is C:Chl taxa-specific? **YES**

(= relationship between Chl/POC and taxa from in situ samples)

1pre) Are samples taxa-specific? *(can samples be attributed to one taxon?)* **only ~ 50%**

2) Are fluo / beamc / bbp proxies for Chl / C? **YES for fluo, NOT REALLY for beamc, NOT SURE for bbp**

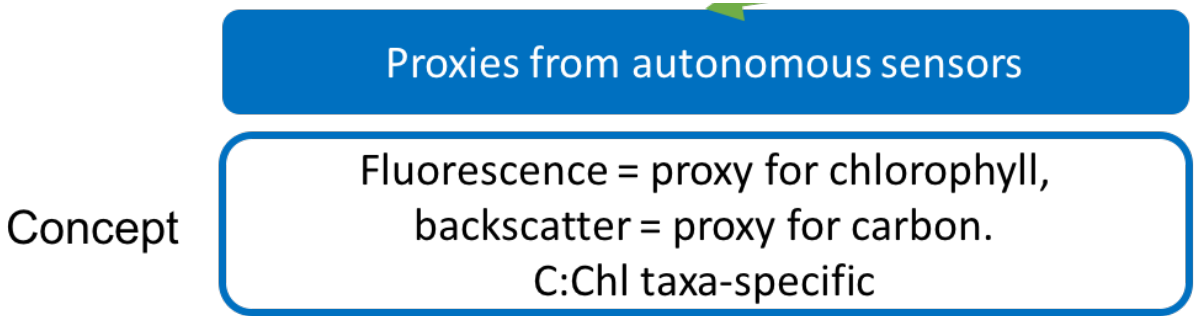
(= relationship between fluo/Chl and Cproxy/POC, where Cproxy = beamc or bbp)

2pre) Is the mooring dataset reliable? *(QC / interdeployment calibration)*

QC / calibration difficult → small dataset

3) Can fluo / beamc or fluo / bbp be used to predict taxonomy? **MAYBE**

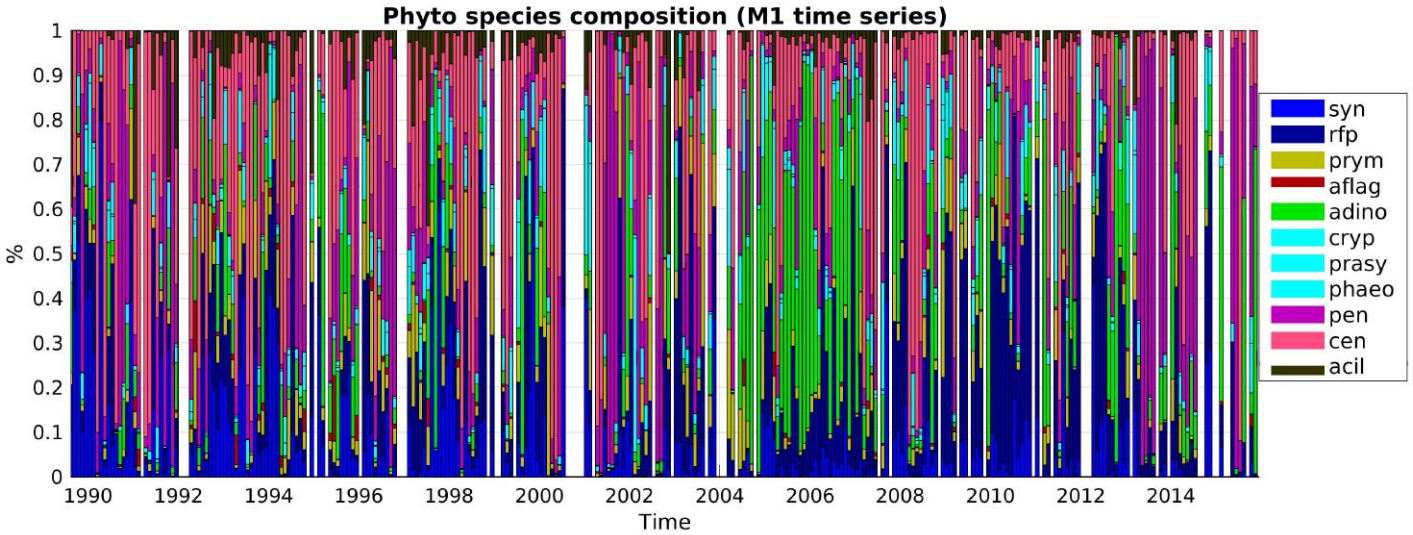
(= relationship between fluo/Cproxy and taxa)

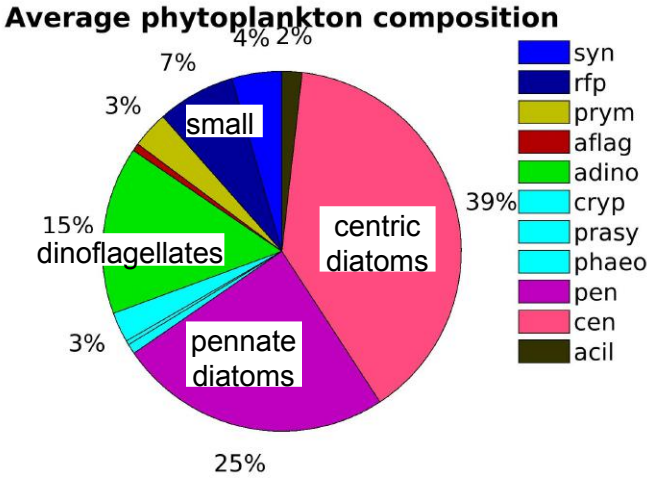


Proxies from autonomous sensors

In situ dataset only
(Chl, POC, taxonomy)
1989-2015, N = 435

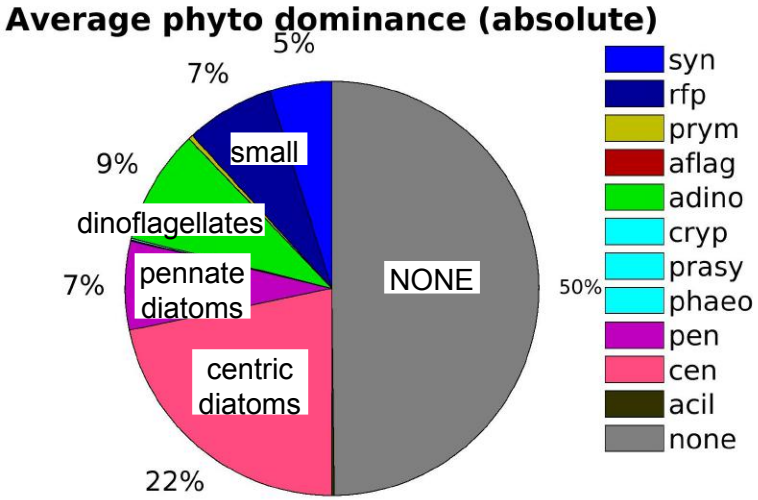
1pre) Phytoplankton community

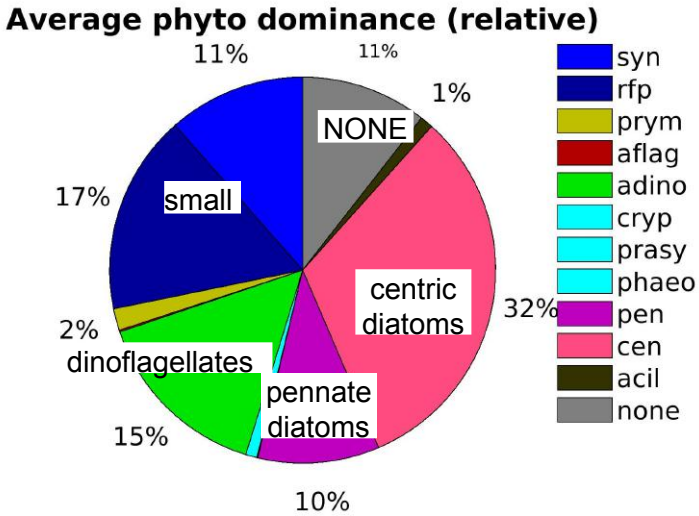




Most samples are a mix of species, not a lot of samples dominated by dinos.

- *absolute dominance:* species >= 50% of the biomass
- *relative dominance:* species is the most abundant and represents > 30% of the biomass



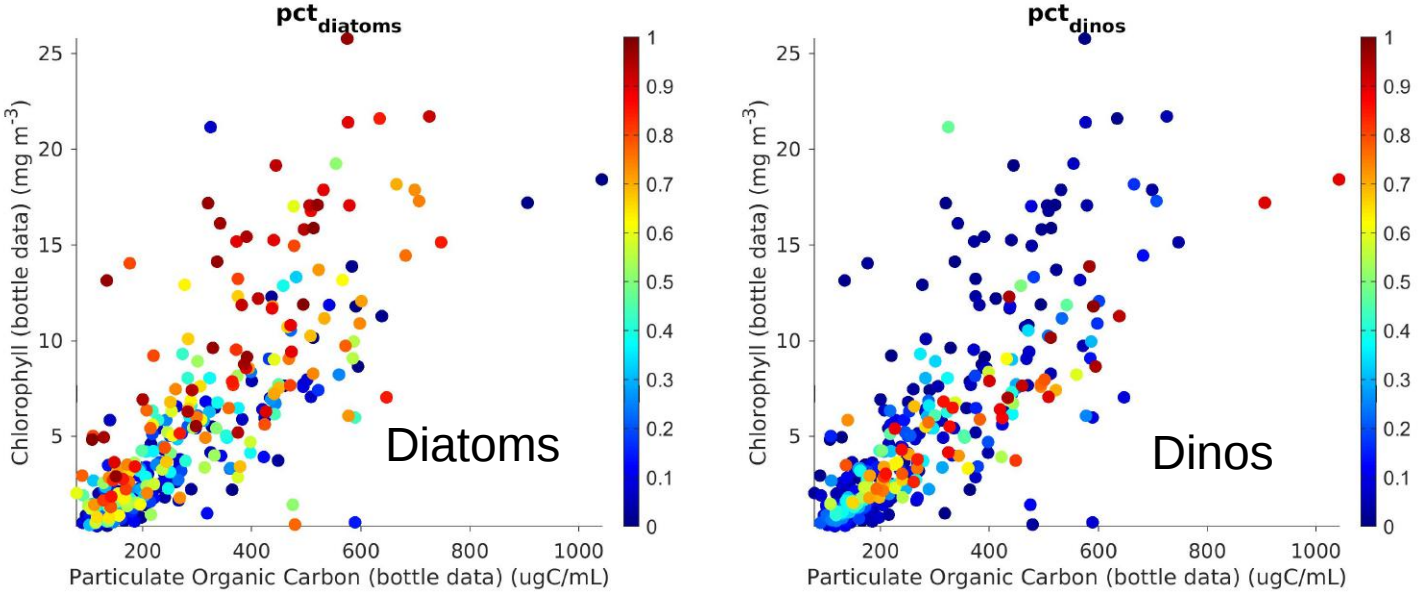


1) Is C:Chl taxa specific?

Looking at in situ (bottle) data only.
Chl: measured at the same time as plankton data
C: trickier. 2 measures:
- total biomass = sum(plankton biomass), very uncertain & noisy*.
- particulate organic carbon (**POC**, independent), might contain heterotrophs too.

Expected relationship: C:Chl is very high for picoplankton (low biomass anyways), high for dinos, low for diatoms.

Yaxis = Chl



No clear separation when considering all samples.

color = pct biomass

Xaxis = POC

(all available BOG data)

**Both relationships with taxonomy and with beamc are worse for total biomass than for POC.*

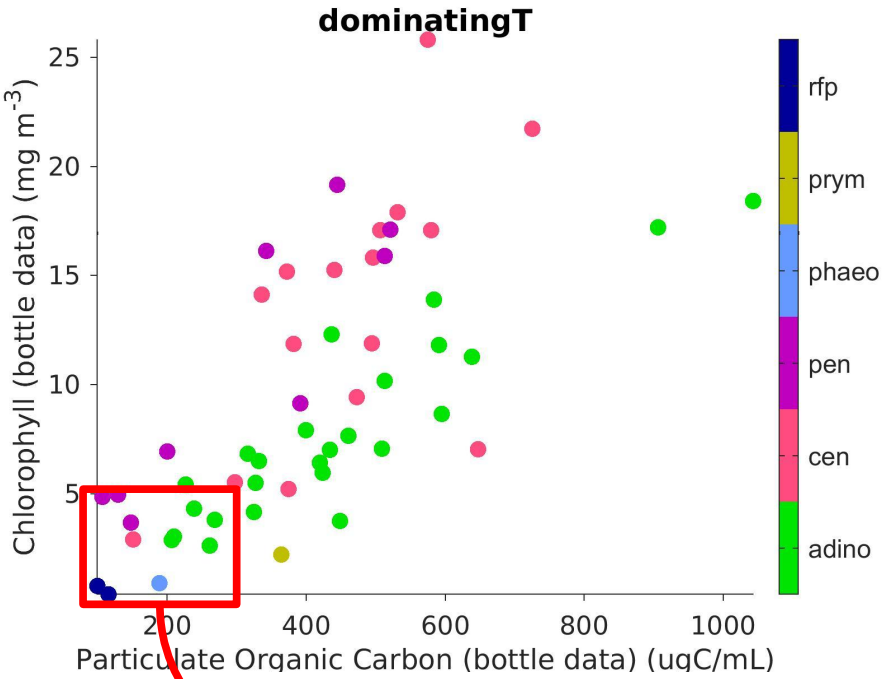
1) Is C:Chl taxa specific?

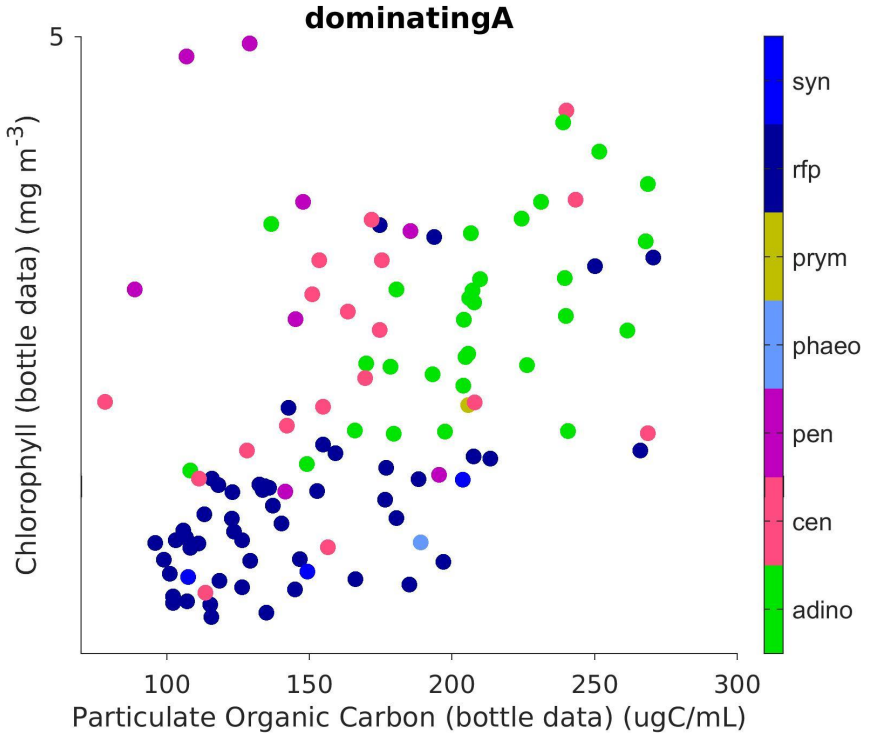
BUT samples strongly dominated by one taxon are separable in Chl/POC space.

Dominating = **above 80%**

Dominating = **above 50%**

Yaxis = Chl





Xaxis = POC

zoom

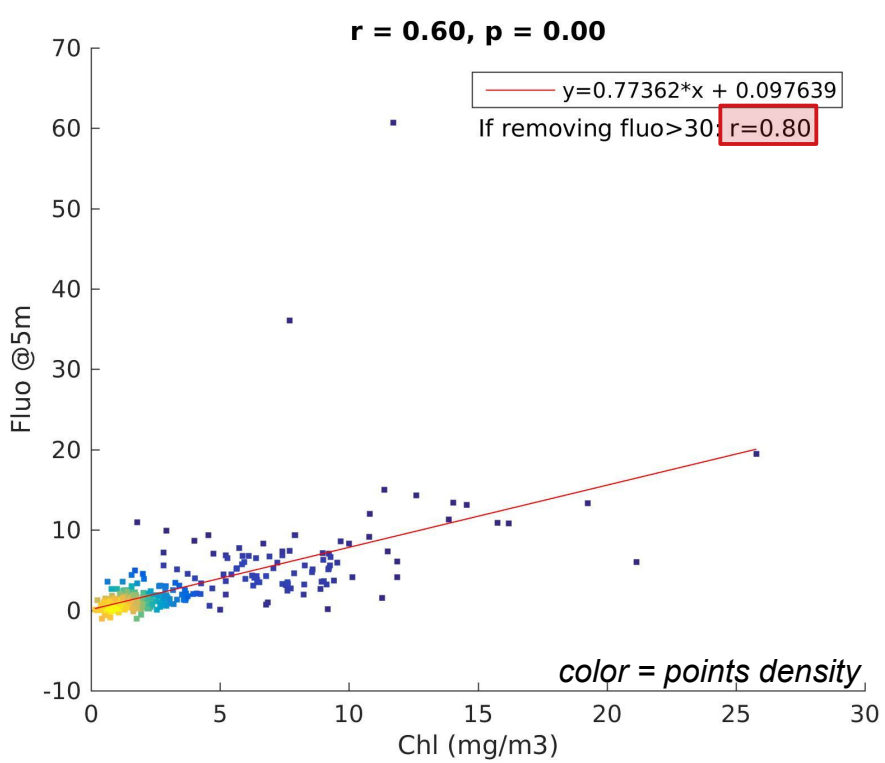
(only samples dominated by one group)

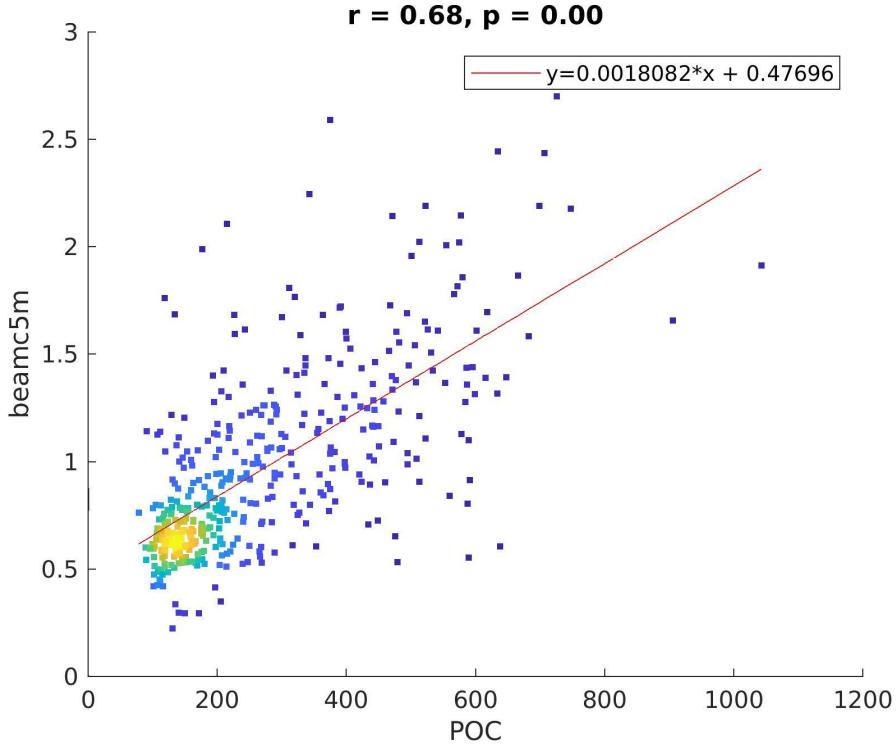
Proxies from autonomous sensors

CTD dataset (fluo, beamc)
vs taxonomy
1989-2015, N = 1228

2) Fluorescence / beam-c as proxies for Chl / C

Autonomous sensors @5 m





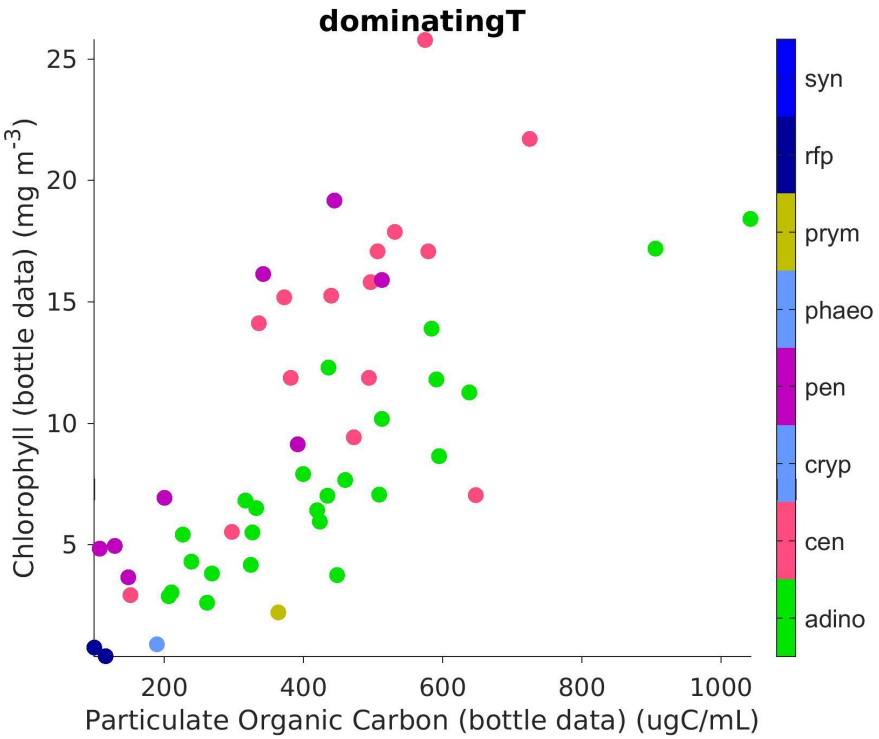
In situ surface bottle measurements

beamc is not a great proxy for biomass.

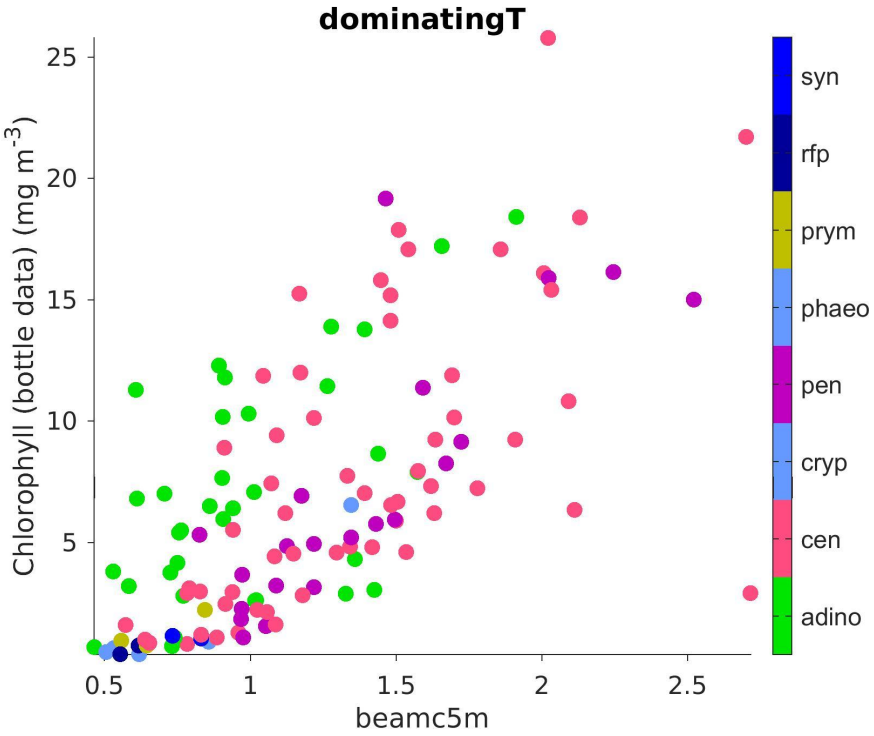
(A lot worse than published relationships in the open ocean, e.g., $r^2 = 0.92$ Graff et al 2015)

3) Taxonomy = f°(Chl, beamc @5m)

Yaxis = Chl



Xaxis = POC

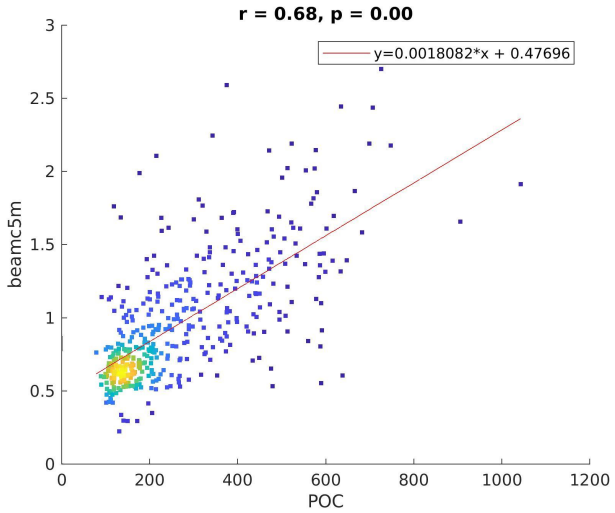


Xaxis = beamc @5m

C:Chl higher for dinos – as expected
(same plot as slide 8)

beamc:Chl lower for dinos

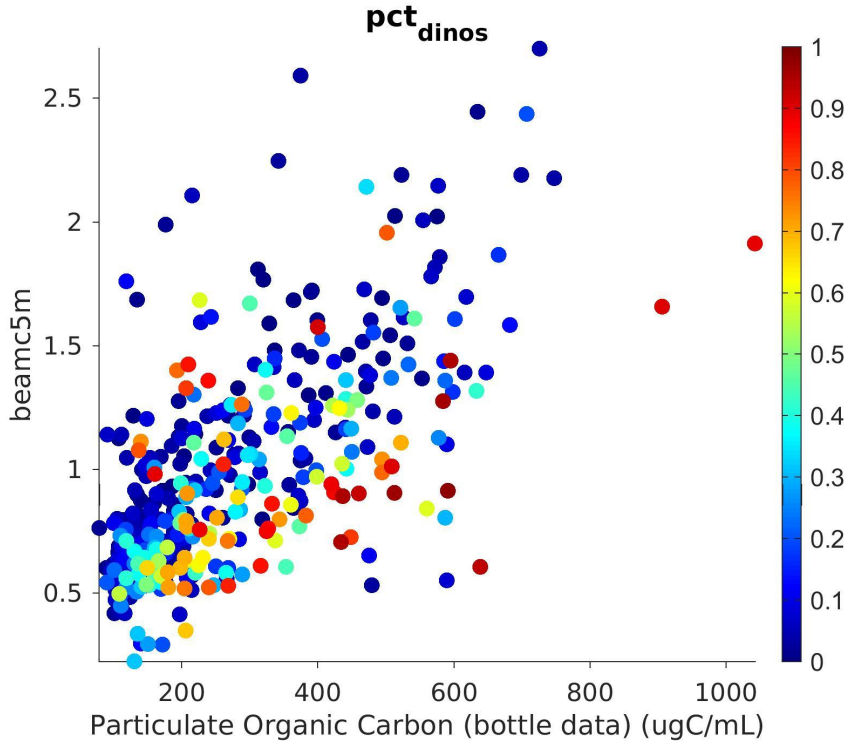
opposite to expected relationship



Beam-c vs. POC

Correlation POC / beamc @5m	
All samples	r = 0.68
pct_dinos > 0.5	r = 0.50
pct _dinos < 0.5	r = 0.74
pct_diatoms > 0.5	r = 0.70
pct_diatoms < 0.5	r = 0.64

Yaxis = beam-c @5m



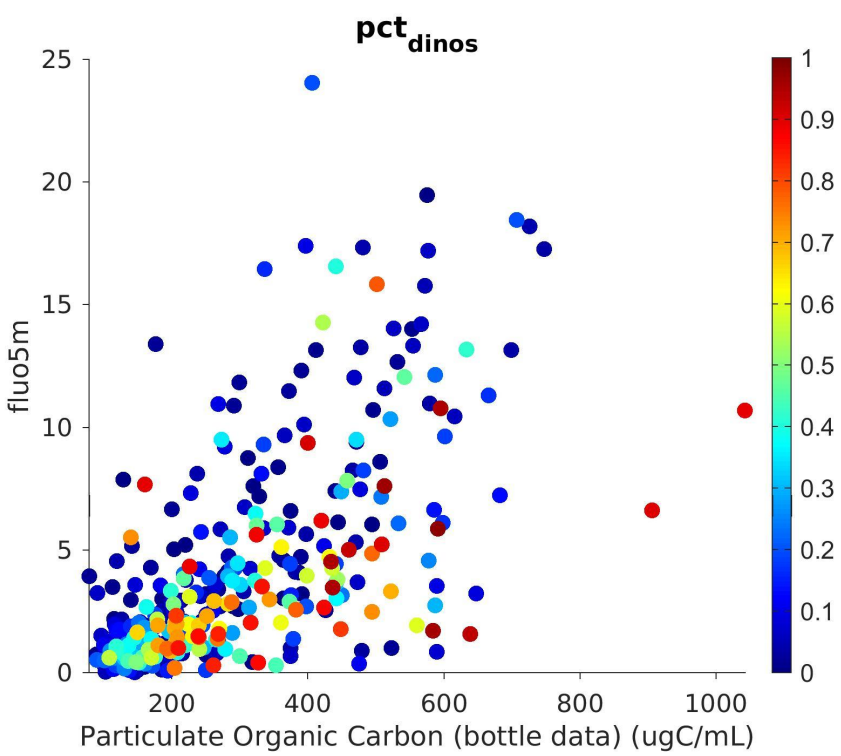
Xaxis = POC

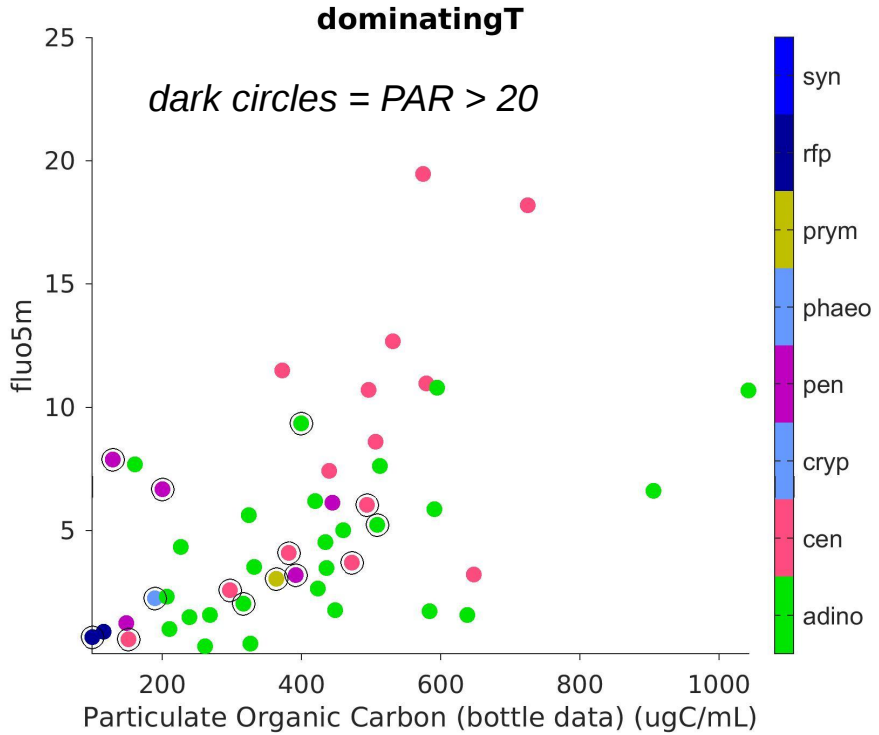
→ relationship POC / beamc breaks down for dinos.

(beamc lower than expected for dinos)

Fluo vs. POC

Yaxis = fluo





Xaxis = POC

The relationship POC / fluo is (surprisingly) driven by taxonomy more than by quenching.
r(Chl, fluo @5m) = 0.78

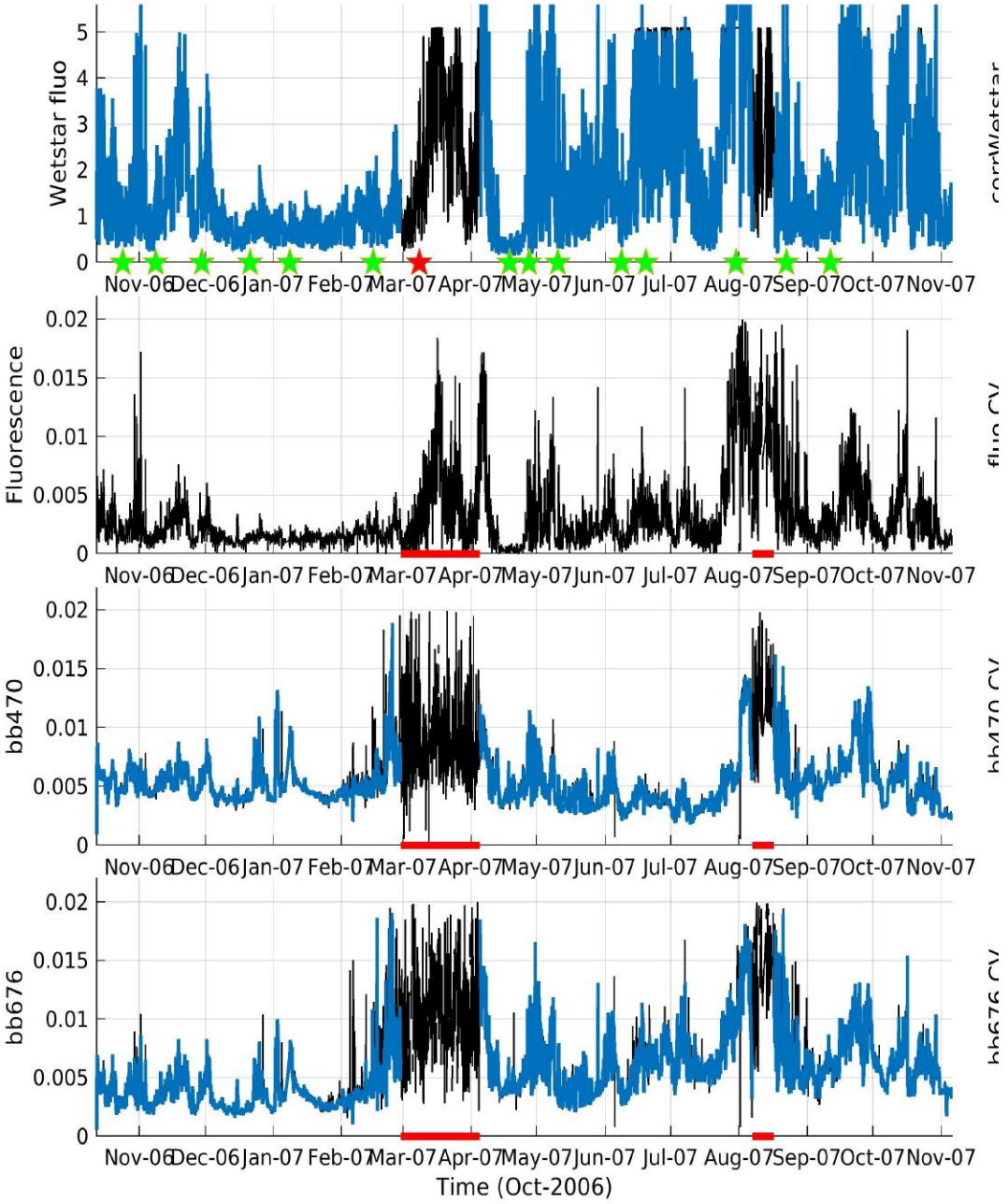
→ the real issue is with beamc.

Proxies from autonomous sensors

Mooring dataset (fluo, bbp470, bbp676) vs taxonomy

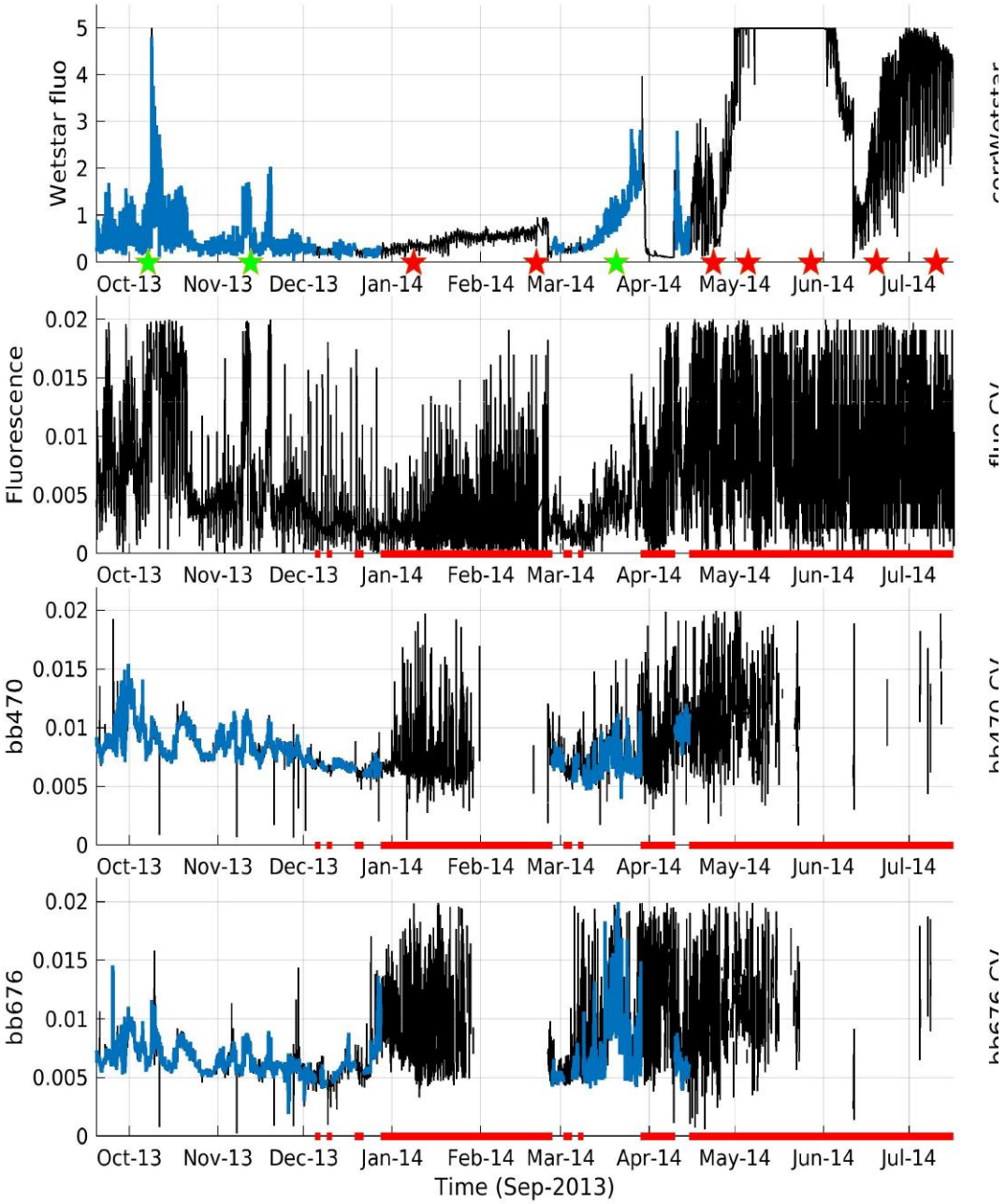
2004-2014, N = 84 (after QC)

2pre) Mooring QC



Example of good deployment (200610).
Stars = in situ taxa counts, red = removed.

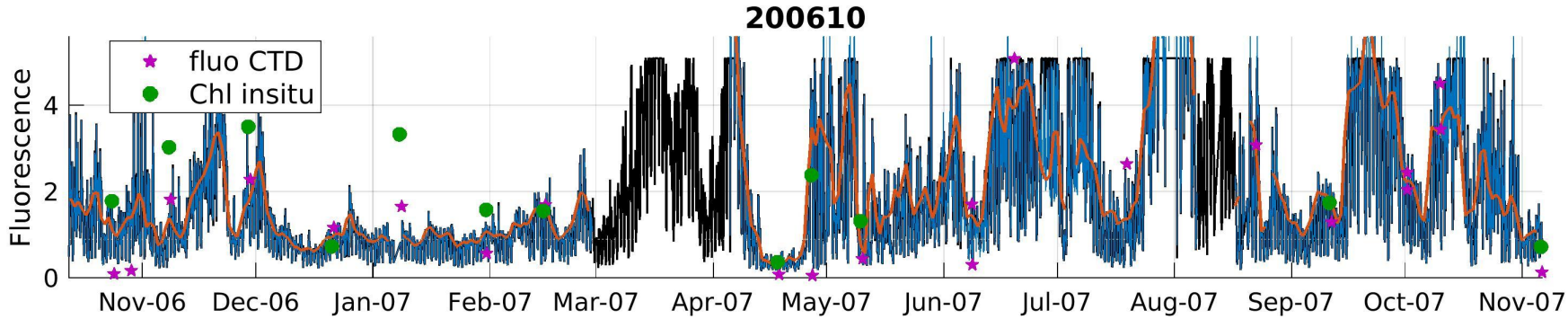
2pre) Mooring QC



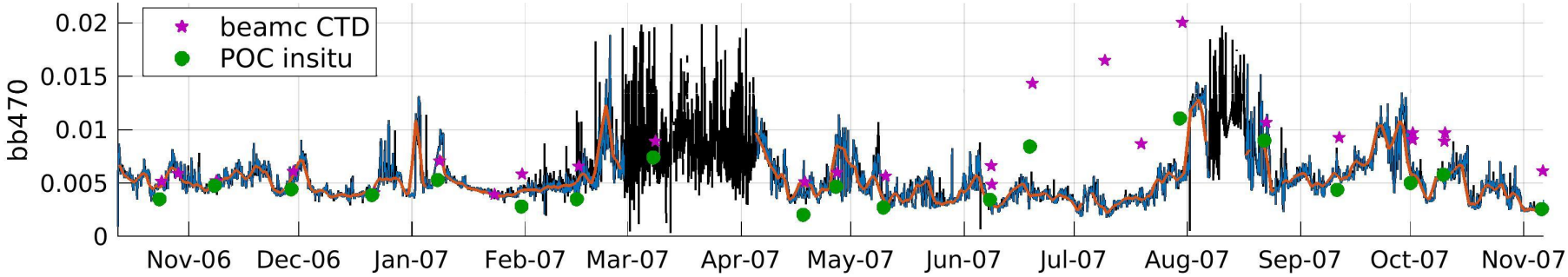
Example of bad deployment (201309).
Stars = in situ taxa counts, red = removed.

2pre) Mooring QC

fluo



bbp



Even for good deployments, fluo mooring / fluo CTD / Chl insitu (top) and bbp mooring / beamc CTD / POC in situ (bottom) do not agree very well.

+ issue of fluorescence intercalibration between deployments.

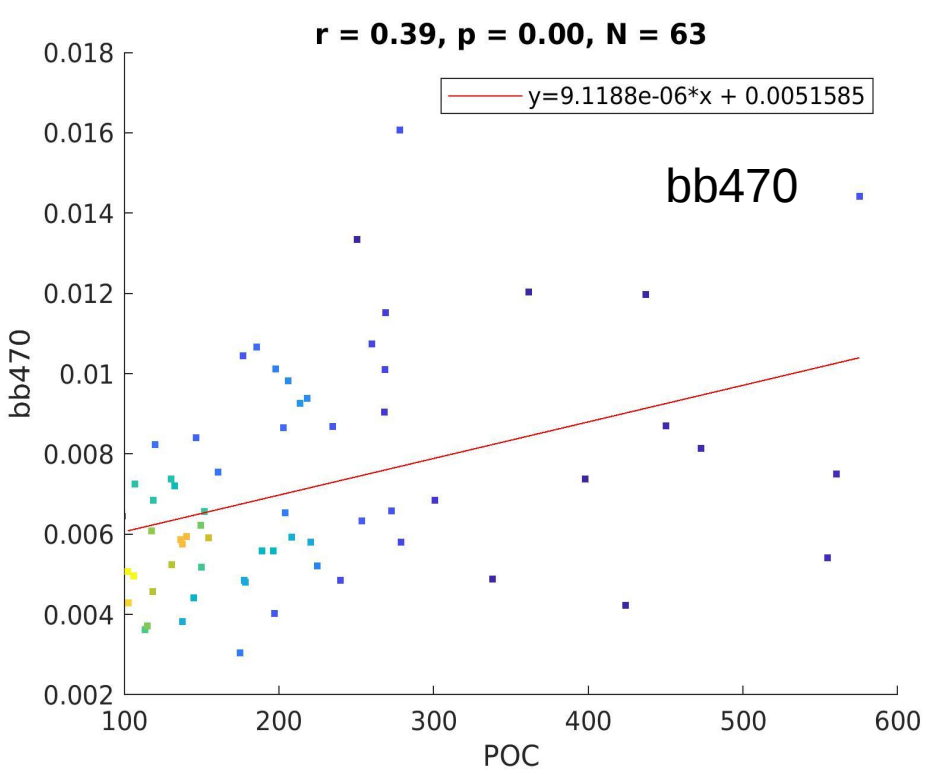
Tested based on: (1) concurrent fluo CTD, (2) concurrent Chl insitu, (3) fluo/bb676 correlation. (2) gives the best results (used hereafter) but correlation is not always great.

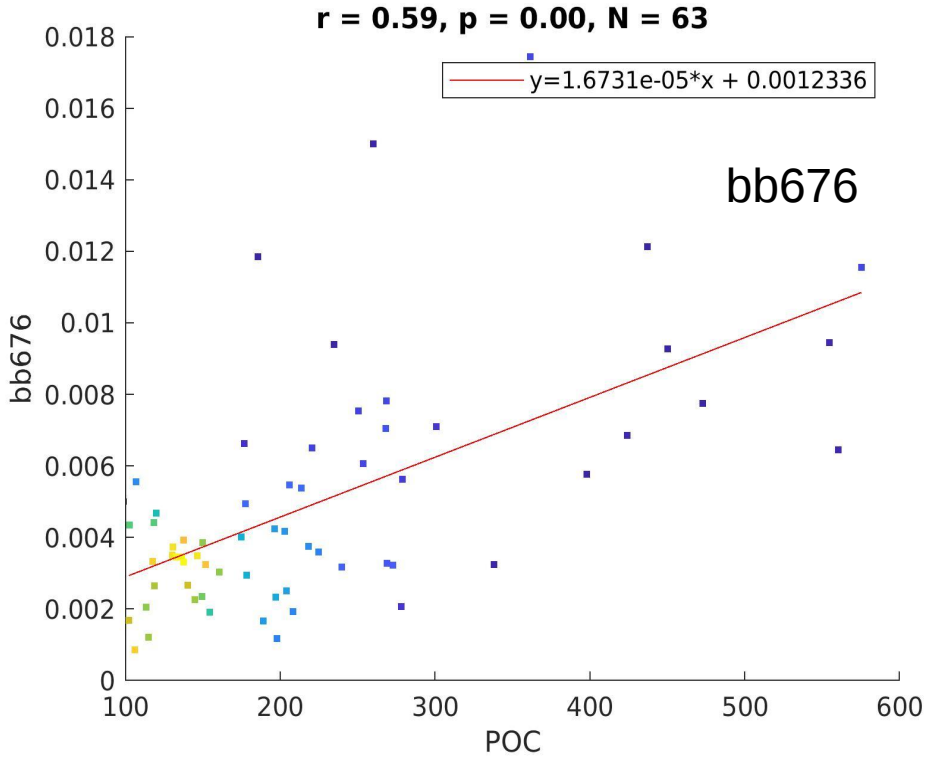
→ choice of subdataset (5 deployments)

2) bbp as proxy for C

based on the entire mooring dataset (10 deployments) since bbp doesn't require calibration

Surface mooring backscatter





In situ POC surface bottle measurements

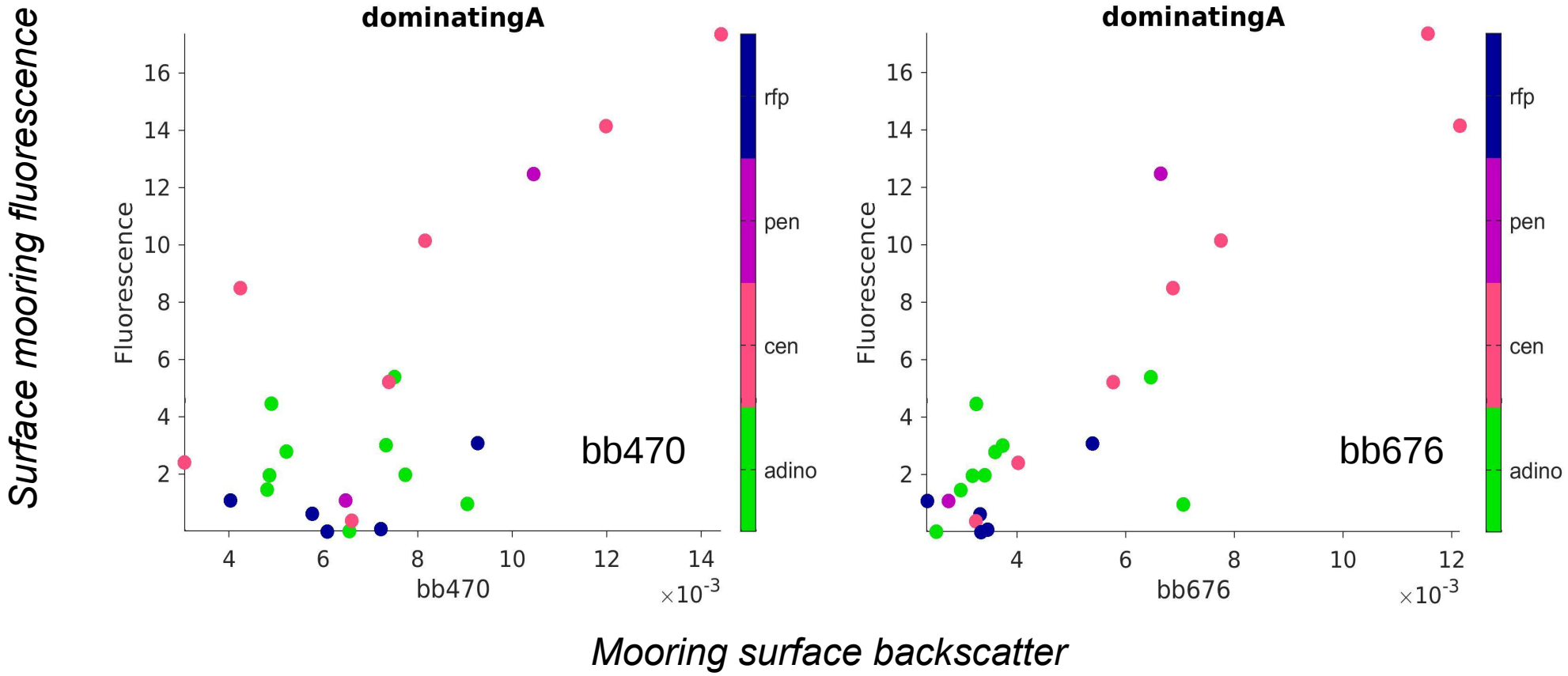
Correlations POC/bbp are not great...

(A lot worse than published relationships in the open ocean, e.g., $r^2 = 0.74$ for bb470 Graff et al 2015)

… but neither are correlations fluo/Chl ie. there are not enough data points to conclude

(r=0.54 for Chl/fluo on the same dataset (no outliers), vs 0.80 on the CTD dataset when removing fluo>30)

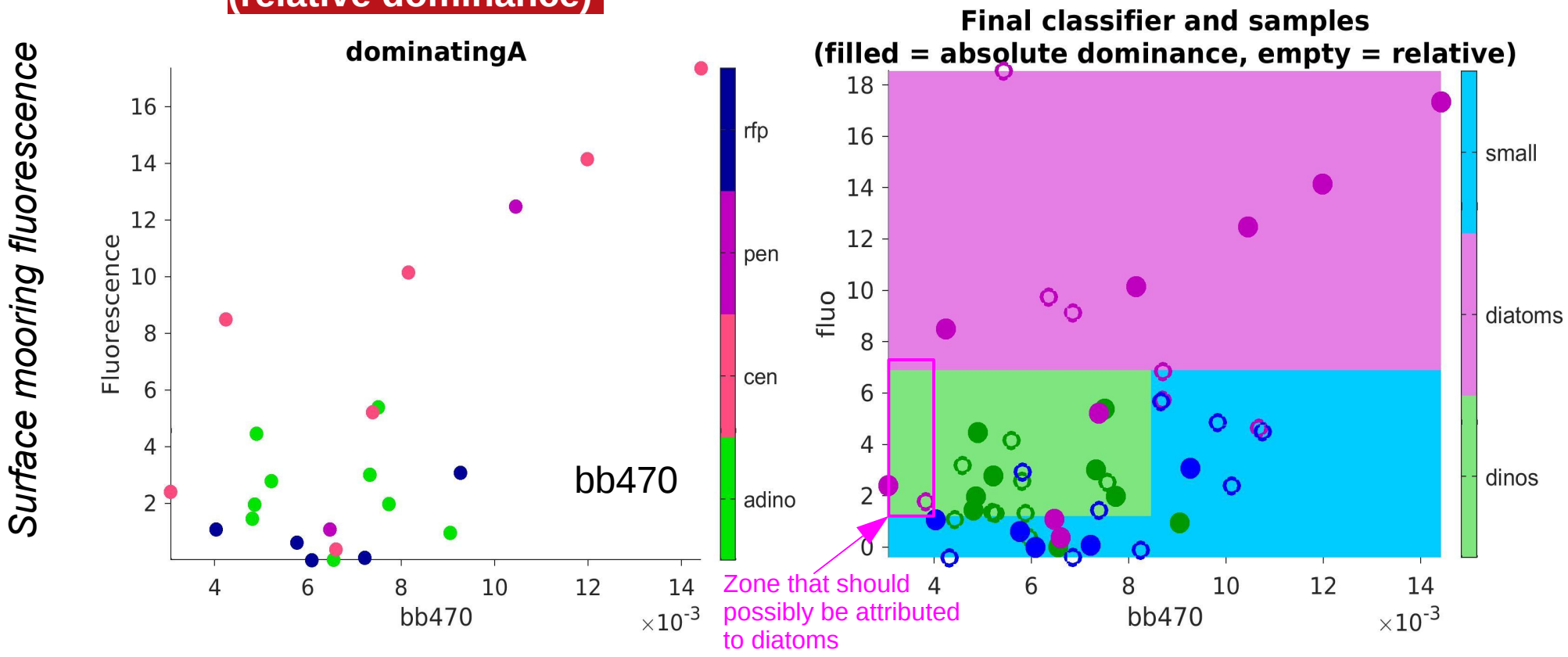
3) fluo/bbp as proxies for taxonomy



Nothing obvious… *note that this is dominatingA (50%) and not dominatingT (80%) as with the CTD dataset (few samples, all dominatingT are diatoms)*

3) fluo/bbp as proxies for taxonomy

… however **machine learning tree algorithm succeeds in predicting taxonomy (relative dominance)**



Algorithm trained on absolute dominance (> 50%, filled circles, N=23) and evaluated on relative dominance (open circles, N=26): 55% accuracy on training dataset, **65% on evaluation dataset** (only predictors = fluo & bb470).

Proxies from satellite (PHYSAT)

Evaluate taxonomic groups proxies (e.g. diatoms, dinoflagellates, picoplankton)
by comparison with BOG time series

Proxies from satellite (PHYSAT)

Concept

Water-leaving radiance (Ra) spectra varies with Chl (first order) and taxa (second order). PHYSAT classifying Ra anomalies.

Approach

1- Do PHYSAT groups match *in situ* groups?
2- Custom calibration with *in situ* data.

Proxies from satellite (PHYSAT)

Goal: evaluate outputs from the PHYSAT algorithm, that predicts taxonomy from space (dominant species at each pixel).

1) PHYSAT only (spatio-temporal patterns)
2) PHYSAT in comparison with BOG data

Main conclusions:

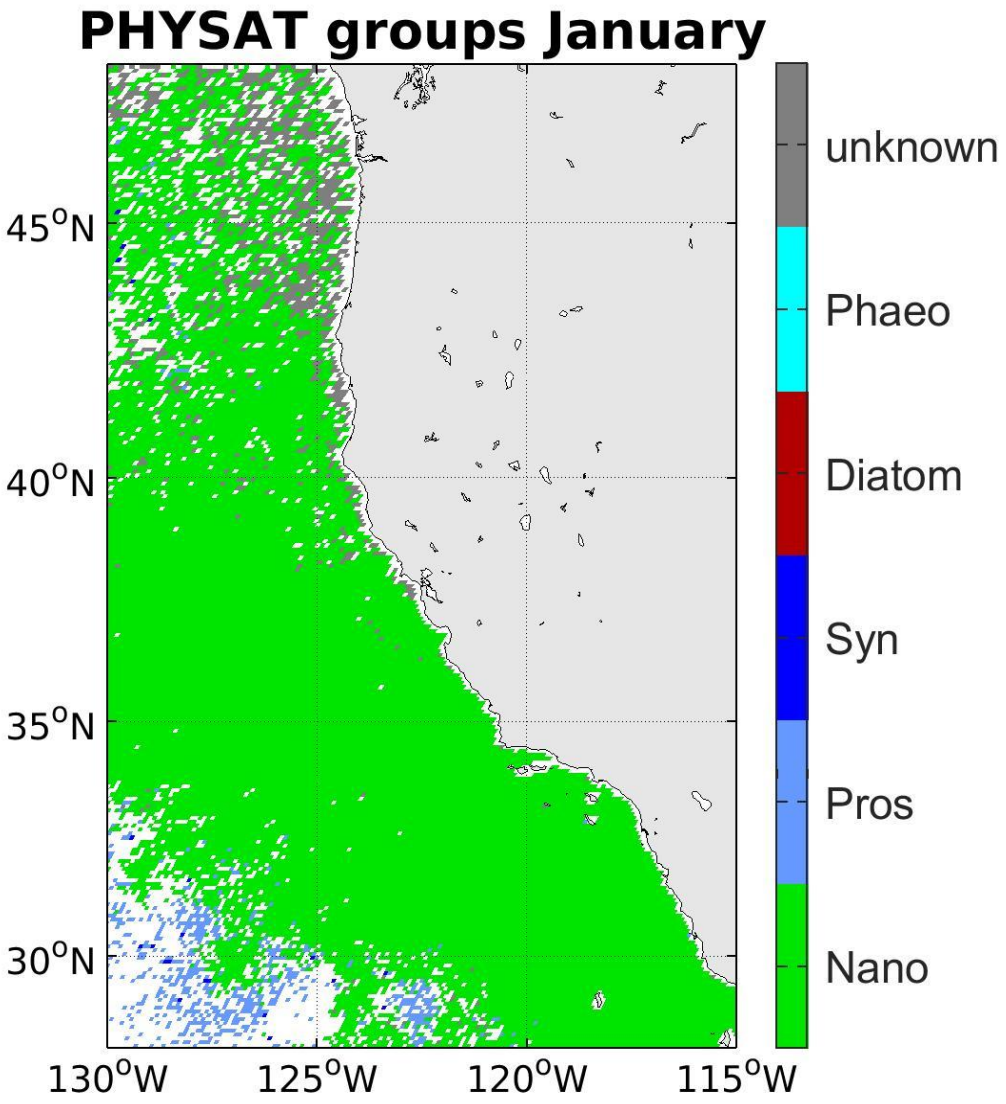
- regional patterns look OK, noting that PHYSAT mostly finds nanoflagellates in winter
- there are a LOT of missing data nearshore, so that MB patterns are off
- comparison with BOG data is not conclusive.
- in general Nanos are likely overrepresented (ie some PHYSAT "nanos" are likely diatoms for instance)

→ doesn't appear to work, at least locally (too many data gaps?)

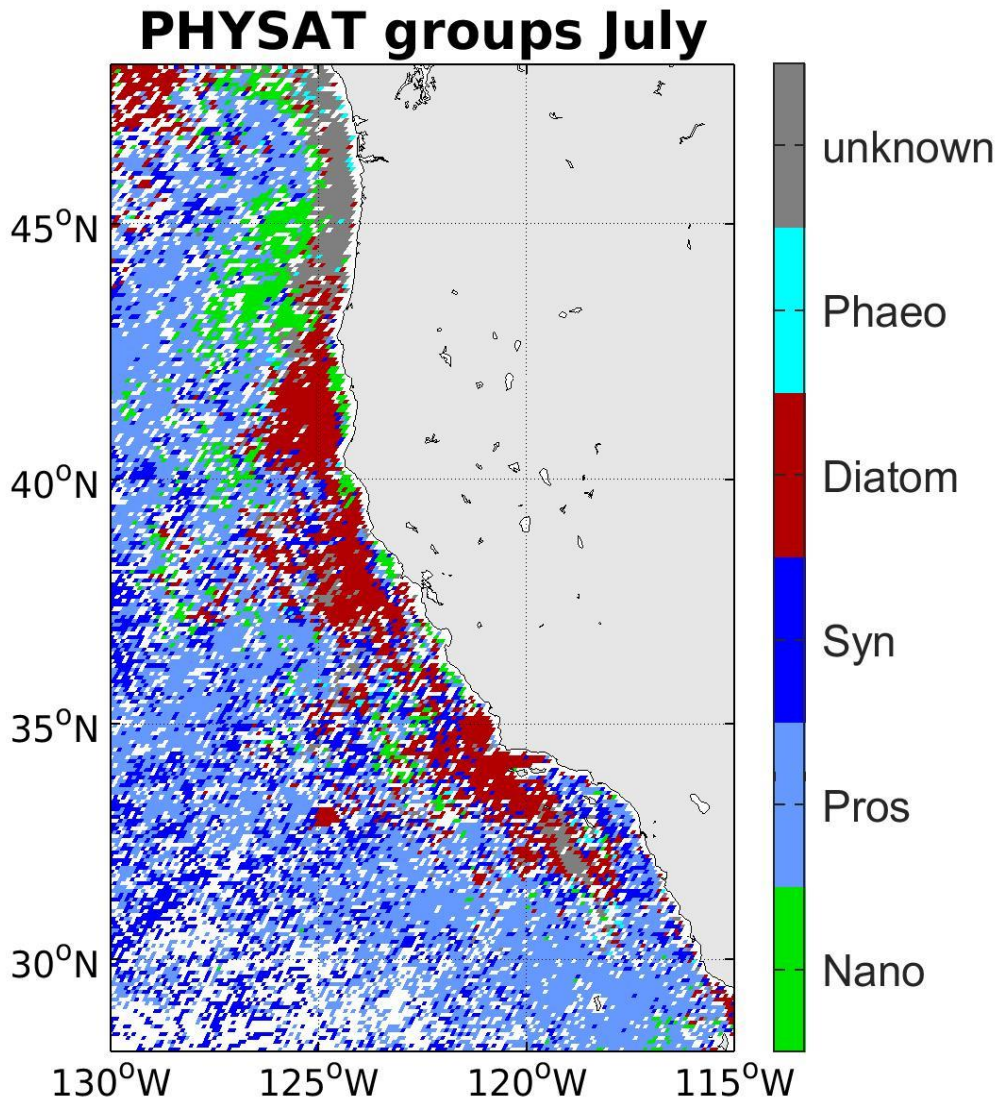
Note that this is based on SeaWiFS only, not MODIS – also likely to work better regionally.

1) PHYSAT patterns

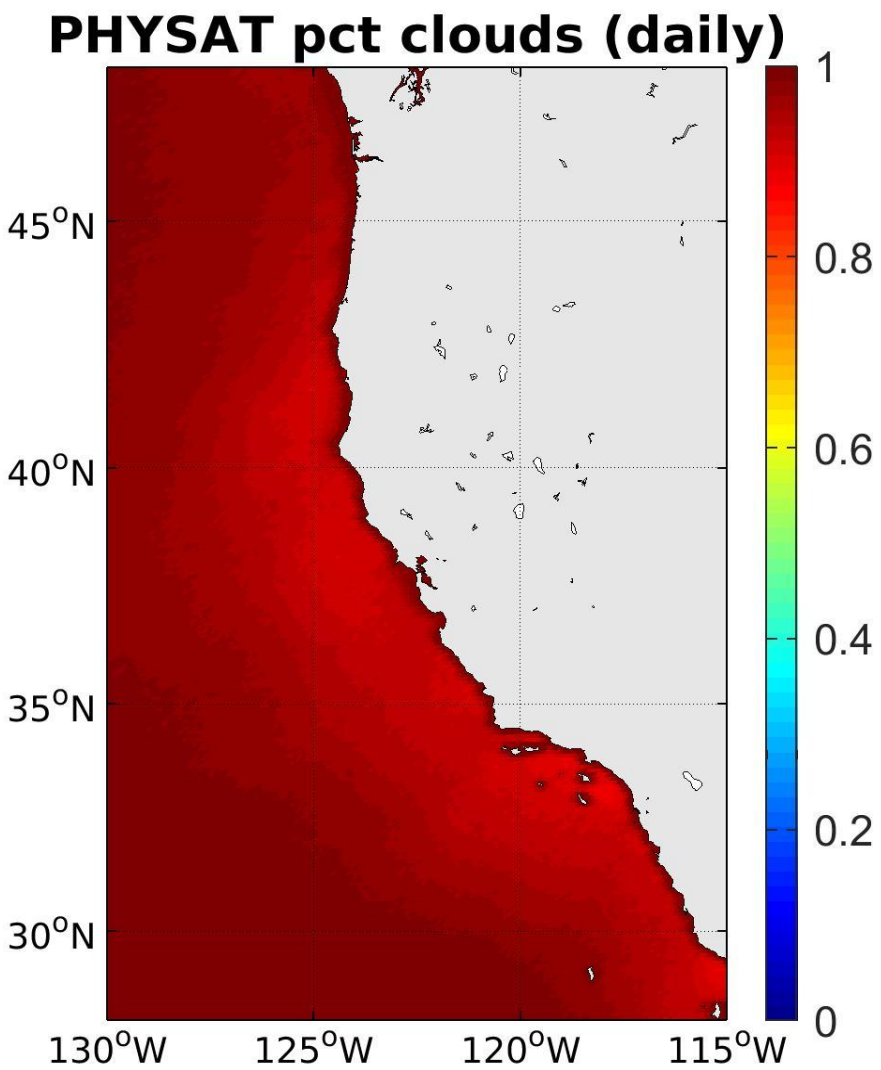
WINTER

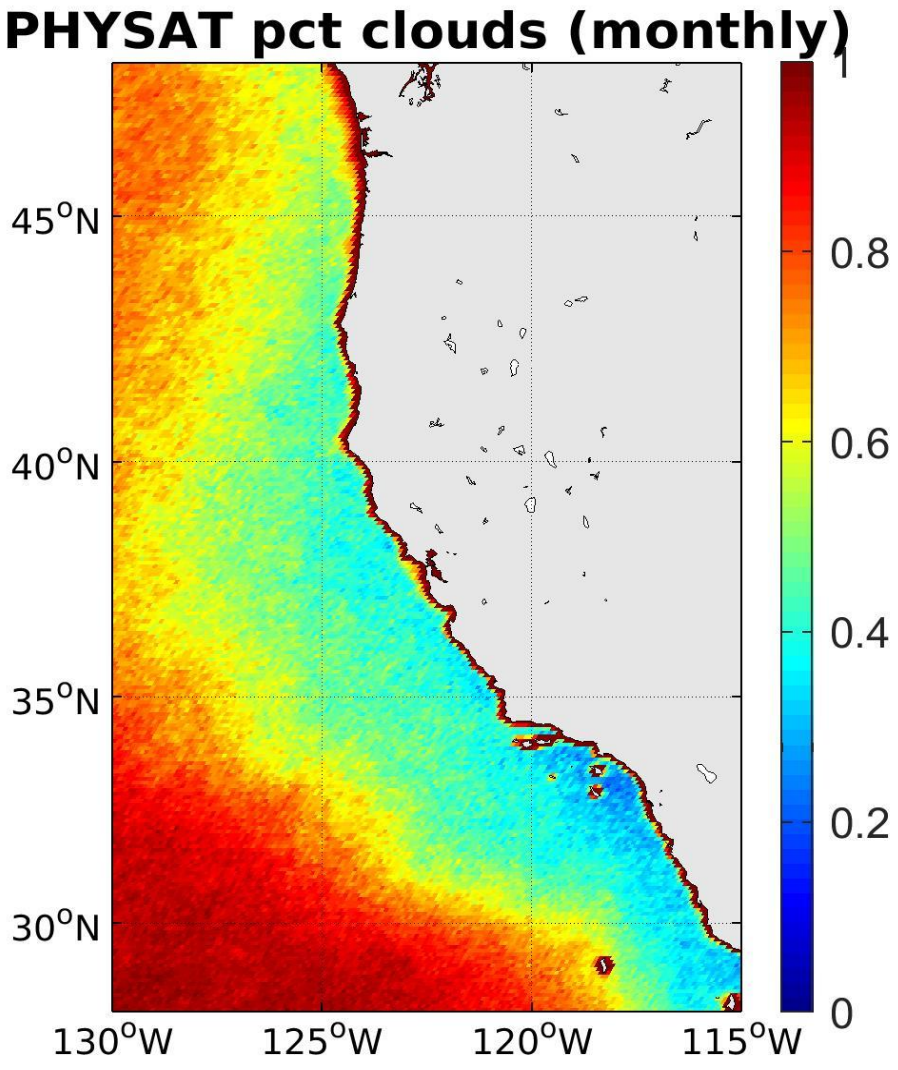


SUMMER



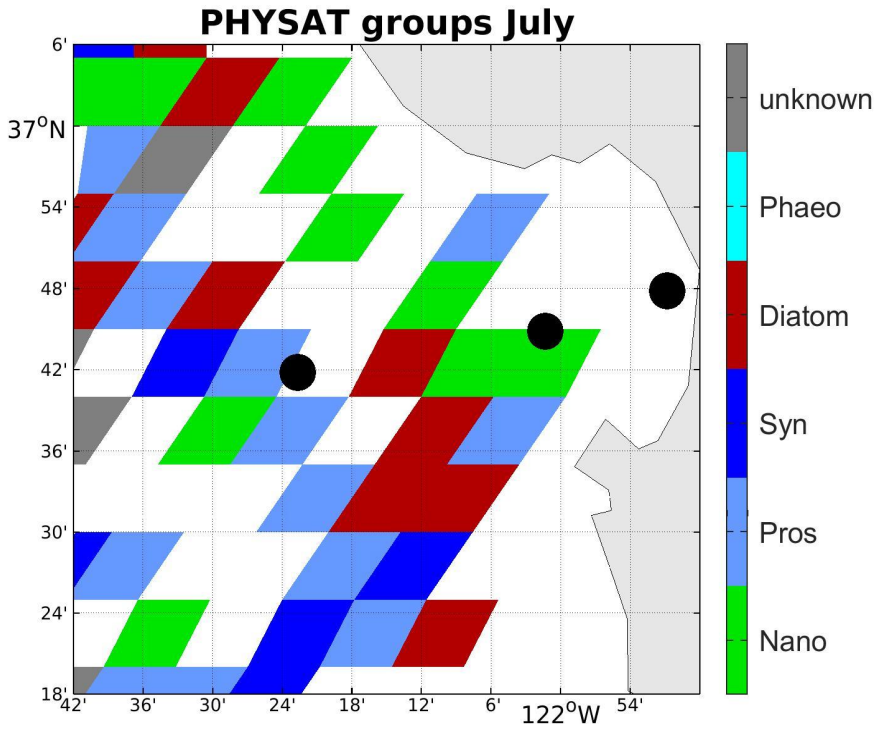
1) PHYSAT patterns: data gaps

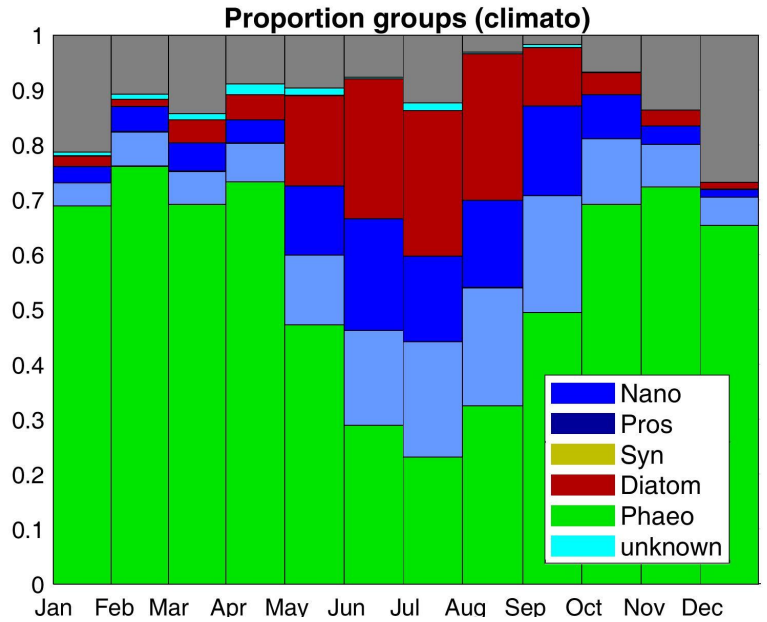


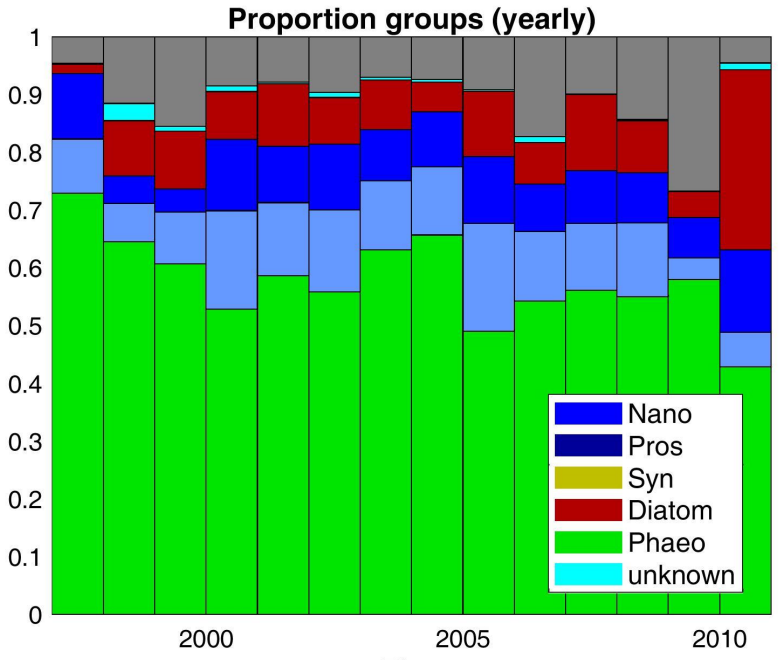


1) PHYSAT patterns: Monterey Bay

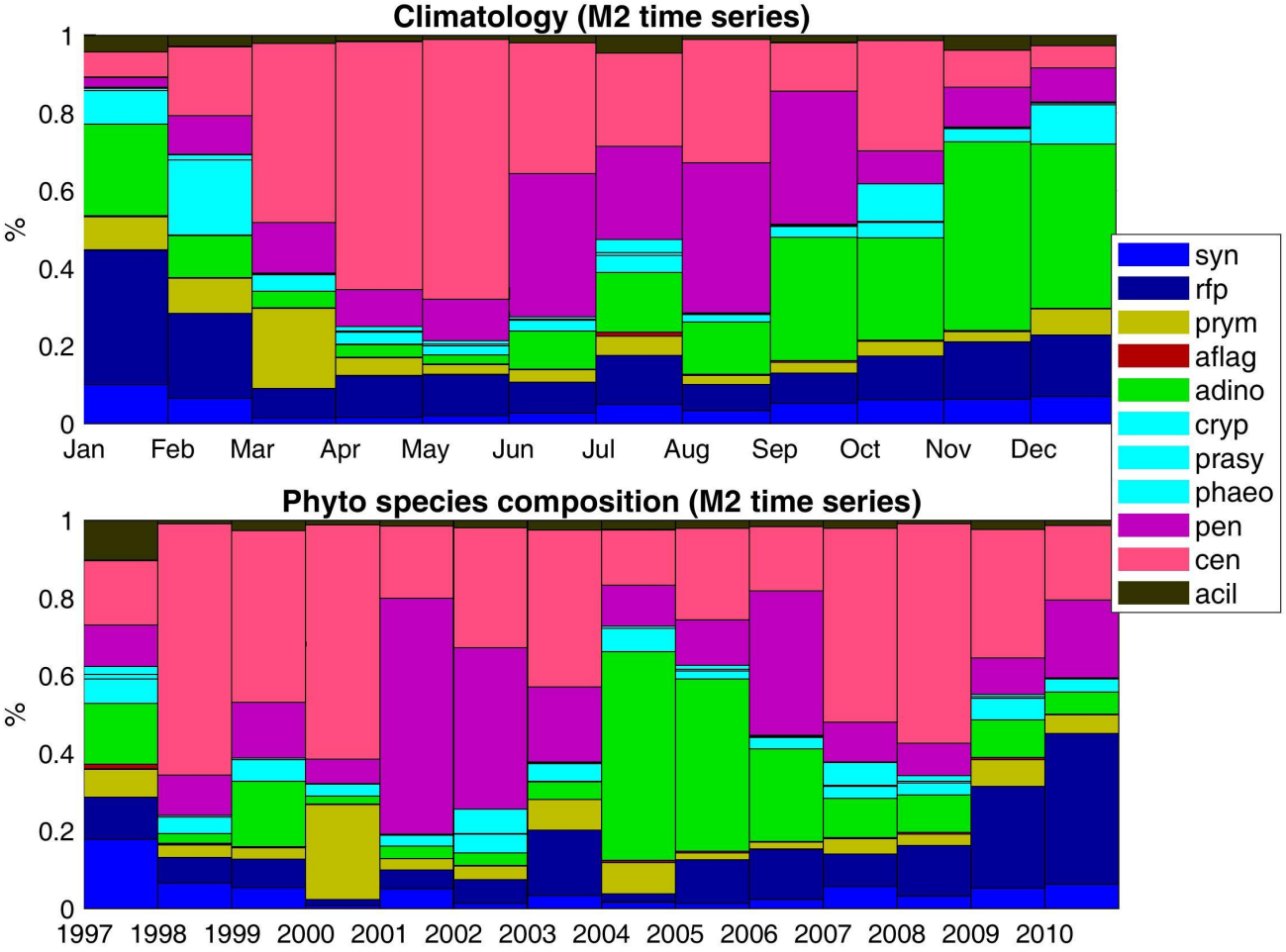
Gaps due to:
- clouds
- PHYSAT algorithm not identifying dominance
- no dominance for a given pixel over the years! (eg same number of 2 groups)

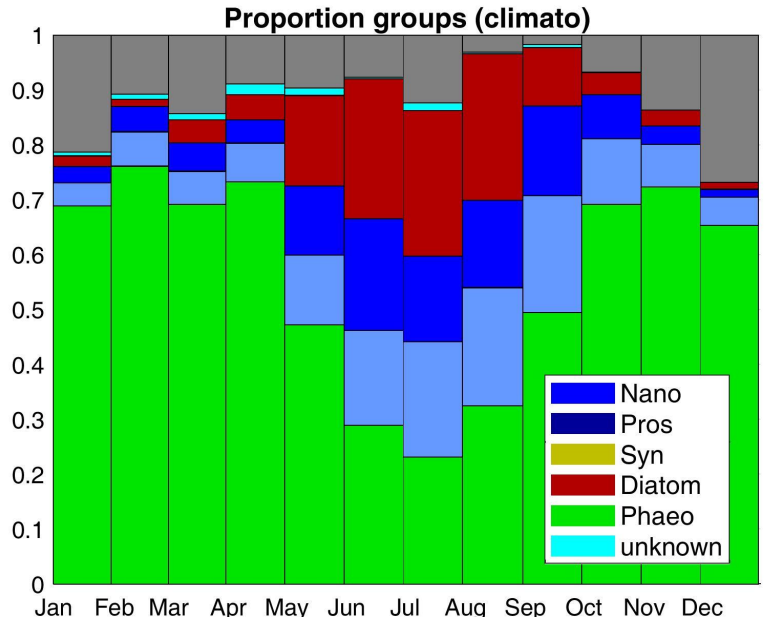


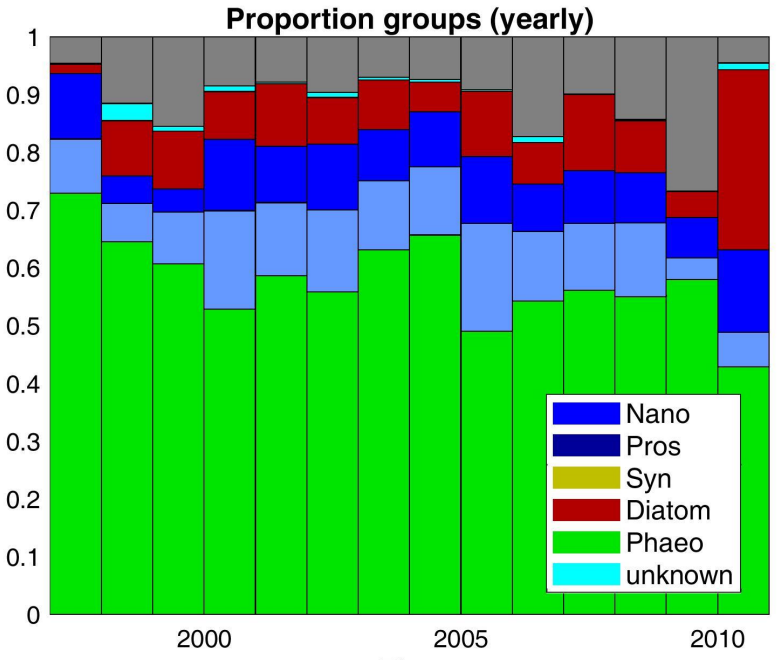




1) Comparison with BOG





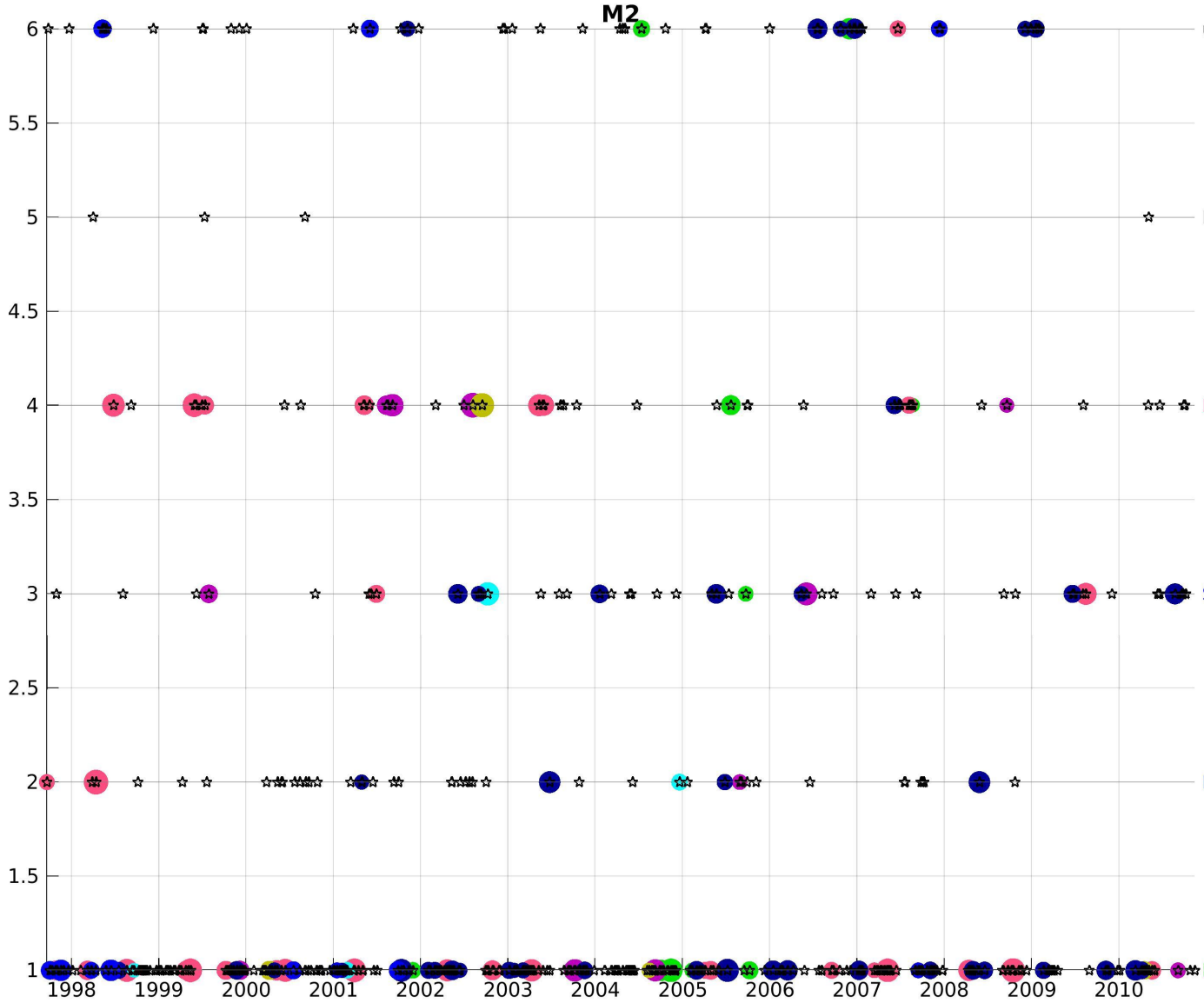


M2 = station most offshore, likely most representative of PHYSAT conditions, restricted to 1997-2010

2) Comparison with BOG

pixel closest to M2
(less clouds than M1),
PHYSAT data within 7 days

Stars = PHYSAT data, colors = matching BOG sample



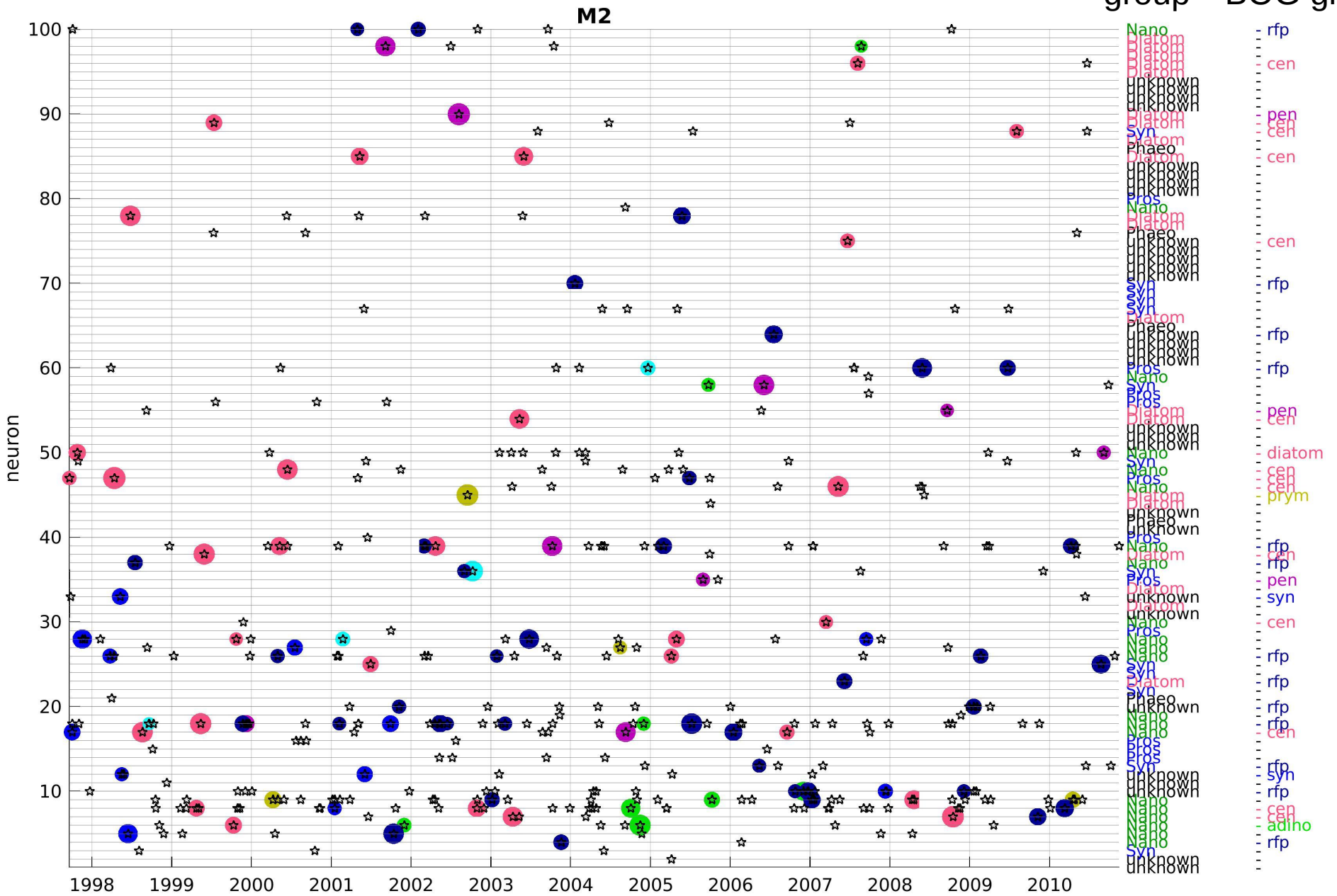
not too bad

but most PHYSAT pixels are nano

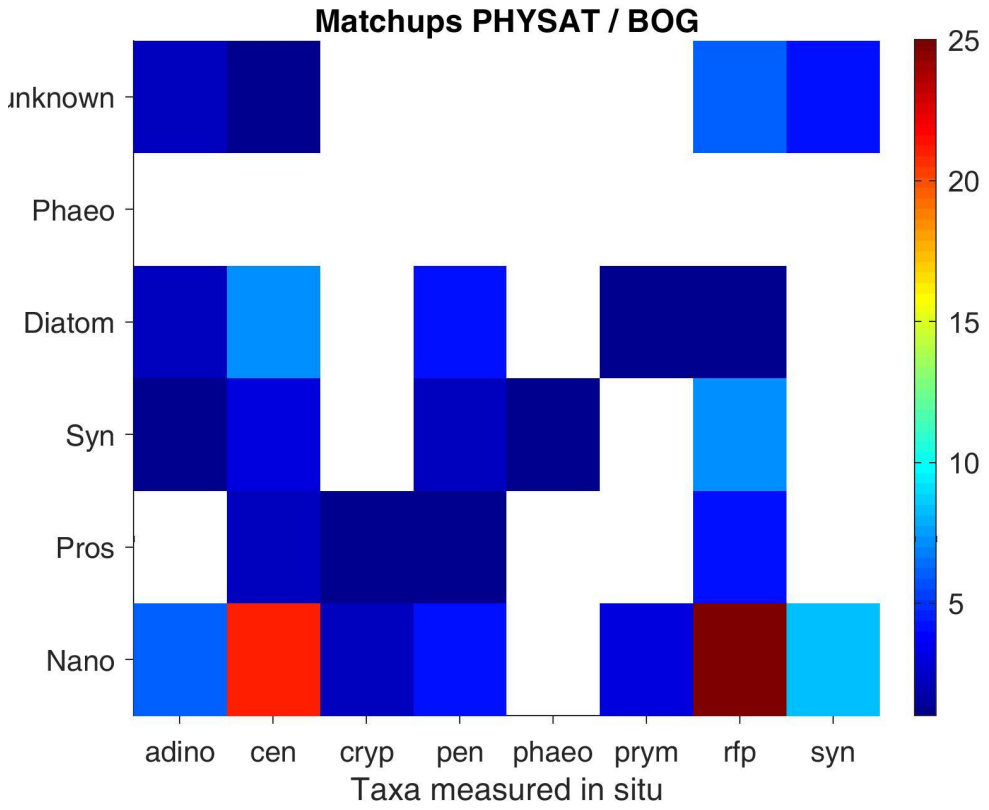
2) Comparison with BOG

pixel closest to M2 (less clouds), PHYSAT data within 7 days

Neurons = most basic PHYSAT output (then attributed to groups)



2) Comparison with BOG



→ not very conclusive.

For instance, PHYSAT “diatoms” do seem to pick up mostly diatoms; however, most diatoms are labelled “Nano” by PHYSAT.