Reconciling the carbon budget in the ocean's twilight zone

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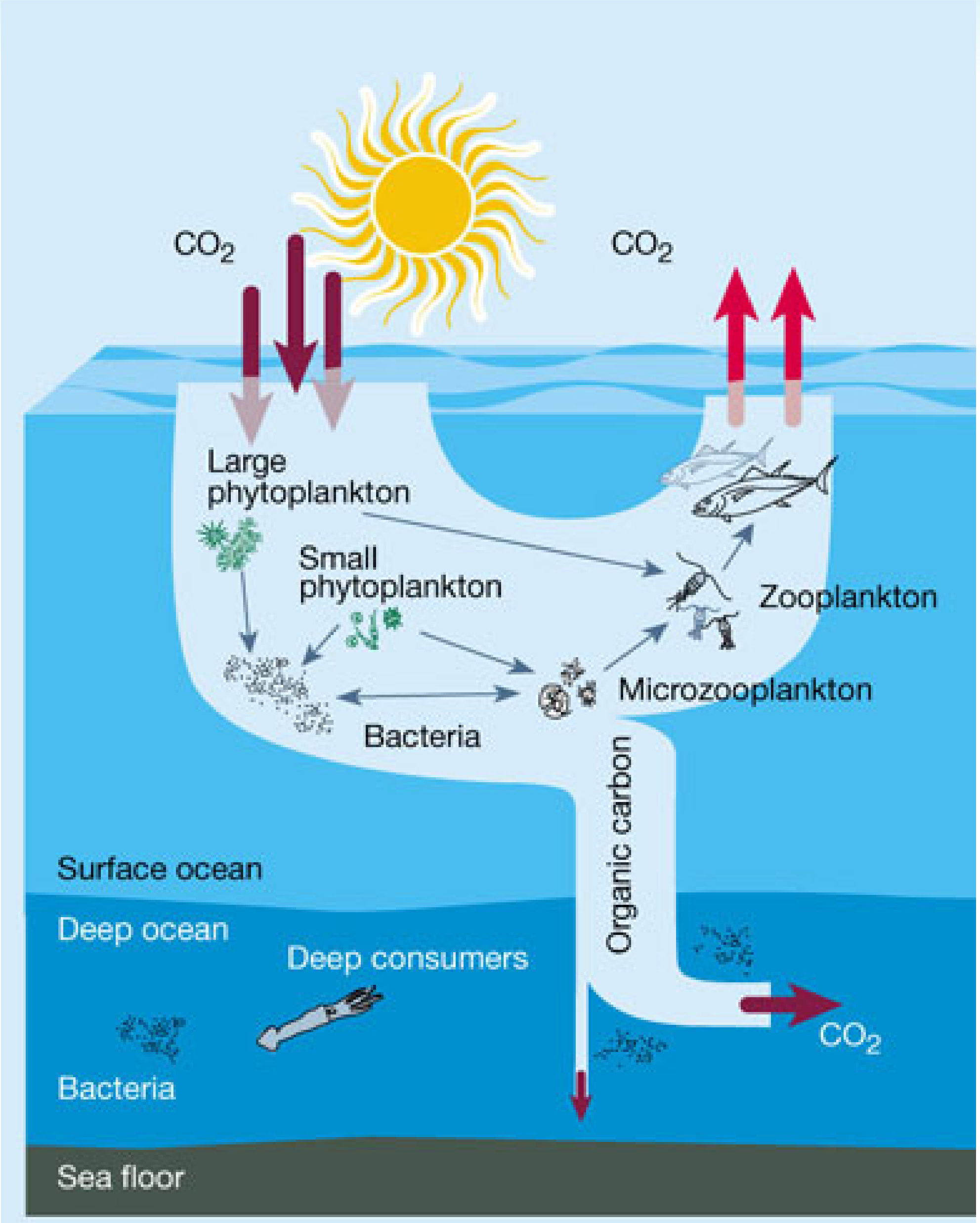
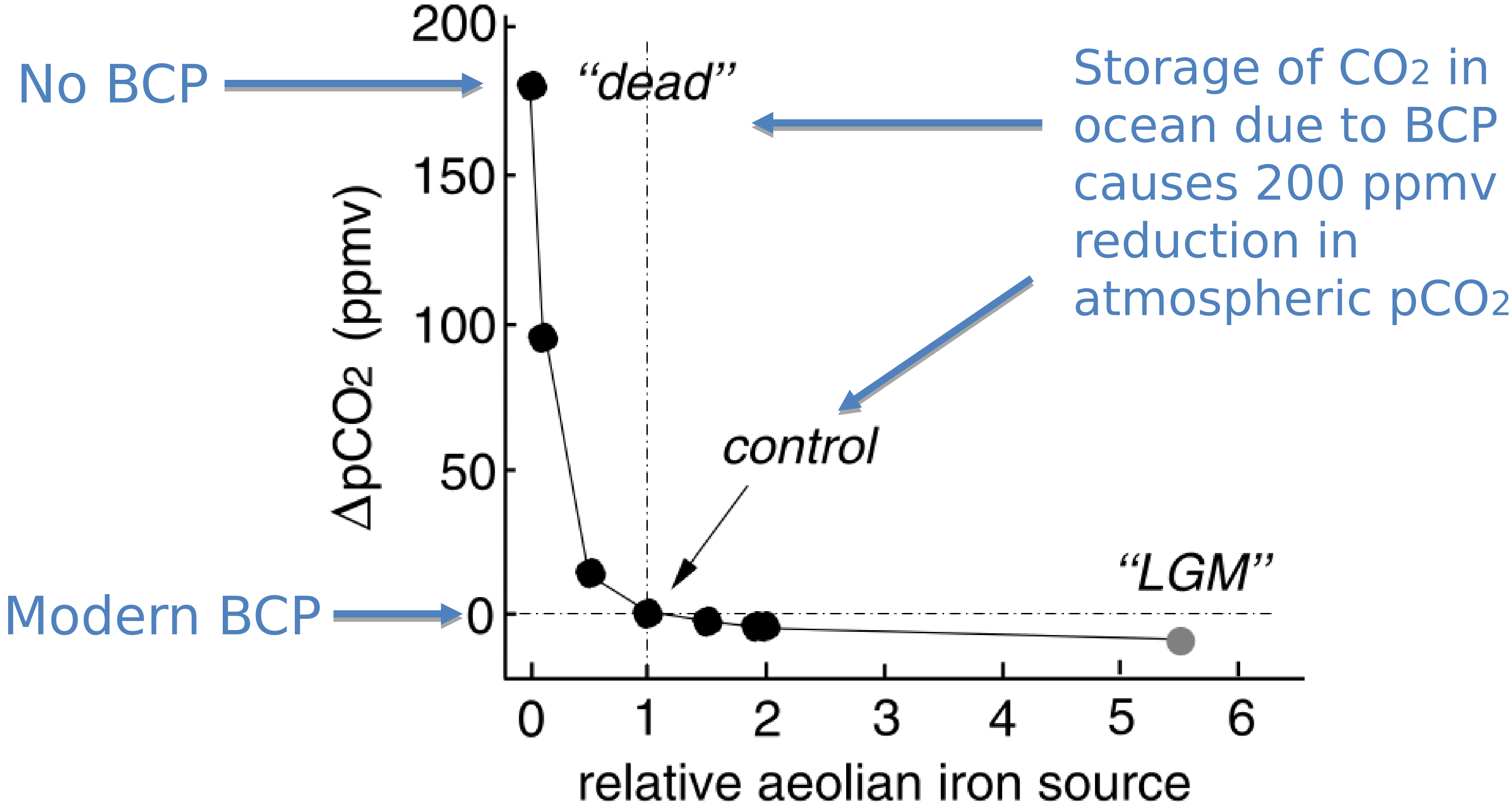


CO_2
CO_2
Large phytoplankton
Small phytoplankton
Zooplankton
Microzooplankton
Bacteria
Organic carbon
Surface ocean
Deep ocean
Deep consumers
CO_2
Bacteria
Sea floor

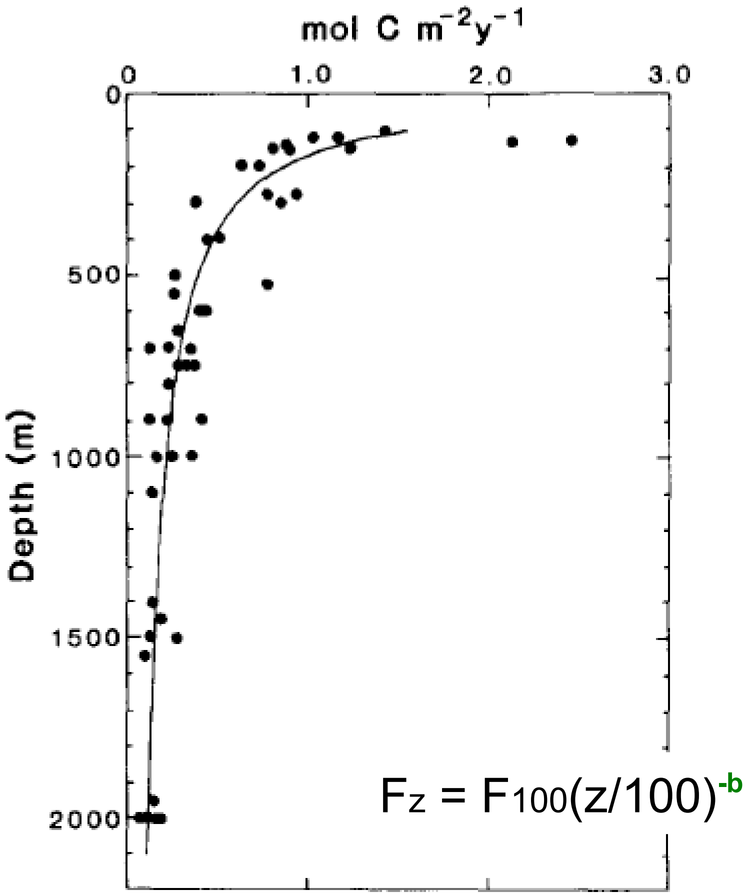
(US JGOFS)

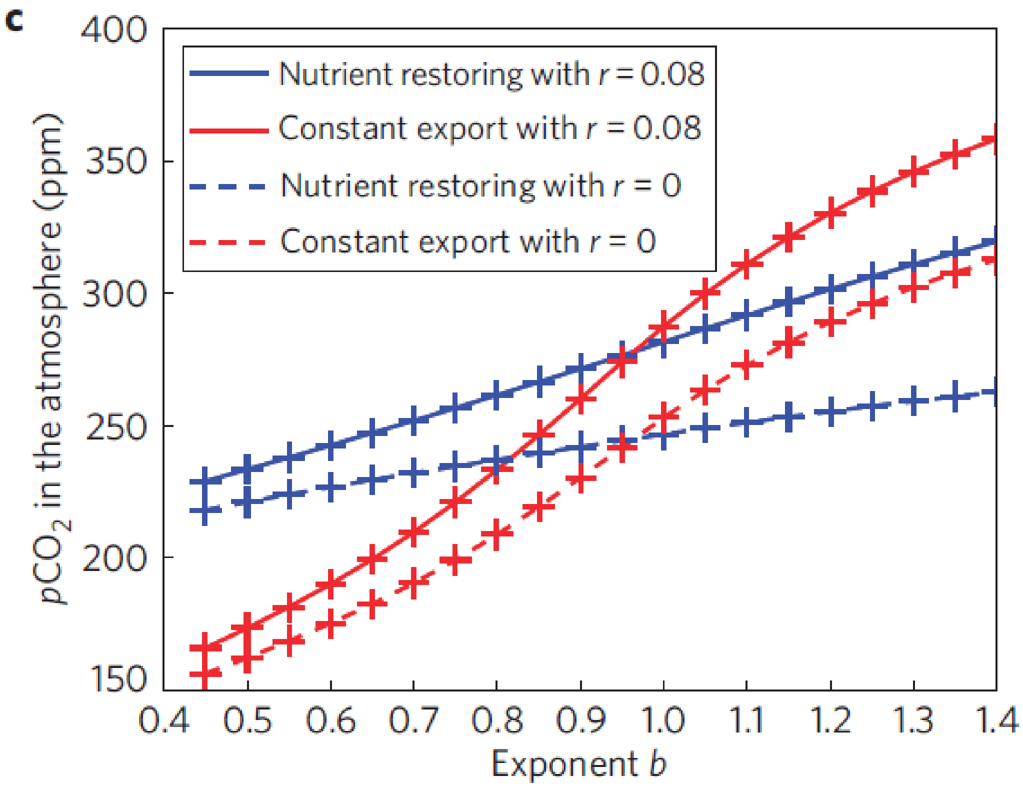
Ocean Biology – A valuable Ecosystem Service



(Parekh et al. 2006, GRL)

Role of Flux attenuation in regulating climate





(Kwon et al. 2009, Nature Geoscience

Martin et al. 1987, DSR)

Understanding *b* & what controls it key to understanding climate

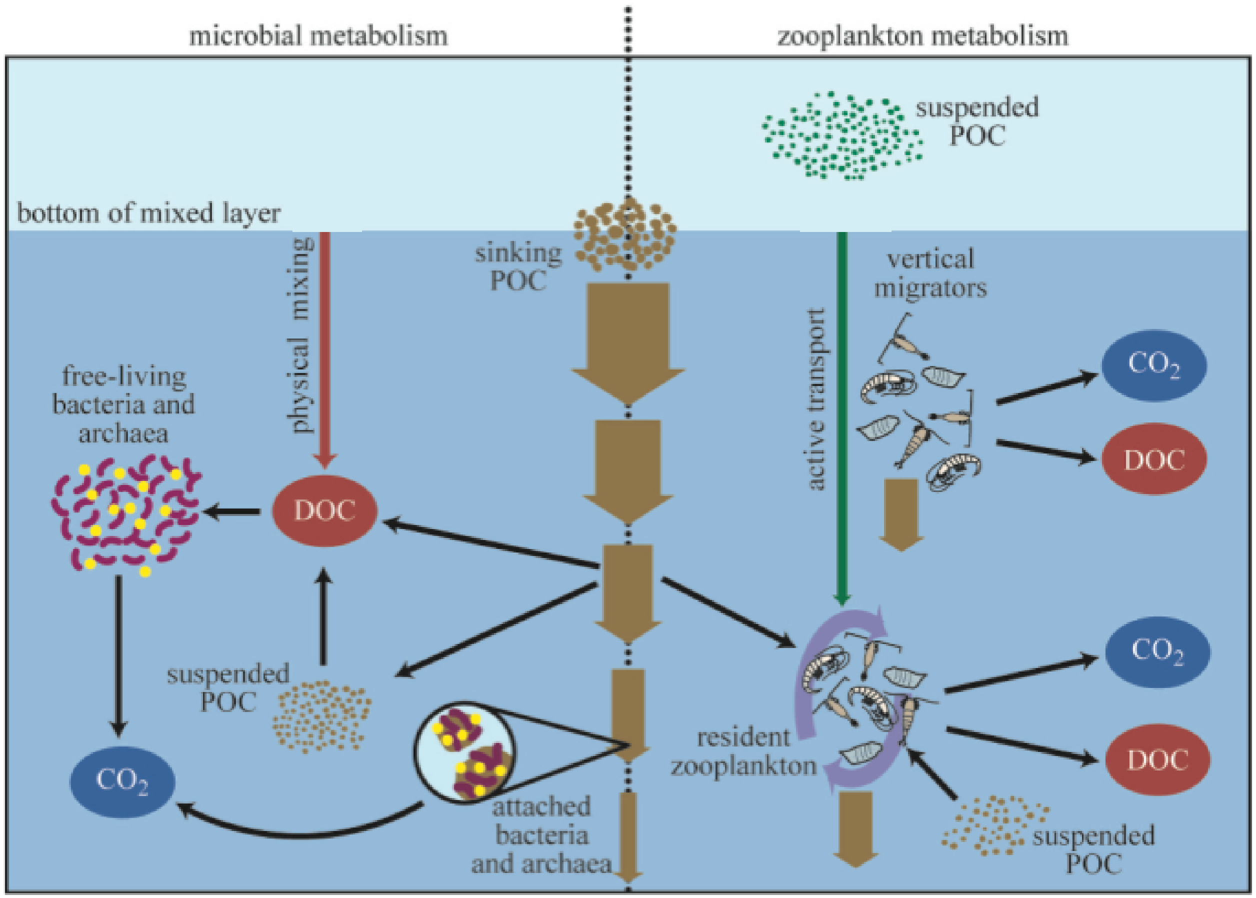


Fig. 1. Models of mesopelagic microbial (bacteria and archaea) and zooplankton metabolism.

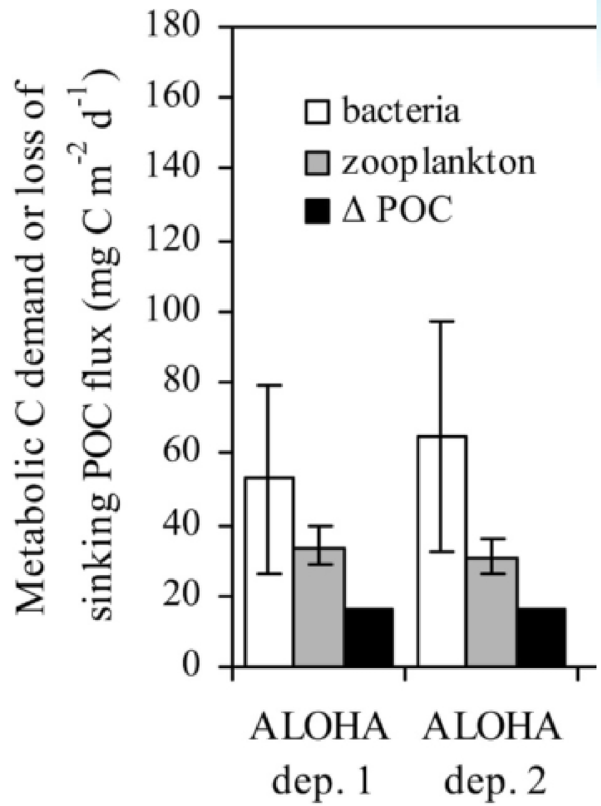
b = biology

(Steinberg et al. 2008, L&O)

If we understood the mesopelagic

- Then, at steady state
  - The consumption of POC in the mesopelagic, measured as the difference in flux at the top and base
  - Should equal zooplankton and bacterial carbon demand

It does not balance!



Station in the subtropical Pacific
(Steinberg et al. 2008)

	Depth range (m)	Source	Carbon demand	ΔPOC	Missmatch
NE Pacific	100 - 1000	Boyd et al. 1999	232-688	58	**4-12**
N Atlantic	100-1000	Reinthaler et al. 2006	5232P	978	**5**
Tropical N Atlantic	250-500	Balter et al. 2009	15-37P	0.3-12	**>2**

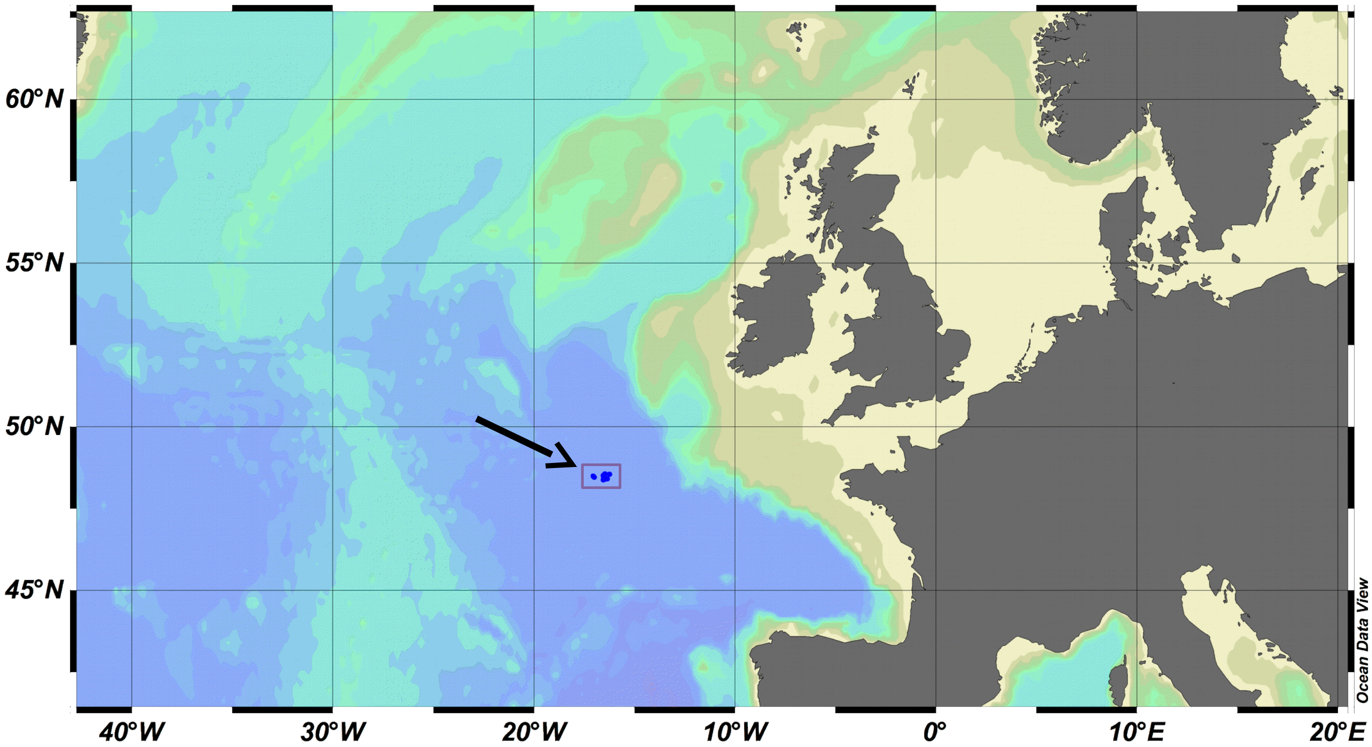
P: based on prokaryotic heterotrophs only

National Oceanography Centre, Southampton
UNIVERSITY OF SOUTHAMPTON AND NATURAL ENVIRONMENT RESEARCH COUNCIL

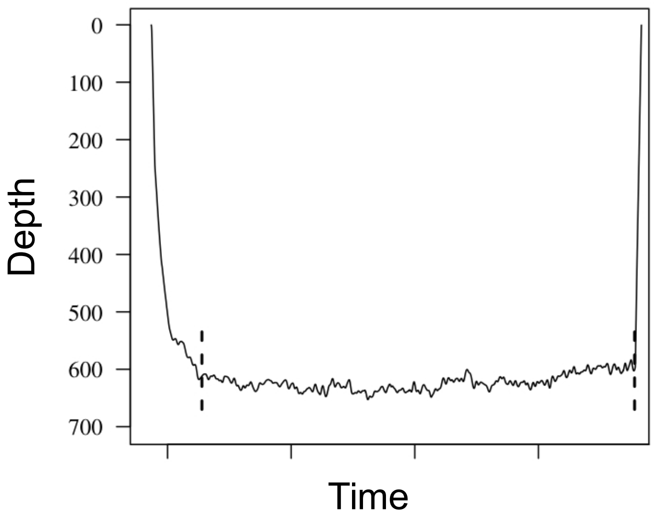
“Where are we going wrong?”

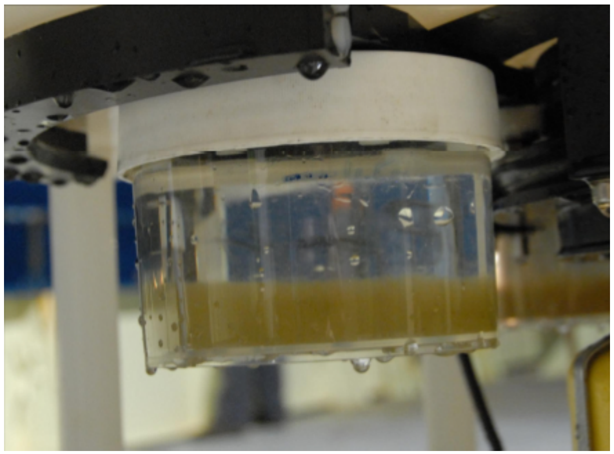
PAP site 2009

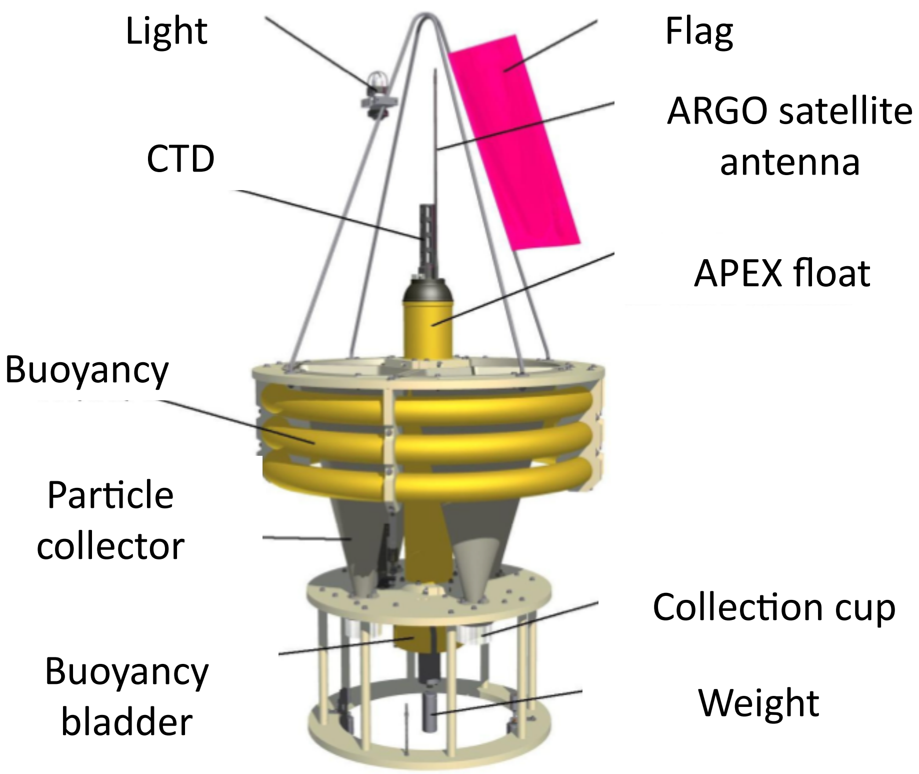
- Measure flux attenuation
- Compare to estimates of mesozooplankton and bacterial metabolism



PELAGRA
Neutrally buoyant sediment trap





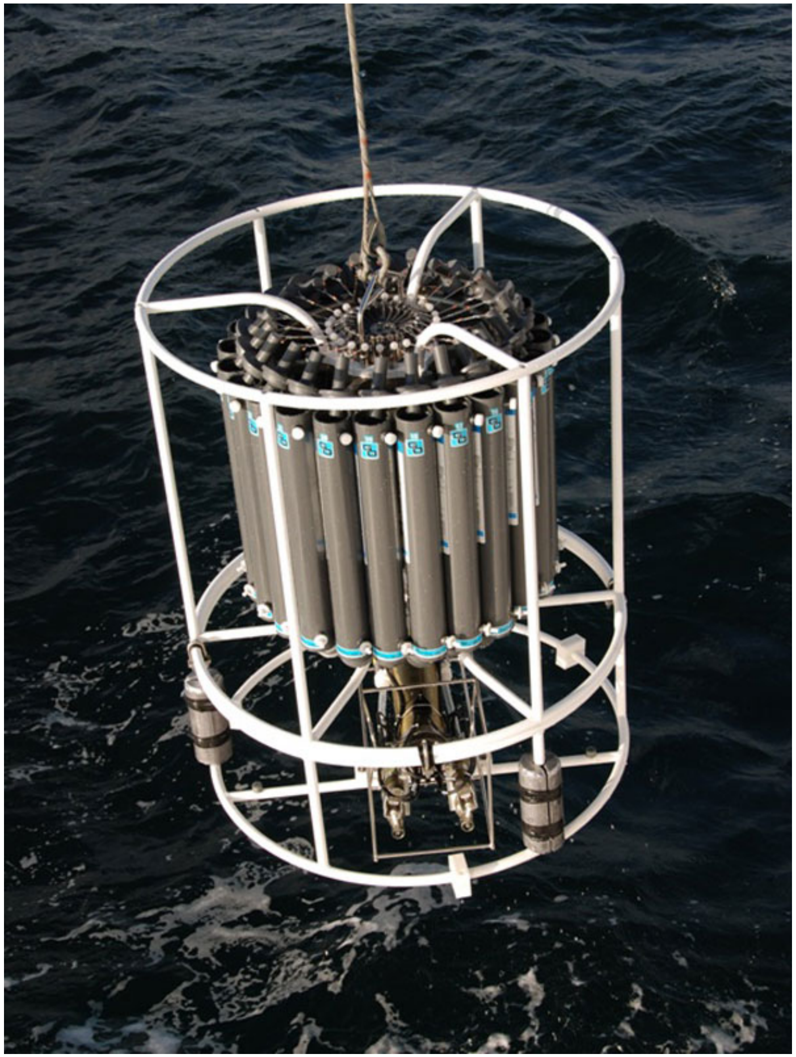


ARIES

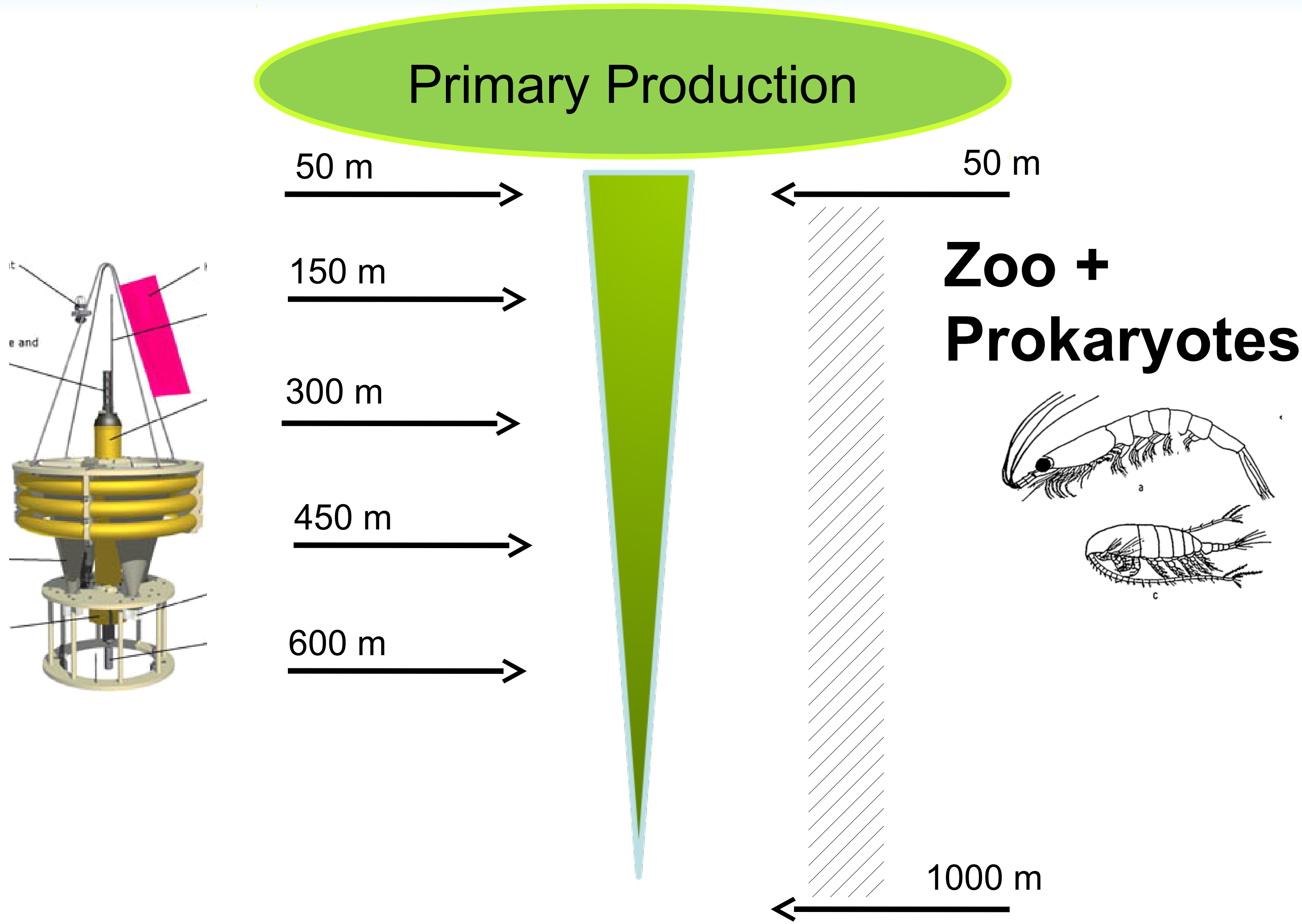
Autosampling & Recording Instrumented Environmental Sampling System

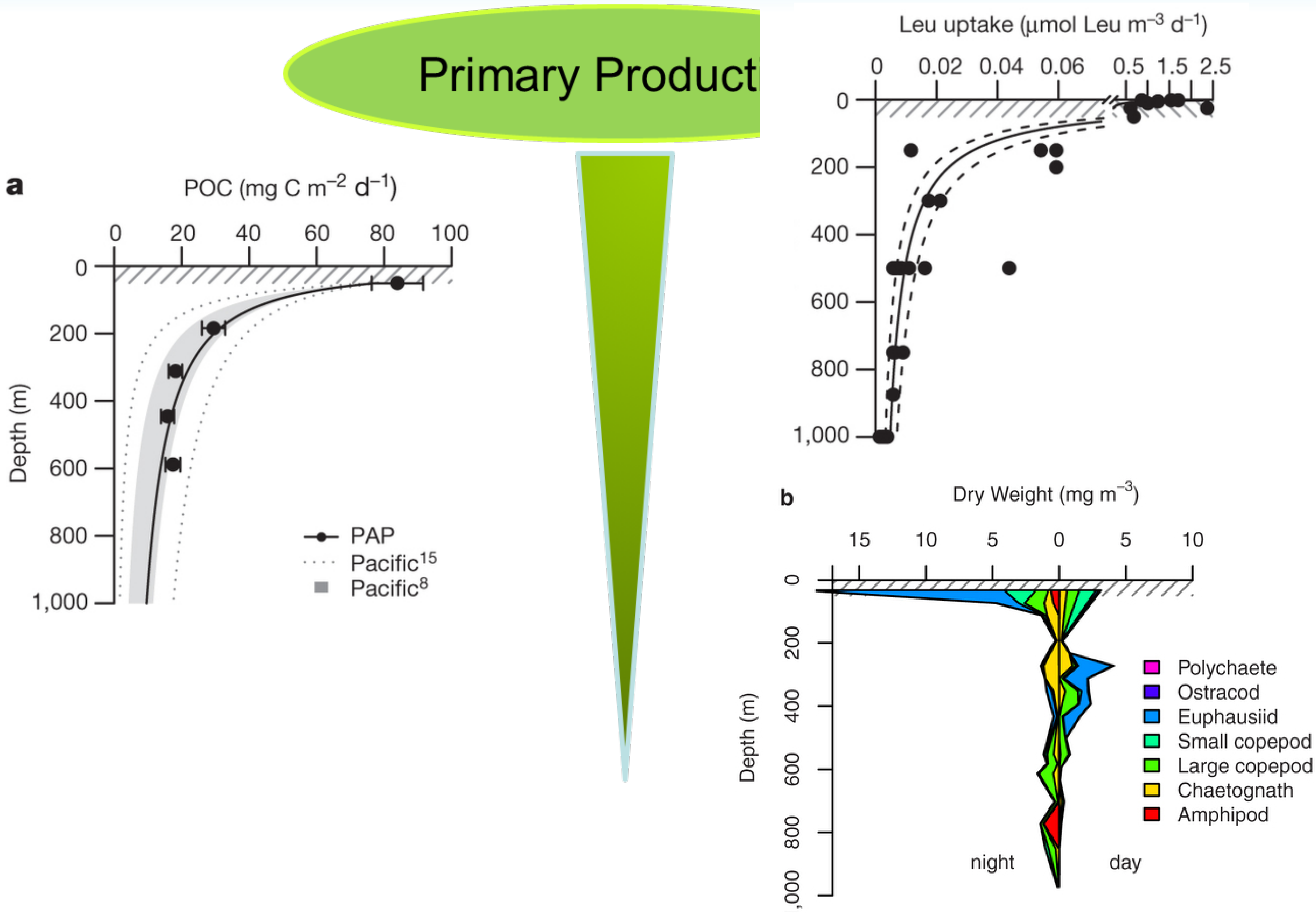
- towed behind the ship
- 110 samples from 55 discrete depth intervals
- converted using allometric equations

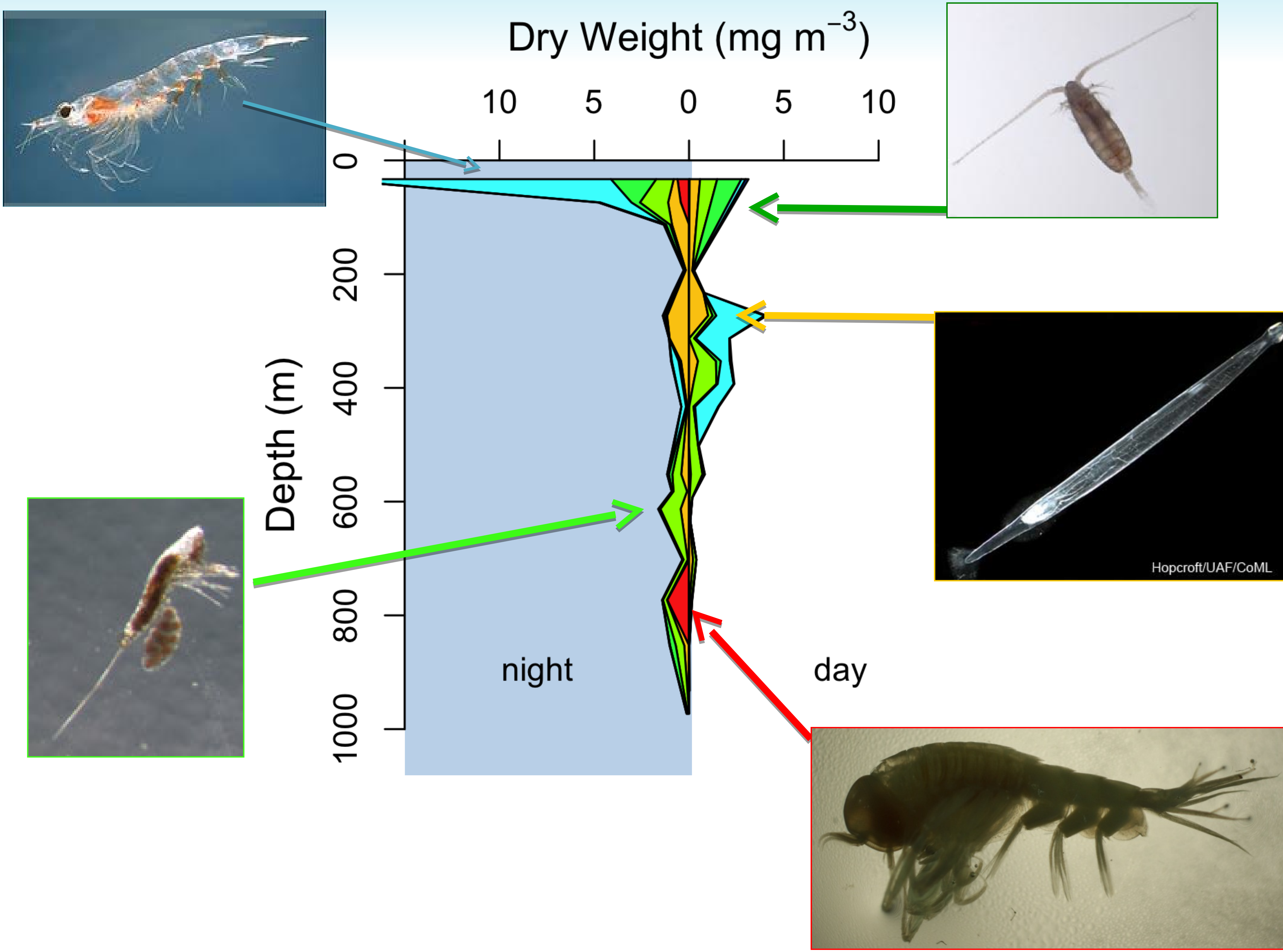
Prokaryotic activity



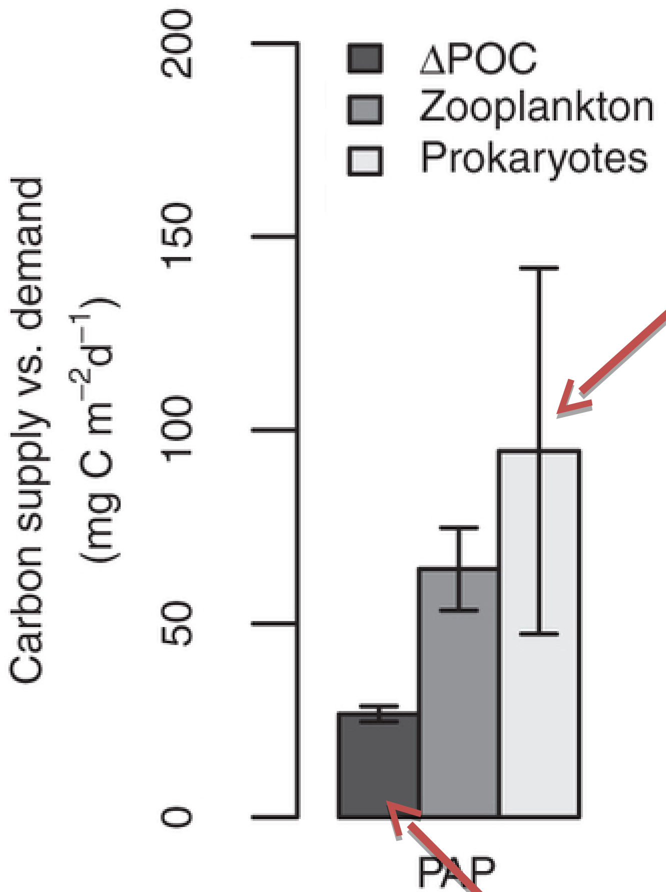
- Uptake of labelled amino acid leucine (^{3}H-leucine)
- 37 samples from 0-1000 m depth
- Converted to respiration and biomass production


Primary Production
50 m
150 m
300 m
450 m
600 m
50 m
Zoo +
Prokaryotes
1000 m


Primary Product
a
POC (mg C m^{-2} d^{-1})
0 20 40 60 80 100
Depth (m)
0 200 400 600 800 1,000
PAP
Pacific[15]
Pacific[8]
Leu uptake (µmol Leu m^{-3} d^{-1})
0 0.02 0.04 0.06 0.5 1.5 2.5
0 200 400 600 800 1,000
b
Dry Weight (mg m^{-3})
15 10 5 0 5 10
Depth (m)
0 200 400 600 800 1,000
Polychaete
Ostracod
Euphausiid
Small copepod
Large copepod
Chaetognath
Amphipod
night
day

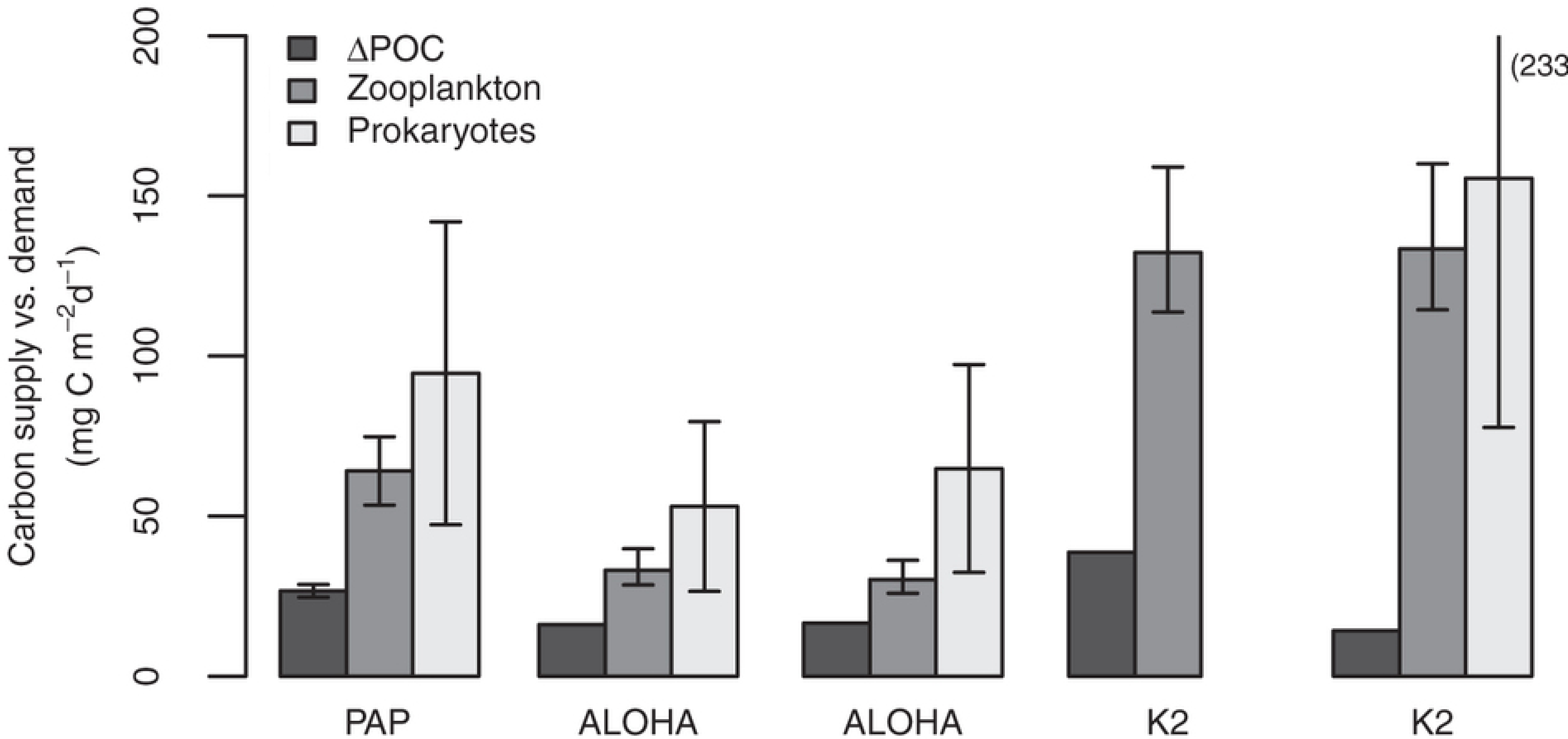

Dry Weight (mg m^{-3})
10
5
0
5
10
Depth (m)
0
200
400
600
800
1000
night
day
Hopcroft/UAF/CoML

Does it balance at PAP?



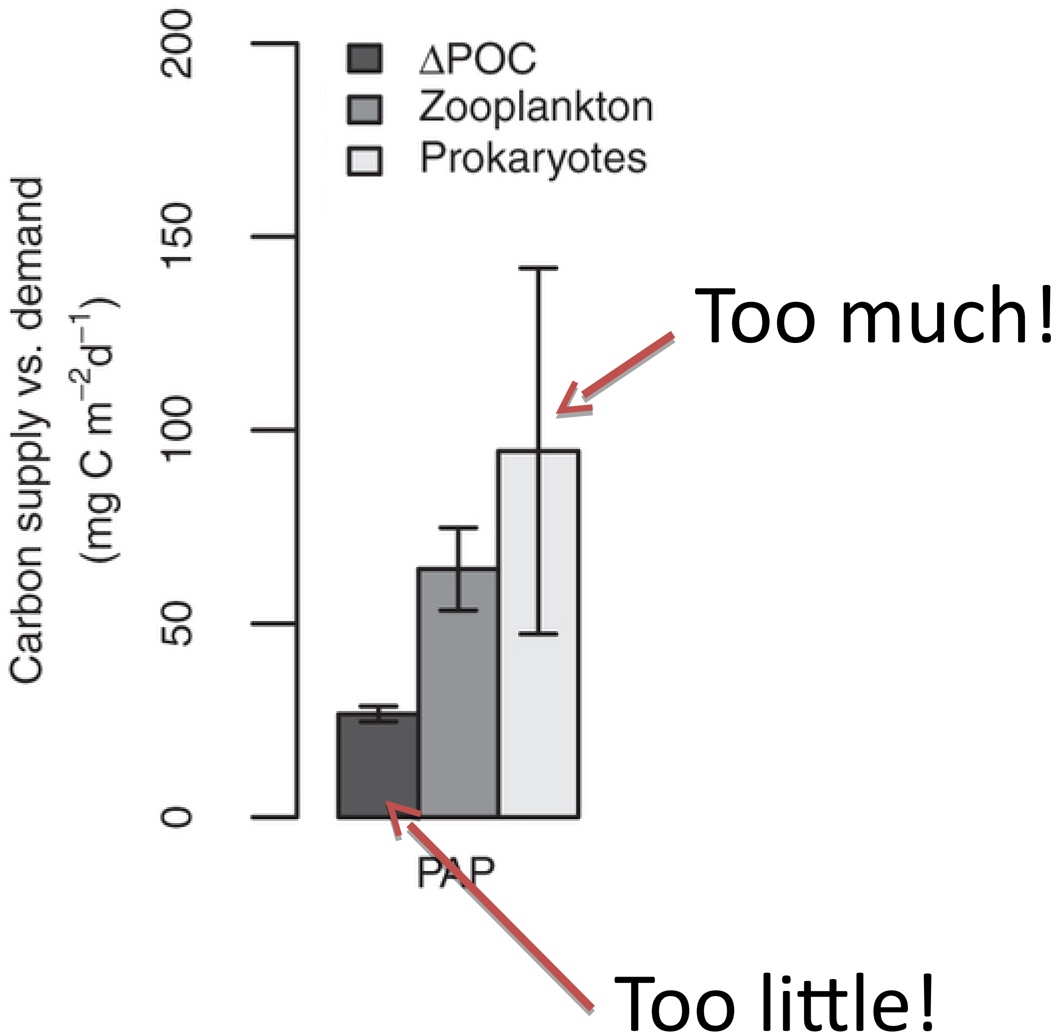
Too much!

Too little!

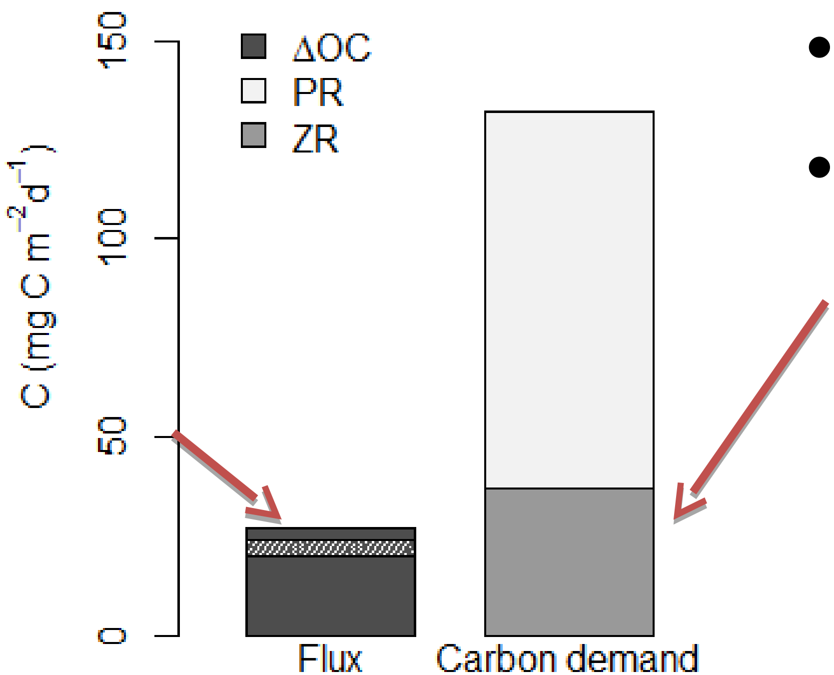


(Steinberg et al. 2008, L&O)

Innovations needed

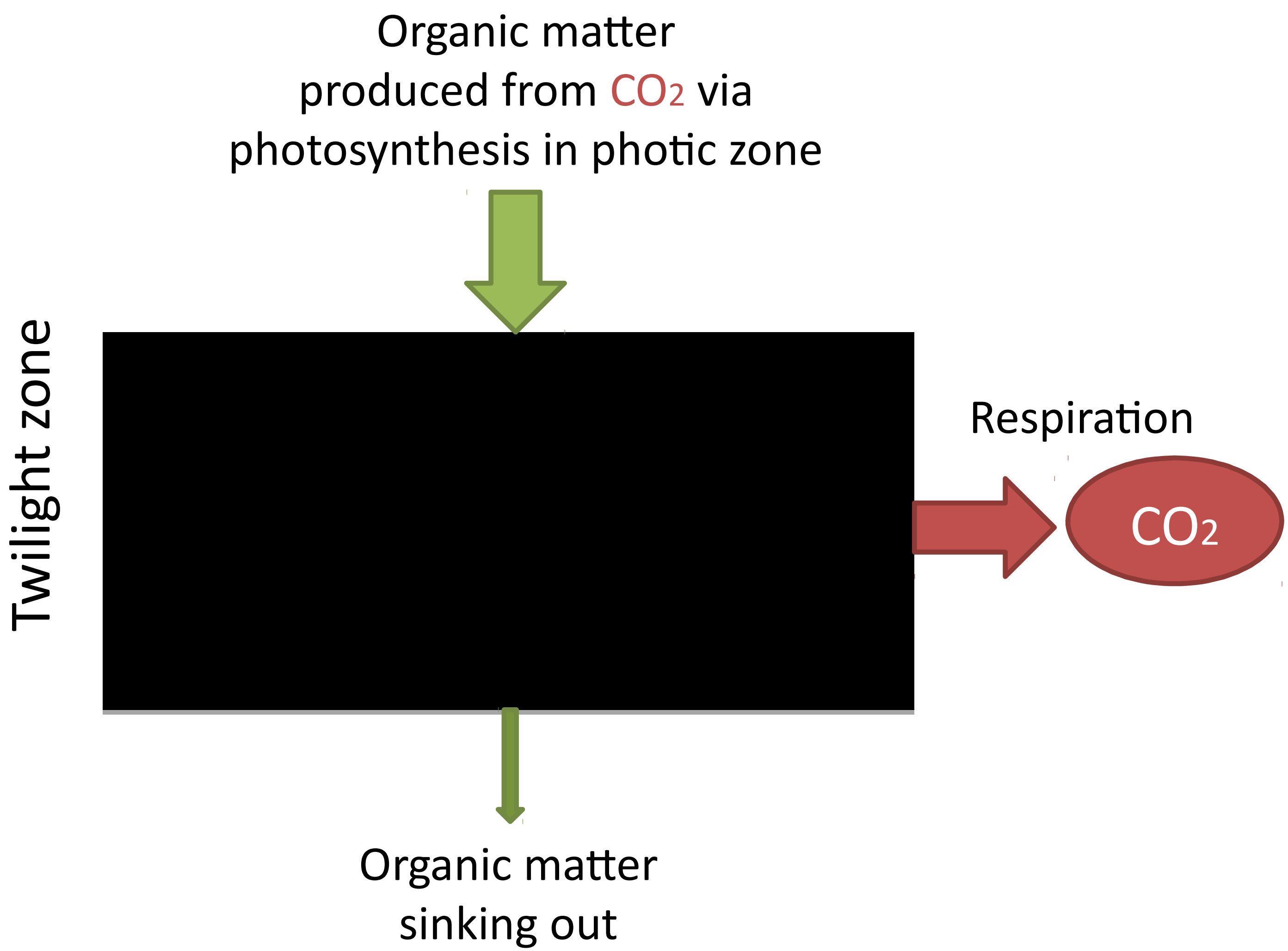


Innovations needed



- Add DOC
- Add active transport
- Assume vertical migrators consume at the surface

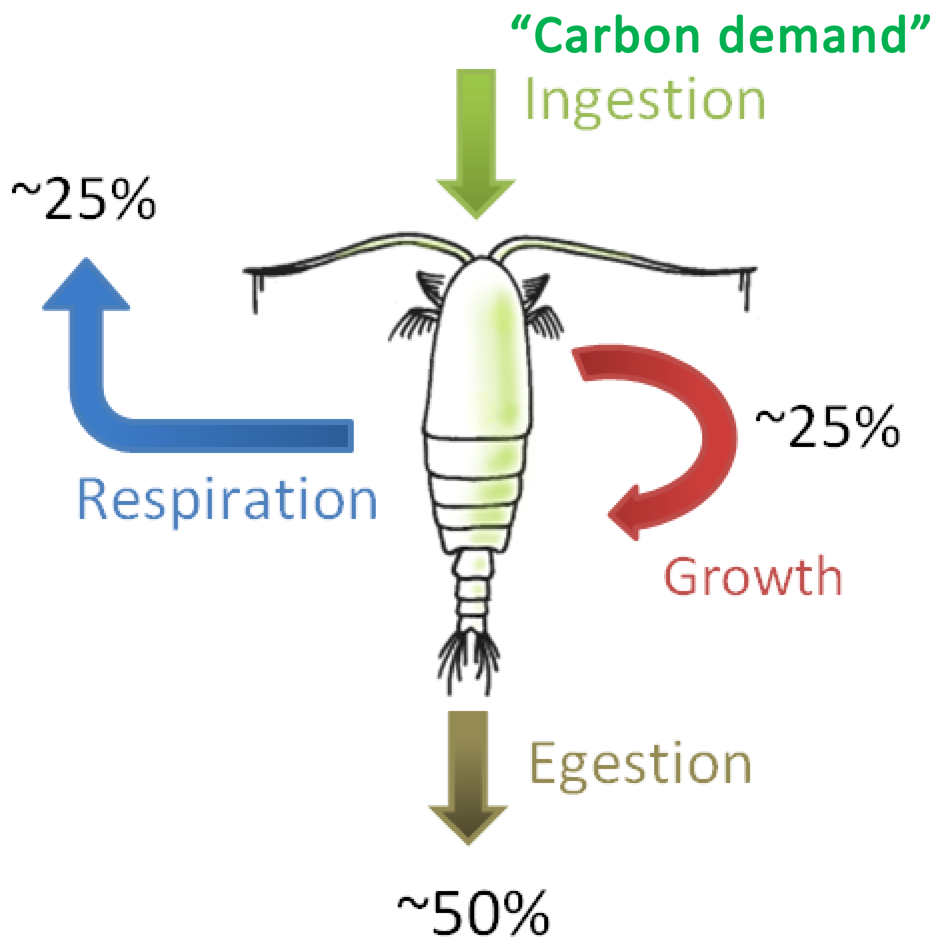
Simple mass balance



Correct estimates of 'output' term

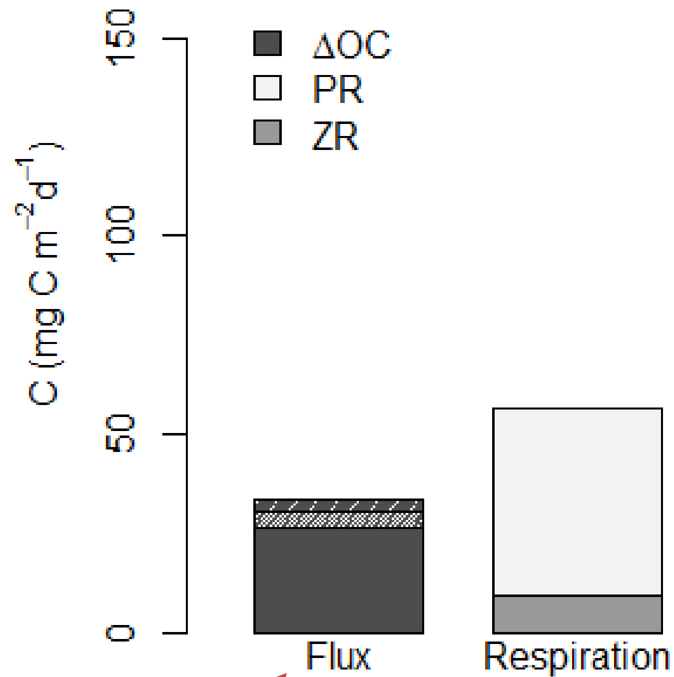
Microbial carbon demand =

Respiration + Production

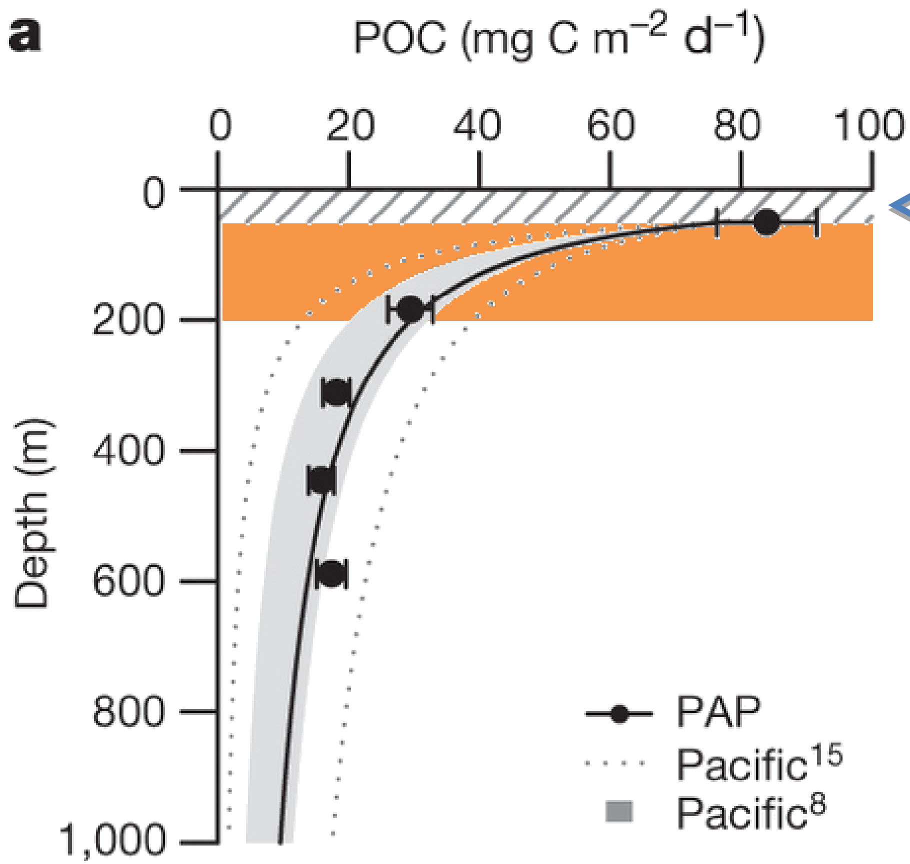


Innovations needed

- Consider **respiration** rather than carbon demand!



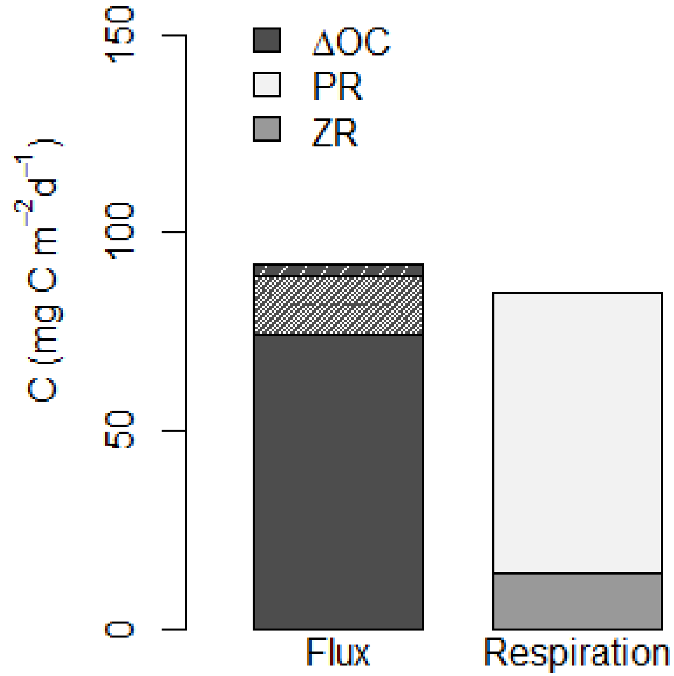
Better!



Mixed layer
(50 m deep)

Innovations needed

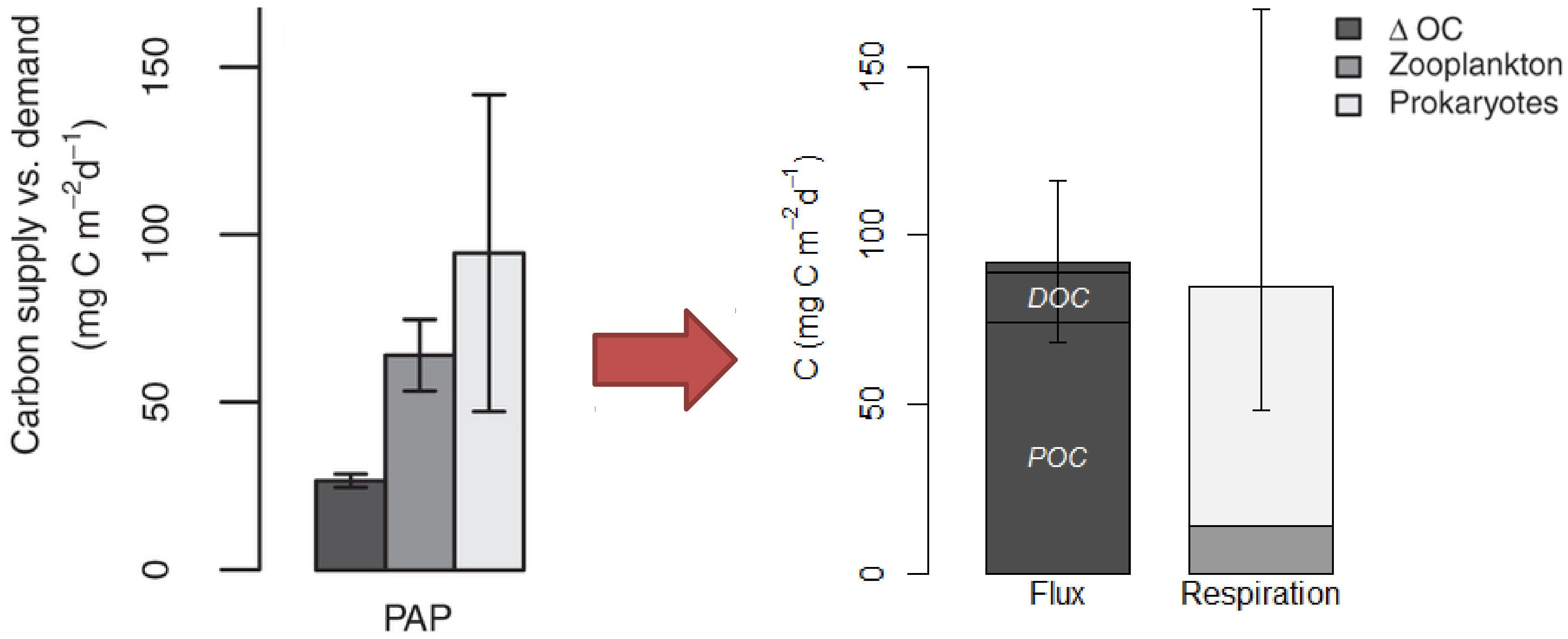
- Integrate over different depth range:
- 50 - 1000 m



Wow!

(Giering et al. 2014, Nature)

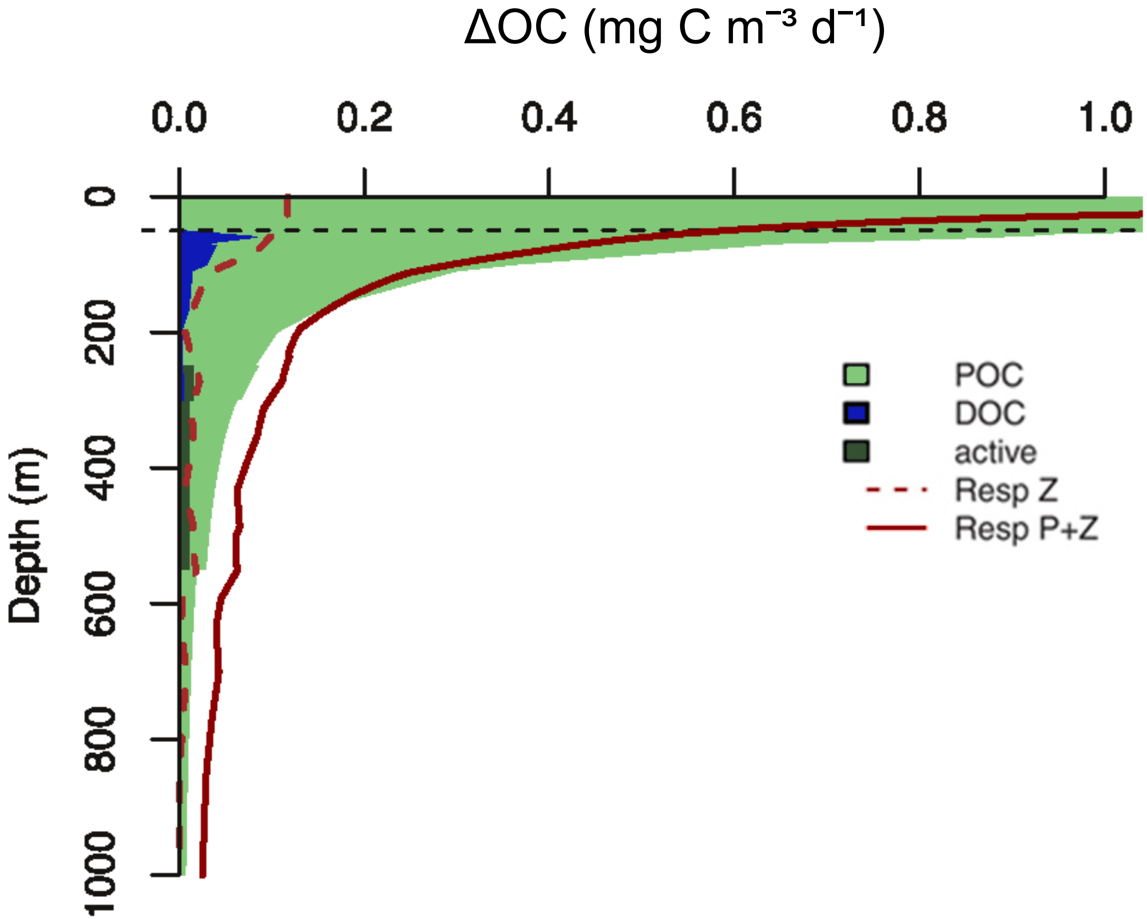
All changes matter



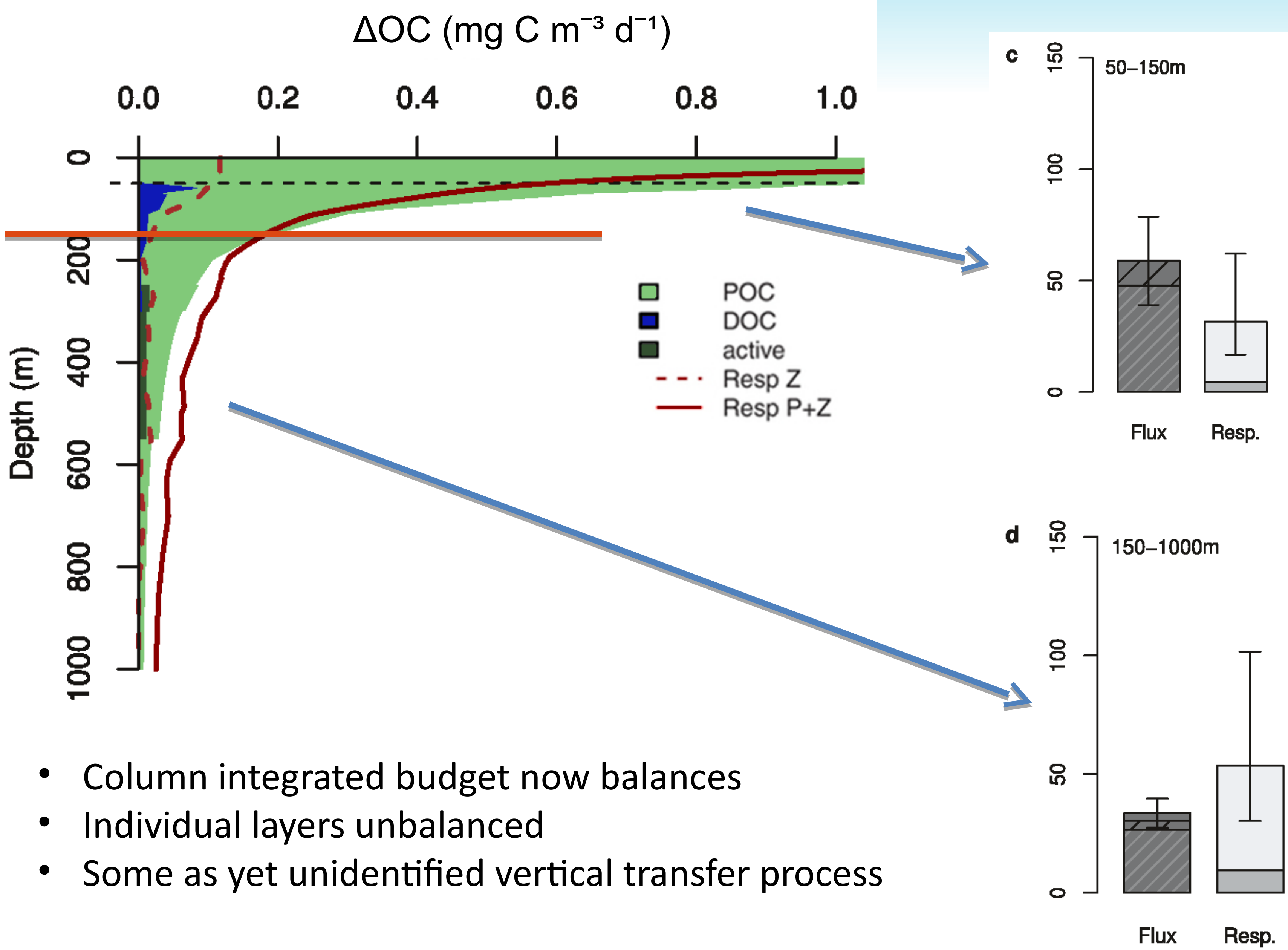
1. OC supply multiplies by ~4 (25 vs. 100) due to inclusion of extra flux (50-150 m) + DOC + active flux)

2. Zooplankton term decreases by ~4 despite greater biomass in target range (50 vs. 15)

3. Prokaryotic term respiration increases owing to extra depth range (75 vs. 90)



- Column integrated budget now balances



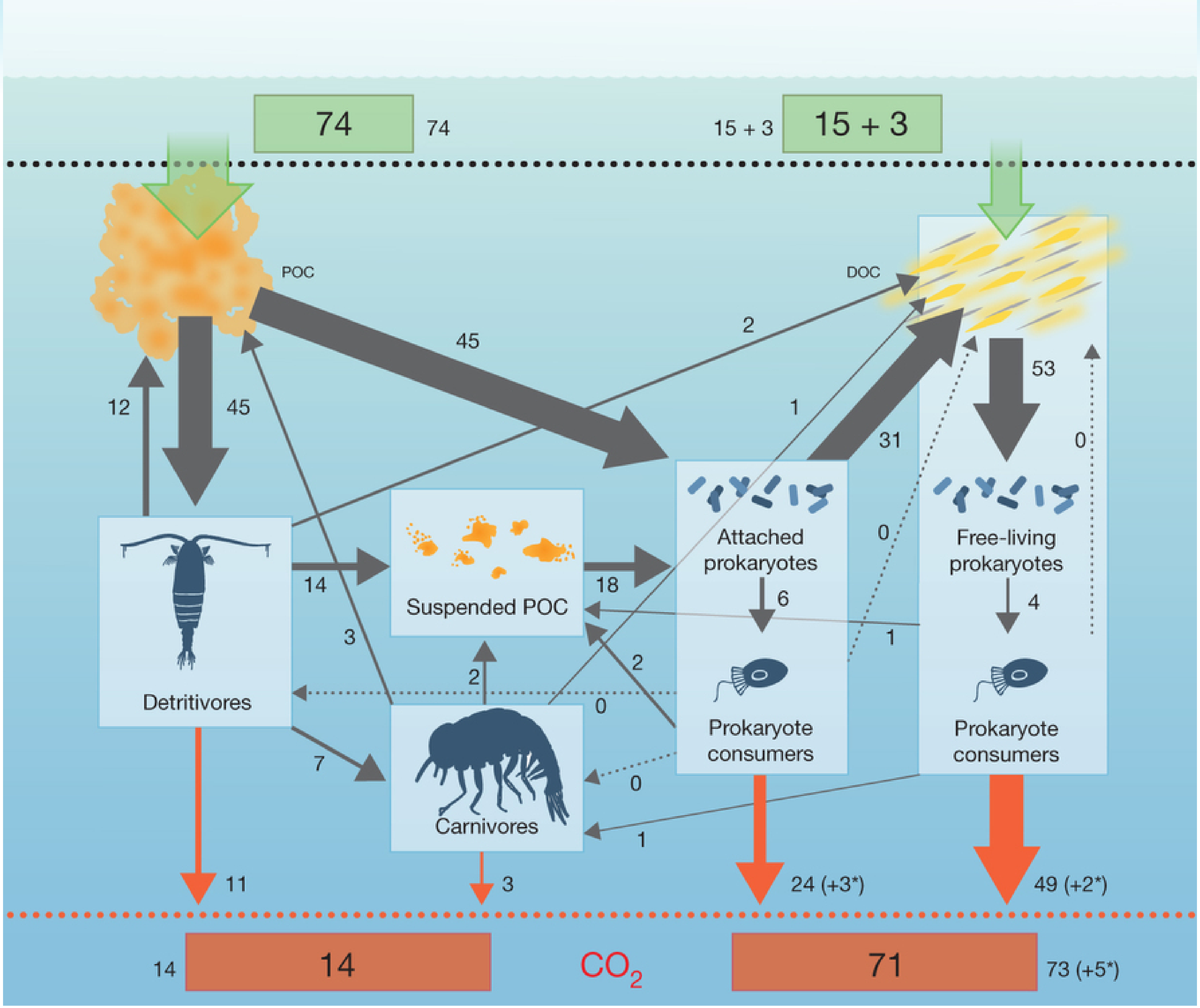
- Column integrated budget now balances
- Individual layers unbalanced
- Some as yet unidentified vertical transfer process

- Or miss-estimated bacterial respiration and problem still unsolved?

Conclusions

- Have achieved a balanced carbon budget for mesopelagic
- Respiration (not carbon demand)
- Integrating from base of mixed layer
- Vertical migrators graze at surface
- Include DOC

- Vertical imbalance persists
- Need better estimate of prokaryotic activity



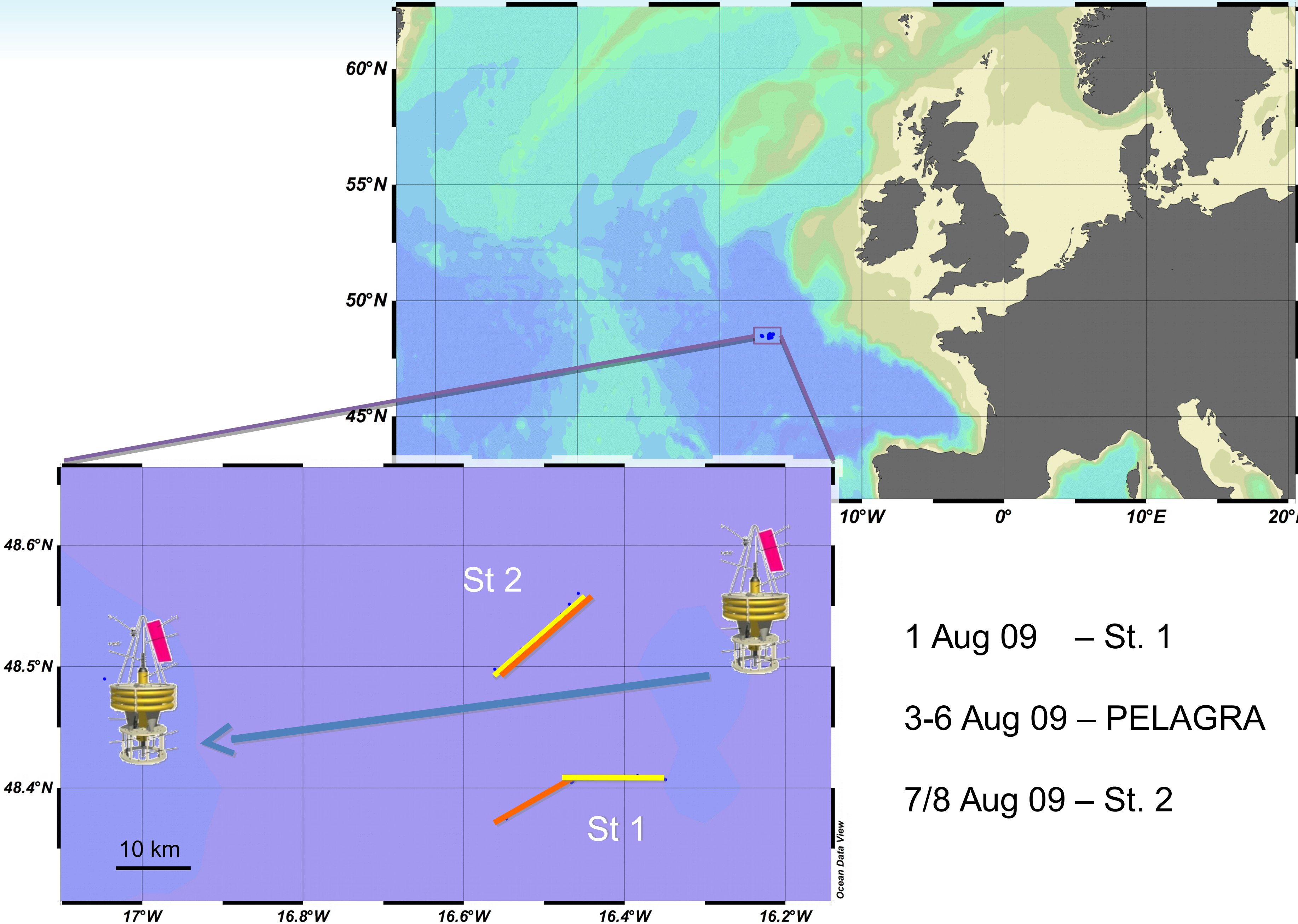
(Giering et al. 2014, Nature)

Questions

- How can we decrease uncertainties?
- What is going on between 50 and 200m?
- What about microzooplankton and higher trophic levels?
- What controls rate of flux attenuation?

Acknowledgements

- Thanks to the captain, crew & scientists of the RRS Discovery and cruise D341
- Jim Hunter, Sam Ward & Thom Cornulier
- OSCAR Project & BODC for data
- Oceans 2025, EURO-BASIN, ANR-POTES programme & NERC for funding

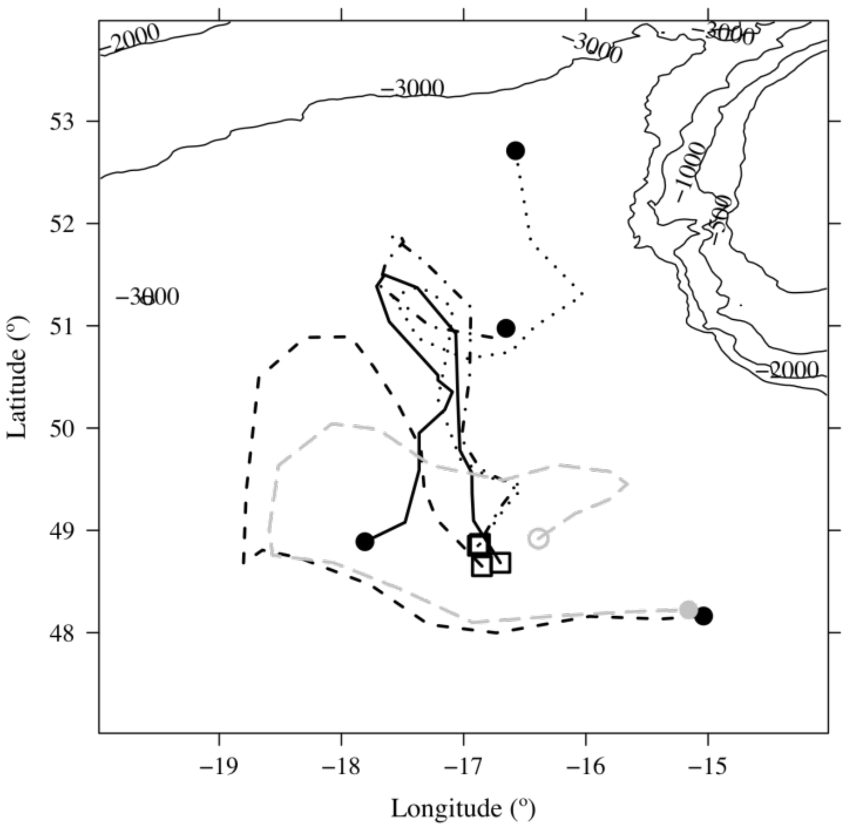


1 Aug 09 – St. 1

3-6 Aug 09 – PELAGRA

7/8 Aug 09 – St. 2

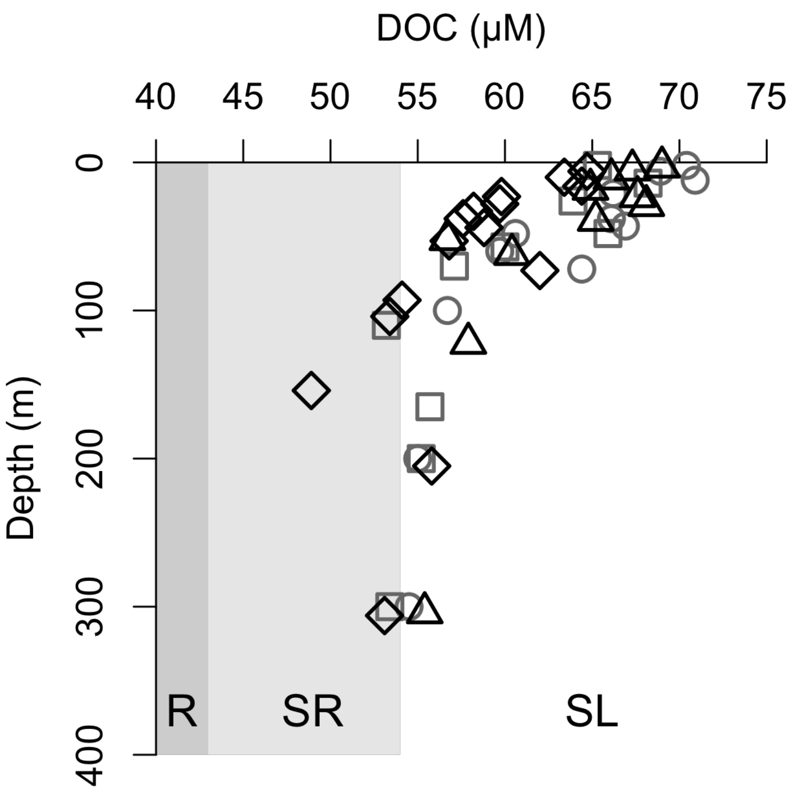
Lateral advection



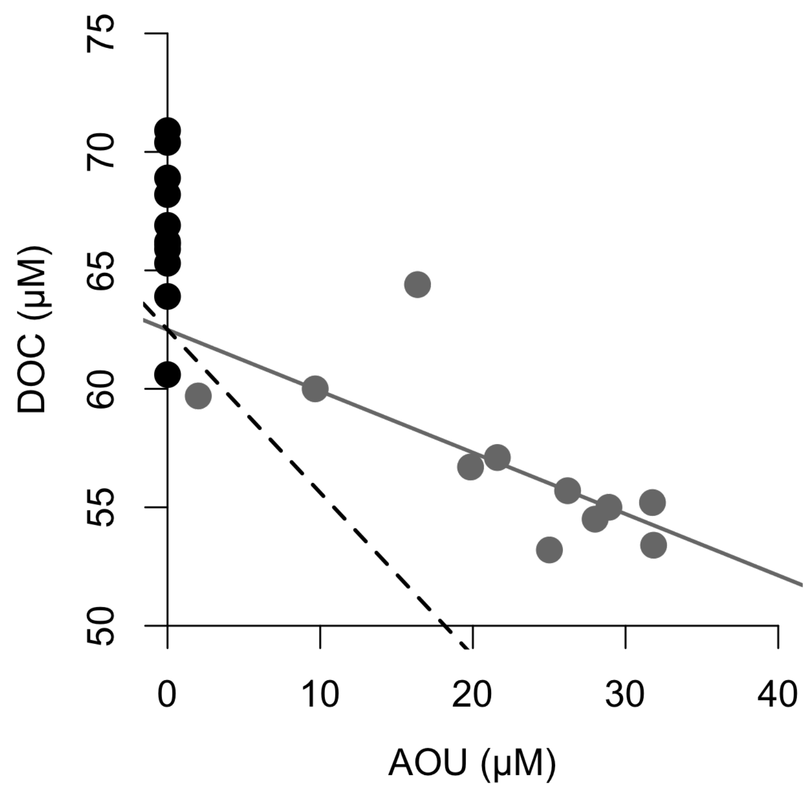
Advection of OC into the region:
0 mg C m-2 d-1

Surface particle back trajectories of the water masses sampled using PELAGRA (grey) and ARIES (back)

i. DOC



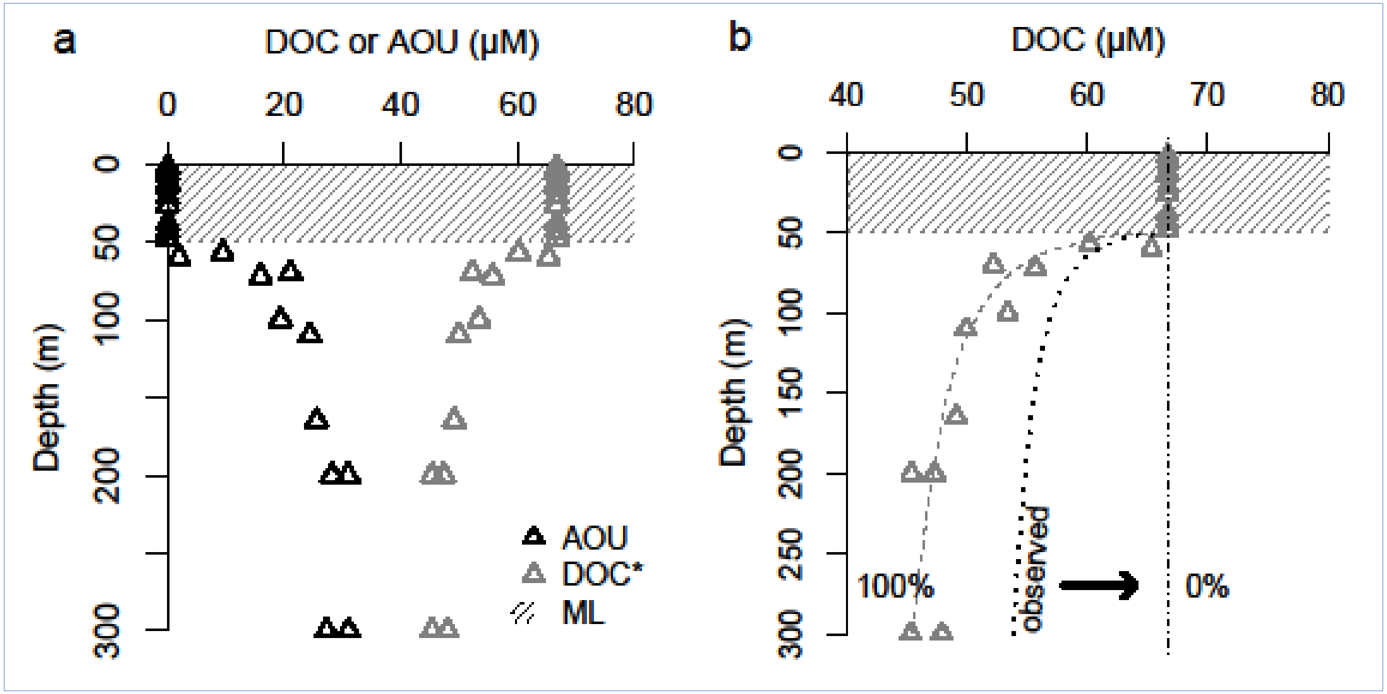
Measured during two previous cruises at the PAP site



DOC input via vertical mixing:

15 mg C m-2 d-1

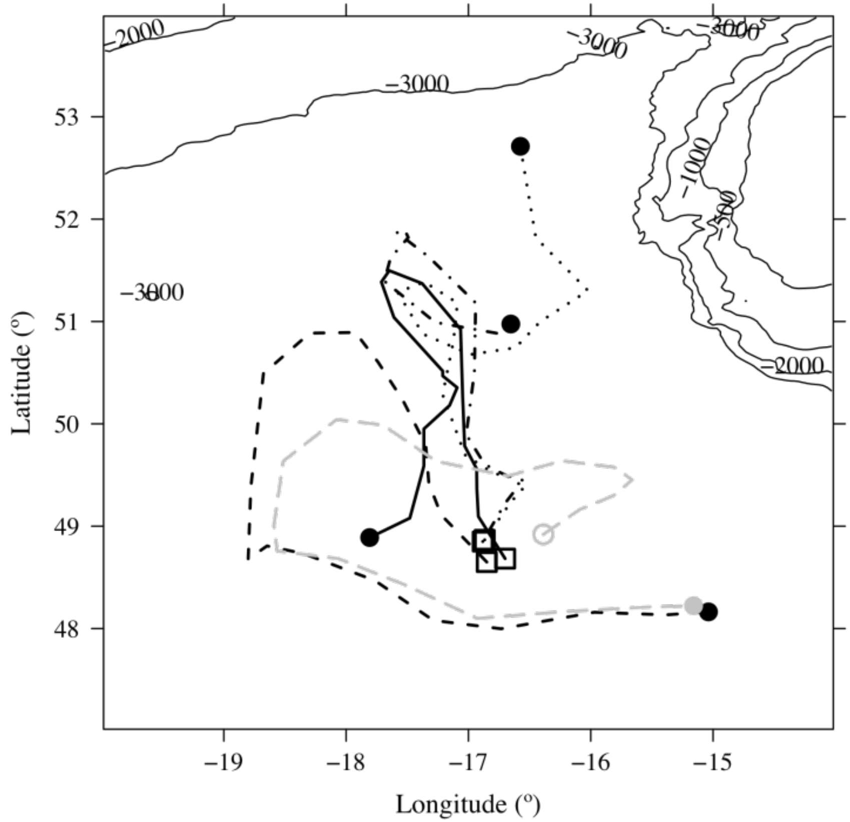
Theory behind AOU:DOC calculations



(**a**) Depth profiles of apparent oxygen utilization (AOU) and theoretical DOC concentration that would be observed if all respiration were due to the consumption of DOC (DOC*). DOC* concentrations in the mixed layer (ML; shaded area) are the average of measured DOC at the PAP site.

(**b**) Depth profiles for concentrations of DOC*, observed DOC, and theoretical DOC if none of the AOU were due to DOC consumption. Internal recycling of DOC (e.g. via dissolution of POC) will increase observed DOC concentrations (arrow) and lead to an underestimation of the relative importance of DOC for interior respiration.

Lateral advection



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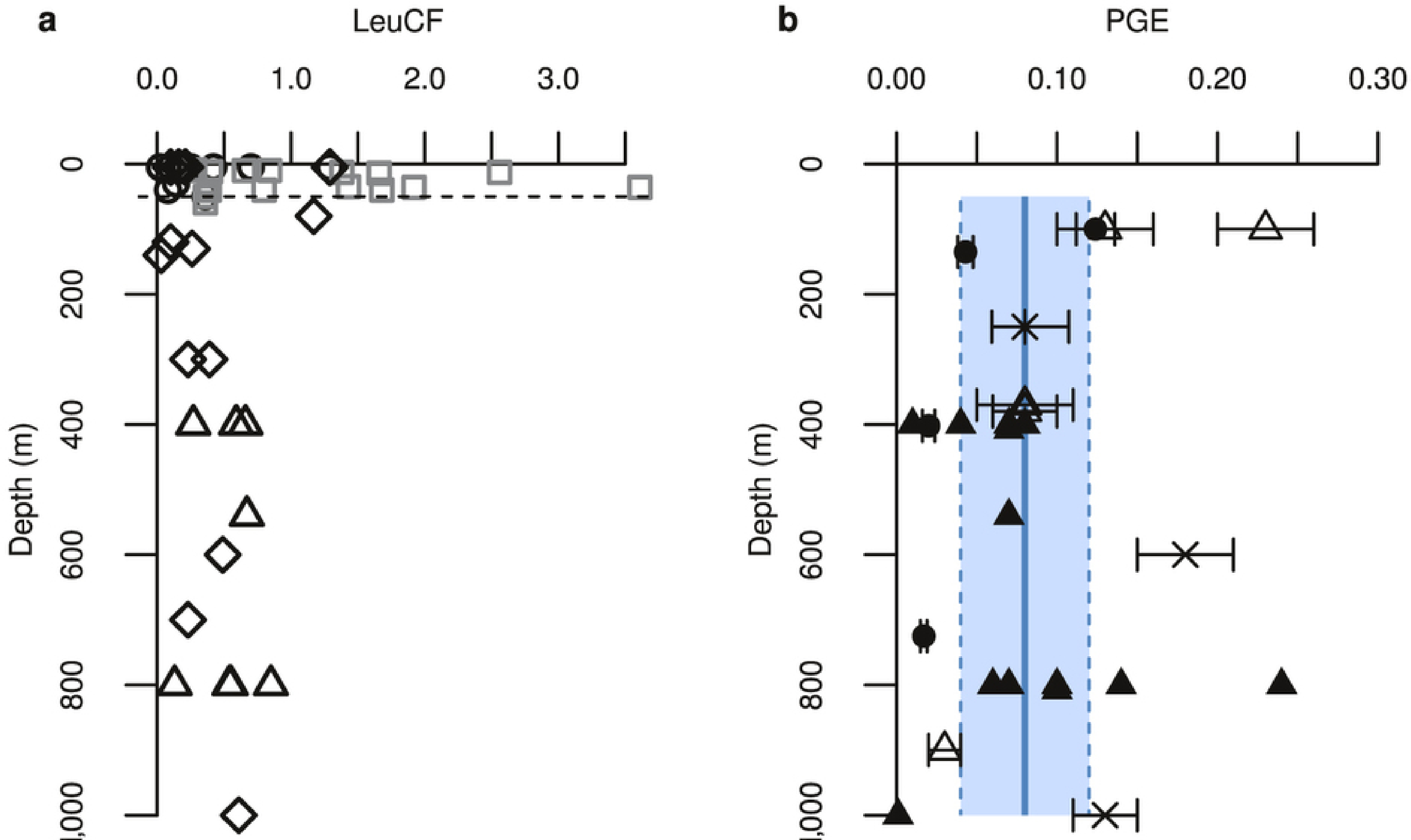
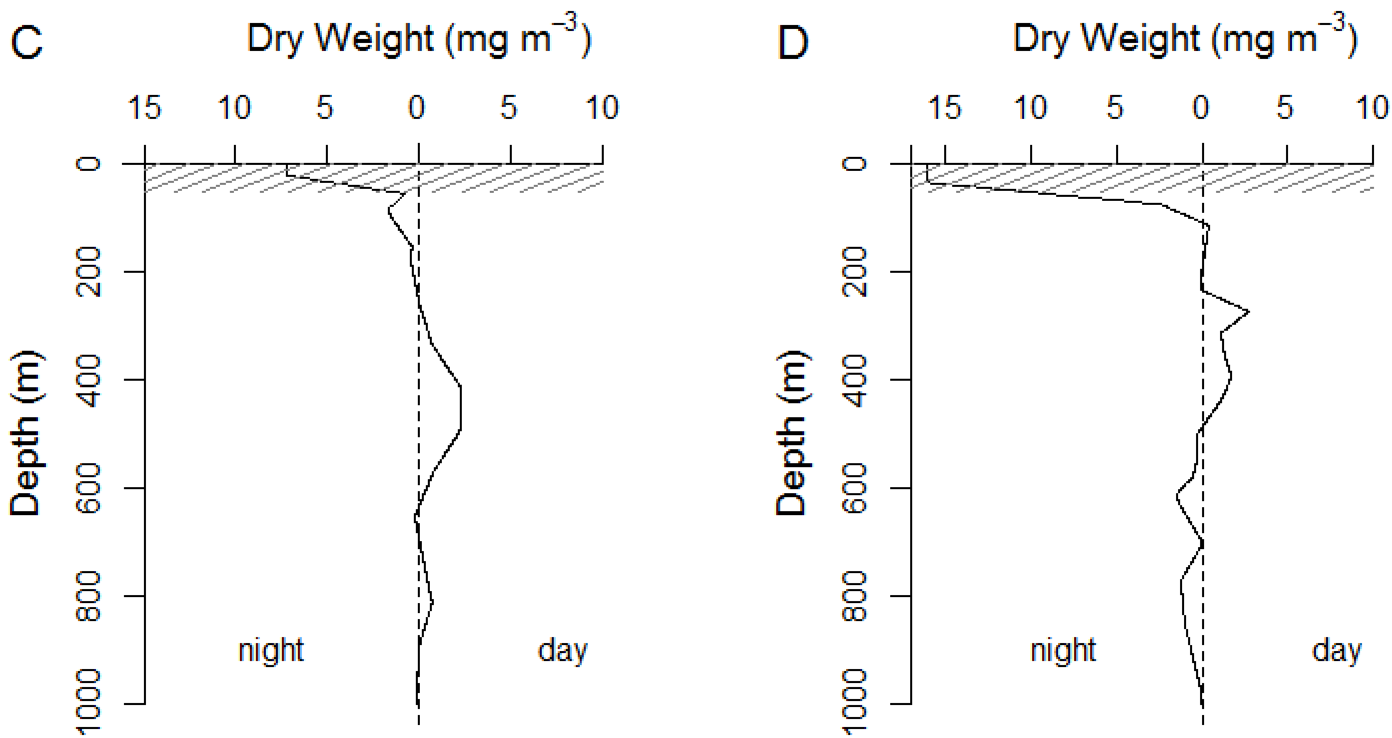
Surface particle back trajectories of the water masses sampled using PELAGRA (grey) and ARIES (back)



a
LeuCF
0.0
1.0
2.0
3.0
Depth (m)
0
200
400
600
800
1,000
b
PGE
0.00
0.10
0.20
0.30
Depth (m)
0
200
400
600
800
1,000

iii. Active transport

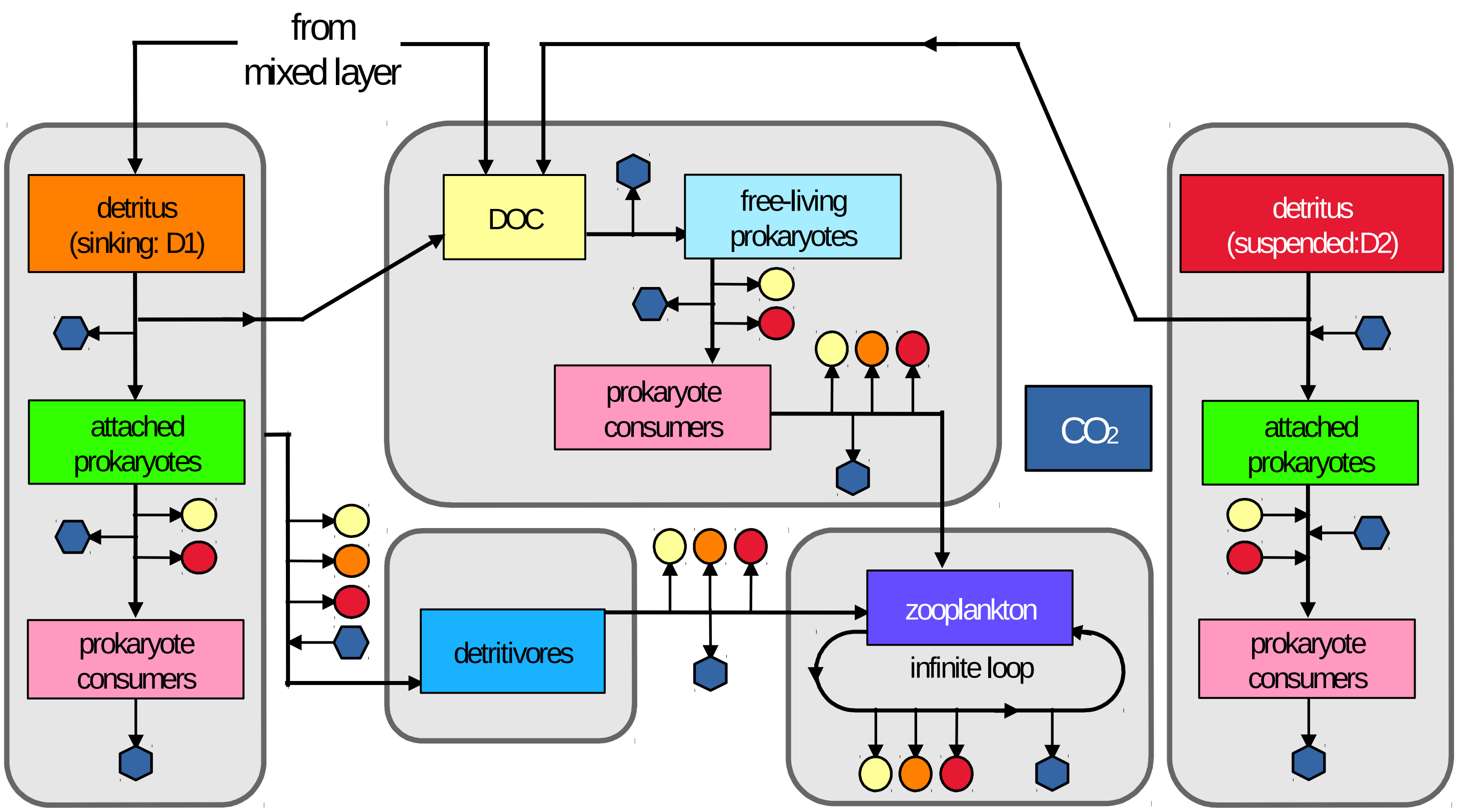


Active DOC export □ 31% of respiration of migrators between 50 – 1000 m:

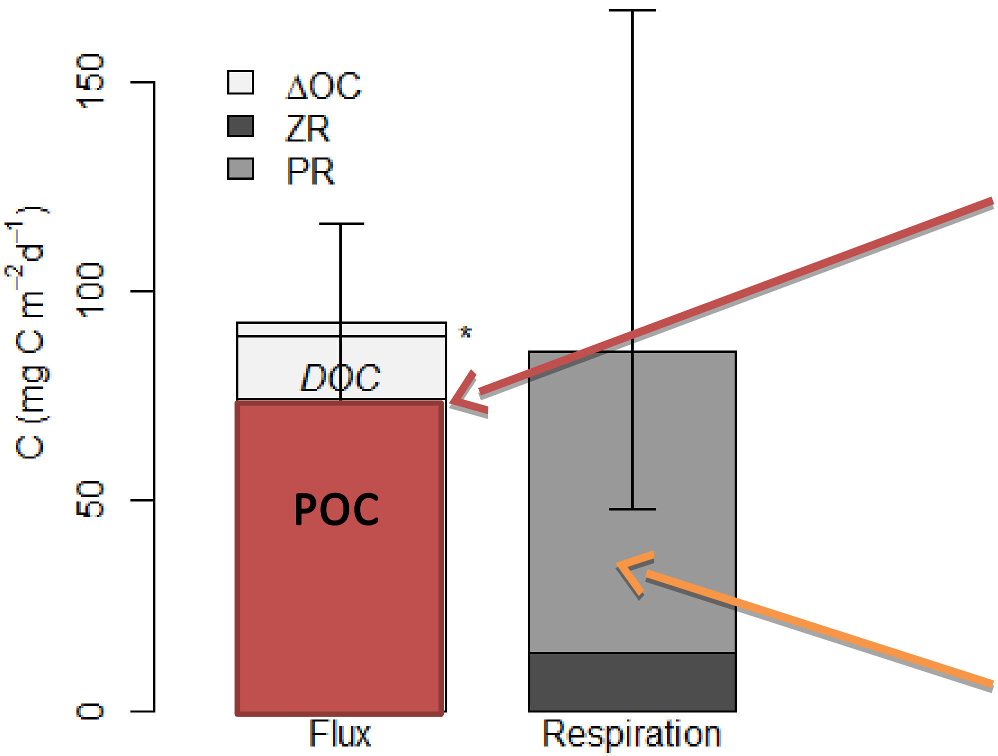
3 mg C m-2 d-1

A food-web model

(based on Anderson & Tang 2010)



How does the budget work?



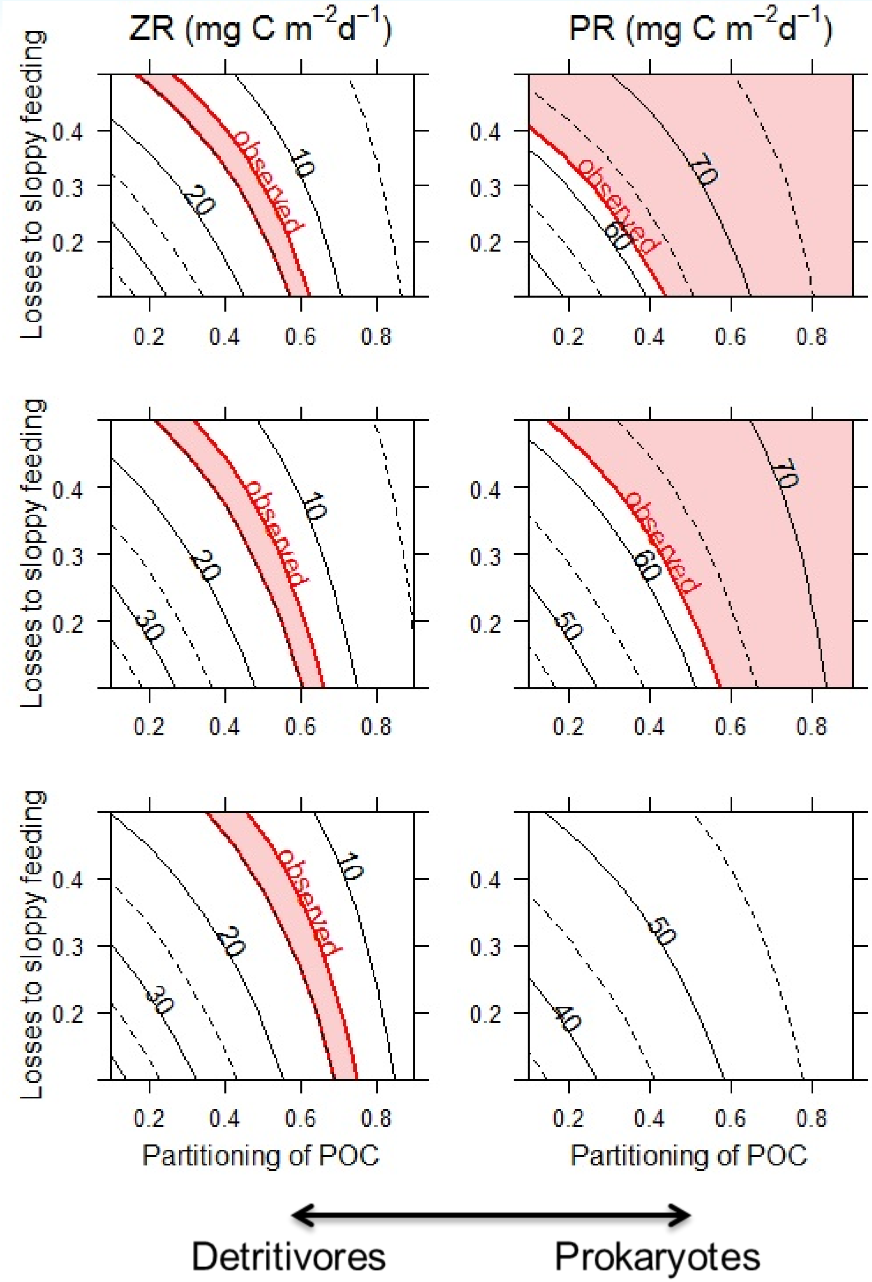
80% of available carbon is available to zooplankton

> 85% of respiration is microbial!

PGE = 0.1

PGE = 0.2

PGE = 0.4



The model is relatively robust to changing model parameter.

Interestingly, with a higher the prokaryotic growth efficiency more ‘sloppy feeding’ is needed to arrive at the observed rates.