

Kill-the-Winner in four environments

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Overview

- Kill-the-Winner
- Microbial loop
- Methods and results
- Conclusions

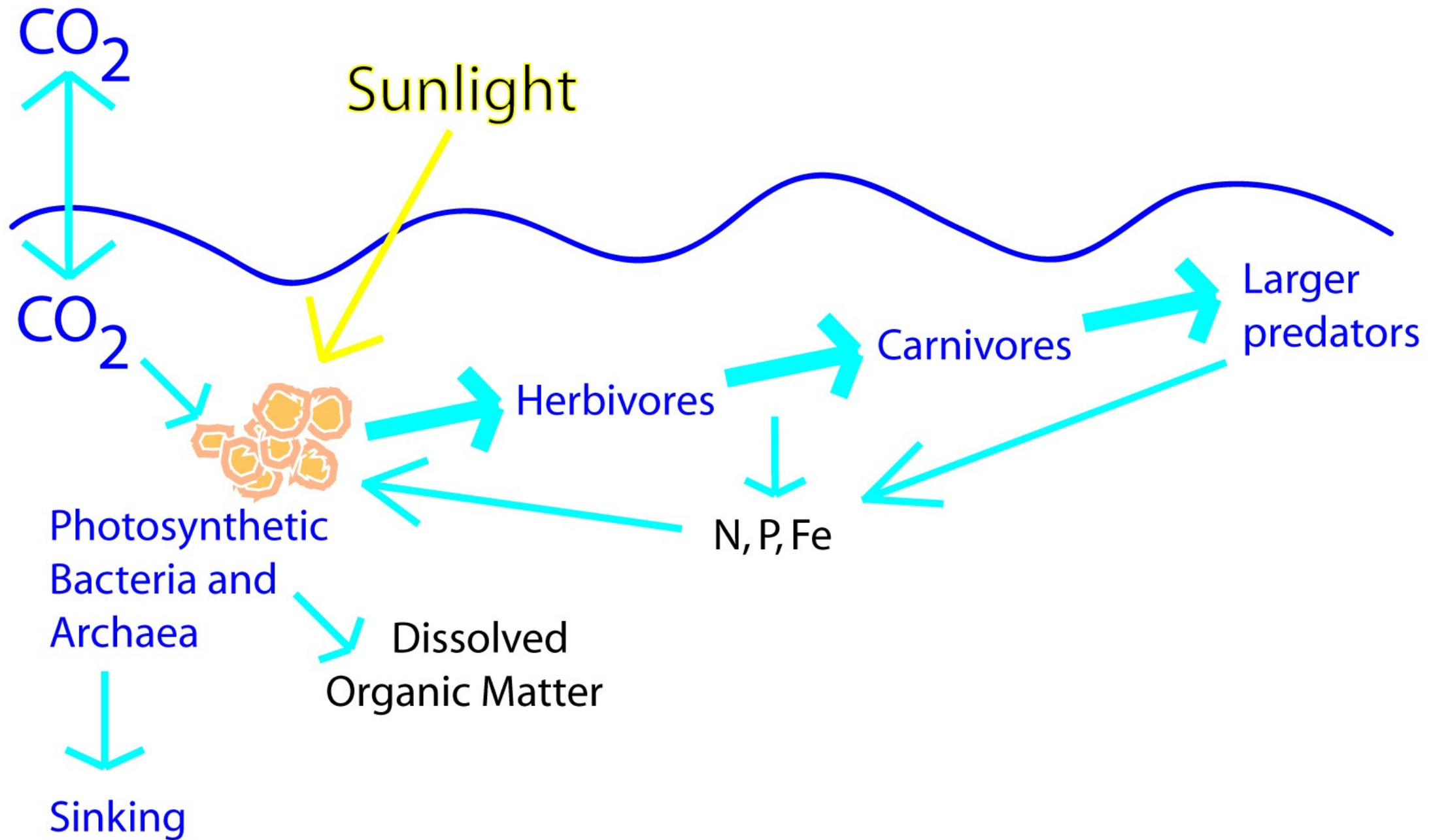
Hypothesis driven research : Kill-the-Winner

- Viral-mediated killing of dominant microbes
- Leads to community structure changes

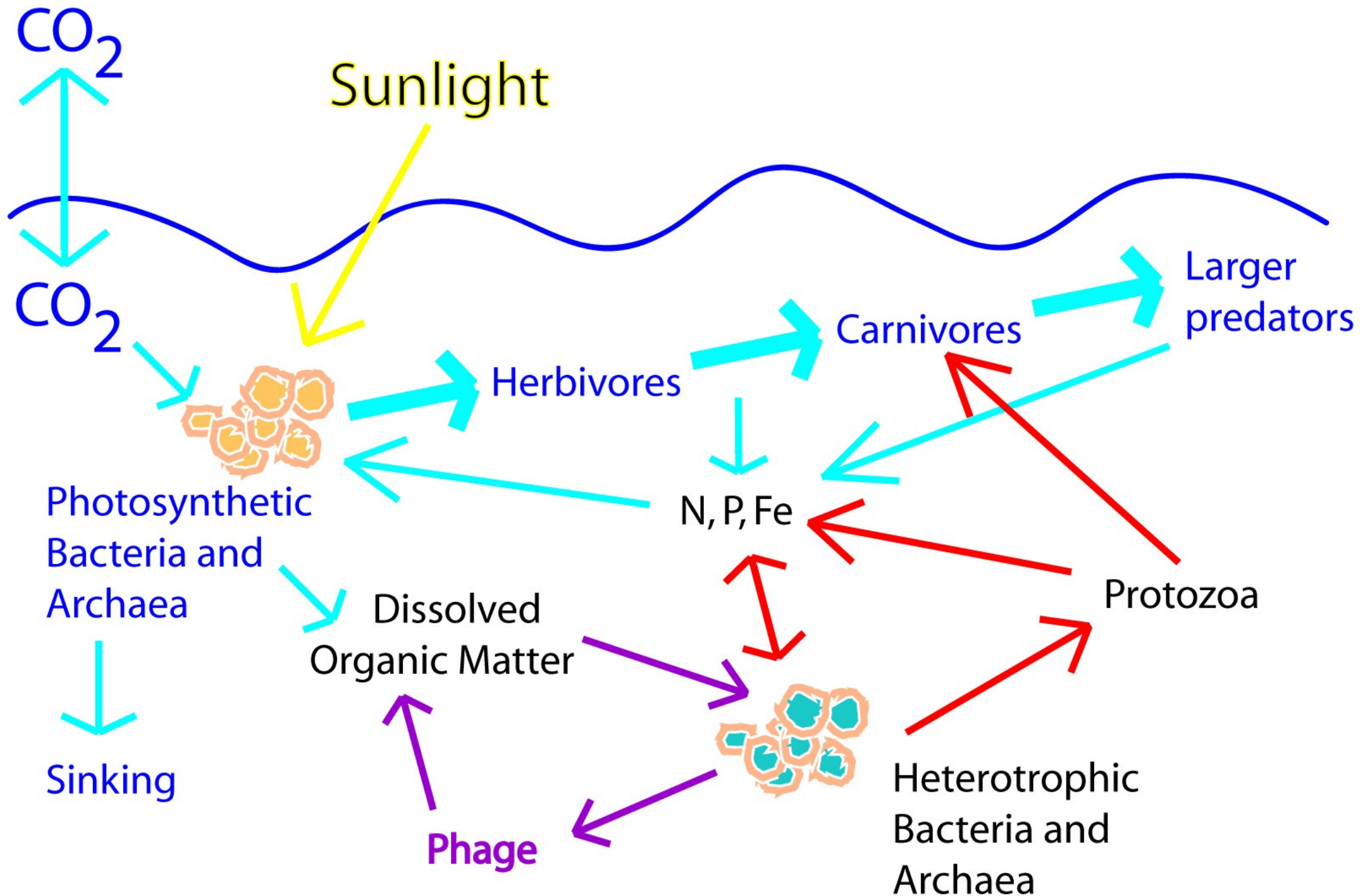
Mic r o b e s ?
B a c t e r i o p h a g e s ?
W h a t ? !

- Q: Why do we even care?
- A: Evolutionary theory.
- A: Estimated to be 10^{30} and 10^{31} on Earth
- A: Carbon cycle surprise. Microbes range between 10^4 ml^{-1} and 10^6 ml^{-1} in oceanic waters and effect greatly the oceanic biogeochemical cycles.

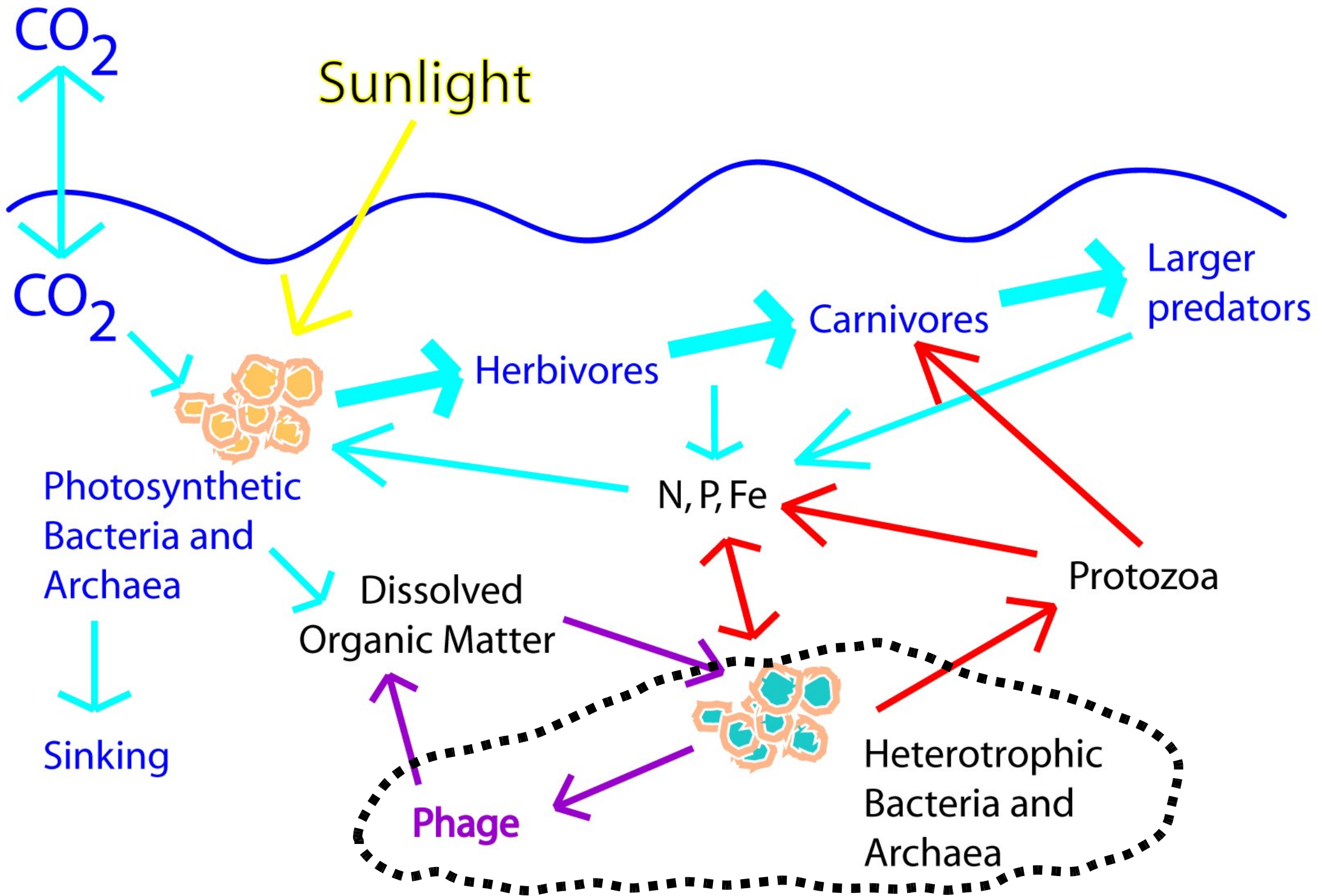
Global Carbon Cycling



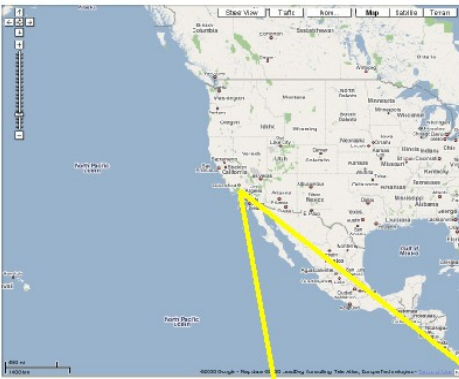
Global Carbon Cycling



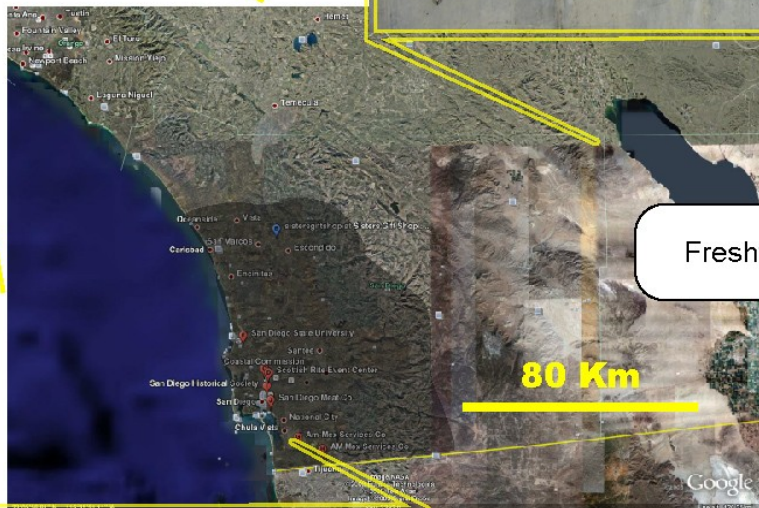
Global Carbon Cycling



Sampling locations



**San Diego,
California,
USA**



Freshwater Samples

80 Km

- Two sites: Kent Sea Tech's fish farm, Bay Saltworks' solar saltern

- 3 ponds in the solar saltern

- 2 ponds in the fish farm



Low Salinity

High Salinity

Medium Salinity

1 Km

Saltern Samples

C o a r s e - g r a i n e d a n a l y s e s

- NCBI's sequenced genome database
- Phage Proteomic Tree (PPT)
- SEED
- XIPE

Results – time series

I - All

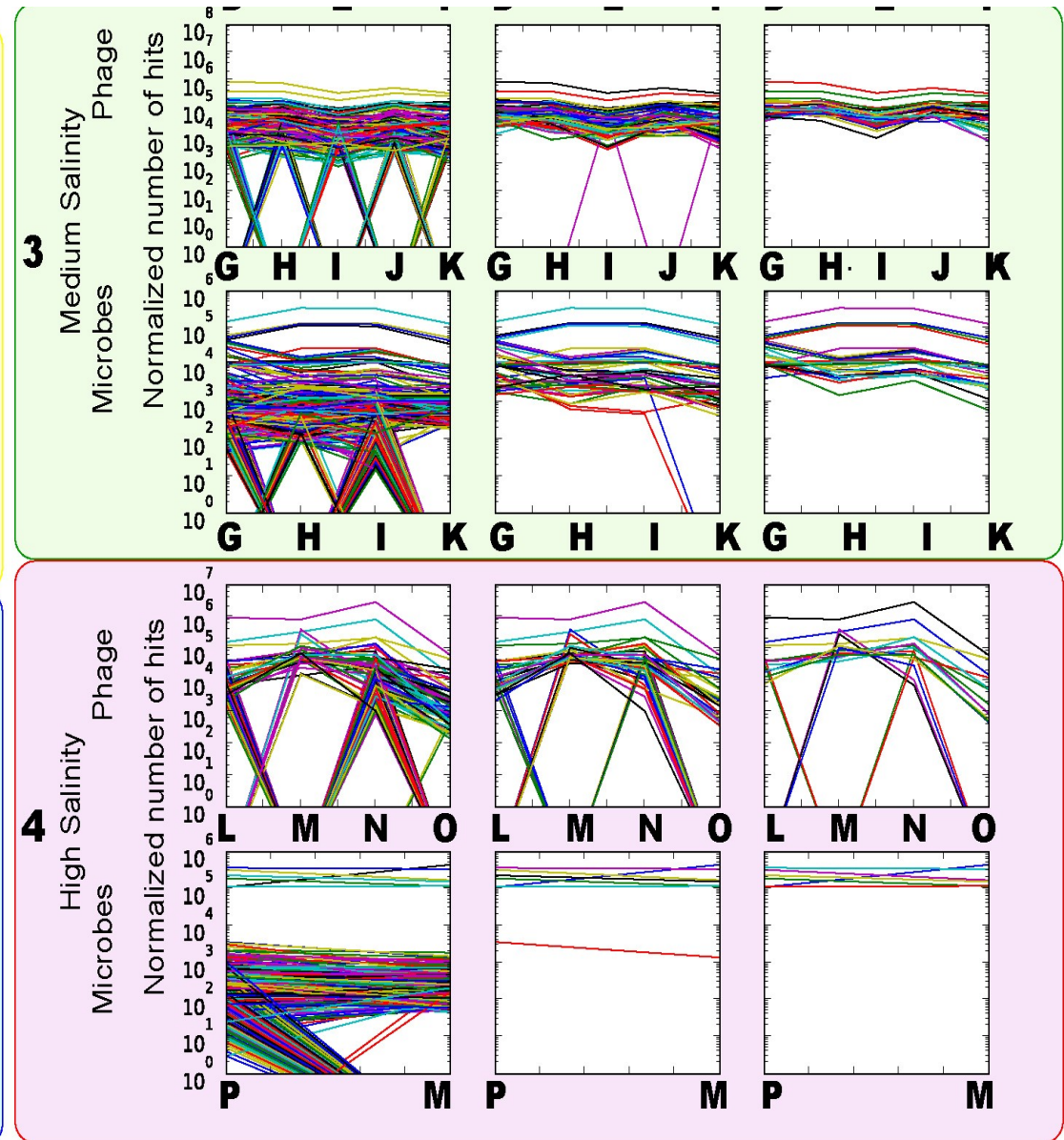
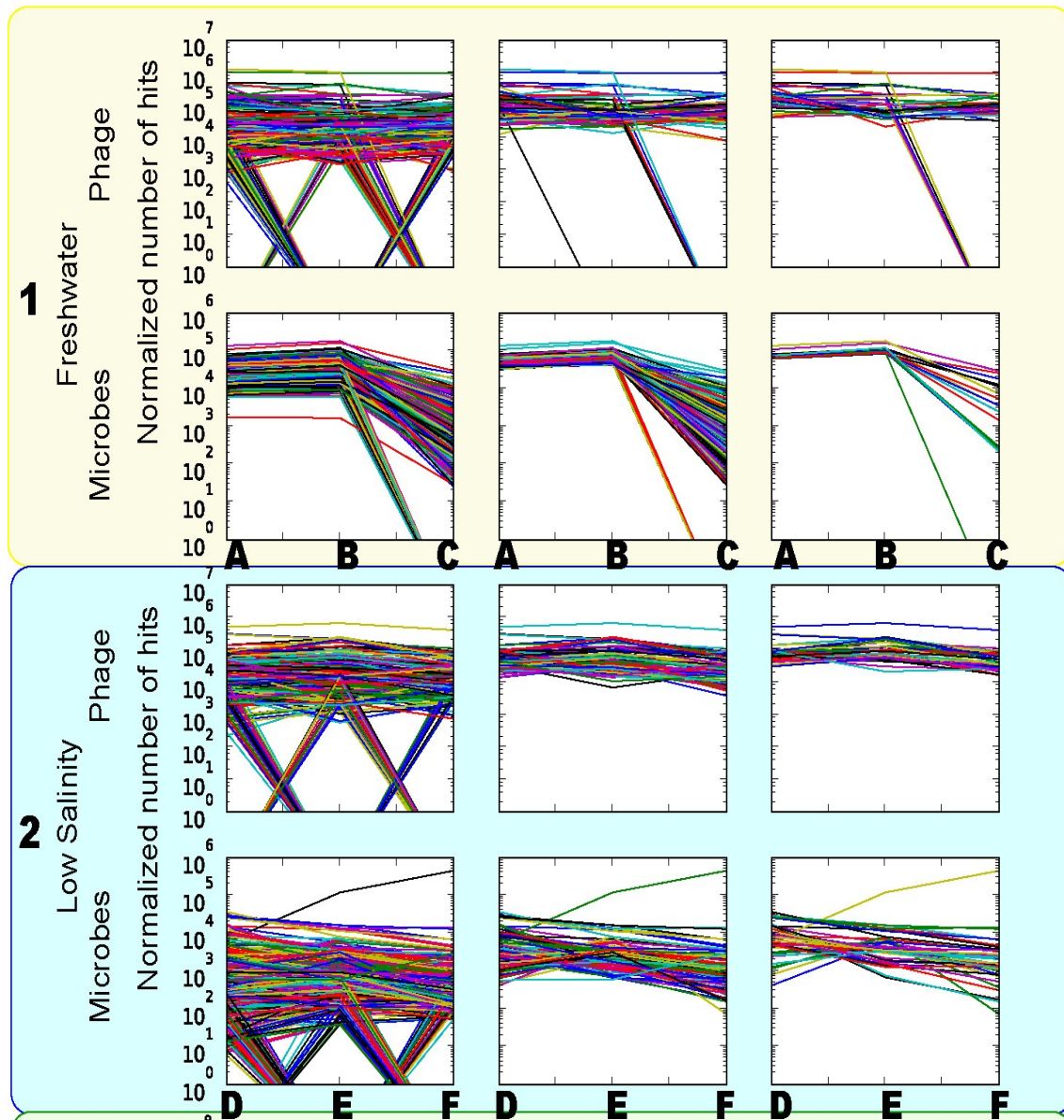
II
Average >
Mean abundance

III
Average > 2X
Mean abundance

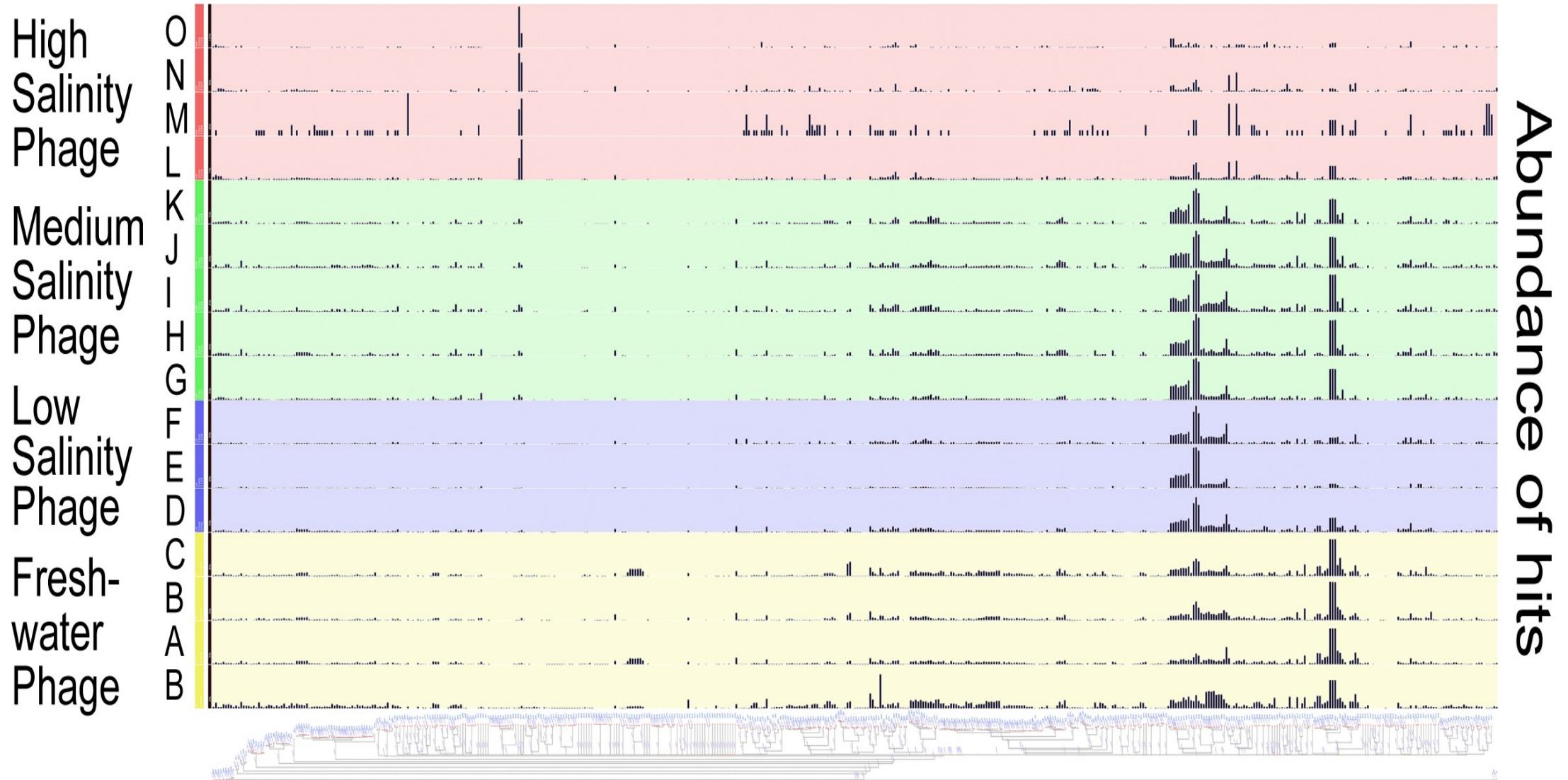
I - All

II
Average >
Mean abundance

III
Average > 2X
Mean abundance



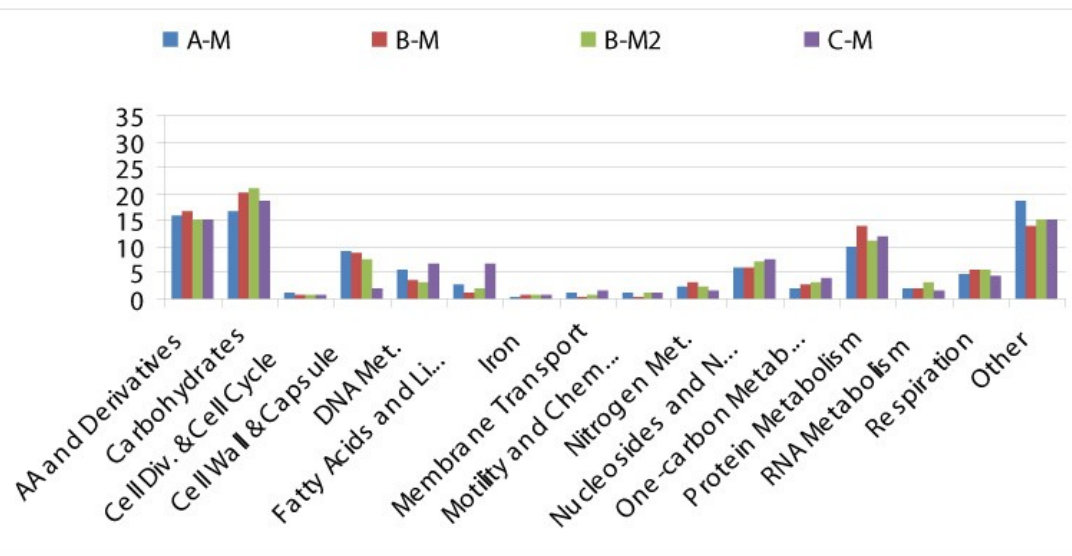
PPT and environmental signatures



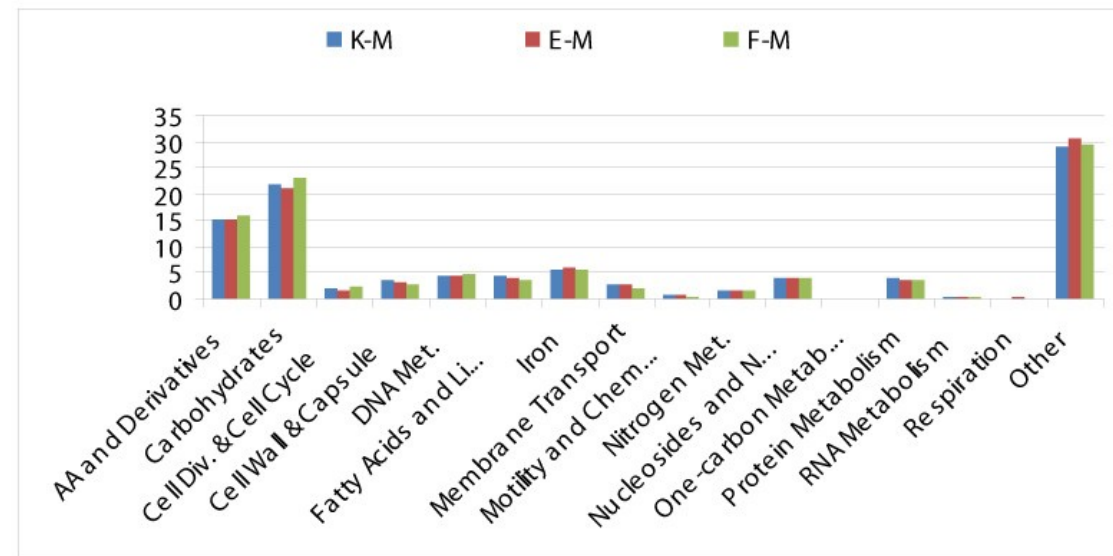
Phage Proteomic Tree

SEED and environmental signatures

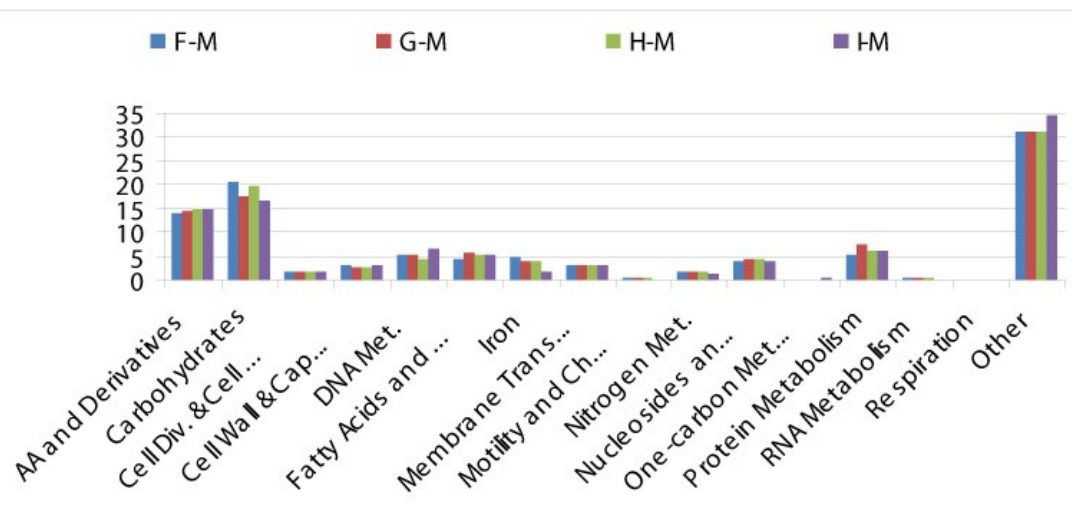
(A) Freshwater microbiomes



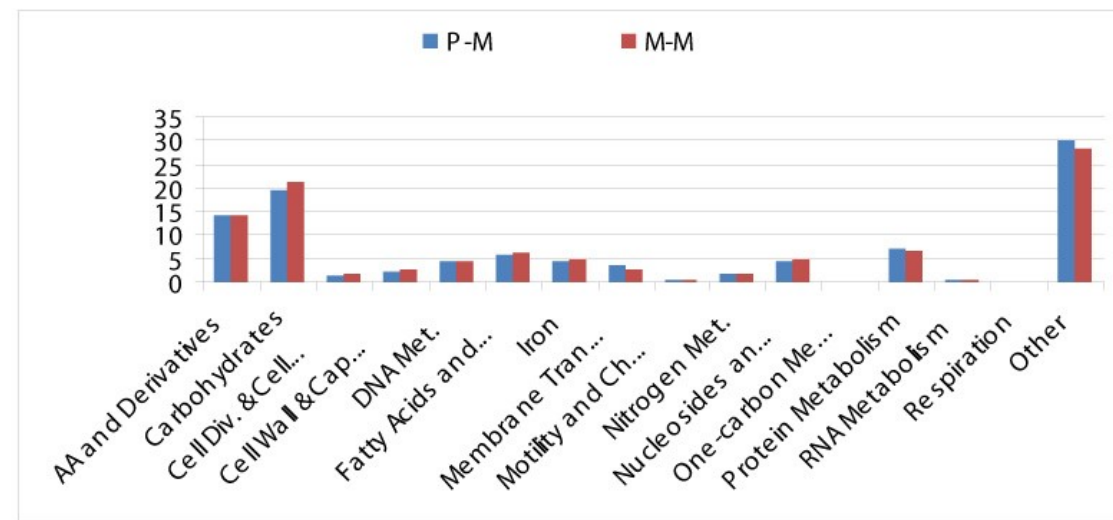
(B) Low salinity microbiomes



(C) Medium salinity microbiomes

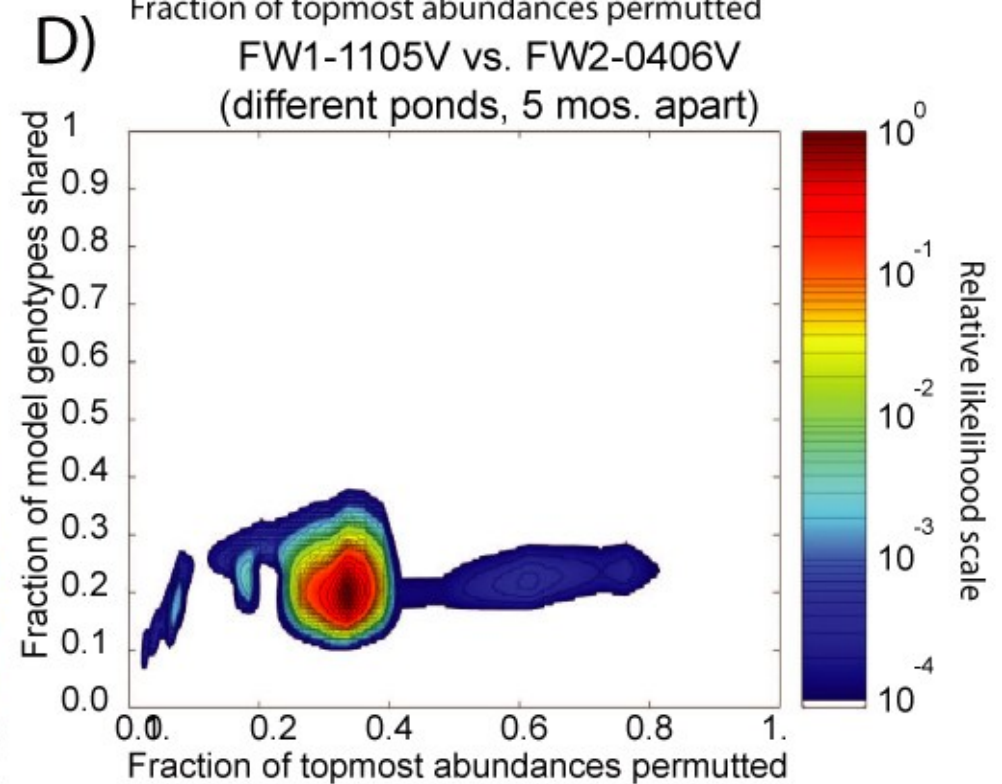
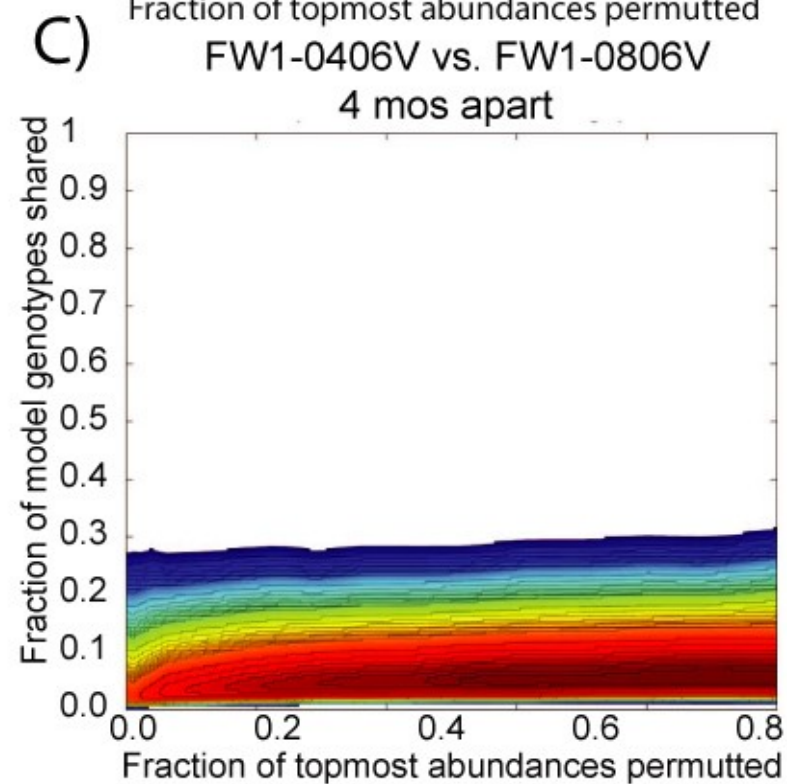
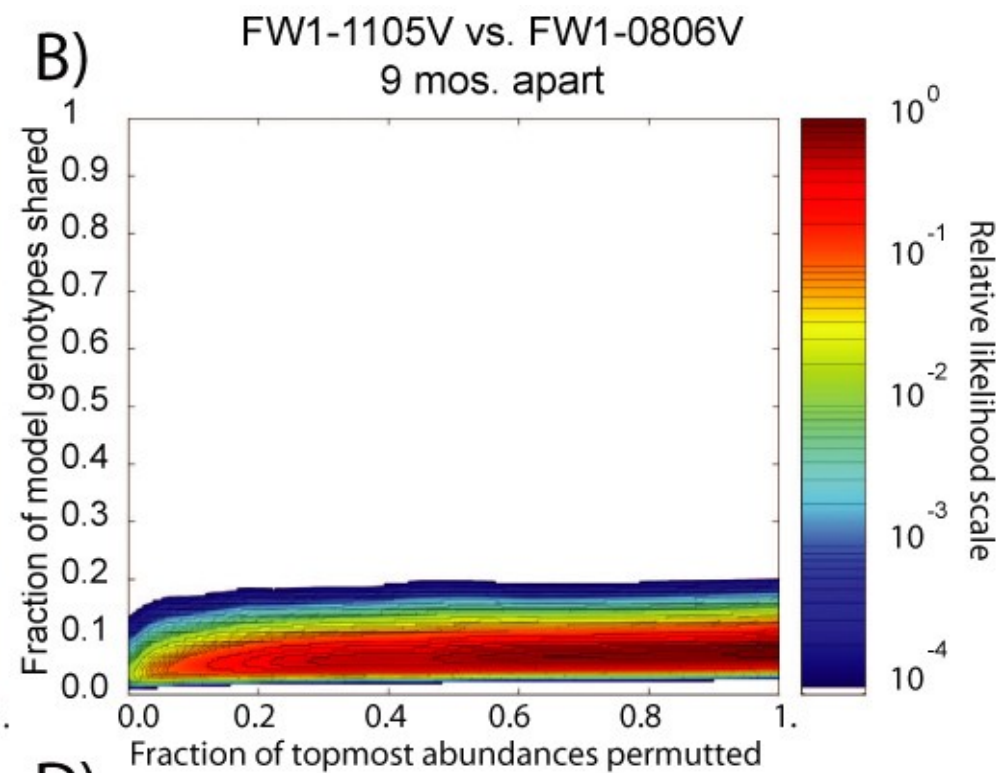
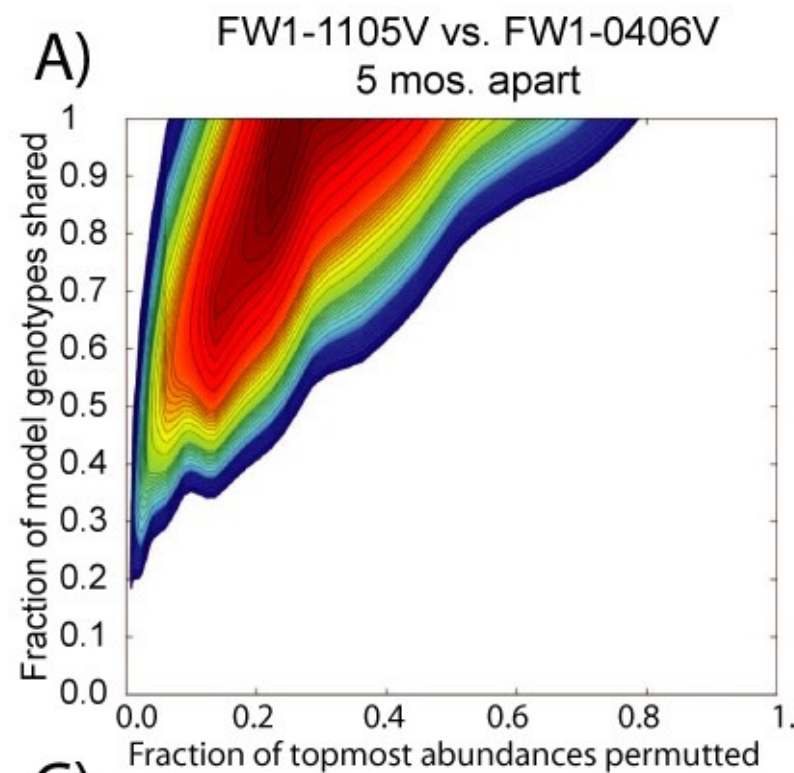


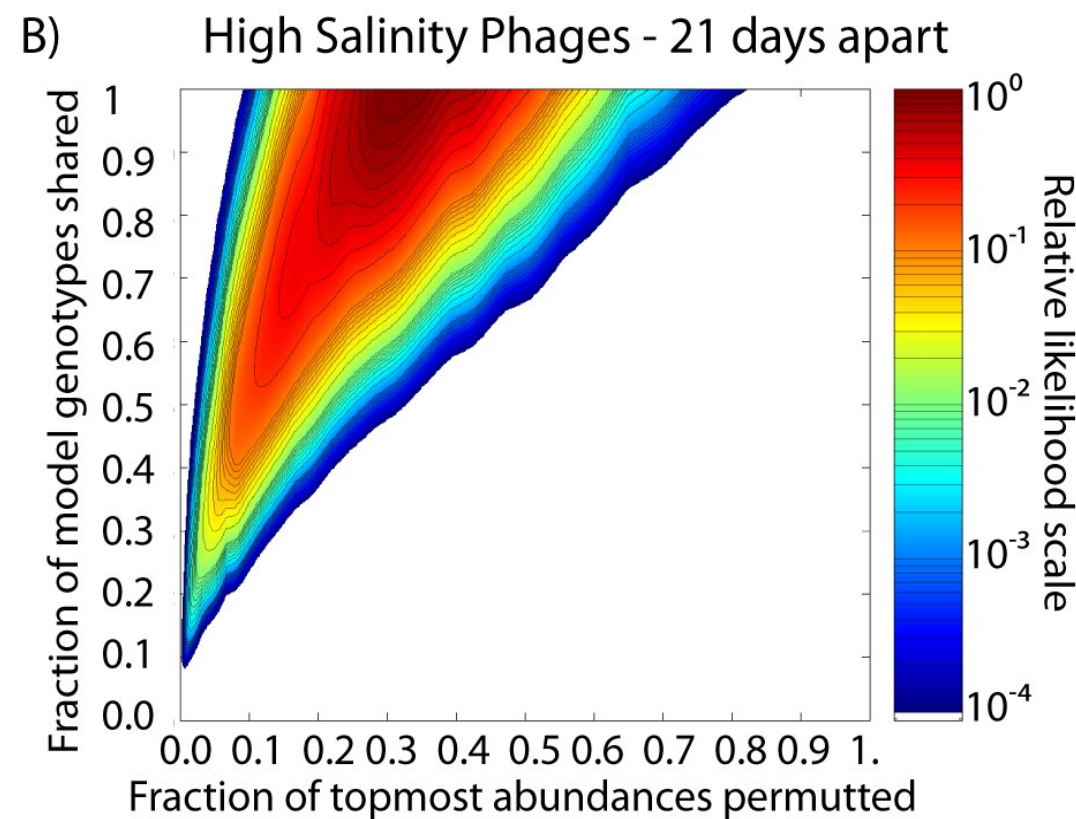
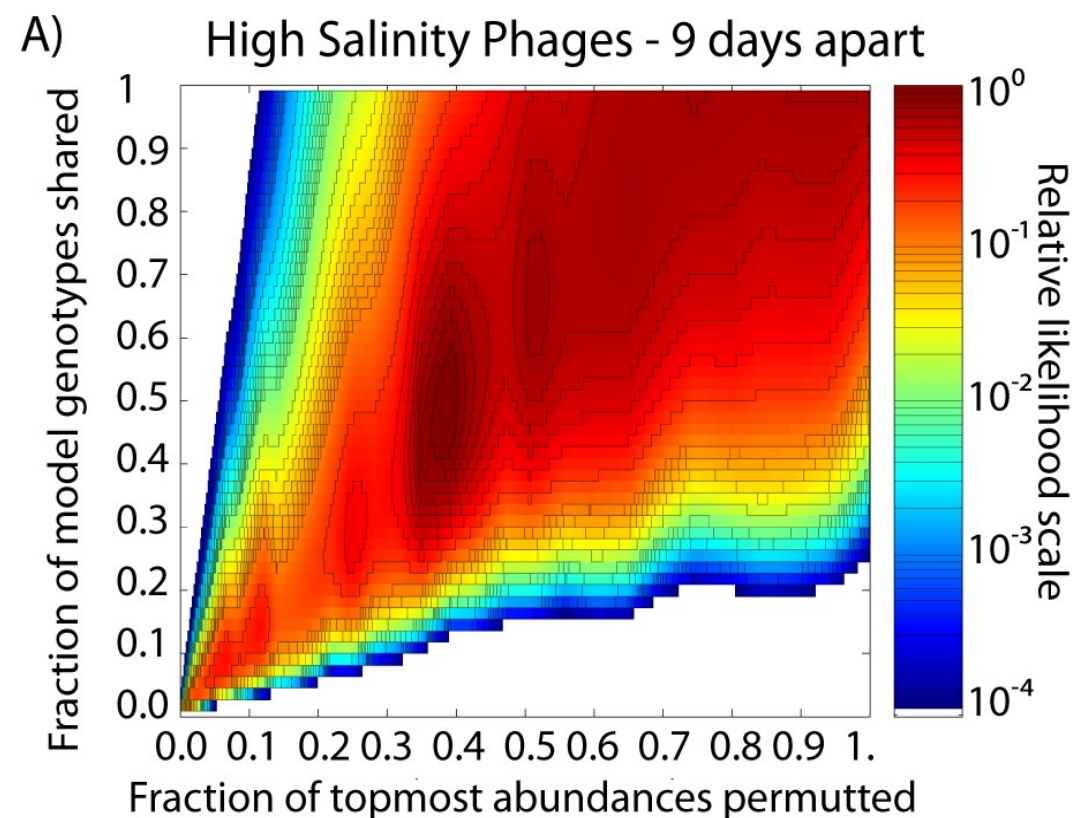
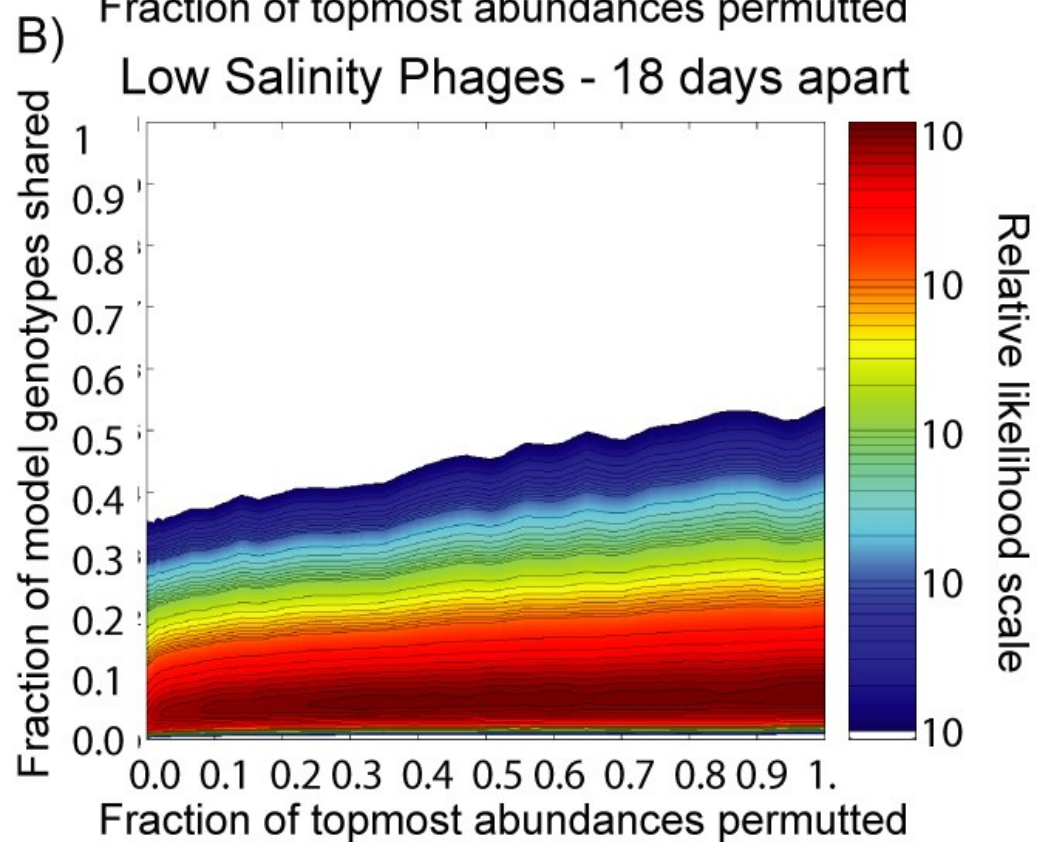
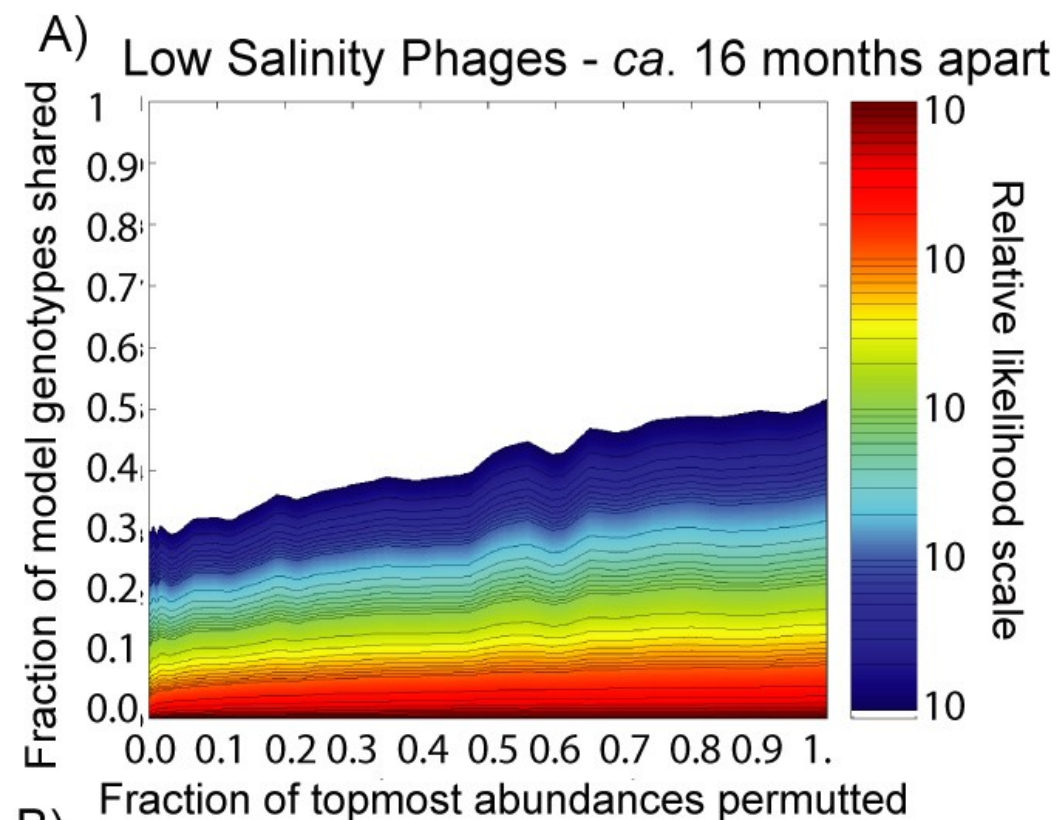
(D) High salinity microbiomes



Fin e-g r a i n e d a n a l y s e s

- Assembly, cross-assembly
- Taxi-phi





↑
% shared

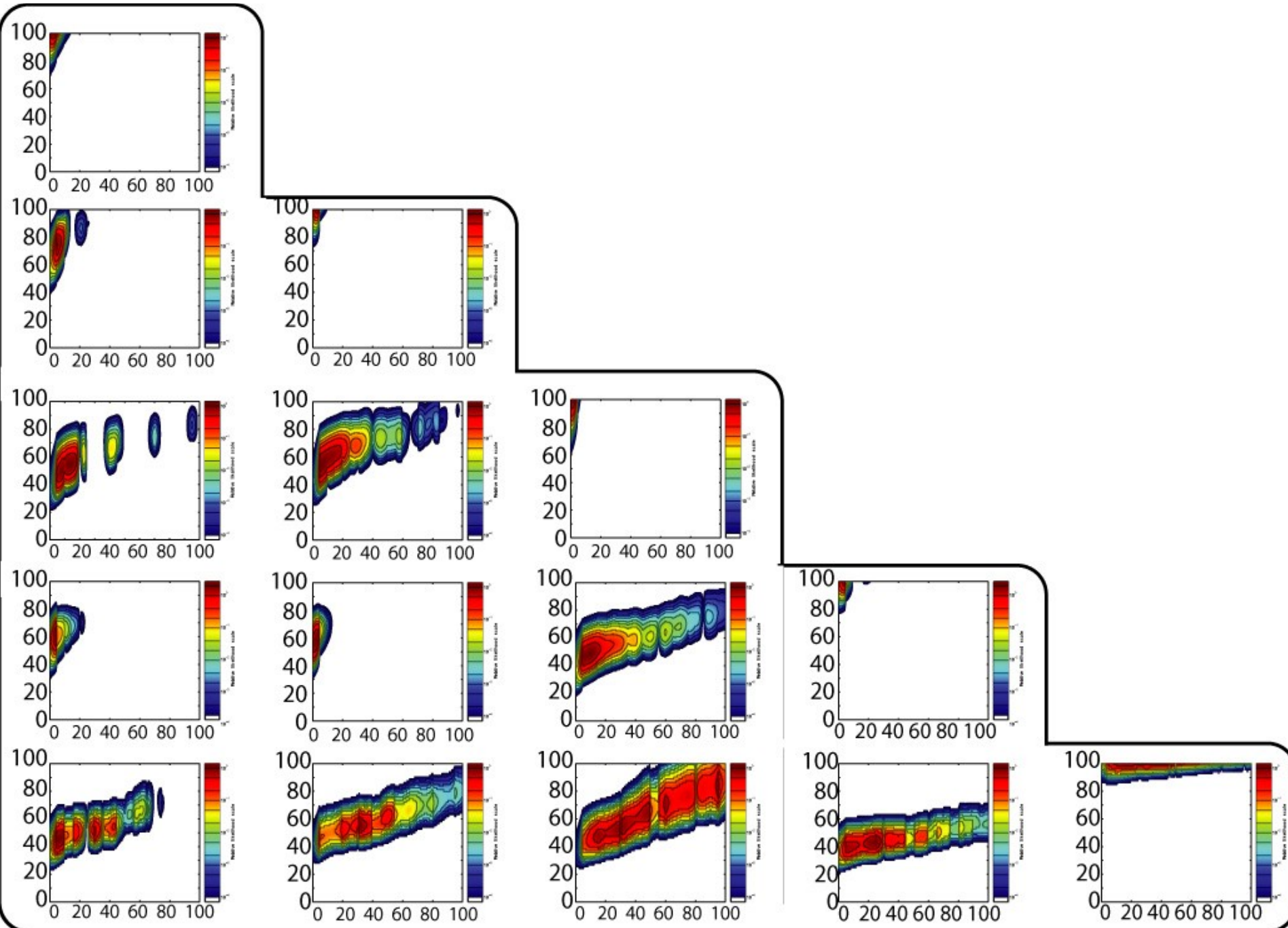
Nov 10
(G-V)

Nov 11
(H-V)

Nov 16
(I-V)

Nov 20
(J-V)

Nov 28
(K-V)



Nov 10
(G-V)

Nov 11
(H-V)

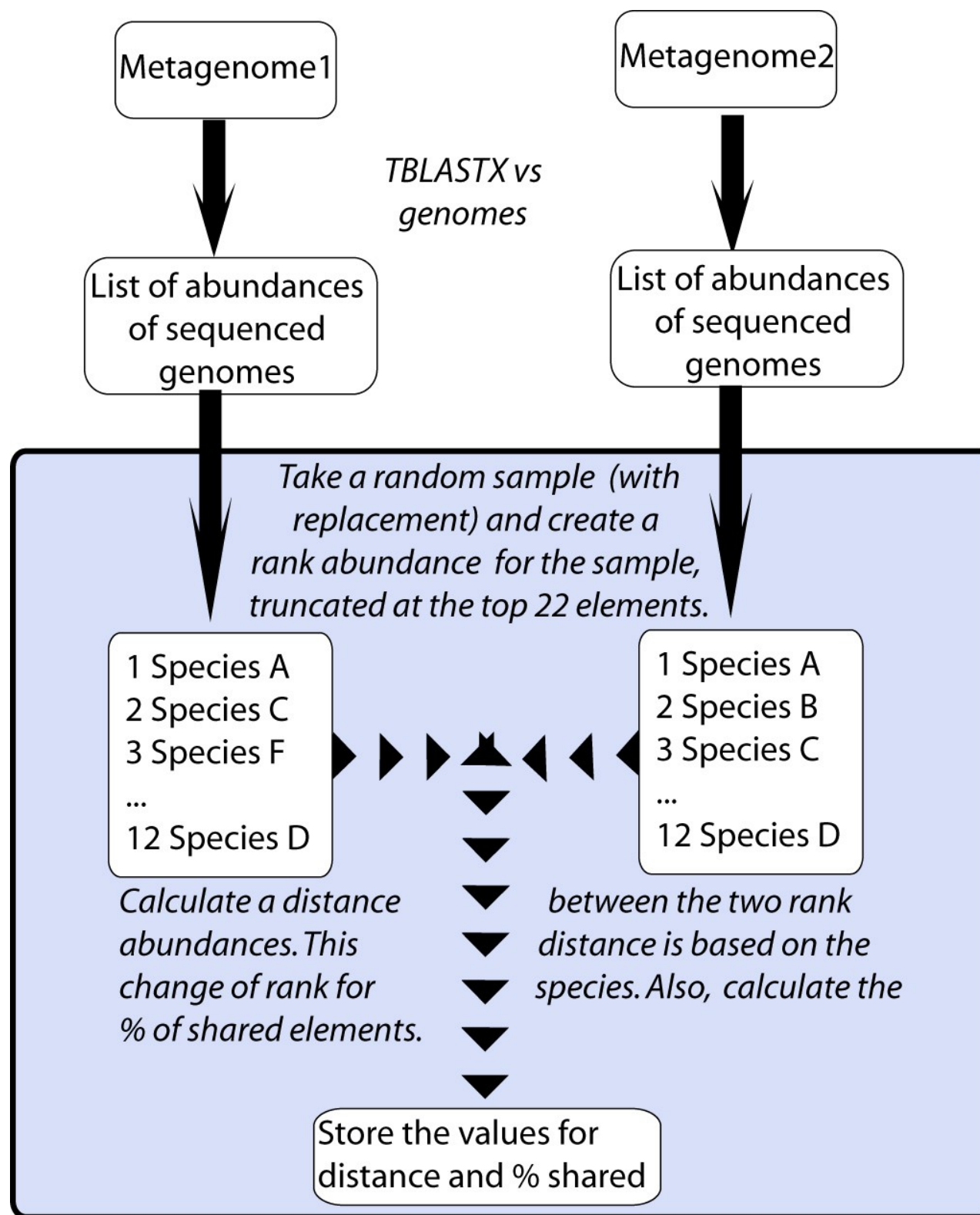
Nov 16
(I-V)

Nov 20
(J-V)

Nov 28
(K-V)

% permuted →

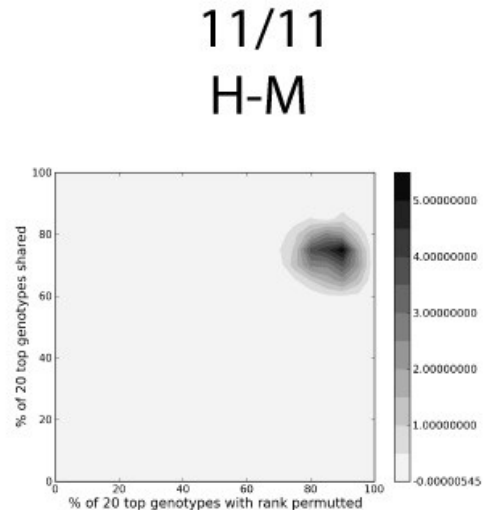
H o w a b o u t t h e m i c r o b e s ?



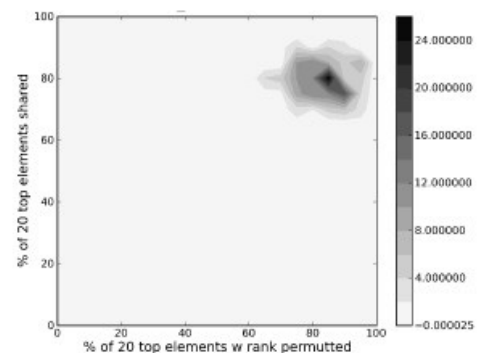
Repeat 5'000 times, plot the density of distances, %-shared pairs

11/10
G-M

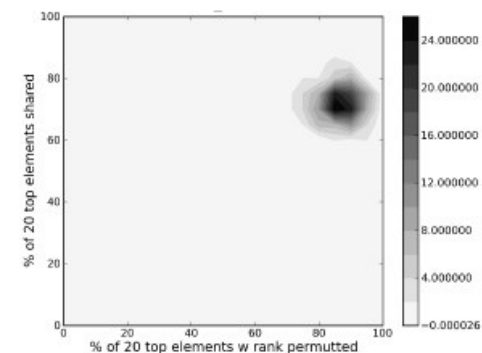
11/10
G-M



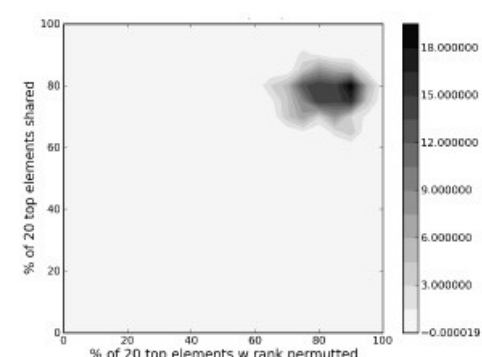
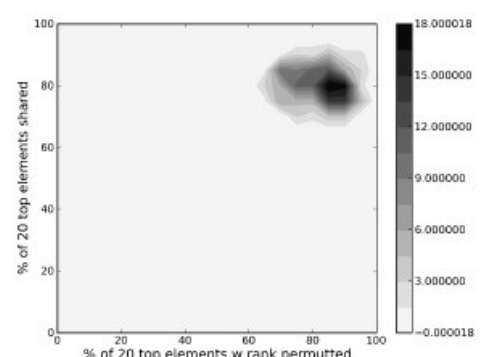
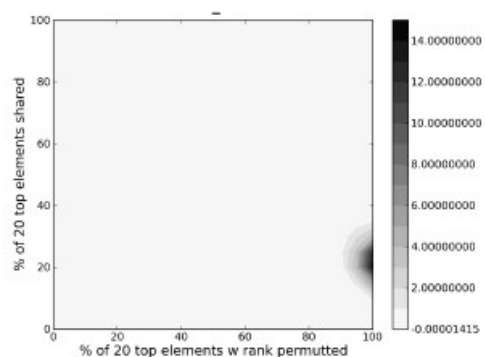
11/20
J-M



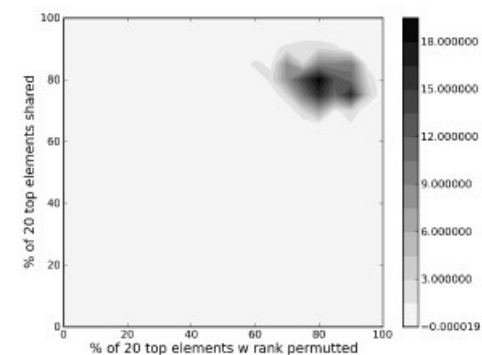
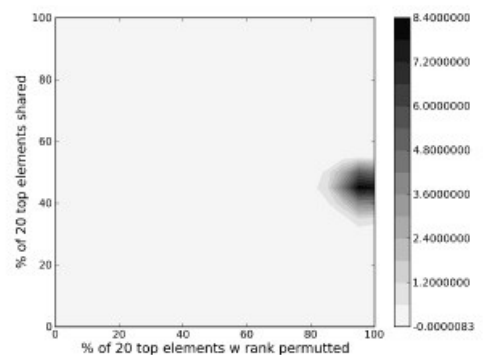
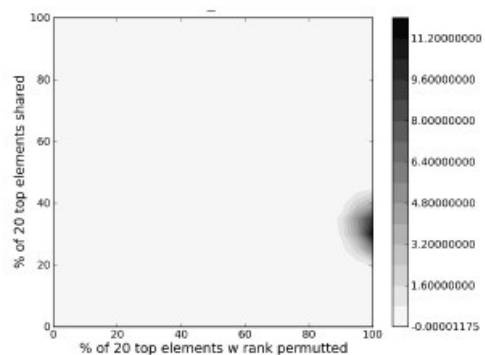
11/28
K-M



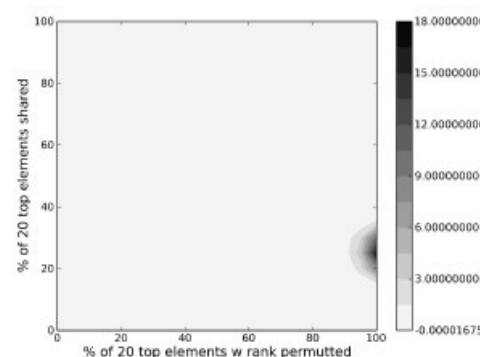
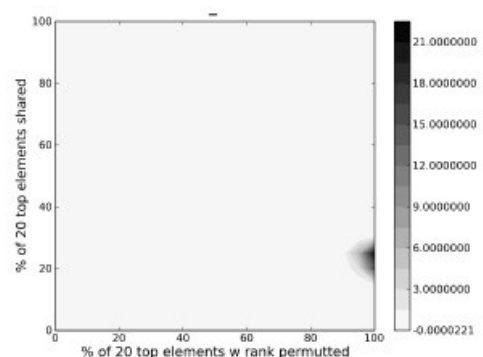
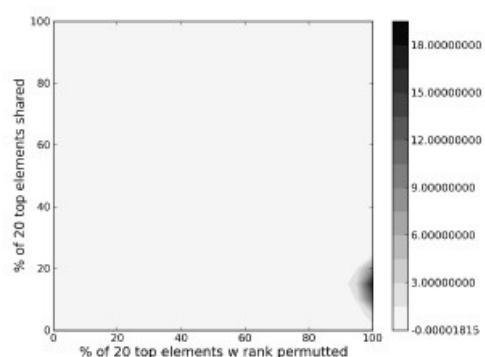
11/11
H-M



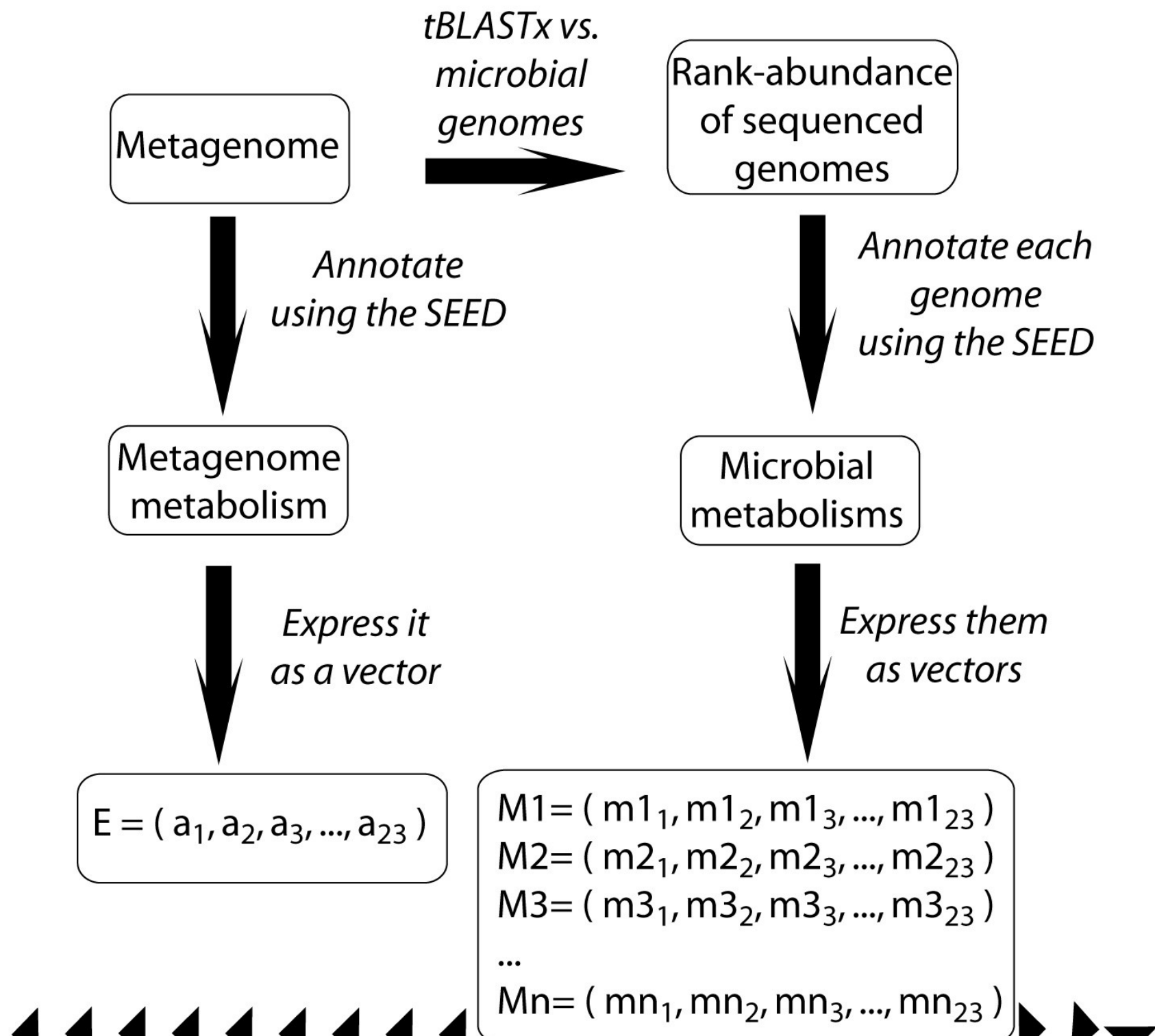
11/20
J-M



11/28
K-M



Connecting community
structure and metabolism, a
weighted linear combination of
the top ranked genomes



$$E = (a_1, a_2, a_3, \dots, a_{23})$$

$$M_1 = (m_{11}, m_{12}, m_{13}, \dots, m_{123})$$

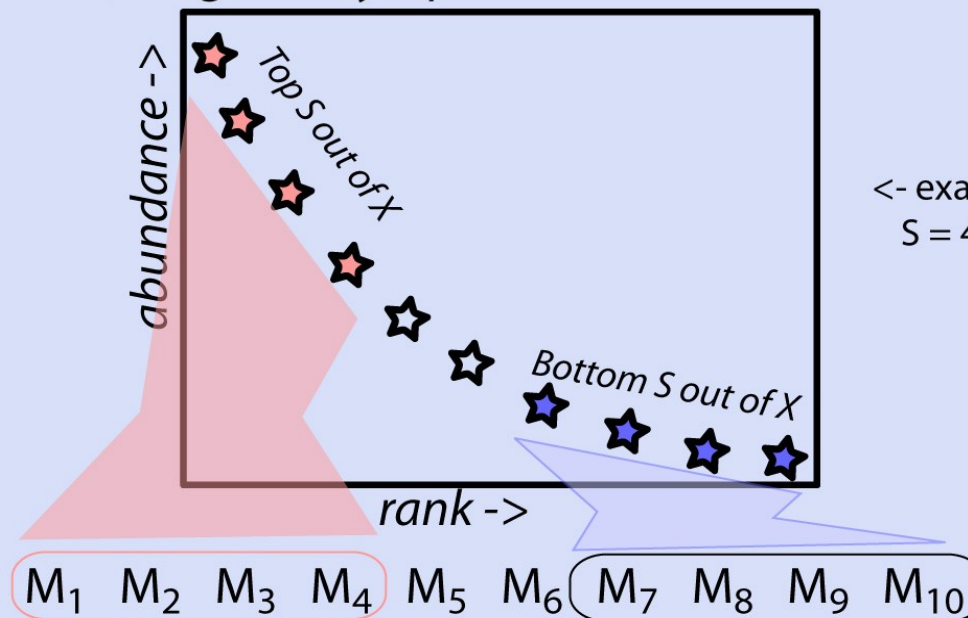
$$M_2 = (m_{21}, m_{22}, m_{23}, \dots, m_{223})$$

$$M_3 = (m_{31}, m_{32}, m_{33}, \dots, m_{323})$$

$$\dots$$

$$M_n = (m_{n1}, m_{n2}, m_{n3}, \dots, m_{n23})$$

Take elements from the top and bottom of the rank abundance curve, shuffle them at random, and calculate their linear combination, weighted by a power-law rank abundance curve (W_i)



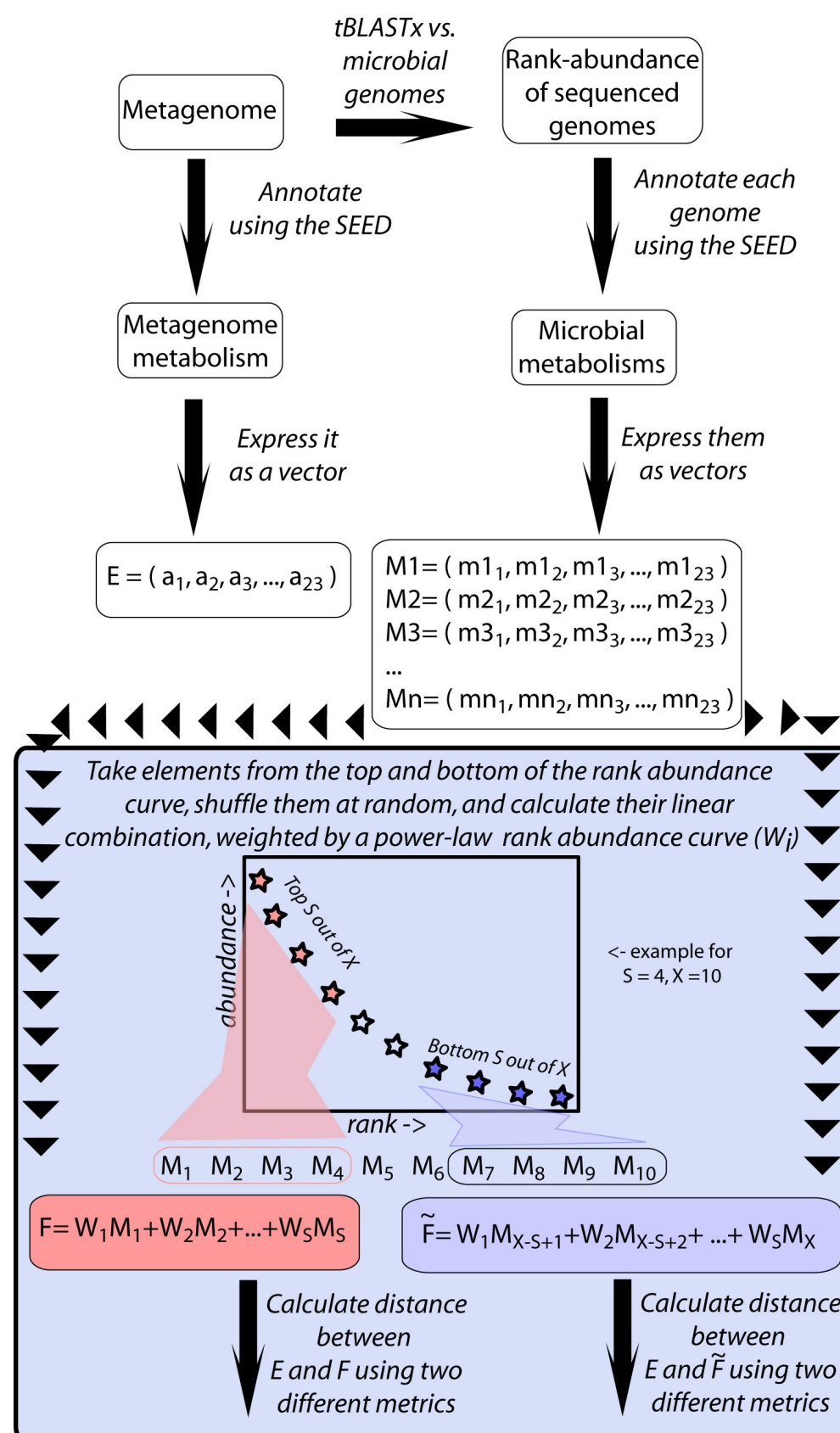
<- example for
 $S = 4, X = 10$

$$F = W_1 M_1 + W_2 M_2 + \dots + W_S M_S$$

$$\tilde{F} = W_1 M_{X-S+1} + W_2 M_{X-S+2} + \dots + W_S M_X$$

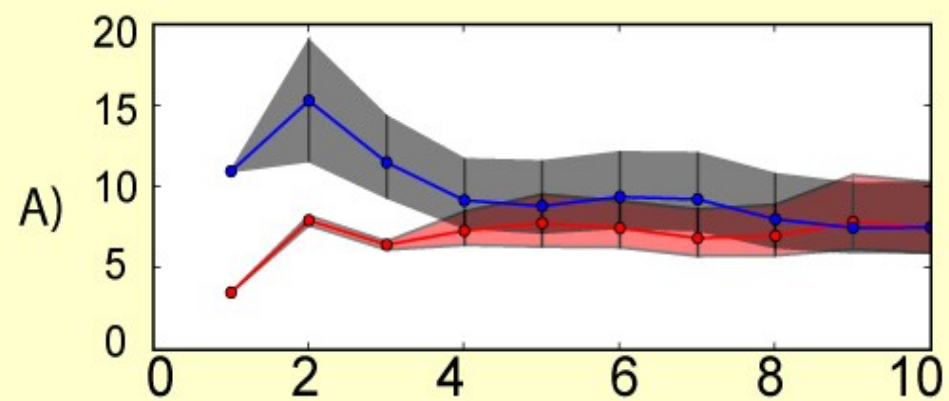
Calculate distance
between
 E and F using two
different metrics

Calculate distance
between
 E and $\tilde{F}$ using two
different metrics

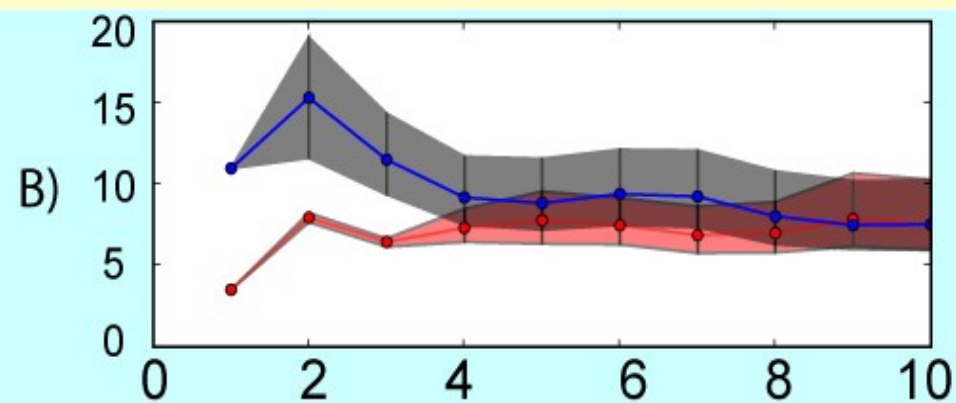


Distance to the reference metagenome

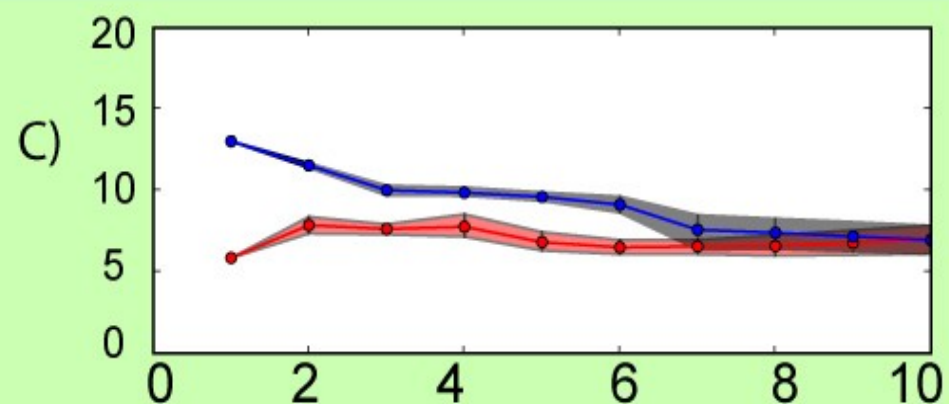
Fresh-
water
microbes



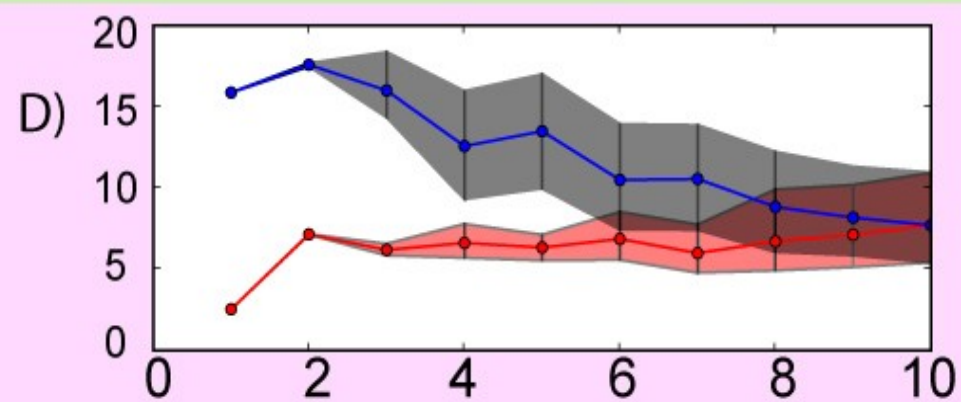
Low
salinity
microbes



Medium
salinity
microbes



High
salinity
microbes



A model for the phage-host community

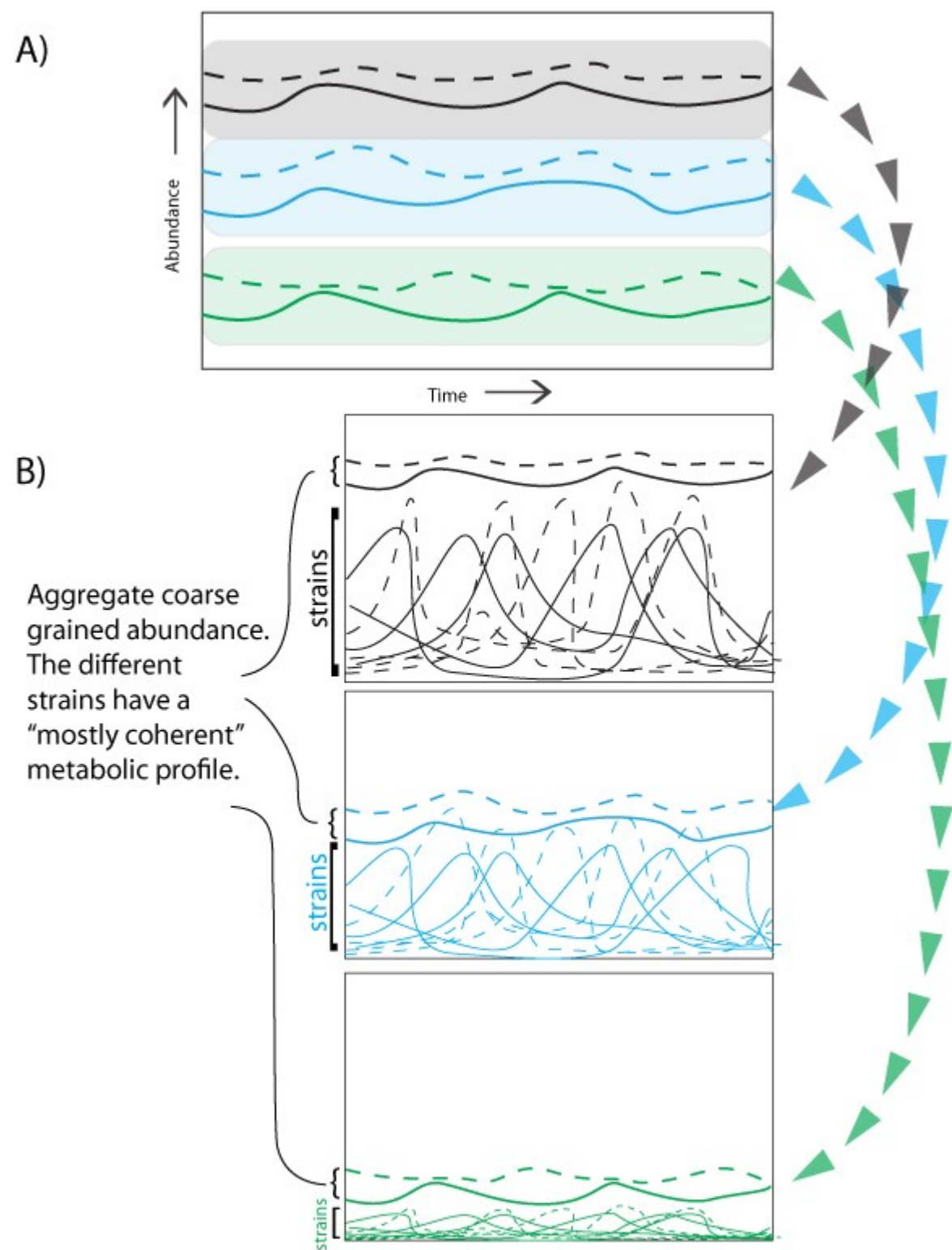


Figure 7
Rodriguez-Brito, Li, et al., 2009

Kill-the-Winner seems to be happening mostly at the strain level, with the species having some KTW dynamics, but not necessarily dominant

Natural Systems seem to be self-similar (sort of, depending on the proper time)

F u t u r e w o r k

- I'd like to have a flying lizard
- I'd like to to swim (for days)

G r a c i a s

- I'd like to thank lots and lots of people that made this possible, in particular Profs. Rohwer, Segall, Edwards, Breitbart, Rodriguez-Valera. Also all the people at the Rohwer Lab, specially Linda and Mike and Matt, as well as many many others.
-

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