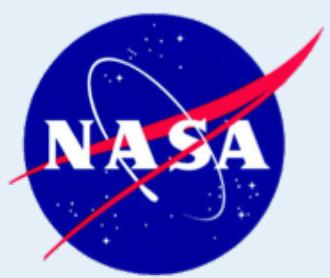


Global surface ocean phytoplankton community structure determined from co-variability in phytoplankton pigment concentrations



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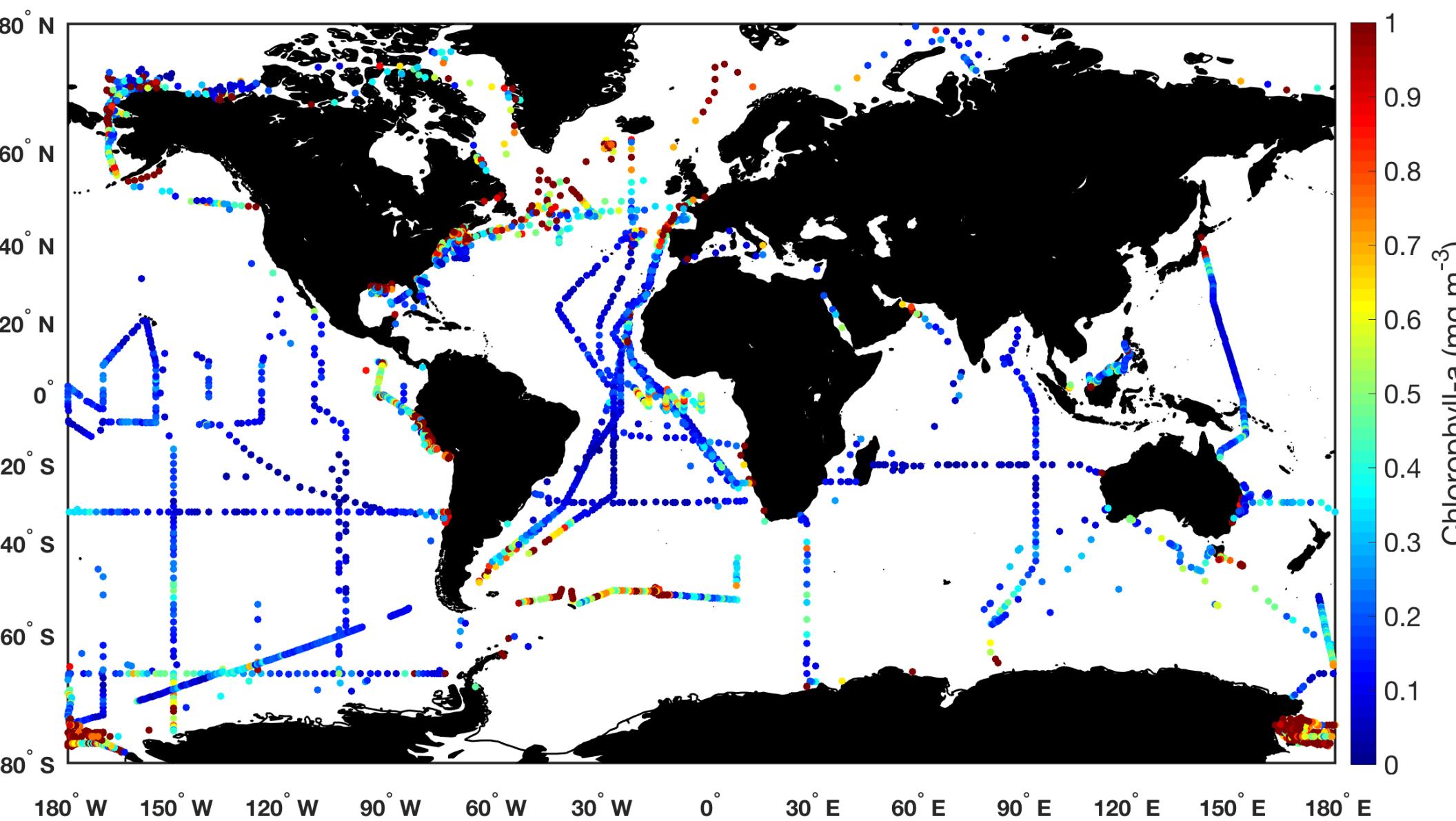
Research Goals

- Describe the global distribution and co-variability of phytoplankton pigments
- Use associations between groups of phytoplankton pigments to distinguish between groups of phytoplankton
- Explore the global patterns of groups and size classes of phytoplankton based on the results of clustering, EOF, and network analyses on varying spatial scales

Data & Methods

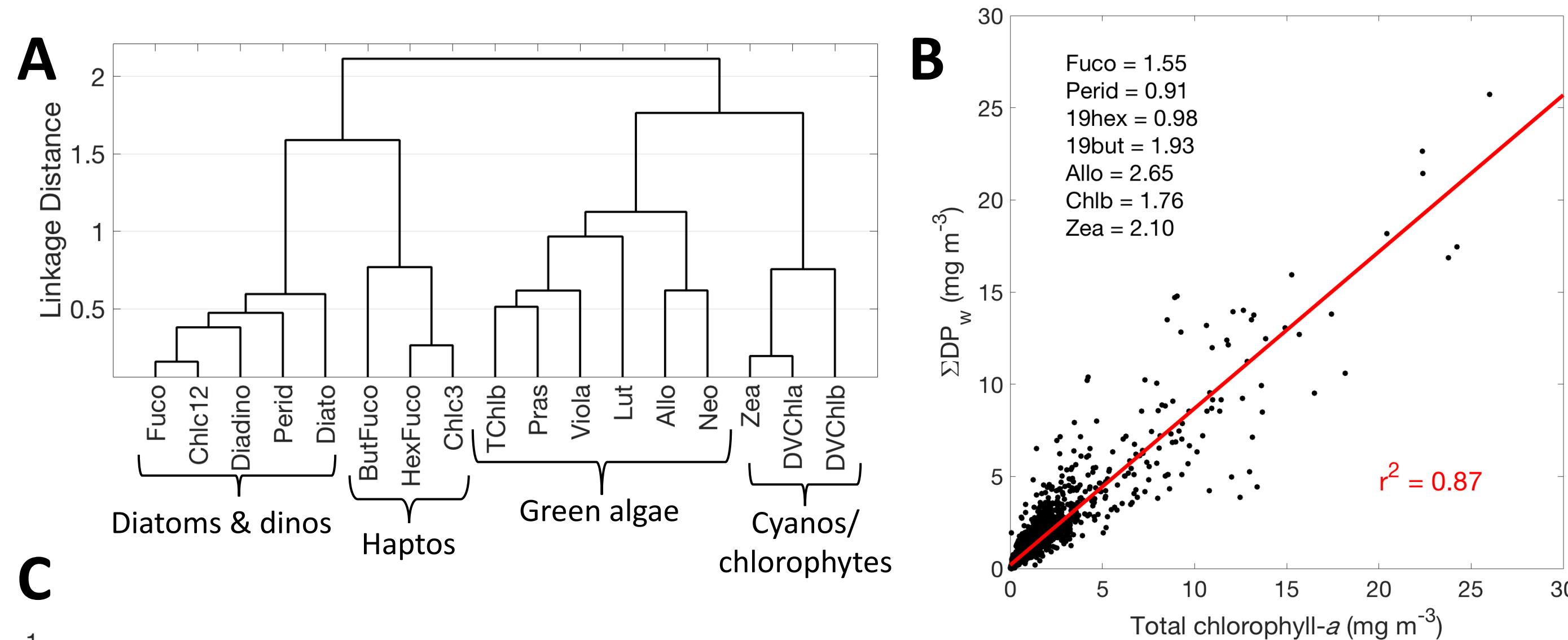
Data summary:

- 4,124 distinct data points from 40+ cruises in 5 major ocean basins
- 6 labs performed analysis: Horn Point, NASA GSFC, LOV, CSIRO, AWI, DiTullio



Methods:

- All pigment values below NASA GSFC detection limit set to zero; pigments normalized to total chlorophyll-a concentration for all analyses
- Hierarchical cluster analysis using correlation distance & Ward's linkage
- Optimized coefficients for diagnostic pigment analysis (Vidussi, Uitz): weighted sum of 7 pigments to equal total chlorophyll-a concentration
- Empirical orthogonal function analysis



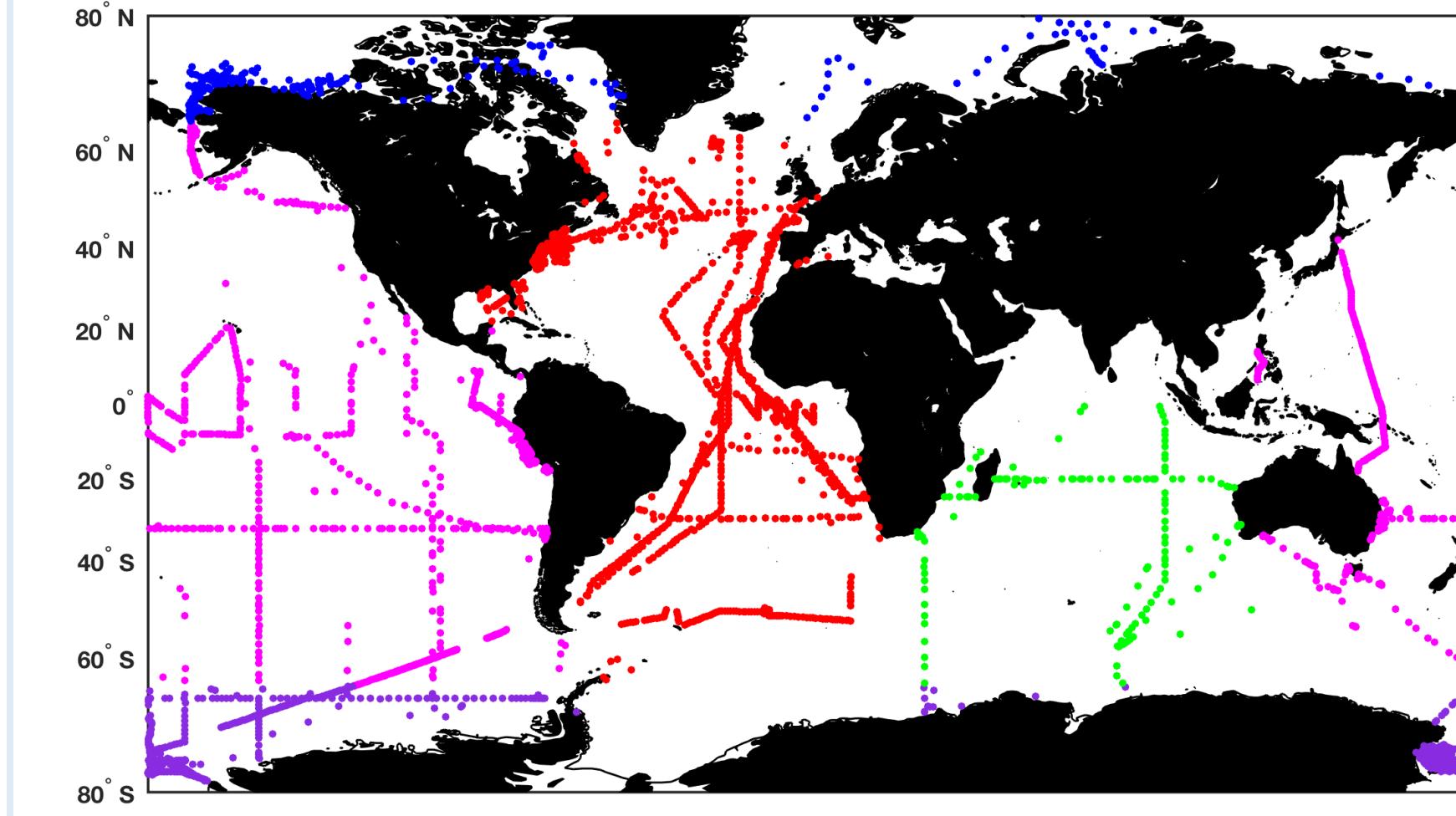
(A) Hierarchical clustering analysis results. (B) Mode 1 of empirical orthogonal function analysis: loadings show the strength of the correlation between each pigment and Mode 1. Sum of first six modes explains 72% of total variance in the dataset. (C) Re-optimized diagnostic pigment analysis.

Results of Cluster, EOF, and DPA Analyses on Varying Spatial Scales

Ocean basins:

Variance explained by EOF modes 1-6: **72.19%**

Mode 1+temp. $r^2 = -0.14$, Mode 1+sal. $r^2 = 0.12$

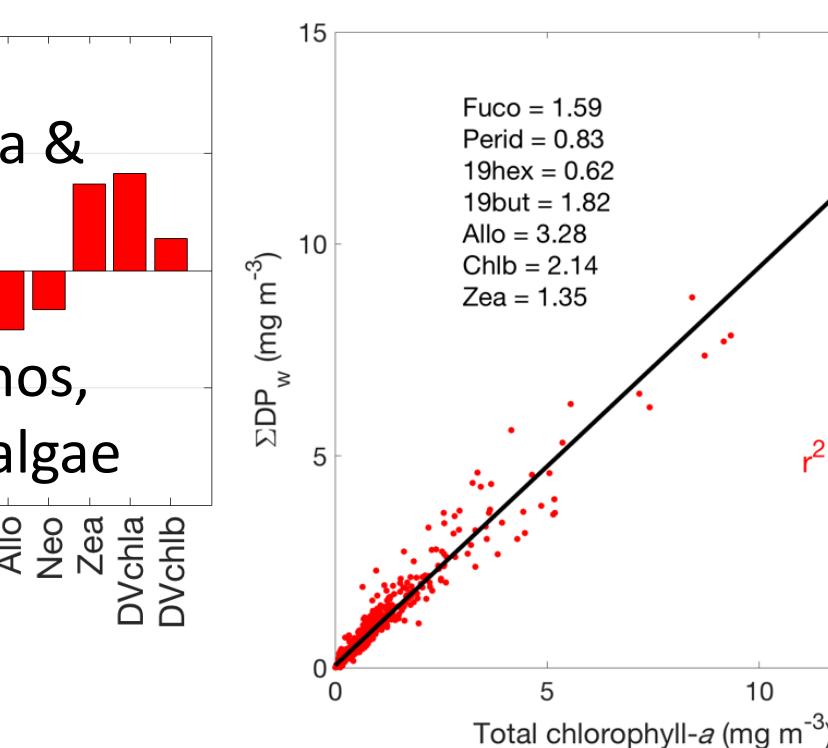


Atlantic

Mode 1: 26.1%

+ = cyanobacteria & chlorophytes

- = diatoms, dinos, haptos, green algae

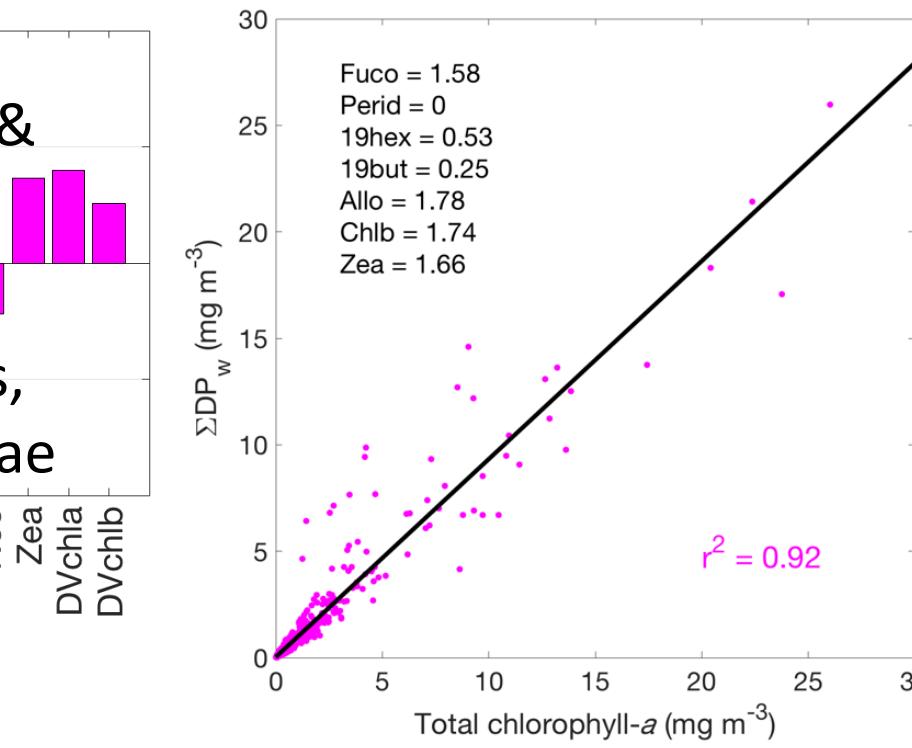


Pacific

Mode 1: 24.8%

+ = cyanobacteria & chlorophytes

- = diatoms, dinos, haptos, green algae



Variance explained by modes 1-6: **71.24%**

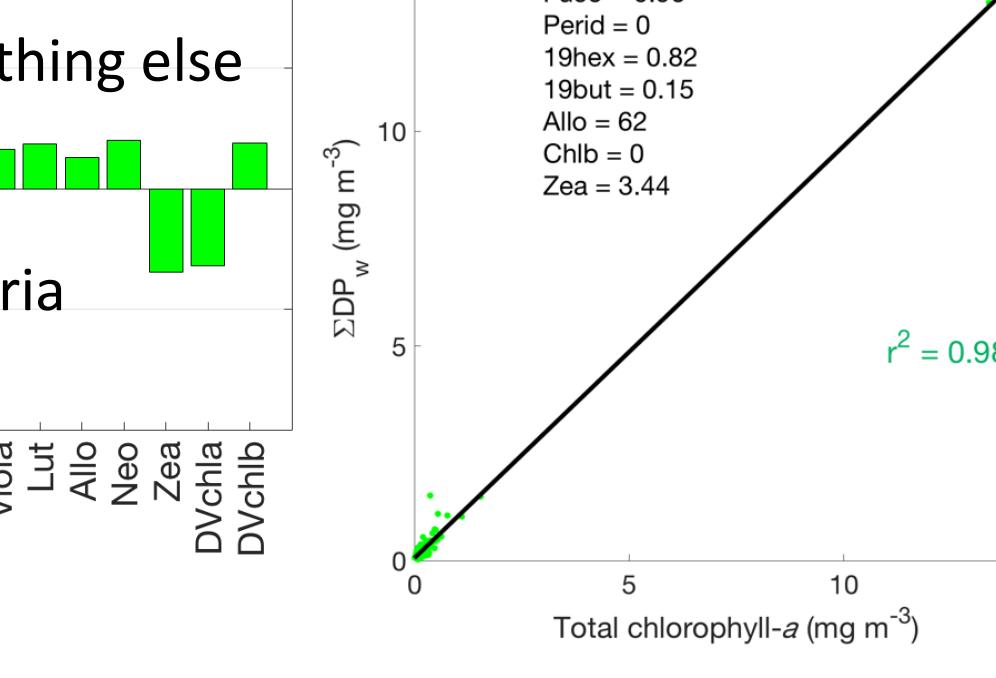
Mode 1+temp. $r^2 = 0.008$, Mode 1+sal. $r^2 = 0.52$

Indian

Mode 1: 35.5%

+ = everything else

- = cyanobacteria

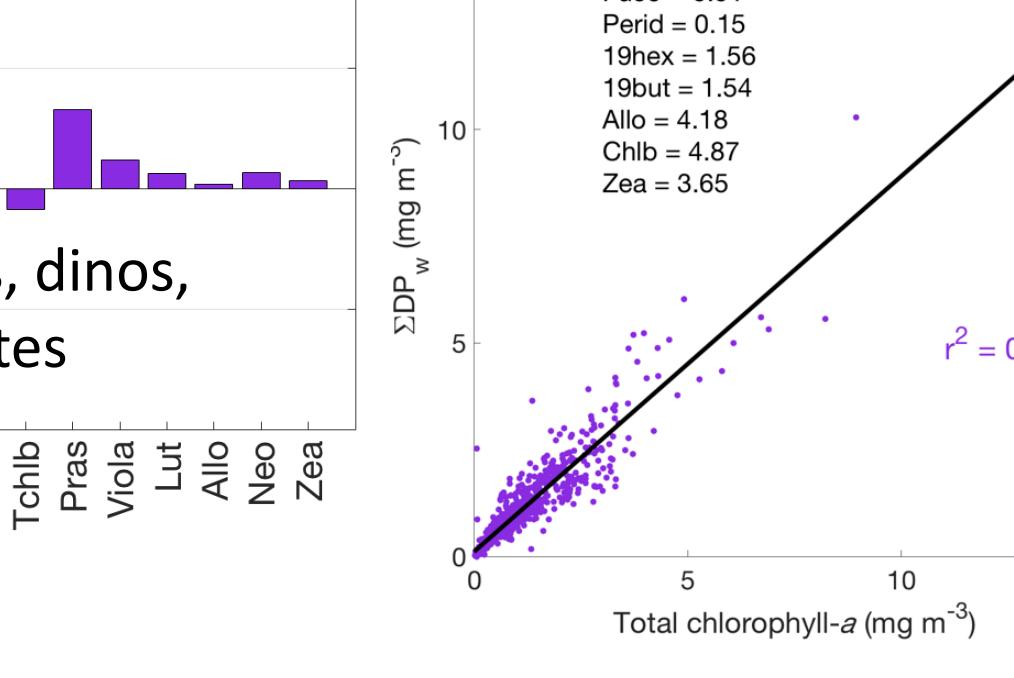


Southern

Mode 1: 28.1%

+ = diatoms, dinos, prasinophytes

- = cyanobacteria

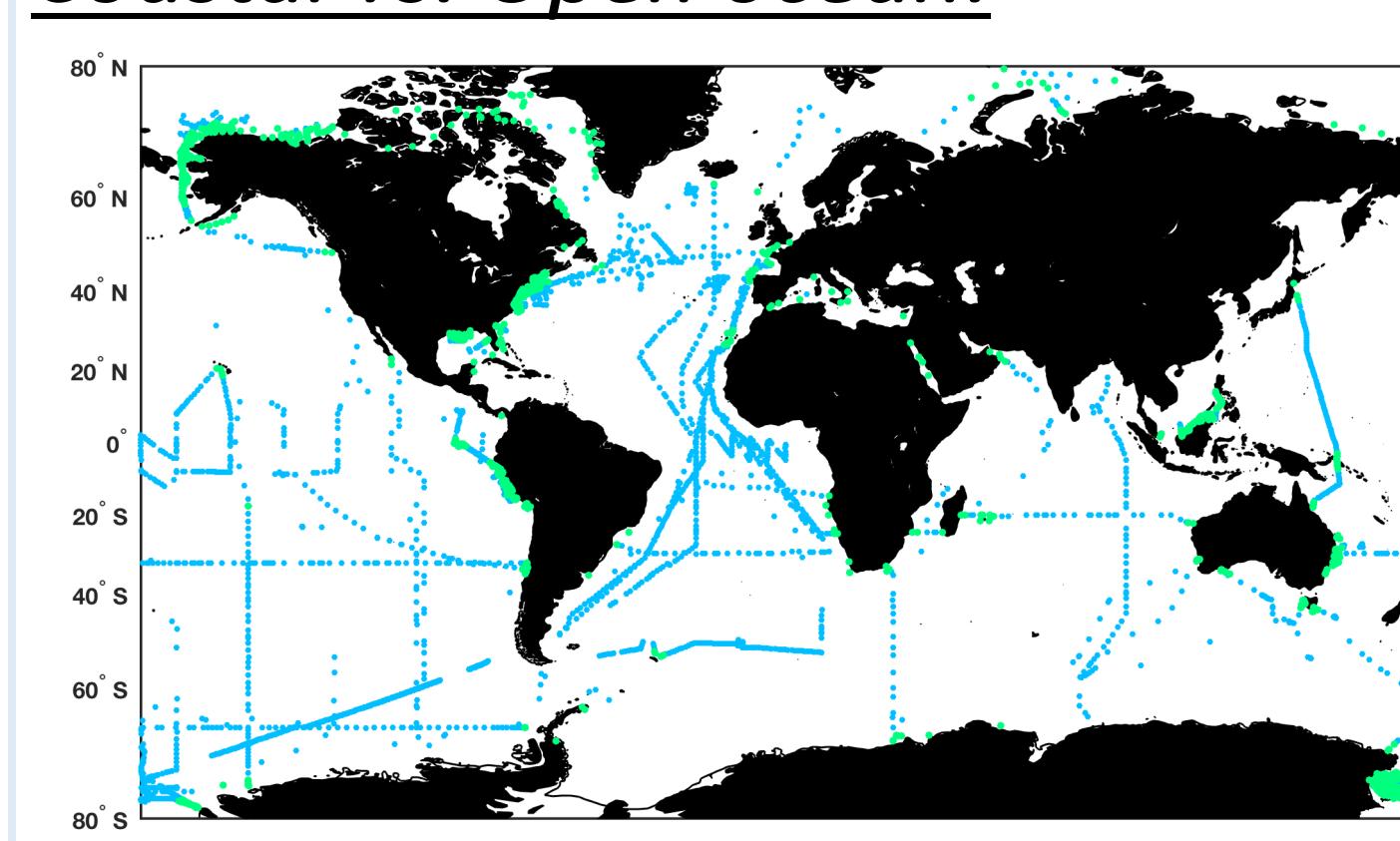


Variance explained by modes 1-6: **81.77%**

Mode 1+temp. $r^2 = -0.17$, Mode 1+sal. $r^2 = -0.61$

Mode 1 of EOF analysis generally more highly correlated with salinity than with temperature: water mass seems to dictate pigment assemblage.

Coastal vs. Open ocean:



Coastal (within 100 km. of coastline):

Variance explained by modes 1-6: **75.67%**

Mode 1+temp. $r^2 = -0.24$, Mode 1+sal. $r^2 = 0.008$

Open ocean:

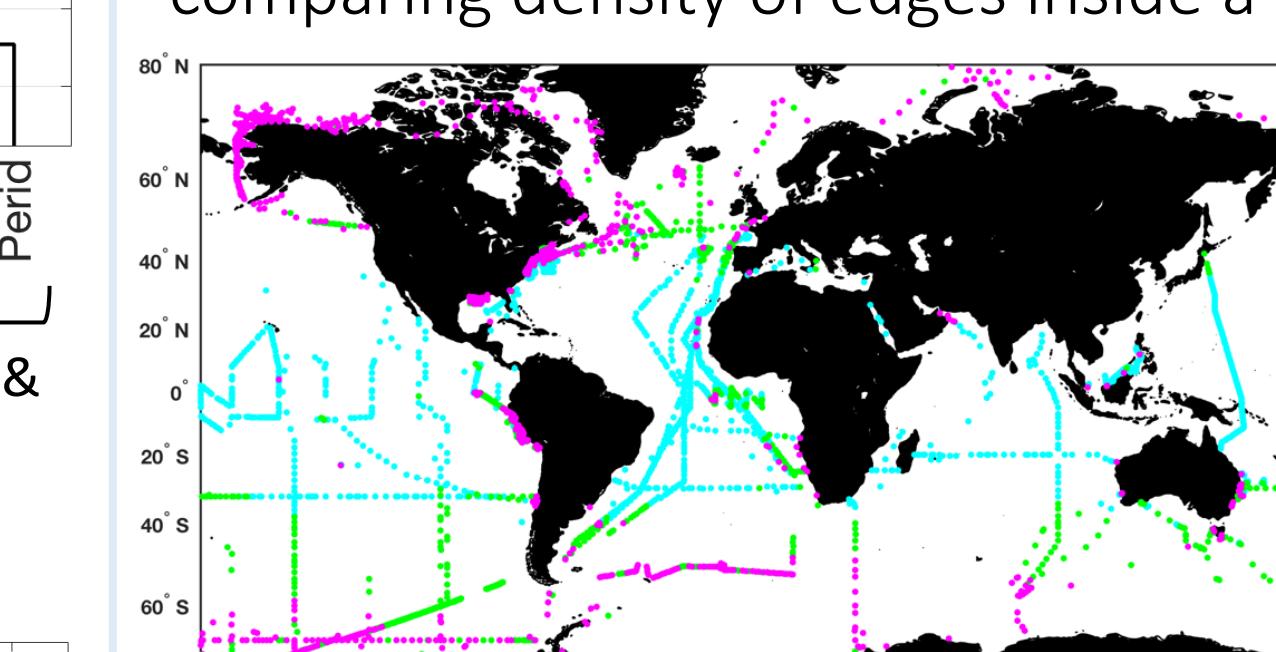
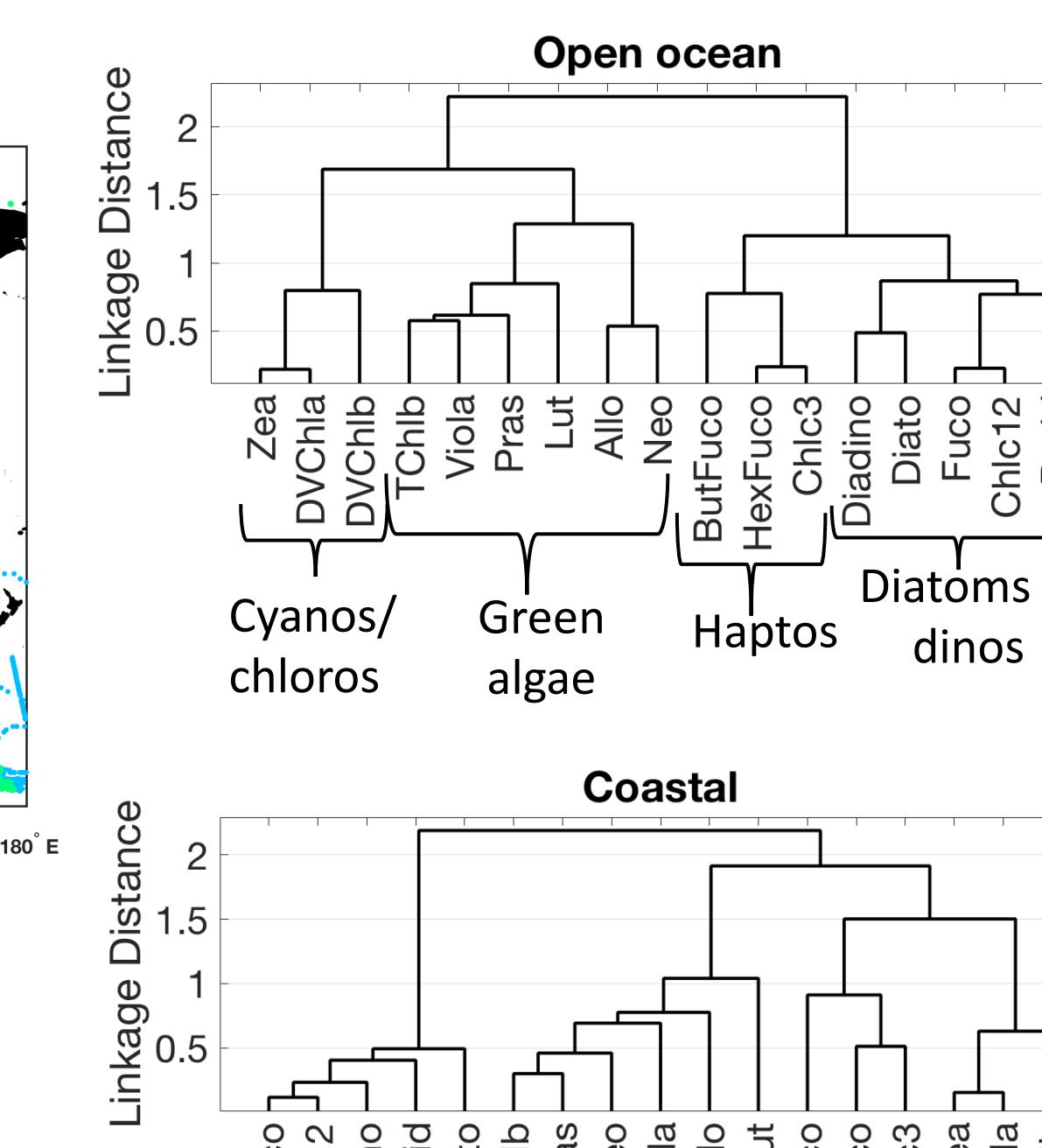
Variance explained by modes 1-6: **70.96%**

Mode 1+temp. $r^2 = -0.48$, Mode 1+sal. $r^2 = -0.06$

Blooms in coast dominated by micros; blooms in open ocean dominated by picos.

Preliminary network results:

Generalized Louvain network for community detection: groups nodes by comparing density of edges inside a community to edges outside a community.



Louvain network results: Algorithm balances speed with performance. 3 communities detected based on the modularity of the weighted correlation adjacency matrix, $a_{ij} = |\text{corrcoef}(x_i, x_j)|^\beta$

Optimized diagnostic pigment analysis: Phytoplankton size classes as a fraction of chl-a where pink >50% micro, green >50% nano, cyan >50% pico, and yellow = multiple groups but no dominant group.

Lucas G. S. Jeub, Marya Bazzi, Inderjit S. Jutla and Peter J. Mucha, "A generalized Louvain method for community detection implemented in MATLAB," [http://netwkit.amath.unc.edu/GenLouvain \(2016\).](http://netwkit.amath.unc.edu/GenLouvain (2016).)

Conclusion & Future Work

- Size emerges as a dominant source of variation in the assemblage of phytoplankton pigments across all analyses (cluster, EOF, DPA, and networks) on both global and basin/coastal scales
- Plan to determine local communities within global dataset of pigments using random walks
- Compare other phytoplankton community metrics (absorption, genomics, IFCB imagery, etc.)

Acknowledgements

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