Identifying the “rules” that govern the ocean’s chemical-microbe network

Sonya Dyhrman

Professor of Earth and Environmental Sciences, Columbia University

Co-PI, NSF STC: Center for Chemical Currencies of a Microbial Planet

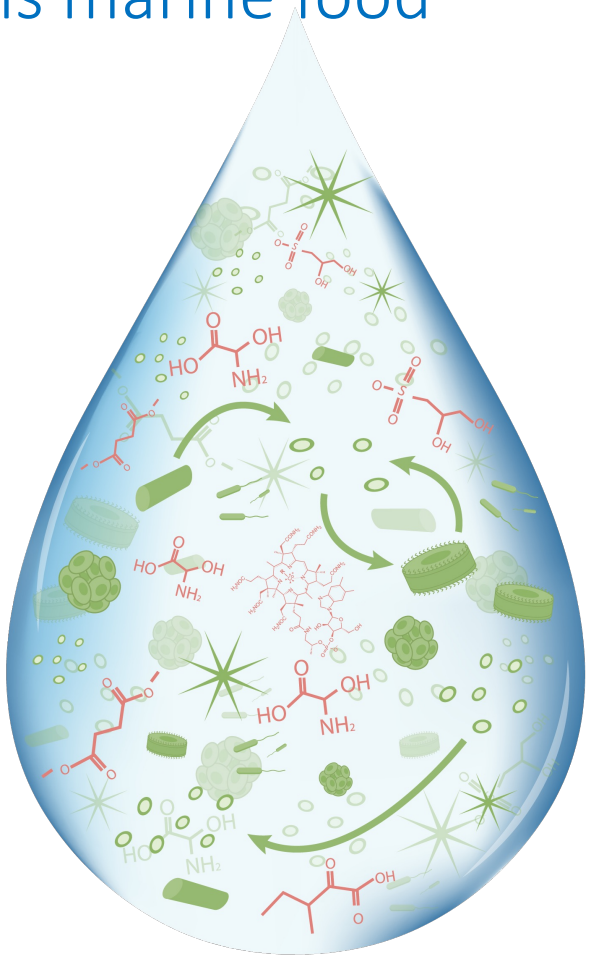
COLUMBIA UNIVERSITY
IN THE CITY OF NEW YORK
LAMONT-DOHERTY EARTH OBSERVATORY

CENTER FOR
CHEMICAL CURRENCIES
OF A MICROBIAL PLANET

Images: WHOI Graphics unless otherwise noted

A vast chemical-microbe network underpins marine food webs and biogeochemical cycling

1. In every 1mL of seawater, there are **10^6 microbes**, (phytoplankton, bacteria and protists) and 10^{10} viruses
2. There are **~100,000 different molecules** of varying concentrations (femtomolar to nanomolar) acting as substrates and signals
3. There are **myriad interactions** within this network- many of which have not been resolved



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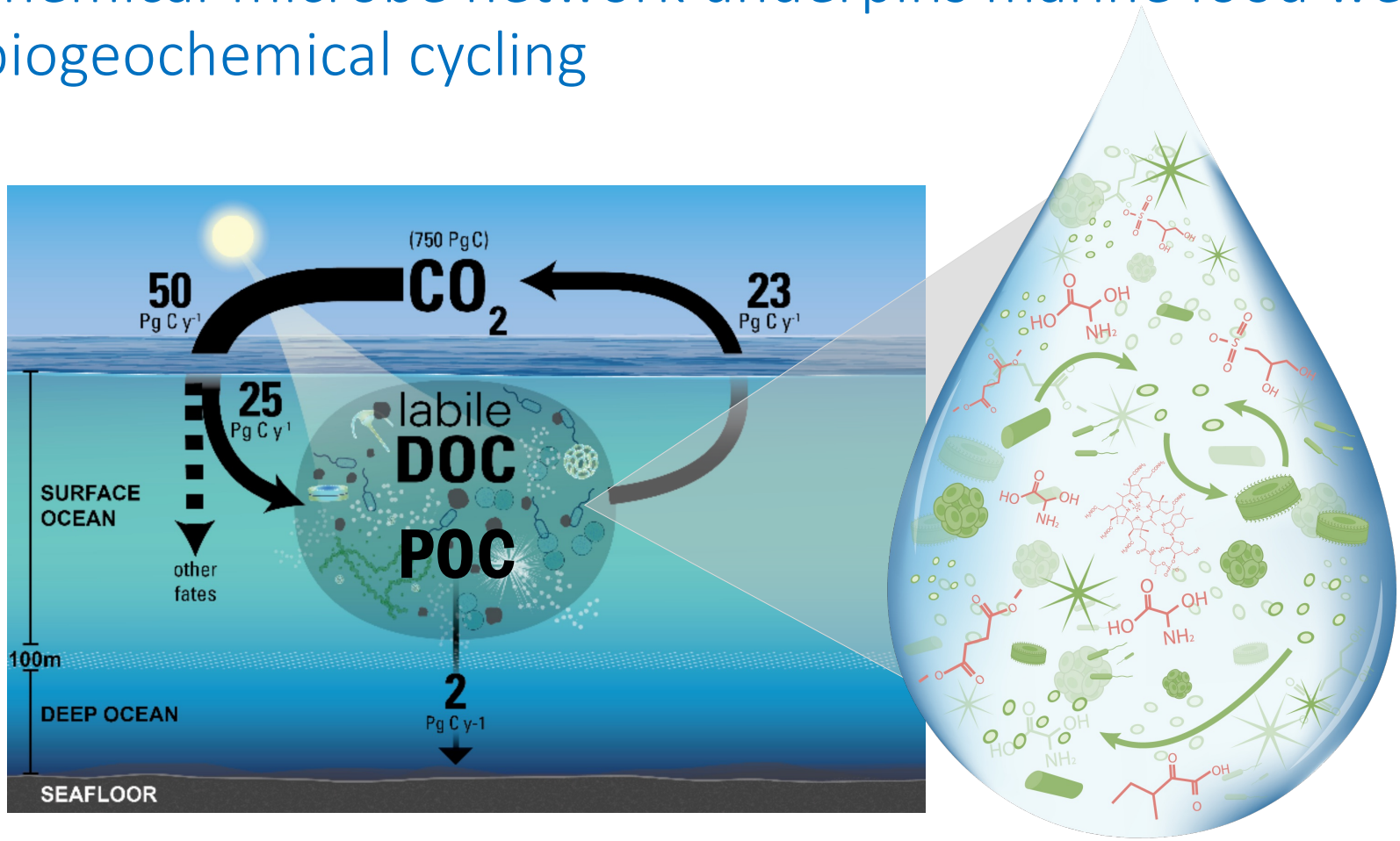
The chemical-microbe network underpins marine food webs and biogeochemical cycling



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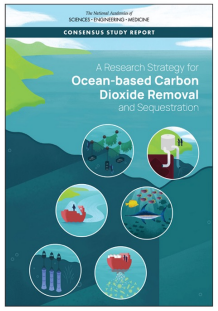
Ocean Carbon Dioxide Removal (CDR) strategies all intersect with the chemical-microbe network and its functions

Consensus Study Report

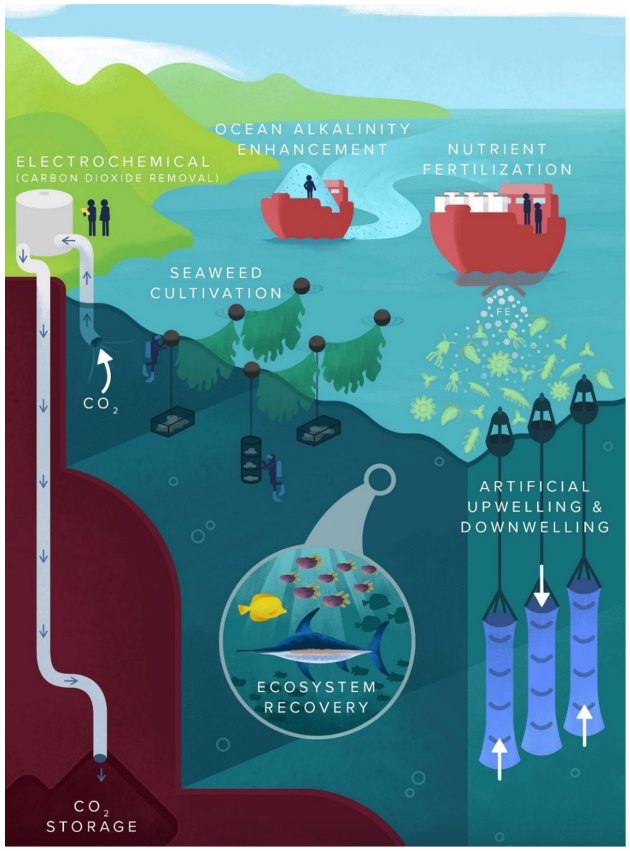
DECEMBER 2021

HIGHLIGHTS



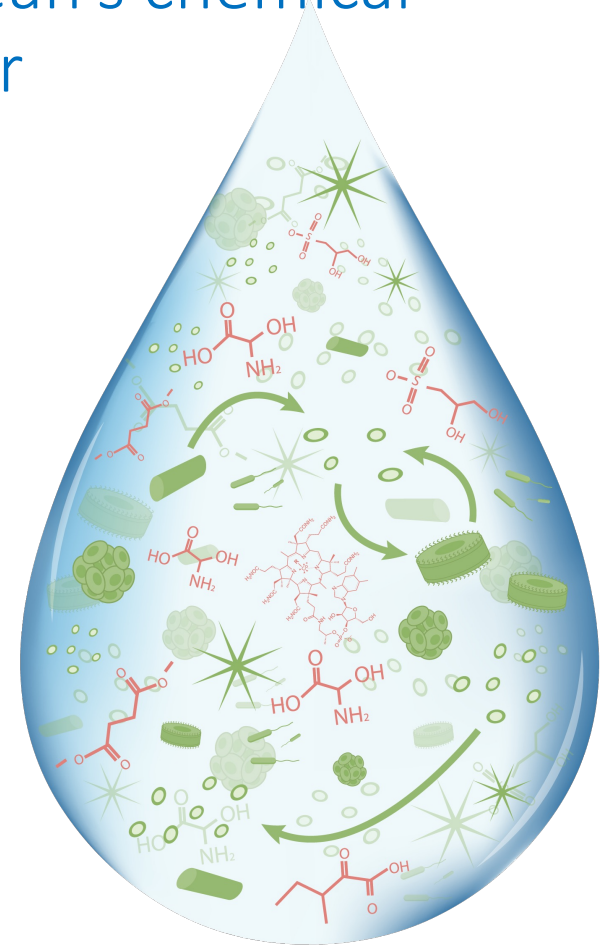
A RESEARCH STRATEGY FOR OCEAN-BASED CARBON DIOXIDE REMOVAL AND SEQUESTRATION

https://www.nationalacademies.org/our-work/a-research-strategy-for-ocean-carbon-dioxide-removal-and-sequestration#sectionPublications

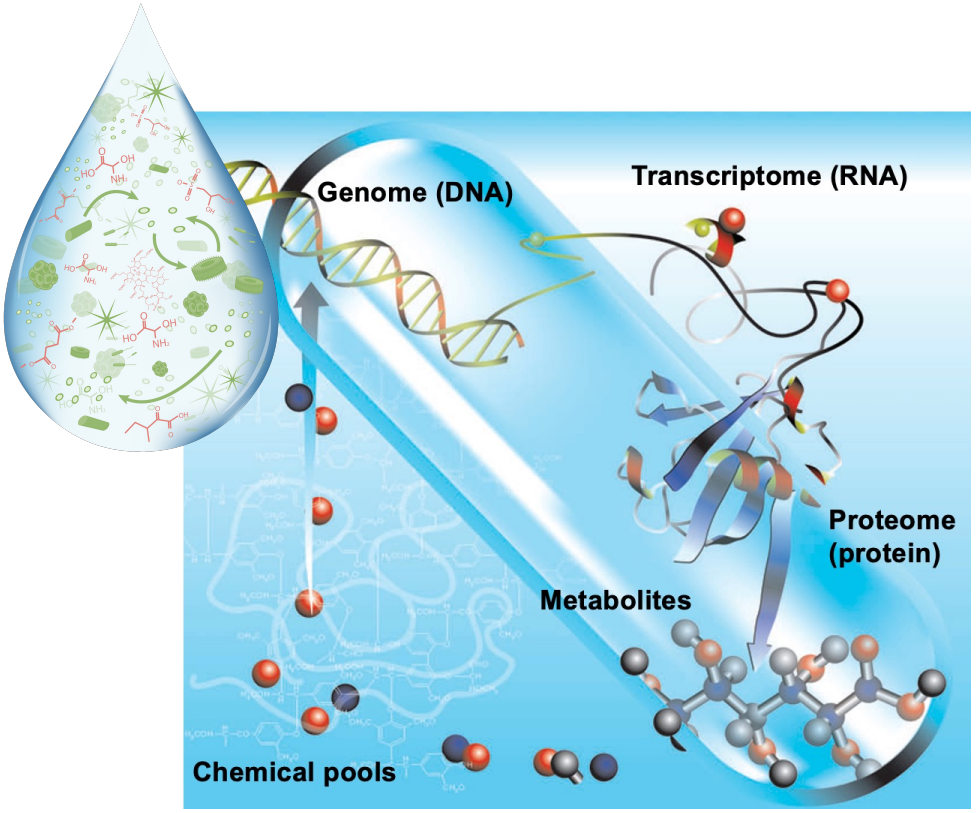


Identifying the “rules” that govern the ocean’s chemical-microbe network to build predictive power

To understand this globally important network we must move beyond inventories to **process-level knowledge**; requiring integrated observational and experiment studies in **chemistry**, **biology** and **modeling** to build predictive power.



Evolving ‘omics methods allow new progress



Kujawinski et al. (2011) *Annual Review Marine Science*

(Meta) genomics = Organisms present and the functions* they carry

(Meta) transcriptomics = The abundance of functions* expressed (turned on) by different organisms

(Meta) proteomic = The abundance of proteins. Dependent on measurements above

(Endo/Exo) metabolome = The abundance of metabolites in cells or seawater.

* Functions are determined based on databases comparisons with distantly related microbes (*E. coli*)

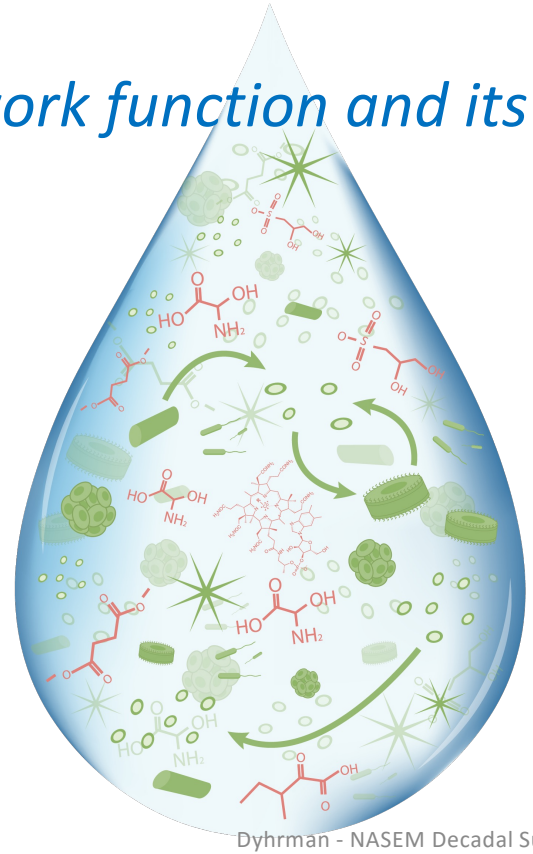
Challenge: The chemical-microbe network underpins ocean ecosystem functions and the earth's biogeochemical cycles, but we lack predictive power on a changing planet.

Opportunity: Identify the rules that govern network function and its sensitivities

1. Investment in **methods and model systems** for resolving the network

2. Expand capacity to **observe the network** across time scales for linking with models

3. Capacity building in **data infrastructure and integration**



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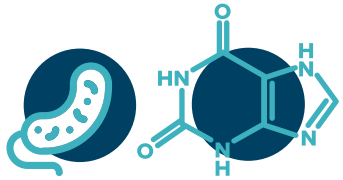
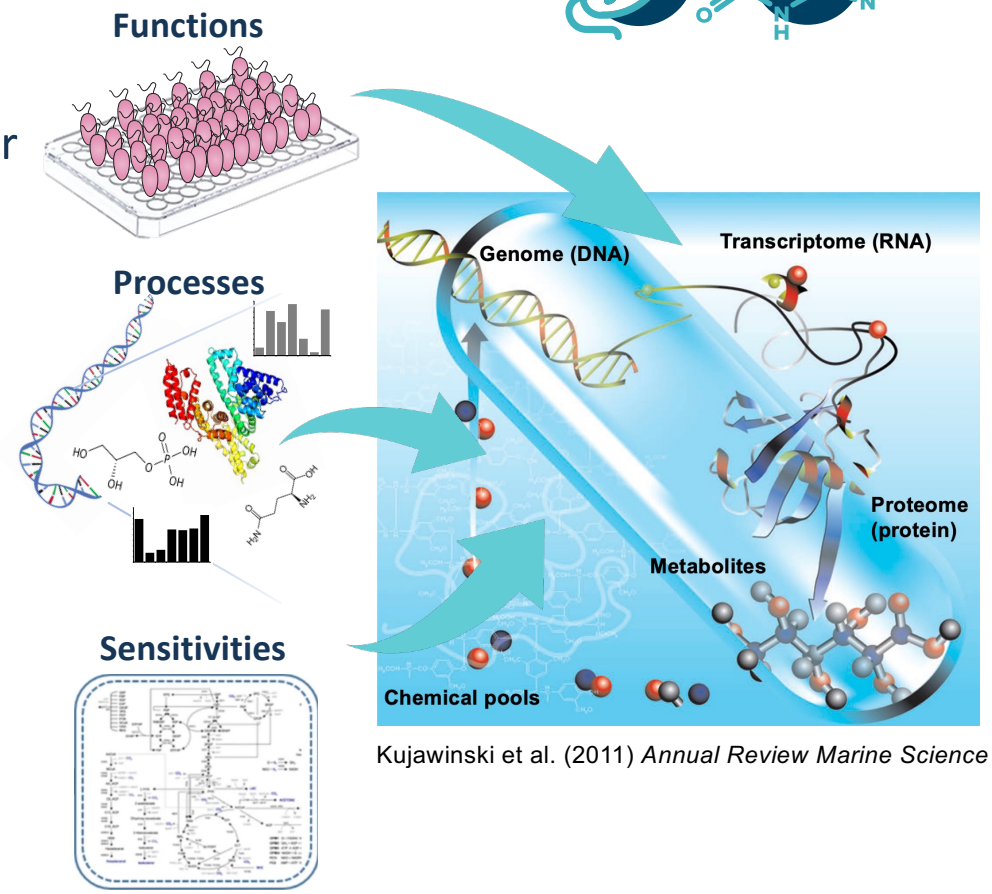
1. Investment in methods and model systems for resolving the network



A Fund development of genetic systems for marine "*E. coli's*", to **resolve marine microbial functions**

B Support continued chemical method development and **link metabolites to production and uptake processes**

C Test **network sensitivities** with model communities in the lab for feeding into models across scales



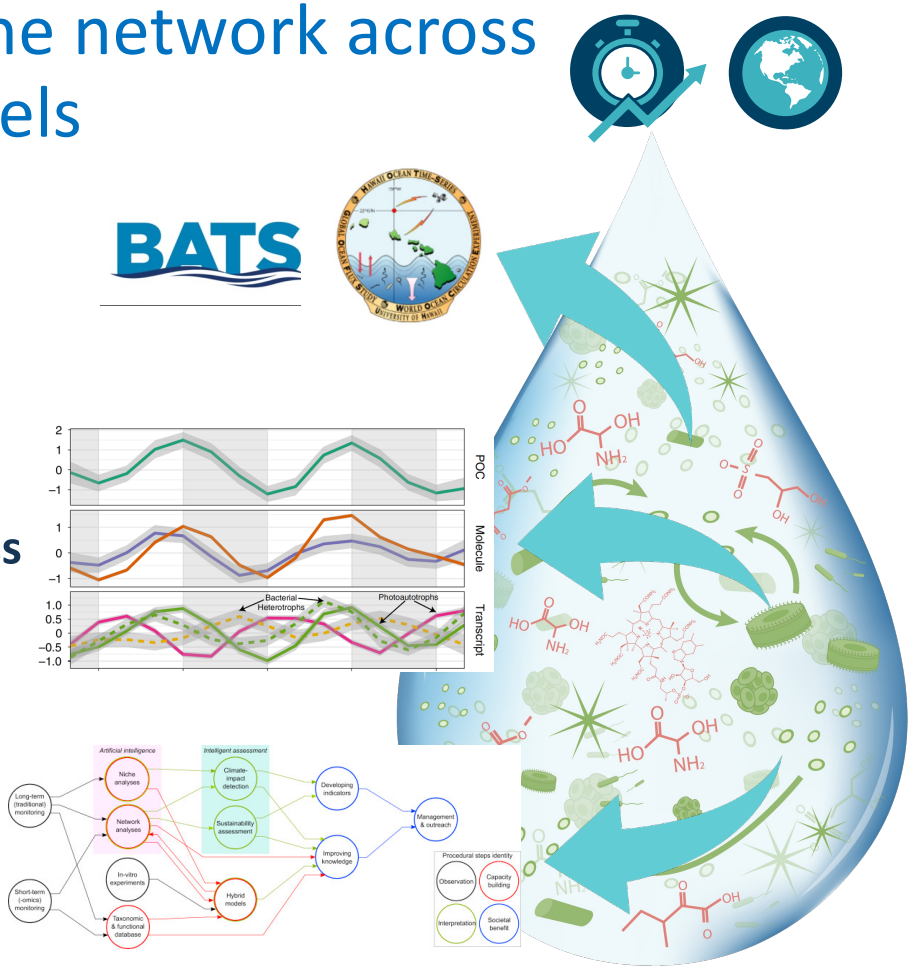
Kujawinski et al. (2011) *Annual Review Marine Science*

2. Expand capacity to observe the network across time scales for linking with models

A Support coincident **multi 'omic measurements** as a core component of the **time-series** (e.g. BATS, HOT)

B Identify **network sensitivities with process studies** (e.g. incubations, diel sampling)

C **Integrate models across scales** to better predictive capacity



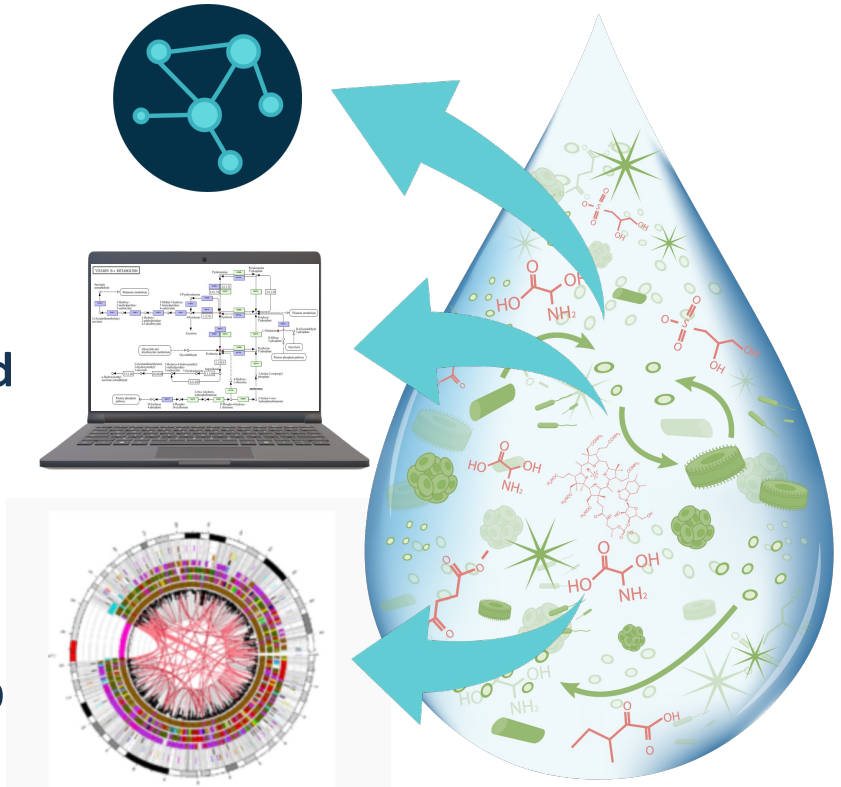
Muratore, Boysen, Harke et al. (2022) *Nature Ecol. Evol.;* D'Alelio et al. (2019) *Curr. Op. Sys. Biol.*

3. Capacity building in data infrastructure and integration

A Support method **intercalibration**, and **data integration** tools

B Expand frameworks for **discoverable derived data products**

C **Training** in computational biology for ECR (e.g. postdoctoral fellowships, Bridge to PhD Fellows, training programs)



2024 Workshop on Genomics

Evomics.org; https://www.us-ocb.org/metat-intercomparison/

Partnership opportunities

- Cross-directorate: BIO
- Interagency:
  - DOE - JGI, KBase, EMSL, E3SM
  - NIH – NCBI
  - NASA
  - NOAA
- Private US:
  - Simons, Gordon and Betty Moore
- Public/Private – International consortia:

U.S. National Science Foundation

SIMONS FOUNDATION

GORDON AND BETTY MOORE FOUNDATION

Partnership opportunities

Intercalibration

Meta-eukomic: Intercomparison of metatranscriptomic methods for characterizing microbial eukaryote contributions to the biological carbon pump

Analysis

Discoverable

Vernette et al. (2022) *Nucleic Acids Res.*

Summary

Confluence of need and opportunity to more fully resolve the rules which govern the chemical – microbe network.

Collectively, this knowledge will help better predict ***ocean resiliency*** on a changing planet.