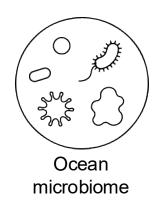
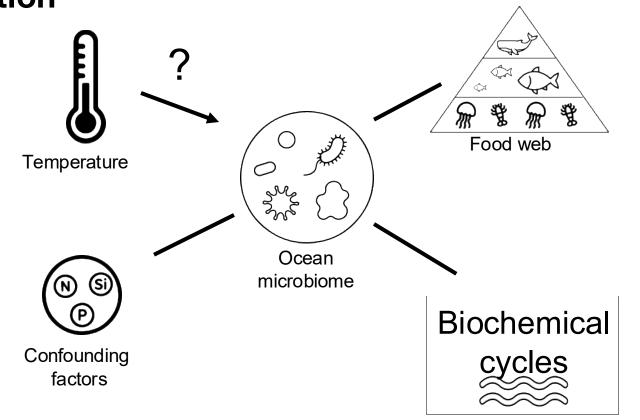


The ocean microbiome plays a central role in climate regulation

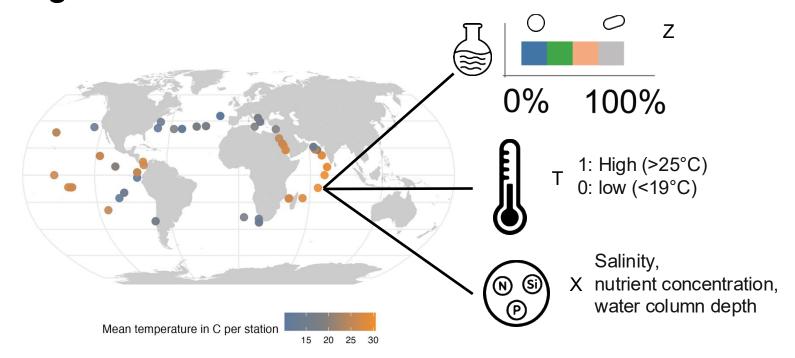


The ocean microbiome plays a central role in climate regulation

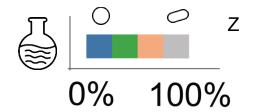
Food web Ocean microbiome **Biochemical** The ocean microbiome plays a central role in climate regulation



Global ocean survey enable us to study those microorganisms in more detail



Outcomes of interest



Let Z be the compositional data matrix with n rows and p species.

Community effects:

- Observed richness: $\sum_{j=1}^{p} \mathbb{I}(Z_{ij} > 0)$ Alpha diversity with Shannon entropy: $-\sum_{i=1}^{p} Z_{ij} ln(Z_{ij})$

Individual species effect:

For each taxa Z_{i} we applied LinDA, a robust regression model to test for a significant association with the treatment variable while controlling for multiple testing

Rubin causal model (RCM)

Unit i	Y _i (1)	Y _i (0)	Individual causal effect $ au$
1	100	10	90
2	1000	100	900
3	1000	90	910
4	1200	300	900

Rubin causal model (RCM)

	Treated	Untreated	
Unit i	Y _i (1)	Y _i (0)	Individual causal effect $ au$
1	100	10	90
2	1000	100	900
3	1000	90	910
4	1200	300	900

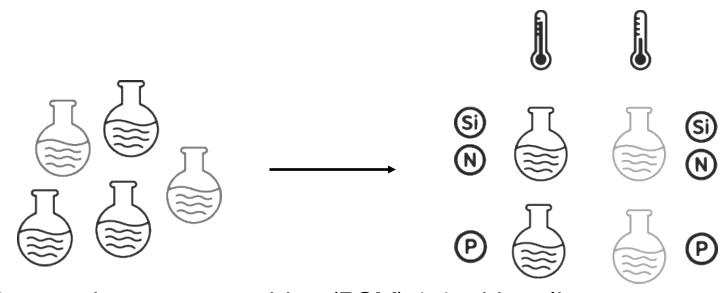
Rubin causal model (RCM)

Rubin causal model frames causal inference as a "missing data" problem: We can only observe one of the potential outcomes

Unit i	Y _i (1)	Y _i (0)	Individual causal effect $ au$
1	100	?	?
2	?	100	?
3	1000	?	?
4	?	300	?

If we assume stable unit treatment value, positivity, and ignorability assumption: $ATT = E[Y_i(1) - Y_i(0)|T_i = 1]$.

We want to find comparable units



- Propensity score matching (PSM) 1:1 with caliper
- Bipartite matching (BM)

Paul R Rosenbaum and Donald B Rubin. Constructing a control group using multivariate matched sampling methods that incorporate the propensity score. The American Statistician, 39(1):33–38, 1985.

Alice J Sommer, Annette Peters, Martina Rommel, Josef Cyrys, Harald Grallert, Dirk Haller, Christian L Müller, and Marie-Abèle C Bind. A randomization-based causal inference framework for uncovering environmental exposure effects on human gut microbiota. PLoS computational biology, 18(5):e1010044, 2022.

Matching results in better covariate balance

We evaluated the covariance balancing with the standardized mean difference $(\overline{X_t} - \overline{X_c})/(\sqrt{s_t^2} + \sqrt{s_c^2})/2$

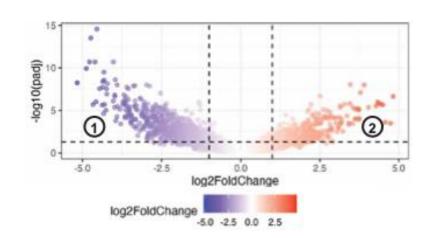
	Unmatched (N = 72, p = 7213)	PSM (N = 36, p = 6594)	BM (N = 32, p = 6547)
Salinity	<u>0.059</u>	0.216	0.163
Phosphate	0.665	0.023	<u>0.018</u>
Nitrate + Nitrite	0.693	0.118	0.003
Depth (SRF)	0.884	0.00	0.00
Depth (DCM)	0.296	0.00	0.00
Depth (MES)	0.843	0.00	0.00

Negative effect on diversity

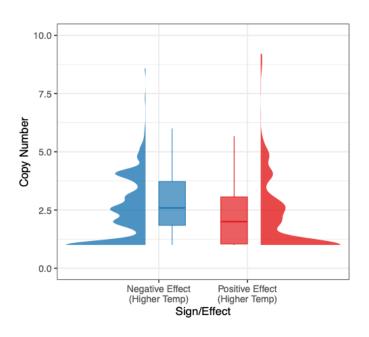
Method	Richness	Shannon
Baseline (Unmatched)	-801.9 ± 153	-0.23 ± 0.06
PSM	-426.5 ± 178	-0.23 ± 0.05
BM	-514.3 ± 199	-0.15 ± 0.07

Effect on individual taxa

Method	Negative	Positive
Baseline (Unmatched)	1718	1546
PSM	1 986	432 (2)
BM	613	239



Warmer temperature favors slower-growing bacteria



Summary and outlook

- Causal inference framework to estimate the causal effect on temperature on ocean microbial communities from large scale surveys
- Extending the idea to continuous treatment variables and a larger dataset
- Conducting a more formal sensitivity analysis