

Metabolic time rescaling predicts coastal microbial dynamics

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Temperature is a primary regulator of marine microbial communities and functioning, yet it is commonly treated as an external covariate acting on a fixed calendar time scale. An alternative view is that temperature accelerates or slows the underlying biogeochemical processes based on the metabolic theory of ecology (MTE), such that the effective pace of community change varies through time. Here we test whether reparameterizing community time series on a temperature-adjusted metabolic time scale improves prediction and interaction inference in a coupled microbial food web. We analyze a 100-day coastal record comprising daily abundances of heterotrophic bacteria, viruses, heterotrophic nanoflagellates, and *Synechococcus*, together with daily nutrients and a co-located 30-minute temperature series. We use the high-frequency temperature data to construct a forward-looking, temperature-adjusted clock, and compare forecasting skill and inferred interaction structure under this metabolic time versus calendar time. Performance is benchmarked against conventional models that incorporate temperature as an external covariate. This framework provides a mechanistically grounded test of whether short, multitrophic microbial dynamics become more predictable and yield coherent interaction pathways when abundance change per unit calendar time is scaled to metabolic time.

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