

Phytoplankton traits from long-term oceanographic time-series

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This file contains MCMC diagnostic plots (traceplots and autocorrelation plots) for the functional group biomass data analysis, along with a report on the simulation study conducted to evaluate the performance of our model in terms of prediction and inference.

I. Diagnostic plots for convergence of the Markov chains

Figures S1–S3 show the traceplots and autocorrelation functions for the model fitting to the functional group biomass. The good mixing of the Markov chains is apparent from the traceplots which show the MCMC sampler jumping freely around the parameter space. Having caterpillar-like traceplots of Markov chains sampling from the same region of the parameter space as in Figs S1–S3 is an indication that the chains have converged to the same limiting distribution. In addition, the autocorrelation functions (ACF) plotted in Figs S1–S3 indicate that the selected thinning period has resulted in a substantially low autocorrelation in the MCMC samples.

II. Report on the simulation study

We simulated data mimicking the biomass dynamics of a two-functional group system, to evaluate the performance of our model in terms of inference and prediction. More specifically, we extracted from the L4 functional group biomass data the biomass of diatoms and phytoflagellates (the two functional groups with no missing data over the time series), and fitted our model to the data with all environmental variables (temperature, irradiance and nitrogen concentration) assuming the observed values at L4 Station over the time series. We used the posterior predictive mean biomass over the time series as simulated data from the hypothetical two functional group system under our model with underlying parameter values given by the posterior mean estimates. We subsequently fed the simulated data back to the model to evaluate the model's ability to retrieve the underlying parameter values. Figures S4 & S5 show the posterior distributions of the model parameters for diatoms and phytoflagellates respectively, with the solid vertical lines indicating the underlying parameter values. As can be seen from these

Figures, all underlying parameter values lie well within the range of the corresponding posterior distributions, implying that the simulated data are consistent with the actual data, and that the model is effective at retrieving the underlying parameter values.

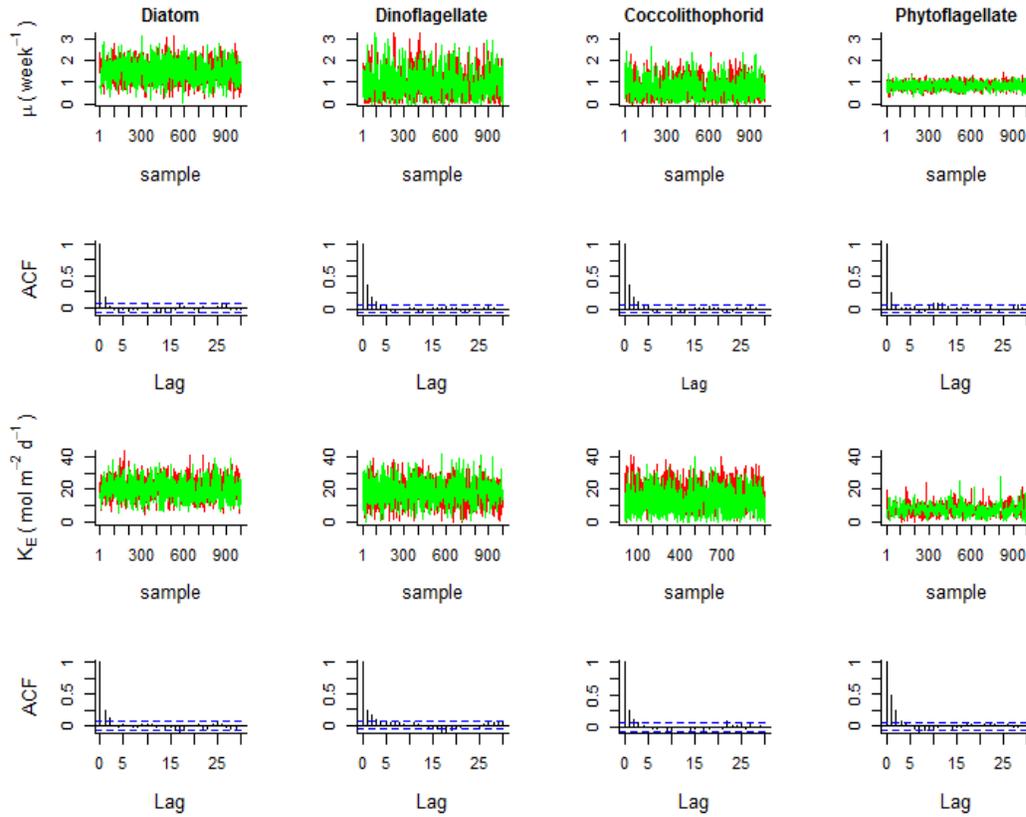


Fig. S1: Traceplots showing 1000 MCMC samples and corresponding autocorrelation functions for the net growth rates and irradiance half-saturation constants. For each parameter, the y-axis scaling is the same to facilitate comparison.

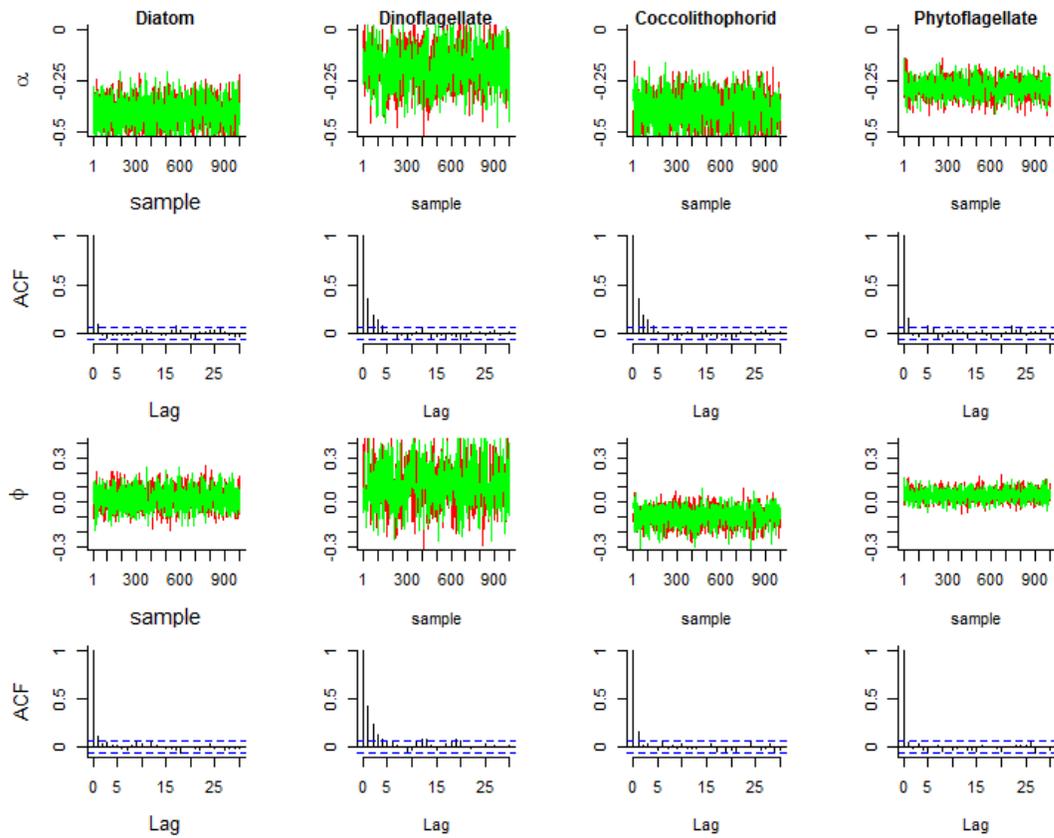


Fig. S2: Trace plots showing 1000 MCMC samples and corresponding autocorrelation functions for the density feedback parameters. For each parameter, the y-axis scaling is the same to facilitate comparison.

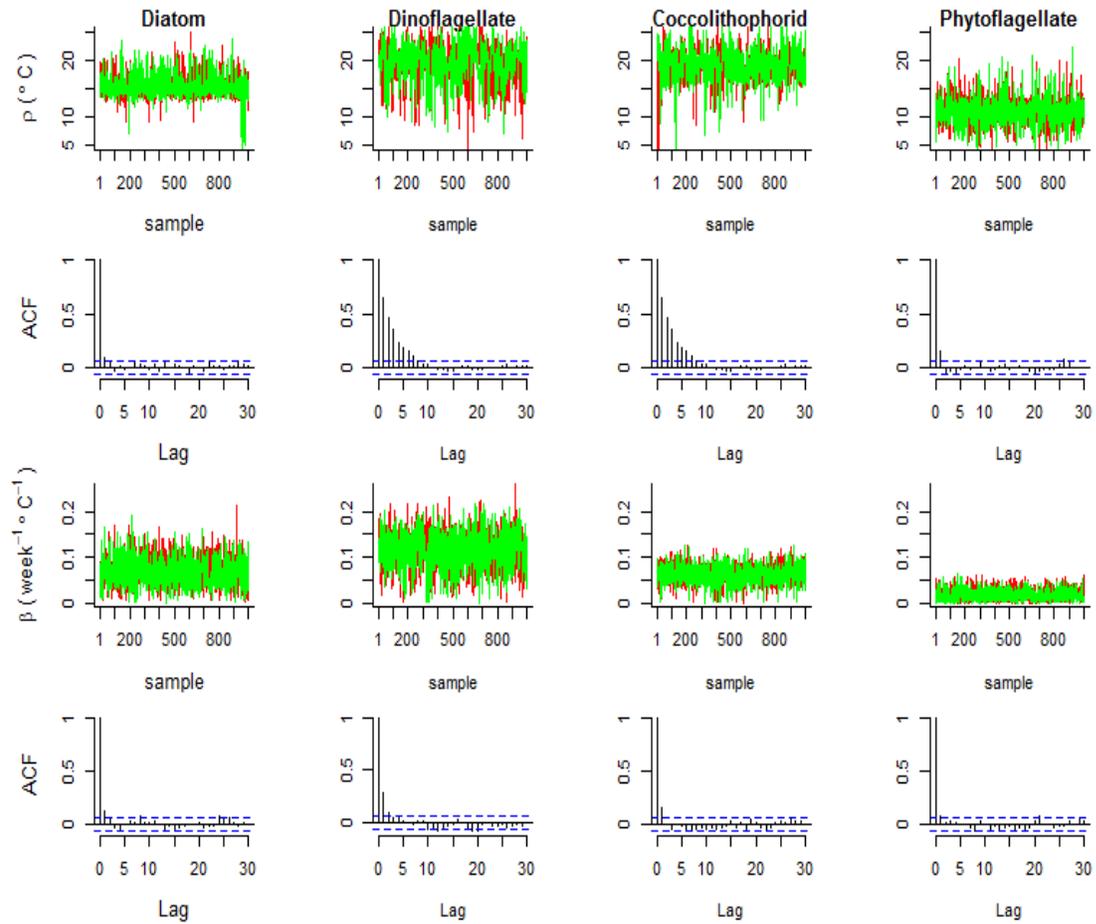


Fig. S3: Trace plots showing 1000 MCMC samples and corresponding autocorrelation functions for the optimal growth temperatures and the temperature sensitivity parameters. For each parameter, the y-axis scaling is the same to facilitate comparison.

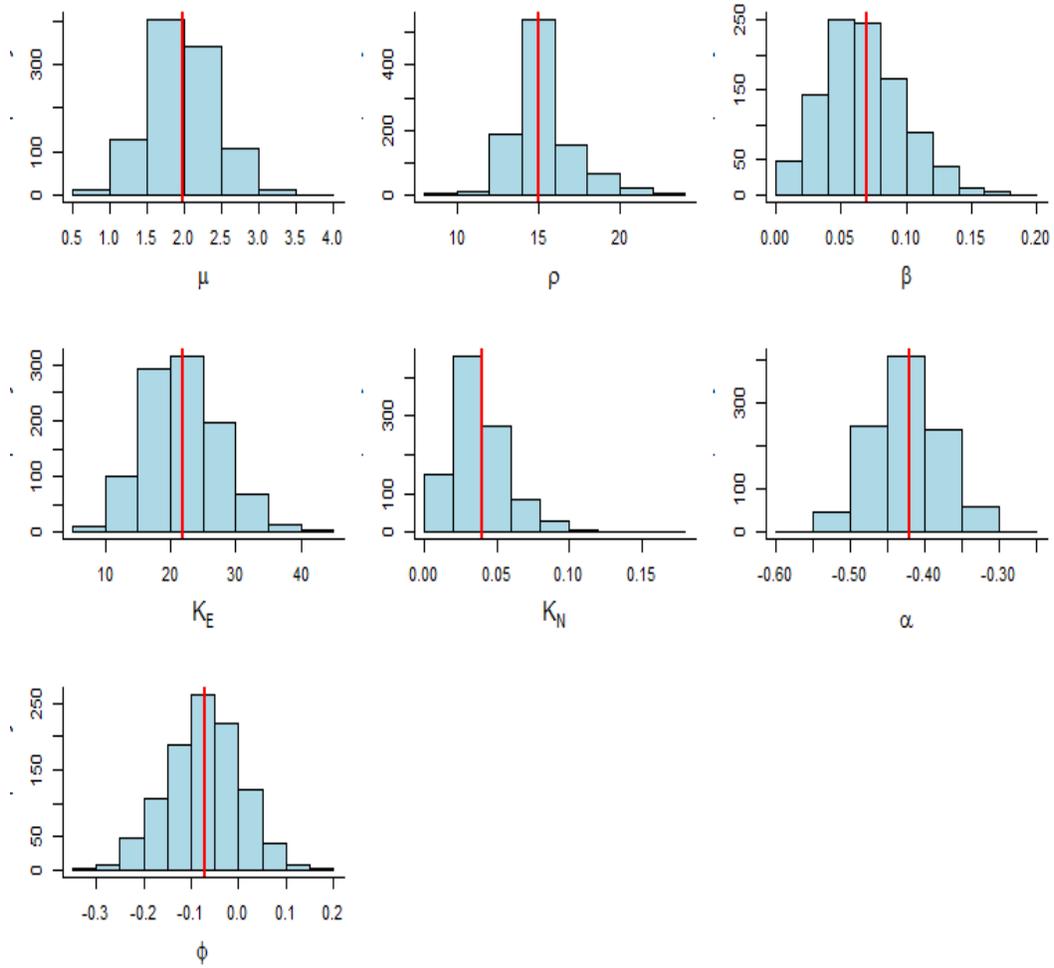


Fig. S4: Histograms of the posterior distributions of the model parameters for simulated diatom biomass, with the solid vertical line indicating the parameter values underlying the data generating process.

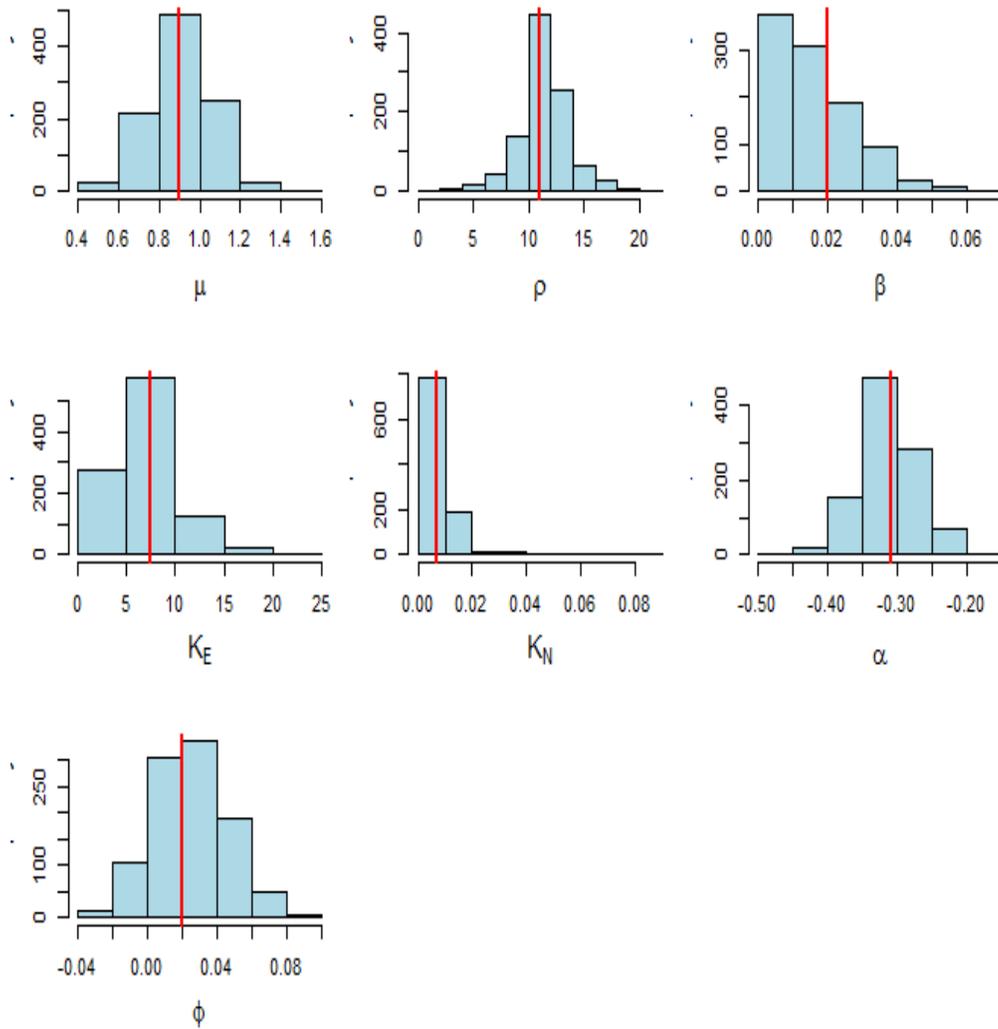


Fig. S5: Histograms of the posterior distributions of the model parameters for simulated phytoplankton biomass, with the solid vertical line indicating the parameter values underlying the data generating process.