

SupplementaryInformation Two: Supplementary figures

Case Study: Application to PoMS data

We load the data and functions needed to plot the supplementary figures.

Convergence checks

Estimates of community hyperparameters

Community mean

Warning: Removed 12 rows containing missing values (``geom_point()``).

Community variance

Warning: Removed 7 rows containing missing values (``geom_point()``).

Overdispersion parameter

Posterior predictive checks

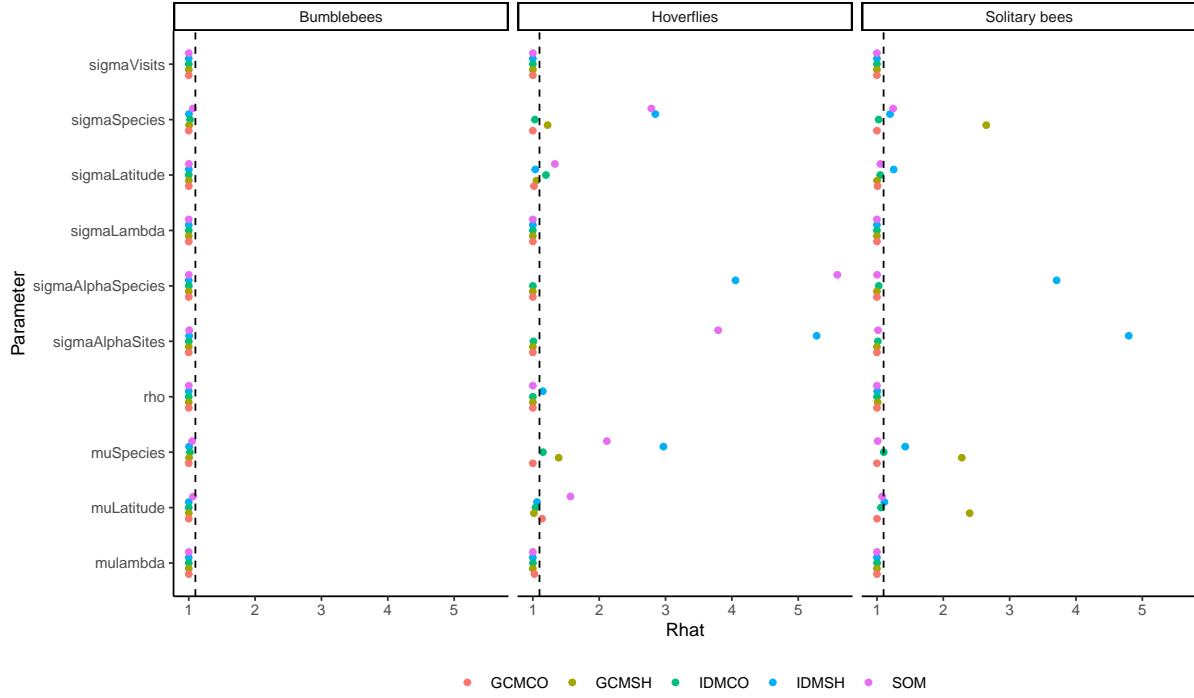


Figure S2-1: Rhat estimates for the Markov chain Monte Carlo samples for each of models used in this study. A model was considered to have converged if the r-hat estimates were less than or equal to 1.1 (corresponding to the left side of the dashed line.)

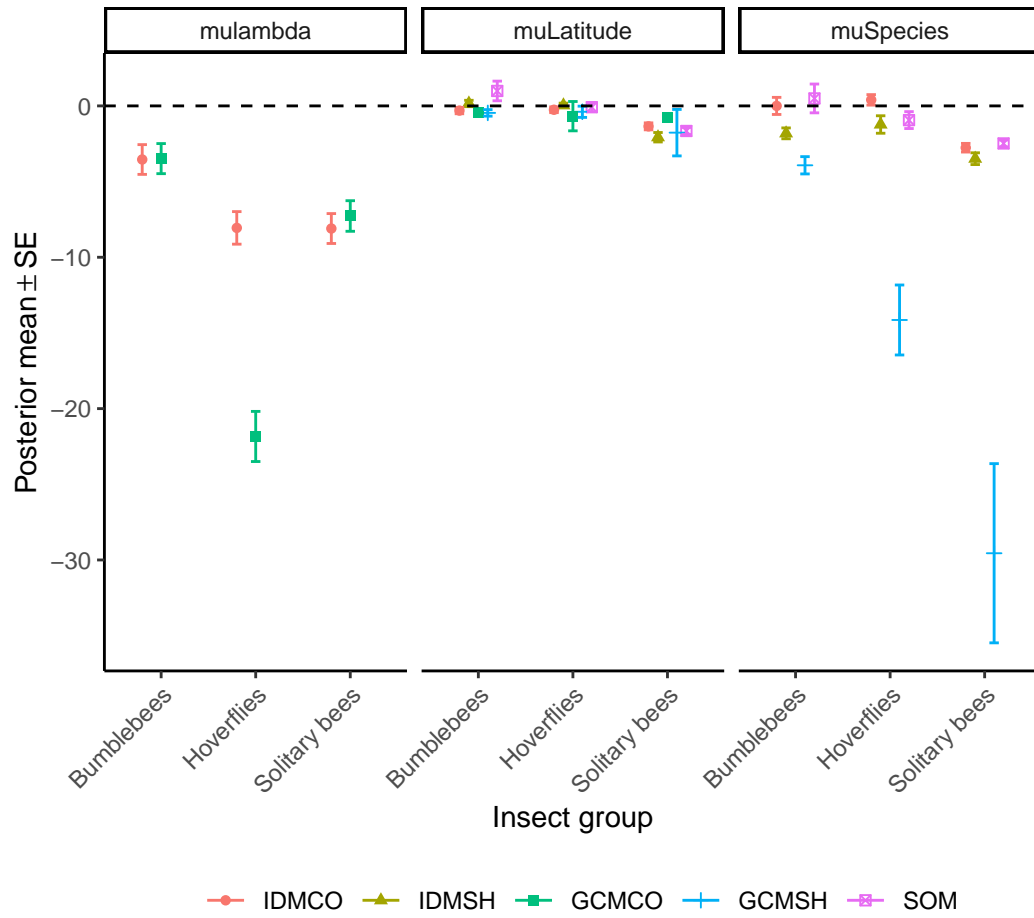


Figure S2-2: Community mean estimated from the five models in this study for intercept (mulambda and muSpecies) and latitudinal effect (muLatitude) from the PoMS case study.

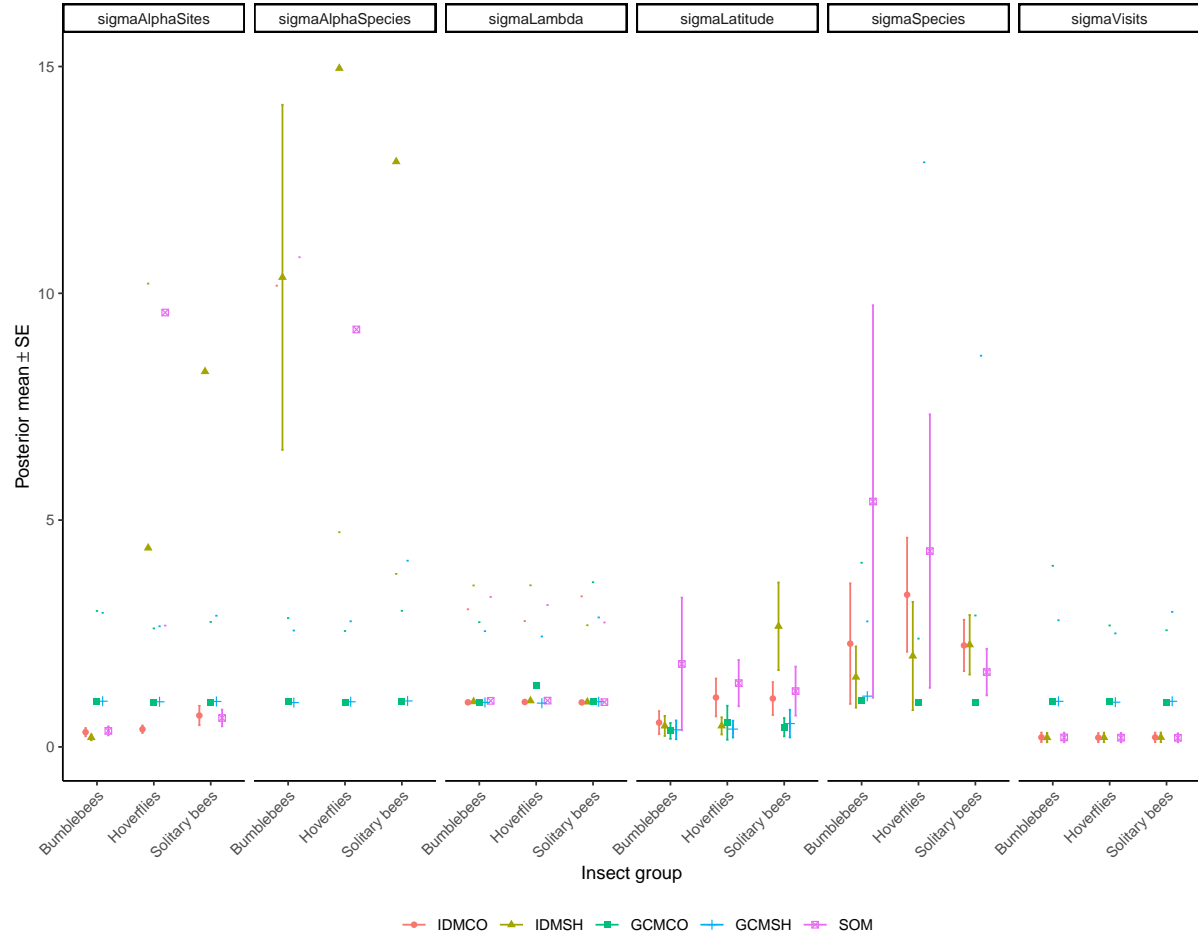


Figure S2-3: Community variance estimated from the five models in this study for the detection probability (sigmaAlphaSpecies, sigmaAlphaSites, sigmaAlphaVisits), and the observation process (intercept: sigmaLambda, sigmaSpecies and latitudinal effect: sigmaLatitude) from the PoMS case study.

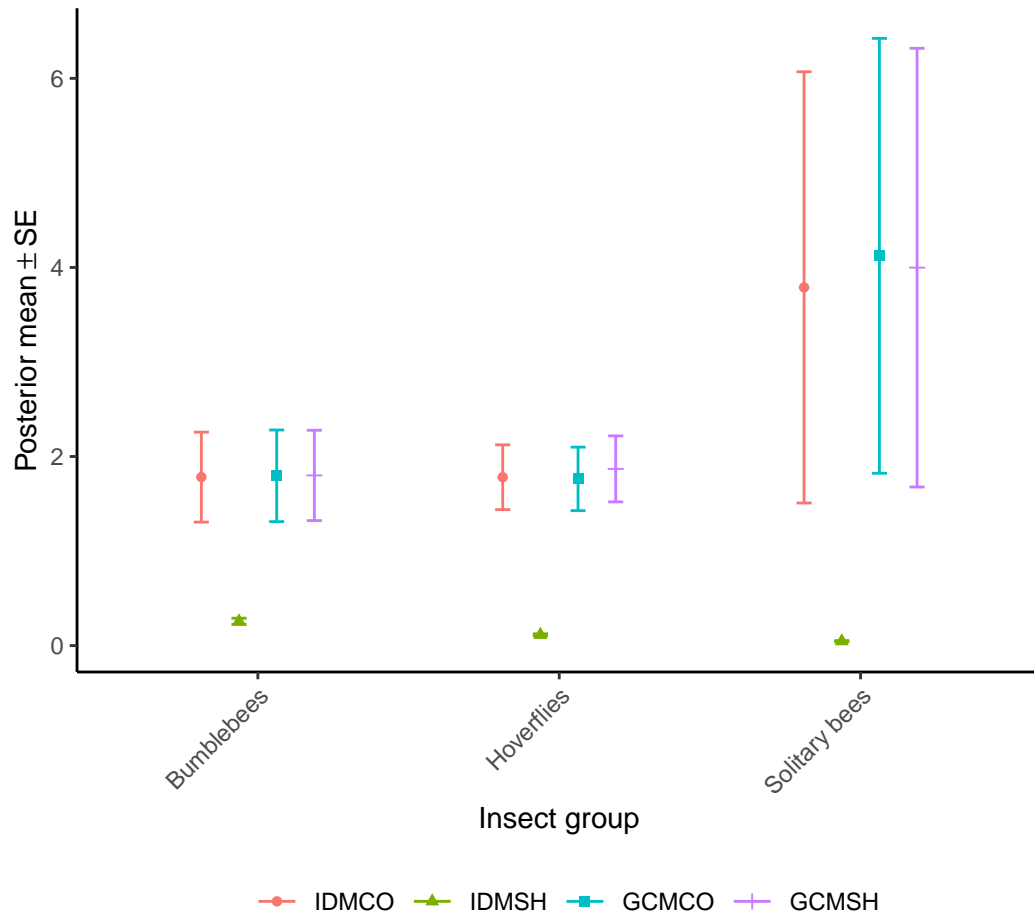


Figure S2-4: Overdispersion parameter (η) estimated from the models that included the FIT count data.

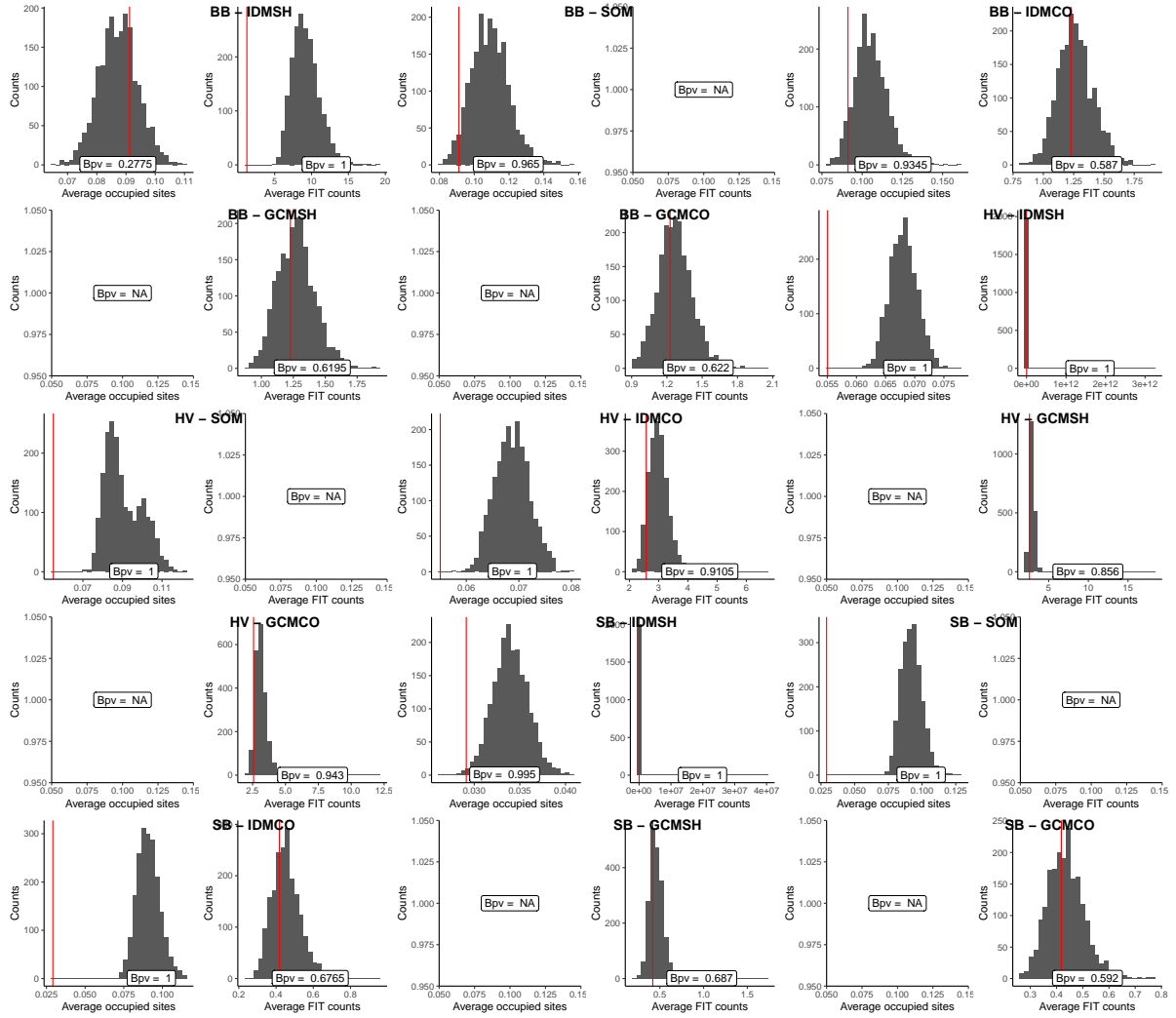


Figure S2-5: Histogram of the test statistic used for the posterior predictive checks for the case study. Each of the models used in the study has two histograms: one for the Pantrap data and the other is for the FIT count data. For each pair of plots, the title is named with the insect group as the prefix: BB for bumblebees, HV for hoverflies and SB for solitary bees. The suffix of the title is named after the insect group used to model the data: integrated distribution model with shared likelihood structure (IDMSH), integrated distribution model with covariate likelihood structure (IDMC0), species occupancy model (SOM), group count model with shared likelihood structure (GCM SH) and group count model with covariate likelihood structure (GCMC0). The value of the test statistic from the original data is coloured in the red vertical lines and the Bayesian p-value (Bpv) is presented in each of the histograms. The models that do not model a particular dataset has empty histograms and the Bayesian p-value is NA.