

Appendix A: Additional analyses of DECEMS simulations

Here we summarize the effect of detection error on metacommunity structure classification. We explored the influence of the mean species-specific detection rate, p_i , and that of incidence matrix size, which scales with gamma diversity.

A.1 Structure-specific results

Table A1 summarizes the misclassification of metacommunity structure with 12 species and mean $p_i = 0.5$, as well as the sample size (n) observed for each structure. These results are qualitatively similar to simulations with increasing mean detection probability. Due to detection errors Gleasonian structures were more often misclassified as Clementsian structures than quasi-Gleasonian structures (and vice versa). This indicates that EMS methods are particularly sensitive to false absences at the range boundaries. The DECEMS method was much more likely to correctly classify structures in these instances, as demonstrated in the main text. Our method of simulating metacommunities did not result in an equal distribution of sample sizes for the various metacommunity structures.

We found that DECEMS was not equally effective for all structure types. For instance, it was easiest for DECEMS to correctly match the true metacommunity structures of Clementsian metacommunities, followed closely by Gleasonian (Fig. A1). The model had more variable results for other structures. However, this is likely influenced by the lower sample sizes for the other types of structures. Additionally, as the mean p_i increased, the differences in the performance of DECEMS between structure types diminished (Fig. A1). It is worth noting that Figure A1 represents the percentage of cases in which the structure of \mathbf{Z}_{post} matches that of \mathbf{Z} perfectly. If we count the instances where \mathbf{Z}_{post} , for instance, is either Gleasonian or quasi-

Gleasonian and the corresponding \mathbf{Z} structure is Gleasonian, then the performance of DECEMS improves even more still.

TABLE A1. Structure misclassification rates by structure type. Indicated is the percentage of cases in which a known structure (left) appears as a particular observed structure (top) due to detection errors. The number of simulations for which a particular known structure was observed (n) is also shown. This is the case for with 12 species and mean $p_i = 0.5$.

		Observed Structures								n
		Gleasonian	Quasi-Gleasonian	Clementsian	Quasi-Clementsian	Nested	Quasi-Nested	Evenly Spaced	Random	
Known Structures	Gleasonian	0.389	0.023	0.503	0.048	-	0.003	0.006	0.028	352
	Quasi-Gleasonian	-	0.091	0.273	0.136	-	0.273	-	0.227	22
	Clementsian	0.090	0.002	0.765	0.058	-	0.006	-	0.080	536
	Quasi-Clementsian	-	-	0.333	0.233	-	0.200	-	0.233	30
	Nested	-	-	-	-	-	-	-	1	1
	Quasi-Nested	-	-	0.111	0.167	-	0.500	-	0.222	18
	Evenly Spaced	0.600	-	0.400	-	-	-	-	-	5
	Random	0.023	-	0.159	0.068	-	-	-	0.750	44

Because all misclassification errors are not equally detrimental to biological understanding, we wanted to determine how often egregious errors occurred. First, we looked at how often coherent structures were misclassified as non-coherent (random) structures. Overall 7% of our simulations in the worst-case scenario (mean $p_i = 0.5$) resulted in an incorrectly assigned random structured for the observed metacommunity \mathbf{Y} . It seemed that Clementsian structures tended to be most prone to this type of misclassification, although this error occurred at least once for all generated structures. Second, we determined whether positively coherent structures were ever misclassified as negatively coherent (i.e. checkerboard pattern). This never happened in our worst-case scenario simulation. Third, we looked at how often communities with negative turnover (e.g. nested) were incorrectly classified as having positive turnover (e.g. Gleasonian or Clementsian). This occurred in 5 out of 19 possible nested/quasi-nested structures,

which is a relatively high frequency, but the sample size is admittedly low. Fourth, we looked at the opposite case, where communities with positive turnover were classified with negative turnover. While this did occur, it only happened in <2% of cases, with a much larger sample size to support this finding. Finally, we determined how often communities with clumped boundaries were classified as having over-dispersed boundaries; however, this never happened in the simulation.

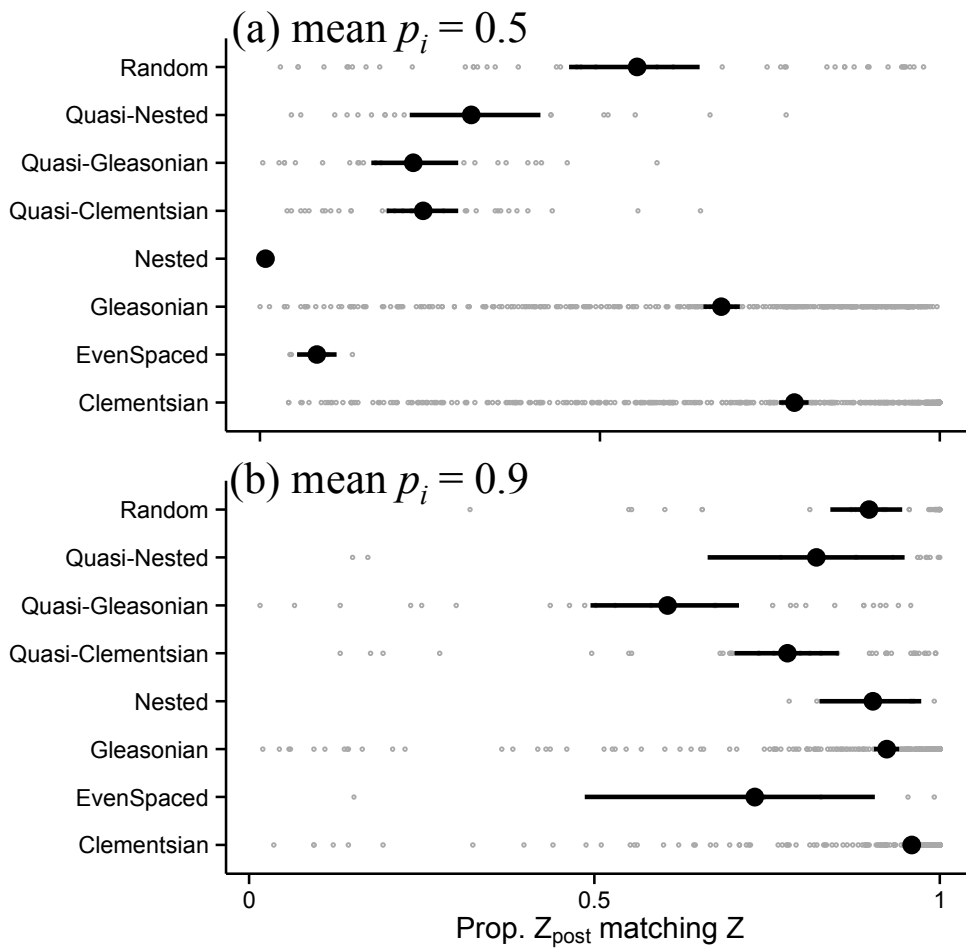


FIG. A1. Performance of DECEMS by structure type. Labeled on the left are the known structures of Z . Dark points and lines represent the mean and 95% bootstrapped confidence intervals of the percentage of times the 500 Z_{post} structures matched the structure of Z . Lighter

circles represent each data point. Note the difference in sample size for each structure type.

A.2 Manipulating metacommunity-wide species richness

Here, we wanted to determine if the gamma diversity of our metacommunity (i.e., the total number of species observed across all sites) influenced our results. To accomplish this, we conducted the same simulation of metacommunities, changing the total number of species to 24 and 36. Because of the increase computation time with additional species, we had to restrict the number of simulated communities to 120 for each value of gamma diversity. We only simulated these metacommunities with a mean $p_i = 0.5$. Then, as in the main text, we determined the percentage of cases in which the observed metacommunity structure (that of \mathbf{Y}) differed from that of \mathbf{Z} . We compared this to the median value for the percentage of cases where the structures of \mathbf{Z}_{post} matched those of \mathbf{Z} . We found that the gamma diversity of the metacommunity did not substantially influence the performance of DECEMS. Although standard EMS approach performed incrementally better with increasing gamma diversity, in each case, the median percentage of \mathbf{Z}_{post} matching those of \mathbf{Z} was significantly greater, demonstrating that DECEMS still outperformed standard EMS methods (Fig. A2).

Unsurprisingly, however, when we increased the number of species in the metacommunity, the likelihood of simulating observed matrices, \mathbf{Y} , with non-coherent structures due to detection error fell substantially, with no such structures found with 36 species (although our sample size was not large). Also, as gamma diversity increased, using our methods, it was difficult to simulate any structures that did not have positive turnover. Thus, most simulated structures were Gleasonian or Clementsian (or quasi-structures of these types).

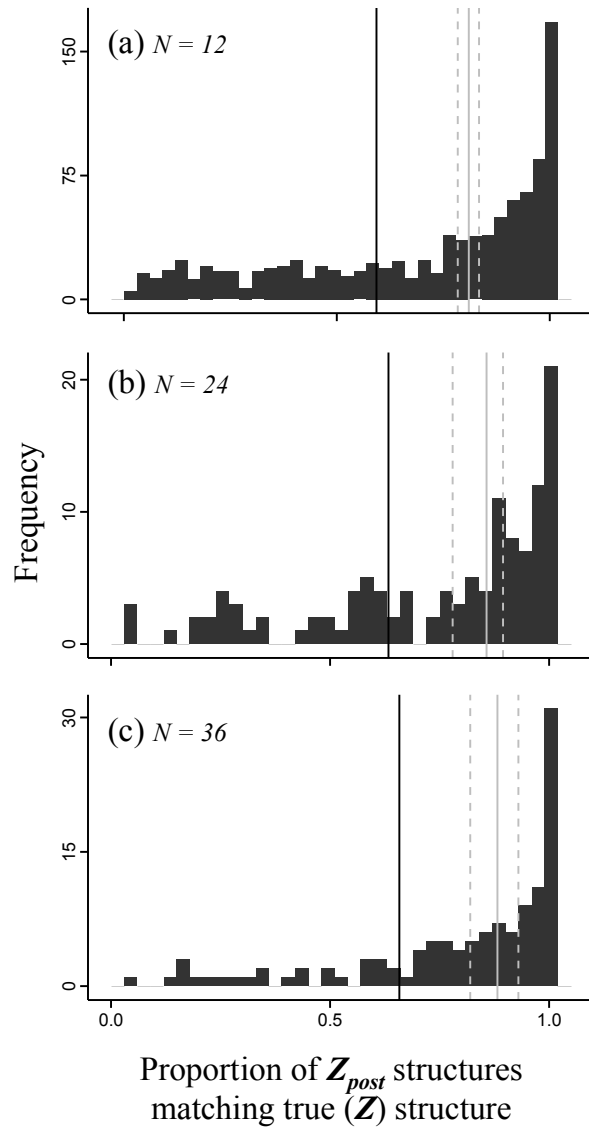


FIG. A2. Performance of standard EMS and DECEMS with increasing gamma diversity (N). As in the main text, black vertical lines represent the point estimate of the proportion of 1000 simulations for which the observed metacommunity, \mathbf{Y} , structure matched the known metacommunity, \mathbf{Z} , structure. Solid and dashed gray vertical lines represent the median and bootstrapped 95% confidence intervals for the proportion of 500 estimated \mathbf{Z}_{post} structures that match the known metacommunity, \mathbf{Z} , structure. For all panels mean $p_i = 0.5$.

It should also be noted that we tried using a more conservative method of creating null matrices ('quasiswap') for low species richness ($N=12$). This method improved the performance of the standard EMS approach slightly; however, there was a concomitant performance improvement in DECEMS (unpublished data). Thus, overall, changing the null matrix generator method did not change our main result that DECEMS outperforms standard EMS approach with detection error.

A.3 Additional Discussion

These additional results further demonstrate the applicability and utility of DECEMS, but also highlight important areas of future research. While we see that detection error can lead to many types of errors, some structures might be more prone to the effects of false absences than others. Additionally, it does not seem that detection error causes many egregious errors in misclassification, but when it does, DECEMS corrects these errors. However, DECEMS does not seem as effective for all types of misclassification errors, although this discrepancy diminishes as the detection error rate declines. Finally, as the gamma diversity of the metacommunity increases, determining coherence is less susceptible to detection error, but false absences at species' range boundaries still cause high misclassification rates using standard EMS methods, which DECEMS is able to correct.

Our results suggest that Morisita's Index and potentially the turnover statistic (measured by species replacements) are quite sensitive to detection error. This is shown by the propensity of false absences at species range boundaries to cause Gleasonian structures to be misclassified as Clementsian structures (and vice versa). This is also seen by quasi-nested structures showing Clementsian or Gleasonian structures. Coherence is also sensitive to detection error, but this

sensitivity declines as the gamma diversity of the metacommunity increases. While not being particularly egregious errors, these misclassifications still bias and misconstrue our understanding of the system's biology. These errors also suggest that assignment of metacommunity structure is more affected by detection errors further down the decision tree (Fig. 1). It will be important for future research to understand how detection errors affecting turnover influence the assignment of quasi-structures and subsequently our biological interpretation of communities. This is particularly relevant because even with perfect detection, quasi-structures arise due to indistinguishable patterns of turnover. Thus, other mechanisms might interact with detection error to influence misclassification of quasi-structures.

We believe that while some of the results discussed in this Appendix are likely general, some of the specifics are likely influenced by our method of simulating coherent metacommunities. In order to simulate different metacommunity structures we manipulated the distributions of covariate values across space and the distribution of species-specific covariate effects. This allowed us to generate many different structures, however, not all structures were equally represented in our simulations. For instance, the majority of metacommunities showed positive turnover. This is because we assumed one environmental covariate and in most cases groups of species responded to the covariate strongly, either positively or negatively, leading to positive turnover.

In future studies, it will be interesting and important to determine the various ways that certain structures arise, which is a great advantage of this occupancy model framework. For instance, we did not assume that species interacted with one another or that, in general, species distributions were non-independent. However, recent work developing joint species distribution models could be easily incorporated into the occupancy modeling framework (Ovaskainen et al.

2010, Pollock et al. 2014). Using these models in simulation studies would reveal the different ways that non-independence in species distributions can affect resulting metacommunity structures.

Using the DECEMS framework as a basis of simulation, we should be able to obtain a better grasp of the processes that lead to specific metacommunity structures, allowing us to better understand how metacommunities arise in nature. This approach will also allow us to determine whether the same processes can lead to the different metacommunity structures, an understanding that is currently lacking. This is a very important next step of this research. Additionally, we will be able to better evaluate the efficacy of DECEMS for each metacommunity structure and more concisely determine if any biases exist. However, we are confident that the benefits of using DECEMS in all cases outweigh the potential uncertainties.

A.4 Literature Cited

- Ovaskainen, O., J. Hottola, and J. Siitonen. 2010. Modeling species co-occurrence by multivariate logistic regression generates new hypotheses on fungal interactions. *Ecology* 91:2514–2521.
- Pollock, L. J., R. Tingley, W. K. Morris, N. Golding, R. B. O’Hara, K. M. Parris, P. a. Vesk, and M. a. McCarthy. 2014. Understanding co-occurrence by modelling species simultaneously with a Joint Species Distribution Model (JSDM). *Methods in Ecology and Evolution* 5:397–406.