

# **Supp. mat. for *The dissimilarity of species interactions networks***

## **S1 From pairwise to multiple-sites**

When the realizations of a metaweb are not situated alongside an environmental gradient, the pairwise comparison method can be replaced by a multi-site approach, *i.e.* a measure of the global variability between the different realizations. In the main text, we expose why simply adapting multiple-sites measures is not satisfactory when there is a high turnover of species. In this appendix, we propose an alternative approach to the problem of multi-site network dissimilarity. We define the *metaweb* as being the aggregation of all species and their interactions at the regional scale. Assuming that the system is well sampled enough, this metaweb can be a proxy of the regional pools of species and interactions. In this perspective, it is easy to measure how much a given site differs from the metaweb, which effectively accounts for its differences with all possible interactions found regionally. In our framework (see Tab. 1 from main text), this is encompassed by the  $\beta'_{os}$  value. The `beta.os_prime` function in the companion R package to this paper automates the process and returns the distribution of  $\beta'_{os}$  values for a list of realizations. In this section, we provide guidances for its measurement and interpretation.

Given  $T$  realizations of size  $S_1^2$  to  $S_T^2$  (*i.e.* the  $i^{th}$  network has  $S_i$  species), if the total number of species across all these realizations is  $n$ , then the resulting metaweb is of size  $n^2$ . If these realizations have a total number of unique inter-

actions  $L$ , then the metaweb will have  $L$  interactions, hence its connectance is  $L/n^2$ . To reconstruct this metaweb, we loop through all the realizations, and when two species are found to interact in at least one site, we report this interaction in the metaweb (see Fig. 1 in main text for a visual model of it).

To calculate  $\beta'_{os}$  for a given realization, one simply extract the interactions established by the species found in the realization from the metaweb, and compare it to the interactions observed within the realization. If all potential (found in the metaweb) interactions are also found in the current realization, then  $\beta'_{os}$  equals 0, indicating perfect similarity.

Since a value of  $\beta'_{os}$  can be generated from each realization, it is possible to look at the *distribution* of dissimilarities across the whole dataset, rather than just having a single value to sum up the multiple- site dissimilarity. Assuming that we are working with a measure of distance between communities, having a distribution of the  $\beta'_{os}$  values close to 0 means that there is a low local selection of interactions (nearly all regional interactions are found in the realizations), whereas having a distribution with a mean close to 1 indicates a strong local selection of interactions (only a few of the regional interactions are found in each realization). It is possible to look for temporal or spatial autocorrelation in these values, or to identify which networks experience more or less link selection than expected by chance. In the context of a spatial analysis, this distribution should be standardized through the use of a  $Z$ -score in place of the raw values. With  $D$  the distribution of values of  $\beta'_{os}$ , then  $Z_D = (\bar{D} - \mu_D)/\sigma_D$ . Realizations with  $Z$  values higher than 0 vary more than the average realization, and realizations with  $Z$  values lower than 0 vary less. As the  $Z$  score is dimensionless, it eases the task of comparing the spatial structure of the variations of realizations across multiple metawebs, notably when the distributions of  $\beta'_{os}$  differ.

In Fig. 1, we present the result of this approach on the host– parasite data used in main text. We calculated the  $\beta'_{os}$  distribution and its  $Z$ -score transformation. The distribution  $D$  does not significantly deviates from normality ( $W$

$= 0.99$ ,  $p = 0.8$  – Shapiro-Wilk test). The mean of  $D$  is 0.3, and its standard deviation is  $9 \times 10^{-2}$ . As showed in the top panel of the figure, the values of  $D$  are relatively close to 0. This indicates that although there are some differences between local realizations and the corresponding part of the metaweb, the structure of the networks is, regionally, rather well conserved.

We propose that the overall dissimilarity within the dataset be measured by the coefficient of variation of the  $D$  distribution (for the same reason we advanced to use  $Z$  scores in place of raw values – this effectively standardizes for the fact that some systems will have different variabilities). As the sample size is likely to be low or moderate in most cases (*i.e.* there are a limited number of realizations available), an unbiased estimate of the sample coefficient of variation should be used (Sokal & Rohlf 1994). The variability of the networks across  $T$  sites is thus expressed as  $CV_D = (1 + 1/(4 \times T)) \times (\sigma_D / \mu_D)$ . Koopmans *et al.* (1964) provide corrections for low sample size when the distribution deviates significantly from normality. In our case,  $CV_D = 0.2974$ , which, being a dimensionless coefficient of variation, can be expressed as the percent relative standard deviation, with  $RSD_D = 29.74\%$  in our case.

The use of the coefficient of variation has the additional desirable property of being applicable even when the species turnover is extremely high. To show this, we extracted 5 random realizations from a large metaweb, and measured the network multi-site dissimilarity either as proposed in main text, and by the sample-size corrected coefficient of variation. For each group of five realizations, we randomly removed links. The sizes of the realizations were kept constant, and only the multi-site taxonomic  $\beta$ -diversity ( $\beta_S^T$ ) varied. The results are presented in Fig. 2. Past a certain level of species turnover, only the coefficient of variation of  $\beta'_{OS}$  is measurable. One additional advantage of the coefficient of variation is that when it takes values above unity, this is a strong indication that variability in the dataset is extremely high, and there is a really low signal in the data.

While these developments are preliminary, we showed that it is possible

to use the metaweb as a tool to investigate the overall dissimilarity across several realizations, and to express these values in a way which facilitates cross-system comparison. It should be noted that, when the realizations are located alongside an environmental gradient, the pairwise approach is sufficient. Future developments of these methods should focus on laying out a robust methodology for hypothesis testing through the use of null models.

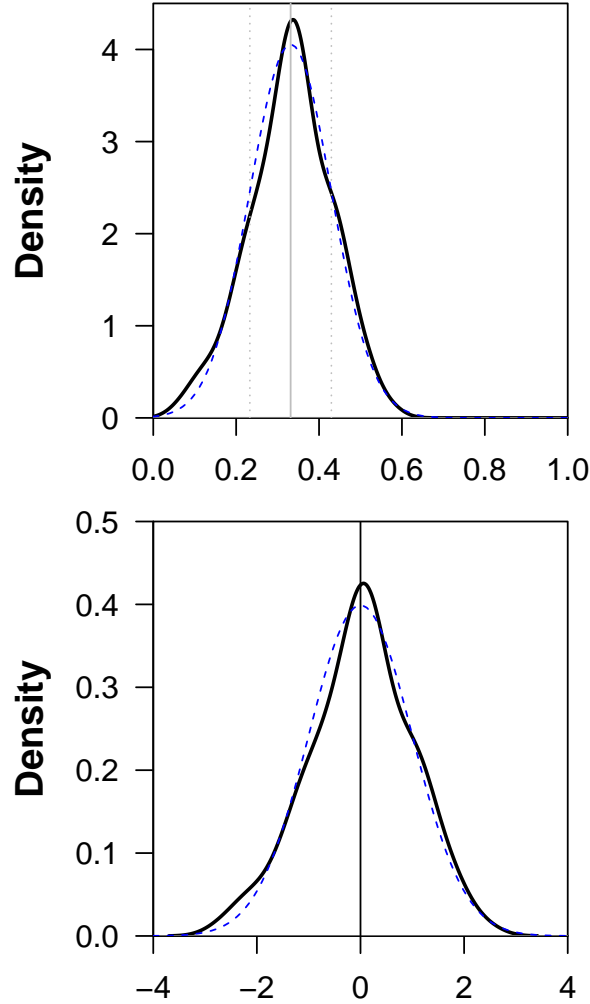


Fig. 1: **Top:** raw values of the distribution of  $\beta'_{os}$  for the 113 networks of hosts and parasites. The solid grey line indicates the mean value, and the dashed grey lines are one standard deviation on either side of the mean. The blue dashed line is a normal distribution with the same mean and standard deviation as the empirical values of  $\beta'_{os}$ . **Bottom:** distribution of the Z-scores for the raw values. This transformation results in a dimensionless measure of the deviation from the corresponding part of the metaweb. The dashed blue line is the probability density of a standard normal deviate.

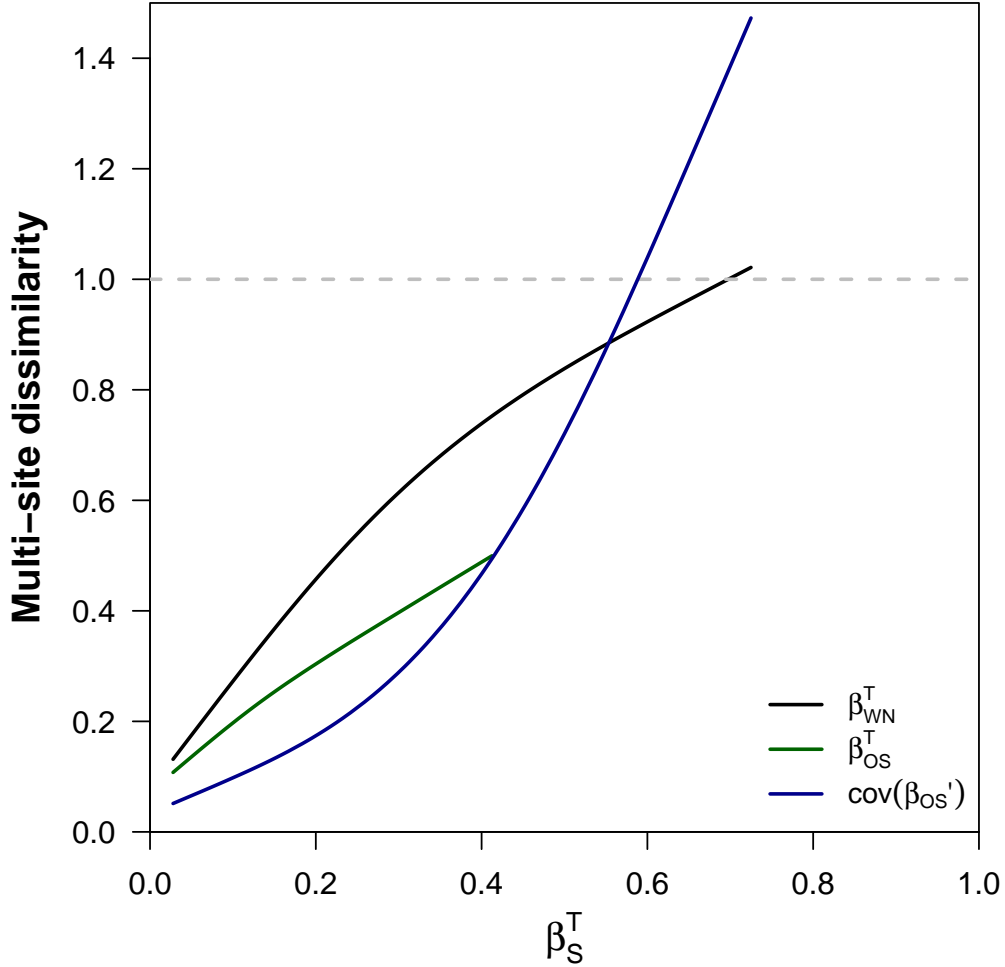


Fig. 2: Values of three different multi-site ( $T = 5$ ) network dissimilarity measures. When the species turnover across realizations is too high (here  $\beta_S^T > 0.4$ ), it becomes impossible to measure  $\beta_{OS}^T$ . However, the coefficient of variation of the distribution of  $\beta_{OS}'$  can still be measured – this measure is more general than the multi-site extension of  $\beta_{OS}^T$ , as it encompasses cases of extreme taxonomic turnover. Note that (i) the line for  $\beta_S^T$  appears to go above one due to the loess smoothing method used, and (ii) the coefficient of variation can actually take values above unity, in which case it indicates that the signal is extremely low.

## S2 Robustness to sampling of both species and links

This section presents additional results to the analysis of the robustness of our framework to incomplete sampling of both species and their interactions, a situation which is likely to arise in practice. We use an approach similar to the one presented in main text. We generate a metaweb of 50 species and 825 interactions using the niche model. Two realizations of 40 species (each species has at least one interaction) are randomly extracted from this metaweb. We calculate the ‘true’ dissimilarity between these realizations. In each realization, we start by simulating the subsampling of species. We set a probability to miss a species,  $P_S$ , which varies between 0 (perfect sampling) and 0.9 (one tenth of the species are sampled), with 100 evenly spaced values. We use this probability to randomly remove species through a Bernoulli process. Once this step is done, we simulate the lack of detection of links between detected species. We set a probability to miss a link,  $P_L$ , which varies between 0 and 0.9, with 100 evenly spaced values. For each existing link, we randomly remove it from the realization with probability  $P_L$ . Once these two steps are done, we remove species with no links.

The main simplifying assumptions of this approach are that (i) the sampling effort is the same across the two realizations, *i.e.* the probability of not detecting a species or an interaction is similar across environments, and (ii) all species and interactions have an equal probability of not being sampled. In empirical situations, (i) is likely to be violated if the environments in which the realizations are sampled differ, *e.g.*, in their ease of access, and (ii) will be sensitive to interaction frequency and local species abundance. However, for the purpose of this analysis, both are acceptable simplifications, in that we are interested in testing the response of our framework, not in simulating the outcome of empirical studies. This procedure is replicated 100 times for each combination of probabilities, *i.e.* there are 1000000 replicates in the figures presented below. At the end of each replicate, and as in main text, for each component of network dissimilarity, we calculate the relative error term, as

beign  $\varepsilon = (N - N')^2$ , where  $N$  is the value of the component between the two fully sampled networks, and  $N'$  is the same value on uncorrectly sampled networks.

The results are presented in Fig. 3. As in main text,  $\beta_{OS}$  is relatively robust to low detection power of interactions (see main text for a discussion of what the values of error terms means). It is also extremely robust to low species detection (*i.e.* for a given value of  $P_L$ , changing the value of  $P_S$  does not strongly affects the error on  $\beta_{OS}$ ). As in main text,  $\beta_{WN}$  reacts to both of them. There seems to exist a point beyond which, when the probability to miss a species increases, the error decreases, both for  $\beta_{WN}$  and  $\beta_{OS}$ . This is explained by the fact that, for high probabilities to miss a species during sampling, the resulting realizations are really small, and the results are thus not meaningful. This is confirmed by the fact that at this point, the error on  $\beta_{ST}$ , which is otherwise constant for increasing probability of missing an interaction (see main text), varies rapidly. At this point, species are so sparsely sampled that the chance of observing overlapping species between any two realizations decreases, or the realizations are of such small size than any comparison is meaningless.

In conclusion, these results show that, assuming that species are not too sparsely sampled (*i.e.* as long as the sampling results in networks large enough, which can be assessed through simulation as in *e.g.* Poisot *et al.* (2011)),  $\beta_{OS}$  is robust to partial species sampling. Furthermore, the impact of species turnover on network turnover,  $\beta_{ST}$ , is robust as well, meaning that our framework performs well when either or both species or interactions are not fully sampled.



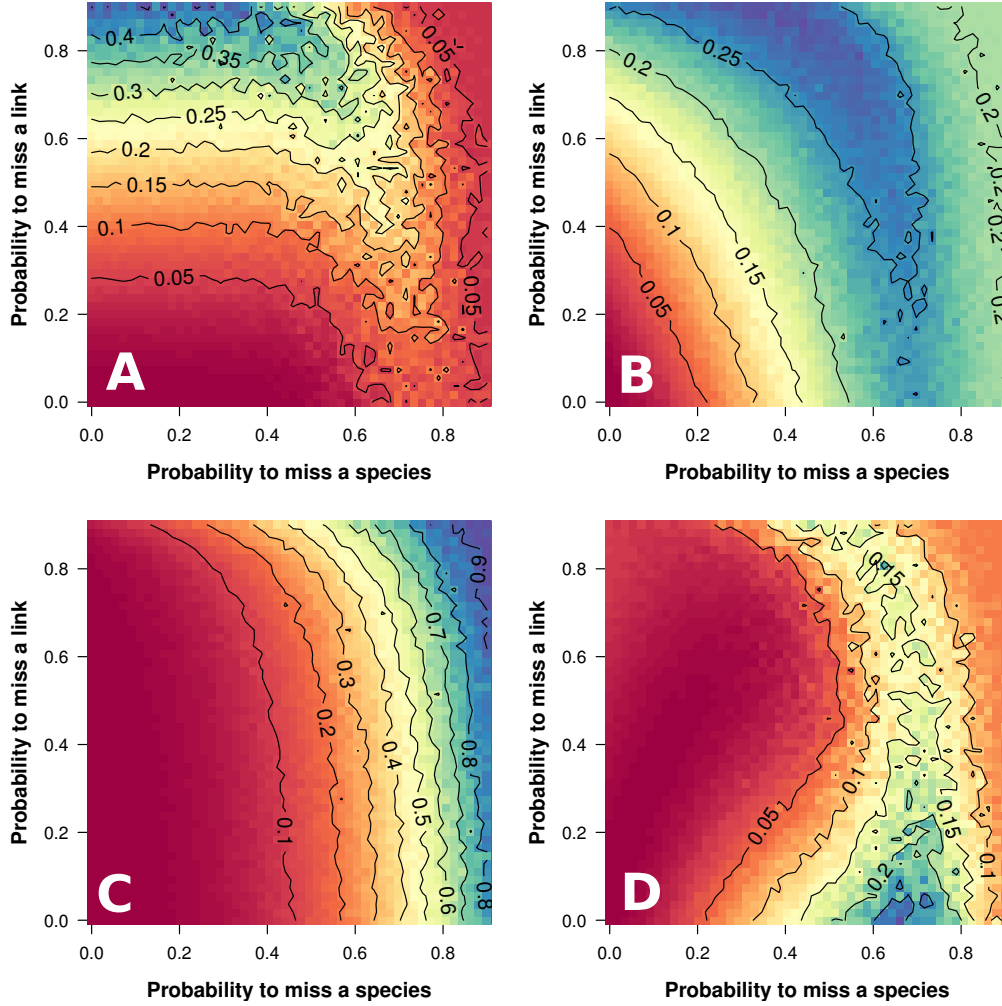


Fig. 3: Results of the simulations, accumulation of error from the true dissimilarity between two realizations when the probability of missing a species or an interaction increases. **A:** Overlapping species dissimilarity,  $\beta_{OS}$ . **B:** Whole network dissimilarity,  $\beta_{WN}$ . **C:** Species composition dissimilarity,  $\beta_S$ . **D:** Contribution of species turnover to network dissimilarity,  $\beta_{ST}$ .

## References

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