

# Supplement to “Community assembly on isolated islands: Macroecology meets evolution”

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# 1 Compilation of networks and metric validation

We compiled plant-herbivore networks from published sources as described in the main text. Table 1 lists publications used in compiling these networks.

Researchers have put forward to set of “network metrics,” including nestedness (Bascompte *et al.*, 2003; Ulrich *et al.*, 2009) and modularity (Newman & Girvan, 2004; Olesen *et al.*, 2007), to understand the complex structure of ecological networks. Null models are used to evaluate the statistical significance of these metrics and to compare between networks of different size Ulrich *et al.* (2009). We compare the results derived from two common null models: the “probabilistic null” of Bascompte *et al.* (2003) using the relative degree distributions of plants and herbivores as weights while randomizing links and suffers from high Type II error (Ulrich *et al.*, 2009); the “fixed-fixed null” (Ulrich *et al.*, 2009) maintains the exact number of links assigned to each species while randomizing which interactors fill the requisite set of links and suffers from high Type I error (Ulrich *et al.*, 2009). We find that using these different null models does not change any trends in our network statistics across the Hawaiian chronosequence but different null models do influence the sign and significance of the network metrics (Fig. 1). We therefore do not interpret the sing or significance of the metrics but only their relative trends across site age.

Because these networks are based on opportunistic data associated with species descriptions, and not based on standardized ecological surveys, we cannot interpret patterns in network metrics without evaluating possible sampling biases (Nielsen & Bascompte, 2007; Gibson *et al.*, 2011; Rivera-Hutinel *et al.*, 2012). To do so we rarefy networks by the number of Hemiptera species included and, for each subsampled network, re-calculate nestedness and modularity z-scores. This rarefaction procedure shows that nestedness is very sensitive to network size (Fig. 3), a known property of nestedness (Nielsen & Bascompte, 2007; Gibson *et al.*, 2011; Rivera-Hutinel *et al.*, 2012). However the relative nestedness z-scores across networks remain qualitatively similar to those observed for the complete networks (Fig. 3). Modularity depends on network size in a more variable way (Fig. 3). Modularity

is expected to decrease with network size (Rivera-Hutinel *et al.*, 2012) and so the marked increase in modularity with network size on Haleakala is unexpected. However in light of the large number of highly specialized taxa this pattern is more reasonable—if most species only have within module links then removing these species through subsampling will only reduce overall modularity. Thus this pattern speaks to the high level of specialization on Haleakala, and to a lesser extent at Kokee which also shows a slight increase in modularity with network size (Fig. 3).

## References

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## 2 Supplemental Figures

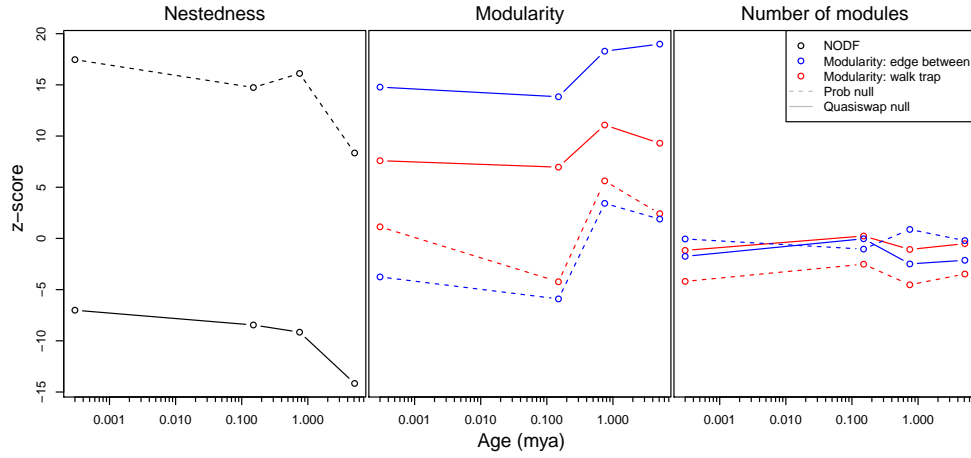


Figure 1: Comparison of different null models (“Prob” and “Quasiswap”) used to standardize network metrics and comparison of different algorithms for assessing modularity (“edge between” and “walk trap”). Choice of null model has a strong influence on the sign and magnitude of metrics but not on their relative trends. The different modularity algorithms lead to largely similar qualitative patterns.

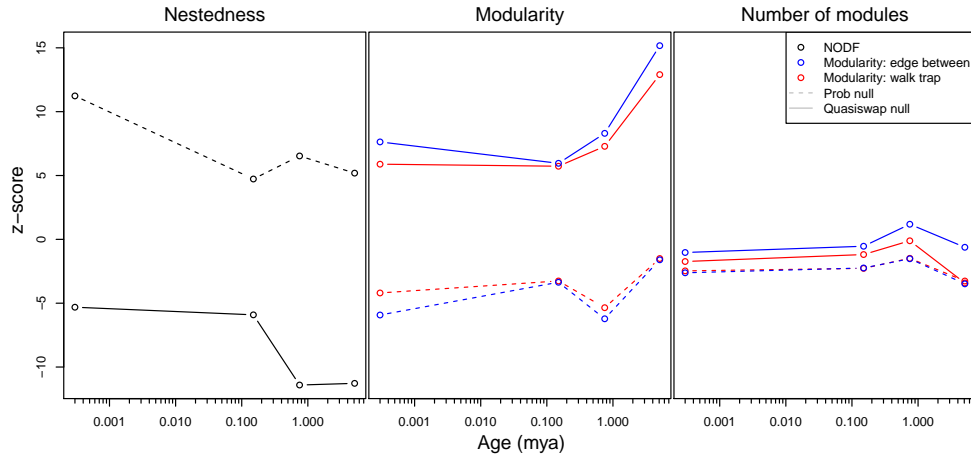


Figure 2: Metrics NODF and modularity calculated for networks based on more biogeographically conservative assignment of Hemiptera to localities. Colors and metric specifics as in Figure 1.

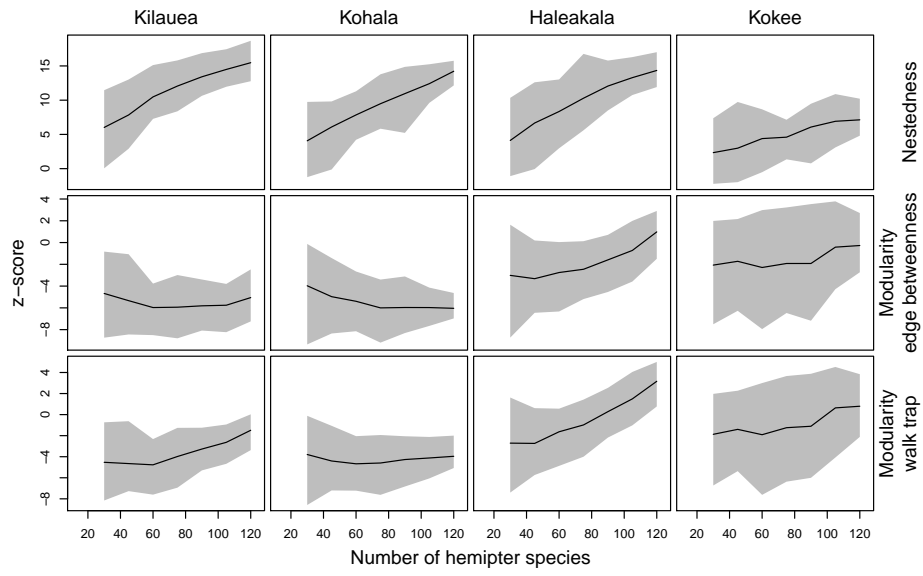


Figure 3: Result from rarification analysis showing sensitivity of network metrics to number of Hemiptera sampled.

## Supplemental Tables

Upon acceptance we will make available our compiled list of Hemiptera and their plant hosts from published sources.

Table 1: Published sources of trophic information used to construct networks.