

Null models

We tested whether our observed β -diversity values among levels of protection were larger or smaller than expected under a random assembly model. For each protected area and for each iteration of the bootstrap, we generated 1000 random species assemblages using the curveball algorithm. This algorithm maintains species frequency and sample species richness while shuffling species co-occurrences across cells.

The large majority of SES values are positive and significantly higher than expected by chance for total species dissimilarity and turnover (Fig. 3) suggesting that the differences in species composition between levels of protection are not simply due to a random distribution of species among sites. However, turnover in reef fish species between restricted areas and non-protected areas is not significantly different than expected by chance highlighting that only strictly protected areas play a key and unique role in sustaining regional fish biodiversity (Fig. 3, G).





