

Appendix C: Residual diagnostics and analysis for cover and taxonomic models

The figures in this appendix show diagnostic plots for residuals from the cover analysis (Figs. C1 – C2) and the taxonomic analysis (Figs. C3 – C4). The MAR model assumes that the vector-valued residuals are serially independent and identically distributed. Thus, residual plots such as these are useful for diagnosing whether or not the variance of the residuals changes with time, or is different for large or small fitted values.

Few features stand out in the residual plot for the cover analysis, except for perhaps the occasional residual with a very large absolute value. Residuals from the taxonomic analysis seem to occasionally demonstrate banding characteristic of log-transformed data for that is below the limit of detection. For example, *Montastrea* was not observed at site RS-5 for 1992 – 2004, and was only detected at small densities in three of the years thereafter. Such banding suggests that, for those coral genera that were frequently below the detection limit from one or more sites (namely, *Montastrea*), sensitivities to hurricanes and sea temperature may be near zero simply because environment will have no observed impact on the growth rates of an undetected coral.

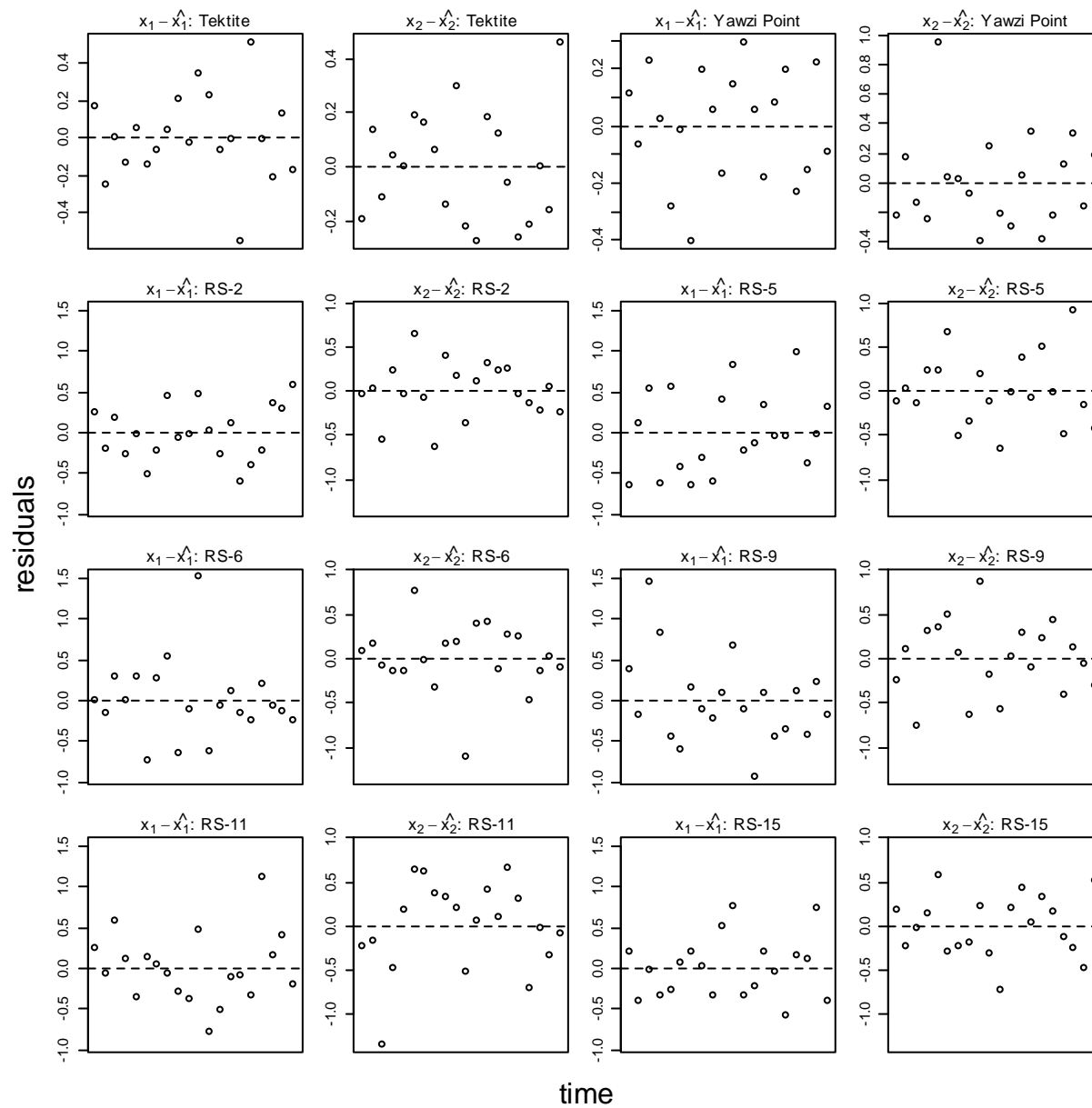


Figure C1. Plots of residuals vs. time for ilr-transformed compositions at Tektite, Yawzi Point, and the random sites.

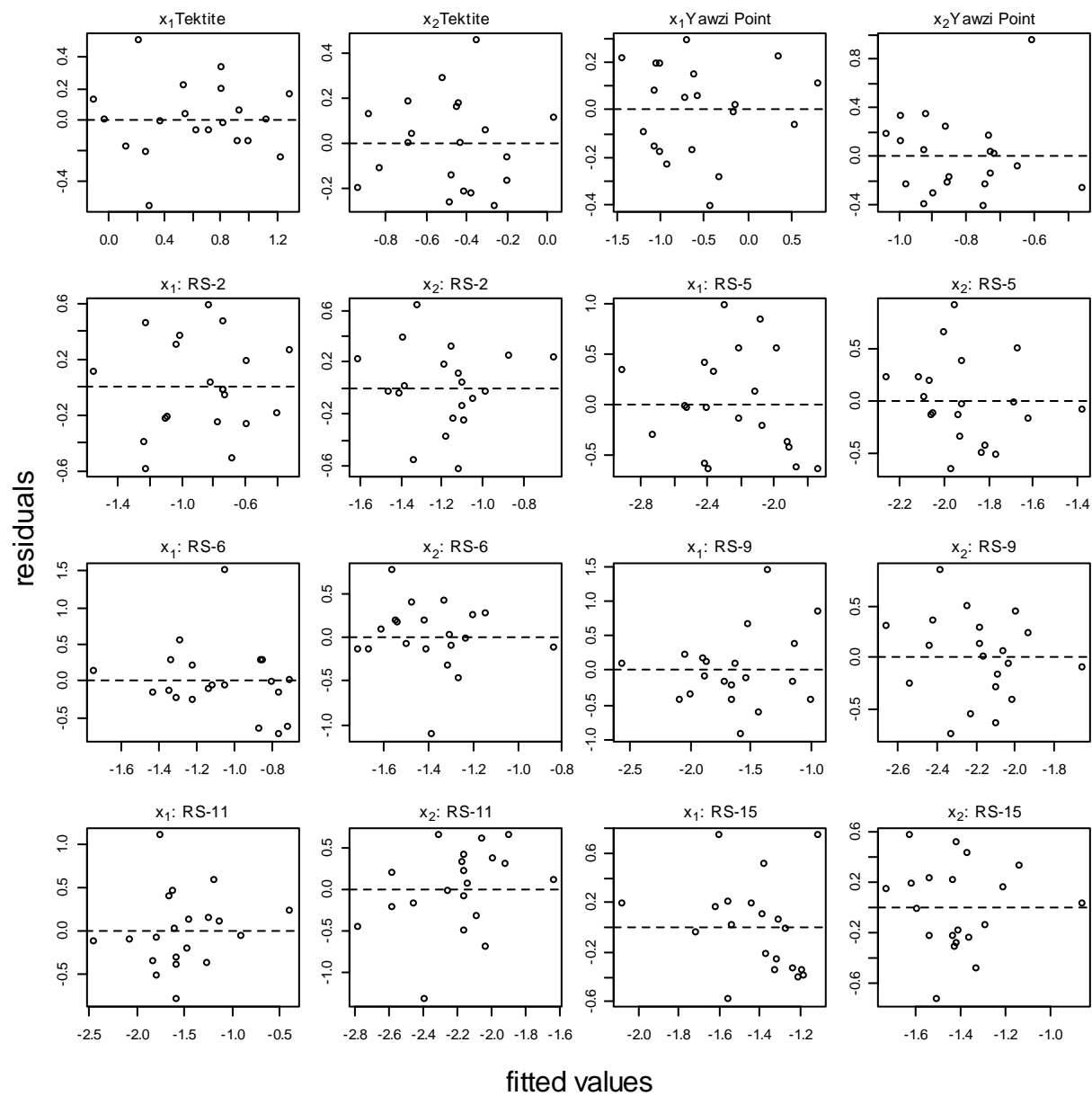


Figure C2. Plots of residuals vs. fitted values for ilr-transformed compositions at Tektite, Yawzi Point, and the individual random sites.

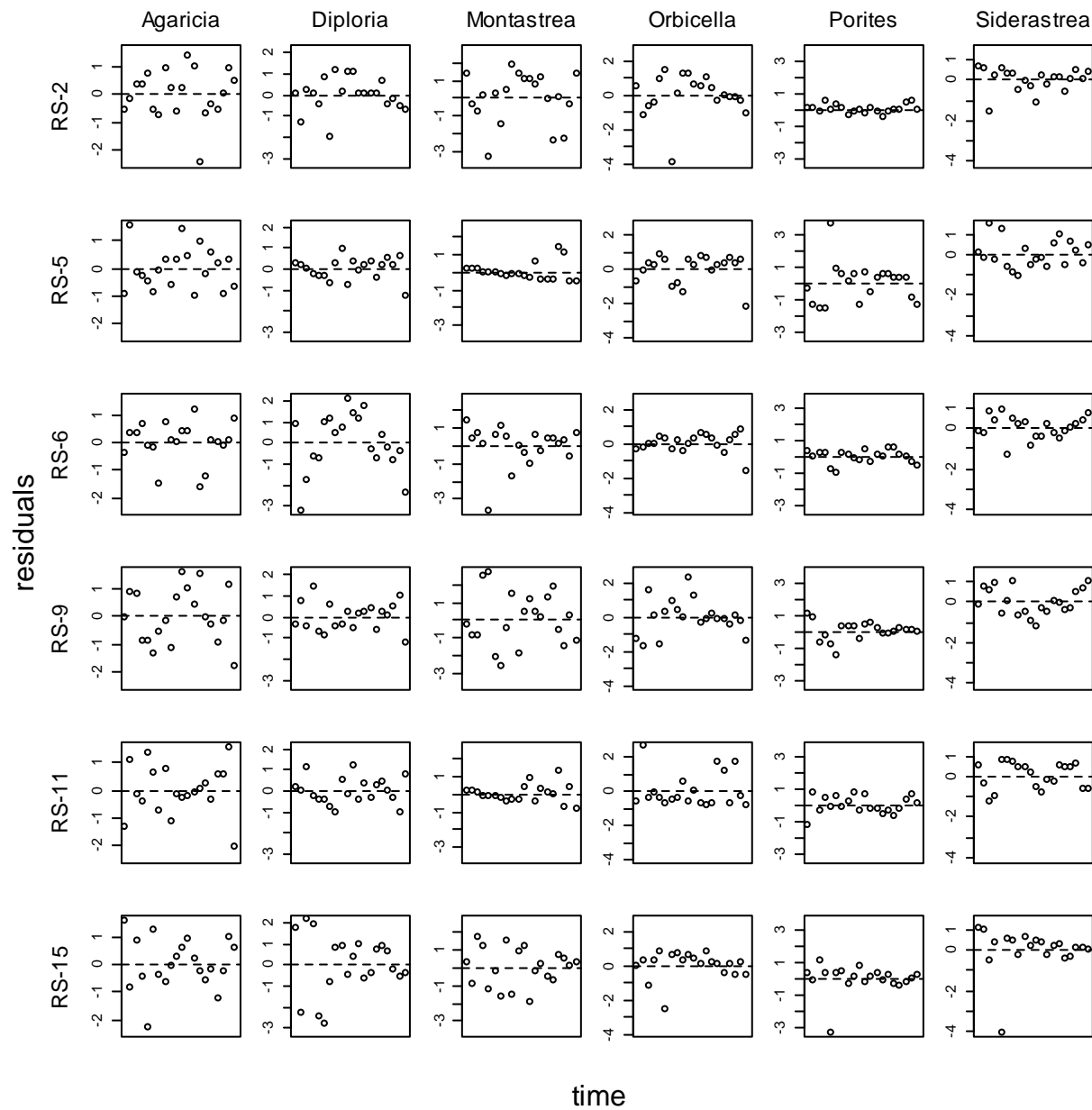


Figure C3. Plots of residuals vs. time for coral genera at individual random sites.

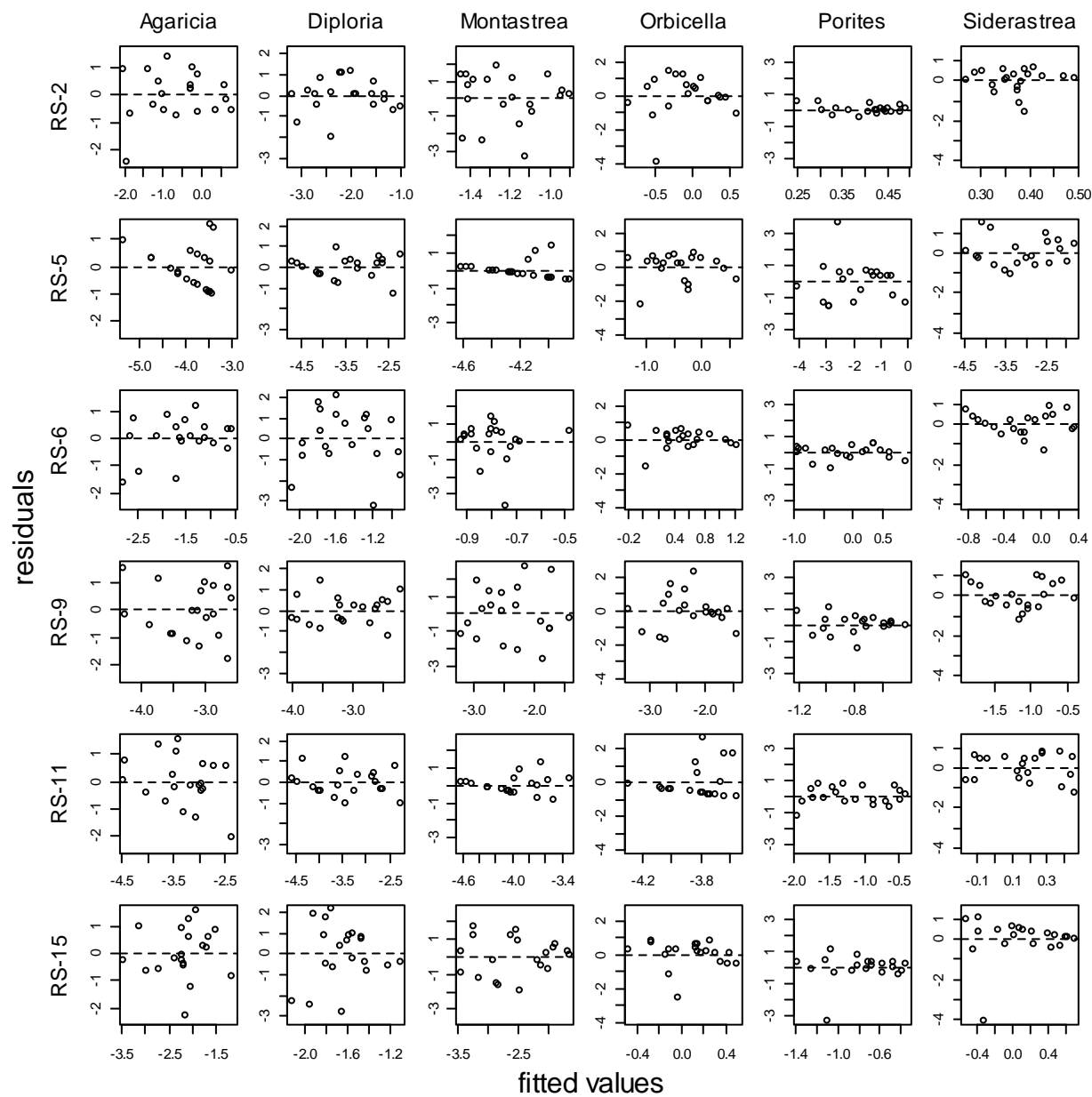


Figure C4. Plots of residuals vs. fitted values for coral genera at individual random sites.