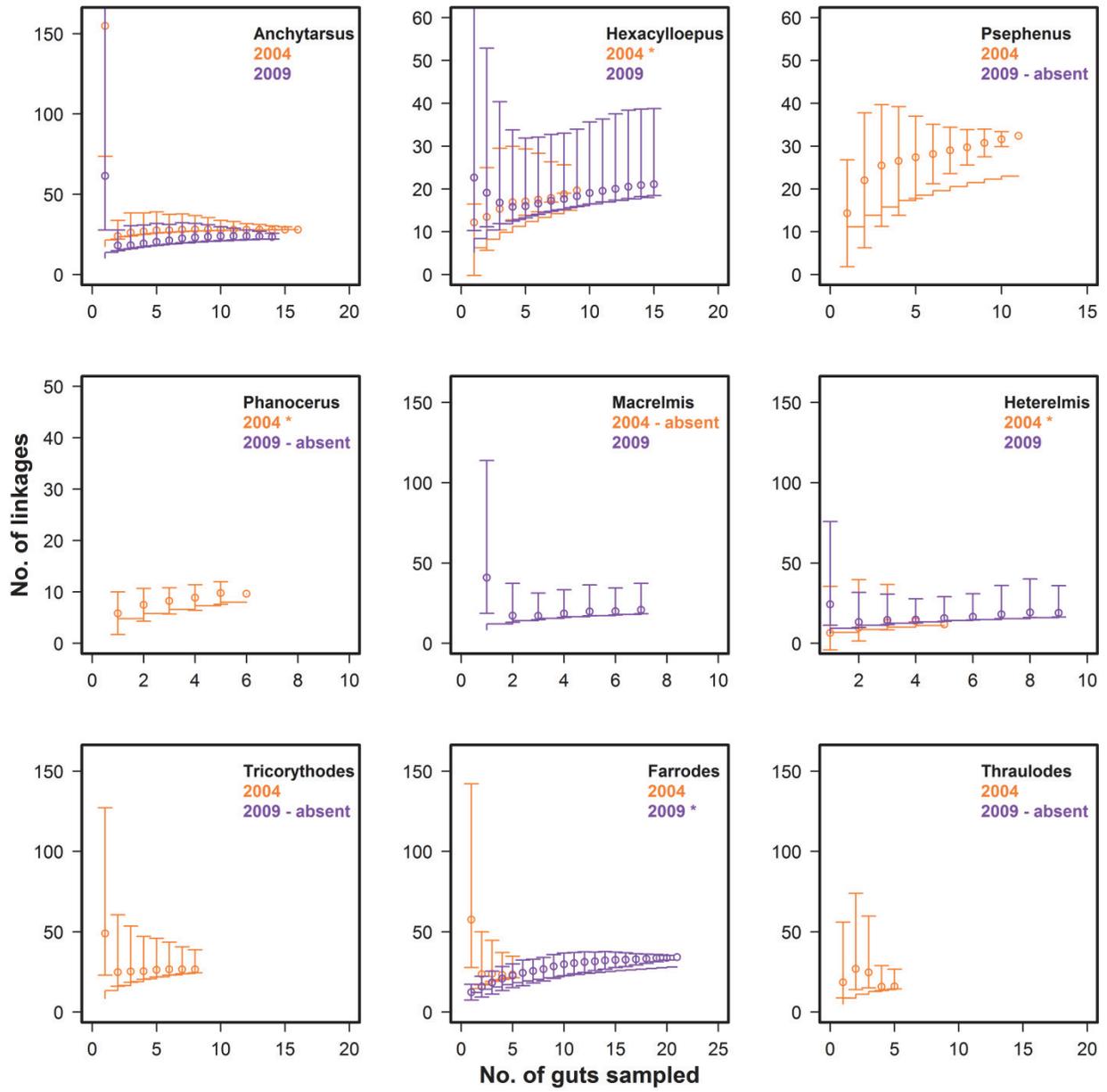
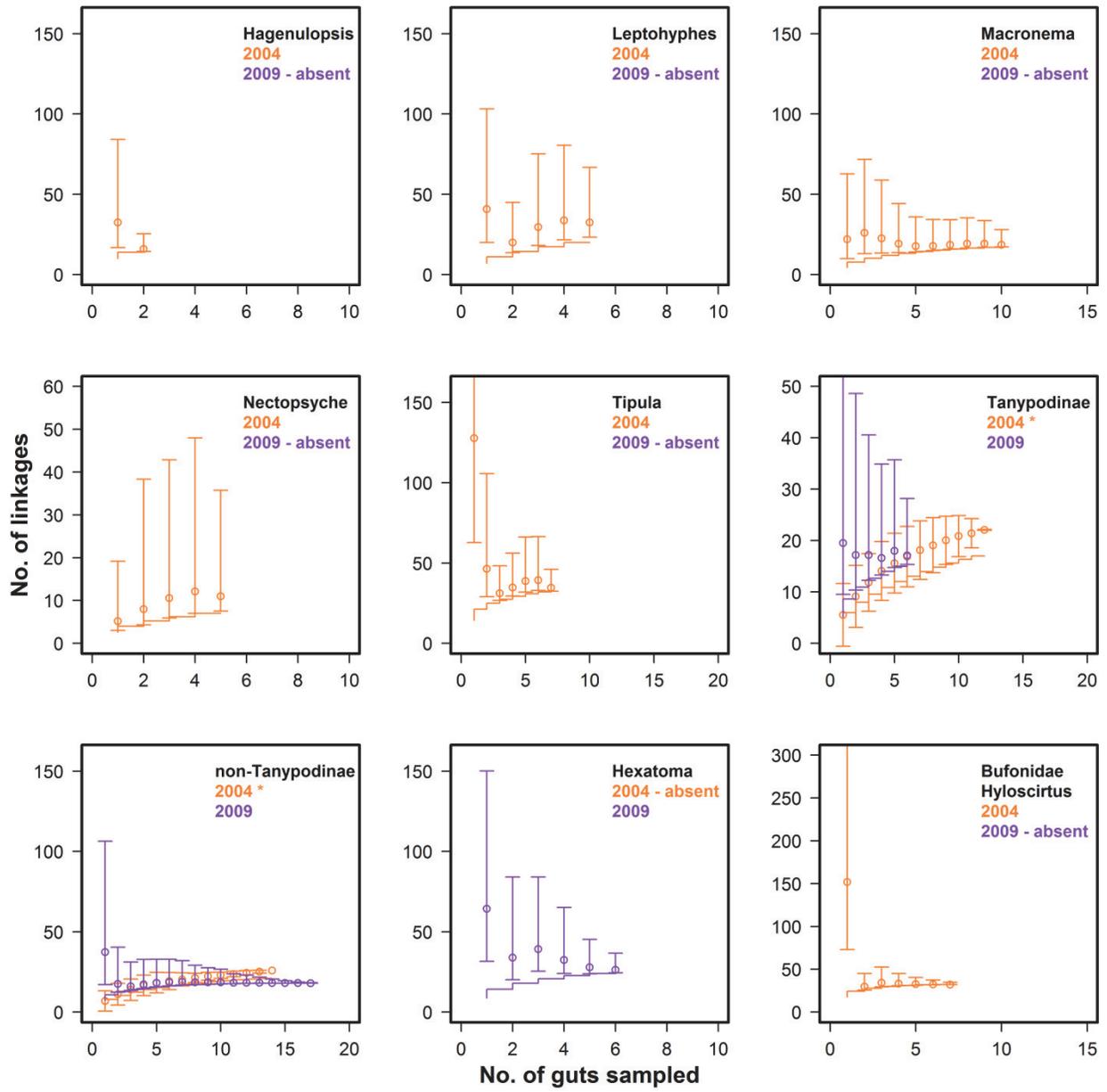
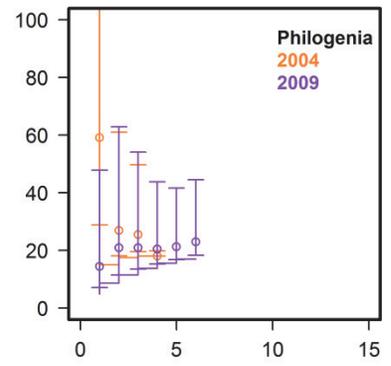
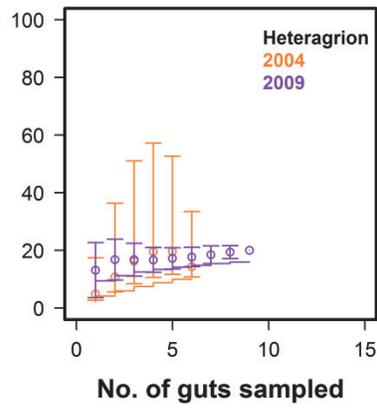
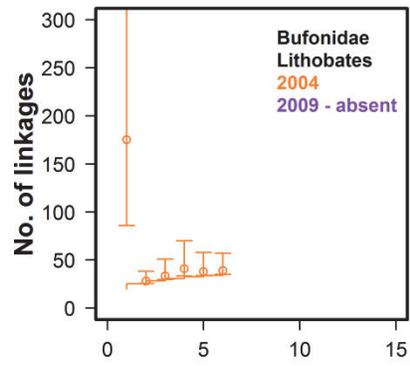


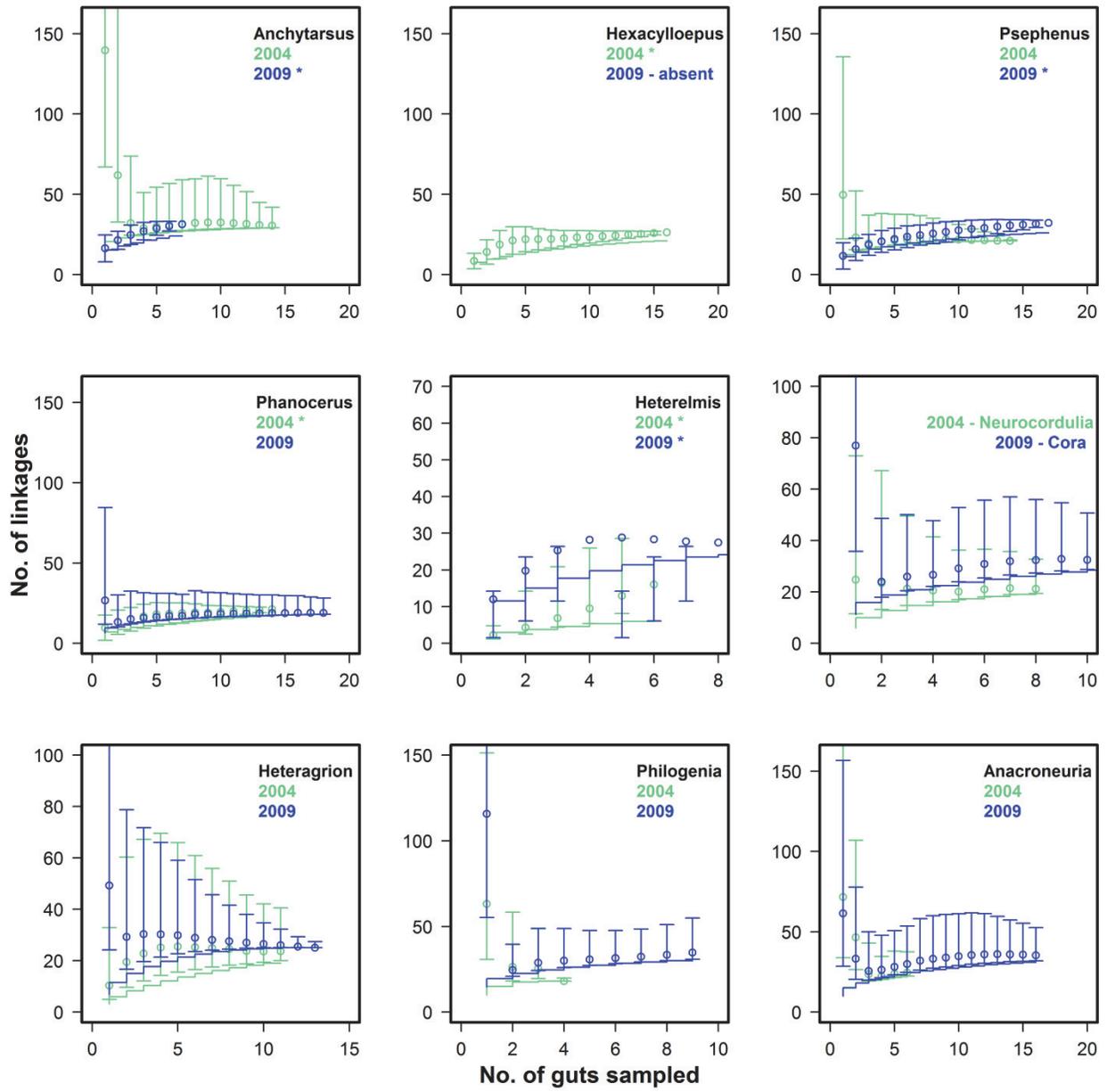
Appendix C.

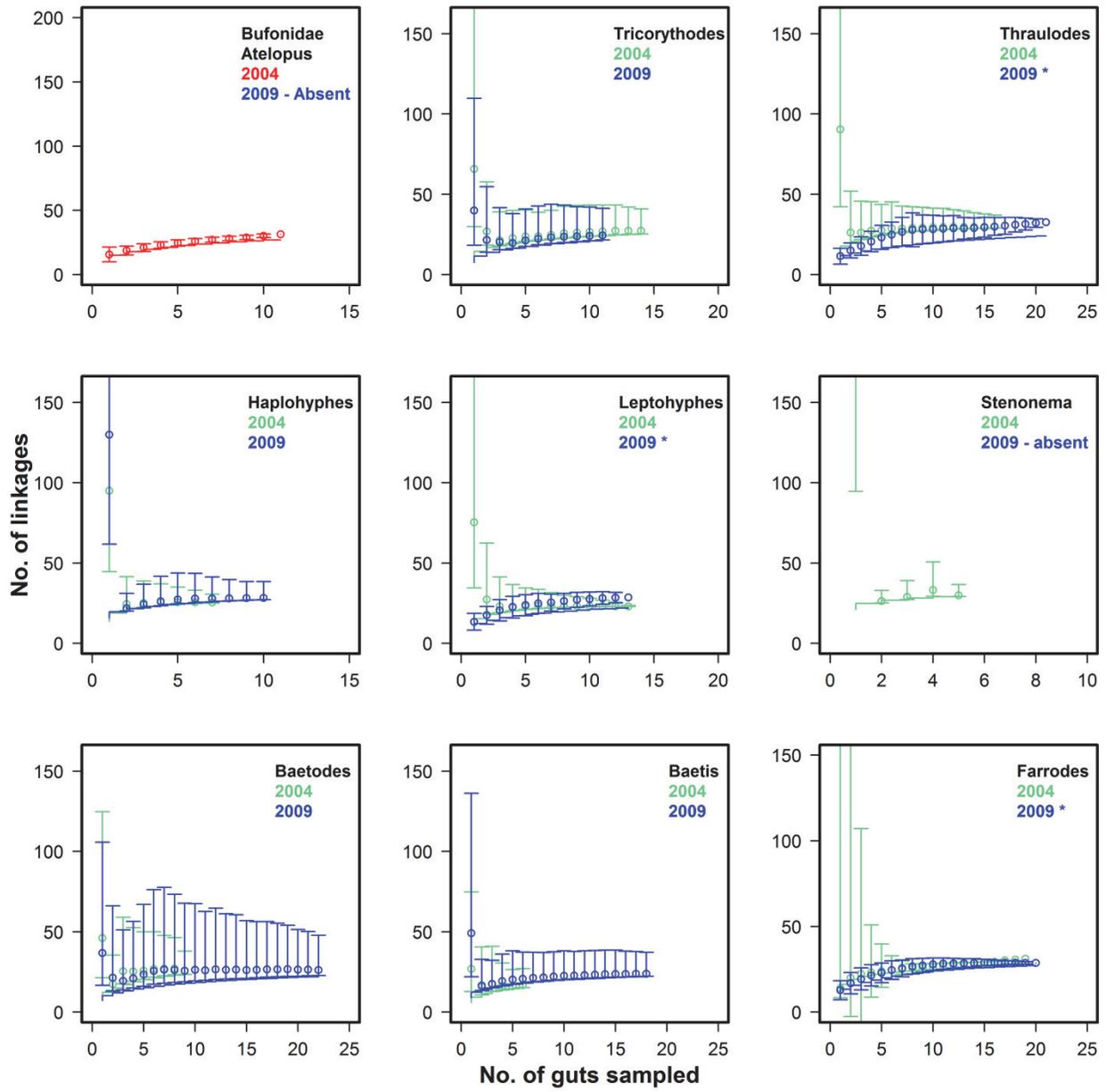
Rarefaction curves (solid lines) of the taxa sampled for gut content analysis from two habitats (riffles and pools) and two points in time (2004 and 2009). A species estimator curve (hollow circles with error bars) using either the Chao1 or Abundance Based Coverage Estimator (ACE) was used to estimate how many additional linkages would be identified with additional sampling. An asterisk next to the taxon name indicates that the coefficient of variation (CV) is greater than 0.5 and that the Classic estimator was used instead of the Bias-Corrected estimator to estimate abundance-based richness using the greater value of the Chao 1 or ACE estimator (Shen et al. 2003). Error bars are SE for 500 runs in EstimateS 8.2 (Colwell 2013). Taxa from pools are in purple and orange, while taxa from riffles are in green and blue. Taxa where the species estimator curve meets the rarefaction curve indicates that further sampling of that taxon would be unlikely to yield any new linkages. Taxa where the species estimator curve does not meet the rarefaction curve suggests that taxon is a specialist, with many singletons and doubletons observed. Additional linkages that were not observed were not factored into the food web analysis because it was unknown where the linkage would connect (e.g. would the prey be an insect or diatom?).

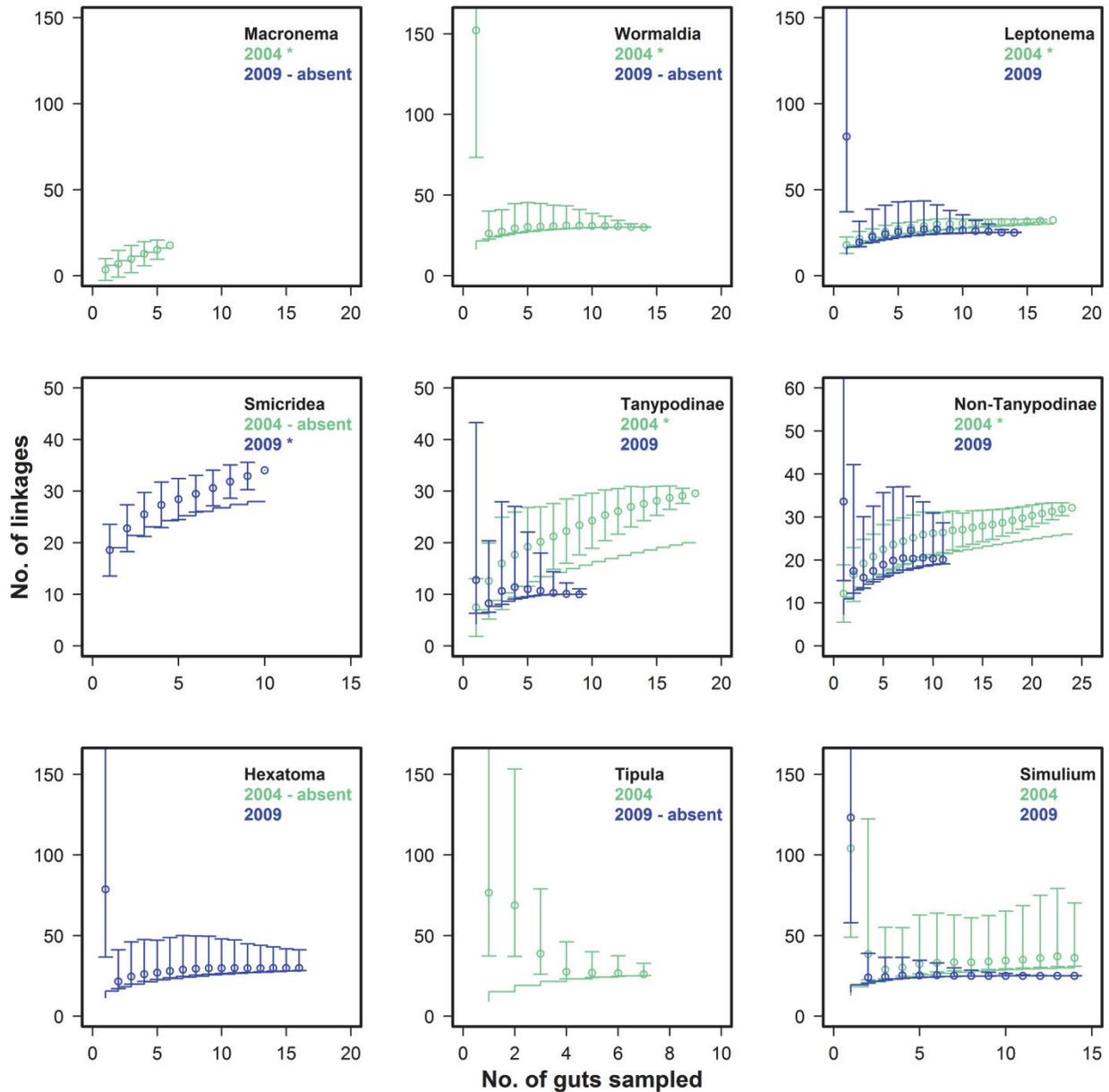












Literature Cited

- Colwell, R. K. 2013. EstimateS: Statistical estimation of species richness and shared species from samples. Version 9. User's Guide and application published at: <http://purl.oclc.org/estimates>.
- Shen, T.-J., A. Chao, and C.-F. Lin. 2003. Predicting the number of new species in further taxonomic sampling. *Ecology* 84:798-804.