The data here includes character matrices and phylogenetic trees used in the analysis outlined at github.com/S-Majoros/Phylogenetic\_Community\_Structure\_Code.r. A family-level phylogenetic tree, i.e. treating each family as one tip, was created using the phylogenetic hypothesis provided in Zhang *et al.* (2018) based upon 95 protein-coding genes. A genus-level tree was created using Zhang *et al.* (2018) and some additional trees (Michat et al. (2017) was used for Dytiscidae, Nie et al. (2017) for Chrysomelidae, and Gusarov (2018) for Staphylinidae). All trees were constructed manually using Mesquite (Maddison & Maddison 2019).

Character matrices were built for each analysis. Characters/traits were found for each family based on the literature (references are available in Appendix 3 of the paper and are also uploaded here). The traits that describe the majority of members of a given family were used; this included habitat (terrestrial or aquatic) and feeding mode (predaceous, phytophagous, or fungivorous). We defined terrestrial as taxa that live primarily in land habitats and aquatic as taxa that live primarily in water bodies and habitats. Predaceous taxa were defined as those who prey on other insects or animals, phytophagous taxa as those who feed primarily on plant material, and fungivores as those who feed primarily on fungi. Each character matrix contains the family or genus name, NRI/NTI value, habitat, adult diet and larval diet.

All information needed for reuse of this dataset, as well as additonal files, is available at github.com/S-Majoros/Phylogenetic\_Community\_Structure\_Code.r. For character matrices: the Churchill family matrices are Coleoptera\_Matrix\_NRI.csv and Coleoptera\_Matrix\_NTI.csv, the Churchill genus matrices are Genus\_NRI\_Matrix\_Churchill.csv and Genus\_NTI\_Matrix\_Churchill.csv, the Guelph family matrices are Guelph\_Matrix\_NRI.csv and Guelph\_Matrix\_NTI.csv, and the Guelph genus matrices are Guelph\_Genus\_Matrix\_NRI.csv and Guelph\_Genus\_Matrix\_NTI.csv. For the phylogenetic trees, the Churchill family tree is Coleoptera\_Tree\_2020, the Churchill genus tree is Churchill\_Genus\_Tree, the Guelph family tree is Guelph\_Tree\_2, and the Guelph genus tree is GGTree.

## References

- Gusarov, V.I. (2018). Phylogeny of the family Staphylinidae based molecular data: a review. In Betz, O., Irmler, U. & Klimaszewski, J. (Eds.), *Biology of rove beetles (Staphylinidae): Life history, evolution, ecology and distribution* (pp. 7-25). Springer International Publishing, Switzerland
- Maddison, W.P. & Maddison, D.R. (2019). Mesquite: a modular system for evolutionary analysis. Version 3.61. <u>http://www.mesquiteproject.org</u>
- Michat, M.C., Alarie, Y & Miller, K.B. (2017). Higher-level phylogeny of diving beetles (Coleoptera: Dytiscidae) based on larval characters. *Systematic Entomology*, 42(4), 734-767. doi: 10.1111/syen.12243
- Nie, R-E, Breeschoten, T., Timmermans, M.J.T.N., Nadein, K., Xue, H-J., Bai, M., Huang, Y., Yang, X-K & Vogler, A.P. (2018). The phylogeny of Galerucinae (Coleoptera:

Chrysomelidae) and the performance of mitochondrial genomes in phylogenetic inference compared to nuclear rRNA genes. *Cladistics*, *34*(2), 113-130. doi: 10.1111/cla.12196

Zhang, S.-Q., Che, L.-H., Li, Y., Liang, D., Pang, H., Ślipiński, S.A. & Zhang, P. (2018). Evolutionary history of Coleoptera revealed by extensive sampling of genes and species. *Nature Communications*, 9(1), 1-11. doi: 10.1038/s41467-017-02644-4