

20.12: Phylogenetically independent contrasts

Introduction

Assumption of independence among the subjects in a study is a key assumption. Comparisons among species are a common experimental approach in evolutionary biology. Typical statistical approaches include use of ANOVA or linear regression approaches. A basic assumption of ANOVA is that sampling units are independent ([13.1 – ANOVA assumptions](#)). Prior to the 1980s, it was rarely appreciated in comparative analysis that species are not independent sample units (Harvey and Pagel 1991); evolution produced nested hierarchical relationships among the species. We recognize this with phylogenies (Felsenstein 1985, Harvey and Pagel 1991, Martins 1996, Garland et al 2005). Mice and rats share a more recent common ancestor, and cattle and pigs share a more recent common ancestor, than do mice and cattle, for example. Felsenstein (1985, 1988) is largely credited for making the argument that Type I error is likely if phylogeny is ignored, and, importantly, provided an algorithm: **Phylogenetic Independent Contrasts, PIC**, which provided a simple way to correct for phylogenetic nonindependence. Felsenstein's landmark 1985 paper has been cited more than ten thousand times (Feb 2024). However, like most innovations, PIC should not be blindly applied in all comparative analysis (e.g., unreplicated evolutionary events, Uyeda et al 2018).

Logic of PIC

Treating comparative data, e.g., species, as a collection of independent samples implies that the evolutionary history was a spontaneous burst, or star-like phylogeny.

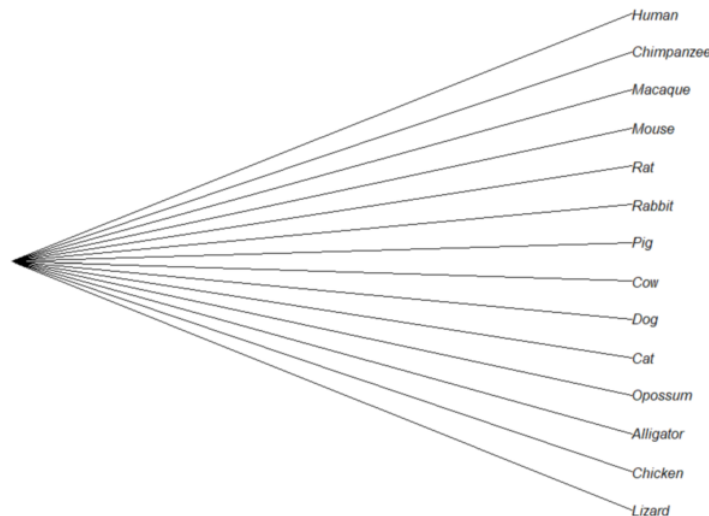


Figure 20.12.1: Star phylogeny (same image shown in Figure 20.11.5).

But what nature provides is nonindependence (Fig. 20.12.2 for more about star phylogeny in PIC see discussion in Garland et al 2005), which should be accounted for during statistical analysis.

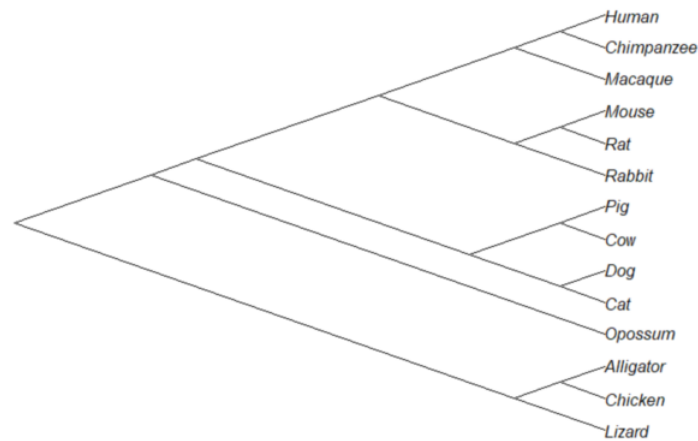


Figure 20.12.2: A cladogram for same species, showing the hierarchical, nested relationships among taxa, what nature actually provides (same image shown Figure 20.11.2).

R package, [phytools](#) , [ape](#)

Lots of good references on this important subject. For now, see

Chapter 4.2, [Estimating rates using independent contrasts](#), by Dr Luke Harmon

and a tutorial from same author, available at

<https://lukejharmon.github.io/ilhabela/instruction/2015/07/02/phylogenetic-independent-contrasts/>

Questions

[pending]

References and suggested readings

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