phylogenetic analyses: summary

The four analysis functions in this chapter take the same inputs: a tree as a `phylo` object, and a long table of traits with one column of species names that match the tree's tip labels exactly. Choosing among the analyses is a matter of choosing the question. **Phylogenetic signal** asks whether related species share similar trait values. **Independent contrasts** remove the effects of shared ancestry before two traits are compared. **Ancestral trait reconstruction** estimates the trait values of ancestors at the tree's nodes. It is not the same as `buildTree()`'s `ancestral_states` in the phylogenies chapter, which computes ancestral sequences.

Function	Question it answers	Settings students vary
`runPhylogeneticAnalyses()`	the comparative analyses in one call	`traits`, `column_w_names_of_tiplabels`, `column_w_names_of_traits`, `column_w_values_for_traits`, `tree`
`phylogeneticSignal()`	do close relatives have similar trait values?	the same five arguments
`independentContrasts()`	are two traits related once shared ancestry is removed?	the same five arguments
`ancestralTraits()`	what trait values did the ancestors have?	the same five arguments
`geom_ancestral_pie()`	pie charts of the ancestral estimates at each node of a `ggtree()` plot	`data = filter(anc_traits_tree, isTip == FALSE)`, `pie_size`, `pie_alpha`

The long trait table is made with `pivot_longer()`, and a tree passed to `ggtree()` for ancestral pies first needs duplicate nodes removed with `distinct(anc_traits_tree, node, .keep_all = TRUE)`.