Overview

The goal of this document is to list the types of questions one might ask from comparative data, and the tools most typically used. The list is by no mean comprehensive. It is arranged by data types.

Continuous data

Regression and correlation	Brownian motion (BM) model. Phylogenetically independent contrasts (PIC) or equivalently, phylogenetic generalized least squares (PGLS).
Phylogenetic signal	Permutation tests to compare with a non-phylogenetic model. Branch length transformation (ex: Pagel's λ, Grafen's ρ, OU's $d = e^{-\alpha}$, ADCD's g).
Ancestral states reconstruction	
Detect shift in mean or in rate	Ornstein-Ühlenbeck (OU) process with selection strength α. Possibly different selection regimes (or different rates) on different branches. Likelihood ratio test (LRT) to compare models.

Discrete data

Ancestral state reconstruction	Parsimony and variants (e.g. Dollo's law)
with posterior probabilities	Likelihood methods (ML or Bayesian, character mapping), Markov models with rates of change (ex: gain/loss)
Correlation between traits	LRT to compare models. Independence: equality between certain rates. Bayesian approach with character mapping.
Correlation trait & diversification	Models combining Markov evolution for traits, and birth/death process for lineage diversification: BiSSE, MuSSE, QuaSSE, etc.

Both continuous and discrete

Continuous dependent variable	Phylogenetic ANOVA, Phylogenetic Principal Component Analysis (PCA)
Binary dependent variable	Phylogenetic logistic regression, phylogenetic generalized estimating equations (GEE), phylogenetic generalized linear mixed models