

Computational Biology HW 5

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Question 1

It cannot be used as it assumes independent observations at the tips. Assuming this, we neglect the phylogenetic background (common ancestral history) and our analysis will be biased due to relatedness as there is no independent character evolution.

Question 2

We want to use linear regression to see if there is correlation between the contrasts. In order to satisfy the assumptions of linear regression we need the contrasts (variables) to be independent of each other and have identical error variance in the response variable.

Question 3

We calculate the contrast of trait j for a node with children i (X_i^j) and l (X_l^j) through $Z_k^j = \frac{X_i^j - X_l^j}{\sqrt{t'_i + t'_l}}$. The independence of the contrast is ensured by the subtraction $X_i^j - X_l^j$. The normalization with corrected branch lengths (division by $\sqrt{t'_i + t'_l}$) is used to define contrasts with identical variance.

Question 4

They could have evolved in correlated way depending on their diet, namely if an ape is an herbivore, it most likely does not need super long claws and high canines, whereas if it is an omnivore and also predatory claws and canines can be useful for fights and also to eat. An example for independent evolution could be that long claws are required for both fighting but also climbing trees, so their diet (linked to canine height) can be independent of claw length. The traits would show a correlation if they evolve in a correlated way and would show correlated normalized contrasts if they evolved in an independent way.

Question 5

We want to count character changes on the tree branches to fill in the contingency table. But there could be a problem to map those changes on the tree branches as the mapping could be ambiguous (there could be multiple options of exact evolution of certain traits on the branches).