Homework 5 - Theory Questions

1)

Fisher's exact test cannot be directly used to check for correlation on the values of discrete traits at the tips of a phylogenetic tree, because the analysis could be biased due to relatedness of the individuals, which is not displayed in the tips alone. The traits are not independent. We could detect false correlation due to relatedness, which we need to avoid.

2)

This is done to overcome interdependencies of the evolutionary trait. This then allows us to perform a linear regression on the contrasts. The values at the internal nodes are just estimates.

To be able to compare contrasts, their variances need to be equal, which is why we normalize.

If species/individuals evolved on a phylogeny, one must correct for the common evolutionary trajectories before comparing characters.

But in a nutshell, independence and equal variance are assumptions of linear regression, which is a model we aim to build off of the contrasts.

3)

Independent variables are created, when we calculate the difference between two traits.

The step that ensures equal variance, is when we divide the above-mentioned trait difference by the square root of the sum of updated branch lengths of the respective nodes.

Both of these steps take place in the calculate_contrast() function of the algorithm.

4)

An argument for correlation is that when defending attacks from other animals, larger teeth and claws are required to scare them off.

They could also evolve in a correlated way, to facilitate cleaning and sharpening of the teeth, as longer teeth require longer claws to get around them and more claw that can be eroded away when sharpening the teeth.

Though generally one must consider that all primates, except humans, have enlarged canine teeth.

On the other hand, they could evolve in an uncorrelated way, if there are no predators, so the apes don't need the longer canine teeth, but still need large claws to climb trees.

If the traits evolved in a correlated way, we would see correlation in the raw traits and the normalized contrasts.

On the other hand, if the traits evolved in an uncorrelated way, we would not see correlation in the raw traits or the normalized contrasts. Though, we could see correlation in the raw traits due to their shared ancestry.

5)

The problem that would arise here, is that we only have the values at the tips, but we don't know what the any data from the rest of the tree. So, we can't tell the number of character changes per branch.

Additionally, we don't know anything about branch lengths.