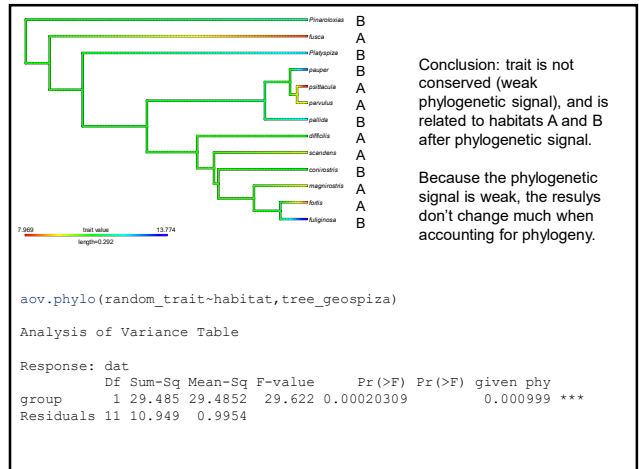
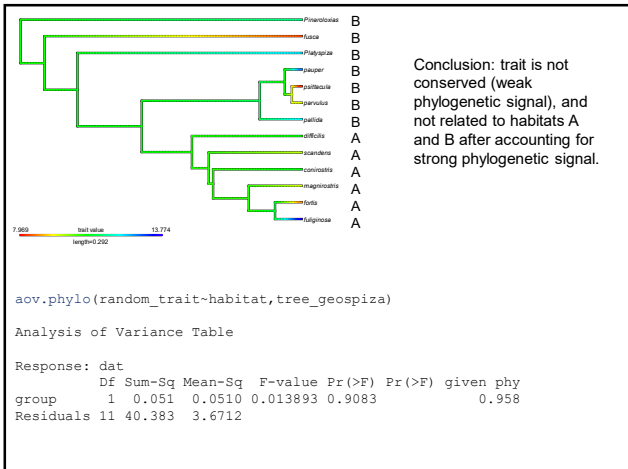
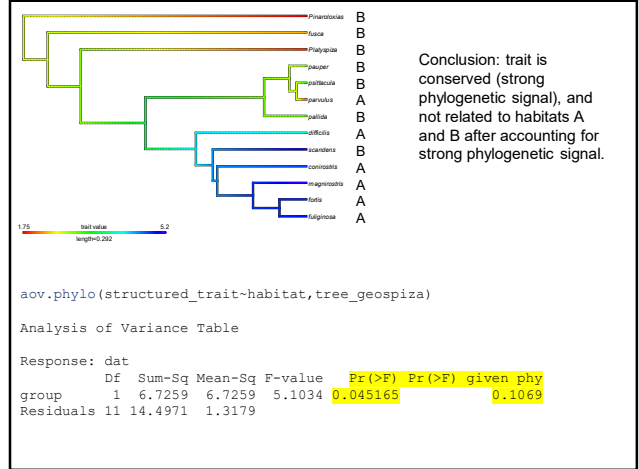
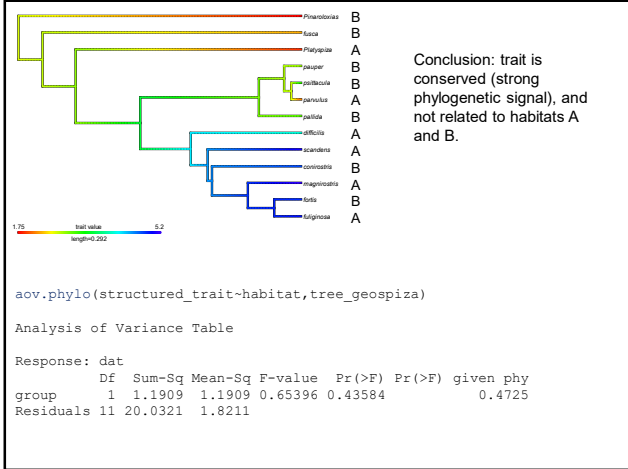


Phylogenetic Anova

- Function `aov.phylo` in geiger package
 - `aov.phylo(response~predictor, phylogeny, nsim=10000)`
- Response variables can be single (ANOVA) or multiple (MANOVA).
- First performs a standard ANOVA/MANOVA testing the hypothesis response~predictor (standard R formula)
- Then, simulates response variables based on phylogeny (using a Brownian motion model).

```

Response: dat
      group Df Sum-Sq Mean-Sq F-value Pr(>F) Pr(phy)
1         1 0.24026 0.240257   6.456 0.027438 0.1765
Residuals 11 0.40936 0.037215
    
```



Loading Phylogeny

- One standard form is a nexus file:

```
#NEXUS
Begin taxa;
  Dimensions ntax=63;
  Taxlabels
    Moxostoma_erythrurum
    Moxostoma_macrolepidotum
    Moxostoma_duquesnii
    Semotilus_atromaculatus
  ...
Begin trees;
  Translate
    1 Moxostoma_erythrurum,
    2 Moxostoma_macrolepidotum,
    3 Moxostoma_duquesnii,
    4 Semotilus_atromaculatus
  ...

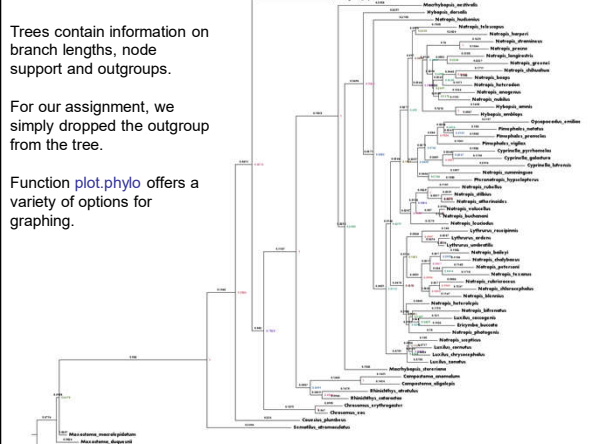
tree TREE1 = [&R]
  (((((5&height_95%_HPD=[0.5065998729999999,1.043333511199999
  7]length_range=[0.1050592,0.6082173],height_median=0.765794867
  8999995,length_95%_HPD=[0.1623718,0.3906135]
  ...
```

- Simplest representation is just the topology
 - Tree TREE1 = ((sp1,sp2),sp3,(sp4,sp5))
- Function `read.nexus` in ape package.

Trees contain information on branch lengths, node support and outgroups.

For our assignment, we simply dropped the outgroup from the tree.

Function `plot.phylo` offers a variety of options for graphing.



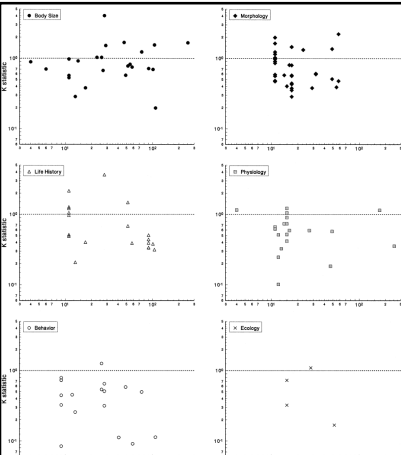
TESTING FOR PHYLOGENETIC SIGNAL IN COMPARATIVE DATA: BEHAVIORAL TRAITS ARE MORE LABILE

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Given the limitations of existing methods (see Discussion), our first purpose is to provide a new test for phylogenetic signal in continuous-valued characters, based on simple randomization procedures. This test allows us to address how common phylogenetic signal really is. Second, we provide a descriptive statistic, *K*, to gauge the amount of phylogenetic signal. Such a statistic is important because it allows com-

Function `fitContinuous` (Geiger package)

- Description of *K* statistic
- Randomization test
 - Observed statistic (*K* or variance in PIC)
 - Compare to permuted values calculated from randomizing traits across tips of phylogeny



K=1 – value expected under Brownian motion evolution model.

K>1 – species more similar, consistent with stabilizing selection.

K<1 – species less similar, consistent with strong selection, measurement error.

Review showed body size and morphology tended to have larger *K* (~1) than life history and behavior traits.