What questions are we trying to ask?

1. Are we trying to control for phylogeny? i.e., if we take a model selection approach using something like family/life history traits etc as an explanatory variable, we could then use phylogeny to control for autocorrelation. Software to do this exists – CAIC package for R

2. Are we trying to use phylogenetic topology as an explanatory variable? This question might need to be fleshed out more before we proceed further. Tom suggested a useful proof of concept exercise where we consider how much of variation in fungal response is explained by phylogenetic distance; do more closely related plants respond more similarly to fungi than distantly related ones? We could run a simple regression using distance between pairs and var in response. If there is no pattern, maybe then there is no phylogenetic signal. This could also be done by calculating Pagel's λ.

Citations (attached):

- Freckleton et al, Phylogenetic Analysis and Comparative Data: A Test and Review Of Evidence. AmNat 2002. This paper describes how to calculate pagel's λ, which is a widely used measure of phylogenetic association., and provides many ecological examples.
- Blomberg et al, Testing for phylogenetic signals in comparative data: behavioral traits are more labile, Evolution 2002. This paper describes another method for calculating phylogenetic signals, and includes a Matlab package to do this. It also includes a discussion of alternative methods to calculate signals.

Useful tools:

- TreeSnatcher: this program takes a tree and outputs a text file with the branch lengths in newick format (this can be read by R); http://www.cs.uni-duesseldorf.de/AG/BI/Software/treesnatcher/
- APE: This is an R package for reading in, drawing, and manipulation phylogenetic trees; http://cran.r-project.org/web/packages/ape/index.htm. APE contains methods to calculate various phylogenetic comparisons (Pagel's λ, lots of others

R packages:

Package	Functionality
Lme4	This package is designed for mixed effect models in R; however it does not seem to allow for arbitrary covariance matrices of random factors.
metafor	This is a package specific for meta-analysis in R; includes fixed and random effect models (as well as mixed models). Does not seem to allow arbitrary covariance matrices. Functionality described here: http://mail.orn.mpg.de/documents/kempenaers/Kemp_66.pdf

APE	Phylogenetic analysis package; methods for viewing and analyzing trees. Includes several well cited methods for phylogenetic association tests. Broadly applicable to many types of trees.
PhylogR	Similar to ape; includes methods for independent contrast but not as well cited. Has some nice plotting functions to visualize phylogenetic relationships, but much of this package is very specific to the developer's own research. Probably not what we want to use.

It is possible that we could manipulate lme4 or metafor to specify arbitrary covariance matrices – we'd have to spend some time looking at how the functions work and see if we could add methods to work with the ones already developed.