Intro to `evolspec`

Jose Eudardo Meireles and Brian O'Meara

2016-10-13

Installing `evolspec`

The easiest way to install `evolspec` directly from github using `devtools`

```r
# If you don't already have `devtools`
install.packages("devtools")

library("devtools")

# Install `evolspec`
devtools::install_github("meireles/evolspec")
```

Using `evolspec`

Datasets

Spectra

We provide the spectral dataset of ASD measurements of Oaks from Cavender-Bares et al. 2016 as an example dataset.

```r
library(evolspec)

## The oak_spec_dataet has "species" as the first column.
oak_spec_jcb2016[ 1:3, 1:5 ]
```

```
##             species        400        401        402        403
## 1    quercus_lyrata 0.04020742 0.03938670 0.04016407 0.04119308
## 2  quercus_garryana 0.03333427 0.03390132 0.03366042 0.03332556
## 3 quercus_douglasii 0.04184950 0.04129001 0.04186536 0.04270853
```

The `oak_spec_jcb2016` has many individuals measured per species, hence many more rows than species names. If you want to aggregate data by species, the function `aggregate_by_species` will return aggregated means `$mean`, standard deviation `$sd` and standard errors `$se` for each wavength.

```r
oak_spec_by_sp = evolspec::aggregate_by_species(oak_spec_jcb2016)
names(oak_spec_by_sp)
```

```
## [1] "mean" "sd"   "se"
```

You may want to manipulate spectral data with base R too, for instance, to get wavelength labels or resample the spectra.

```r
## To get a matrix with spectra only and get the wavelength labels, do
oak_spec_only = oak_spec_jcb2016[ , -1]
wlavelengths  = colnames(oak_spec_only)
```

```
## You can also resample the original oak data at a certain resolution,
## for instance, 10 nm
wl_subset_10nm    = as.character( seq(400, 2400, by = 10) )
oak_spec_10nm     = oak_spec_jcb2016[ , c("species", wl_subset_10nm)]
oak_spec_only_10nm = oak_spec_only[ , wl_subset_10nm ]

## Finally you can also aggregate by species the resamples spectra at 10nm resolution
oak_spec_by_sp_10nm_mu =  evolspec::aggregate_by_species(oak_spec_10nm)$mean
```
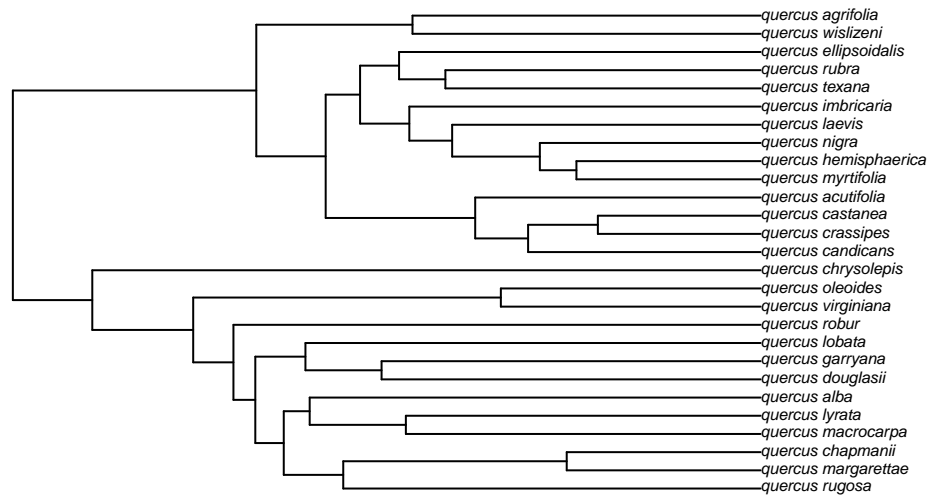
Phylogenetic tree

We also provide the Oak phylogenetic tree `oak_tree` that matches the example spectral data.

```
library("evolspec")
```

```
plot(oak_tree, cex = 0.5)
```


Phylogenetic signal

```
spec_phylosig_lambda = evolspec::phylo_signal(oak_tree,
                                              oak_spec_by_sp$mean,
                                              method = "lambda")
```

```
## Loading required package: phytools

## Loading required package: ape

## Loading required package: maps
```

```r
spec_phylosig_k        = evolspec::phylo_signal(oak_tree,
                                                oak_spec_by_sp$mean,
                                                method = "K")


par(mfrow = c(1, 2))

plot(x = wlavelengths,
     y = spec_phylosig_lambda$lambda,
     ylab = "Pagel's lambda", cex = 0.5,
     col = ifelse(spec_phylosig_lambda$pval <= 0.05, "red", "black"))

plot(x = wlavelengths,
     y = spec_phylosig_k$K,
     ylab = "Bloombergs's K", cex = 0.5,
     col = ifelse(spec_phylosig_k$pval <= 0.05, "red", "black"))
```