Changing tip labels using morTipLabels

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The function morTipLabels is a pretty rudimentary method for relabeling tips for our own lab data, mainly the trees generated from RAD-seq data... but it's generalizable. To run it, first make sure you have installed ape, magrittr, and openxlsx. Then, you'll need to grab the function off of GitHub:

source('https://raw.githubusercontent.com/andrew-hipp/mor-systematics/master/AAA.LAB/morTipLabels.R')

This reads the function into R. It also assumes you might want to use some of the specimen metadata files from the T: drive, so it *tries* to read those in; it should work fine even if it doesn't succeed. To see whether it has succeeded, look at the contents of your workspace:

ls()

## [1] "a" "dat.acer" "dat.malus" "dat.tilia" "morTipLabels" "tidyName" "tr"

You should see dat.acer, dat.malus, and dat.tilia in your workspace. If you do, then hooray! If not, then the T: drive was probably not mounted at the time that you sourced in the file.