Phylogenetic Independent Contrasts in R

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April 8, 2013

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1 Introduction

This document introduces you to a variety of tools and approaches to analyzing phylogenetic data with R.

There is detailed information on phylogenetic analysis with R at both the R phylo wiki and the CRAN task page for phylogenetics.

Make sure that you have the most recent version of R installed. For the analyses below, you will need to install the following libraries in R: * ape * geiger
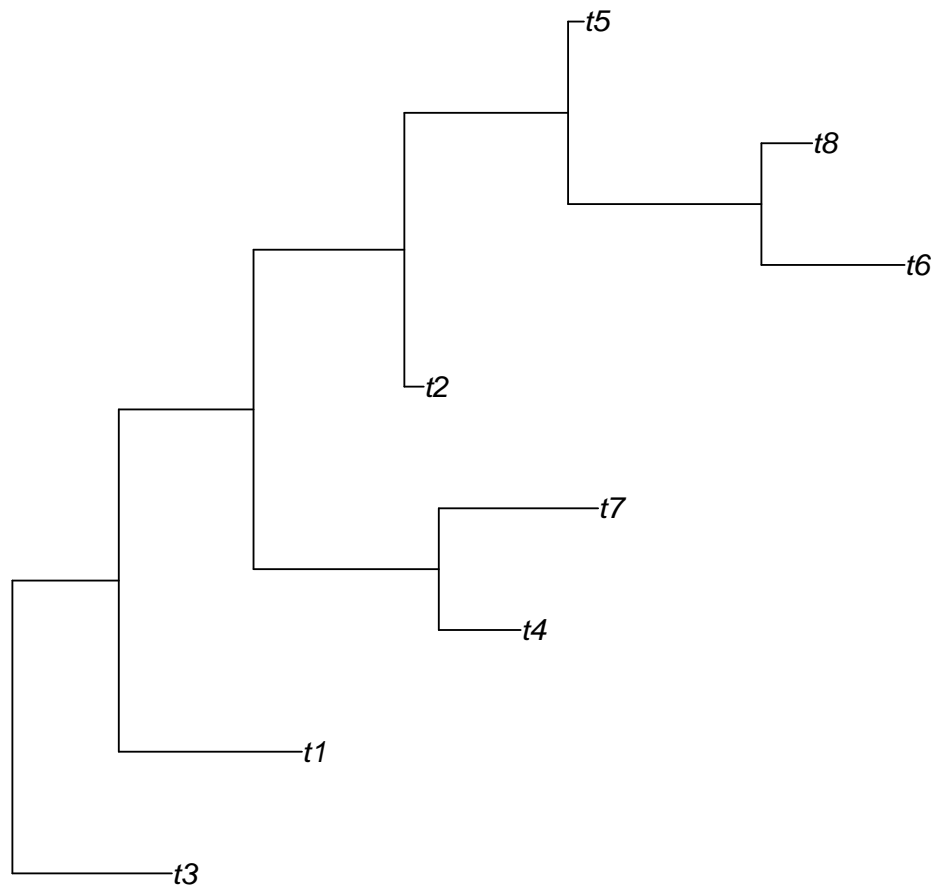
Update them if they are not the latest version.

2 Simulating trees

First, load ape:

```
library(ape)
```

The simplest way to generate a random tree is with the rtree() function:

```
plot(rtree(8))
```

The only required argument is the number of taxa. Unless otherwise specified, the branch lengths are drawn from a uniform distribution between 0 and 1.

3   How this document was made

This document is a computable data report compiled directly from the data. To recreate this file from the data, you will need to install:

- R (`http://www.r-project.org`). This document was generated with version 2.15.2.

- The R package knitr (`http://yihui.name/knitr/`), which can be installed from within R.

This document was generated with version 0.9.

- pdflatex, which comes with LaTeX distributions (`http://www.latex-project.org/ftp.html`). This document was generated with version 3.1415926-2.4-1.40.13.

From within the knitr directory, launch R and run:

```
library(knitr)
knit("comparative_r.Rnw")
quit()
```

This will generate a new tex file. To compile this tex file into a pdf file, run the following at the shell command line:

```
pdflatex comparative_r.tex
```

In addition to recreating this document as-is, you can directly edit and add to the analyses in the .Rnw source file. You can also copy the R source code from the .Rnw file.