How to take a sample of Pastis output species trees

Beatriz Willink   Rachel Blow

May 2020

Set your working directory to the parent directory containing all of your MCMC analyses

```
knitr::opts_knit$set(root.dir = '..' )
```

1) Call the "ape" package for reading trees

```
require(ape)
```

2) Read in the species tree files

```
tres <- read.nexus("SM_pastis/IschnuraExpanded.nexus.t")
```

3) Take random sample of 1000 trees for ancestral state reconstruction

```
random.1000.trees <- sample(tres, size = 1000, replace = T)
write.nexus(random.1000.trees, file = "SM_BayesTraits/sample.1000.trees",
    translate = T)
```