

How to take a sample of StarBEAST output species trees combined from two independent runs

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NB: First combine species trees output from the two independent chains using LogCombiner which is available as part of BEAST

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 combined species tree file from both StarBEAST runs

```
tres <- read.nexus("StarBEAST2/combined.species.tree")
```

- 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 = "BayesTraits/sample.1000.trees",
  translate = T)
```

- 4) Take random sample of 2100 trees for investigation of polymorphism correlates

```
random.2100.trees <- sample(tres, size = 2100, replace = T)
write.nexus(random.2100.trees, file = "MCMCglmm/sample.2100.trees",
  translate = T)
```