# **babette**: BEAST2 from R

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```
library(babette)
```

**babette** is an R package to work with BEAST2
1) configure and run BEAST2
2) analyze BEAST2 results

One or more DNA alignments

**BEAST2** is a popular and versatile Bayesian phylogenetics tool. BEAST2 is accompanied by multiple graphical user interface tools. Clicking through each of these tools is tedious and error prone. **babette** is an R package replaces all these tools in a user-friendly way
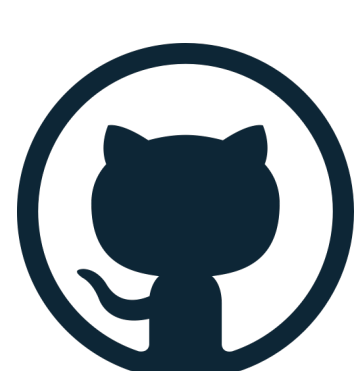
**BEAUti** is a graphical user interface tool to create a BEAST2 configuration file. It is used to select one or more alignments, site models, clock models, tree priors and prior distributions. **babette** can do the same from an R function call. This allows iteration over multiple alignments, site models, clock models, tree priors and prior distributions. <u>Novel</u>: only in `babette`, posterior crown age can be fixed

**DensiTree** is a graphical user interface tool to view posterior's phylogenies. **babette** gives access to those phylogenies directly and supplies the same visualization
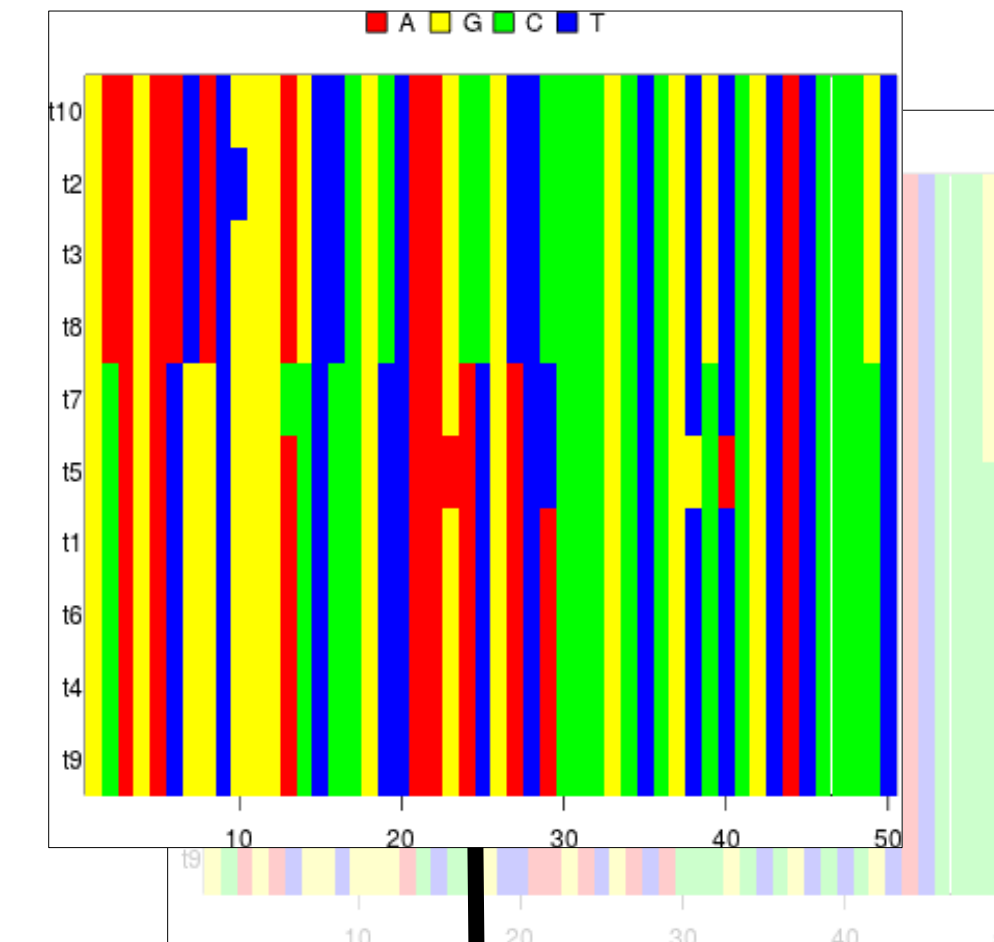
**Tracer** is a graphical user interface tool to view posterior parameter estimates. **babette** gives access to these values directly and allows to calculate the same statistics from an R function call. This allows for scripted posterior quality assessment, inference on summary statistics of multiple runs, and plotting your data in your own funky way

**babette** does the same as these four tools combined, from R

## 1. Run

Specify assumptions
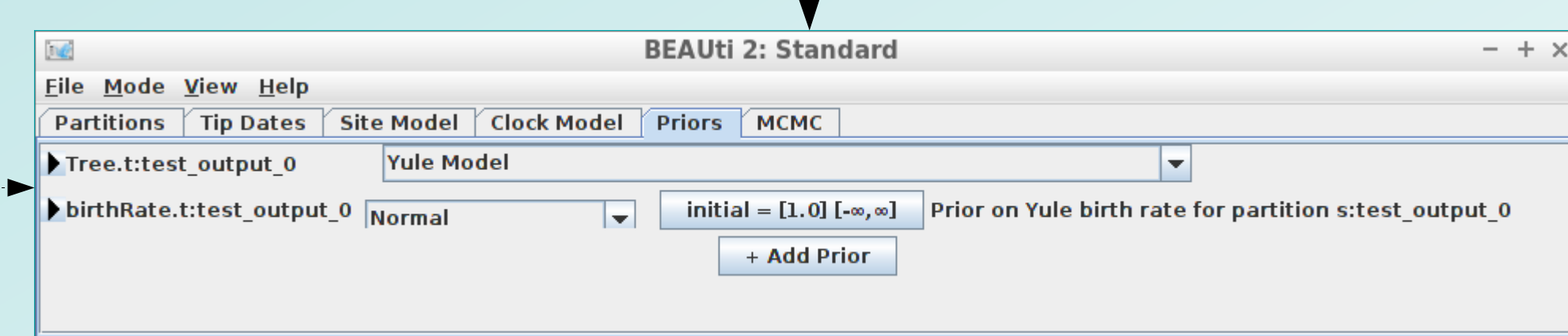
Run BEAST2

```
out <- run_beast2(
  "my.fasta"
)
```
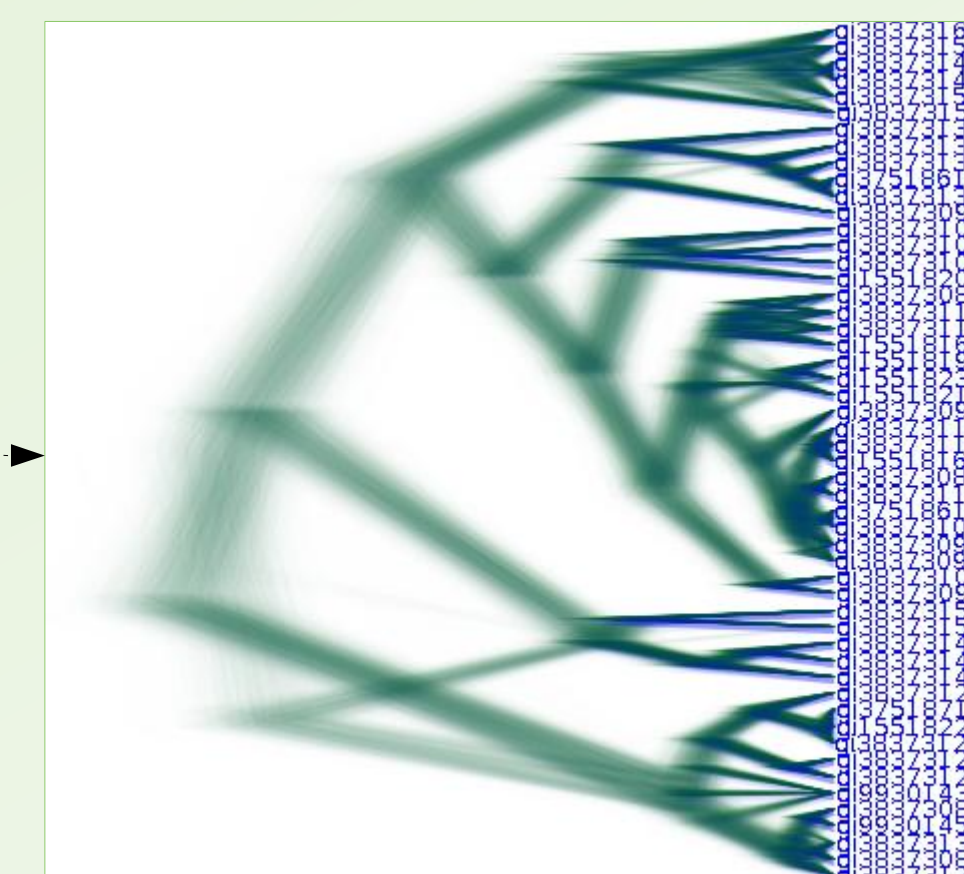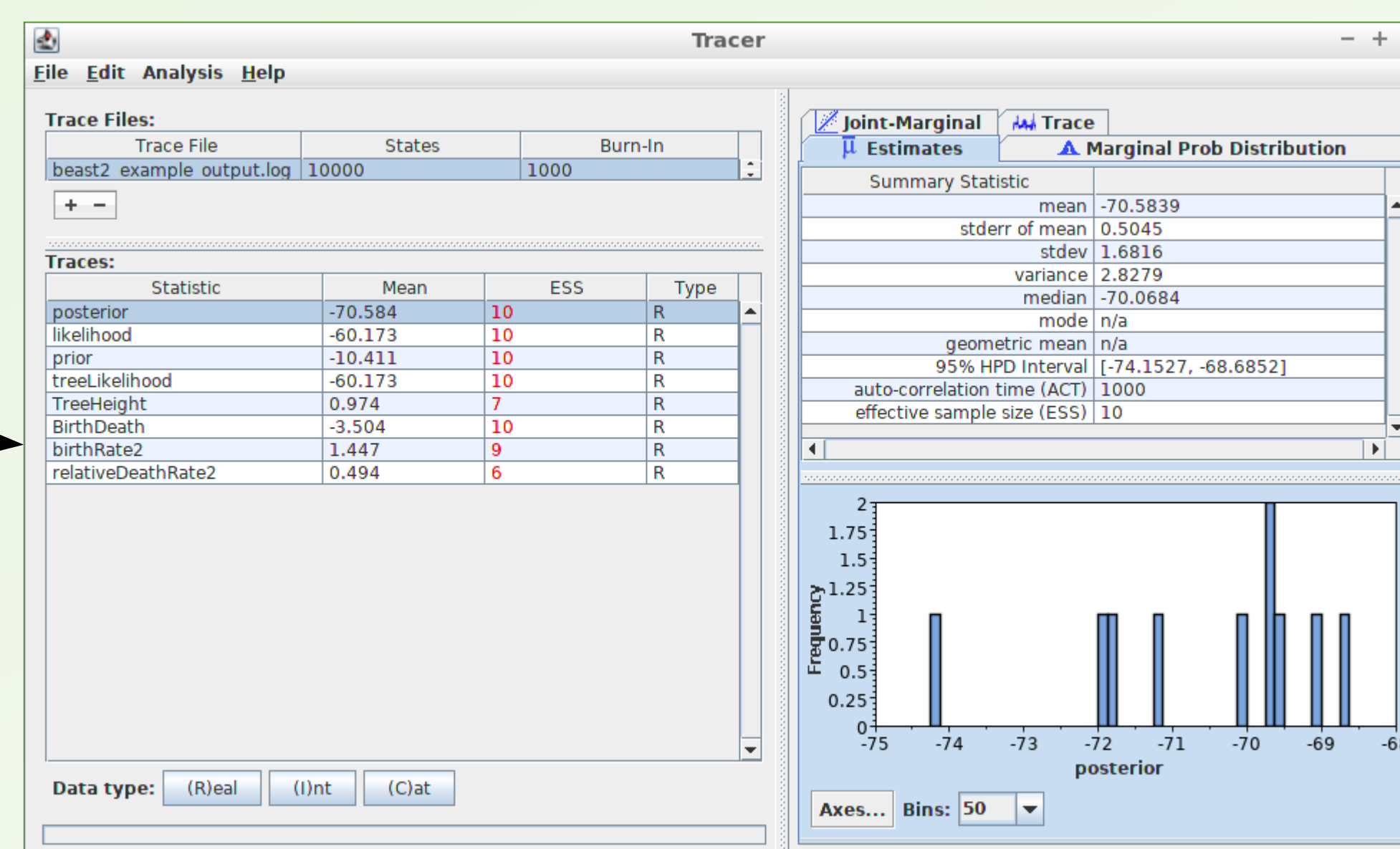
## 2. Analyze results

### 2a. Posterior phylogenies

```
densitree(out$trees)
```

### 2b. Posterior estimates

```
esses <- calc_esses(
  out$estimates,
  sample_interval = 1000
)
```

```
ggplot(
  data = out$estimates),
  aes(posterior)
) + geom_histogram()
```

```
sum_stats <- calc_sum_stats(
  out$estimates$posterior,
  sample_interval = 1000
)
```

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https://github.com/richelbilderbeek/babette