

# babette: BEAST2 from R

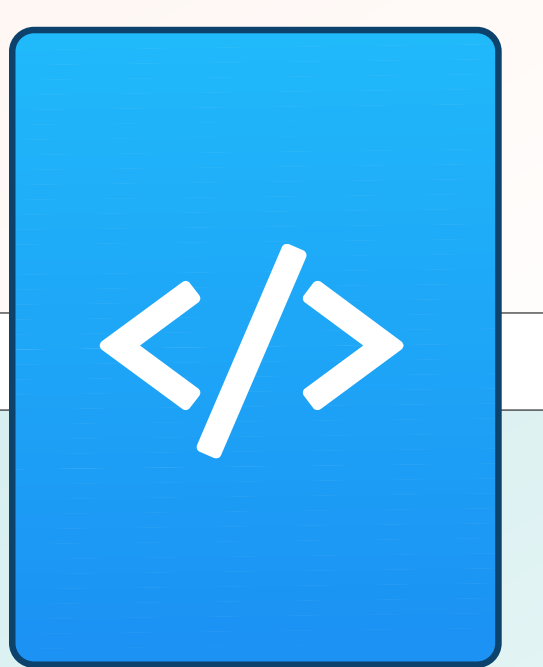
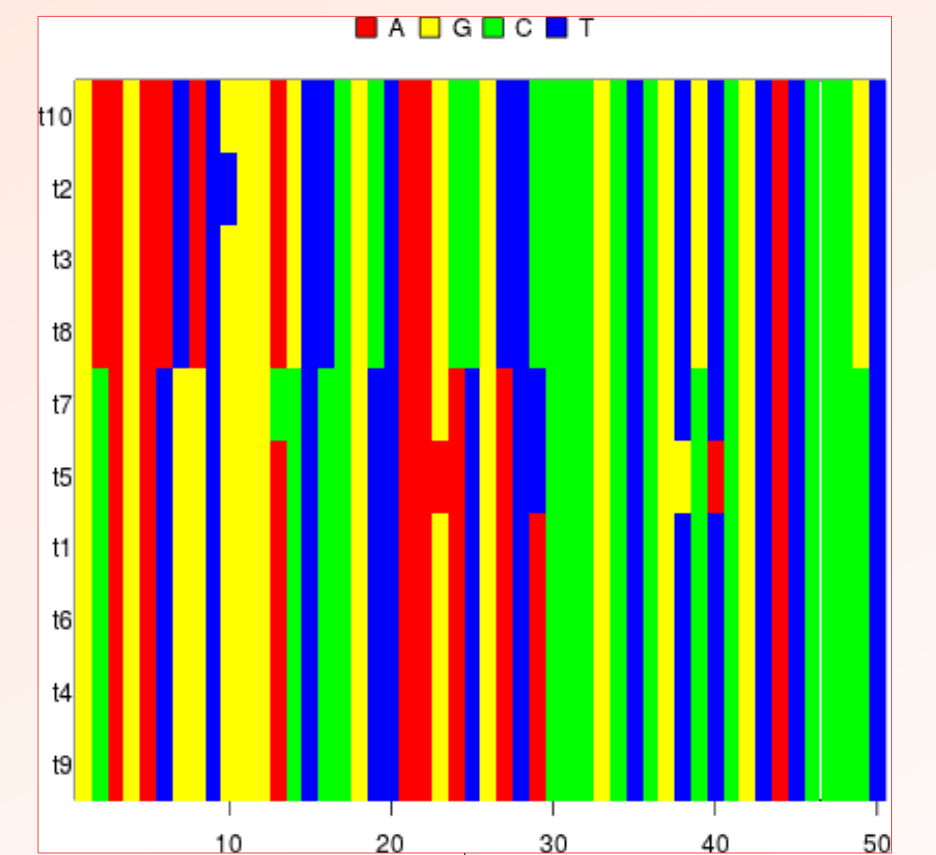
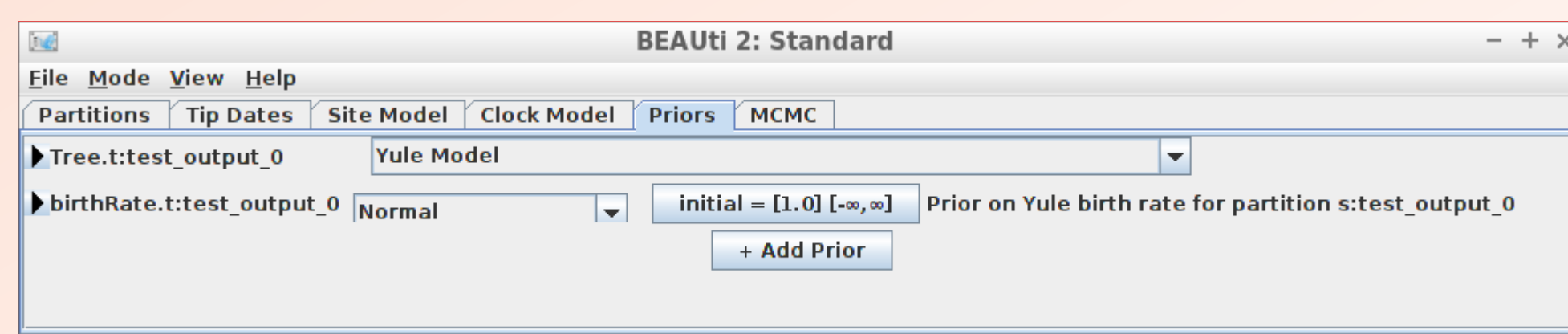


- babette is an R package suite to work with BEAST2:
- 1) beautier: 'BEAUti 2 for R': create BEAST2 input files
  - 2) beastier: run BEAST2 from R
  - 3) tracerer: 'Tracer for R': analyze BEAST2 results

## 1. Create BEAST2 input file



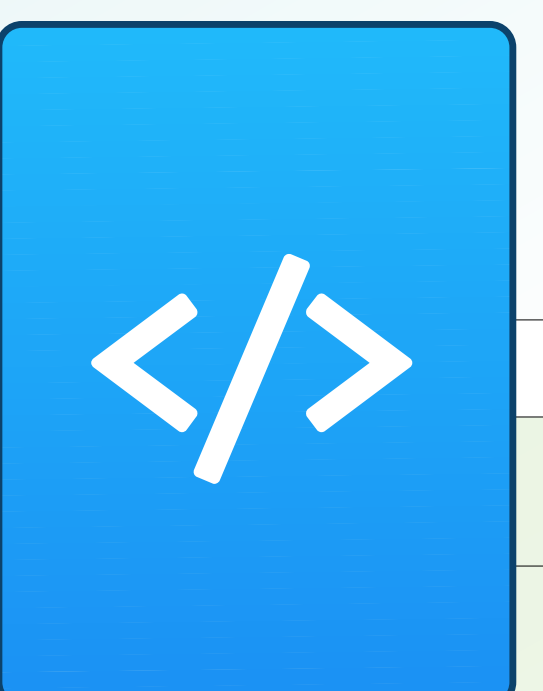
```
create_beast2_input_file(
  "my.fas",
  "beast2.xml"
)
```



## 2. Run BEAST2



```
out <- run_beast2(
  "beast2.xml"
)
```

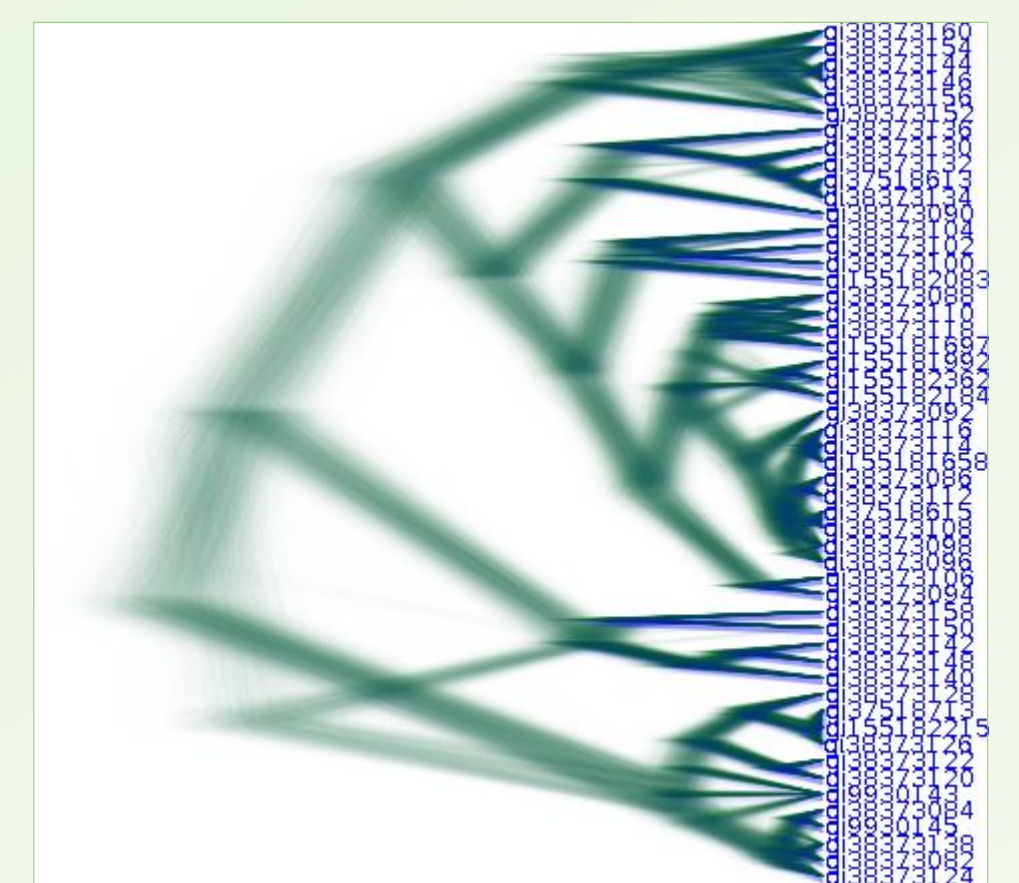


## 3. Analyze results



### 3a. Posterior phylogenies

```
densiTree(out$trees)
```

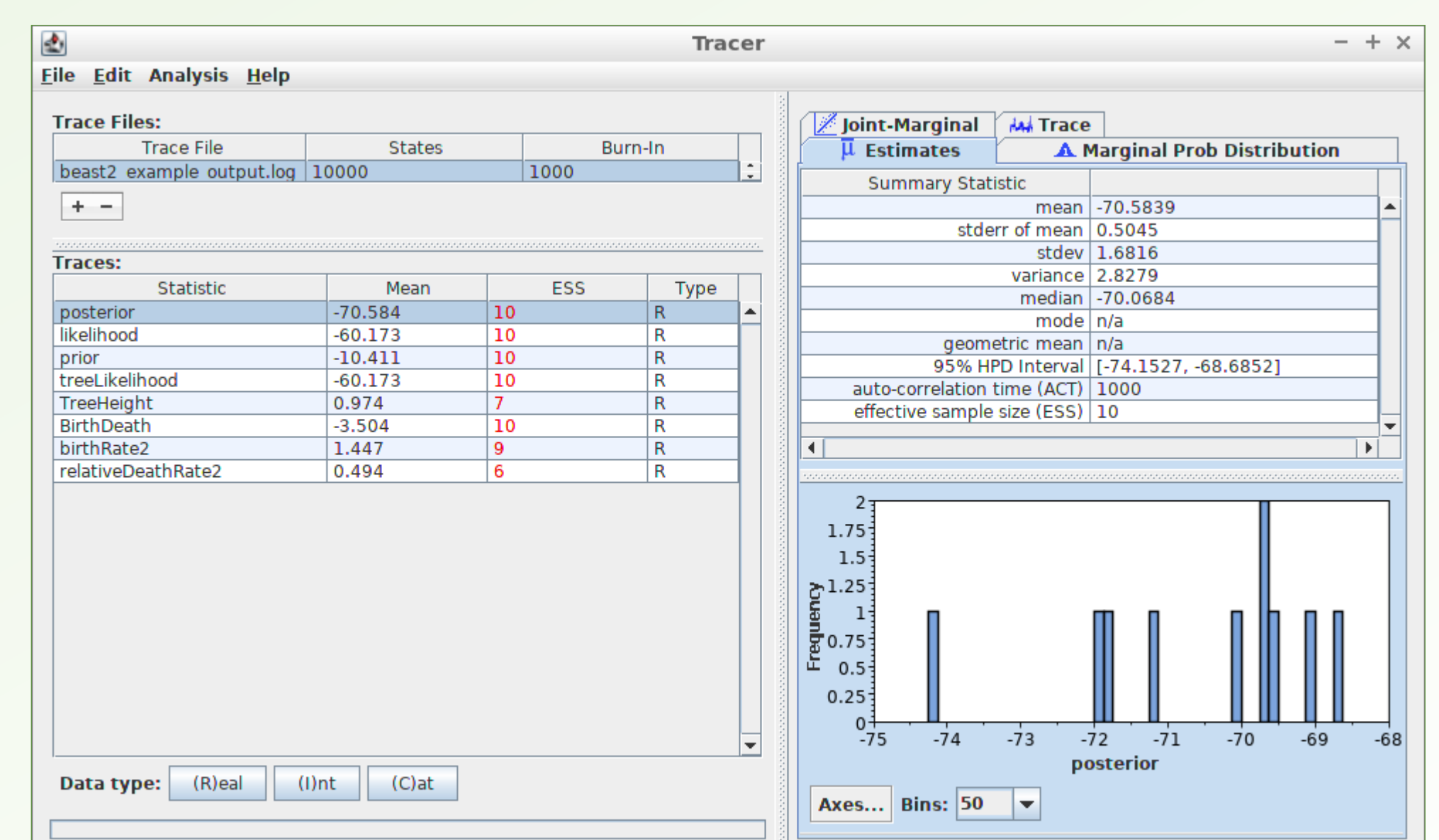


### 3b. Posterior estimates

```
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>