

babette: BEAST2 from R

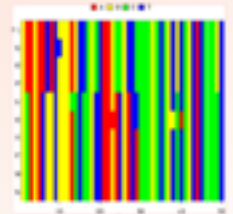
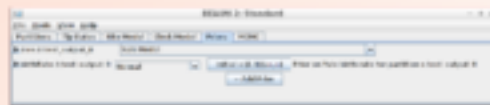


- babette is an R package suite to work with BEAST2:
- 1) beautier: 'BEAUti 2 for R': create BEAST2 input files
 - 2) beastier: run BEAST2 from R
 - 3) tracerer: 'Tracer for R': analyze BEAST2 results

1. Create BEAST2 input file



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



2. Run BEAST2



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



BEAST2 is a popular and versatile Bayesian phylogenetics tool. BEAST2 is accompanied by multiple graphical user interface tools. For bigger theoretical experiments, clicking through each of these tools is tedious and error prone. babette is an R package suite that can replace all these tools in a user-friendly way.

3. Analyze results

3a. Posterior phylogenies



```
denslTree(out$trees)
```

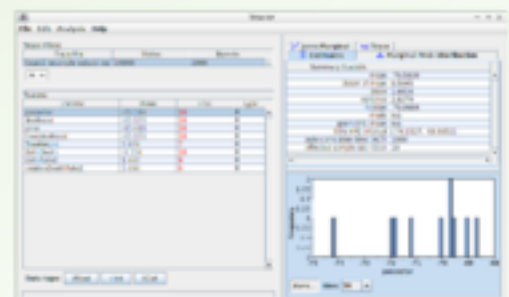


3b. Posterior estimates

```
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>

