



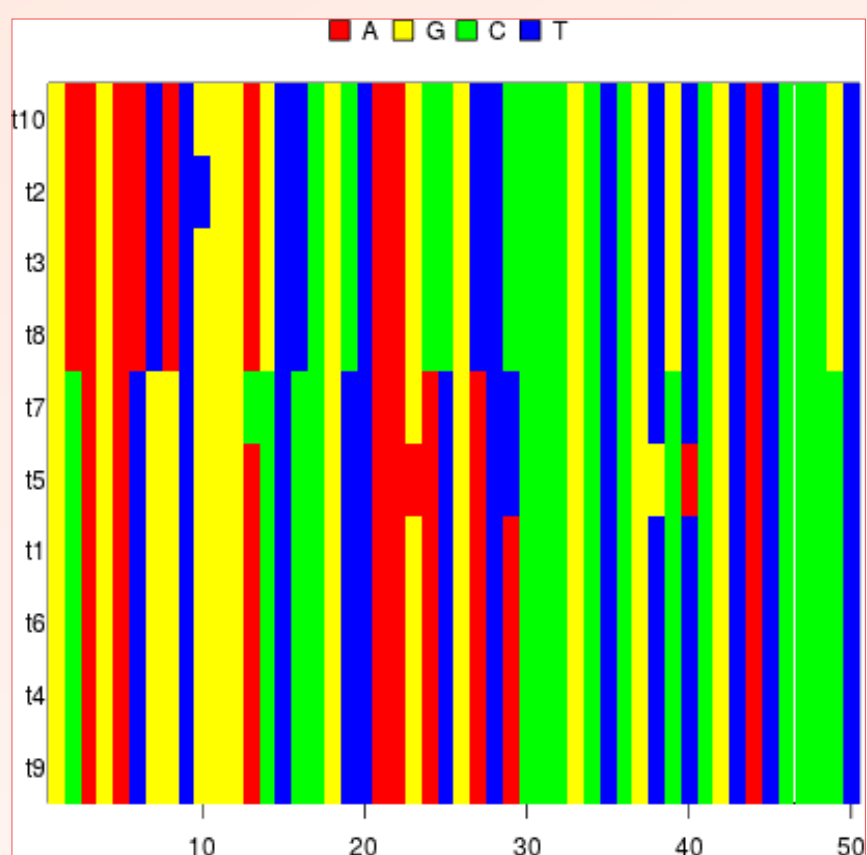
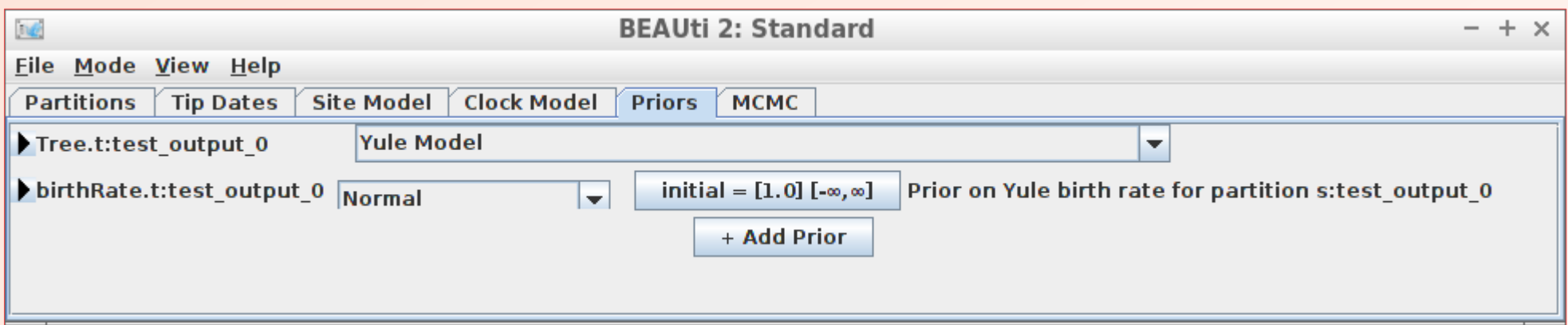
'babette' is an R package suite to work with BEAST2.

babette: BEAST2 from R

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  
)
```

