

# 1 babette: BEAUti 2, BEAST2 and Tracer for R

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## 6 Summary

7 **1.** In the field of phylogenetics, BEAST2 is one of the most widely  
8 used software tools. It comes with the graphical user interfaces BEAUti  
9 2, DensiTree and Tracer, to create BEAST2 configuration files and to in-  
10 terpret BEAST2's output files. However, when many different alignments  
11 or model setups are required, a workflow of graphical user interfaces is  
12 cumbersome.

13 **2.** Here, we present a free, libre and open-source package, **babette**:  
14 'BEAUti 2, BEAST2 and Tracer for R', for the R programming language.  
15 **babette** creates BEAST2 input files, runs BEAST2 and parses its results,  
16 all from an R function call.

17 **3.** We describe **babette**'s usage and the novel functionality it provides  
18 compared to the original tools and we give some examples.

19 **4.** As **babette** is designed to be of high quality and extendable, we  
20 conclude by describing the further development of the package.

21  
22 **Keywords:** computational biology, evolution, phylogenetics, BEAST2, R

# 1 Introduction

Phylogenies are commonly used to explore evolutionary hypotheses. Not only can phylogenies show us how species (or other evolutionary units) relate to each other, but we also estimate relevant parameters such as extinction and speciation rates. There are many phylogenetics tools available to obtain an estimate of the phylogenetic tree of a given set of species. BEAST2 (Bouckaert *et al.* 2014) is one of the most widely used ones. It creates a posterior of jointly-estimated phylogenies and model parameters, from one or more DNA, RNA or amino acid alignments (see figure 1 for an overview of the workflow). It has a graphical and a command-line interface, that both need a configuration file containing alignments and model parameters. BEAST2 is bundled with BEAUti 2 (Drummond *et al.* 2012) ('BEAUti' from now on), a desktop application to create a BEAST2 configuration file. BEAUti has a user-friendly graphical user interface, with helpful default settings. As such, BEAUti is an attractive alternative to manual and error-prone editing of BEAST2 configuration files.

However, BEAUti cannot be called from a command-line script. This implies that when the user wants to explore the consequences of various settings, this must be done manually. This is the common workflow when using a few alignments and doing a superficial analysis of sensitivity of the reconstructed tree to model settings. For exploring many trees (for instance from simulations) and for more thorough sensitivity analysis, one would like to loop through multiple (simulated) alignments, nucleotide substitution models, clock models and tree priors. One such tool to replace BEAUti is **BEASTmaster** (Matzke 2015), which focuses on morphological traits and tip-dating, but also supports DNA data. **BEASTmaster**, however, takes hundreds of lines of R code to setup the BEAST2 model configuration and a Microsoft Excel file to specify alignment files.

BEAST2 is also associated with Tracer (Rambaut & Drummond 2007) and

50 DensiTree (Bouckaert & Heled 2014). Both are desktop applications to ana-  
51 lyze the output of BEAST2, each with a user-friendly graphical user interface.  
52 Tracer’s purpose is to analyze the parameter estimates generated from a BEAST  
53 2 run. It shows, among others, the effective sample size (ESS) and time series  
54 (‘the trace’, hence the name) of each variable in the MCMC run. Both ESS and  
55 trace are needed to assess the strength of the inference. DensiTree visualizes the  
56 phylogenies of a BEAST2 posterior, with many options to improve the display  
57 of many phylogenies.

58 However, for exploring the output of many BEAST2 runs, one would like a  
59 script to collect all parameters’ ESSes, parameter traces and posterior phyloge-  
60 nies. There is no single package that offers a complete solution, but examples  
61 of R packages that offer a partial solution are **BEASTmasterR**, **rBEAST** (Ratmann  
62 2015) and **RBeast** (Faria & Suchard 2015). **BEASTmasterR** and **RBeast** are in-  
63 complete packages, where **rBEAST** does not aim to be a package to be used by  
64 most BEAST2 users.

65 Here, we present **babette**: BEAUti 2, BEAST2 and Tracer for R, which  
66 creates BEAST2 configuration files, runs BEAST2, and analyzes its results, all  
67 from an R function call. This will save time, tedious mouse clicking and reduces  
68 the chances of errors in such repetitive actions. The interface of **babette** mimics  
69 the tools it is based on. This familiarity helps both beginner and experienced  
70 BEAST2 users to make the step from those tools to **babette**. **babette** enables  
71 the creation of a single-script pipeline from sequence alignments to posterior  
72 analysis in R.

## 73 2 Description

74 **babette** is written in the R programming language (R Core Team 2013) and en-  
75 ables the full BEAST2 workflow from an R function call, in a similar way to what

76 BEAUti, DensiTree and Tracer do. **babette**'s main function is `run_beast2`,  
77 which configures BEAST2, runs it and parses its output. `run_beast2` needs  
78 at least the name of a FASTA file containing a DNA alignment. The default  
79 settings for the other arguments of `run_beast2` are identical to BEAUti's and  
80 BEAST2's default settings. Per alignment, a site model, clock model and tree  
81 prior can be chosen. Multiple alignments can be used, each with its own (un-  
82 linked) site model, clock model and tree prior.

83 **babette** currently has 61 exported functions to set up a BEAST2 configura-  
84 tion file. **babette** is an alternative for a majority of BEAUti use cases. Because  
85 of BEAUti's high number of plugins, **babette** uses a software architecture that  
86 is designed to be extended. Furthermore, **babette** has 7 exported function to  
87 run and help run BEAST2. One function is used to run BEAST2, others al-  
88 low the user to check if a BEAST2 configuration file is indeed valid. Finally,  
89 **babette** has 20 exported function to parse the BEAST2 output files and analyze  
90 the created posterior. **babette** gives the same ESSes and summary statistics  
91 as Tracer. The data is formatted as such, that it can easily be visualized using  
92 `ggplot2` (for a trace, similar to Tracer) or `phangorn` (Schliep 2011) (for the  
93 phylogenies in a posterior, similar to DensiTree).

94 Currently, **babette** does not replace all functionality in BEAUti, as it does  
95 not provide 3 out of 7 tree priors, nor does it support RNA alignments or  
96 use of morphological data. The many plug-ins of BEAUti are not yet sup-  
97 ported by **babette**. **babette** does not support all command-line arguments of  
98 BEAST2, does not provide the more specialized Tracer analysis options, nor is it  
99 as feature-rich in plotting options as DensiTree. Up until now, the **babette** fea-  
100 tures implemented are those requested by users. Further extension of **babette**  
101 will be based on future user requests.

### 102 3 Usage

103 In R, the functions of a package need to be loaded in the global namespace first:

```
104 library(babette)
```

105 BEAUti, and likewise **babette**, needs at least a FASTA filename to produce a  
106 BEAST2 configuration file. In BEAUti, this is achieved by loading a FASTA file,  
107 then saving an output file using a common save file dialog. After this, BEAST2  
108 needs to be applied to the created configuration file. It creates multiple files  
109 storing the posterior. These output files must be parsed by either Tracer of  
110 DensiTree. In **babette**, all this is achieved by:

```
111 out <- run_beast2("anthus_aco.fas")
```

112 This code will create a (temporary) BEAST2 configuration file, from the FASTA  
113 file with name **anthus\_aco.fas** (which is supplied with the package, from  
114 (Van Els & Norambuena 2018)), using the same default settings as BEAUti,  
115 which are, among others, a Jukes-Cantor site model, a strict clock, and a Yule  
116 birth tree prior. **babette** will then execute BEAST2 using that file, and parses  
117 the output. The returned data structure, named **out**, is a list of parameter  
118 estimates (called **estimates**), posterior phylogenies (called **anthus\_aco\_trees**,  
119 named after the alignment's name) and MCMC operator performance (**operators**).  
120 An example of using a different site model, clock model and tree prior is:

```
121 out <- run_beast2(  
122   "anthus_aco.fas",  
123   site_models = create_hky_site_model(),  
124   clock_models = create_rln_clock_model(),  
125   tree_priors = create_bd_tree_prior()  
126 )
```

127 This code uses an HKY site model, a relaxed log-normal clock model and a birth-

death tree prior, each with their default settings in BEAUti. Table 1 shows an overview of all functions to create site models, clock models and tree priors. Note that the arguments' names `site_models`, `clock_models` and `tree_priors` are plural, as each of these can be (a list of) one or more elements. Each of these arguments must have the same number of elements, so that each alignment has its own site model, clock model and tree prior. An example of two alignments, each with its own site model, is:

```

135 out <- run_beast2(
136   c("anthus_aco.fas", "anthus_nd2.fas"),
137   site_models = list(
138     create_tn93_site_model(),
139     create_gtr_site_model()
140   )
141 )

```

`babette` also uses the same default prior distributions as BEAUti for each of the site models, clock models and tree priors. For example, by default, a Yule tree prior assumes that the birth rate follows a uniform distribution, from minus infinity to plus infinity. This assumption implies that negative and positive birth rates are just as likely, where a negative birth rate is biologically impossible (note that in practice, this usually works out just fine). One may prefer an exponential distribution instead, as this would assume only positive birth rates, and makes high birth rates unlikely. To do this in `babette`:

```

150 out <- run_beast2(
151   "anthus_aco.fas",
152   tree_priors = create_yule_tree_prior(
153     birth_rate_distr = create_exp_distr()
154   )
155 )

```

156 Within this same example, one may specify the initial shape parameters of the  
157 exponential distribution. In BEAST2's implementation, an exponential distri-  
158 bution has one shape parameter: its mean, which can be set to any value with  
159 BEAUti. Within **babette**, to set the mean value of the exponential distribution  
160 to a fixed (non-estimated) value, do:

```
161 out <- run_beast2(  
162   "anthus_aco.fas",  
163   tree_priors = create_yule_tree_prior(  
164     birth_rate_distr = create_exp_distr(  
165       mean = create_mean_param(  
166         value = 1.0,  
167         estimate = FALSE  
168       )  
169     )  
170   )  
171 )
```

172 Our initial motivation to create **babette** was that we wanted to fix the crown  
173 age of a phylogeny. BEAUti assumes that a phylogeny has a crown age that  
174 needs to be jointly-estimated with the phylogeny and other parameters. It does  
175 not allow for fixing the crown age. Without **babette**, one needs to manually edit  
176 the BEAST2 configuration file (Bouckaert & Vaughan 2017), which is tedious  
177 and prone to errors. Fixing the crown ages is especially useful for theoretical  
178 experiments, as this allows for one less source of variation. This is how to specify  
179 a fixed crown age with **babette**:

```
180 out <- run_beast2(  
181   "anthus_aco.fas",  
182   posterior_crown_age = 15  
183 )
```

184 **babette** allows for the same functionality as Tracer. Tracer works on the val-  
185 ues of the parameter estimates sampled in the BEAST2 run. This is called  
186 the "trace" (hence the name). The start of the trace is usually discarded, as  
187 an MCMC algorithm (such as used by BEAST2) first has to converge to its  
188 equilibrium. The start of the trace, called the "burn-in", will be removed, as  
189 its parameter estimates are not representative. By default, Tracer discards the  
190 first 10% of all the parameter estimates. To remove a 20% burn-in from all  
191 parameter estimates in **babette**, the following code can be used:

```
192 traces <- remove_burn_ins(  
193   out$estimates ,  
194   burn_in_fraction = 0.2  
195 )
```

196 Tracer shows the ESSes of each posterior's variables. These ESSes are important  
197 to determine the strength of the inference. As a rule of thumb, an ESS of 200 is  
198 acceptable for any parameter estimate. To calculate the effective sample sizes  
199 (of all estimated variables) in **babette**:

```
200 esses <- calc_esses(  
201   traces ,  
202   sample_interval = 1000  
203 )
```

204 Tracer displays multiple summary statistics for each estimated variable: the  
205 mean and its standard error, standard deviation, variance, median, mode, geo-  
206 metric mean, 95% highest posterior density interval, auto-correlation time and  
207 effective sample size. It displays these statistics per variable. In **babette**, these  
208 summary statistics are collected for all estimated parameters at once:

```
209 sum_stats <- calc_summary_stats(  
210   traces ,
```



```
211   sample_interval = 1000
```

```
212 )
```

213 **babette** allows for the same functionality as **DensiTree**. **DensiTree** displays the  
214 phylogenies in a posterior at the same time scale, drawn one over one another,  
215 allowing to see the uncertainty in topology and branch lengths. Within the  
216 object **out**, the posterior phylogenies are stored as **anthus\_aco\_trees**, and can  
217 be plotted as such:

```
218 plot_densitree(out$anthus_aco_trees)
```

## 219 4 **babette** resources

220 **babette** is free, libre and open source software available from the official R pack-  
221 age archive at <http://cran.r-project.org/src/contrib/PACKAGES.html#babette>  
222 and is licensed under the GNU General Public License v3.0. **babette** uses the  
223 Travis CI (<https://travis-ci.org>) continuous integration service, which is  
224 known to significantly increase the number of bugs exposed (Vasilescu *et al.*  
225 2015) and increases the speed at which new features are added (Vasilescu *et al.*  
226 2015). **babette** has a 100% code coverage, which correlates with code quality  
227 (Horgan *et al.* 1994; Del Frate *et al.* 1995). **babette** follows Hadley Wickham's  
228 style guide (Wickham 2015), which improves software quality (Fang 2001).  
229 **babette** depends on multiple packages, which are **ape** (Paradis *et al.* 2004),  
230 **beautier** (Bilderbeek 2018b), **beastier** (Bilderbeek 2018a), **devtools** (Wick-  
231 ham & Chang 2016), **geiger** (Harmon *et al.* 2008), **ggplot2** (Wickham 2009),  
232 **knitr** (Xie 2017), **phangorn** (Schliep 2011), **rmarkdown** (Allaire *et al.* 2017),  
233 **seqinr** (Charif & Lobry 2007), **stringr** (Wickham 2017), **testit** (Xie 2014)  
234 and **tracerer** (Bilderbeek 2018c).

235 **babette**'s development takes place on GitHub, <https://github.com/richelbilderbeek/>

236 **babette**, which accommodates collaboration (Perez-Riverol *et al.* 2016) and im-  
237 proves transparency (Gorgolewski & Poldrack 2016). **babette**'s GitHub facili-  
238 tates feature requests and has guidelines how to do so.

239 **babette**'s documentation is extensive. All functions are documented in the  
240 package's internal documentation. For quick use, each exported function shows  
241 a minimal example. For easy exploration, each exported function's documen-  
242 tation links to related functions. Additionally, **babette** has a vignette that  
243 demonstrates extensively how to use it. The GitHub documentation helps to get  
244 started, with a dozen examples of BEAUti screenshots with equivalent **babette**  
245 code.

## 246 5 Citation of babette

247 Scientists using **babette** in a published paper can cite this article, and/or cite  
248 the **babette** package directly. To obtain this citation from within an R script,  
249 use:

```
250 > citation("babette")
```

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Name	Description
run_beast2	Run BEAST2
create_gtr_site_model	Create a GTR site model
create_hky_site_model	Create an HKY site model
create_jc69_site_model	Create a Jukes-Cantor site model
create_tn93_site_model	Create a TN93 site model
create_rln_clock_model	Create a relaxed log-normal clock model
create_strict_clock_model	Create a strict clock model
create_bd_tree_prior	Create a birth-death tree prior
create_cbs_tree_prior	Create a coalescent Bayesian skyline tree prior
create_ccp_tree_prior	Create a coalescent constant-population tree prior
create_cep_tree_prior	Create a coalescent exponential-population tree prior
create_yule_tree_prior	Create a Yule tree prior
create_beta_distr	Create a beta distribution
create_exp_distr	Create an exponential distribution
create_gamma_distr	Create a gamma distribution
create_inv_gamma_distr	Create an inverse gamma distribution
create_laplace_distr	Create a Laplace distribution
create_log_normal_distr	Create a log-normal distribution
create_normal_distr	Create a normal distribution
create_one_div_x_distr	Create a 1/X distribution
create_poisson_distr	Create a Poisson distribution
create_uniform_distr	Create a uniform distribution

Table 1: babette’s main functions

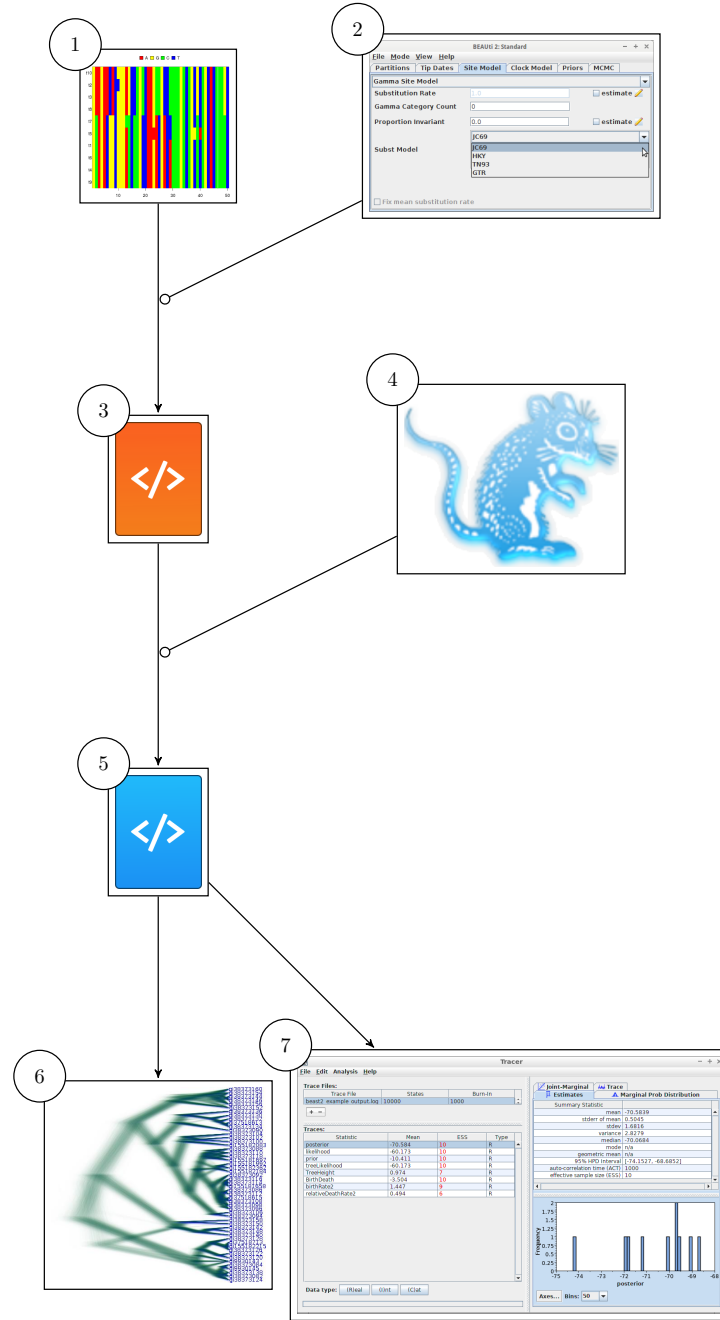


Figure 1: Workflow using GUI tools. From an alignment (1) and BEAUti (2), a BEAST2 configuration file (3) is created. BEAST2 (4) uses that file to infer a posterior, storing it in multiple files (5). These results are visualized using DensiTree (6) and Tracer (7). babette allows for the same workflow, all from an R function call.