# Bayesian inference for the logistic growth model

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### 1 Preliminaries

This vignette illustrates the steps needed to perform inference for an ODE model, the logistic growth model. A detailed description of the rationale behind the Bayesian inference approach for differential equations can be found in the preprint describing the deBInfer package (Boersch-Supan and Johnson 2016). The vignette also illustrates how to simulate noisy observations from an existing DE model. Conducting inference on a model with known parameters is good practice, when developing models for actual data, as it provides validation of the inference procedure.

This examples assumes that deBInfer is installed and loaded. If this is not the case it needs to be installed from github, which requires the devtools package (Wickham and Chang 2016).

```
install.packages("devtools")
#Load the devtools package.
```

Then deBInfer can be installed from github.

```
install_github("pboesu/debinfer")
```

library(deBInfer)

library(devtools)

# 2 Defining the DE model

We define a logistic growth model

$$\frac{dN}{dt} = rN\left(1 - \frac{N}{K}\right). \tag{1}$$

and implement it for deSolve::ode (Soetaert, Petzoldt, and Setzer 2010):

```
library(deSolve)
logistic_model <- function (time, y, parms) {
    with(as.list(c(y, parms)), {
        dN <- r * N * (1 - N / K)
        list(dN)
        })
}</pre>
```

We then pick a set of parameter values (r = 0.1, K = 10) and an initial condition (N = 0.1) and solve the model for these values.

```
y \leftarrow c(N = 0.1)

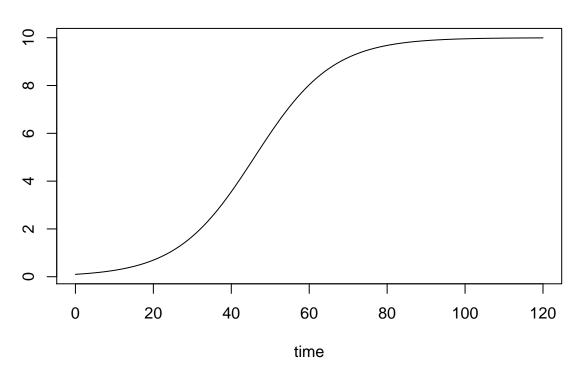
parms \leftarrow c(r = 0.1, K = 10)

times \leftarrow seq(0, 120, 1)

out \leftarrow ode(y, times, logistic_model, parms, method='lsoda')
```

We can plot this numerical solution.

N



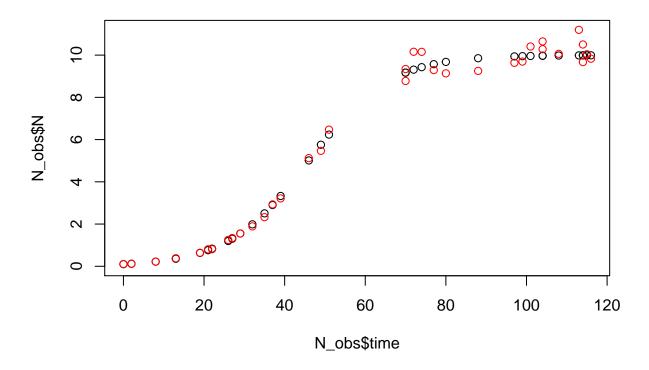
## 3 Simulating observations

Next we simulate a noisy dataset from this equation. We do this by sampling a random subset from the integration output

```
set.seed(143)
#force include the first time-point (t=0)
N_obs <- as.data.frame(out[c(1,runif(35, 0, nrow(out))),])</pre>
```

and we "add" lognormal noise with a known "observation" standard deviation  $\sigma_{obs}^2 = 0.05$ .

```
# add lognormal noise
  parms['sdlog.N'] <- 0.05
  N_obs$N_noisy <- rlnorm(nrow(N_obs), log(N_obs$N),parms['sdlog.N'])
#observations must be ordered for solver to work
N_obs <- N_obs[order(N_obs$time),]
#Plot true and noisy observations
plot(N_obs$time, N_obs$N, ylim=c(0, max(N_obs$N,N_obs$N_noisy)))
points(N_obs$time, N_obs$N_noisy, col="red")</pre>
```



## 4 Defining an observation model and parameters for inference

The appropriate log-likelihood for these data takes the form

$$\ell(\mathcal{Y}|\boldsymbol{\theta}) = \sum_{t} \ln \left( \frac{1}{\tilde{N}_{t} \sigma_{obs} \sqrt{2\pi}} \exp \left( -\frac{(\ln \tilde{N}_{t} - \ln(N_{t} + \varepsilon))^{2}}{2\sigma_{obs}^{2}} \right) \right)$$
(2)

where  $\tilde{N}_t$  are the observations, and  $N_t$  are the predictions of the DE model given the current MCMC sample of the parameters  $\boldsymbol{\theta}$ . Further,  $\varepsilon$  is a small correction needed, because the DE solution can equal zero (or less, depending on numerical precision) (L. R. Johnson, Pecquerie, and Nisbet 2013). We chose  $\varepsilon = 10^{-6}$ , which is on the same order as the numerical precision of the default solver (deSolve::ode) with {method = "lsoda"}.

This can be translated into an observation model function for deBInfer. The observation model function must have three named arguments data, sim.data, and samp, as these are used by the MCMC procedure to pass in the data (as a data.frame, i.e. indexed using the \$ operator and the column names of the input data), the current state of the Markov chain (as a named vector), and the associated DE model solution (as a matrix-like object of class deSolve, i.e. indexed using the [ ] operator and the declared names of the state variables). We can access these inputs to define the data likelihood.

The user specifies the observation model such that it returns the summed log-likelihoods of the data. In this example the observations are in the data frame column N\_noisy, and the corresponding predicted states are in the column N of the matrix-like objectsim.data

All parameters that are used in the DE model and the observation model need to be declared for the inference procedure using the debinfer\_par() function. The declaration describes the variable name, whether it is a DE or observation parameter and whether or not it is to be estimated. If the parameter is to be estimated, the user also needs to specify a prior distribution and a number of additional parameters for the MCMC procedure. debinfer currently supports priors from all probability distributions implemented in base R, as well as their truncated variants, as implemented in the truncdist package (Novomestky and Nadarajah 2012).

We declare the DE model parameter r, assign a prior  $r \sim \mathcal{N}(0,1)$  and a random walk sampler with a Normal kernel (samp.type="rw") and proposal variance of 0.005. Similarly, we declare  $K \sim \ln \mathcal{N}(1,1)$  and  $\ln(\sigma_{obs}^2) \sim \mathcal{N}(0,1)$ . Note that we are using the asymmetric uniform proposal distribution  $\mathcal{U}(\frac{a}{b}\theta^{(k)}, \frac{b}{a}\theta^{(k)})$  for the variance parameter (samp.type="rw-unif"), as this ensures strictly positive proposals.

Lastly, we provide an initial value  $N_0 = 0.1$  for the DE:

```
N <- debinfer_par(name = "N", var.type = "init", fixed = TRUE, value = 0.1)
```

The declared parameters are then collated using the setup\_debinfer function. Note that for models with more than one state variable, the initial values must be entered in the same order, as they are specified in the DE model function, as the solver matches these values by position, rather than by name. More details can be found in ?deSolve::ode. The remaining parameters can be entered in any order.

```
mcmc.pars <- setup_debinfer(r, K, sdlog.N, N)</pre>
```

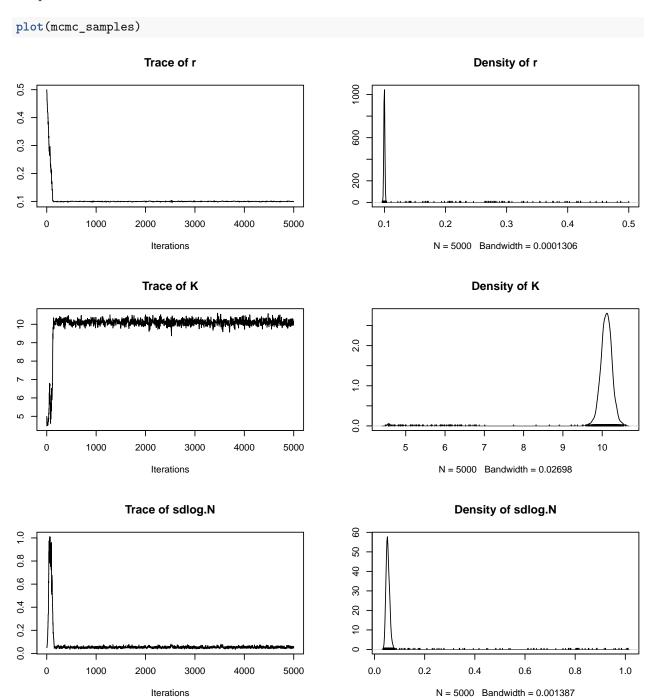
#### 5 Conduct inference

Finally we use deBInfer to estimate the parameters of the original model. de\_mcmc is the workhorse of the package and runs the MCMC estimation. The progress of the MCMC procedure can be monitored using the cnt, plot and verbose options: Every cnt iterations the function will print out information about the current state, and, if plot=TRUE, traceplots of the chains will be plotted. Setting verbose=TRUE will print additional information. Note that frequent plotting will substantially slow down the MCMC sampler, and should be used only on short runs when tuning the sampler.

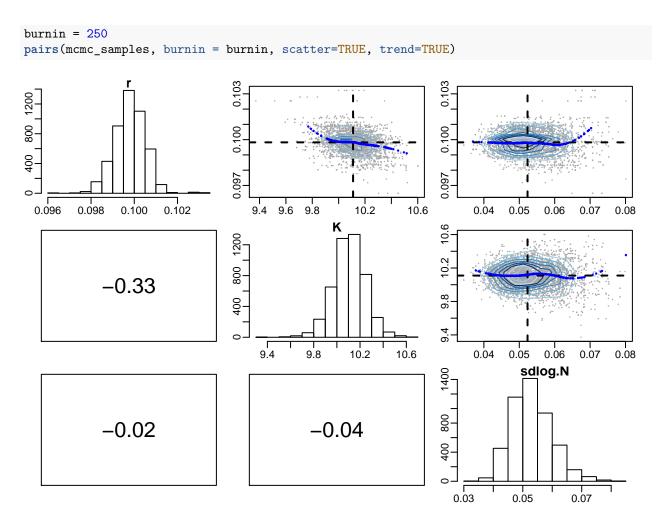
```
# do inference with deBInfer
# MCMC iterations
iter = 5000
# inference call
mcmc_samples <- de_mcmc(N = iter, data=N_obs, de.model=logistic_model,</pre>
```

```
obs.model=logistic_obs_model, all.params=mcmc.pars,
Tmax = max(N_obs$time), data.times=N_obs$time, cnt=500,
plot=FALSE, solver="ode")
```

We plot and summarize the MCMC chains

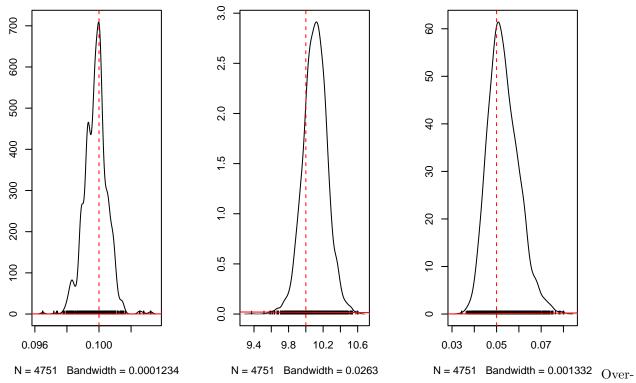


From the traceplot we can see that the burnin period is about 250 samples. We can remove the burnin and have a look at parameter correlations using pairs.debinfer\_result.



And we can look at the overlap between the posterior and prior densities using post\_prior\_densplot.

```
par(mfrow=c(1,3))
post_prior_densplot(mcmc_samples, burnin = burnin, param="r")
abline(v=0.1, col="red", lty=2)
post_prior_densplot(mcmc_samples, burnin = burnin, param="K")
abline(v=10, col="red", lty=2)
post_prior_densplot(mcmc_samples, burnin = burnin, param="sdlog.N")
abline(v=0.05, col="red", lty=2)
```



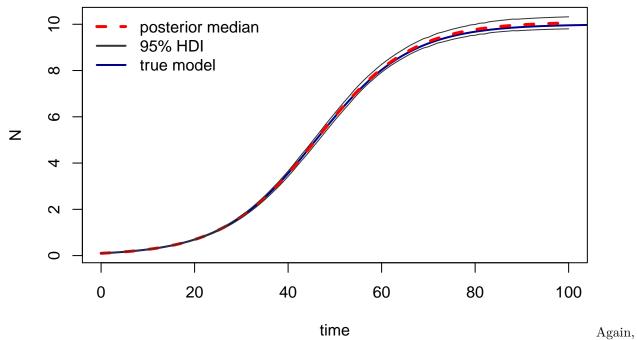
lay the true underlying parameter values as vertical dashed lines shows that our estimation is doing a pretty good job.

### 6 Posterior simulations

We then simulate DE model trajectories from the posterior and calculate the 95% highest posterior density interval for the deterministic part of the model.

```
post traj <- post sim(mcmc samples, n=500, times=0:100, burnin=burnin, output = 'all', prob = 0.95)
```

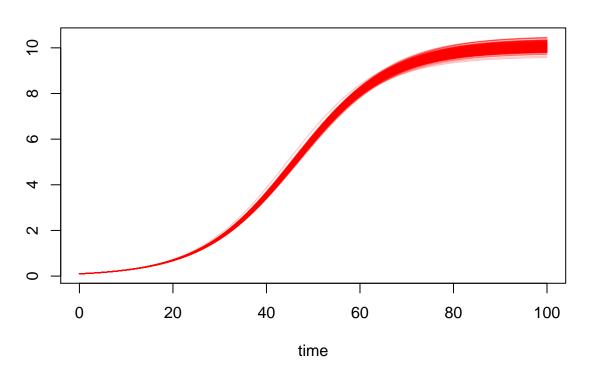
We can visualise the median posterior trajectory and the associated highest posterior density interval using plot.type="medianHDI". The panel.first option can be used to add the trajectory of the true model, which is stored in out.



this confirms that the inference procedure does indeed recover the true model.

Lastly, we can plot an ensemble of posterior trajectories using plot.type="ensemble"

# N



## References

Boersch-Supan, Philipp, and Leah Johnson. 2016. "deBinfer: Bayesian Inference for Dynamical Models of Biological Systems." ArXiv~[Q-Bio.QM]~1605.00021. https://arxiv.org/abs/1605.00021.

Johnson, Leah R, Laure Pecquerie, and Roger M Nisbet. 2013. "Bayesian Inference for Bioenergetic Models." *Ecology* 94 (4). Eco Soc America: 882–94.

Novomestky, Frederick, and Saralees Nadarajah. 2012. Truncdist: Truncated Random Variables. http://CRAN.R-project.org/package=truncdist.

Soetaert, KER, Thomas Petzoldt, and R Woodrow Setzer. 2010. "Solving Differential Equations in R: Package DeSolve." Journal of Statistical Software 33 (9): 1-25.

Wickham, Hadley, and Winston Chang. 2016. Devtools: Tools to Make Developing R Packages Easier. http://CRAN.R-project.org/package=devtools.