# Simulation and Parameter Estimation for Biomass Crops

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**Abstract**

Demonstration of the use of the `r2bugs.distributions` function.

## 1 Introduction

A simple example follows, using a normal distribution, $N(\mu = 10, \sigma = 2)$ we will compare a random sample from the R and BUGS implementation of the distribution.

```
> r.distn <- data.frame(distn = "norm", parama = 10, paramb = 2)
> Y.R <- do.call(paste("r", r.distn$distn, sep = ""),
+                list(n.iter/4, r.distn$parama, r.distn$paramb))
> bugs.dist <- r2bugs.distributions(r.distn)
> Y.BUGS <- r2bugs::bugs.rdist(bugs.dist, n.iter = n.iter)

Compiling model graph
   Resolving undeclared variables
   Allocating nodes
   Graph Size: 4

Initializing model
```

Simple tests show that the mean and variance of the two samples are similar. Indeed, this is done for five parameterizations of each of seven distributions (Normal, log-Normal, Weibull, Gamma, $\chi^2$, Binomial, and Negative-Binomial in the tests that are written for the `r2bugs` package. These tests and can be found in the file `/inst/tests/test.r2bugs.distributions.R`.

Here, we can visually compare the similarity of the density of 25000 samples from the same distribution implemented in R (black) and then JAGS (red).

**density.default(x = Y.R)**

N = 25000   Bandwidth = 0.2372