Dugong – HW 9

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Due March 29, 2022

These data concern growth of dugongs (sometimes called sea cows, an aquatic mammal found primarily in the Indo-West Pacific). The data file is called 'dugong.dat' and contains two columns, the age of the animal in years, and the length of the animal in meters for 27 individuals. If you plot the data, you will see that growth is faster for young animals and then seems to stop in older animals. This type of growth is called nonlinear growth, and the simplest curve to describe such growth is:

$$y_i = a - bg^{x_i}, \tag{1}$$

where y_i represents the length of the animal and x_i represents the age of the animal. As you can see, there are three parameters to estimate, a, b, and g. 'a' represents the asymptote or value at which growth stops, 'b' is constrained to be positive, and 'g' is constrained to be between 0 and 1.

You have two tasks:

1. Determine parameter estimates for the growth curve.
2. Compare the results from JAGS to those from Stan.

After making sure chains have converged appropriately, you will compare the results by examining both equal tail and HPD interval estimates of the parameters (and functions thereof) that matter.

You should hand in a no more than a one page summary of your results that should include at least one plot. Make sure to address all appropriate model diagnostics and convergence, but note that you might not be able to fit code output in your one page summary. All code should come in as an appendix to your one page summary.

Summary

I first ran the model in JAGS, and obtained the following results:

```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 27
##    Unobserved stochastic nodes: 4
##    Total graph size: 128
##
## Initializing model
```

```
## Inference for Bugs model at "model1.txt", fit using jags,
##  4 chains, each with 50000 iterations (first 2000 discarded)
```

```
##  n.sims = 192000 iterations saved
##          mu.vect sd.vect    2.5%     25%     50%     75%   97.5%  Rhat n.eff
## a          2.658   0.077   2.529   2.606   2.651   2.701   2.831 1.001 36000
## b          0.982   0.080   0.829   0.929   0.980   1.032   1.146 1.001 31000
## g          0.863   0.034   0.786   0.845   0.867   0.886   0.919 1.001 11000
## s2error    0.011   0.004   0.006   0.008   0.010   0.013   0.020 1.001 75000
## deviance -48.609   3.474 -52.935 -51.161 -49.405 -46.897 -39.792 1.001 30000
##
## For each parameter, n.eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
##
## DIC info (using the rule, pD = var(deviance)/2)
## pD = 6.0 and DIC = -42.6
## DIC is an estimate of expected predictive error (lower deviance is better).
```

```
##                  lower        upper
## a          2.518030089   2.81303670
## b          0.823503674   1.13881610
## deviance -53.417501091 -41.79498584
## g          0.795065576   0.92426316
## s2error    0.005212471   0.01835893
## attr(,"Probability")
## [1] 0.95
```

```
##     2.5%    97.5%
## 2.529287 2.831464
```

```
##      2.5%     97.5%
## 0.8294786 1.1459334
```

```
##      2.5%     97.5%
## 0.7864701 0.9186779
```

```
##        2.5%       97.5%
## 0.005984892 0.020167184
```

It seems like there is a high level of autocorrelation for the JAGS output, so using a different sampler would help solve the issue.

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## Running MCMC with 4 parallel chains...
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## Chain 1 finished in 5.9 seconds.
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## Chain 2 finished in 6.4 seconds.
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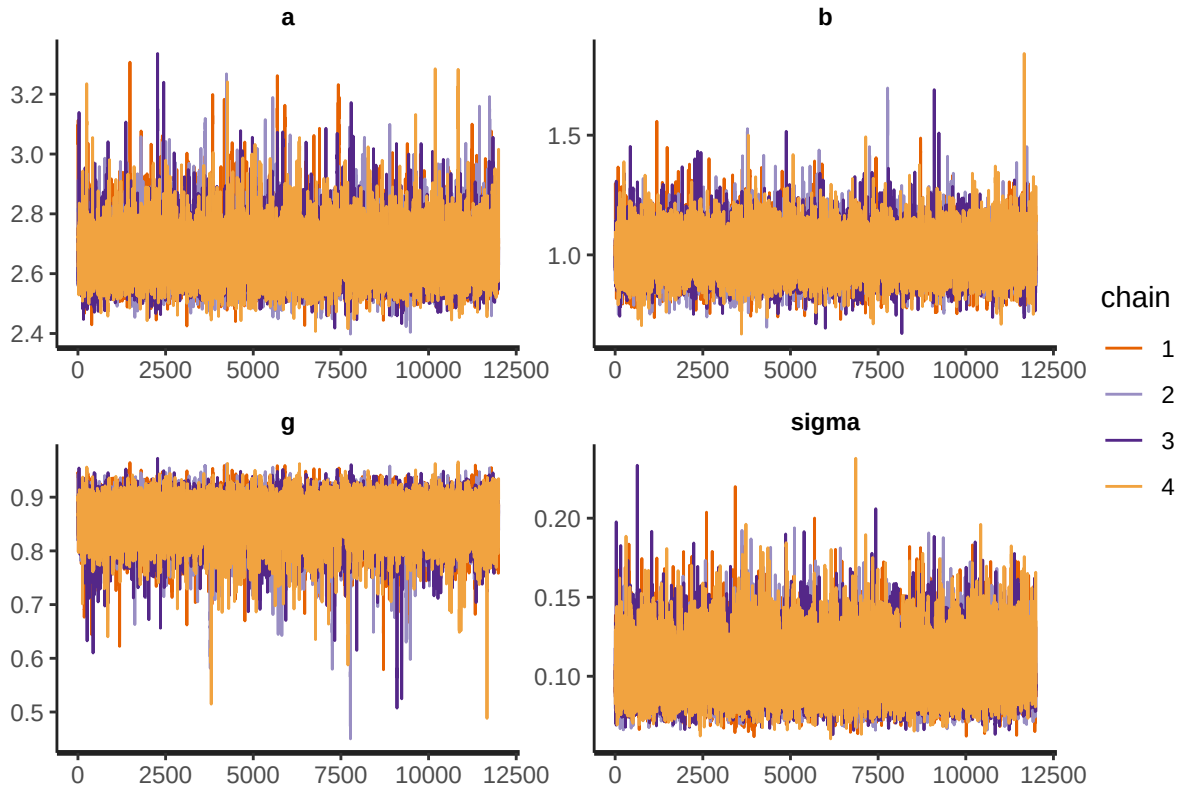
## Chain 3 Iteration: 14000 / 14000 [100%]  (Sampling)
## Chain 3 finished in 6.6 seconds.
##
## All 4 chains finished successfully.
## Mean chain execution time: 6.1 seconds.
## Total execution time: 7.3 seconds.

## # A tibble: 5 x 10
##   variable   mean median     sd    mad      q5    q95  rhat ess_bulk ess_tail
##   <chr>     <dbl>  <dbl>  <dbl>  <dbl>   <dbl>  <dbl> <dbl>    <dbl>    <dbl>
## 1 lp__     40.3   40.7   1.59   1.36   37.2    42.2    1.00   13987.   17560.
## 2 a         2.67   2.66  0.0841 0.0741  2.55    2.82   1.00   13759.   11269.
## 3 b         1.01   1.00  0.0842 0.0781  0.877   1.15   1.00   18602.   18475.
## 4 g         0.863  0.867 0.0368 0.0319  0.800   0.914  1.00   14404.   13412.
## 5 sigma     0.104  0.102 0.0168 0.0156  0.0804  0.135  1.00   21901.   22257.
```

Using the NUTS sampler provided with Stan, we have the following traceplots:



It appears to be doing pretty well. Lets compare the variables:

```
## # A tibble: 4 x 3
##   variable `2.5%` `97.5%`
##   <chr>     <dbl>   <dbl>
## 1 a         2.53    2.86
## 2 b         0.853   1.18
## 3 g         0.780   0.922
## 4 sigma     0.0772  0.142
```

```
##         lower  upper
## sigma 0.07501 0.1384
## a     2.51200 2.8320
## b     0.84360 1.1700
## g     0.78890 0.9267
## attr(,"Probability")
## [1] 0.95
```

Appendix

```
knitr::opts_chunk$set(echo = FALSE, fig.align = 'center', message = FALSE, eval = FALSE)
library(rstan)
library(R2jags)
```

```
library(cmdstanr)
library(loo)

dugong <- read.table("dugong.dat", header=TRUE)
dugong

plot(dugong, ylim = c(0,2.8))
model1 <- "
model {
for (i in 1:27) {
  y[i] ~ dnorm(mu[i], 1/s2error)
  mu[i] = a - b*g^(x[i])
}
  a ~ dnorm(3, 0.001)
  b ~ dgamma(6, 4)
  g ~ dbeta(5.5, 1.5)
  s2error ~ dgamma(1.1, 0.05)
}
"

writeLines(model1, 'model1.txt')

y <- dugong$length
x <- dugong$age

data.jags <- c('y', 'x')
parms <- c('a', 'b', 'g', 's2error')

dugong.sim <- jags(model.file = 'model1.txt', data = data.jags, parameters.to.save = parms,
                   n.iter = 50000, n.burnin = 2000, n.chains = 4, n.thin = 1, inits = NULL)

dugong.sim
sims <- as.mcmc(dugong.sim)
gelman.diag(sims)
chains <- as.matrix(sims)
sims <- as.mcmc(chains)
raftery.diag(sims)
effectiveSize(sims)
autocorr.diag(sims)
geweke.diag(sims)
HPDinterval(sims, prob = 0.95)
library(dplyr)
quantile(sims[,1], c(0.025, 0.975))
quantile(sims[,2], c(0.025, 0.975))
quantile(sims[,4], c(0.025, 0.975))
quantile(sims[,5], c(0.025, 0.975))
mod <- cmdstan_model(stan_file='hw9.stan')

data_list <- list(x = x,y = y, N = length(dugong$age))
fit <- mod$sample(data_list,
                  chains = 4,
                  parallel_chains = 4,
                  sig_figs = 4,
```

```
                  iter_sampling = 12000,
                  iter_warmup = 2000)

fit$summary(variables = c('lp__','a', 'b', 'g', 'sigma'))
rstan::traceplot(read_stan_csv(fit$output_files()), pars = c('a', 'b', 'g', 'sigma'))
fit$summary(variables = c('a', 'b', 'g', 'sigma'), ~quantile(., probs = c(0.025, 0.975)))

stanfit <- rstan::read_stan_csv(fit$output_files())
samps <- extract(stanfit)
chains <- cbind(samps[[1]], samps[[2]], samps[[3]], samps[[4]])
colnames(chains) <- names(samps[1:4])
sims <- as.mcmc(chains)
HPDinterval(sims, prob = 0.95)
```