Bayesian statistics with R
6. Bayesian analyses in R with the Jags software

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Bayes in practice

Software implementation (R compatible)

Oldies but goodies:

- WinBUGS, OpenBUGS: Where it all began.
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The new kids on the block:

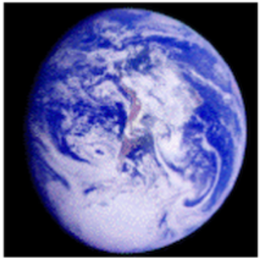
- Nimble: What I'm going for these days.
- Stan: Entirely different algorithmic approach.
- Greta: Dunno anything about it.

Introduction to JAGS (Just Another Gibbs Sampler)

Martyn Plummer

Real example

Impact of climatic conditions on white stork breeding success



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- We need to specify priors for parameters.

Read in the data

```
nbchicks <- c(151,105,73,107,113,87,77,108,118,122,112,120,122,89,69,71,
              53,41,53,31,35,14,18)

nbpairs <- c(173,164,103,113,122,112,98,121,132,136,133,137,145,117,90,80,
             67,54,58,39,42,23,23)

temp <- c(15.1,13.3,15.3,13.3,14.6,15.6,13.1,13.1,15.0,11.7,15.3,14.4,14.4
          12.7,11.7,11.9,15.9,13.4,14.0,13.9,12.9,15.1,13.0)

rain <- c(67,52,88,61,32,36,72,43,92,32,86,28,57,55,66,26,28,96,48,90,86,
          78,87)

datax <- list(N = 23, nbchicks = nbchicks, nbpairs = nbpairs,
              temp = (temp - mean(temp))/sd(temp)
```

Write down the model

$$\begin{aligned}
\text{nbchicks}_i &\sim \text{Binomial}(\text{nbpairs}_i, p_i) && \text{[likelihood]}\\
\text{logit}(p_i) &= a + b_{temp}\,\text{temp}_i + b_{rain}\,\text{rain}_i && \text{[linear model]}\\
a &\sim \text{Normal}(0, 1000) && \text{[prior for } a\text{]}\\
b_{temp} &\sim \text{Normal}(0, 1000) && \text{[prior for } b_{temp}\text{]}\\
b_{rain} &\sim \text{Normal}(0, 1000) && \text{[prior for } b_{rain}\text{]}
\end{aligned}$$

Build the model

```
{
# Likelihood
    for( i in 1 : N){
        nbchicks[i] ~ dbin(p[i],nbpairs[i])
        logit(p[i]) <- a + b.temp * temp[i] + b.rain * rain[i]
        }
# ...
```

Specify priors

```
# Priors
a ~ dnorm(0,0.001)
b.temp ~ dnorm(0,0.001)
b.rain ~ dnorm(0,0.001)
}
```

Warning: Jags uses precision for Normal distributions (1 / variance)

You need to write everything in a file

```
model <-
paste("
model
{
    for( i in 1 : N)
        {
        nbchicks[i] ~ dbin(p[i],nbpairs[i])
        logit(p[i]) <- a + b.temp * temp[i] + b.rain * rain[i]
        }
a ~ dnorm(0,0.001)
b.temp ~ dnorm(0,0.001)
b.rain ~ dnorm(0,0.001)
    }
")
```

Alternatively, you may write a R function

```
logistic <- function() {
    for( i in 1 : N)
        {
        nbchicks[i] ~ dbin(p[i],nbpairs[i])
        logit(p[i]) <- a + b.temp * temp[i] + b.rain * rain[i]
        }

# priors for regression parameters
a ~ dnorm(0,0.001)
b.temp ~ dnorm(0,0.001)
b.rain ~ dnorm(0,0.001)
    }
```

Let us specify a few additional things

```
# list of lists of initial values (one for each MCMC chain)
init1 <- list(a = -0.5, b.temp = -0.5, b.rain = -0.5)
init2 <- list(a = 0.5, b.temp = 0.5, b.rain = 0.5)
inits <- list(init1,init2)

# specify parameters that need to be estimated
parameters <- c("a","b.temp","b.rain")

# specify nb iterations for burn-in and final inference
nb.burnin <- 1000
nb.iterations <- 2000
```

Run Jags

```r
# load R2jags
library(R2jags)
# run Jags
storks <- jags(data  = datax,
               inits = inits,
               parameters.to.save = parameters,
               model.file = "code/logistic.txt",
               # model.file = logistic, # if a function was written
               n.chains = 2,
               n.iter = nb.iterations,
               n.burnin = nb.burnin)
storks
```

Inspect parameter estimates

```
#> Compiling model graph
#>    Resolving undeclared variables
#>    Allocating nodes
#> Graph information:
#>    Observed stochastic nodes: 23
#>    Unobserved stochastic nodes: 3
#>    Total graph size: 181
#>
#> Initializing model
#> Inference for Bugs model at "code/logistic.txt", fit using jags,
#>  2 chains, each with 2000 iterations (first 1000 discarded)
#>  n.sims = 2000 iterations saved
#>          mu.vect sd.vect    2.5%     25%     50%     75%   97.5%  Rhat n.eff
#> a          1.557   0.086   1.438   1.527   1.563   1.597   1.668 1.254  2000
#> b.rain    -0.152   0.063  -0.264  -0.194  -0.154  -0.110  -0.026 1.005   400
#> b.temp     0.031   0.061  -0.083  -0.011   0.033   0.074   0.143 1.027    67
#> deviance 206.476  32.889 201.803 202.790 203.847 205.437 212.562 1.076  2000
```

Your turn

Practical

- Run the stork analysis yourself.
- Does it seem like there is an effect of rainfall or temperature on breeding success?

Assess convergence

Reminder – MCMC Algorithm

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- For the MCMC algorithm, the posterior distribution is only needed to be known up to proportionality.
- Once the stationary distribution is reached we can regard the realisations of the chain as a (dependent) sample from the posterior distribution (and obtain Monte Carlo estimates).
- We consider some important implementation issues.

MCMC – Proposal Distribution

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- This typically involves
    - specifying a given distribution family (e.g. normal, uniform), and then,
    - setting the parameters of the given distribution.
- Although the exact distribution specified is essentially arbitrary – it will have a significant effect on the performance of the MCMC algorithm.

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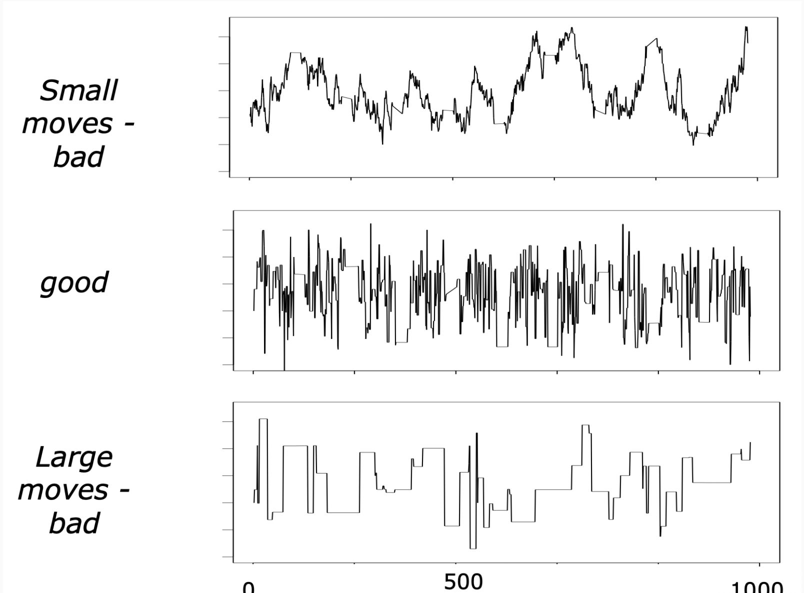
- In order to balance the size of the proposed moves with the chance of accepting them the proposal variance is often tuned to obtain a mean acceptance probability of $20 - 40\%$.
- Automatic in Jags – ouf!
- The movement around the parameter space is often referred to as **mixing**.

Good/Bad Traces



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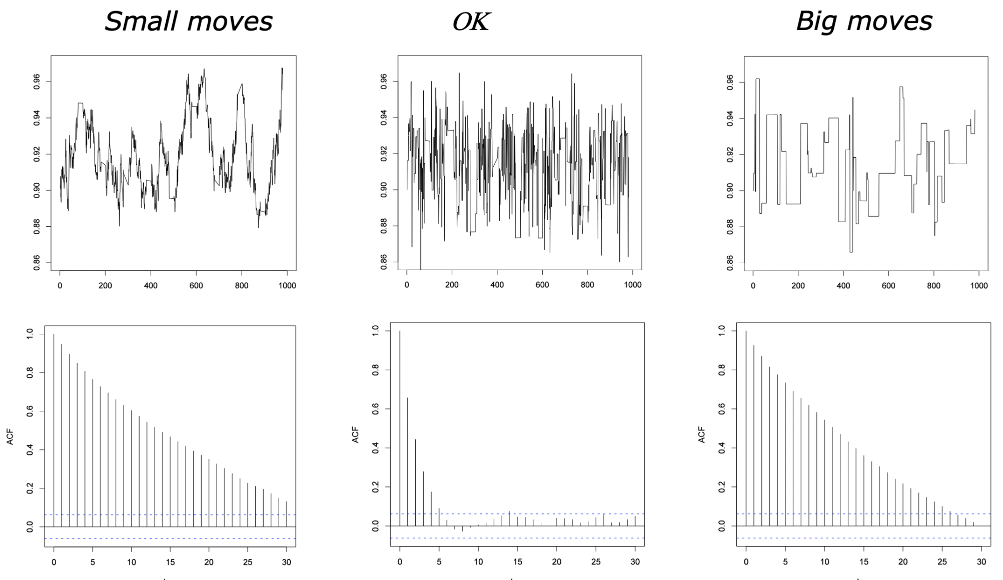
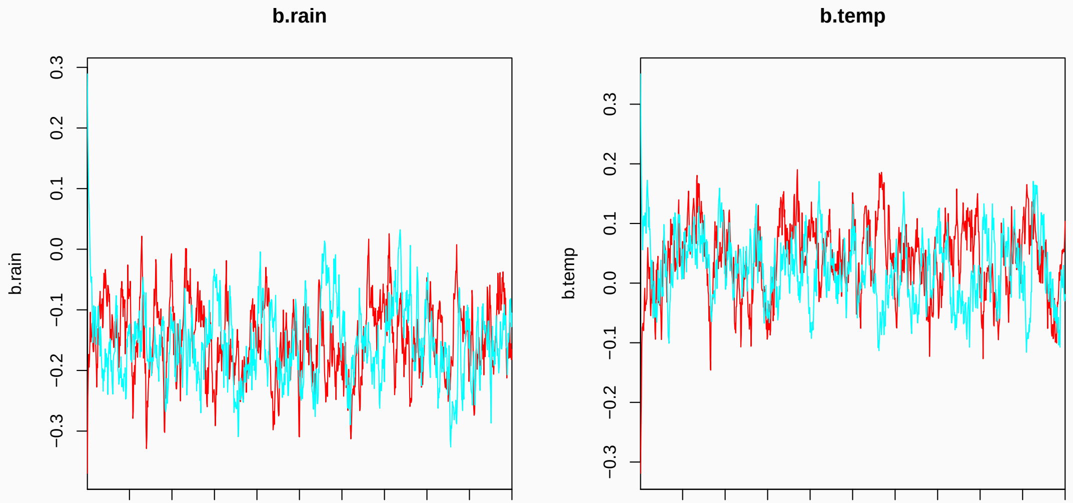
- Autocorrelation function (ACF) plots are a convenient way of displaying the strength of autocorrelation in the given sample values.
- ACF plots provide the autocorrelation between successively sampled values separated by k iterations, referred to as lag, (i.e. $\text{cor}(\theta_t, \theta_{t+k})$) for increasing values of k.

ACFs



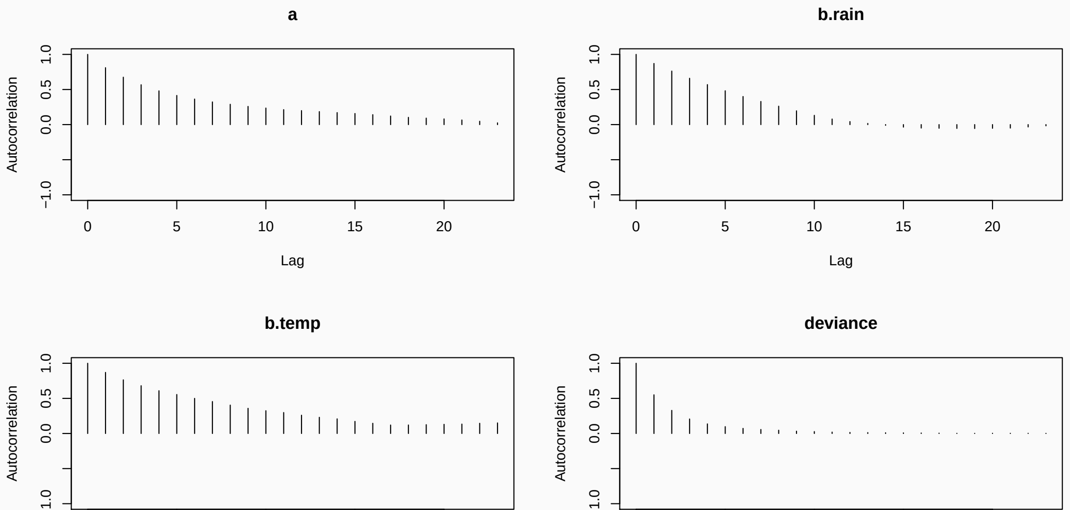
Traceplots for the storks

```
traceplot(storks,mfrow = c(1, 2), varname = c('b.rain','b.temp'), ask = FA
```



Autocorrelation for the storks

```
autocorr.plot(as.mcmc(storks),ask = FALSE)
```



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- Once there, explore efficiently: The post-convergence sample size required for suitable numerical summaries.

Convergence assessment

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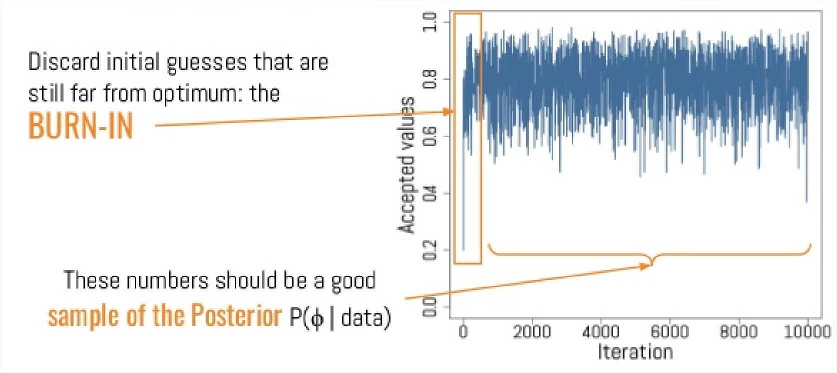
- In practice, we must discard observations from the start of the chain and just use observations from the chain once it has converged.
- The initial observations that we discard are referred to as the **burn-in**.
- The simplest method to determine the length of the burn-in period is to look at trace plots.

Burn-in (if simulations cheap, be conservative)



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  - `n.eff` is less than the number of MCMC iterations.
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  - `n.eff` is less than the number of MCMC iterations.
  - Check the `n.eff` of every parameter of interest.
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- We need n.eff $\geq$ 100 independent steps.

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- Values near 1 indicates likely convergence, a value of ≤ 1.1 is considered acceptable.
- Necessary condition, not sufficient; In other words, these diagnostics cannot tell you that you have converged for sure, only that you have not.

n.eff and $\hat{R}$ for the storks

```
storks
#> Inference for Bugs model at "code/logistic.txt", fit using jags,
#>  2 chains, each with 2000 iterations (first 1000 discarded)
#>  n.sims = 2000 iterations saved
#>          mu.vect sd.vect   2.5%     25%     50%     75%   97.5%  Rhat
#> a          1.557   0.086   1.438   1.527   1.563   1.597   1.668 1.254
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#> deviance 206.476  32.889 201.803 202.790 203.847 205.437 212.562 1.076
#>
#> For each parameter, n.eff is a crude measure of effective sample size,
#> and Rhat is the potential scale reduction factor (at convergence, Rhat=
#>
#> DIC info (using the rule, pD = var(deviance)/2)
```

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- Run multiple chains from arbitrary starting places (initial values).
- Assume convergence when all chains reach same regime.
- Discard initial burn-in phase.
- Check autocorrelation, effective sample size and $\hat{R}$.

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  - Standardize covariates.
  - Non-centering: $\alpha \sim N(0, \sigma)$ becomes $\alpha = z\sigma$ with $z \sim N(0, 1)$.

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- Something wrong with your model?
  - Start with a simpler model (remove complexities).
  - Use simulations.
- Change your sampler. Upgrade to Nimble or Stan.

MCMC makes you queens and kings of the stats world

Get all values sampled from posteriors

```
res <- as.mcmc(storks) # convert outputs in a list
res <- rbind(res[[1]],res[[2]]) # put two MCMC lists on top of each other
head(res)
#>                 a     b.rain      b.temp  deviance
#> [1,] 0.001453882 -0.3696904 -0.31896604 1330.1117
#> [2,] 0.395127701 -0.2449326 -0.24991008  799.9864
#> [3,] 0.650288794 -0.2076239 -0.19215583  550.0958
#> [4,] 0.823172695 -0.1735001 -0.10789538  414.1633
#> [5,] 0.962482487 -0.1944938 -0.07475411  336.1398
#> [6,] 1.057606257 -0.1803931 -0.07201281  295.7432
tail(res)
#>                 a      b.rain       b.temp deviance
#> [1995,] 1.610581 -0.08353296  0.005973991 203.8253
#> [1996,] 1.604299 -0.08593543  0.029785709 203.6425
```

Compute a posteriori $\Pr(\text{rain} < 0)$

```r
# probability that the effect of rainfall is negative
mean(res[,'b.rain'] < 0)
#> [1] 0.988
```

Compute a posteriori $\Pr(\text{temp} < 0)$

```r
# probability that the effect of temperature is negative
mean(res[,'b.temp'] < 0)
#> [1] 0.3065
```

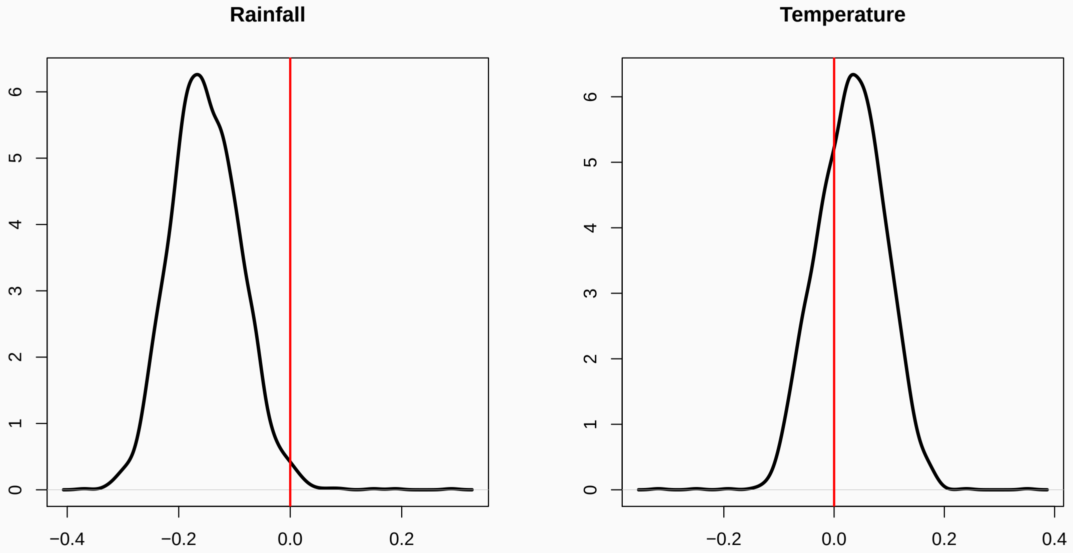
Get credible interval for the rain effect

```
quantile(res[,'b.rain'],c(0.025,0.975))
#>        2.5%       97.5%
#> -0.26365655 -0.02618803
```

Get credible interval for the temperature effect

```
quantile(res[,'b.temp'],c(0.025,0.975))
#>       2.5%      97.5%
#> -0.0829715  0.1432316
```

Graphical summaries



Your turn

A stupid question

- Get the posterior distribution of $b_{rain}^2 + \cos(b_{temp})$

Solution

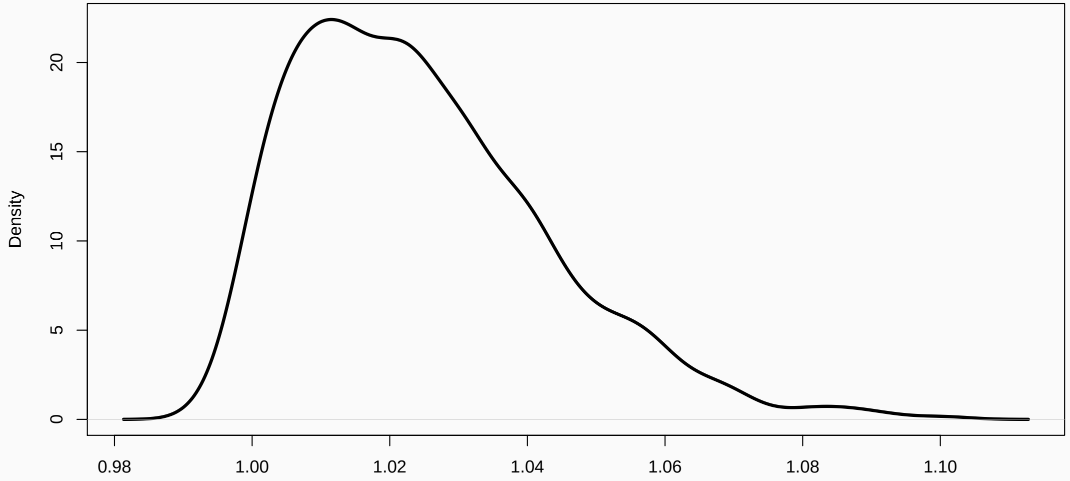
R code

- Evaluate the function for each MCMC iteration

```r
stupid_pd <- res[,'b.rain']^2 + cos(res[,'b.temp'])
head(stupid_pd)
#> [1] 1.086231 1.028927 1.024702 1.024287 1.035035 1.029950
```

- Plot the distribution

```r
plot(density(stupid_pd), xlab = '', main = '', lwd = 3)
```


Density