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

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November-December 2024

Bayes in practice

Software implementation (R friendly)

Oldies but goodies:

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- Jags: What we will use in this course.

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If you're not into coding:

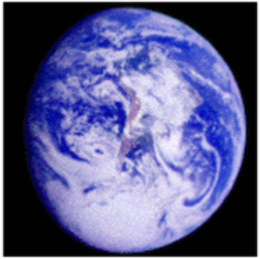
- brms: Bayesian regression models with Stan.
- MCMCglmm: Generalised Linear Mixed Models.
- Check out the CRAN Task View: Bayesian Inference for more.

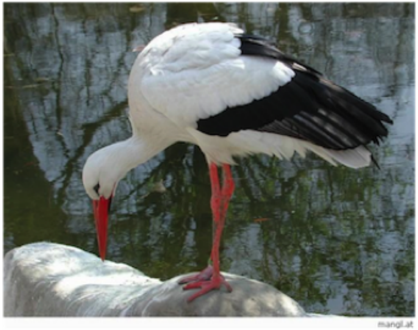
Introduction to JAGS (Just Another Gibbs Sampler)

Martyn Plummer

Real example

Impact of climatic conditions on white stork breeding success





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- We have collected data.
- We need to build a model - write down the likelihood.
- 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)
```

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

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

```r
# 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 <- 10000
nb.iterations <- 20000 # beware: nb.iterations includes nb.burnin!
```

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 20000 iterations (first 10000 discarded)
#>  n.sims = 20000 iterations saved. Running time = 0.397 secs
#>          mu.vect sd.vect    2.5%     25%     50%     75%   97.5%  Rhat n.eff
#> a          1.556   0.056   1.444   1.517   1.555   1.594   1.666 1.001  4800
#> b.rain    -0.159   0.062  -0.280  -0.201  -0.158  -0.116  -0.039 1.003   880
#> b.temp     0.030   0.059  -0.084  -0.011   0.031   0.071   0.145 1.004   470
#> deviance 204.620   2.445 201.797 202.829 203.996 205.758 210.989 1.001  6400
```

Your turn: Practical 5

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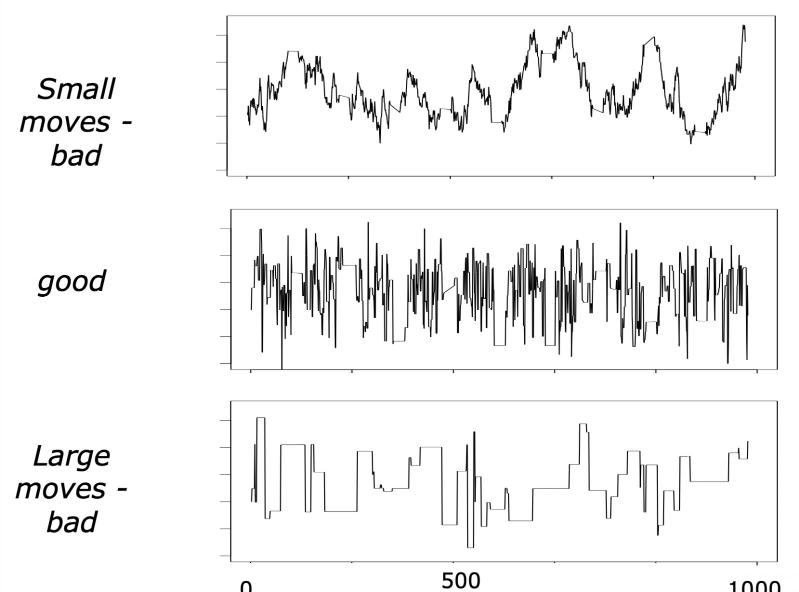
- In order to balance the size of the proposed moves with the chance of accepting them the proposal variance is often tuned to obtain a mean acceptance probability of $20 - 40\%$.
- Automatic in Jags – ouf!
- The movement around the parameter space is often referred to as **mixing**.

Good/Bad Traces



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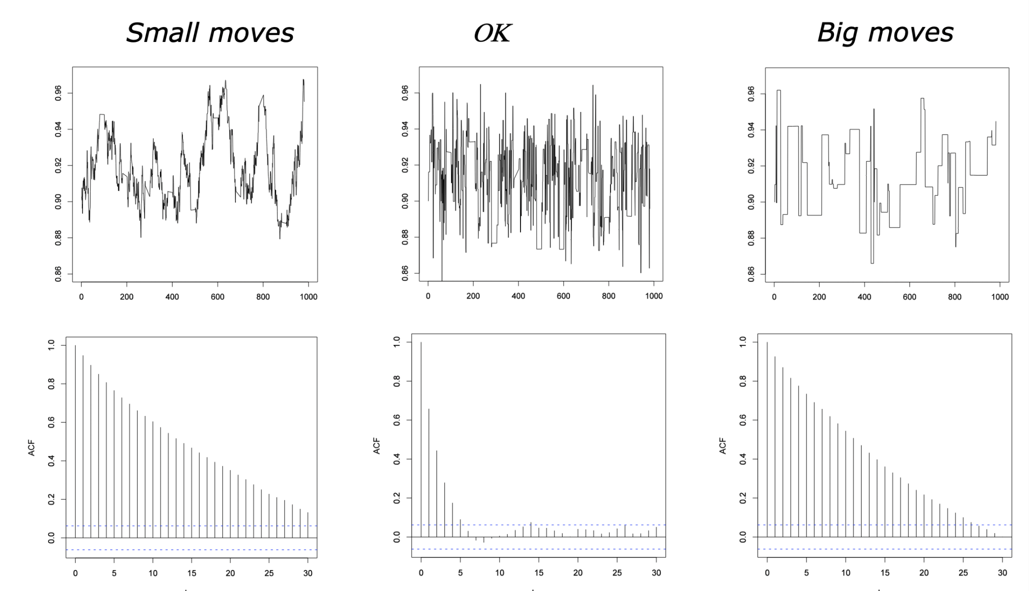
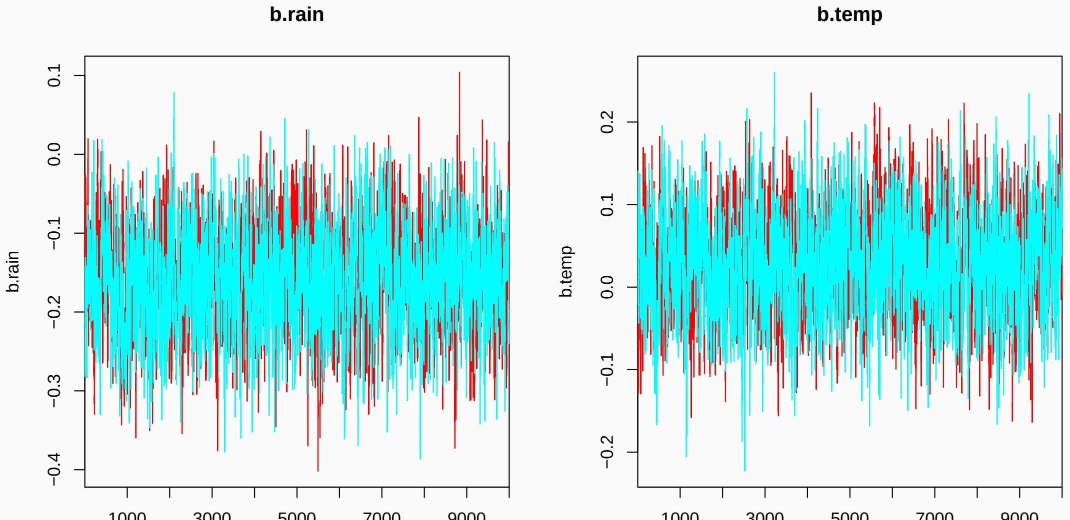
- Strongly correlated observations require large sample sizes and therefore longer simulations.
- Autocorrelation function (ACF) plots are a convenient way of displaying the strength of autocorrelation in the given sample values.
- ACF plots provide the autocorrelation between successively sampled values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

ACFs



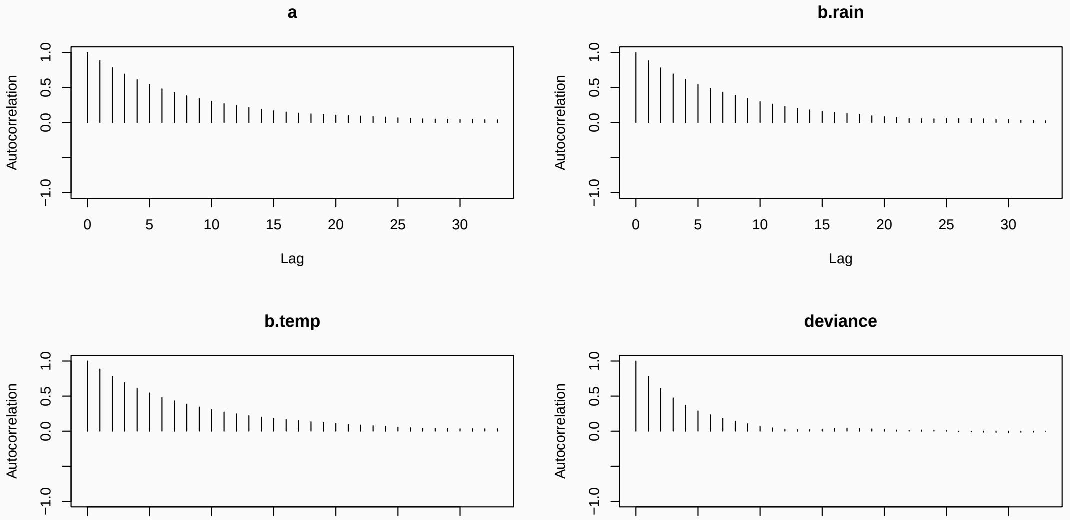
Traceplots for the storks

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



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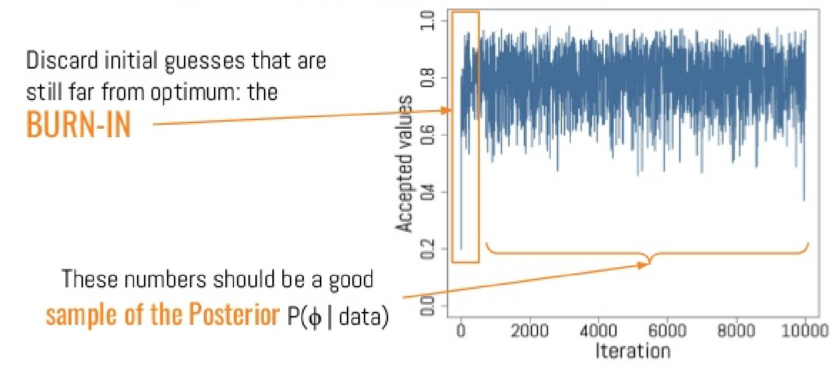
- In practice, we must discard observations from the start of the chain and just use observations from the chain once it has converged.
- The initial observations that we discard are referred to as the **burn-in**.
- The simplest method to determine the length of the burn-in period is to look at trace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

Burn-in (if simulations cheap, be conservative)



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- 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 20000 iterations (first 10000 discarded)
#>  n.sims = 20000 iterations saved. Running time = 0.397 secs
#>          mu.vect sd.vect    2.5%     25%     50%     75%   97.5%  Rhat n.eff
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#>
#> 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: pV = var(deviance)/2)
#> pV = 3.0 and DIC = 207.6
#> DIC is an estimate of expected predictive error (lower deviance is better).
```

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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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- 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

```r
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,] 1.592695 -0.1536290 -0.08196748 205.7059
#> [2,] 1.565114 -0.1430165 -0.07531474 204.8535
#> [3,] 1.562266 -0.1507711 -0.04574838 203.3078
#> [4,] 1.568856 -0.1717589 -0.01386842 202.4108
#> [5,] 1.579275 -0.1555799  0.04397199 201.8867
#> [6,] 1.619766 -0.1632612  0.02921485 203.0722
```

```r
tail(res)
#>                   a     b.rain     b.temp deviance
#> [19995,] 1.537181 -0.2060164 0.14337311 205.4198
#> [19996,] 1.531171 -0.2032037 0.13371735 204.8634
#> [19997,] 1.516007 -0.2136806 0.12462898 204.7411
#> [19998,] 1.555380 -0.1974718 0.10503041 203.3408
#> [19999,] 1.549064 -0.1977094 0.10357682 203.2665
#> [20000,] 1.520648 -0.2096805 0.07060464 202.7861
```

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

```r
# probability that the effect of rainfall is negative
mean(res[,'b.rain'] < 0)
#> [1] 0.9963
```

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

```r
# probability that the effect of temperature is negative
mean(res[,'b.temp'] < 0)
#> [1] 0.3109
```

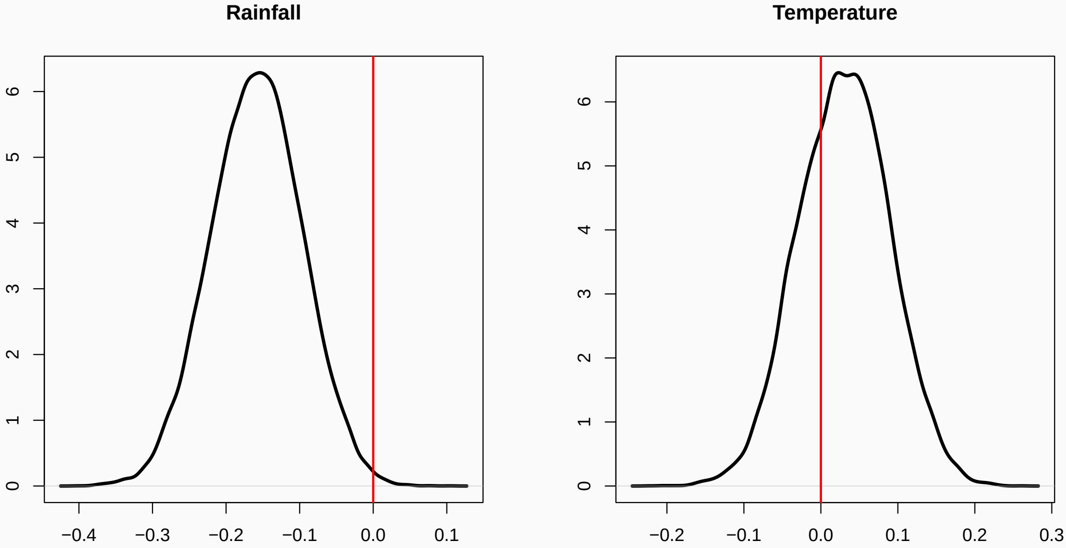
Get credible interval for the rain effect

```r
quantile(res[,'b.rain'],c(0.025,0.975))
#>          2.5%        97.5%
#> -0.28026967 -0.03873445
```

Get credible interval for the temperature effect

```
quantile(res[,'b.temp'],c(0.025,0.975))
#>        2.5%       97.5%
#> -0.08415379  0.14466530
```

Graphical summaries



Your turn: Practical 6