Bayesian statistics for ecology

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.
- Jags: What we will use in this course.

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The new kids on the block:

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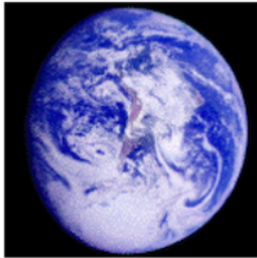- Greta: Dunno anything about it.

Introduction to JAGS (Just Another Gibbs Sampler)

Martyn Plummer

Impact of climatic conditions on white stork breeding success

Let's do a logistic regression on some White stork data

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- We need to specify priors for parameters.

Read in the data

```r
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)
```

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Write down the model

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

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

```r
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 <- 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           1.540   0.086   1.422   1.506   1.546   1.582   1.653 1.037  1000
#> b.rain     -0.154   0.067  -0.273  -0.198  -0.157  -0.116  -0.010 1.003   550
#> b.temp      0.023   0.056  -0.084  -0.015   0.023   0.060   0.125 1.015   110
#> deviance  206.640  34.906 201.791 202.810 203.887 205.507 212.071 1.073  2000
```

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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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- 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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- The movement around the parameter space is often referred to as **mixing**.

Good/Bad Traces

*Small moves - bad*
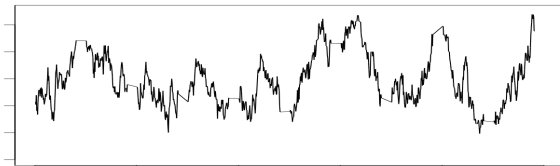
good
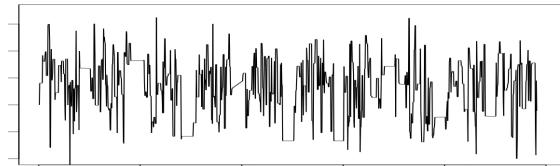
Large moves - bad
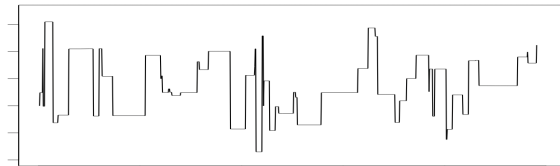
Autocorrelation functions

- Traceplots of for small and big moves provide (relatively) high correlations (known as autocorrelations) between successive observations of the Markov chain.
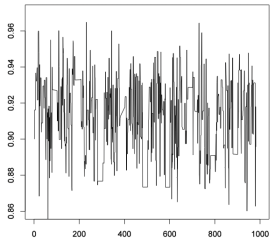
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- Autocorrelation function (ACF) plots are a convenient way of displaying the strength of autocorrelation in the given sample values.

- 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.
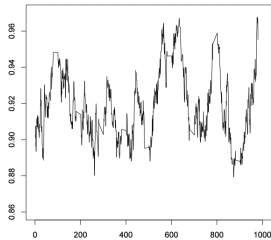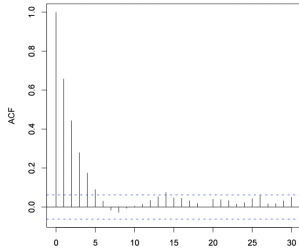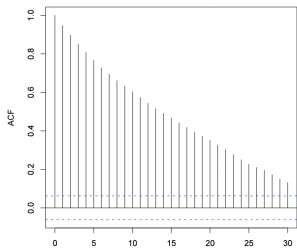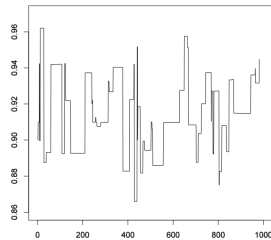
Small moves   *OK*   *Big moves*
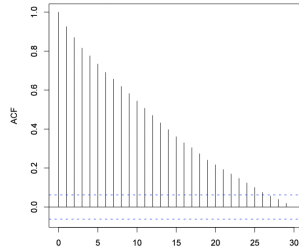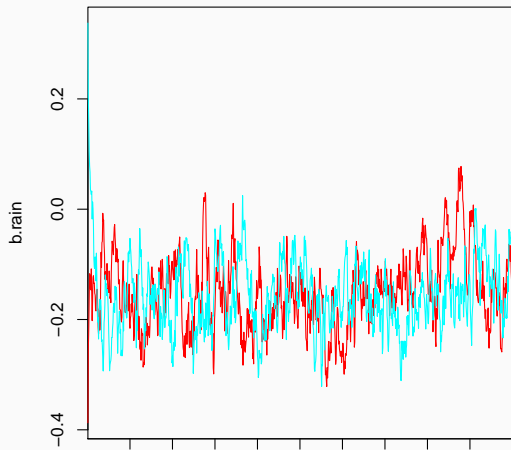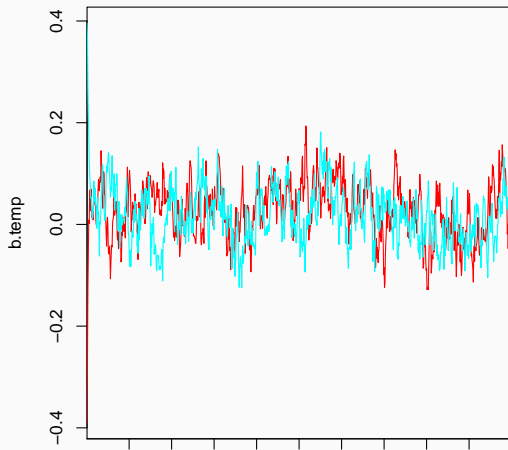
Traceplots for the storks

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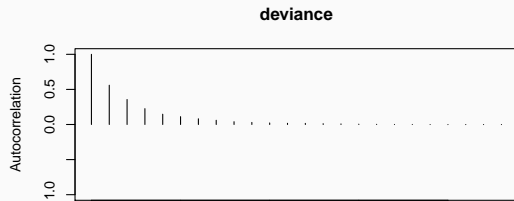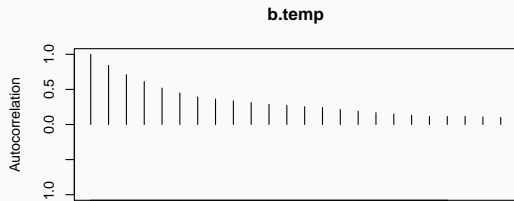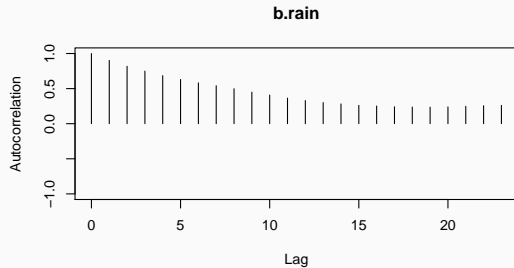
Autocorrelation for the storks

```
autocorr.plot(as.mcmc(storks),ask = FALSE)
```
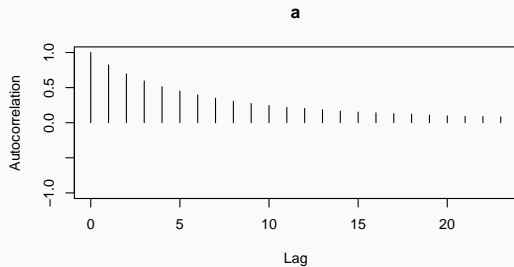
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- Converge to same target distribution: We need to think of the time required for convergence (realisations of the Markov chain have to be discarded before this is achieved).

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

Convergence assessment

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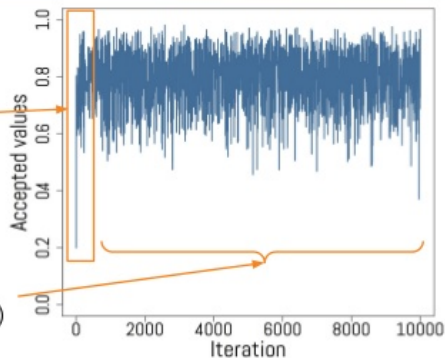- The simplest method to determine the length of the burn-in period is to look at trace plots.

Discard initial guesses that are still far from optimum: the **BURN-IN**

These numbers should be a good **sample of the Posterior** $P(\phi \mid data)$

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- The effective sample size (`n.eff`) measures chain length while taking into account the autocorrelation of the chain.
    - `n.eff` is less than the number of MCMC iterations.
    - Check the `n.eff` of every parameter of interest.
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  - `n.eff` is less than the number of MCMC iterations.
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- We need $n.eff \geq 100$ independent steps.

Potential scale reduction factor

- Gelman-Rubin statistic $\hat{R}$

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- Measures the ratio of the total variability combining multiple chains (between-chain plus within-chain) to the within-chain variability. Asks the question is there a chain effect? Very much alike the F test in an ANOVA.

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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           1.540   0.086   1.422   1.506   1.546   1.582   1.653 1.037
#> b.rain     -0.154   0.067  -0.273  -0.198  -0.157  -0.116  -0.010 1.003
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#> deviance  206.640  34.906 201.791 202.810 203.887 205.507 212.071 1.073
#>
#> 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).

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- 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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- 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,] -0.006902112 -0.3873233 -0.390095753 1381.5274
#> [2,]  0.381949493 -0.2549725 -0.267749235  820.8014
#> [3,]  0.573066002 -0.2166297 -0.125849306  596.9673
#> [4,]  0.758081091 -0.1643545 -0.060360393  448.4008
#> [5,]  0.931419982 -0.1170217  0.008371841  346.3375
#> [6,]  0.996726797 -0.1228979  0.001970008  316.1731
tail(res)
#>                  a      b.rain       b.temp deviance
#> [1995,] 1.546504 -0.05419978 -0.01065592 204.4991
#> [1996,] 1.555810 -0.04977522 -0.02021324 204.7901
```

Compute a posteriori Pr(rain < 0)

```r
# probability that the effect of rainfall is negative
mean(res[,'b.rain'] < 0)
#> [1] 0.979
```

Compute a posteriori Pr(temp < 0)

```
# probability that the effect of temperature is negative
mean(res[,'b.temp'] < 0)
#> [1] 0.338
```

Get credible interval for the rain effect

```
quantile(res[,'b.rain'],c(0.025,0.975))
#>        2.5%        97.5%
#> -0.273069656 -0.009805219
```
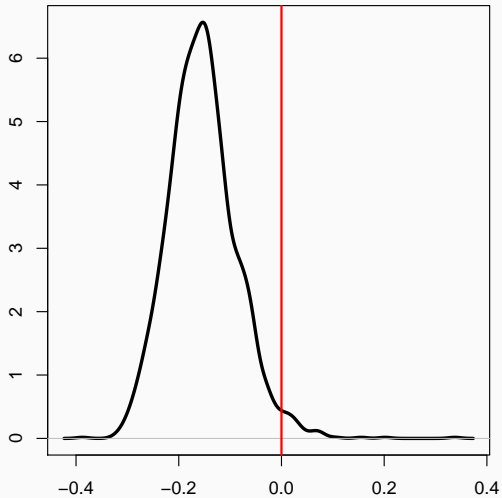
Get credible interval for the temperature effect

```
quantile(res[,'b.temp'],c(0.025,0.975))
#>        2.5%        97.5%
#> -0.08359463   0.12479919
```
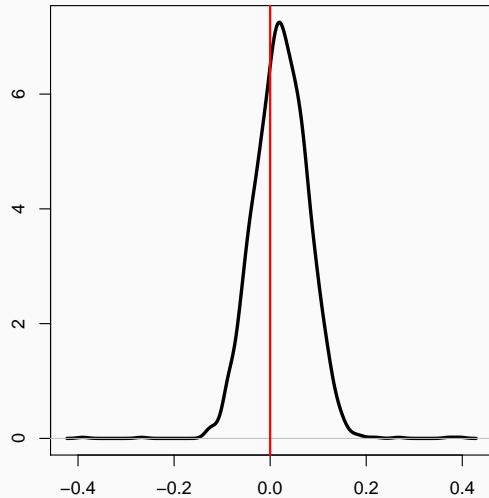
Graphical summaries

Your turn

A stupid question

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

Solution

- Evaluate the function for each MCMC iteration

```r
stupid_pd <- res[,'b.rain']^2 + cos(res[,'b.temp'])
head(stupid_pd)
#> [1] 1.074892 1.029380 1.039020 1.025191 1.013659 1.015102
```

- Plot the distribution

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