Bayesian Data Analysis

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- → BUGS stands for Bayesian Inference Using Gibbs Sampling and began in 1989.
- → Its basic philosophy was to separate the language used to describe a model from the actual programs used to carry out the computations (the engine).
- → This approach has two attractive advantages:
 - → One can easily specify complex models without requiring extensive knowledge of Bayesian computational tools.
 - The language has remained stable and consistent over time, even as the underlying programs which actually do the sampling are constantly changing.

- The syntax of the BUGS language is relatively straightforward. Every line does one of the following things:
 - \hookrightarrow Defines a stochastic node

```
theta~dbeta(1,1)
```

 $\hookrightarrow \ \, \text{Defines a deterministic node}$

```
tau=pow(sigma,-2)
```

→ Provides a comment

```
## Prior
```

 \hookrightarrow Defines a loop

```
for (i in 1:n)
```

- \hookrightarrow Common distributions in the BUGS language are dbin, dpois, dunif, dnorm, dgamma.
- → The normal is parameterised in terms of its mean and precision (=1/ variance).
- → Functions cannot be used as arguments in distributions (one needs to create new nodes).
- → For more details on the distributions and functions available in BUGS, check the online manual.

- → Historically, the most widely used BUGS engine has been a program called WinBUGS. It began in the early 1980s under David Spiegelhalter at the Medical Research Council Biostatistics Unit in Cambridge, UK.
- → Further developments by the developers of WinBUGS, however, have focused on a somewhat different program called OpenBUGS; the features and appearance of the programs are similar, but OpenBUGS is more compatible with different operating systems.
- → Information about WinBUGS and OpenBUGS available at

```
https://www.mrc-bsu.cam.ac.uk/software/bugs/
```

A separate project, JAGS (Just Another Gibbs Sampler), can be thought of as an engine for running BUGS models, although strictly speaking, the language syntax for the two programs is not always identical.

```
http://mcmc-jags.sourceforge.net/
```



 $\hookrightarrow\,$ Another two recent engines are STAN and NIMBLE, whose links are, respectively

http://mc-stan.org/

https://r-nimble.org/nimble-a-new-way-to-do-mcmc-and-more-from-bugs-code-in-r-3

- \hookrightarrow All engines carry out the following steps for fitting BUGS models:
 - Checking model syntax.
 - Reading in data.
 - Compiling the model.
 - Initialising the simulation.
 - Sampling.
 - Report results.

- Go to the File menu and click on New. This opens a window entitled 'untitled1'.
- 2 In this new window specify the model, the data, and starting values for the computations. We will see that, in fact, starting values are not necessarily needed.
- 3 Back in the (Win/Open)BUGS window, open the menu *Model* and click on *Specification*. Highlight model by double-click. Click on *Check model*. Highlight start of data. Click on *Load* data. Click on *Compile*. Highlight start of initial values. Click on *Load* inits. Click on *Gen Inits* if more initial values needed. Note that messages are printed at the bottom left describing whether or not these operations are working.
- Open Update from Model menu, and Samples from Inference menu. Type nodes to be monitored into Sample Monitor, and click set each. Click on Update to generate samples.
- Type * into Sample Monitor, and click stats, etc to see results on all monitored nodes. Perform more updates.

- \hookrightarrow Let us come back to the drug example of lecture and practical 1. Remember that we have assumed $Y \sim \text{Binomial}(n, \theta)$ and $\theta \sim \text{Beta}(a, b)$, with a = 9.2 and b = 13.8. The observed v is 15 and n is 20.
- \hookrightarrow In BUGS, the model syntax is

```
#Model
model{
y~dbin(theta,n)
theta~dbeta(a,b)
}

#Data
list(y=15, n=20, a=9.2, b=13.8)

#Initial values (a different one for each chain, 2 in this case)
list(theta=0.1)
list(theta=0.5)
```

Running WinBUGS/OpenBUGS

→ We can also easily compute the posterior predictive probability as well as the probability of exceeding a critical threshold. For instance, in the first practical, we've computed the probability of observing at least 25 positive responses in 40 new trials. The BUGS model is as follows:

```
#Model
model(
model()
y~dbin(theta,n)
theta~dbeta(a,b)
ypred~dbin(theta,m)
pcit<-step(ypred-ncrit)
}
#Data
list(n=20, y=15,a=9.2, b=13.8, m=40, ncrit=25)</pre>
```

 \hookrightarrow Note that step (a-b) equals 1 if $a - b \ge 0$ and 0 otherwise.

- \hookrightarrow To recap, the basic steps are
 - Specify the model
 - Load the model
 - Load the data
 - Load/generate initial values
 - Run the sampler
 - Monitor nodes
 - Update model
 - Repeat as necessary
- → For further and more detailed instructions we refer to the WinBUGS 14 manual (file winbugs_user_manual14.pdf on Learn).

- One can run WinBUGS/OpenBUGS directly, we don't need
 R installed on our machine to do so, but it's both easier and more useful to use
 R as an interface.
- → Several R interfaces exist, namely R2WinBUGS, BRugs, and R2OpenBUGS.
- → The main problem is that they do not work well (or at all) in MAC computers.
- → Fortunately, JAGS runs smoothly on all operating systems (mac os, windows, unix/linux) and R interface is also available, through the packages R2 jags, rjags, and runjags.
- → We also argue that JAGS is also more contemporaneous and actively maintained (by Martin Plummer).

- → In general, the steps to using JAGS to produce samples are:
 - Download JAGS at

```
http://sourceforge.net/projects/mcmc-jags/files/
```

- Install the rjags package in R, which should automatically find your JAGS installation.
- 3 Specify the statistical model (likelihood and prior) using the model command.
- 4 Compile the model using jags.model.
- 6 Generate samples using update and coda.samples.
- → As it was already mentioned, there are, at least, 3 R interfaces for JAGS. The model syntax is the same for the three interfaces, what changes is how relevant information is extracted. We will stick with rjags, although you are free to choose your preferred interface.

- \hookrightarrow We will learn rjags as we go! As an introductory example, we will go back to the example where we have normally distributed data where both the mean and the variance are unknown, i.e., $Y_i \stackrel{\text{iid}}{\sim} N(\mu, \sigma^2)$, with μ and σ^2 unknown (see R script jags_unknown_mean_and_variance).
- \hookrightarrow Note that BUGS language uses the precision, instead of variance, in the parameterisation of the normal distribution. Therefore, we assume $\mu \sim N(\mu_0, \sigma_0^2)$ and $\sigma^{-2} \sim \text{Gamma}(a, b)$, with $\mu_0 = 0$, $\sigma_0^2 = 100$, and a = b = 0.1.
- → First we must load the rjags package require (rjags)

Running JAGS via rjags

The program specifying the model (BUGS) code must be put in a separate file which is then read by JAGS. When working in ℝ this is most conveniently done by saving the model in an object, e.g., model_string="model{...}" and then using the ℝ function textConnection when passing the model to the jags.model function.

```
model_string <- "model{
    # Likelihood
    for(i in 1:n){
        y[i]~dnorm(mu,inv.var)
    }

    # Prior for mu
    mu~dnorm(mu0,inv.var0)
    inv.var0=1/sigma02

# Prior for the inverse variance
    inv.var~dgamma(a, b)

# Compute the variance
    sigma2=1/inv.var
}"</pre>
```

Running JAGS via rjags

 \hookrightarrow Alternatively we can use the R function cat, to put the model in a file, say, m1. jag

```
cat("model{
# Likelihood
for(i in 1:n) {
y[i] ~dnorm(mu,inv.var)
}
# Prior for mu
mu~dnorm(mu0,inv.var0)
inv.var0=1/sigma02
# Prior for the inverse variance
inv.var~dgamma(a, b)
# Compute the variance
sigma2=1/inv.var
}",
file="ml.jaq")
```

 \hookrightarrow Personally, I prefer the first option.

Running JAGS via rjags

- → The BUGS language is declarative, i.e., it is not executed as the program runs. Instead it is
 a specification of the model structure, and after the model is set up JAGS will decide how
 best to go about the MCMC simulation.

```
data=list(y=y,n=n,mu0=mu0,sigma02=sigma02,a=a,b=b)
```

→ Regarding starting values, we can supply them, although JAGS in most cases will however be able to generate them. In case we want to monitor convergence we will normally run several chains, so in case we supply the initial values, we must supply starting values for each chain. Here, in this example, we use three chains, hence the initial values is a list of three lists. Each os these lists has as elements one named value for each parameter – in this case there two parameters mu (mean) and inv.var (precision).

inits=list(list(mu=mean(y),inv.var=1/var(y)), list(mu=0,inv.var=1), list(mu=10,inv.var=0.1))

Running JAGS via rjags

→ Once the model, the data, and the initial values (in case we want to supply them) we ask JAGS, through the function jags.model to compile and initialise the model.

```
model=jags.model(textConnection(model_string),n.chains=3,data=data,inits=inits)
```

 \hookrightarrow As this step, we obtain the following

```
Compiling model graph
Resolving undeclared variables
Allocating nodes
Graph information:
Observed stochastic nodes: 150
Unobserved stochastic nodes: 2
Total graph size: 160
```

Initializing model

→ In case we have used the function cat to define the model and saved it as file m1. jag, we would instead write

```
model=jags.model("m1.jag",n.chains=3,data=data,inits=inits)
```



- → To get samples from the posterior distribution of the parameters, we use the coda.samples function after first using the update function to run the Markov Chain for a burn-in period of a number of specified iterations (in this case 1000).
- → For coda.samples we must specify
 - → The variables (nodes) that we want to monitor in the subsequent cycles of the chain.

 This is done using the argument variable.names. In our case the variables we want to monitor are called mu and sigma2.
 - \hookrightarrow How many iterations to run the chain (n.iter).
 - How often we sample the specified parameters and retain the results in memory (thin, by default equal to one).

Running JAGS via rjags

\hookrightarrow We thus type

```
update(model,1000,progress.bar="none") res=coda.samples(model,variable.names=c("mu","sigma2"),n.iter=10000, progress.bar="none")
```

→ As always in R, the most useful overview comes from the summary function

```
> summary(res)

Iterations = 12001:22000
Thinning interval = 1
Number of chains = 3
Sample size per chain = 10000
```

 Empirical mean and standard deviation for each variable, plus standard error of the mean:

```
        Mean
        SD Naive SE Time-series SE

        mu
        1.926
        0.2336
        0.001348
        0.001336

        sigma2
        8.215
        0.9591
        0.005537
        0.005640
```

2. Quantiles for each variable:

```
2.5% 25% 50% 75% 97.5%
mu 1.468 1.767 1.926 2.083 2.384
sigma2 6.541 7.541 8.144 8.812 10.283
```

- \hookrightarrow We can also type plot (res) to visualise the traceplots and densityplots.
- → For inspection of the autocorrelation function, type autocorr.plot(res) and for knowing the effective sample size effectiveSize(res). The Gelman Rubin statistics is obtained typing gelman.plot(res) (requires that the number of chains is equal or greater than 2).
- → We can also extract results for each chain and each parameter using the object res. For instance, to obtain the values of mu of the first chain, we type res[[1]][,1], while for obtaining the sigma2 values for chain 2, we do res[[1]][,2].
- \hookrightarrow We can also collect all the posterior samples from the different chains in one matrix by typing resmat=as.matrix(res).