WinBUGS for Beginners

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"A knowledge of Bayesian statistics is assumed..."

The content of this presentation is mainly based on WinBUGS manual

Introduction

BUGS¹: "Bayesian inference Using Gibbs Sampling"

- Project for Bayesian analysis using MCMC methods
- It is not being further developed

WinBUGS^{1,2}

- Stable version
- Run directly from R and other programs

OpenBUGS³

- Currently experimental
- Run directly from R and other programs
- Running under Linux as LinBUGS

¹ MRC Biostatistics Unit Cambridge, ² Imperial College School of Medicine at St Mary's, London ³ University of Helsinki, Finland

WinBUGS

Freely distributed

http://www.mrc-bsu.cam.ac.uk/bugs/welcome.shtml

Key for unrestricted use

http://www.mrc-bsu.cam.ac.uk/bugs/winbugs/WinBUGS14_immortality_key.txt

- WinBUGS installation also contains:
 - Extensive user manual
 - Examples
- Control analysis using:
 - Standard windows interface
 - DoodleBUGS: Graphical representation of model
- A closed form for the posterior distribution is not needed
- Conditional independence is assumed
- Improper priors are not allowed

Inputs

- Model code
 - Specify data distributions
 - Specify parameter distributions (priors)

Data

- List / rectangular format
- Initial values for parameters
 - Load / generate

model {

statements to describe model in BUGS language

- Multiple statements in a single line or one statement over several lines
- Comment line is followed by #
- Types of nodes
 - 1. Stochastic
 - Variables that are given a distribution
 - 2. Deterministic / Logical
 - Logical functions of other nodes
 - 3. Constant

- Stochastic and deterministic nodes appears only once on the LHS of a statement (except in data transformation)
- Name nodes
 - Case sensitive
 - Characters allowed: letters, numbers and period
 - Start with a letter
 - No end with a period
 - Maximum 32 characters
- Numbers
 - Standard or exponential notation
 - Include decimal point in the exponential format
 - Notation allowed: .0001 0.0001
 1.0E-4 1.0e-4
 1.E-4 1.0E-04
 - Not allowed: 1E-4

- Stochastic nodes:
 - Assign distributions using ~ ("is distributed as")
 - Help → WinBUGS user manual → Distributions
 - Handle 19 discrete/continuous univariate distributions:
 - eg: Bernoulli, Binomial, Categorical, Negative Binomial, Poisson, Beta, Chi-squared, Exponential, Gamma, Normal, Pareto, Student-t, Uniform, Weibull, etc
 - Handle 5 discrete/continuous multivariate distributions:
 - Multinomial, MVN, Multivariate Student-t, Dirichlet, Wishart
 - No missing data, except for multivariate normal data

- Stochastic nodes:
 - Examples

for (j in 1:J) { y[j] **~ dbin**(p[j], n[j]) }

for (i in 1:N) { Y[i, 1:M] **~ dmnorm**(mu[], Omega[,]) }

Logical nodes:

- Assign logical expressions using <- ("to be replaced by")
- Logical expressions can be built using:
 - Operators: +, -, *, /, unitary minus (-A)
 - Logical functions:

 $\begin{array}{l} \text{Help} \rightarrow \text{WinBUGS user manual} \rightarrow \text{Model Specification} \rightarrow \text{Logical} \\ \text{nodes} \rightarrow \text{Table I: Functions} \end{array}$

Examples:

```
N <- K+2
```

```
mu[i] <- beta0 + beta * z[i] + b[i]
```

```
prec[1:2, 1:2] <- inverse( var.matrix[,] )</pre>
```

```
log( e[i, j] ) <- inprod( beta[1:3] , X[i, j, 1:3] )</pre>
```

Logical nodes:

- Cannot be given data or initial values (except when using the data transformation)
- Link functions that can be used on the left hand side of logical nodes

log	logit	cloglog	probit
logit(mu[i]) <- beta0 + beta * z[i] + b[i]			

- Data transformation:
 - Data y available
 - Want to model sqrt(y)

Arrays and indexing

- Vectors and matrices are indexed within square brackets []
 - n:m represents n,n+1,...,m
 - y[] indicates all values of a vector y
 - y[,3] indicates all values of the *third* column of a twodimensional array y
- Range of the variable must be explicitly defined in multivariate nodes
 - x[1:K] ~ dmnorm(mu[], tau[,])
- Up to three dimensions are currently allowed (?)
- Multidimensional arrays are handled as one-dimensional arrays with a constructed index
 - *y[i, j]*
 - x[i, j, 1:3]

Censoring

- Interval censored: y ~ ddist(theta)l(lower, upper)
- Right censored: y ~ ddist(theta)l(lower,)
- Left censored: y ~ ddist(theta)l(,upper)
- The structure is only use if y has not been observed, otherwise the constraints will be ignored
- If y, theta, lower and upper are not observed, then lower and upper must not be functions of theta

Data

- Available data and constants nodes are specified in a data file
- Format:
 - List (S-Plus/R format)
 - Rectangular: Data in arrays
- Whole array must be specified in a single file
- Missing values are represented as NA
- All variables in a data file must be defined in a model
- It is possible to load a mixture of list and rectangular format data for the same model (see Rats example)

Data: list format

data in a list format

- Scalars and arrays are named and given values in a single structure
- No space between *list* and (
- Example:

list(

```
list(

xbar = 22, N = 3, T = 5,

x = c(8.0, 15.0, 22.0, 29.0, 36.0),

Y = structure(

.Data = c(151, 199, 246, 283, 320,

145, 199, 249, 293, 354,

153, 200, 244, 286, 324),

.Dim = c(3,5)
```

Data: list format

• Example of 3 * 2 * 4 dimensional array:

1	2	3	4
5	6	7	8
9	10	11	12
13	14	15	16
17	18	19	20
21	22	23	24

list(Y = structure(.Data = c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24),.Dim = c(3, 2, 4)

Data: rectangular format

var1[] var2[] varK[] END

- Columns headed by array name
- Arrays of equal size
- Array names must have explicit brackets
- The first index position of any array must be empty
- End file with an '*END*' statement, followed by at least one blank line
- Example:

```
age[] sex[]
26 0
52 1
....
END
```

Data: rectangular format

var1[] var2[] varK[] END

Example of multi-dimensional arrays:

Y[,1]	Y[,2]	Y[,3]	Y[,4]	Y[,5]
151	199	246	283	320
145	199	249	293	354
147	214	263	312	328
153 END	200	244	286	324

Initial values

- Required for all stochastic nodes (without available data)
- Initial values can be:
 - Load
 - Specify initial values following same format as Data
 - Generated
 - Use Specification tool

- Evaluate association between:
 - Respiratory illness and exposure to nitrogen dioxide (NO₂)
- Measurement error in the exposure
- Studied subjects: 103 children
- Data:

Bedroom NO ₂ level in ppb (Z)				
Respiratory illness (y)	<20	20-40	40+	Total
Yes	21	20	15	56
No	27	14	6	47
Total	48	34	21	103

y response variable.

Z observed exposure. 3 categories z_i (j = 1, 2, 3)

 Berkson measurement error model: Association between true exposure (X) and observed exposure (Z)

$$X_{j} = \alpha + \beta Z_{j} + \varepsilon_{j}$$

where $\alpha = 4.48$,

- $\beta = 0.76$ and
- ε j follows a normal distribution with zero mean and variance 81.14
- Observed exposure (Z_i) takes values 10, 30 or 50

A logistic regression model is assumed

 $y_j \sim \text{Binomial}(p_j, n_j)$ logit $(p_j) = \theta_1 + \theta_2 X_j$

where p_j = probability of respiratory illness for children in the j-th exposure group θ_1 and θ_2 are the regression coefficients

 The regression coefficients are given vague independent normal priors

Model

model {
 for(j in 1 : J) {

```
# DISEASE MODEL
y[ j ] ~ dbin(p[ j ], n[ j ])
logit(p[j]) <- theta[1] + theta[2] * X[j]</pre>
```

```
# MEASUREMENT ERROR MODEL
X[ j ] ~ dnorm(mu[ j ], tau)
mu[ j ] <- alpha + beta * Z[ j ]
}</pre>
```

```
# PRIORS
theta[1] ~ dnorm(0.0, 0.001)
theta[2] ~ dnorm(0.0, 0.001)
```

}

Data

list(J = 3, alpha = 4.48, beta = 0.76, tau = 0.01234, n = c(48, 34, 21), Z = c(10, 30, 50),y = c(21, 20, 15))

Initial values

list(theta = c(0.0, 0.0), X = c(0.0, 0.0, 0.0))

Run model

Menu bar \rightarrow Model \rightarrow Specification tool

1. Check model

"model is syntactically correct"

2. Load data

"data loaded"

- 3. Specify num. of chains to be simulated
- 4. Compile model

"model compiled"

- 5. Initial values for each chain
 - Load "model is initialized"
 - Generate *"initial values generated, model initialized"*

check model	loa	ad data
compile	num of c	hains 1
load inits	for chain	1.
den inits		

Update model

Menu bar \rightarrow Model \rightarrow Update tool

1. Specify number of MCMC updates to be carried out

🙀 Update Tool	×
updates 1000	refresh 100
update thin 1	iteration 0
└── over relax	🗆 adapting

- Data have not been stored
- Used for "burn-in" period

Monitor runs

Menu bar \rightarrow Inference \rightarrow Sample monitor tool

Monitor a single node (unknown quantity)

- Type name of node to be monitored
- Click on "set"
- Update model

Generate simulated values of all unknown quantities

- Repeat steps 1 and 2 for all nodes to be monitored
- Type * to select all the nodes
- Update model

Sample monitor tool



- trace
 Plots variable value against iteration number (dynamic)
- history Plots a complete trace
- density Plots a smoothed kernel density estimate / histogram
- **stats** Summary statistics
- coda ASCII representation of the monitored values for use in R
- **quantiles** Plots running mean and 95% CI against iteration num.
- auto cor* Plots/calculates the autocorrelation function of the variable out to lag-50

* Values can be listed by double-clicking on the plot followed by ctrl-left-mouse-click

Sample monitor tool



- bgr diag* Plots/calculates the Gelman-Rubin convergence statistic.
 - Blue: Width of the 80% interval of the pooled runs
 - Green: Average width of the 80% intervals within the individual runs
 - Red: R = pooled / within
 - Interval widths are normalised to have an overall maximum of 1
 - R >1 if starting values are over-dispersed
 - Look for convergence of R to 1, and convergence of pooled and within interval

* Values can be listed by double-clicking on the plot followed by ctrl-left-mouse-click

STATS

- node
 Name of the unknown quantity
- mean
 Posterior mean of the unknown quantity
- sd Posterior standard deviation of the unknown quantity
- MC error Computational accuracy of the mean
- **2.5%** Lower endpoint of the 95% credible interval
- median
 Posterior median
- 97.5% Upper endpoint of the 95% credible interval
- start The starting simulation (after discarding the start-up)
- sample Number of simulations used to approximate the posterior distribution

Output options

- By default WinBUGS opens a new window for each output (stats, history, density, ...)
- All output could be written into single log file:
 - Options menu → Output options → select "log"
- Access to the output:
 - Info menu \rightarrow Open Log

CODA

- CODA: Convergence Diagnostic and Output Analysis.
- Files produced:
 - Output file for each chain: CODA for chain N or (.out file)
 - Contains iteration number and value
 - Description file: CODA index or (.ind file)
 - Indicates which lines of the CODA for chain N file correspond to which variable
- Save files:
 - Menu bar \rightarrow File \rightarrow Save as
 - Select Plain Text (.txt) in Save as type
 - Give a file name, enclose it in quotes, and save it
 - Example:
 - Output files: "AirChain1.out" and "AirChain2.out"
 - Description file: "Air.ind"

Analysis using R

Required library: coda

http://cran.r-project.org/web/packages/coda/coda.pdf

See WinBUGS example in R

Analysis using R

Another option is using library: boa
 Bayesian Output Analysis
 http://www.public-health.uiowa.edu/boa/BOA.pdf

Run directly from R

- Required package for OpenBUGS: BRugs
- Required package for WinBUGS: *R2WinBUGS*
 - Write a Bugs model in a file with a *.bug* extension
 - Go into R
 - Prepare the inputs to the *bugs* function in R and run it
 - A WinBUGS window will pop up and R will freeze up
 - The model will now run in WinBUGS (Log window)
 - When WinBUGS is done, its window will close and R will work again.
 - See example in R

Useful links

- The BUGS Project <u>http://www.mrc-bsu.cam.ac.uk/bugs/welcome.shtml</u> <u>http://www.mrc-bsu.cam.ac.uk/bugs/documentation/contents.shtml</u>
- Woodworth, George G. Biostatistics: A Bayesian Introduction. Introduction to WinBUGS. 2004 <u>http://www.stat.uiowa.edu/~gwoodwor/BBIText/AppendixBWinbugs.</u> pdf
- Sturtz S, Ligges U, Gelman A (2005). R2WinBUGS: A Package for Running WinBUGS from R. Journal of Statistical Software, 12(3), 1-16.

<u>http://cran.r-</u> project.org/web/packages/R2WinBUGS/vignettes/R2WinBUGS.pdf

Useful links

- Plummer M, Best N, Cowles K and Vines K. (2006). CODA: Convergence Diagnosis and Output Analysis for MCMC. R News. 6(1), 7-11 http://cran.r-project.org/doc/Rnews/Rnews_2006-1.pdf
- Running WinBugs and OpenBugs from R <u>http://www.stat.columbia.edu/~gelman/bugsR/</u>

Selected references

- Brooks SP and Gelman A (1998) Alternative methods for monitoring convergence of iterative simulations. Journal of Computational and Graphical Statistics. 7, 434-455.
- Lunn DJ, Thomas A, Best N, and Spiegelhalter D (2000) WinBUGS -- a Bayesian modelling framework: concepts, structure, and extensibility. Statistics and Computing, 10:325--337.
- Ntzoufras, I (2009) Bayesian modeling using WinBUGS. John Wiley and Sons.