7 WinBUGS

$\boxed{\text{WinBUGS} = \textbf{B}\text{ayesian inference }\textbf{U}\text{sing }\textbf{G}\text{ibbs }\textbf{S}\text{ampling}}$

WinBUGS is a computer program aimed at making MCMC available to applied researchers. Its interface is fairly easy to use, and it can also be called from programs such as R. WinBUGS is free and can be found on the website:

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

OpenBUGS program, found at: http://mathstat.helsinki.fi/openbugs/

Given a likelihood and prior distribution, the aim of WinBUGS is to sample model parameters from their posterior distribution. After the parameters have been sampled for many iterations, parameter estimates can be obtained and inferences can be made.

For a given project, three files are used:

1. A program file containing the model specification.
2. A data file containing the data in a specific (slightly strange) format.
3. A file containing starting values for model parameters (optional).

File 3 is optional because WinBUGS can generate its own starting values. There is no guarantee that the generated starting values are good starting values, though.

Advice for new users:

1. Step through the simple worked example in the tutorial.
2. Try other examples provided with this release (see Examples Volume 1 and Examples Volume 2).
3. Edit the BUGS language to fit an example of your own.

Users should already be aware of the background to bayesian Markov chain Monte Carlo methods.

The current Metropolis MCMC algorithm is based on a symmetric normal proposal distribution, whose standard deviation is tuned over the first 4000 iterations in order to get an acceptance rate of between 20% and 40%. All summary statistics for the model will ignore information from this adapting phase. (You'll notice if the 'adapting' box in 'Update Tool'-window is ticked or not).

Strong recommendation: the first step in any analysis should be the construction of a directed graphical model. Briefly, this represents all quantities as nodes in a directed graph, in which arrows run into nodes from their direct influences (parents). The model represents the assumption that, given its parent nodes `pa[v]`, each node `v` is independent of all other nodes in the graph except descendants of `v`, where descendant has the obvious definition. (If the descendants of `v` contain data values, then in the posterior distribution `v` would depend on these data too, but otherwise it depends on its parents only if their values are given).

Nodes in the graph are of three types.

1. Constants are fixed by the design of the study: they are always founder nodes (i.e. do not have parents), and are denoted as rectangles in the graph. They should be specified in a data file. (Although simple data could be assigned within model specification).

2. Stochastic nodes are variables that are given a distribution, and are denoted as ellipses in the graph; they may be parents or children (or both). Stochastic nodes may be observed in which case they are data, or may be unobserved and hence be parameters, which may be unknown quantities underlying a model, observations on an individual case that are unobserved say due to censoring, or simply missing data.

3. Deterministic nodes are logical functions of other nodes.

Quantities are specified to be data by giving them values in a data file, in which values for constants are also given.

7.1 Structure of the model

The syntax and form of a model in WinBUGS follows (nearly) directly from the structure of the required densities in the Bayes formula. Therefore, understanding of the product rule and bayes formula, as well as other basic theorems of probability calculus is as essential as understanding grammatical rules and structure of sentences natural languages. We need a conditional distribution of data, and a prior. And these can consist of several conditional distributions. The whole structure is convenient to draw as a Directed Acyclic Graph (DAG).

The joint posterior density is always fully specified when all these necessary parts are defined. Therefore, WinBUGS is a **declarative** language, as opposed to **procedural** programming languages. (*This is important to remember*). In a procedural language the following code could be valid:

```
X := 1;
Y := 1;
Z := X+Y;
```

but the following would not compute:

```
Z := X+Y;
X := 1;
Y := 1;
```

In WinBUGS, the order of these statements would not matter, because in WinBUGS the logical structure is defined which can be *written out* in any order, as long as all the quantities are defined somewhere and their combination defines a valid model.

In WB, we define a chain of conditional distributions that was obtained from the product rule when writing the Bayes formula. Each variable $v \in V$ in the model can be a 'child node' that is conditionally dependent on its 'parent nodes':

$$\pi(V) = \prod_{v \in V} \pi(v \mid \text{parents}\{v\}),$$

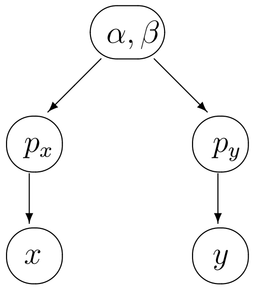
and the last variables in this chain have no further parents, i.e. their conditional distribution does not depend on any further variables - it is the prior distribution. The whole structure specifies a bayesian model. A simple example (assuming data x, y, n, m) could be:

```
model{
x ~ dbin(px,n)
y ~ dbin(py,m)
px ~ dbeta(a,b)
py ~ dbeta(a,b)
a ~ dexp(1)
b ~ dexp(1)
}
```

or a linear model (assuming data x, y):

```
model{
for(i in 1:N){
 y[i] ~ dnorm(mu[i],tau)
 # huom: tau = 1/sigma^2
 mu[i] <- alpha + beta * (x[i]-mean(x[]))
 }
alpha ~ dnorm(0,0.0001); beta ~ dnorm(0,0.0001)
tau ~ dgamma(0.001,0.001)
}
list(N=5,x=c(1,2,3,4,5),y=c(1,3,3,3,5))
```

Full models are often easier to picture graphically as a Directed Acyclic Graph (DAG). In the binomial model above this would be:



A DAG gives the necessary structure for a valid bayesian model as well as for a valid WB code. (The exception is that in WB we can also define Gibbs sampling algorithm directly using 'full conditionals').

A DAG is made of nodes and arrows. In WinBUGS syntax the different node types ((1) constant (data), (2) random or (3) deterministic) have specific coding. Constants are defined either within the code or separately as a list, but because they represent data, it is recommendable to give them as part of the data listing rather than part of the model definition code. Random nodes are defined by stating what their conditional distribution is (coded '$\sim$'). Deterministic nodes are always logical functions of some other nodes (coded '$\leftarrow$').

Since cycles are not allowed in a DAG, then how to define models where some variable has some feedback into itself? For example, the size of a population drives population growth which again determines the population size. The question is: what is the probability model for this? It is a model of a stochastic process. The variables need to be indexed with respect to time, so that the conditional distribution of X_{t+1} depends on X_t, and this can be written as a DAG without cycles. Alternatively, (but this can be more complicated), we could try to solve the conditional probability distribution for the whole set of values $X_1, \ldots, X_t$, given some other parameters of the model. But if the X variables are unknown, their simulation might require block updating which is not possible in WinBUGS which is based on single site updating algorithms (unless there are extensions available). In General, Gibbs sampling theory allows block updating.

Models can be defined in WB either by writing the corresponding WB code, or by drawing the DAG using doodle-BUGS. Once the 'doodle' is defined, the corresponding WB code is automatically generated. But the opposite is not possible: a picture of a DAG cannot be generated from winBUGS code, you need to draw it elsewhere. But the WB language is much more versatile than doodle-BUGS, so it is best to learn to write WB codes, and do drawing of DAGs elsewhere.

7.1.1 Example: different codes, same model

```
p ~ dbeta(1,1)
x ~ dbin(p,n)
```

```
p ~ dbeta(a,b)
a <- x+1 ; b <- n-x+1
```

```
p ~ dunif(0,1)
pr <- exp(logfact(n)-logfact(x)-logfact(n-x)+x*log(p)+(n-x)*log(1-p))
one ~ dbern(pr); one <- 1
```

```
z ~ dnorm(0,1)
p <- phi(z)
x ~ dbin(p,n)
```

```
p ~ dunif(0,1)
for(i in 1:x){
result[i] ~ dbern(p); result[i] <- 1
}
for(j in x+1:n){
result[j] ~ dbern(p); result[j] <- 0
}
```

7.1.2 Ask the posterior

Once we can simulate from the posterior with WB, we can derive answers to several questions, or 'queries', that depend on the unknown parameters described by the posterior. For example, in comparing two populations with unknown prevalences p_1 and p_2, we might be interested in the following probabilities:

$$P(p_1 > p_2 \mid \text{data}), \quad P(|p_1 - p_2| > c \mid \text{data}), \quad P(p_1/p_2 > 1 \mid \text{data}), \quad P(p_1^2 + p_2^2 > c \mid \text{data})$$

The last example could be related to e.g. genetical application in which p_i would be the prevalence of allele i in Hardy-Weinberg equilibrium. The classical statistical approach of hypothesis testing concerning parameters and their transformations is replaced in bayesian context by computation of these probabilities. For example, the posterior density of $\mid p_1 - p_2 \mid$ could be visualized as the simulated empirical distribution from WB, but we could also compute $P(\mid p_1 - p_2 \mid > c \mid \text{data})$ as an answer to the question if the absolute difference is larger than c. This could be done by the following code, using `step`-function:

```
model{
for (i in 1:2){
x[i] ~ dbin(p[i],n[i])
p[i] ~ dbeta(1,1)
}
Pabsdiff <- step( abs(p[1]-p[2])-c)
}
```

Here, `Pabsdiff` is an indicator variable (remember from the preliminaries). When we compute the average of this indicator over the MCMC simulation $i = 1, \ldots, N$ we get an approximation of the required probability:

$$\frac{1}{N}\sum_{i=1}^{N} I_i \approx E(I) = 1 \times P(I = 1) + 0 \times P(I = 0) = P(I = 1)$$

Asking for prediction:

We might also need a prediction for a forthcoming variable x_{new} in some forthcoming sample of size m_1, under unknown prevalence p_1. This could be computed simply by adding the following:

`xnew[1]` $\sim$ `dbin(p[1],m[1])`

In the example of linear regression, we could ask for a prediction of y_6 at the next point x_6. This could be achieved by adding one more step in the loop by setting $N + 1$ instead of N, and by adding `NA` in the data list in place of `y[6]`.

7.2 Data structures

Anything that is not an unknown (random) quantity in the model, has to be fixed value, i.e. given as data or constant. The whole data set is listed separately from the model code, for example:

```
list(x=4,
     y=c(3.5,7.2,9.1),
     z=structure(
       .Data=c(7,3,5,1,8,2),
       .Dim=c(2,3)))
```

which defines a scalar x, vector y and a matrix z of size 2×3. Data matrices can also be defined in this form:

```
 z[,1] z[,2] z[,3]
 7     3     5
 1     8     2
 END
```

so that first index of z needs to be left empty, and there must be an empty line after `END`. You can avoid much trouble if you always check carefully that you have indexed your data correctly. There are no useful tools for checking data inconsistencies within WinBUGS. When data variables have been defined and assigned, there should be a conditional distribution for them in the code. For example, if variable y is given as data, then we might have a model directly for it:

```
y ~ dnorm(mu,tau)
```

Alternatively, we might be interested in modeling some transformation of this variable, which could be done as:

```
 yy <- log(y)
 yy ~ dnorm(mu,tau)
```

Of course, we might have calculated the transformed y already beforehand, and then use that as data. Note that the previous use of transformations within the code is actually against the idea in WB syntax which prohibits multiple definitions of the 'same thing'. Indeed, very often you will see error messages: 'multiple definition of x'.

If data are in some other format in some other software, you have to find out how to make it in WB format. There are some tools that can be used for converting data:

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

For example, for Matlab, some tools are also at:

http://www.cs.ubc.ca/ murphyk/Software/MATBUGS/matbugs.html

7.3 Indexing and looping

Indexing of variables is an efficient way of simplifying and shortening WB code. You just need to be careful in that the indexing is correct. For example:

```
for(i in 1:3){ y[i] ~ dnorm(mu,tau)  }
```

It is also possible to define a distribution of a vector variable:

```
y[1:3] ~ dmnorm(mu[1:3],tau[1:3,1:3])
```

Here, it is sufficient to specify the indexes on the left hand side for y, whereas μ and τ could be written in the form `mu[]` and `tau[,]` which would include the whole vector or matrix. Also, sums could be defined over the whole vector:

```
 s <- sum(theta[])
 s2 <- sum(eta[,1])
```

In setting the limits for a loop `for(i in 1:3)`, it is useful to define the limit(s) by a constant: `for(i in 1:L)`, `L<-3`, or `list(L=3)`. For easier editing of new model versions, all constants should be defined together with data - in a single place. It is also convenient to use nested looping:

```
 for(i in 1:I){
    for(j in 1:J){
    y[i,j] ~ dpois(mu[i,j])
    log(mu[i,j]) <- mu0 + mu1*x1[i] + mu2*x2[j] + e[i,j]
    }
 }
```

The most frequent coding errors with loops are forgetting the braces, "}", or wrong position of the braces, or forgetting the indexing, or wrong indexing. Often this results to an error message: "multiple definition of..."

The range of indexing cannot be random. The following approach might be useful in such case:

```
for(i in 1:N){
 ind[i] <- 1 + step(i-K - 0.01)
 y[i] ~ dnorm(mu[ind[i]],1)
}
```

Here, variable K is unknown, K $\in \{1, \ldots, \mathrm{N}\}$, and it controls which variables y_i are modelled as $N(\mu_1, 1)$. (Can be useful in changepoint-problems).

7.3.1 Example: change point estimation

Assume data about monthly accidents y_i. This can be modeled using Poisson distribution, with parameter μ_1 before the change point and μ_2 after the change point. Prior distribution for the location of the change point could be discrete uniform $1/N$, where N is the number of months. The model assumes that μ_1 applies at least to the first month, and that it could also apply to the last month, in which case there would not be a change point at all.

```
model{
for(i in 1:N){
y[i] ~ dpois(mu[ind[i]])
ind[i] <- 1 +step(i-K-0.01)
pk[i] <- 1/N
}
K ~ dcat(pk[]); mu[1] ~ dgamma(0.01,0.01); mu[2] ~ dgamma(0.01,0.01)
}
```

An example with real data: coal mining accidents in Britain 1851-1962. (Carlin et al: Hierarchical Bayesian Analysis of Changepoint Problems. Appl. Statist. (1992). 41, No. 2, pp.389-405). Did improvement in technology and safety practices have an actual effect of the rate of serious accidents? When did the change actually occur? This could be modeled using the following code.

```
model{
 for(year in 1:N){
 T[year] <- year+1850
 D[year]~dpois(mu[year])
 log(mu[year])<-b[1]+step(year-changeyear)*b[2]
 }
 for(j in 1:2){b[j]~dnorm(0,0.0001)}
 actual<-changeyear+1850
 changeyear ~ dunif(1,N)
 mu1 <- exp(b[1])
 mu2 <- exp(b[1]+b[2])
}
 list(D=c(4, 5, 4, 1, 0, 4, 3, 4, 0, 6,
      3, 3, 4, 0, 2, 6, 3, 3, 5, 4,
      5, 3, 1, 4, 4, 1, 5, 5, 3, 4,
      2, 5, 2, 2, 3, 4, 2, 1, 3, 2,
      1, 1, 1, 1, 1, 3, 0, 0, 1, 0,
      1, 1, 0, 0, 3, 1, 0, 3, 2, 2,
      0, 1, 1, 1, 0, 1, 0, 1, 0, 0,
      0, 2, 1, 0, 0, 0, 1, 1, 0, 2,
      2, 3, 1, 1, 2, 1, 1, 1, 1, 2,
      4, 2, 0, 0, 0, 1, 4, 0, 0, 0,
      1, 0, 0, 0, 0, 0, 1, 0, 0, 1,
      0, 0),N=112)
```

7.4 Logical expressions

Long expressions can be too long for WinBUGS. You would then get the error message: "logical expression too complex". This can be avoided only by using additional variables:

```
a <- g + t + g*u + 7*pow(w,s)
b <- r + sqrt(h) - inprod(z[],zz[]) + e/p
c <- a+b
```

instead of writing the whole expression as a one-liner. Some useful logical functions in WinBUGS are:

```
abs(e)
equals(e1,e2)
step(e)
exp(e)
log(e)
inprod(v1,v2)
inverse(v)
max(e1,e2)
min(e1,e2)
ranked(v,s)
mean(v)
sum(v)
sd(v)
phi(e)
pow(e1,e2)
sqrt(e)
```

Note: there is no function for computing a product. But the summation can be used for doing this, by taking logarithms: $ab = \exp(\log(ab)) = \exp(\log(a) + \log(b))$.

Note: these logical functions calculate a deterministic value that must be assigned to some variable, "$\leftarrow$", and those variables must not have an assigned value as data, nor initial value.

Sometimes we need to have IF-THEN -structures, but these are not part of WinBUGS syntax in the same way as in procedural languages. Remember, WinBUGS is a declarative language. Therefore, if we need something like this:

$$\begin{array}{ll} \text{if } y = 1 & \text{then } x \sim N(\mu_1, 1) \\ & \text{else } x \sim N(\mu_2, 1), \end{array}$$

it has to be coded as:

```
x[1] ~ dnorm(mu[1],1)
x[2] ~ dnorm(mu[2],1)
z <- equals(y,1)*x[1] + (1-equals(y,1))*x[2]
```

This shows how to define mixture distributions by setting y as a Bernoulli-variable. The Bernoulli probability would correspond to weight of the first mixture component, $\mathrm{N}(\mu_1, 1)$. Also `step`-function could be used. Moreover, multiple logical choices could be implemented by using `categorical`-distribution:

```
 a ~ dcat(p[])
 z ~ dnorm(mu[a],1)
```

7.4.1 Example: hypothesis of two models

If the alternative hypotheses can be described as alternative models: $M_1 : N(0,1)$ and $M_2 : N(3,1)$ (with no other choices, so $P(M_1) = 1 - P(M_2)$) and observed data consists of $z = 1$, then the posterior probability of each hypothesis can be modeled as:

```
 model{
 a ~ dcat(p[])
 p[1] <- 0.5; p[2] <- 0.5
 z ~  dnorm(mu[a],1)
 mu[1] <- 0; mu[2] <- 3
 z <- 1
 P1 <- equals(a,1)
 }
```

By computing the average of P1 over the simulation, we can approximate the posterior probability:

$$P(\text{M1} \mid z) = \frac{P(z \mid \text{M1})P(\text{M1})}{P(z \mid \text{M1})P(\text{M1}) + P(z \mid \text{M2})P(\text{M2})}.$$

This can also be interpreted as a classification problem. The observation z belongs to either 'class', so that the simulated average of P1 is an approximation of the posterior probability of belonging to class 1.

7.5 Irregular data structure

Original data are often not in the form of a regular $n \times m$ matrix, but in the form of a ragged array. For example, different individuals can contribute a different number of measurements. Such data could be augmented by symbols of missing data "NA":

```
list(A=structure(
       .Data=c(7,NA,NA,
               9,6,3,
               2,NA,5),
       .Dim=c(3,3)))
```

Alternatively, we could code the data as a single vector, and use auxiliary indexing:

```
 list(A=c(7,9,6,3,2,5),
      person=c(1,2,2,2,3,3))
```

In the model, we can then use nested indexing to pick the right data value for the right model expression:

```
A[i] ~ dnorm(mu[person[i]],tau)
```

If the augmentation by NAs was used, WB will interpret these as missing data, and it will automatically sample these values as any other unknown quantities in the model. In other words: we will get a posterior distribution for the missing values. (Actually, this will be either prior or posterior predictive distribution). It is also possible to use offset-variables, but that technique is more prone to coding errors than the other two approaches.

7.6 Distributions

A list of all available distributions (and also logical functions) is found from the Help-menu. It may be noted that the list is not exhaustive catalogue of all distributions. Usually it is sufficient also when some other distributions are needed, because some distributions are related to each other so that random variables of one distribution can be transformed to random variables of another.

Sometimes, problems occur in special situations. For example, if a binomial distribution becomes defined with $N = 0$. This could happen when the data contain a list of sample sizes in a surveillance scheme and sometimes there have been no samples at all. The error can be avoided by removing such 'data' because there would be no loss of information. Another problem might occur if the binomial N is being estimated. In this case, initial value should be larger than zero, although the resulting posterior will cover also zero. There are some minor differences between different versions of WB which may result in different behaviour in extreme or unusual situations.

As a special case of distributions, censored observations may need to be modeled. This means that instead of an exact observation of X, we only know that $X > L$. Then, instead of the conditional density

$$\pi(X \mid \text{parameters})$$

we need the conditional probability:

$$P(X > L \mid \text{parameters})$$

These are frequently used in survival modeling where the observations are often censored from right $X > L$ or left $X < H$, or both $L < X < H$. In WB, this can be implemented using I-function. For example, with normal density:

```
x ~ dnorm(mu,tau)I(low,)
y ~ dnorm(mu,tau)I(,high)
z ~ dnorm(mu,tau)I(low,high)
```

Here, the limits low and high are not allowed to depend on the parameters to be estimated, mu and tau. The same can be written using 'one's trick'. For example:

```
x ~ dnorm(mu,tau)
one <- 1
one ~ dbern(pr)
pr <- step(x-L)
```

Here, 'one' is an instrumental bernoulli-variable which is defined as 'observed data' telling that $X > L$.

Truncated distribution modeling is different from censored data. For example, a truncated normal distribution $\mathrm{N}(\mu, \tau)$ over the interval $[5, \infty]$ has a probability density that has the same functional form as the original density, apart from a different normalizing constant:

$$\frac{1}{\int_5^\infty \pi(x \mid \mu, \tau)\, \mathbf{d}x}$$

which depends on the unknown parameters μ and τ. If these parameters are to be estimated, the normalizing constant is not constant with respect to these parameters, and we need to include the correct truncated model somehow. In principle, customized own distributions can be defined in WB using 'zero's trick':

```
C <- 10000
for (i in 1:N){
 zeros[i] <- 0
 phi[i] <-   -log(L[i])+C
 zeros[i] ~ dpois(phi[i])
}
```

where `C` needs to sufficiently large so that `phi` would be always positive. The trick is based on observing that the probability of 'zero' in a Poisson model is $P(0) = \exp(-\lambda)$, i.e. $\lambda = -\log(P(0))$. When we replace the probability $P(0)$ as the self defined probability of data point `x[i]`, given here as `L[i]`, the required probability model is obtained in lieu of the 'probability of zero'. If the variable X is discrete, then $-\log(L)$ is automatically positive. Constant `C` is only needed if X is continuous and `L` represents the values of density function that can be larger than one. Then, $-\log(L)$ might not be automatically positive. Alternatively, own distributions could be implemented using 'one's trick':

```
C <- 10000
for (i in 1:N){
 ones[i] <- 1
 p[i] <- L[i]/C
 ones[i] ~ dbern(p[i])
}
```

where `C` has to be enough large so that p < 1. Again, if L is directly a probability (not a value of density function), then this works automatically without constant `C`.

In both tricks, the data are a set of numbers $\{x_1, \ldots, x_N\}$ so that the self defined distribution gives the probabilities (or probability densities) L_i for each data point, and this can be written out as an expression.

Posterior for Dirichlet parameters: Suppose as part of a model there are J probability arrays `p[j, 1:K]`, $j = 1, ..., J$, where K is the dimension of each array and `sum(p[j, 1:K])` $= 1$ for all j. We give each of them a Dirichlet prior:

```
p[j, 1:K] ~ ddirch(alpha[])
```

and we would like to learn about `alpha[]`. However, in WinBUGS the parameters `alpha[]` of a Dirichlet distribution cannot be stochastic nodes. The trick is to note that if `delta[k]` $\sim$ `dgamma(alpha[k], 1)`, then the vector with elements `delta[k] / sum(delta[1:K])`, $k = 1, ..., K$, is Dirichlet with parameters `alpha[k]`, $k = 1, ..., K$. So the following construction should allow learning about the parameters `alpha[]`:

```
for (k in 1:K){
 p[j, k] <- delta[j, k] / sum(delta[j,])
 delta[j, k] ~ dgamma(alpha[k], 1)
 }
```

A prior can be put directly on the `alpha[k]`'s.

7.7 Graphics

Graphics in WB is very basic and there are no attempts to develop more sophisticated graphical tools within WB since there are many other more advanced software already. It is best to take the MCMC sample out from WB and then process the graphics elsewhere. The histogram plots in WB can be modestly edited, though. ('properties').

7.8 Scripts

It may be convenient to run WB using scripts. In this way, we can avoid mouse clicking all the steps in every simulation. The script is a series of commands written in the specific file `script.odc`. This file could be for example:

```
display('log')
check('C:/kurssi/koemalli.odc')
data('C:/kurssi/koemallindata.odc')
compile(3)
gen.inits()
update(500)
set(parameter)
update(1000)
history(parameter)
gr(parameter)
coda(parameter,C:/kurssi/output)
quit()
```

The model code would be written in the file `koemalli.odc`. The script is run by running the file `backbugs.exe`. The specified series of tasks is then done, and the results are written in files, file names starting with 'output'.

7.9 More resources

First aid can be sought here:

- Example codes (Help → examples Vol I & II (& Vol III in OpenBUGS)).
- Help → User manual.
- WB FAQ:
`http://www.mrc-bsu.cam.ac.uk/bugs/faqs/contents.shtml`
- WB mailing list archives:
`http://www.jiscmail.ac.uk/lists/bugs.html`

If nothing helps, you can try WB mailing list.

If you want to use Linux instead of Windows, the open-bugs version could be used:
`http://mathstat.helsinki.fi/openbugs/`

Moreover, there are some extensions as downloadables. For example, GeoBUGS is a special package for spatial modelling that is already included in WB1.4.1. (Menu: map).

WB development interface provides more downloadable extensions, such as Reversible-Jump MCMC.

`http://www.winbugs-development.org.uk/`

By using WBDev, it is possible to build your own 'hardwired' WB functions and distributions, that would otherwise run too slowly if coded as part of the model definition code.

Finally: Always document your WinBUGS code properly! There can never be too many comment lines within the code. Just like with any other programming, after 6 months you will not remember clearly what `xzpred2` is. If the model is going to be used by you or anyone else after a longer time, make sure the code is readable and understandable. After all, it is the mathematical model that should be uniquely and clearly defined. There can be many different WinBUGS implementations for the same model, and the implementation of computer code alone is not a sufficient documentation of the model.