

An Introduction to Using WinBUGS for Cost-Effectiveness Analyses in Health Economics

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Practical 1

Getting started in OpenBUGS / WinBUGS

- Brief comparison WinBUGS / OpenBUGS
- Practical
 - Opening OpenBUGS
 - Entering a model and data
 - Some error messages
 - Starting the sampler
 - Checking sampling performance
 - Retrieving the posterior summaries

WinBUGS / OpenBUGS

- **WinBUGS** was developed at the MRC Biostatistics unit in Cambridge. Free download, but registration required for a licence. No fee and no warranty.
- **OpenBUGS** is the current development of WinBUGS after its source code was released to the public. Download is free, no registration, GNU GPL licence.

WinBUGS / OpenBUGS

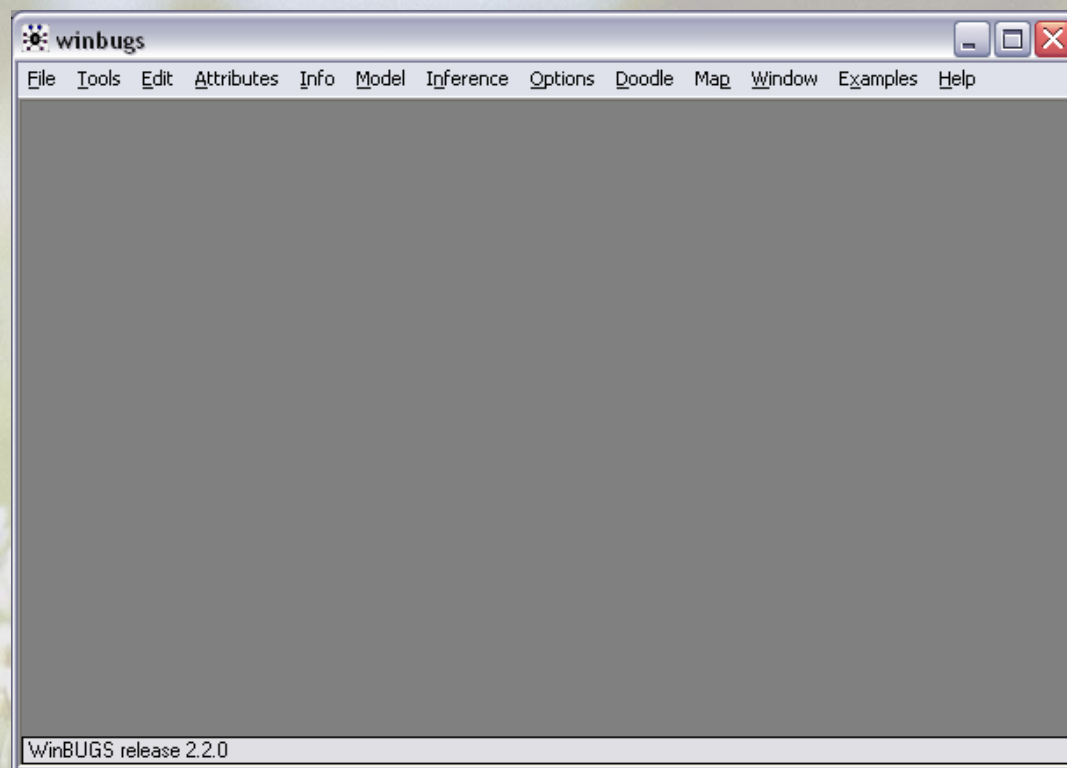
- There are **no major differences** between the latest WinBUGS (1.4.1) and OpenBUGS (2.2.0) releases.
- Minor differences include:
 - OpenBUGS is occasionally a bit slower
 - WinBUGS requires Microsoft Windows OS
 - OpenBUGS error messages are sometimes more informative
- The examples in these slides use OpenBUGS.

Practical 1: Target

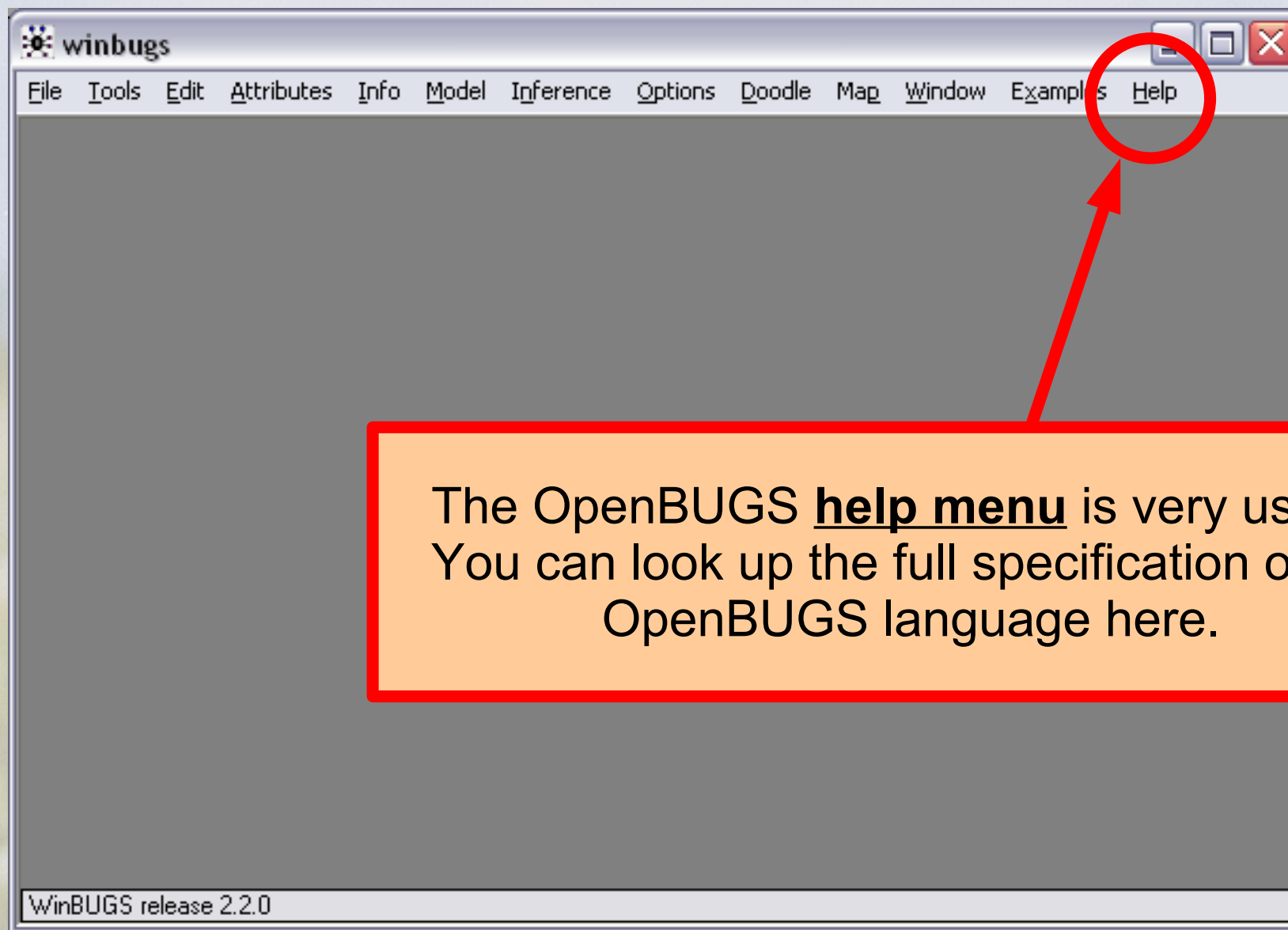
- Start OpenBUGS
- Code the example from health economics from the earlier presentation
- Run the sampler and obtain posterior summaries

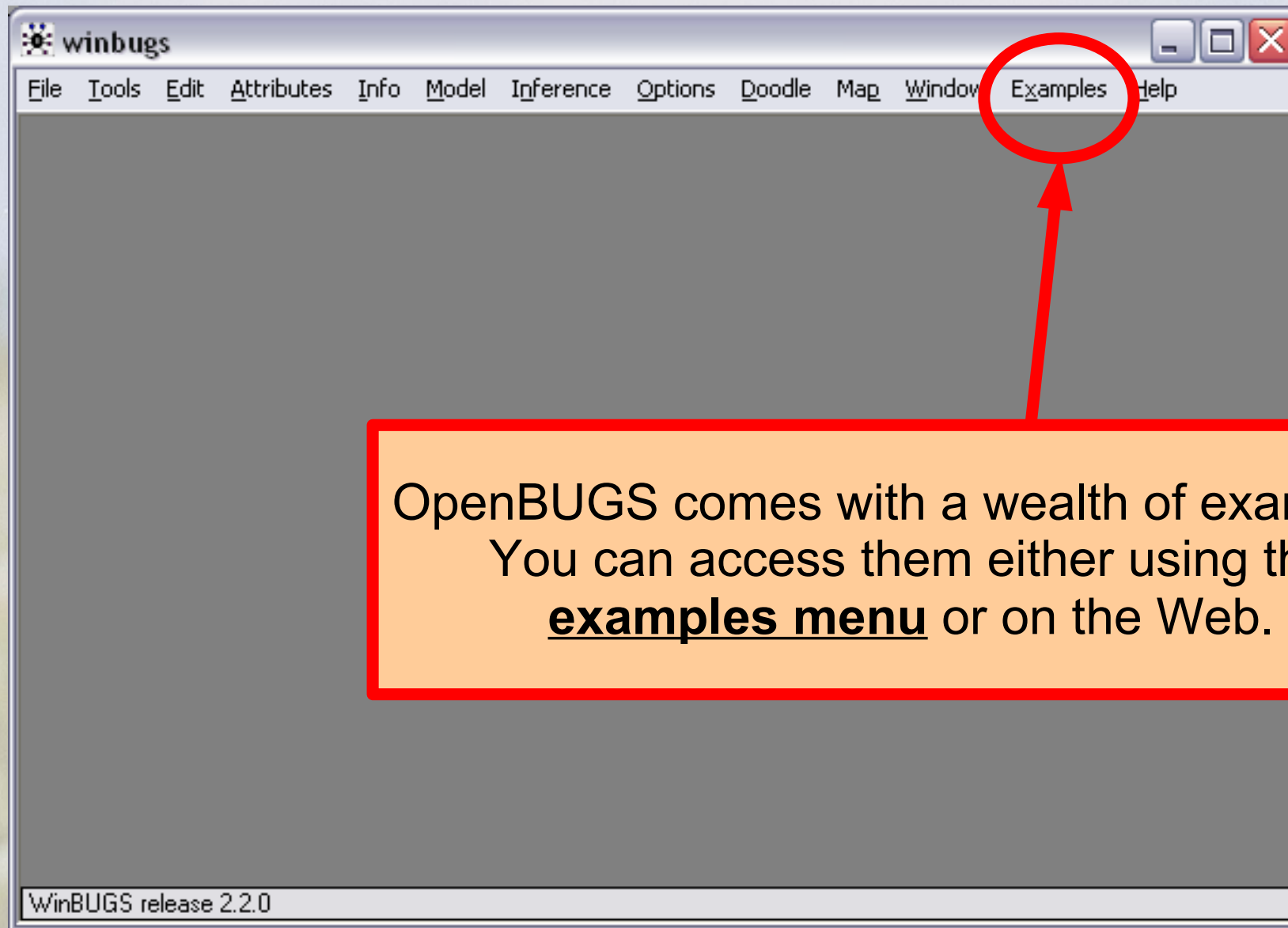
Starting OpenBUGS

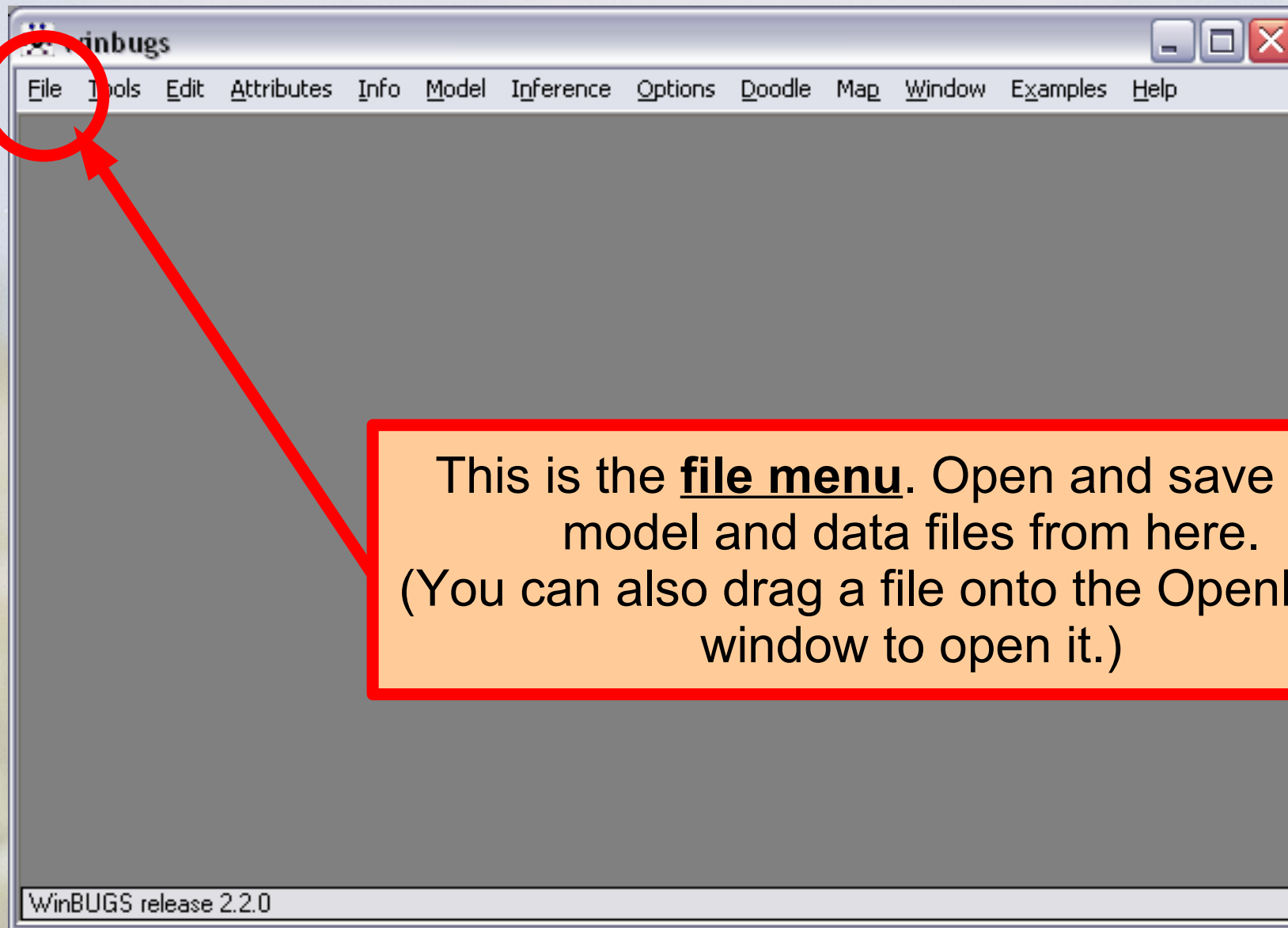
- You can download OpenBUGS from <http://mathstat.helsinki.fi/openbugs/>
- Start the program.



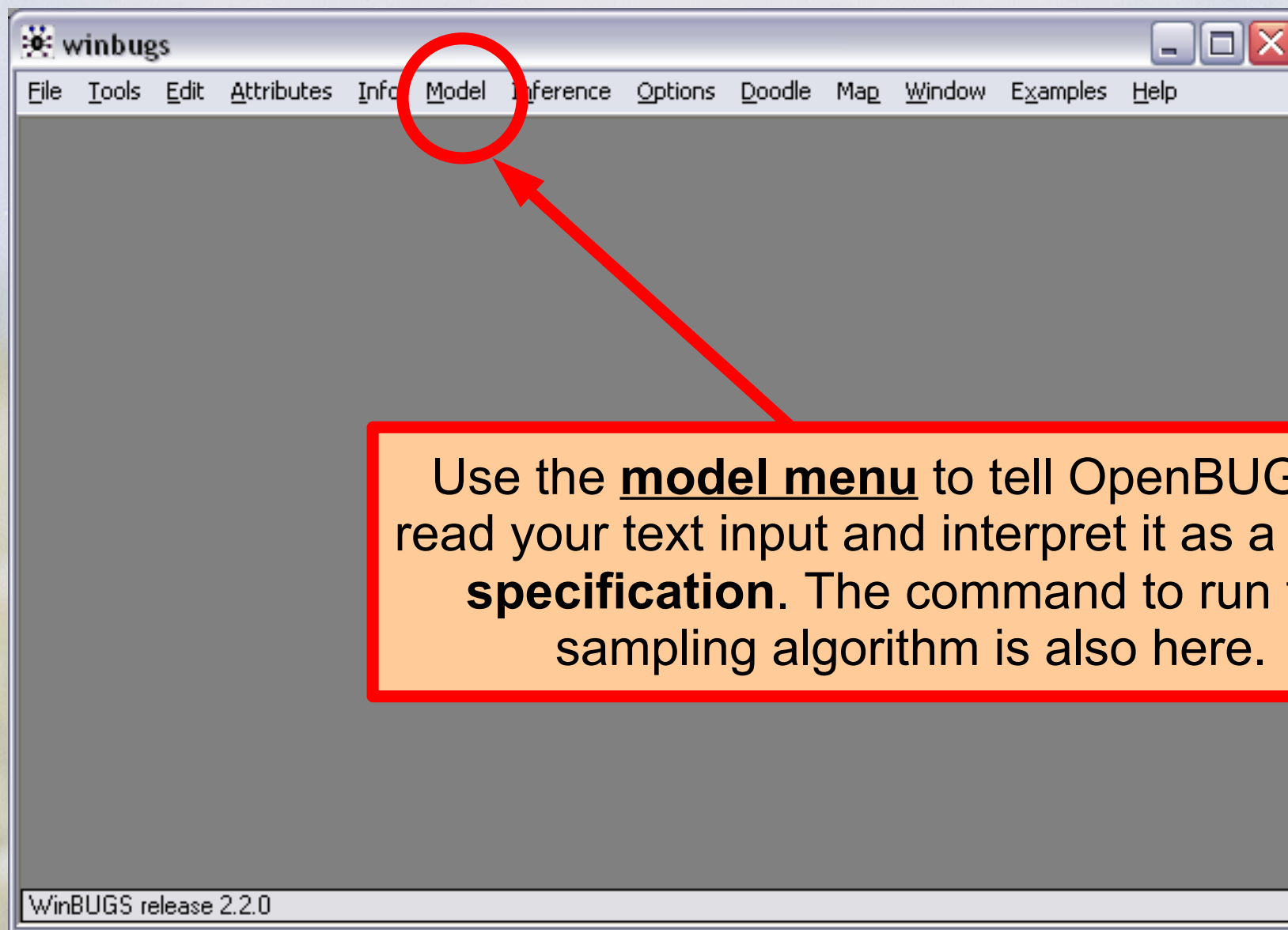


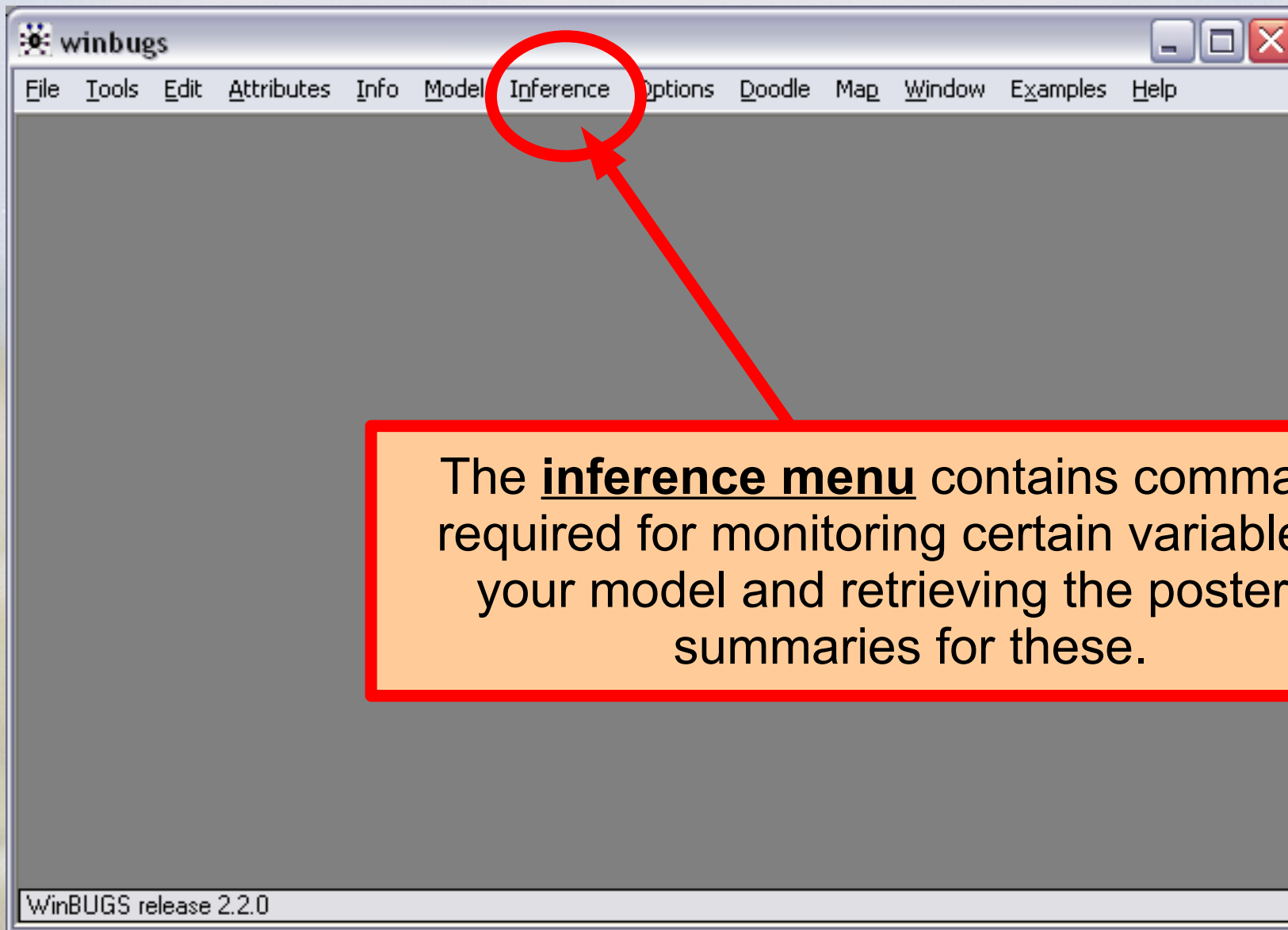


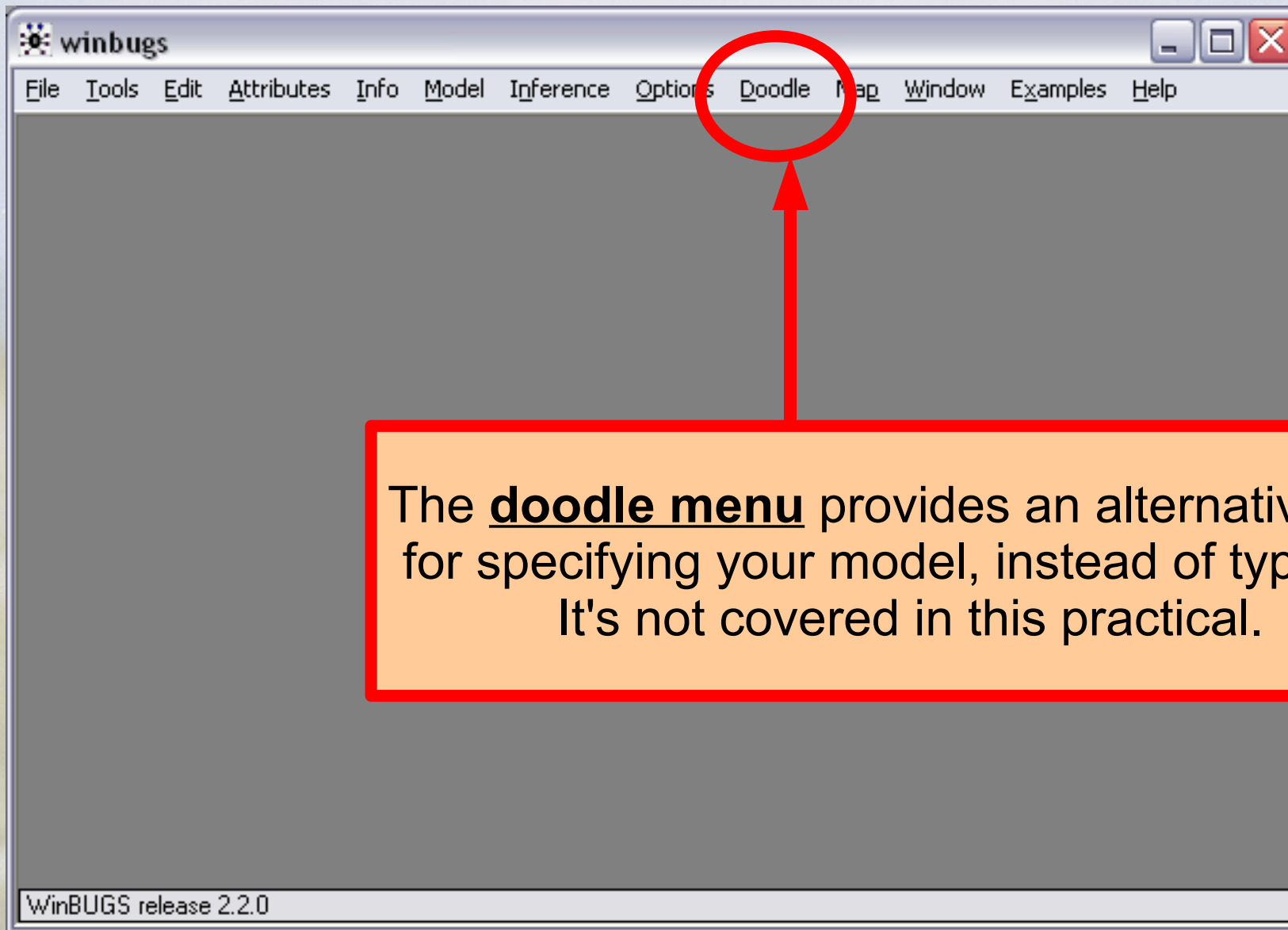


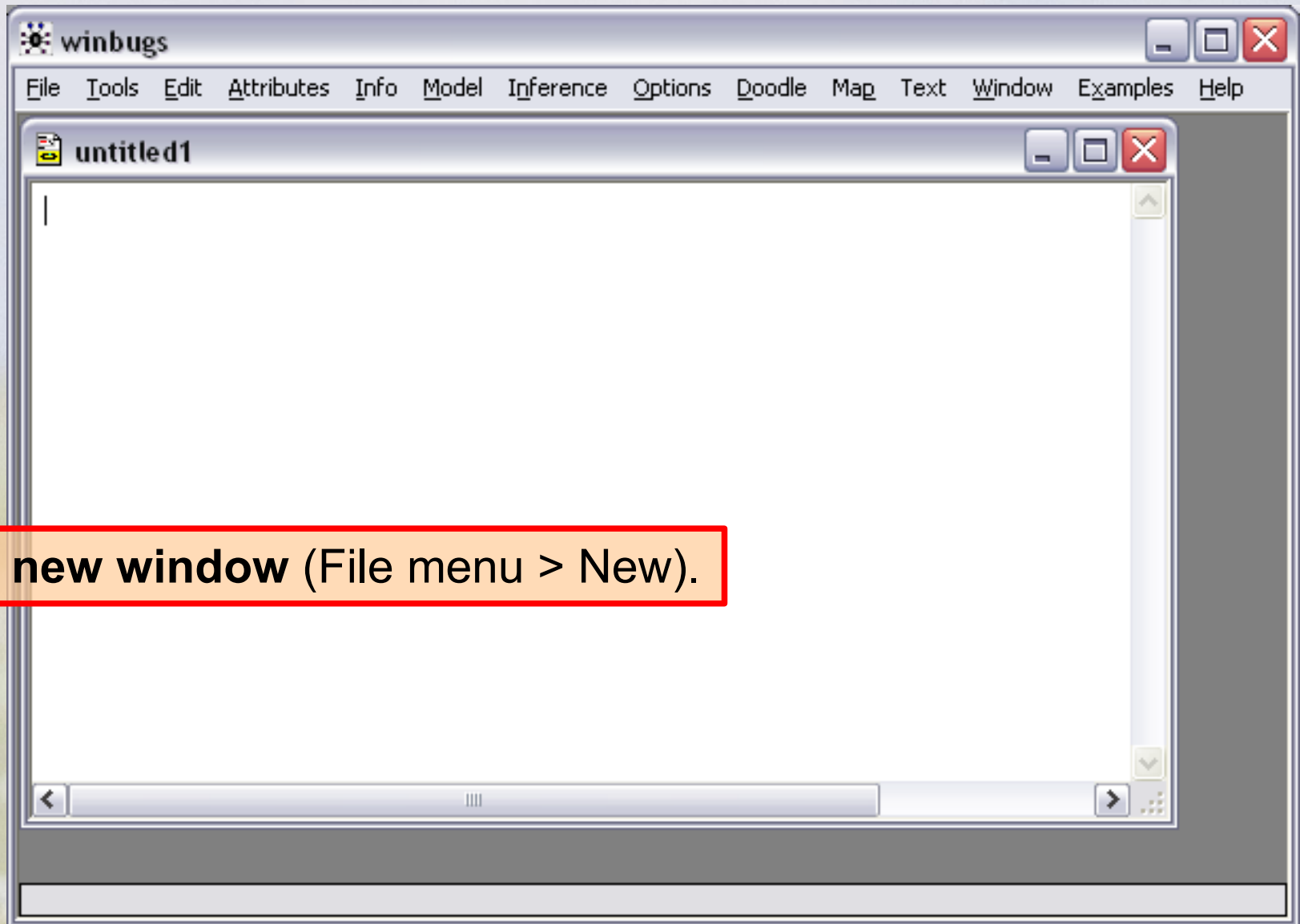


This is the **file menu**. Open and save your model and data files from here.
(You can also drag a file onto the OpenBUGS window to open it.)

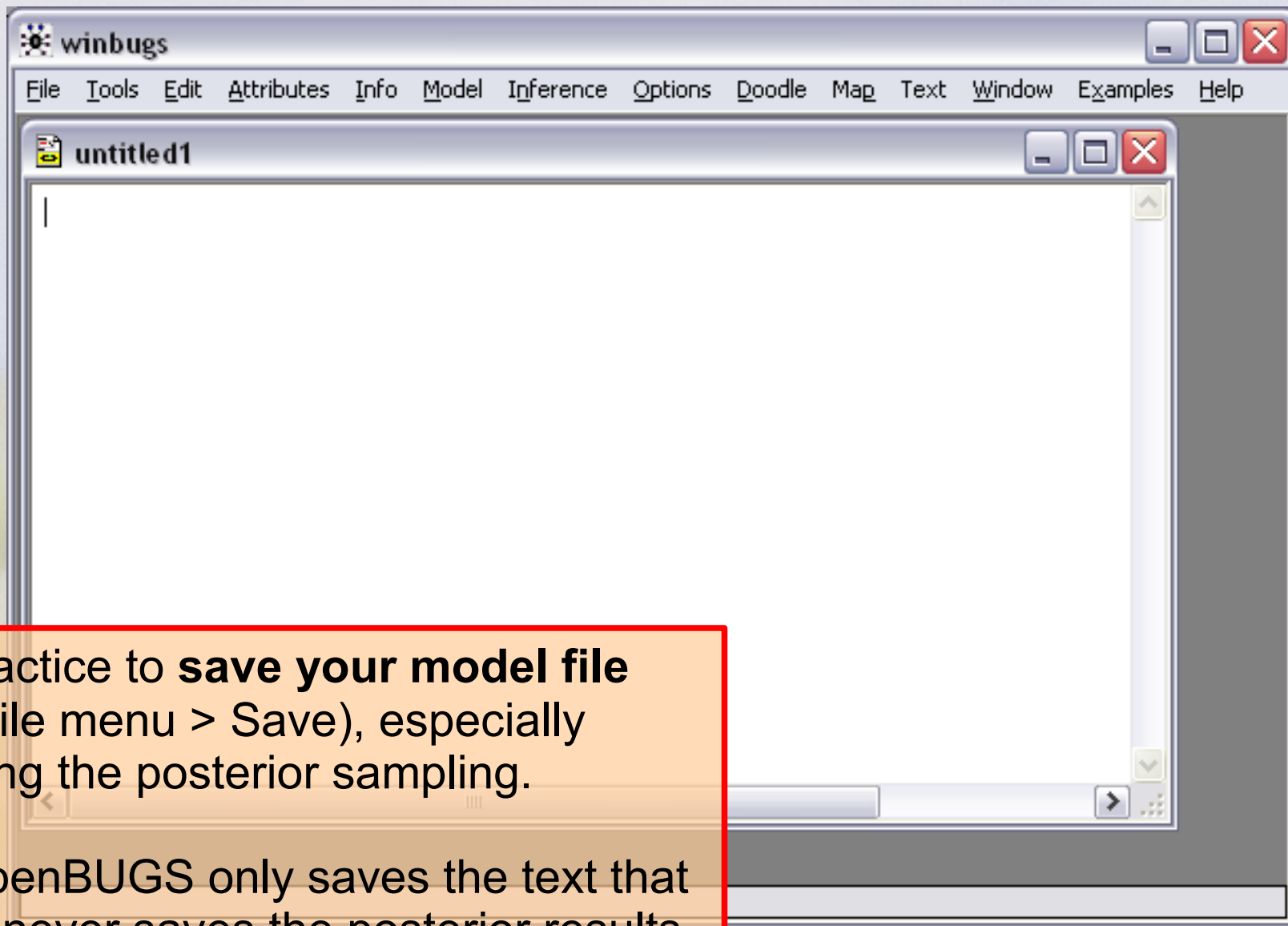








Let's open a **new window** (File menu > New).



It is good practice to **save your model file regularly** (File menu > Save), especially before starting the posterior sampling.

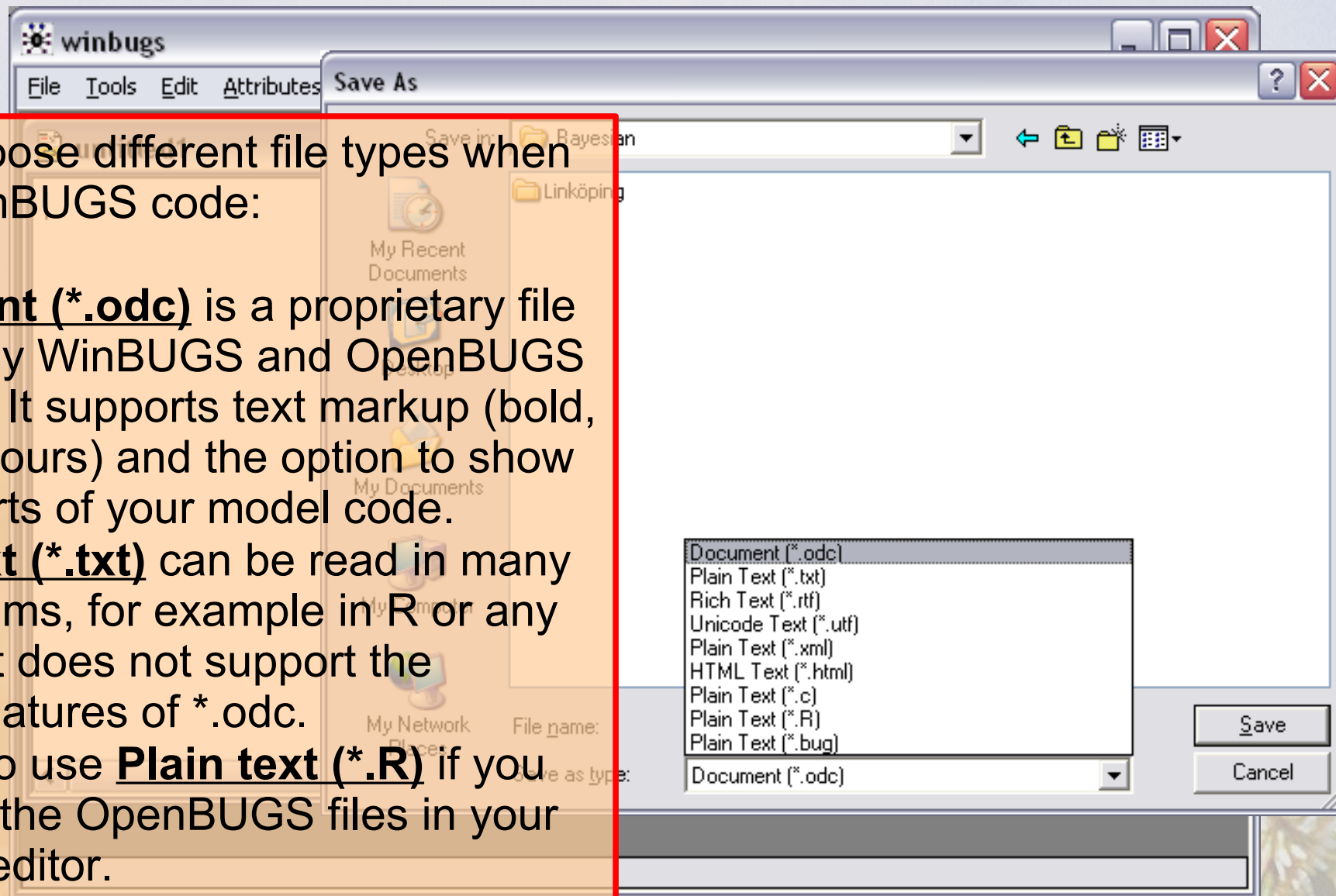
Note that OpenBUGS only saves the text that you enter, it never saves the posterior results.

You can choose different file types when saving OpenBUGS code:

→ **Document (*.odc)** is a proprietary file type that only WinBUGS and OpenBUGS understand. It supports text markup (bold, fontface, colours) and the option to show and hide parts of your model code.

→ **Plain text (*.txt)** can be read in many other programs, for example in R or any text editor. It does not support the advanced features of *.odc.

You can also use **Plain text (*.R)** if you want to edit the OpenBUGS files in your favourite R editor.



Syntax of the OpenBUGS language

Writing OpenBUGS code is similar to writing R code.

- `<-` Define the value of the LHS by a calculation
- `~` Define the value of the LHS by a probability distribution
- `x[5]` Refer to a vector (or array) element

`for (i in 1:20) {` Write a “for” loop like this.
 ...
 }

Syntax of the OpenBUGS language

Note on the use of brackets:

() round brackets

- group mathematical terms in an equation – e.g. $x^*(a+b)$
- submit arguments to a function – e.g. `exp(log(q))`
- are used in special cases like the “for” loop.

[] square brackets index a vector or an array.

{ } curly brackets group statements into blocks.

Syntax of the OpenBUGS language

Important differences to R syntax:

In OpenBUGS the **order of the statements is irrelevant**. Code is not executed from top to bottom.

In OpenBUGS you do **not need to define an array or vector** before you use it. It suffices to indicate on the LHS of an equation that you are assigning to a particular element of an array, e.g. `q[5,3] <- a*b`

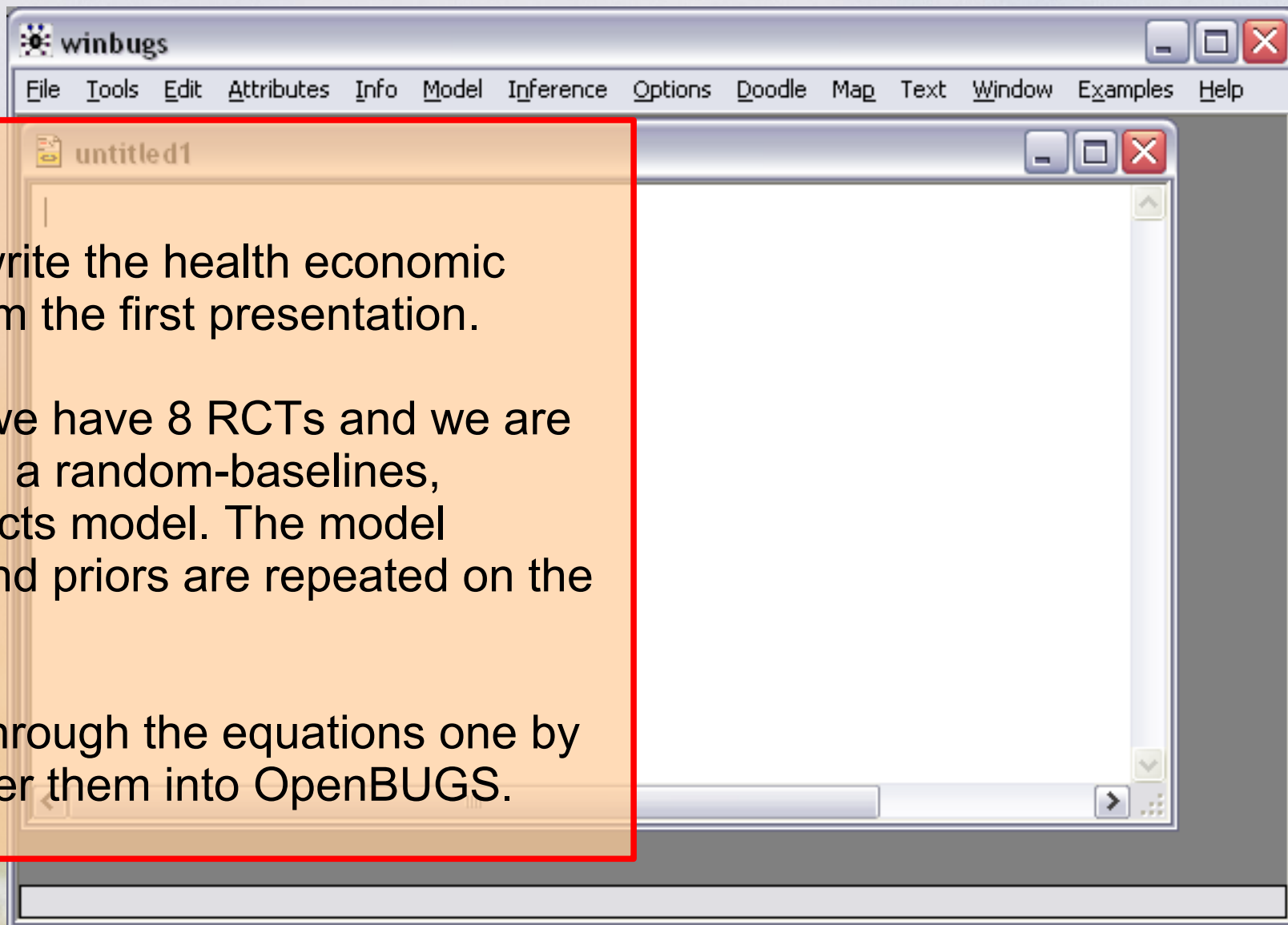
In OpenBUGS if you want to **refer to an entire array**, you must put empty square brackets behind the name, e.g. `q[,]`

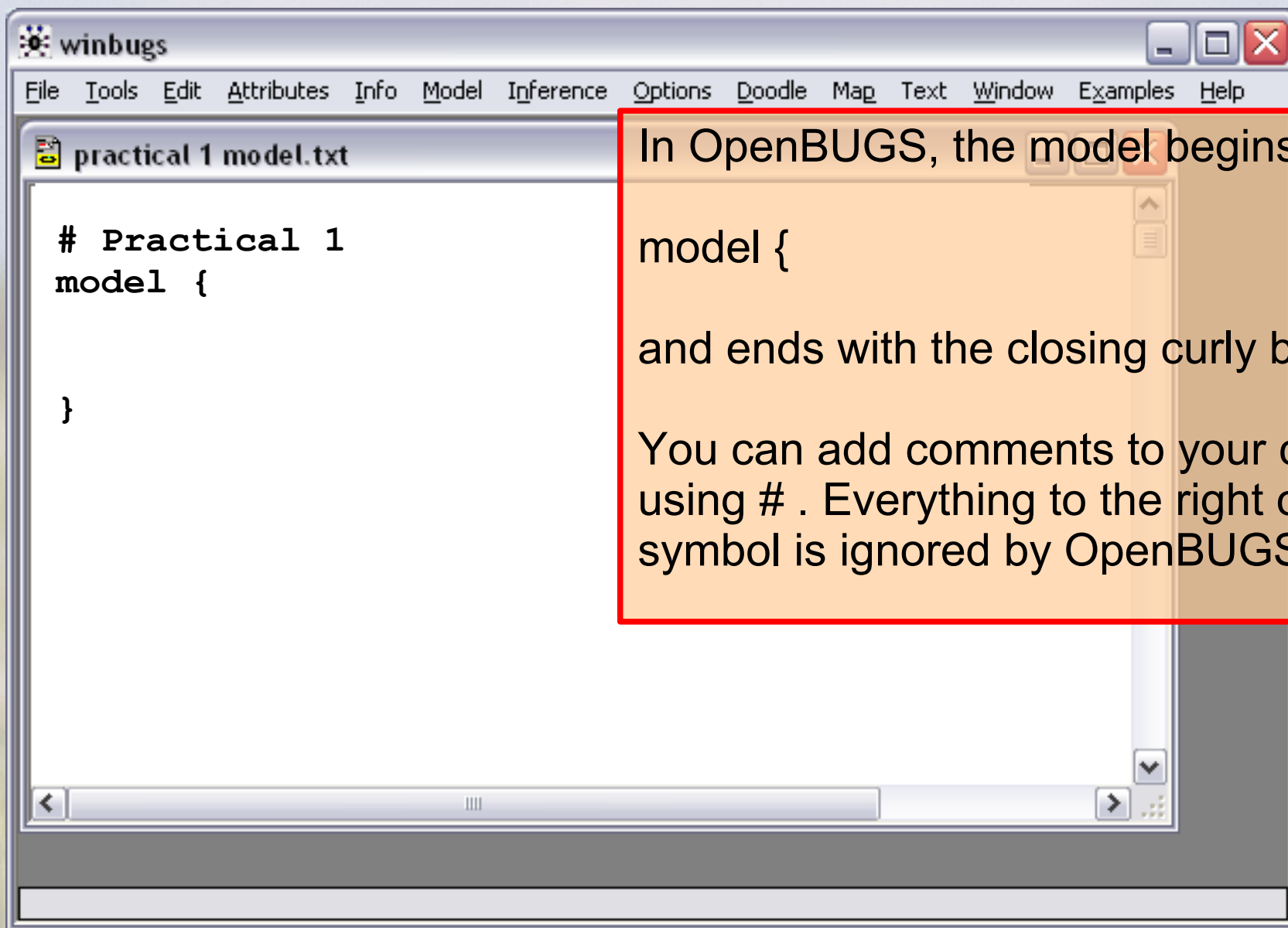
Ready?

Let's try to write the health economic example from the first presentation.

Recall that we have 8 RCTs and we are working with a random-baselines, random-effects model. The model equations and priors are repeated on the next slides.

We will go through the equations one by one and enter them into OpenBUGS.

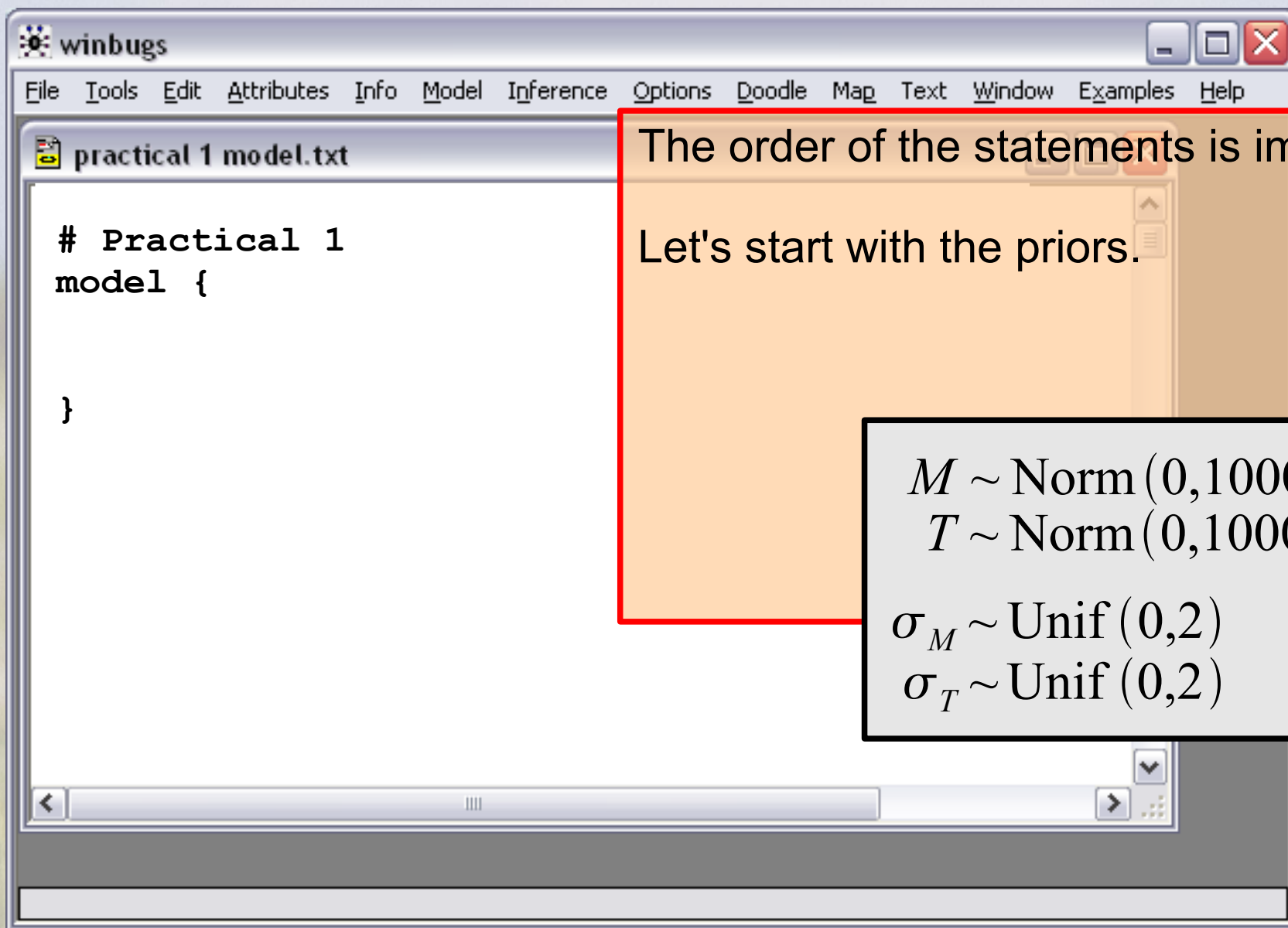




```
winbugs
File Tools Edit Attributes Info Model Inference Options Doodle Map Text Window Examples Help
practical 1 model.txt
# Practical 1
model {

}
```

In OpenBUGS, the model begins with `model {` and ends with the closing curly bracket `}`. You can add comments to your code using `#`. Everything to the right of a `#` symbol is ignored by OpenBUGS.

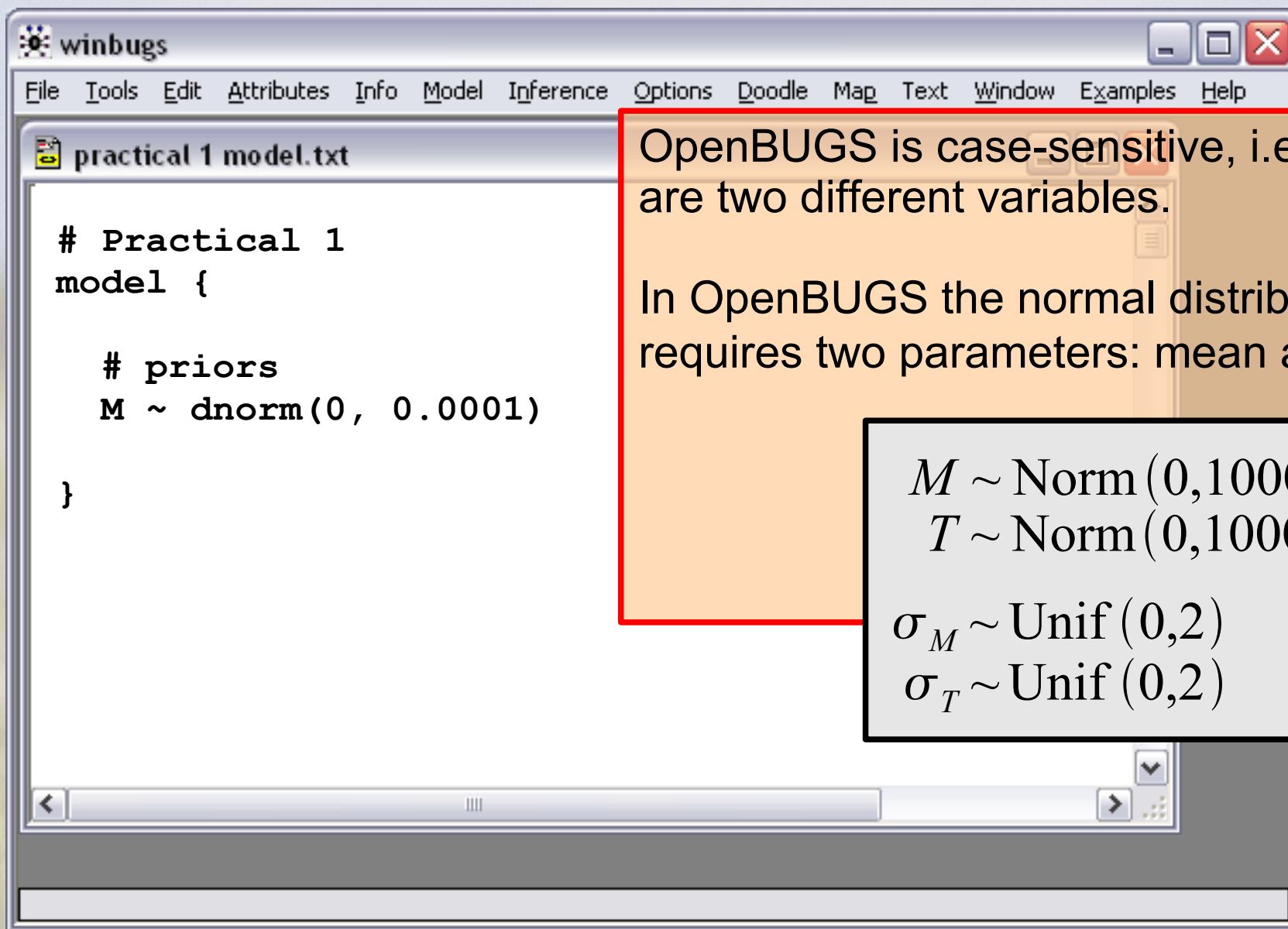


The order of the statements is immaterial.

Let's start with the priors.

$$M \sim \text{Norm}(0, 10000)$$
$$T \sim \text{Norm}(0, 10000)$$

$$\sigma_M \sim \text{Unif}(0, 2)$$
$$\sigma_T \sim \text{Unif}(0, 2)$$



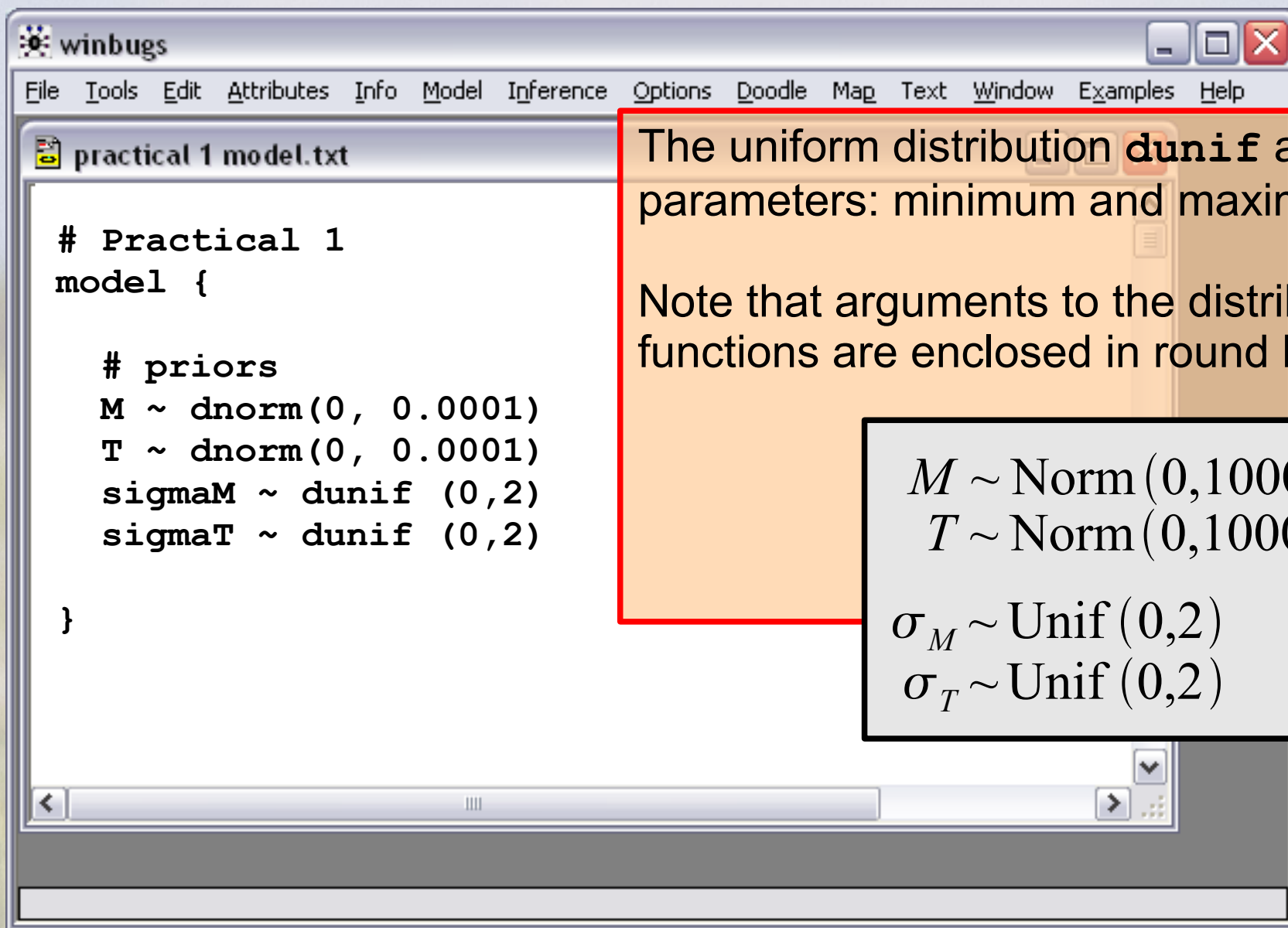
```
winbugs
File Tools Edit Attributes Info Model Inference Options Doodle Map Text Window Examples Help
practical 1 model.txt
# Practical 1
model {
  # priors
  M ~ dnorm(0, 0.0001)
}
```

OpenBUGS is case-sensitive, i.e. M and m are two different variables.

In OpenBUGS the normal distribution **dnorm** requires two parameters: mean and precision.

$$M \sim \text{Norm}(0, 10000)$$
$$T \sim \text{Norm}(0, 10000)$$

$$\sigma_M \sim \text{Unif}(0, 2)$$
$$\sigma_T \sim \text{Unif}(0, 2)$$



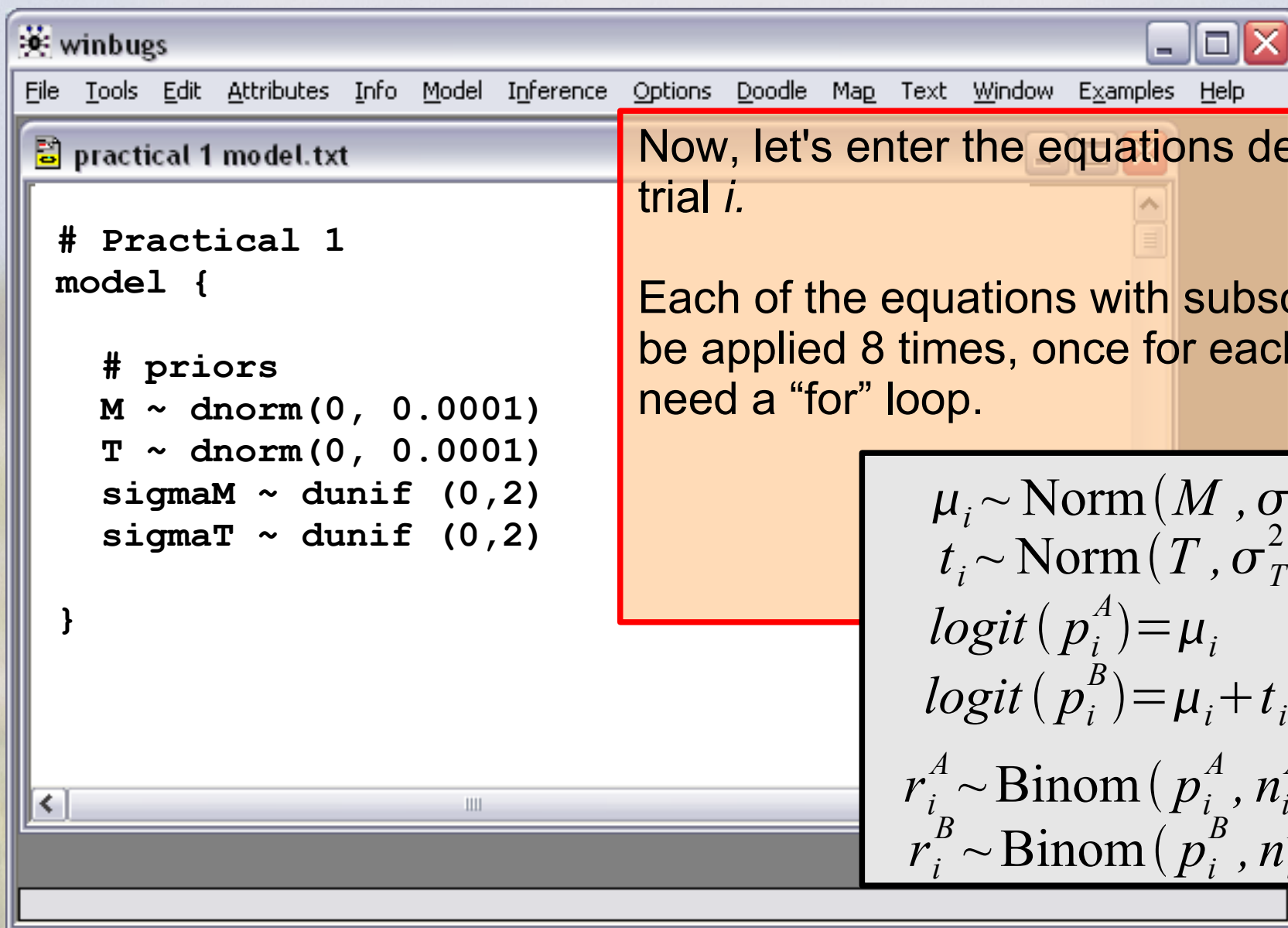
```
winbugs
File Tools Edit Attributes Info Model Inference Options Doodle Map Text Window Examples Help
practical 1 model.txt
# Practical 1
model {
  # priors
  M ~ dnorm(0, 0.0001)
  T ~ dnorm(0, 0.0001)
  sigmaM ~ dunif (0,2)
  sigmaT ~ dunif (0,2)
}
```

The uniform distribution `dunif` also takes two parameters: minimum and maximum.

Note that arguments to the distribution functions are enclosed in round brackets ().

$$M \sim \text{Norm}(0, 10000)$$
$$T \sim \text{Norm}(0, 10000)$$

$$\sigma_M \sim \text{Unif}(0, 2)$$
$$\sigma_T \sim \text{Unif}(0, 2)$$

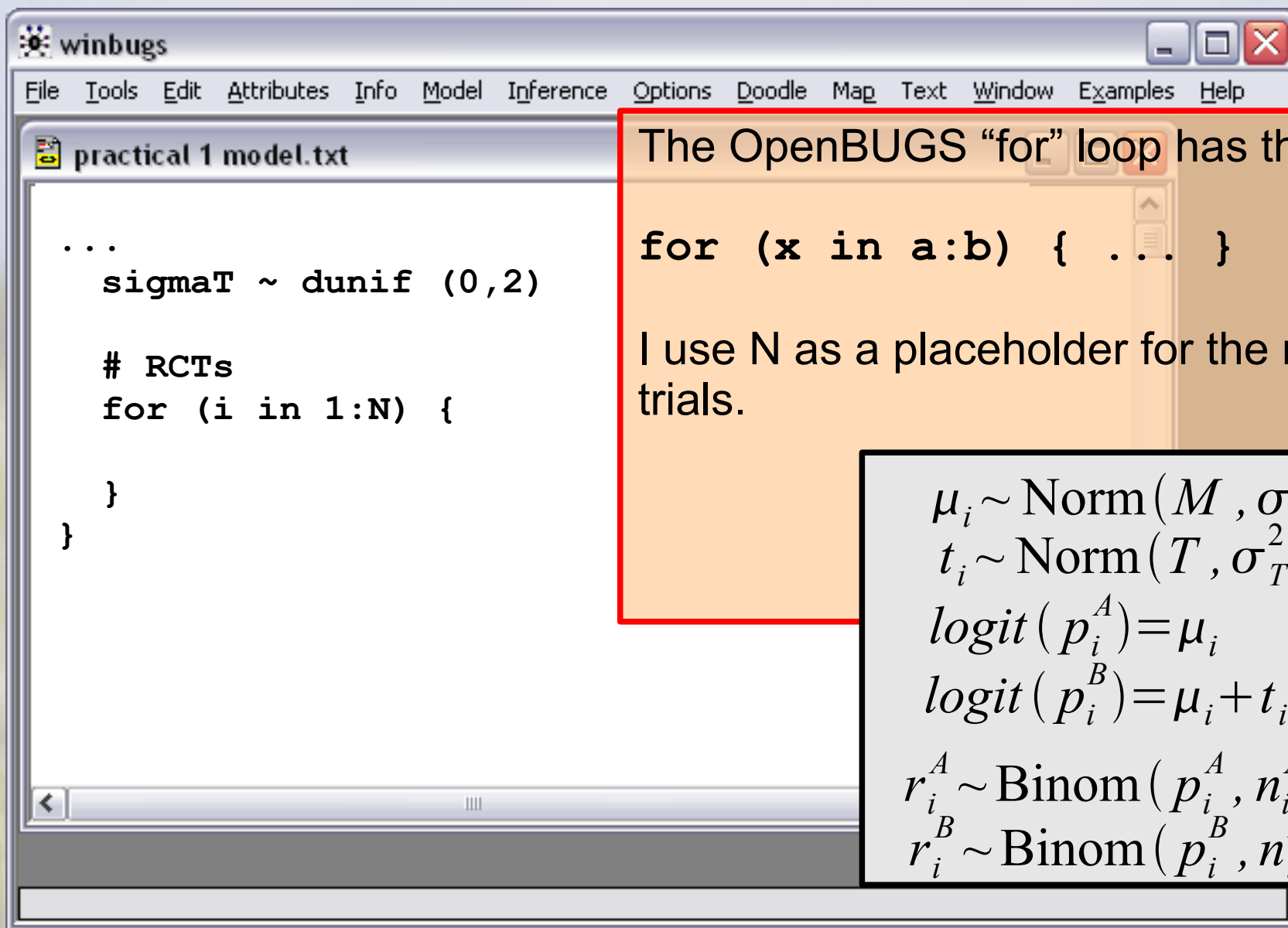


```
winbugs
File Tools Edit Attributes Info Model Inference Options Doodle Map Text Window Examples Help
practical 1 model.txt
# Practical 1
model {
  # priors
  M ~ dnorm(0, 0.0001)
  T ~ dnorm(0, 0.0001)
  sigmaM ~ dunif(0,2)
  sigmaT ~ dunif(0,2)
}
```

Now, let's enter the equations describing each trial i .

Each of the equations with subscript i has to be applied 8 times, once for each trial. We need a “for” loop.

$$\begin{aligned}\mu_i &\sim \text{Norm}(M, \sigma_M^2) \\ t_i &\sim \text{Norm}(T, \sigma_T^2) \\ \text{logit}(p_i^A) &= \mu_i \\ \text{logit}(p_i^B) &= \mu_i + t_i \\ r_i^A &\sim \text{Binom}(p_i^A, n_i^A) \\ r_i^B &\sim \text{Binom}(p_i^B, n_i^B)\end{aligned}$$



```
winbugs
File Tools Edit Attributes Info Model Inference Options Doodle Map Text Window Examples Help
practical 1 model.txt
...
sigmaT ~ dunif (0,2)

# RCTs
for (i in 1:N) {

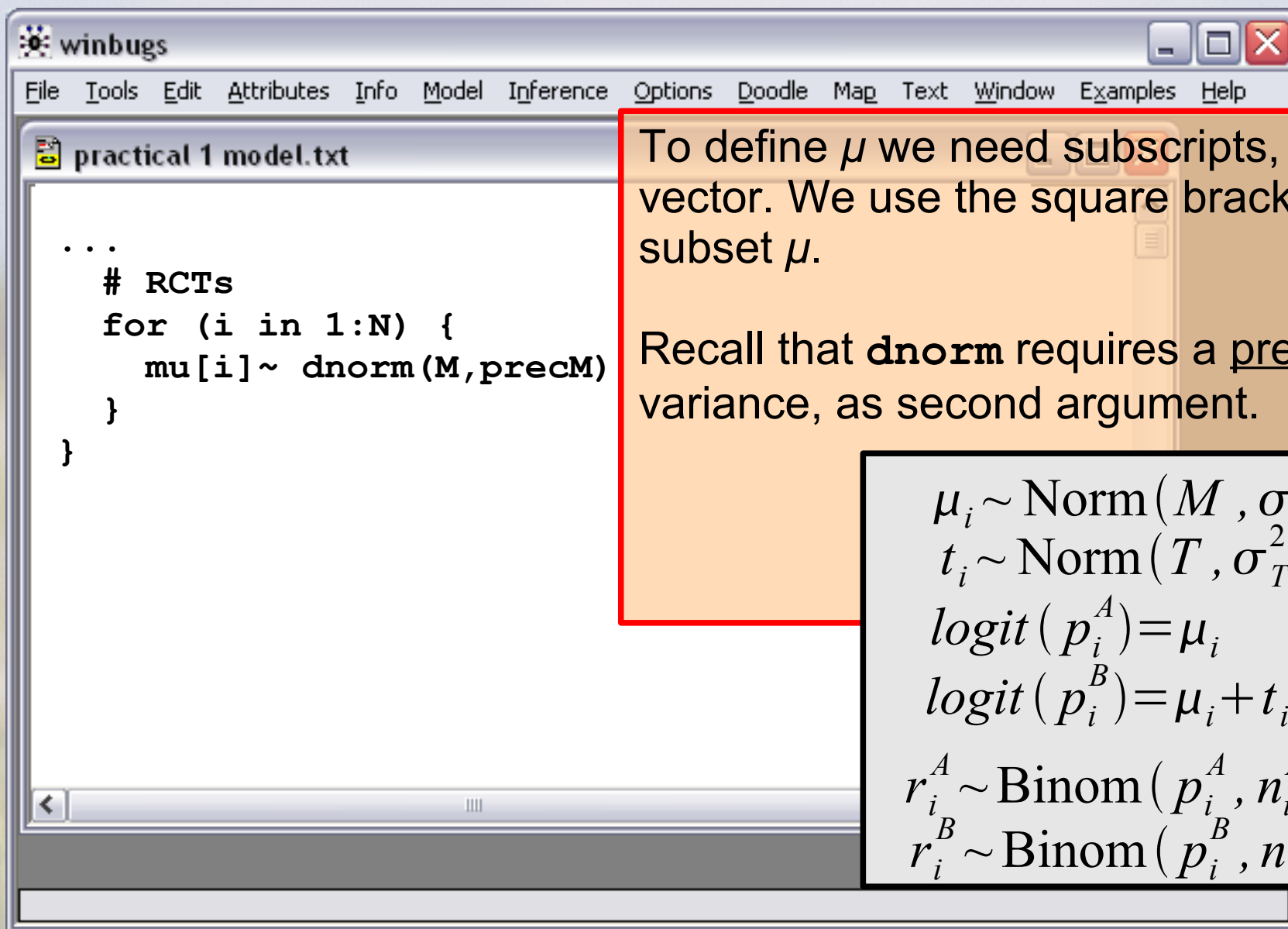
}
}
```

The OpenBUGS “for” loop has this syntax:

```
for (x in a:b) { ... }
```

I use N as a placeholder for the number of trials.

$$\begin{aligned}\mu_i &\sim \text{Norm}(M, \sigma_M^2) \\ t_i &\sim \text{Norm}(T, \sigma_T^2) \\ \text{logit}(p_i^A) &= \mu_i \\ \text{logit}(p_i^B) &= \mu_i + t_i \\ r_i^A &\sim \text{Binom}(p_i^A, n_i^A) \\ r_i^B &\sim \text{Binom}(p_i^B, n_i^B)\end{aligned}$$



```
winbugs
File Tools Edit Attributes Info Model Inference Options Doodle Map Text Window Examples Help
practical 1 model.txt
...
# RCTs
for (i in 1:N) {
  mu[i] ~ dnorm(M, precM)
}
}
```

To define μ we need subscripts, i.e. μ is a vector. We use the square brackets $[]$ to subset μ .

Recall that **dnorm** requires a precision, not a variance, as second argument.

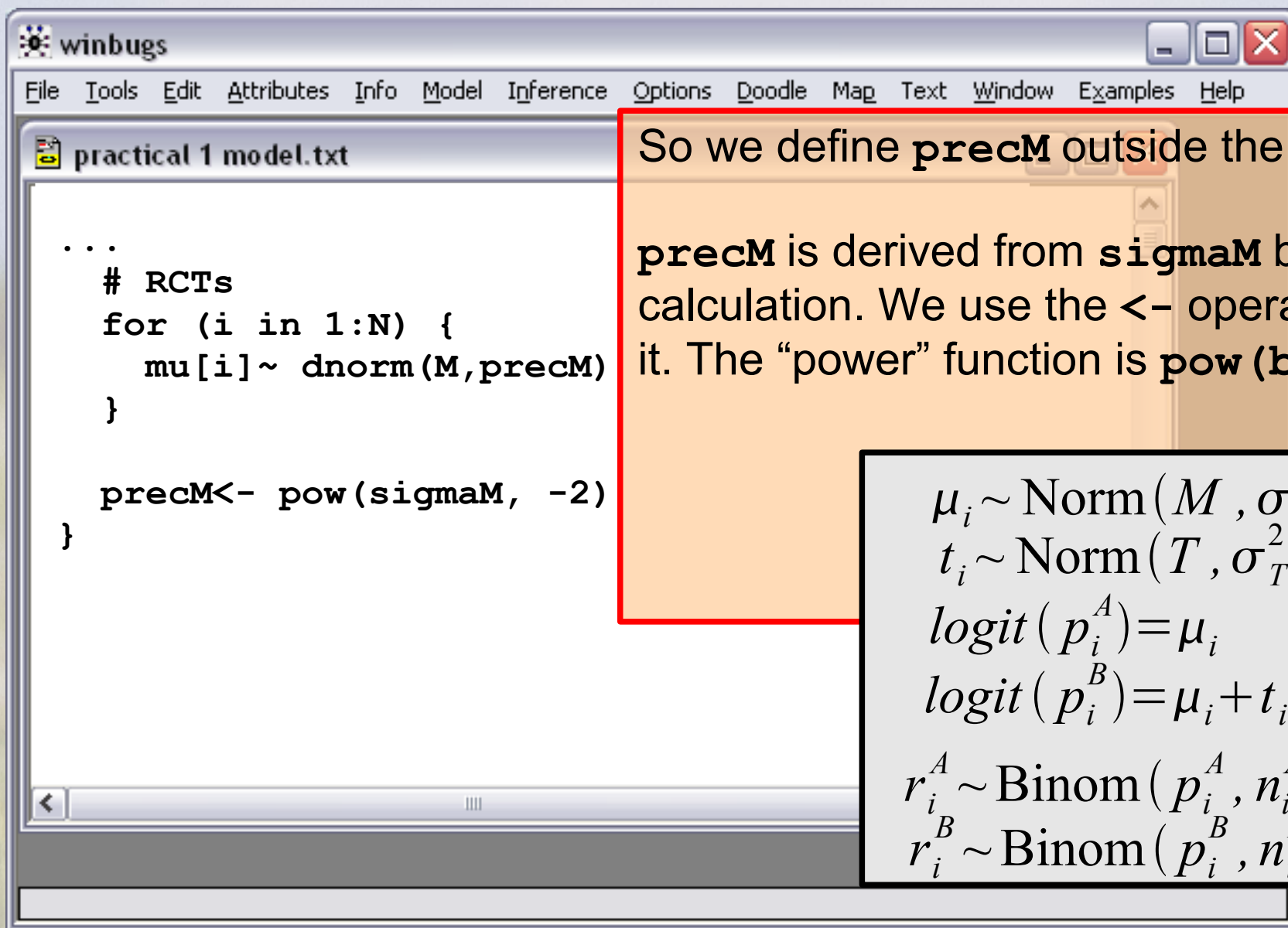
$$\begin{aligned}\mu_i &\sim \text{Norm}(M, \sigma_M^2) \\ t_i &\sim \text{Norm}(T, \sigma_T^2) \\ \text{logit}(p_i^A) &= \mu_i \\ \text{logit}(p_i^B) &= \mu_i + t_i \\ r_i^A &\sim \text{Binom}(p_i^A, n_i^A) \\ r_i^B &\sim \text{Binom}(p_i^B, n_i^B)\end{aligned}$$

```
...
# RCTs
for (i in 1:N) {
  mu[i] ~ dnorm(M, precM)
}
}
```

In OpenBUGS you are not allowed to write calculations into the arguments of the distribution functions, i.e. we cannot write $\text{dnorm}(M, 1/(\text{sigmaM} * \text{sigmaM}))$

So we define **precM** outside the “for” loop.

$$\begin{aligned} \mu_i &\sim \text{Norm}(M, \sigma_M^2) \\ t_i &\sim \text{Norm}(T, \sigma_T^2) \\ \text{logit}(p_i^A) &= \mu_i \\ \text{logit}(p_i^B) &= \mu_i + t_i \\ r_i^A &\sim \text{Binom}(p_i^A, n_i^A) \\ r_i^B &\sim \text{Binom}(p_i^B, n_i^B) \end{aligned}$$



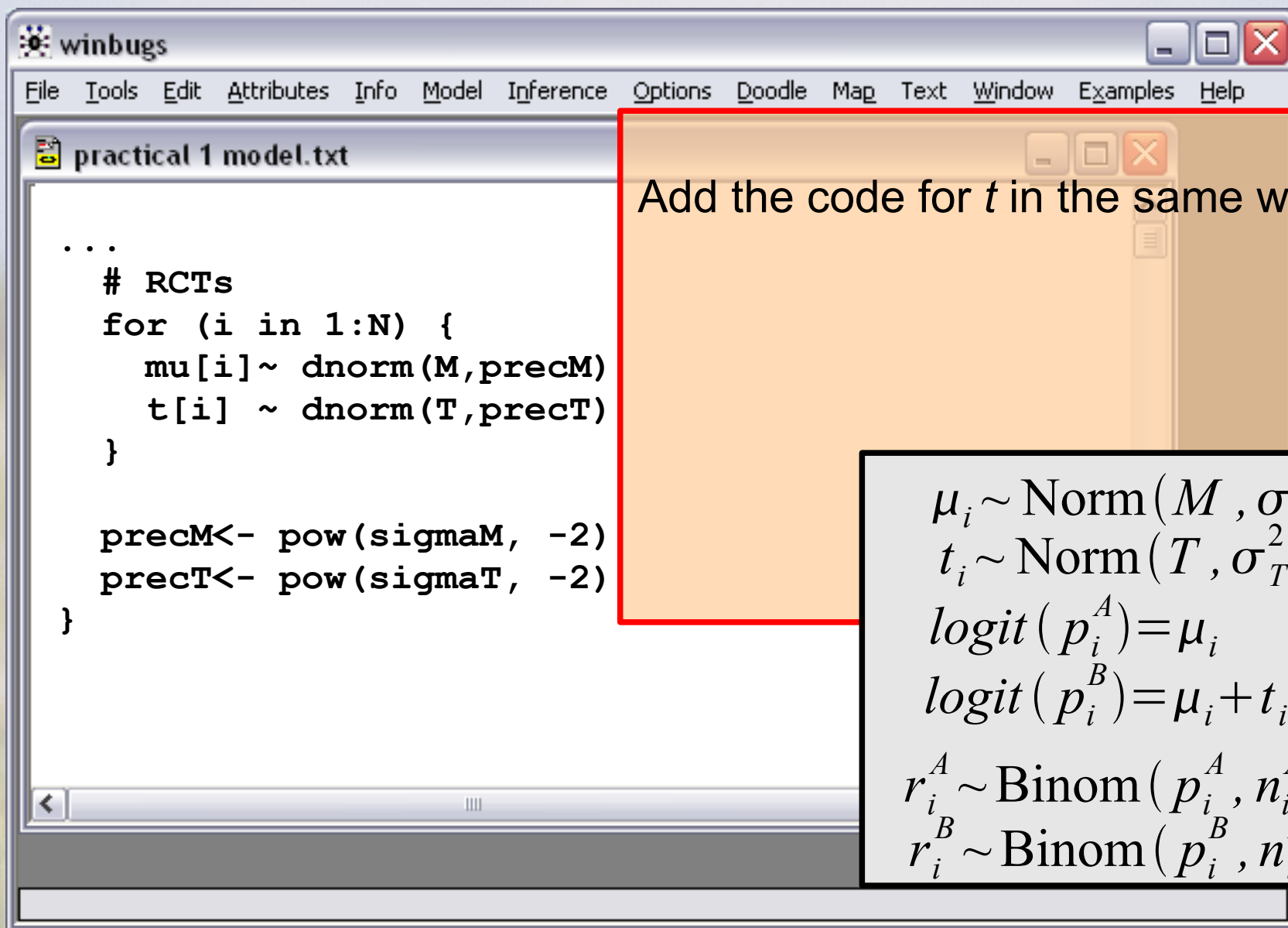
```
winbugs
File Tools Edit Attributes Info Model Inference Options Doodle Map Text Window Examples Help
practical 1 model.txt
...
# RCTs
for (i in 1:N) {
  mu[i] ~ dnorm(M, precM)
}

precM <- pow(sigmaM, -2)
}
```

So we define **precM** outside the “for” loop.

precM is derived from **sigmaM** by simple calculation. We use the **<-** operator to define it. The “power” function is **pow(base, exp)**.

$$\begin{aligned}\mu_i &\sim \text{Norm}(M, \sigma_M^2) \\ t_i &\sim \text{Norm}(T, \sigma_T^2) \\ \text{logit}(p_i^A) &= \mu_i \\ \text{logit}(p_i^B) &= \mu_i + t_i \\ r_i^A &\sim \text{Binom}(p_i^A, n_i^A) \\ r_i^B &\sim \text{Binom}(p_i^B, n_i^B)\end{aligned}$$



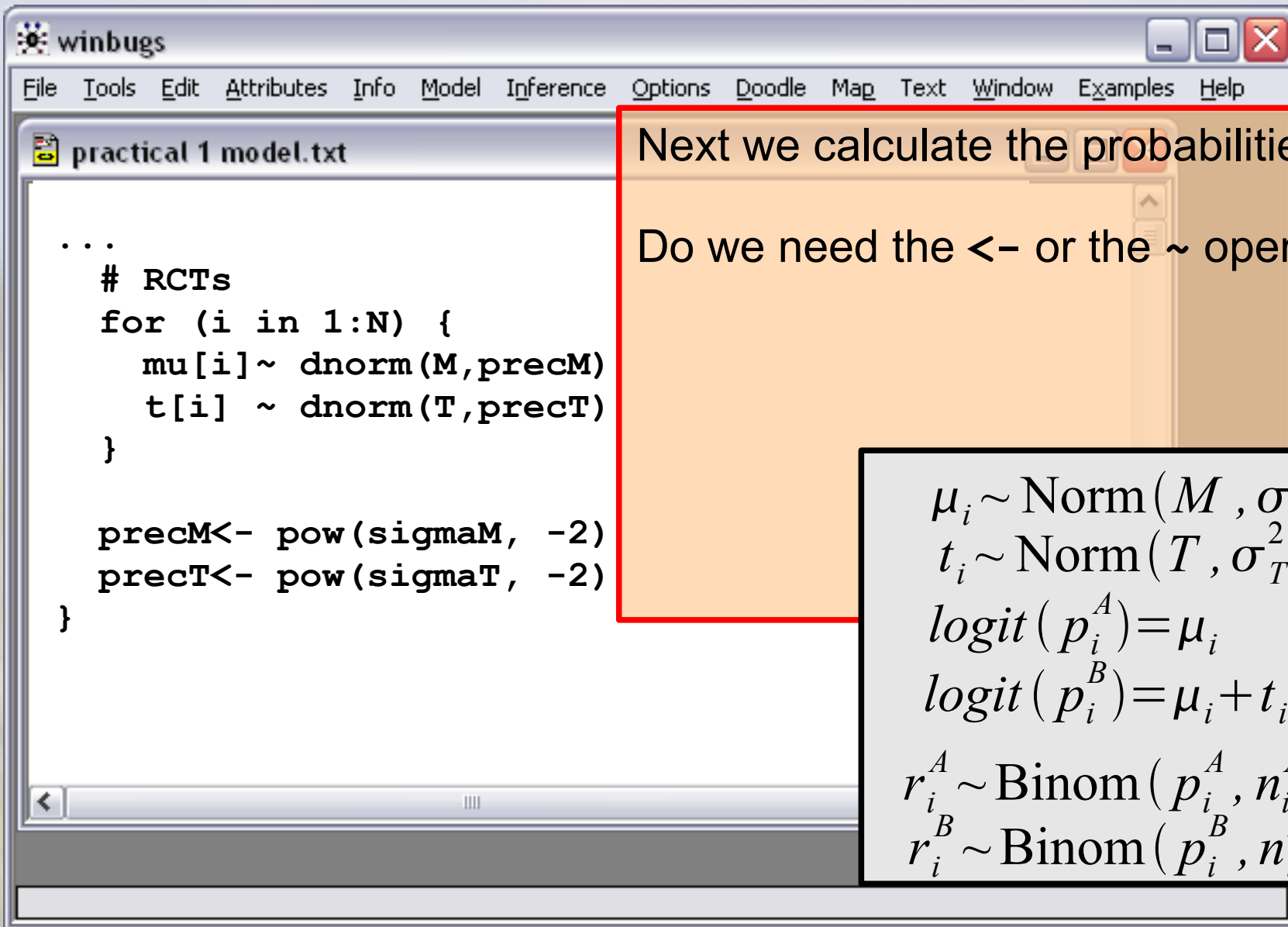
The screenshot shows the winbugs application window. The menu bar includes File, Tools, Edit, Attributes, Info, Model, Inference, Options, Doodle, Map, Text, Window, Examples, and Help. The active window is titled 'practical 1 model.txt' and contains the following code:

```
...
# RCTs
for (i in 1:N) {
  mu[i] ~ dnorm(M, precM)
  t[i] ~ dnorm(T, precT)
}

precM<- pow(sigmaM, -2)
precT<- pow(sigmaT, -2)
}
```

Add the code for t in the same way.

$$\begin{aligned}\mu_i &\sim \text{Norm}(M, \sigma_M^2) \\ t_i &\sim \text{Norm}(T, \sigma_T^2) \\ \text{logit}(p_i^A) &= \mu_i \\ \text{logit}(p_i^B) &= \mu_i + t_i \\ r_i^A &\sim \text{Binom}(p_i^A, n_i^A) \\ r_i^B &\sim \text{Binom}(p_i^B, n_i^B)\end{aligned}$$



```
winbugs
File Tools Edit Attributes Info Model Inference Options Doodle Map Text Window Examples Help
practical 1 model.txt
...
# RCTs
for (i in 1:N) {
  mu[i] ~ dnorm(M,precM)
  t[i] ~ dnorm(T,precT)
}

precM<- pow(sigmaM, -2)
precT<- pow(sigmaT, -2)
}
```

Next we calculate the probabilities p^A and p^B .

Do we need the \leftarrow or the \sim operator?

$$\begin{aligned}\mu_i &\sim \text{Norm}(M, \sigma_M^2) \\ t_i &\sim \text{Norm}(T, \sigma_T^2) \\ \text{logit}(p_i^A) &= \mu_i \\ \text{logit}(p_i^B) &= \mu_i + t_i \\ r_i^A &\sim \text{Binom}(p_i^A, n_i^A) \\ r_i^B &\sim \text{Binom}(p_i^B, n_i^B)\end{aligned}$$

```
...
# RCTs
for (i in 1:N) {
  mu[i] ~ dnorm(M, precM)
  t[i] ~ dnorm(T, precT)
  logit(pA[i]) <- mu[i]
}

precM <- pow(sigmaM, -2)
precT <- pow(sigmaT, -2)
}
```

Next we calculate the probabilities p^A and p^B .

We need the `<-` operator, because we can calculate the probabilities from the μ and t .

In OpenBUGS it's ok to put `logit` on the LHS.

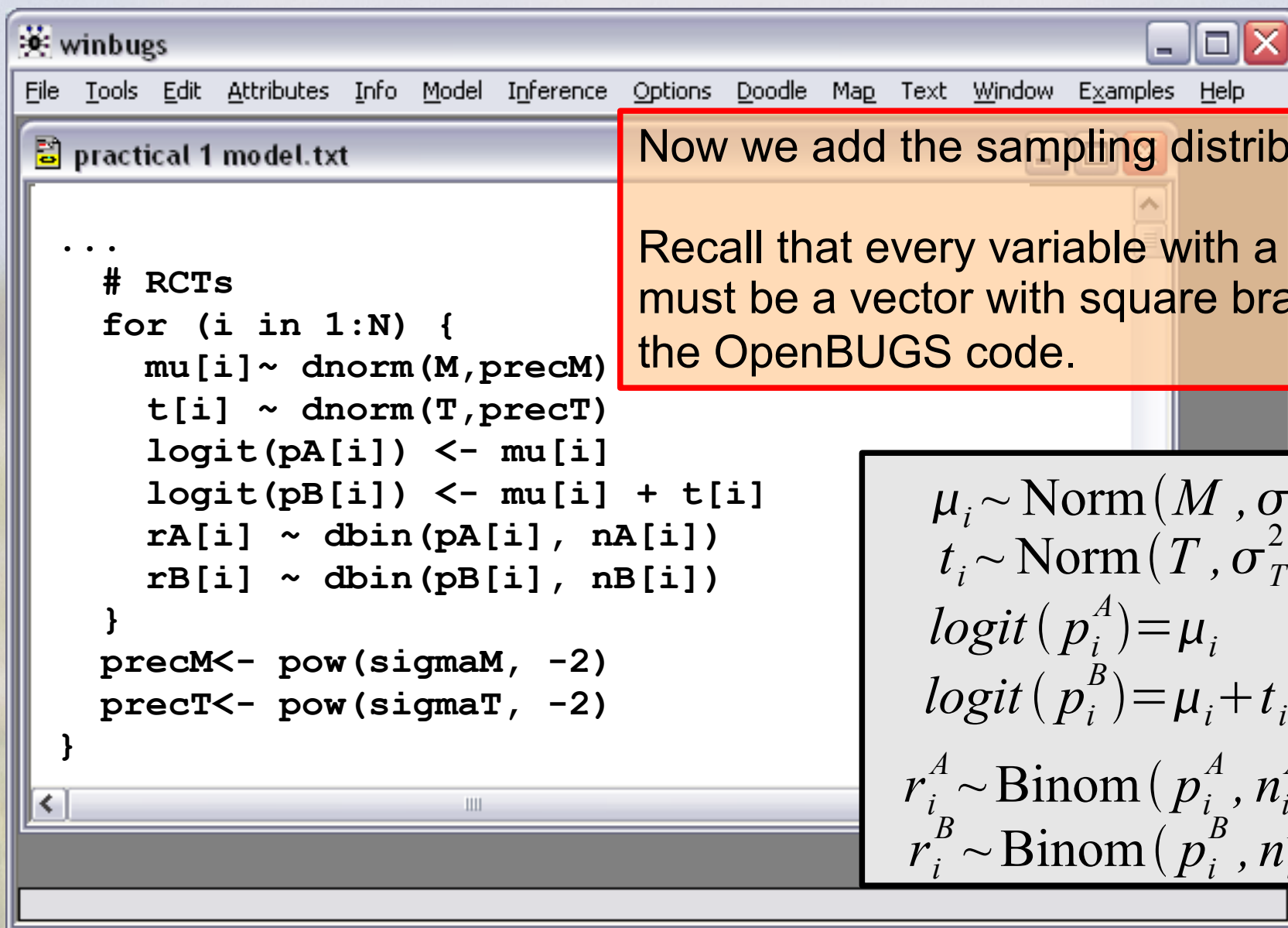
$$\begin{aligned}\mu_i &\sim \text{Norm}(M, \sigma_M^2) \\ t_i &\sim \text{Norm}(T, \sigma_T^2) \\ \text{logit}(p_i^A) &= \mu_i \\ \text{logit}(p_i^B) &= \mu_i + t_i \\ r_i^A &\sim \text{Binom}(p_i^A, n_i^A) \\ r_i^B &\sim \text{Binom}(p_i^B, n_i^B)\end{aligned}$$


```
winbugs
File Tools Edit Attributes Info Model Inference Options Doodle Map Text Window Examples Help
practical 1 model.txt
...
# RCTs
for (i in 1:N) {
  mu[i] ~ dnorm(M, precM)
  t[i] ~ dnorm(T, precT)
  logit(pA[i]) <- mu[i]
  logit(pB[i]) <- mu[i] + t[i]
}

precM <- pow(sigmaM, -2)
precT <- pow(sigmaT, -2)
}
```

Define p^B in a similar fashion.

$$\begin{aligned} \mu_i &\sim \text{Norm}(M, \sigma_M^2) \\ t_i &\sim \text{Norm}(T, \sigma_T^2) \\ \text{logit}(p_i^A) &= \mu_i \\ \text{logit}(p_i^B) &= \mu_i + t_i \\ r_i^A &\sim \text{Binom}(p_i^A, n_i^A) \\ r_i^B &\sim \text{Binom}(p_i^B, n_i^B) \end{aligned}$$

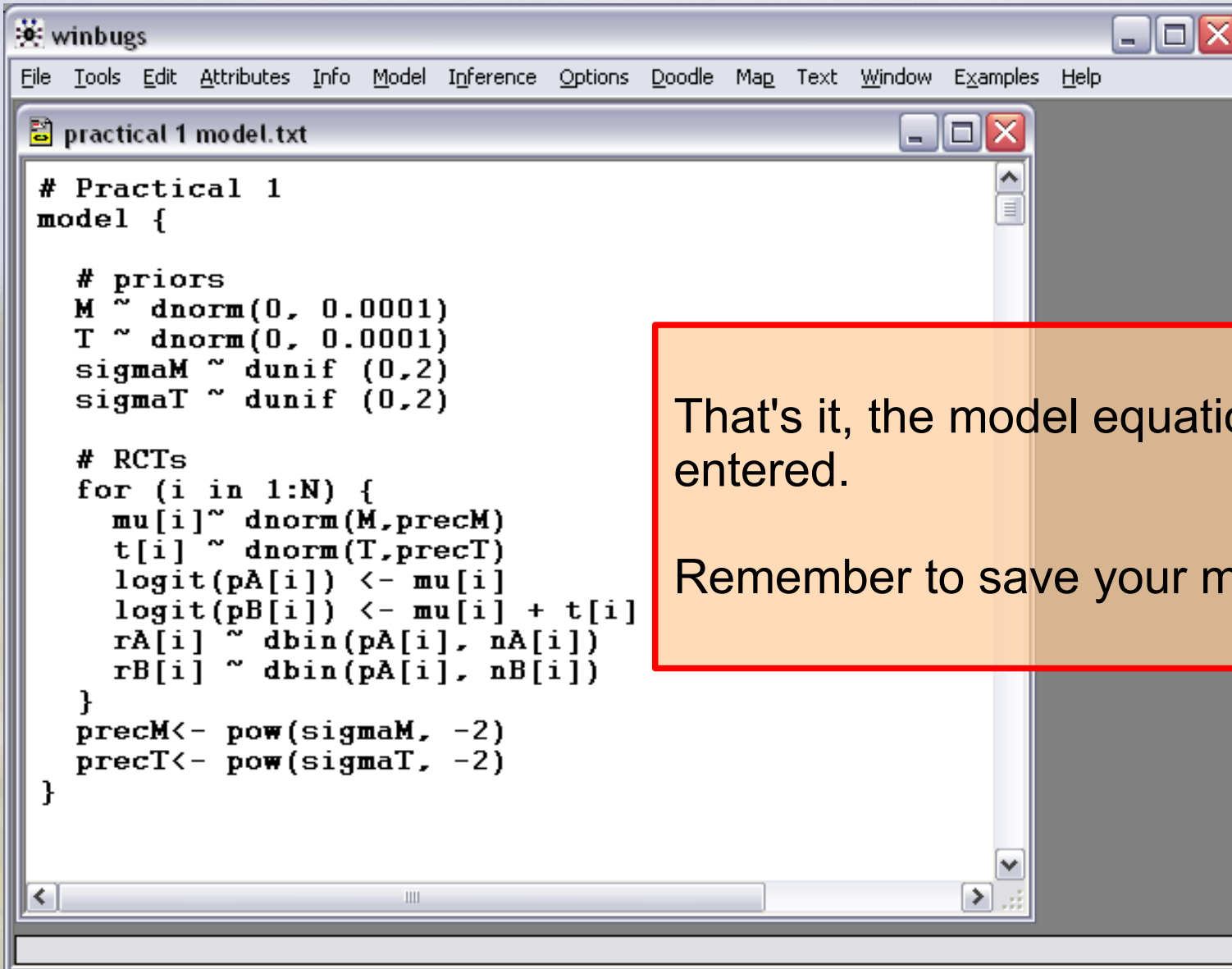


```
...
# RCTs
for (i in 1:N) {
  mu[i] ~ dnorm(M, precM)
  t[i] ~ dnorm(T, precT)
  logit(pA[i]) <- mu[i]
  logit(pB[i]) <- mu[i] + t[i]
  rA[i] ~ dbin(pA[i], nA[i])
  rB[i] ~ dbin(pB[i], nB[i])
}
precM <- pow(sigmaM, -2)
precT <- pow(sigmaT, -2)
}
```

Now we add the sampling distributions.

Recall that every variable with a subscript i must be a vector with square brackets $[i]$ in the OpenBUGS code.

$$\begin{aligned} \mu_i &\sim \text{Norm}(M, \sigma_M^2) \\ t_i &\sim \text{Norm}(T, \sigma_T^2) \\ \text{logit}(p_i^A) &= \mu_i \\ \text{logit}(p_i^B) &= \mu_i + t_i \\ r_i^A &\sim \text{Binom}(p_i^A, n_i^A) \\ r_i^B &\sim \text{Binom}(p_i^B, n_i^B) \end{aligned}$$



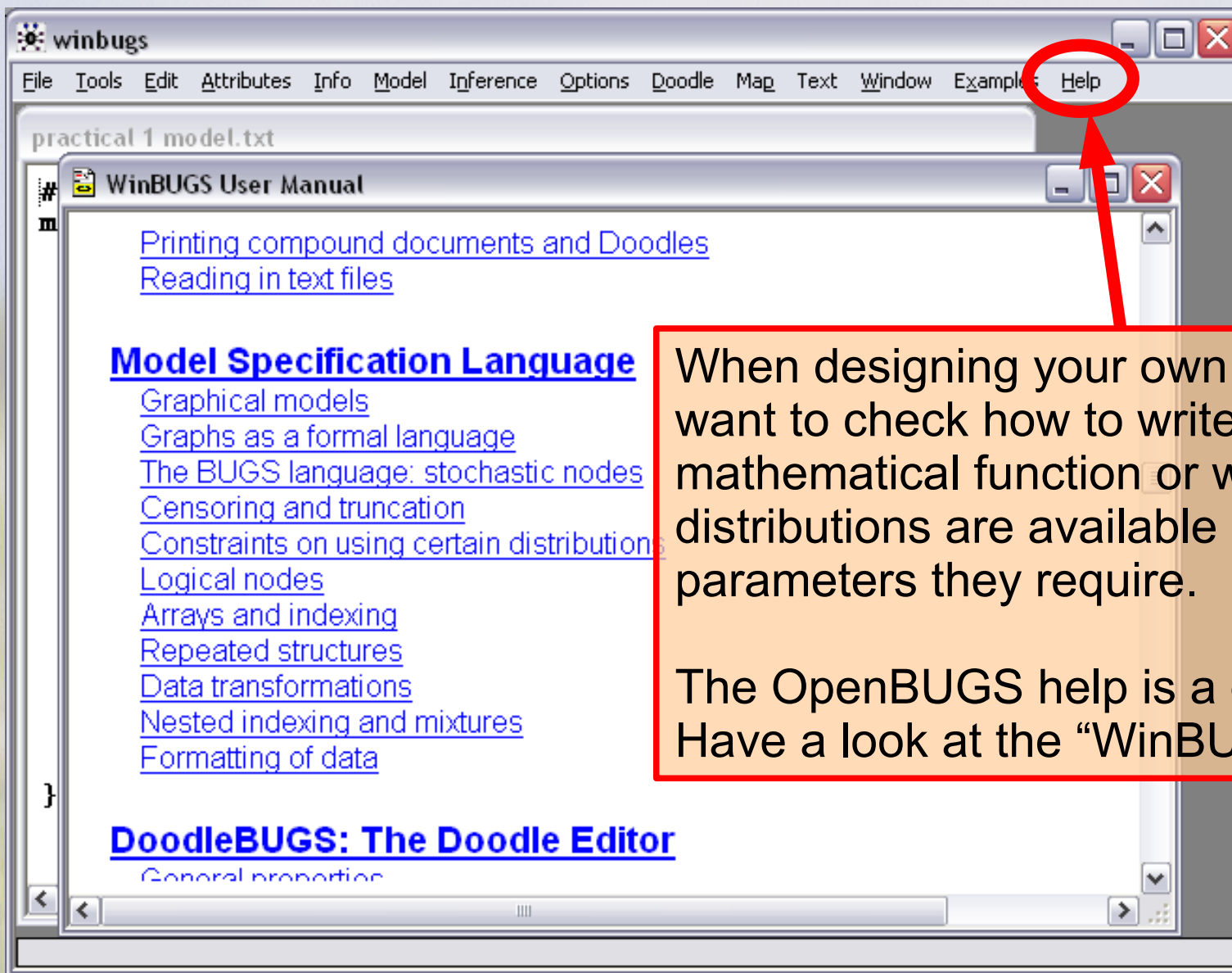
```
# Practical 1
model {

  # priors
  M ~ dnorm(0, 0.0001)
  T ~ dnorm(0, 0.0001)
  sigmaM ~ dunif (0,2)
  sigmaT ~ dunif (0,2)

  # RCTs
  for (i in 1:N) {
    mu[i]~ dnorm(M,precM)
    t[i] ~ dnorm(T,precT)
    logit(pA[i]) <- mu[i]
    logit(pB[i]) <- mu[i] + t[i]
    rA[i] ~ dbin(pA[i], nA[i])
    rB[i] ~ dbin(pA[i], nB[i])
  }
  precM<- pow(sigmaM, -2)
  precT<- pow(sigmaT, -2)
}
```

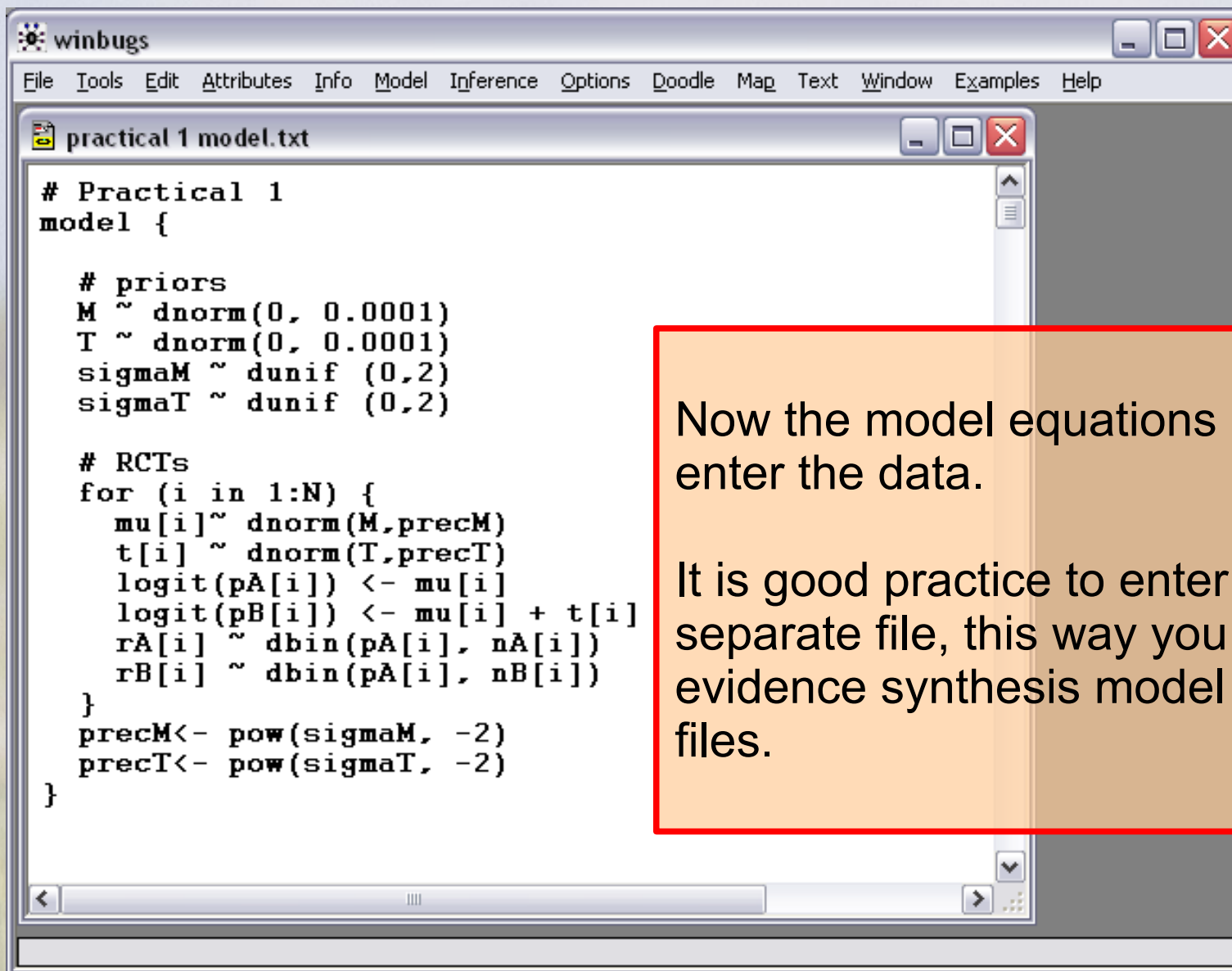
That's it, the model equations have been entered.

Remember to save your model!



When designing your own models, you may want to check how to write a particular mathematical function or which probability distributions are available and what parameters they require.

The OpenBUGS help is a great place to start. Have a look at the “WinBUGS User Manual”!



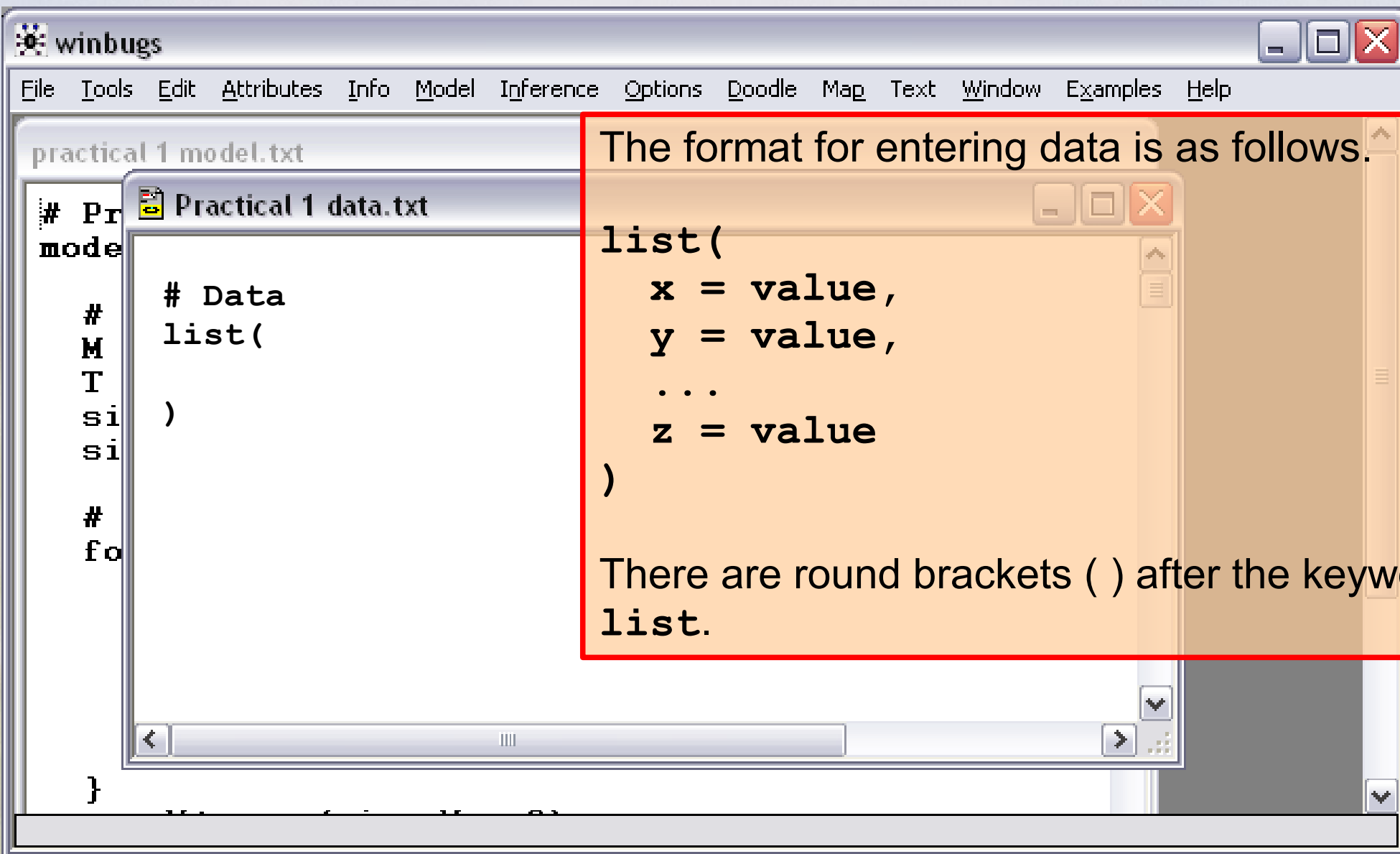
```
# Practical 1
model {

  # priors
  M ~ dnorm(0, 0.0001)
  T ~ dnorm(0, 0.0001)
  sigmaM ~ dunif (0,2)
  sigmaT ~ dunif (0,2)

  # RCTs
  for (i in 1:N) {
    mu[i]~ dnorm(M,precM)
    t[i] ~ dnorm(T,precT)
    logit(pA[i]) <- mu[i]
    logit(pB[i]) <- mu[i] + t[i]
    rA[i] ~ dbin(pA[i], nA[i])
    rB[i] ~ dbin(pA[i], nB[i])
  }
  precM<- pow(sigmaM, -2)
  precT<- pow(sigmaT, -2)
}
```

Now the model equations are done, next we enter the data.

It is good practice to enter your data into a separate file, this way you can reuse one evidence synthesis model with different data files.



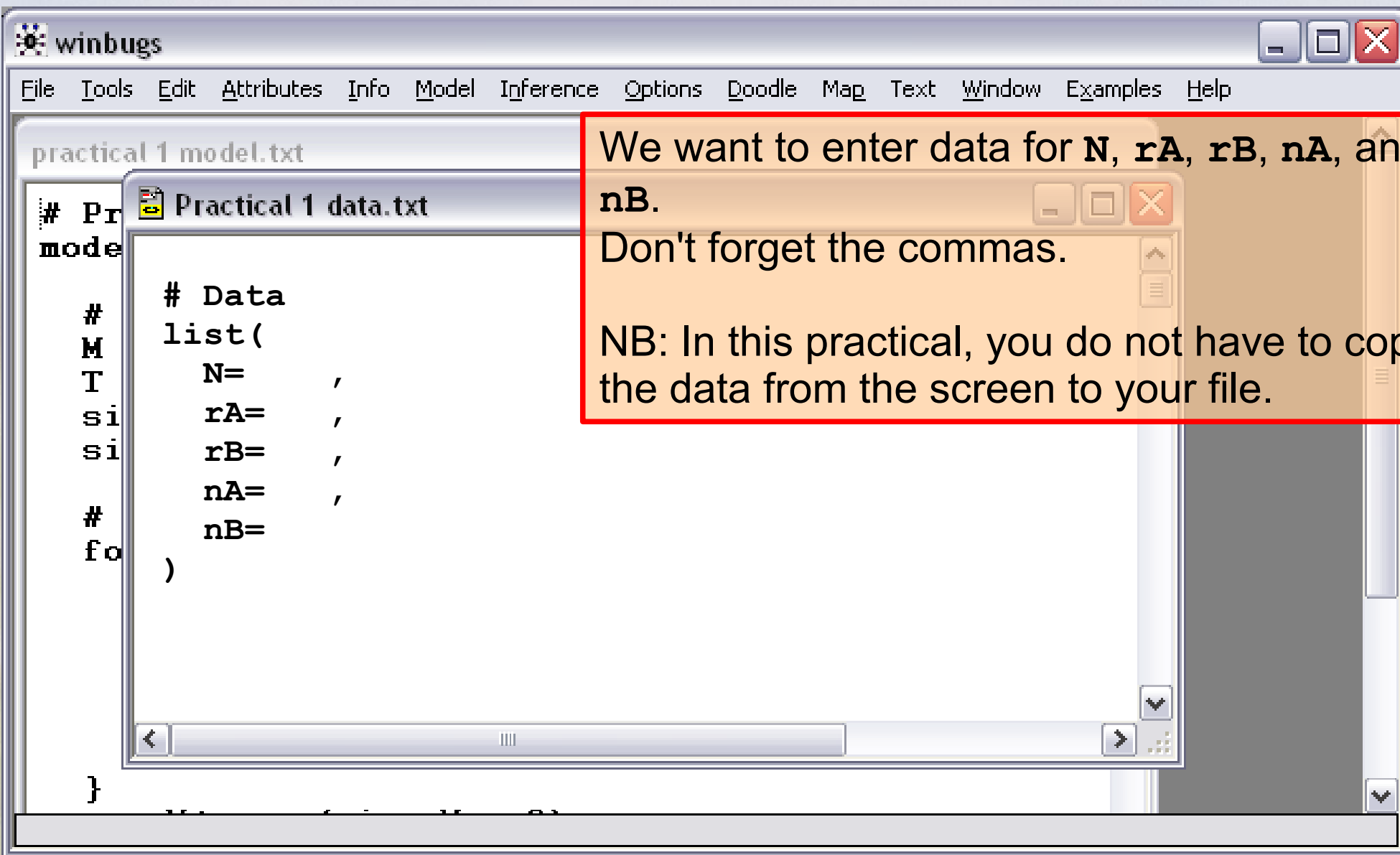
The screenshot shows the winbugs application window. The main window displays a file named 'practical 1 model.txt' with the following code:

```
# Pr  
mode  
  
#  
# Data  
# M  
# T  
# si  
# si  
  
# fo
```

An inset window titled 'Practical 1 data.txt' is open, showing the following code:

```
list(  
  x = value,  
  y = value,  
  ...  
  z = value  
)
```

The inset window is highlighted with a red border. Text overlaid on the inset window reads: 'The format for entering data is as follows.' and 'There are round brackets () after the keyword list.'



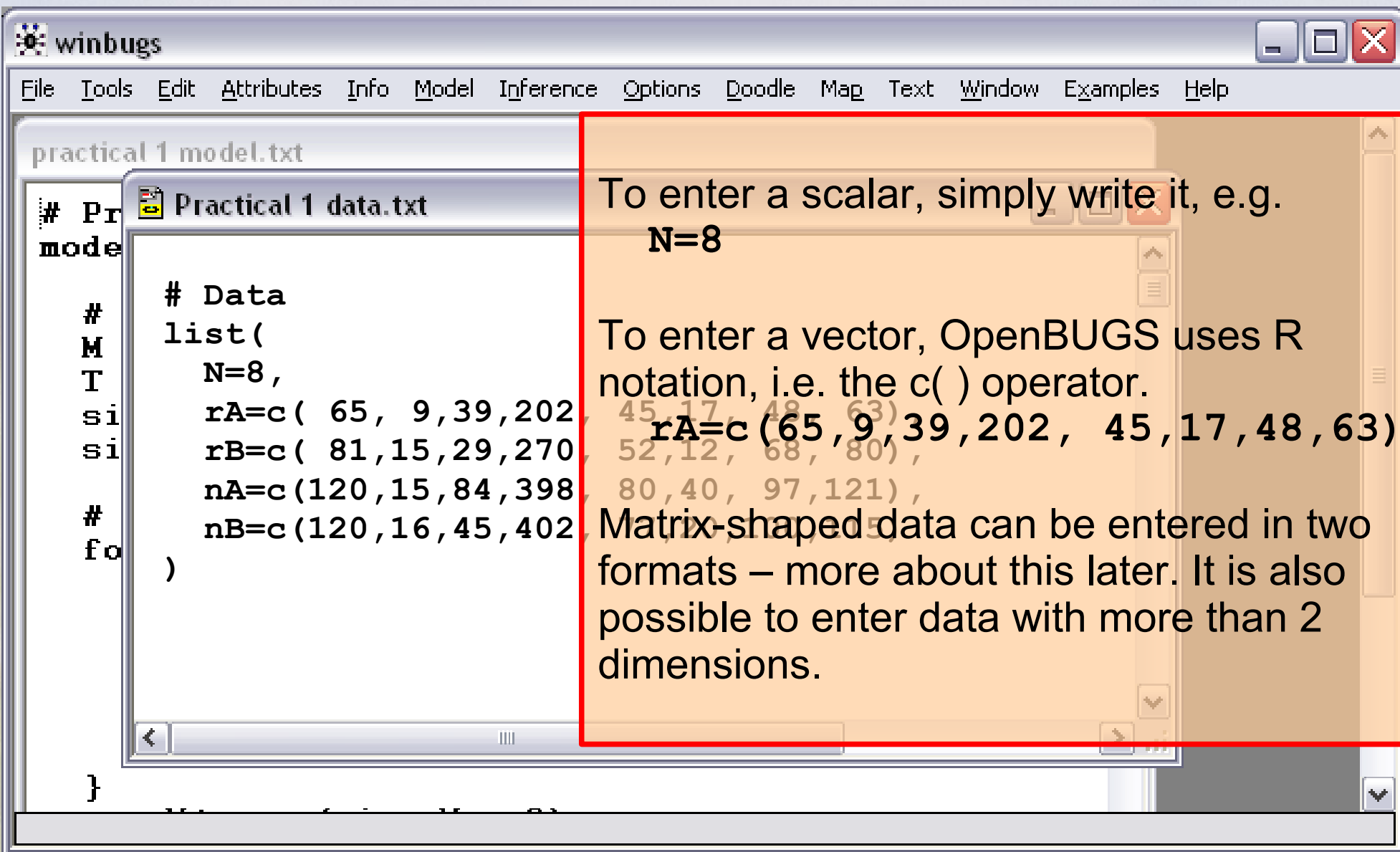
The screenshot shows the winbugs application window. The main window displays a file named 'practical 1 model.txt'. A smaller window titled 'Practical 1 data.txt' is open over it, showing the following code:

```
# Pr  
mode  
  
# Data  
list(  
  N=      ,  
  rA=     ,  
  rB=     ,  
  nA=     ,  
  nB=     ,  
fo  
)  
  
}
```

We want to enter data for **N**, **rA**, **rB**, **nA**, and **nB**.

Don't forget the commas.

NB: In this practical, you do not have to copy the data from the screen to your file.



The screenshot shows the OpenBUGS software interface. The main window displays a file named 'practical 1 model.txt' with the following code:

```
# Pr  
mode  
  
#  
M  
T  
si  
si  
#  
fo  
)  
}
```

A secondary window titled 'Practical 1 data.txt' is open, showing the following code:

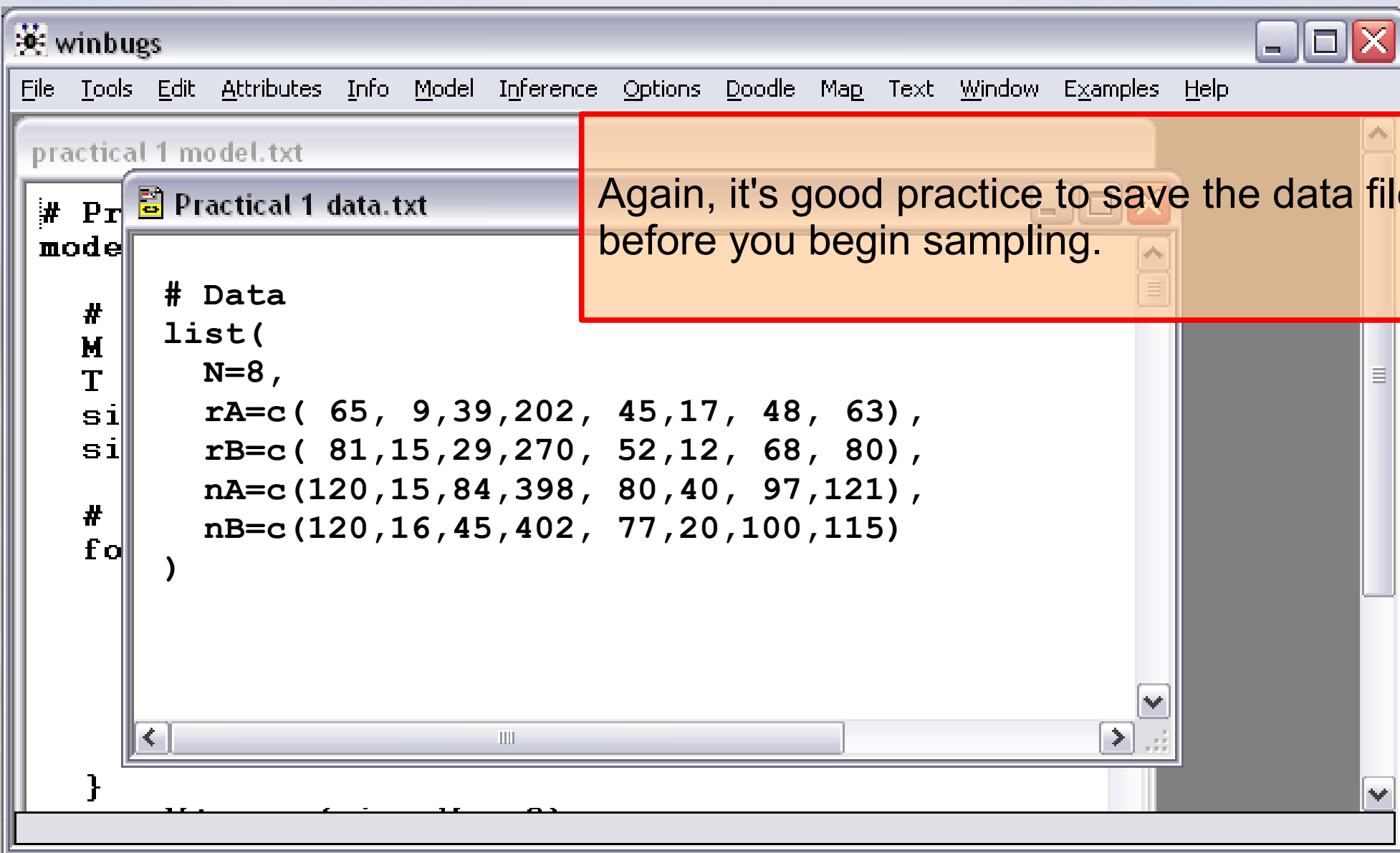
```
# Data  
list(  
  N=8,  
  rA=c( 65, 9, 39, 202,  
  rB=c( 81, 15, 29, 270,  
  nA=c(120, 15, 84, 398,  
  nB=c(120, 16, 45, 402,  
)
```

Overlaid on the right side of the screenshot is a red-bordered box containing the following text:

To enter a scalar, simply write it, e.g.
N=8

To enter a vector, OpenBUGS uses R notation, i.e. the `c()` operator.
rA=c(65, 9, 39, 202, 45, 17, 48, 63)

Matrix-shaped data can be entered in two formats – more about this later. It is also possible to enter data with more than 2 dimensions.



The screenshot shows the winbugs application window. The title bar reads 'winbugs'. The menu bar includes 'File', 'Tools', 'Edit', 'Attributes', 'Info', 'Model', 'Inference', 'Options', 'Doodle', 'Map', 'Text', 'Window', 'Examples', and 'Help'. The main window displays a file named 'practical 1 model.txt'. A secondary window titled 'Practical 1 data.txt' is open, showing the following R code:

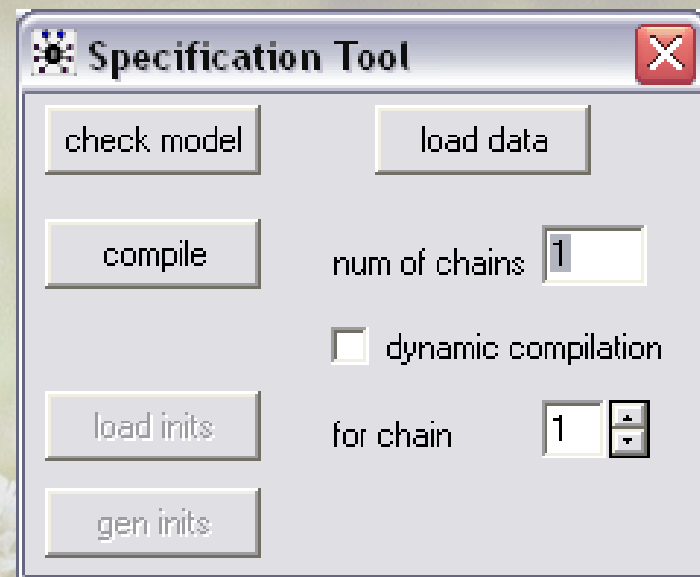
```
# Pr  
mode  
  
# Data  
list(  
  N=8,  
  rA=c( 65, 9, 39, 202, 45, 17, 48, 63),  
  rB=c( 81, 15, 29, 270, 52, 12, 68, 80),  
  nA=c(120, 15, 84, 398, 80, 40, 97, 121),  
  nB=c(120, 16, 45, 402, 77, 20, 100, 115)  
)
```

Again, it's good practice to save the data file before you begin sampling.

Overview of model specification

- When you have entered the model and the data, open the “Specification Tool” on the “Model” menu.

1. “Check” the model
2. “Load” the data
3. “Compile” the model
4. Load or generate initial values



The screenshot shows the 'winbugs' application window. The main text area contains the following code:

```
# Practical 1
model {

# priors
M ~ dnorm(0, 0.0001)
T ~ dnorm(0, 0.0001)
sigmaM ~ dunif (0,2)
sigmaT ~ dunif (0,2)

# RCTs
for (i in 1:N) {
  mu[i] ~ dnorm(M, precM)
  t[i] ~ dnorm(T, precT)
  logit(pA[i]) <- mu[i]
  logit(pB[i]) <- mu[i] + t[i]
  rA[i] ~ dbin(pA[i], nA[i])
  rB[i] ~ dbin(pA[i], nB[i])
}
```

Overlaid on the right is the 'Specification Tool' dialog box with the following controls:

- Buttons: check model, load data, compile, load inits, gen inits
- num of chains: 1
- dynamic compilation
- for chain: 1

A red-bordered box highlights the word 'model' in the code and the 'check model' button in the dialog. A text box next to it contains the instruction:

1. Highlight the word **model** in the model file, and click on the button "Check model".

The screenshot shows the 'winbugs' application window. The main text area contains the following code:

```
# Practical 1
model {

# priors
M ~ dnorm(0, 0.0001)
T ~ dnorm(0, 0.0001)
sigmaM ~ dunif (0,2)
sigmaT ~ dunif (0,2)

# RCTs
for (i in 1:N) {
  mu[i] ~ dnorm(M, precM)
  t[i] ~ dnorm(T, precT)
  logit(pA[i]) <- mu[i]
  logit(pB[i]) <- mu[i] + t[i]
  rA[i] ~ dbin(pA[i], nA[i])
  rB[i] ~ dbin(pA[i], nB[i])
}
```

A 'Specification Tool' dialog box is open, featuring buttons for 'check model', 'load data', 'compile', 'load inits', and 'gen inits'. It also includes a 'num of chains' input field set to 1, a 'dynamic compilation' checkbox, and a 'for chain' dropdown menu set to 1.

A red box highlights the status bar at the bottom of the main window, which displays the message: 'model is syntactically correct'.

Check the status bar – if you see an error message, fix your model code.

The screenshot shows the winbugs application window. The main text area displays the contents of 'practical 1 data.txt', which includes a list of data points for variables rA, rB, nA, and nB. The word 'list' is highlighted in the code. A 'Specification Tool' dialog box is open, showing buttons for 'check model', 'load data', 'compile', 'load inits', and 'gen inits'. The 'load data' button is highlighted with a red box. The status bar at the bottom left shows 'data loaded' and is also circled in red.

```
#data
list(
N=8,
rA=c( 65, 9,39,202, 45,17, 48, 63),
rB=c( 81,15,29,270, 52,12, 68, 80),
nA=c(120,15,84,398, 80,40, 97,121),
nB=c(120,16,45,402, 77,20,100,115)
)
```

2. Highlight the word **list** in the data file, and click on the button "Load data".

The screenshot shows the winbugs application window. The main window displays a file named 'practical 1 model.txt' containing the following code:

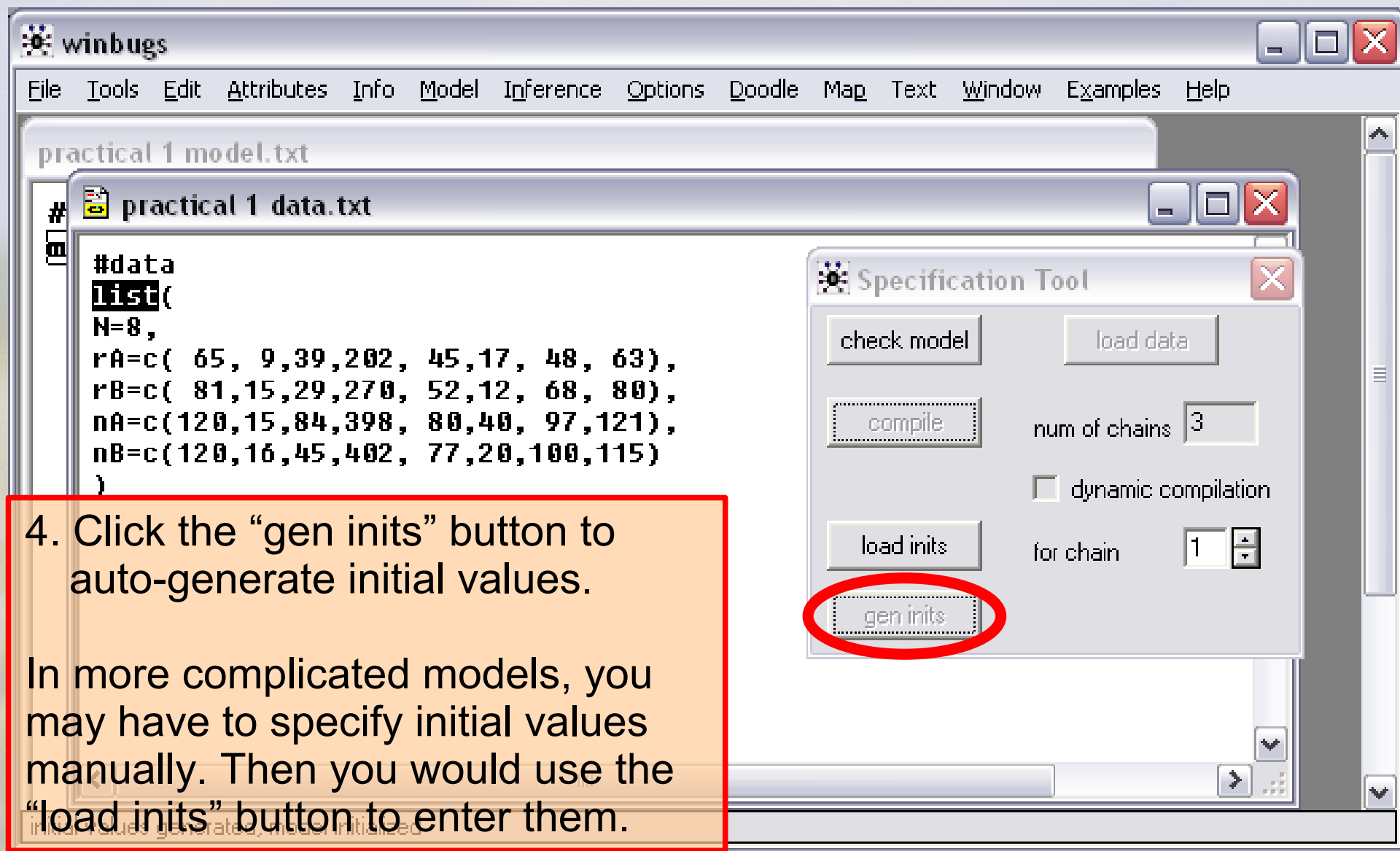
```
#data
list(
N=8,
rA=c( 65, 9,39,202, 45,17, 48, 63),
rB=c( 81,15,29,270, 52,12, 68, 80),
nA=c(120,15,84,398, 80,40, 97,121),
nB=c(120,16,45,402, 77,20,100,115)
)
```

Overlaid on the main window is a 'Specification Tool' dialog box. It contains several buttons: 'check model', 'load data', 'compile', and 'load inits'. A text input field labeled 'num of chains' contains the value '1' and is circled in red. Below this field is a checkbox for 'dynamic compilation' which is unchecked. At the bottom of the dialog, there is a 'for chain' label and a spinner control set to '1'. A red box highlights the 'num of chains' field and the 'compile' button.

3. Enter a number of chains and click "Compile".

It's a good idea to use more than 1 chain. I usually set this to 3.

data loaded



The screenshot shows the winbugs application window. The main window displays a text editor with the following content:

```
practical 1 model.txt  
# practical 1 data.txt  
#data  
list(  
N=8,  
rA=c( 65, 9,39,202, 45,17, 48, 63),  
rB=c( 81,15,29,270, 52,12, 68, 80),  
nA=c(120,15,84,398, 80,40, 97,121),  
nB=c(120,16,45,402, 77,20,100,115)  
)
```

Overlaid on the main window is the "Specification Tool" dialog box. It contains several buttons: "check model", "load data", "compile", "load inits", and "gen inits". The "gen inits" button is circled in red. To the right of the buttons are input fields: "num of chains" set to 3, a checkbox for "dynamic compilation" which is unchecked, and "for chain" set to 1.

4. Click the “gen inits” button to auto-generate initial values.

In more complicated models, you may have to specify initial values manually. Then you would use the “load inits” button to enter them.

The screenshot shows the winbugs application window. The main window displays a text editor with the following code in 'practical 1 model.txt':

```
#data
list(
N=8,
rA=c( 65, 9,39,202, 45,17, 48, 63),
rB=c( 81,15,29,270, 52,12, 68, 80),
nA=c(120,15,84,398, 80,40, 97,121),
nB=c(120,16,45,402, 77,20,100,115)
)
```

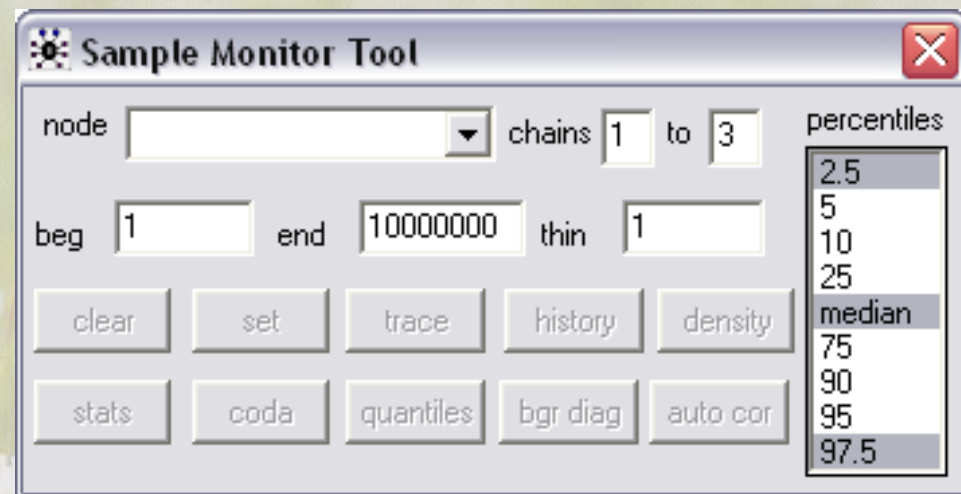
A 'practical 1 data.txt' window is also open, showing the same code. A 'Specification Tool' dialog box is overlaid on the right, with buttons for 'check model', 'load data', and 'compile'. It also has a 'num of chains' field set to 3 and a 'dynamic compilation' checkbox. A red box highlights the text: "That's it! If you do not see the status text 'initial values generated, model initialized', an error message should have told you what the problem is." At the bottom of the winbugs window, the status bar displays "initial values generated, model initialized", which is circled in red.

Common errors

- After “Check model”
 - Syntax errors like commas and () and [] and { }
 - Using the same variable name sometimes as scalar and sometimes as array
- After “Load data”
 - Loading data for variables that are defined by <-
 - Loading data of the wrong shape for a vector or array
- After “Compile”
 - Defining a variable twice or forgetting to specify some required data
 - Leaving out the correct [] indices for variables that are defined inside a “for” loop

Overview of the sampling steps

- After compiling and initialising your model, open the “Sample Monitor Tool” on the “Inference” menu
 1. Set monitors for the parameters of interest
 2. Using the “Update tool”, simulate draws from the posterior
 3. Check for issues like burn-in and convergence
 4. Retrieve sample summary or histograms, or export draws to another program



The screenshot shows the winbugs software interface. The main window displays a model file named 'practical 1 model.txt' with the following code:

```
# Practical 1
model {

# priors
M ~ dnorm(0, 0.0001)
T ~ dnorm(0, 0.0001)
sigmaM ~ dunif (0,2)
sigmaT ~ dunif (0,2)

# RCTs
for (i in 1:N) {
  mu[i] ~ dnorm(M, prec[i])
  t[i] ~ dnorm(T, prec[i])
  logit(pA[i]) <- mu[i]
  logit(pB[i]) <- mu[i] + t[i]
  rA[i] ~ dbin(pA[i], nA[i])
  rB[i] ~ dbin(pB[i], nB[i])
}
```

Overlaid on the model file is the 'Sample Monitor Tool' dialog box. The 'node' field is set to 'M', and the 'set' button is highlighted. The dialog also shows 'chains 1 to 3', 'beg 1', 'end 10000000', and 'thin 1'. A list of percentiles (2.5, 5, 10, 25, median, 75, 90, 95, 99.5) is visible on the right.

Setting the monitors allows you to pick which variables are of interest and avoids generating data streams for other variables. Here, let's monitor M and T . So, enter M into the "node" field and click "set". Then do the same with T .

The screenshot shows the OpenBUGS software interface. The main window displays a text editor with the following code:

```
# Practical 1
model {
  # RCTs
  for (i in 1:N) {
    mu[i] ~ dnorm(M, precM)
    t[i] ~ dnorm(T, precT)
    logit(pA[i]) <- mu[i]
    logit(pB[i]) <- mu[i] + t[i]
    rA[i] ~ dbin(pA[i], nA[i])
    rB[i] ~ dbin(pA[i], nB[i])
  }
}
```

Overlaid on the main window are two smaller windows:

- Update Tool:** A dialog box with a red border. It contains input fields for 'updates' (set to 10000), 'refresh' (set to 100), 'thin' (set to 1), and 'iteration' (set to 0). There are 'update' and 'iteration' buttons, and checkboxes for 'over relax' and 'adapting'.
- Sample Monitor Tool:** A window showing monitoring options. It includes a dropdown menu set to 'M', 'chains' set to 1 to 3, 'end' set to 100000000, and 'thin' set to 1. It also has buttons for 'set', 'trace', 'history', 'density', 'stats', 'coda', 'quantiles', 'bgr diag', and 'auto cor'. A 'percentiles' table is visible on the right.

The 'percentiles' table in the Sample Monitor Tool shows the following values:

percentiles
2.5
5
10
25
median
75
90
95
97.5

Now, open the “Update tool” from the “Model” menu. Enter 10000 for the number of updates, and click “Update”.

Common errors during “Update”

If you get error messages while OpenBUGS is generating draws from the posterior, these are usually displayed in the form of cryptic “trap” messages. It can be difficult to figure out what went wrong.

The most common problems are unsuitable initial values, a model that leaves part of posterior parameter space undefined, or a model that is too complex for OpenBUGS.

Hopefully you do not run into any of these during this first practical!

The screenshot shows the winbugs application window. The main window displays a model file named 'practical 1 model.txt' with the following code:

```
# Practical 1
model {
  # RCTs
  for (i in 1:N) {
    mu[i] ~ dnorm(M, precM)
    t[i] ~ dnorm(T, precT)
    logit(pA[i]) <- mu[i]
    logit(pB[i]) <- mu[i] + t[i]
    rA[i] ~ dbin(pA[i], nA[i])
    rB[i] ~ dbin(pA[i], nB[i])
  }
}
```

An 'Update Tool' dialog box is open, showing 'updates' set to 10000 and 'iteration' set to 10000. The 'iteration' field is circled in red. The 'Sample Monitor Tool' window is also visible, showing a table of percentiles for parameter M:

percentiles
2.5
5
10
25
median
75
90
95

The status bar at the bottom of the winbugs window displays the message '10000 updates took 10 s', which is also circled in red.

Note that OpenBUGS can be unresponsive while it is updating. Patience!

When OpenBUGS is ready, you should see a message like "10000 updates took 10s" in the status bar.

Some basic checks

Sampling Bayesian posteriors through a numerical method like MCMC (e.g. with OpenBUGS) can go wrong if the sampler does not explore model space well.

In this practical we will check 3 diagnostics. You should always check them.

Trace The simultaneous chains should wiggle in the same area in posterior model space.

BGR The red line should be very close to 1 at the RHS.

Auto-correlation Most of the bars in these graphs should be small.

The screenshot shows the winbugs application window. The main window displays a model file named 'practical 1 model.txt' with the following code:

```
# Practical 1
model {
  # RCTs
  for (i in 1:N) {
    mu[i] ~ dnorm(M, precM)
    t[i] ~ dnorm(T, precT)
    logit(pA[i]) <- mu[i]
    logit(pB[i]) <- mu[i] + t[i]
    rA[i] ~ dbin(pA[i], nA[i])
    rB[i] ~ dbin(pA[i], nB[i])
  }
}
```

At the bottom of the window, a status bar indicates '10000 updates took 10 s'.

Overlaid on the main window are two dialog boxes:

- Update Tool:** A dialog box with input fields for 'updates' (10000) and 'refresh' (100). It has buttons for 'update', 'thin' (1), and 'iteration' (10000). There are also checkboxes for 'over relax' and 'adapting'.
- Sample Monitor Tool:** A dialog box with a 'node' dropdown menu set to '*', 'chains' from 1 to 3, and a 'percentiles' list containing 2.5, 5, 10, 25, median, 75, 90, 95, and 97.5. It also has input fields for 'beg' (1), 'end' (10000000), and 'thin' (1). Buttons include 'clear', 'set', 'trace', 'history', 'density', 'stats', 'coda', 'quantiles', 'bgr diag', and 'auto cor'.

Now, click on the “Sample monitor tool” to bring it back (or open it from the “Inference” menu).
Enter * into the node box, then click “Trace”.

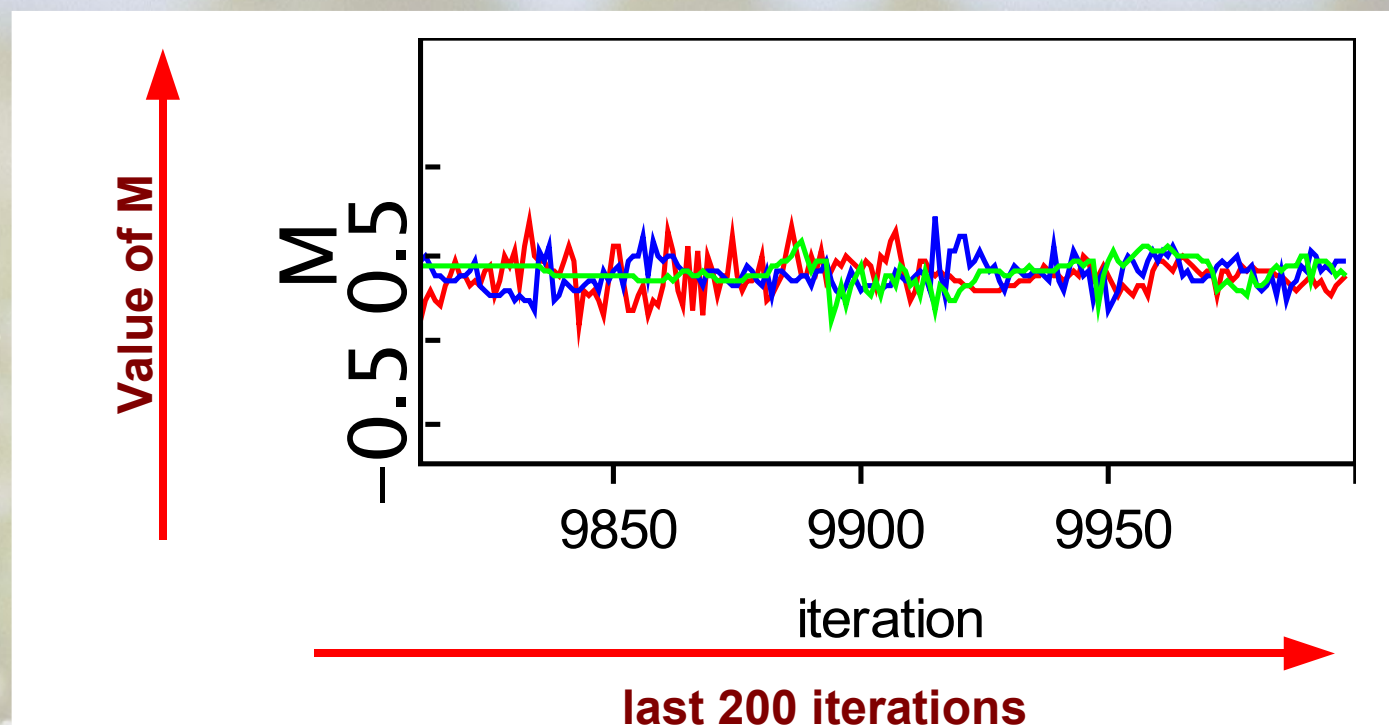
The screenshot shows the 'winbugs' application window. At the top is a menu bar with options: File, Tools, Edit, Attributes, Info, Model, Inference, Options, Doodle, Map, Text, Window, Examples, Help. Below the menu bar are several tool windows:

- Update Tool:** Contains input fields for 'updates' (10000), 'refresh' (100), 'update', 'thin' (1), and 'iteration' (10000). There are also checkboxes for 'over relax' and 'adapting'.
- Sample Monitor Tool:** Shows a tree view of nodes (node, beg, end, chains, percentiles) and a list of statistics: 10, 25, median, 75, 90, 95, 97.5. Buttons for 'clear', 'set', 'trace', 'history', 'density', 'stats', 'coda', 'quantiles', 'bgr diag', and 'auto cor' are visible.
- Dynamic trace:** Contains two side-by-side line plots. The left plot is for parameter 'M', with the y-axis ranging from -0.5 to 0.5 and the x-axis labeled 'iteration' from 9850 to 9950. The right plot is for parameter 'T', with the y-axis ranging from -600.0 to 0.0 and the x-axis labeled 'iteration' from 9850 to 9950. Both plots show multiple colored lines representing different chains, fluctuating around a central value.

A red-bordered text box is overlaid on the Sample Monitor Tool window, containing the text: "You should see something like this plot in the 'Dynamic trace' window."

You should see something like this plot in the “Dynamic trace” window. Each colour represents one of the chains in the posterior sample.

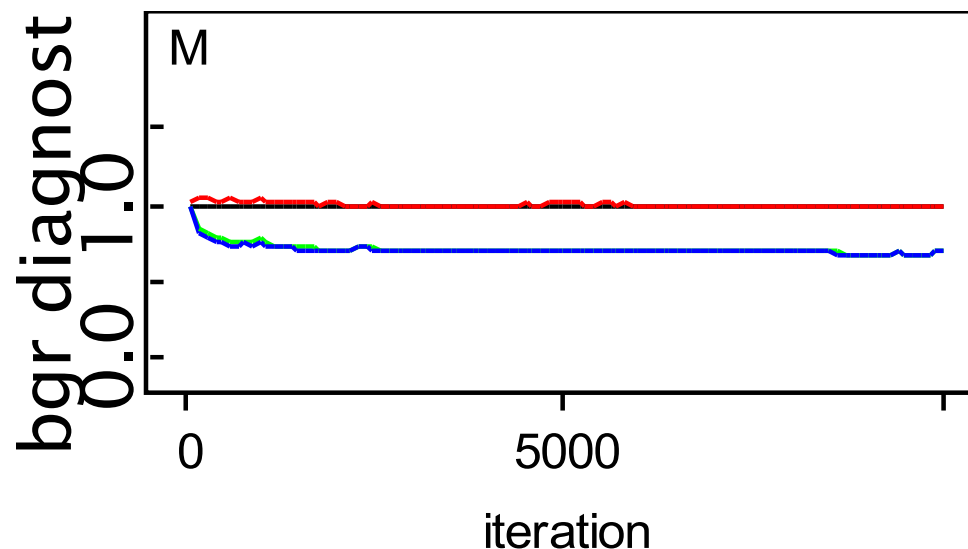
Check the trace to see that all chains “wiggle” and that they overlap well. The plot below looks quite good.



Now create the BGR plot for all monitors *.

Note that the colours in this plot do not represent the three different chains. There are always three colours (red, green, blue), the red line matters in this test.

The red line should be very close to 1.0 on the right-hand side. This plot looks excellent.

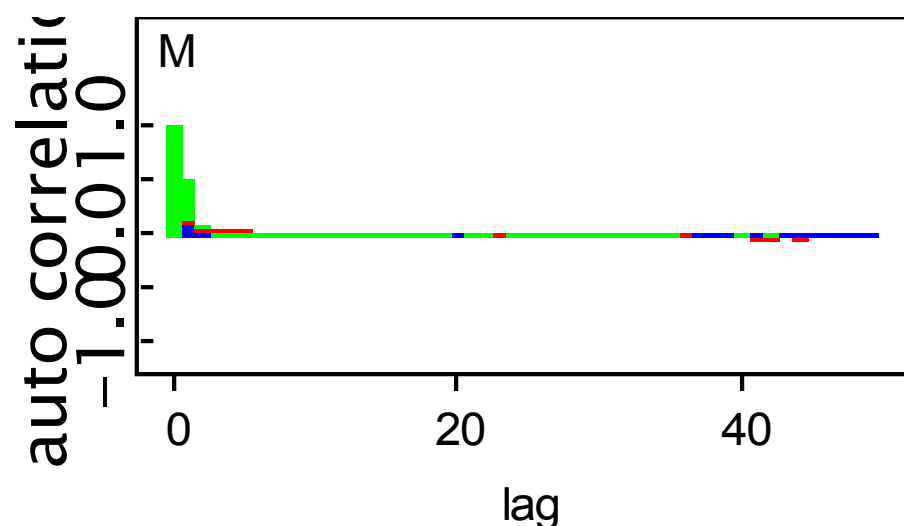


Third, click on the “auto cor” button to look at the within-chain autocorrelation. (The colours correspond to the individual chains here.)

Ideally, autocorrelation should be noticeable only for a lag of 1, indicating that the chain moves randomly from one iteration to the next.

In this case the sampler on the “green” chain performed slightly less well than the others.

But autocorrelation is not apparent in any chain for lags above 3. This plot looks ok.

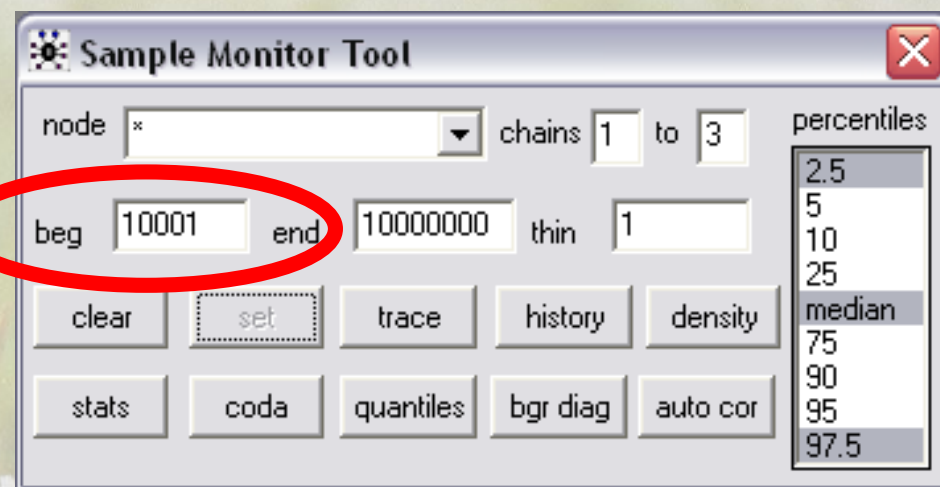


Burn-in and convergence

We have looked at 3 basic diagnostics and the posterior sampler appears to be sampling well after 10,000 iterations. There was no sign that the initial values were still influencing the output.

So if we delete these first 10,000 draws as “burn-in”, we should get good draws from now on.

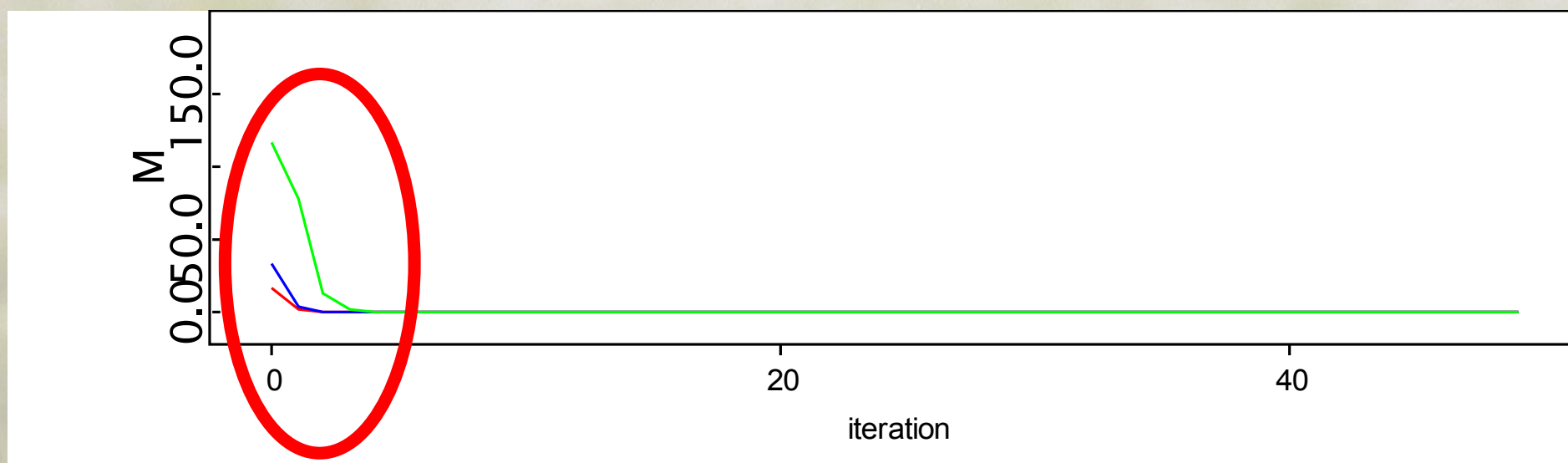
Write 10,001 into the *beg* field on the “Sample monitor tool”. Then use the “Updater” to generate the 10,000 samples that we will use.



How many draws to discard?

In this simple example, it is probably a waste of computing time to throw away 10,000 draws for burn-in. Actually it took around 5 iterations to move away from the initial values.

But we checked the statistics after 10,000 draws so we are safe only if we discard all of these for burn-in.



How many draws to generate?

This depends on your application. People often use 10,000 draws but there is no magic number.

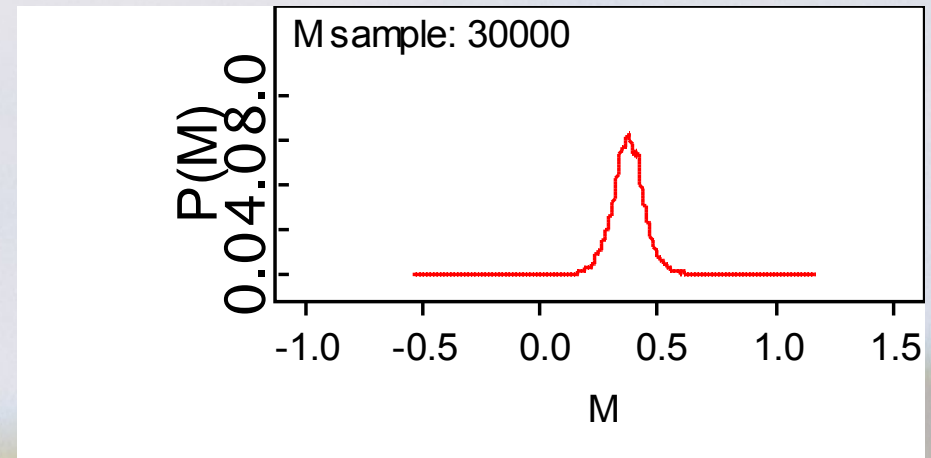
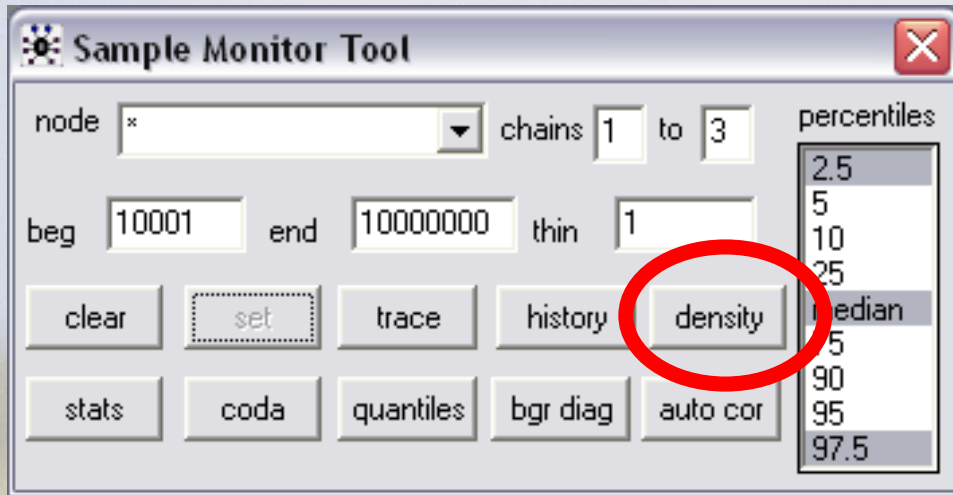
When you generate more draws, the resulting means, standard deviations, credibility intervals etc. will be more accurate. Histograms and other graphs will appear smoother.

Running 3 chains, you actually end up with $3 \times 10,000$ draws.

The screenshot shows the 'winbugs' application window with two sub-windows open: 'Update Tool' and 'Sample Monitor Tool'. The 'Update Tool' window has fields for 'updates' (10000), 'refresh' (100), 'iteration' (20000), and 'thin' (1). It also has checkboxes for 'over relax' and 'adapting'. The 'Sample Monitor Tool' window has a 'node' dropdown menu, 'chains' (1 to 3), 'beg' (10001), 'end' (10000000), and 'thin' (1) fields. It features buttons for 'clear', 'set', 'trace', 'history', 'density', 'stats', 'coda', 'quantiles', 'bgr diag', and 'auto cor'. A 'percentiles' list is visible on the right side of the 'Sample Monitor Tool' window, showing values: 2.5, 5, 10, 25, median, 75, 90, 95, 97.5. At the bottom of the main window, a status bar displays '10000 updates took 10 s'.

Now we have generated 20,000 draws each, in 3 chains, out of which we are discarding the first 10,000 as burn-in. With 3 chains, the posterior summaries will thus be based on 30,000 draws.

This is a brief overview of the inferences you can do within OpenBUGS.



The “**Density**” button shows partial posterior histograms, i.e. the posterior probability distribution for an individual parameter regardless of the values of other parameters.

As with all posterior summaries, if higher accuracy is desired, generate more draws. You should generate more draws if the posterior density looks “rugged” or has unexplainable spikes.



The “**Stats**” button creates a table with posterior mean, standard deviation, MC error, 95%-credibility interval and median.

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
M	0.04836	0.08293	0.002087	-0.1076	0.04576	0.2129	10001	30000
T	0.7127	0.1249	0.00317	0.481	0.7105	0.9601	10001	30000



The posterior mean and standard deviation. Note that you can compare these to the prior mean and standard deviation – this gives you an idea of the information content of your likelihood function, compared to the prior.

The “**Stats**” button creates a table with posterior mean, standard deviation, MC error, 95%-credibility interval and median.

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
M	0.04836	0.08293	0.002087	-0.1076	0.04576	0.2129	10001	30000
T	0.7127	0.1249	0.00317	0.481	0.7105	0.9601	10001	30000



The MC error is an estimate of how much of the variation in the posterior sample is due to the noise generated in the sampler.

Its value should be very small relative to the sd.

The “**Stats**” button creates a table with posterior mean, standard deviation, MC error, 95%-credibility interval and median.

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
M	0.04836	0.08293	0.002087	-0.1076	0.04576	0.2129	10001	30000
T	0.7127	0.1249	0.00317	0.481	0.7105	0.9601	10001	30000



The posterior median and 95% credibility interval

To change the percentiles you can use the controls in the “Sample Monitor Tool” before you click on the “Stats” button.

The “**Stats**” button creates a table with posterior mean, standard deviation, MC error, 95%-credibility interval and median.

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
M	0.04836	0.08293	0.002087	-0.1076	0.04576	0.2129	10001	30000
T	0.7127	0.1249	0.00317	0.481	0.7105	0.9601	10001	30000



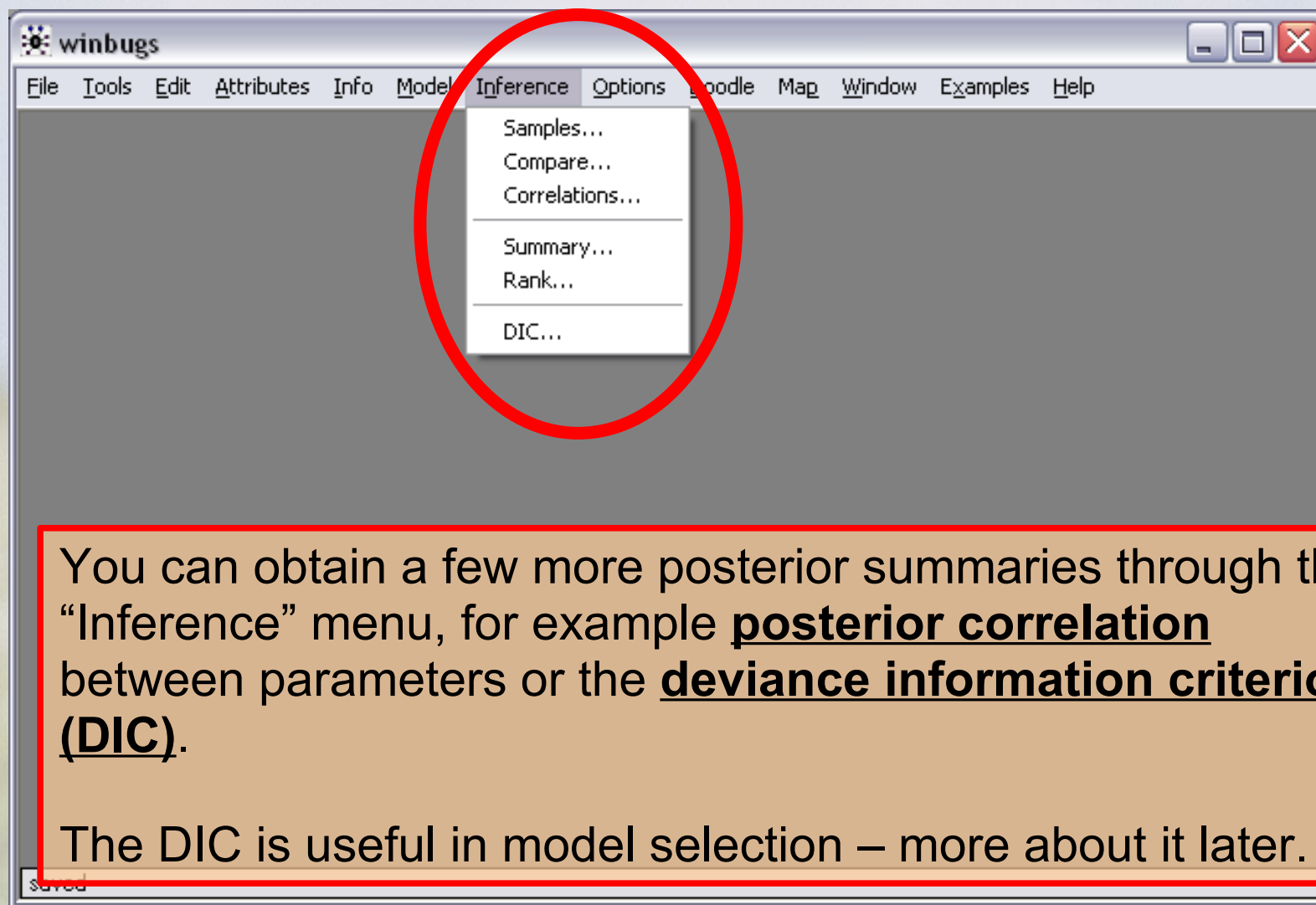
Some information on the number of draws that went into this table.

The “**Stats**” button creates a table with posterior mean, standard deviation, MC error, 95%-credibility interval and median.

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
M	0.04836	0.08293	0.002087	-0.1076	0.04576	0.2129	10001	30000
T	0.7127	0.1249	0.00317	0.481	0.7105	0.9601	10001	30000

Some comments

- It is instructive to compare the posterior means and standard deviations to your priors – to see whether, through the likelihood function, the data have contributed information to all parameters.
- In this case we notice no abnormalities in the posterior densities or summaries. If for example you had found signs of a bimodal posterior distribution or unreasonably wide credible intervals, you should rethink your model design.



You can obtain a few more posterior summaries through the “Inference” menu, for example **posterior correlation** between parameters or the **deviance information criterion (DIC)**.

The DIC is useful in model selection – more about it later.

Summary

- Now you have entered and run your first OpenBUGS model. You know how to
 - code a model in OpenBUGS language
 - load data
 - run the numerical sampling algorithm
 - check for convergence and discard burn-in iterations
 - produce a few useful posterior summaries
- If you want to practice more examples on your own, check out the “**Examples**” menu!