- The basic idea is always the same:
 - Firstly: define the (full) likelihood. This is the conditional probability model for all observed data
 - For example: all results from coin tossing modelled as Bernoulli-variables for(i in 1:n){ B_i ~ dbern(theta) }
 - If sufficient statistics exists, then you can summarize all data with that, for example: X ~ dbin(theta,n)
 - Written with sufficient statistics or with individual data points, the likelihood function for the unknown parameter theta is the same. Only this matters!

- The basic idea is always the same:
 - Secondly: define the (full) prior for all parameters (if there are many)
 - For example: theta ~ dbeta(1,1)
 - or for each parameter independently: for(i in 1:k){ theta[i] ~ dbeta(...) }
 - or jointly as a multivariate distribution, e.g. theta[1:k] ~ ddirich(a[1:k])
 - or hierarchically, e.g.
 - theta[1] ~ dunif(0,1); theta[2] <- dunif(0,theta[1])
 - Even in case of prior independence, parameters can still be dependent in the resulting posterior.
 - The same prior can be constructed in different ways too. For example these are equivalent for theta:

```
theta ~ dbeta(1,1)
theta ~ dunif(0,1)
theta <- phi(a); a ~ dnorm(0,1)</pre>
```

- The basic idea is always the same:
 - Thirdly: it helps to figure out the model as a DAG first
 - This helps to keep track of what is in the model, and that each part is defined:
 - All observed data values "X" have a conditional probability model, which depends on parameters "theta". In a DAG this is drawn as "theta → X" for each X.
 - All parameters have assigned priors, or further distributions, which depend on further parameters.
 - No cycles in model definition! It should constitute Acyclic Graph!
 - Keep in mind that you are constructing the logical definition of the elements needed in Bayes theorem: the prior and the likelihood.

- Collect several definitions by using indexing and looping:
 - For example: separate models for each X: for(i in 1:K){ X[i] ~ dbin(theta[i] , N[i]) }
 - For example: models with common parameter for each X:

for(i in 1:K){ X[i] ~ dbin(theta , N[i]) }

- Every definition within "for(i in 1:K){ }" should have index i on the left-hand-side of "~" or "←".
- Can make several nested loops, for "x[i,j]" etc.
- Can use nested indexing, for "x[y[i]]".
- Can use arithmetics in indexing, for "x[i+10]"

• Separate parameters example DAG:



• Common parameter example DAG:



- What distributions and logical functions are available?
 - Check the list from manual/menu.
 - Pay attention to parameterization!
 - A very useful function: step(). This can be used to create indicator variables, to compute probabilities by computing mean of the indicator.
 - What you define should be logically correct and computable in all situations. 1/X should never become 1/0 if X is stochastic.

• Data formatting (every data variable should appear in the model code)

```
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)) )
```

Alternative format

```
z[,1] z[,2] z[,3]
7 3 5
1 8 2
END (Note: empty line after END)
```

 Irregular data can be coded using NA for "missing"

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

BUGS would generate predictions for NAs. Alternatively, use auxiliary indexing: list(z=c(7,9,6,3,2,5),person=c(1,2,2,2,3,3))

 Transformations of original data values can be declared within model code

yy <- log(y)
yy ~ dnorm(mu,tau)</pre>

Here y would be given in data listing.

 Can check your data values from 'info' → 'node info' → 'values' (if you doubt what values were loaded).

- Always think it as a DAG. → hierarchical model structures.
- Fixed data value has to be assigned to a stochastic "~" node in the model code, not "<-". The latter would make 'multiple deterministic definitions' error.
- Ddistr(?,?) ← Parameters, not expressions. Check parameterization !
- Test first with a small number of iterations to see how slowly it runs.
- Give constants in data, not within code.
- Separate clearly what's data, what's model.
- Use comments # there are never too many!

- Collect definitions logically into groups (priors, likelihoods, predictions), easier to read.
- Transformations of data can be defined within code.
- Use indexing, and nested indexing.
- Avoid multiple definitions (e.g. within for-loops!) they are syntax errors.
- Break long expressions into short ones (avoid 'logical expression too complex' error)
- Pay attention to naming of parameters, variables. They should be meaningful at first sight. (or write good explanations in comment lines)

- Constants cannot be monitored, but can check them from the node-info menu button.
- Sooner or later, it will be more convenient to run BUGS from R, try it later...
- For the inbuilt convergence diagnostics, you should pick overdispersed starting values for at least 3 chains.
- Think of identifiability: are there sufficient data? Is something hanging completely from prior? It is deceptively easy to build castles in the clouds....
- Make use of inprod to avoid writing long expressions

 a[1]*X[1]+a[2]*X[2]+... ... And make use of other
 useful functions available (see manual → functions).

 Finally: don't get confused of what is (fixed) data, and what is unknown parameter. It is <u>always</u> about computing posterior distribution of the <u>unknowns</u>, conditionally on the known data:

P(unknowns | known data)

This posterior distribution is what you get from BUGS.