model { }

data { }
- matrices
- vectors
- scalars

initial values { }
- all parameters need to be initialized

we want to model $\begin{cases} Y_i = \beta_0 + \beta_1 X_i + \varepsilon_i, \; i = 1, \ldots, NSUB \\ \varepsilon_i \sim N(0, \sigma_\varepsilon^2) \end{cases}$

```
model
  { # Begin model
    for (i in 1:NSUB)
    { Y[i] ~ dnorm(m[i], tau_eps)
      m[i] <- beta0 + beta1 * x[i]
    }
  # beta0 ~ dnorm(0, 1.0E-6)
  # beta1 ~ dnorm(0, 1.0E-6)
  # tau_eps ~ dgamma(.001, .001)
  }# end model
```

"precision = $1/\sigma_\varepsilon^2$"

"data!"

"auxiliary variable"

parameters

Y[]	X[]
2	.1
1	1
3	0
4	2
5	3

END

list(beta0 = 0, beta1 = 0, tau_eps = 1)

#be sure priors are compatible w/ model

#warning:
WINBUGS is powerful!

So use it with responsibility.

Will run even if not identifiable!

WINBUGS Documentation:

1) The WINBUGS Manual
2) Ciprian Crainiceanu's website
3) Bayesian Statistical Modeling, Peter Congdon
4) MCMC in practice Spiegelhalter et al.
5) JSS → bayesian analysis for P-splines, Crainiceanu

Tricks & Tips (not exhaustive)

1. Nested indexing

Y_{ij} → biomarker for subject i at visit j

X_{ij} → BMI ..... " "

$$Y_{ij} = \beta_0 + b_i + \beta_1 X_{ij} + \varepsilon_{ij}$$

$$b_i \sim N(0, \sigma_b^2)$$

$$\varepsilon_{ij} \sim N(0, \sigma_\varepsilon^2)$$

Need to rearrange the data...

First step: restructure the data

Y	X	subject
2	0	1
3	2	1
2	2	1
1	3	2
24	1	2
3	2	3
⋮	⋮	
END	END	

"unbalanced design"

model

{ # begin model

for (i in 1:NOBS)

{ Y[i] ~ dnorm(m[i], tau_eps)

m[i] ← beta0 + b[subject[i]] + beta1 * x[i]

}

for (R in 1:NSUB)

{ b[R] ~ dnorm(0, tau_b)} ← smoothing parameter

beta0 ~ same as before

beta1 ~ same as before

tau_eps ~ same as before

tau_b ~ same as tau_eps

}# end model

2nd trick

$$\begin{cases} \text{beta0} + b_i \\ b_i \sim N(0, \sigma_b^2) \end{cases} \quad <=> \quad b_i \sim N(B_0, \sigma_b^2)$$

Hierarchical centering

mathematically equivalent

not WINBUGS technically equivalent

Hierarchical centering

take beta0 out of m[i] statement

in previous model block, and

put beta0 in for 0 in dnorm(beta0, tau.b)

1. Convergence of Chains

2. Mixing

3. plot your priors and posteriors
   → you can see if parameters are learning from data

   if there's no change between prior/posterior
   1) could be parameter is weakly or non-identifiable

4. Check whether parameters make any sense / Naive estimates

5. Do simulations
   ↳ the frequentist properties of your Bayesian Analysis

Simplify, Simplify, Simplify.

1. Go back to simple regression.

2. Fix parameters

   tau_b ← 1

   ↖ instead of a distribution.

Arsenic - "As" is bad for you

		threshold
As(III)	Arsenite	.1
As(V)	Arsenate	.5

they'd like to measure Y_{ij}^{k} → true concentration of arsenic for subject i at visit j

R=1 As(III)

R=2 As(V)

C^{R} limit of detection

W_{ij}^{R} → observed concentration

60 subjects, 3 obs. / subject

Data seen:

$$w_{ij}^{R} = \begin{cases} y_{ij}^{R}, & y_{ij}^{k} > C^{R} \\ NA, & \text{otherwise} \end{cases}$$

censoring, but not independent

multilevel, lognormal, ~~probit~~ ... ~~tobit~~ model

$$y_{ij}^{R} = u_{ij}^{k} + b_{i}^{k} + \varepsilon_{ij}^{k}$$

$$\varepsilon_{ij}^{R} \sim N(0, \sigma_{\varepsilon,k}^{2})$$

$$u_{ij}^{R} = x_{ij}^{k} \beta_{R}$$