Bayes Seminar: Part II

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Automating inference using BUGS:

- BUGS allows us to build automated systems to perform posterior sampling
- BUGS constructs a sampler based only on a model description
- BUGS is a descriptive programming language rather than a procedural programming language

- A BUGS interpreter works because MCMC sampling is automatable
- BUGS interpreters often use two types of sampling under the hood:
  - Gibbs sampling is fully automatable for conjugate parts of models
  - Metropolis-Hasting sampling is automatable even without conjugacy

Why use BUGS?

- Separating model descriptions from inference procedures encourages exploration of multiple models
- Novel models can be built from familiar components without thinking about analytic tractability

Some BUGS interpreters:

- WinBUGS
- OpenBUGS
- JAGS

- We'll start with inference in the beta-binomial model we used before

Binomial Model I

```
model
{
  for (i in 1:N)
  {
    x[i] ~ dbern(p)
  }

  p ~ dbeta(alpha, beta)

  alpha <- 1
  beta <- 1
}
```

- Every BUGS model starts with `model`
- Primitive looping is allowed
- Two types of assignment: deterministic and stochastic

- We've used a beta(1, 1) prior
- This is a flat prior over $[0, 1]$

- For inference, BUGS needs to be invoked with data
- We'll use JAGS as our BUGS interpreter
- We'll use R via the rjags package to send data to JAGS

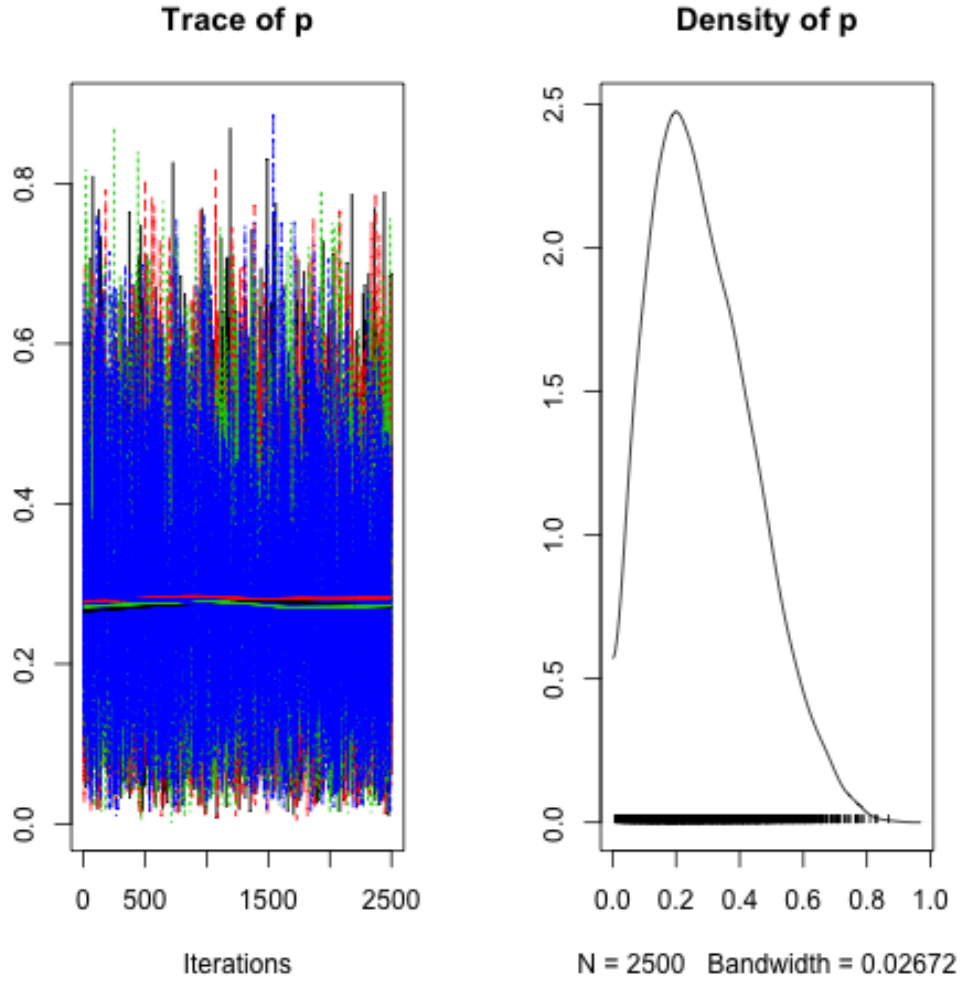
```
library('rjags')

df <- read.csv(file.path('data',
                         'binomial',
                         'binomial.csv'))
```

For the sample data:

- $p = 0.4$
- $n = 5$
- $\hat{p} = 0.2$

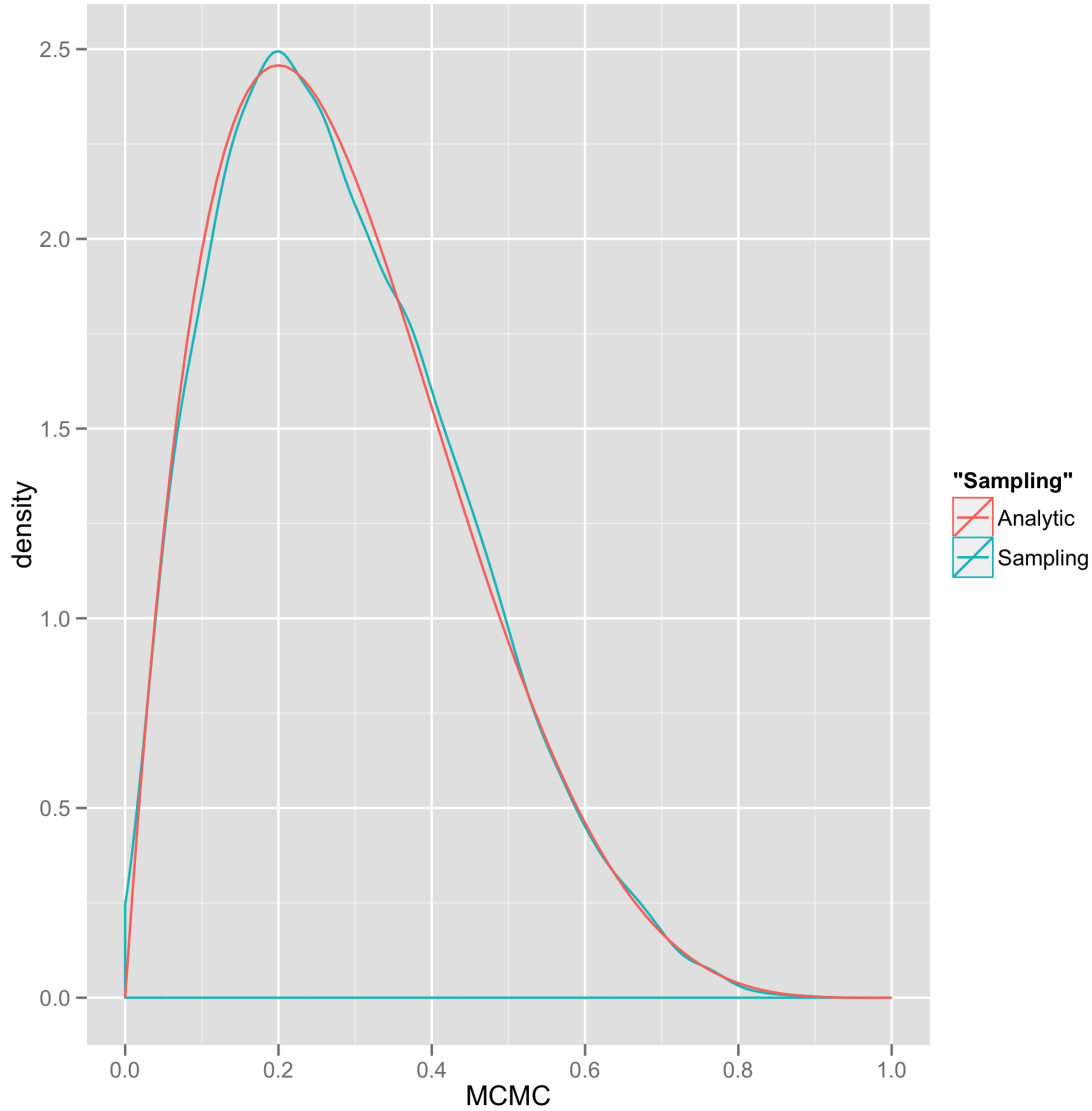
```
"X"
0
0
0
1
0
```

```
jags <- jags.model(file.path('bugs',
                             'binomial',
                             'binomial.bugs'),
                   data = list('x' = with(df, X),
                               'N' = nrow(df)),
                   n.chains = 4,
                   n.adapt = 1000)

mcmc.samples <- coda.samples(jags,
                             c('p'),
                             2500)

plot(mcmc.samples)

summary(mcmc.samples)
```


Trace of p
0.0
0.2
0.4
0.6
0.8
0
500
1500
2500
Iterations
Density of p
0.0
0.5
1.0
1.5
2.0
2.5
0.0
0.2
0.4
0.6
0.8
1.0
N = 2500 Bandwidth = 0.02672

```
Iterations = 1:2500
Thinning interval = 1
Number of chains = 4
Sample size per chain = 2500

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

          Mean             SD       Naive SE Time-series SE
      0.286161       0.159027       0.001590       0.001576

2. Quantiles for each variable:

   2.5%     25%     50%     75%   97.5%
0.04272 0.16242 0.26418 0.39122 0.63907
```

```
alpha <- with(df, sum(X) + 1)
beta <- nrow(df) + 2 - alpha

alpha / (alpha + beta)
#[1] 0.2857143

summary(mcmc.samples)$statistics
#           Mean             SD       Naive SE Time-series S
#   0.286160728    0.159026669    0.001590267    0.0015759
```


2.5
2.0
1.5
1.0
0.5
0.0
density
0.0
0.2
0.4
0.6
0.8
1.0
MCMC
"Sampling"
Analytic
Sampling

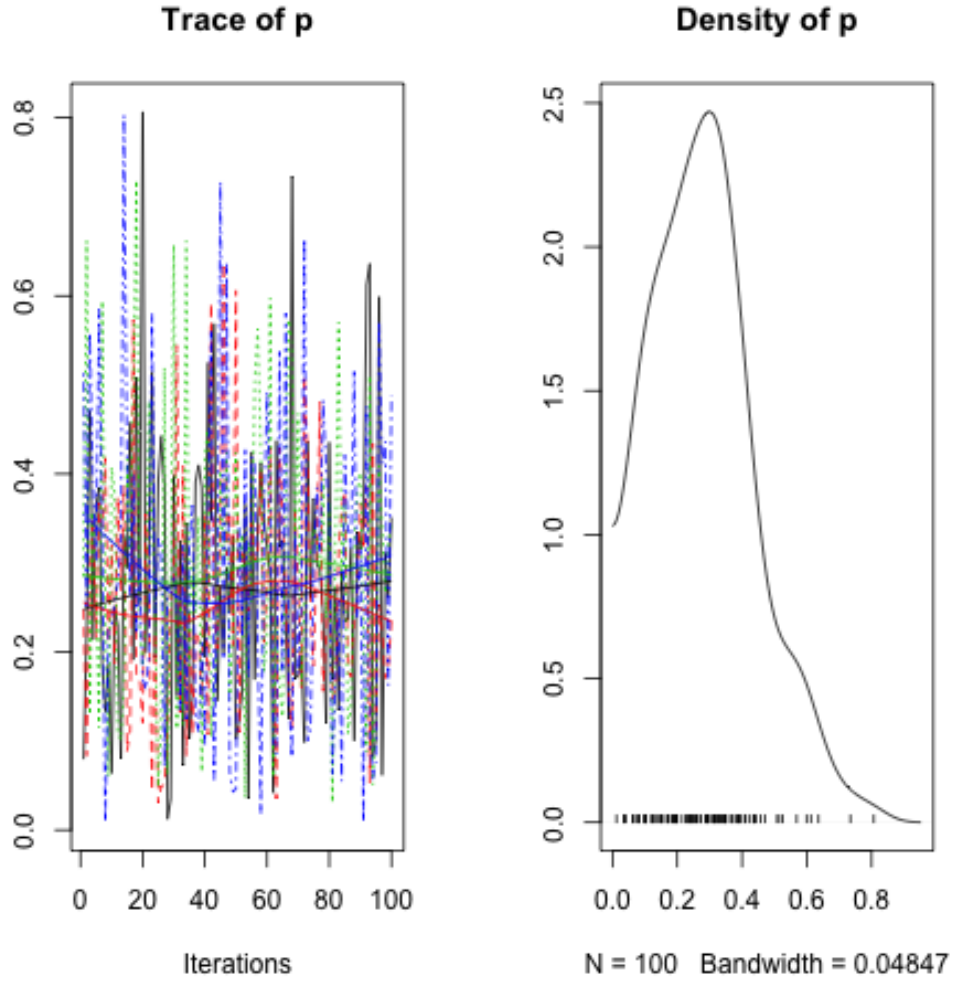
```
binom.test(with(df, sum(X)), nrow(df))$conf.int
#[1] 0.005050763 0.716417936
credible.interval <- c(qbeta(0.025, alpha, beta),
                       qbeta(0.975, alpha, beta))
credible.interval
#[1] 0.04327187 0.64123458
binom.test(with(df, sum(X)) + 1, nrow(df) + 2)$conf.int
#[1] 0.03669257 0.70957914
```

Lessons:

- BUGS has correctly performed inference
- Simulation results closely approximate analytic results
- We get a full posterior, not just a point estimate or CI

- What could we have done wrong?
- Used no adaptive phase
- Gathered too few samples

```
jags <- jags.model(file.path('bugs',
                             'binomial',
                             'binomial.bugs'),
                   data = list('x' = with(df, X),
                               'N' = nrow(df)),
                   n.chains = 4,
                   n.adapt = 0)

mcmc.samples <- coda.samples(jags,
                             c('p'),
                             100)

plot(mcmc.samples)
```


Trace of p
0.0
0.2
0.4
0.6
0.8
0
20
40
60
80
100
Iterations
Density of p
0.0
0.5
1.0
1.5
2.0
2.5
0.0
0.2
0.4
0.6
0.8
N = 100 Bandwidth = 0.04847

- You should play with this example more and try to break it
- In this case, having no adaptive phase turns out not to matter
- Using too few samples gives us a wiggly approximation to the posterior

- Let's move on to inferring the mean of a normal distribution

```
model
{
  for (i in 1:N)
  {
    x[i] ~ dnorm(mu, tau)
  }

  mu ~ dnorm(0, 0.0001)

  sigma <- 3
  tau <- pow(sigma, -2)
}
```

- BUGS uses precision rather than variance to specify normal distributions
- We use a weakly informative Normal prior centered at zero
- We use arithmetic within BUGS to transform variance into precision

For sample data:

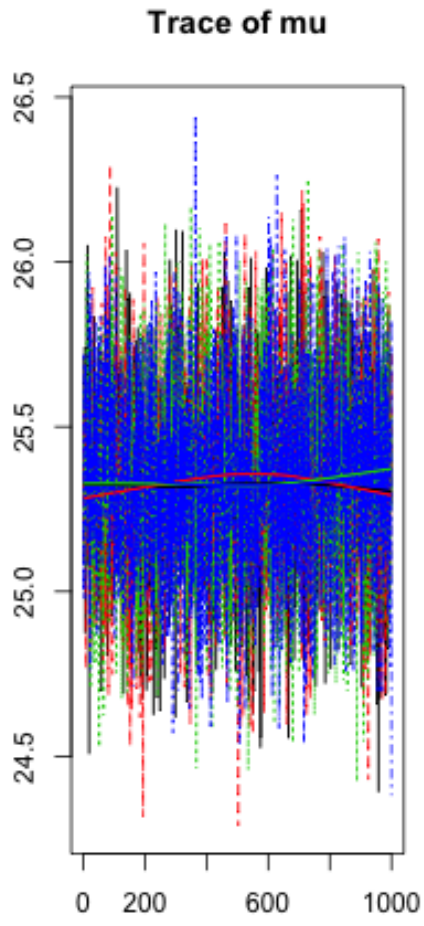
- $\mu = 25$
- $\sigma = 3$
- $n = 100$
- $\hat{\mu} = 25.32666$

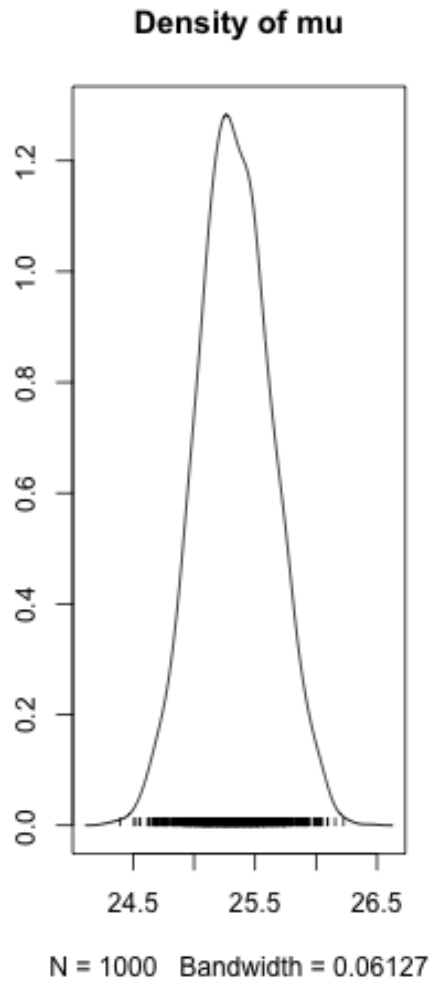
```
"X"
23.120638567773
25.5509299726662
22.4931141627699
...
23.2802037572893
21.3261621553049
23.5797980906821
```

```
library('rjags')

df <- read.csv(file.path('data',
                         'normal',
                         'normal_mean.csv'))
```

```
jags <- jags.model(file.path('bugs',
                             'normal',
                             'normal_mean.bugs'),
                   data = list('x' = with(df, X),
                               'N' = nrow(df)),
                   n.chains = 4,
                   n.adapt = 500)

mcmc.samples <- coda.samples(jags,
                             c('mu'),
                             1000)

plot(mcmc.samples)

summary(mcmc.samples)
```

```
Iterations = 1:1000
Thinning interval = 1
Number of chains = 4
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

          Mean             SD       Naive SE Time-series SE
     25.331926       0.303623       0.004801       0.004849

2. Quantiles for each variable:

 2.5%   25%   50%   75% 97.5%
24.74 25.13 25.32 25.53 25.93
```


Trace of mu
26.5
26.0
25.5
25.0
24.5
0
200
600
1000
Iterations


Density of mu
1.2
1.0
0.8
0.6
0.4
0.2
0.0
24.5
25.5
26.5
N = 1000 Bandwidth = 0.06127

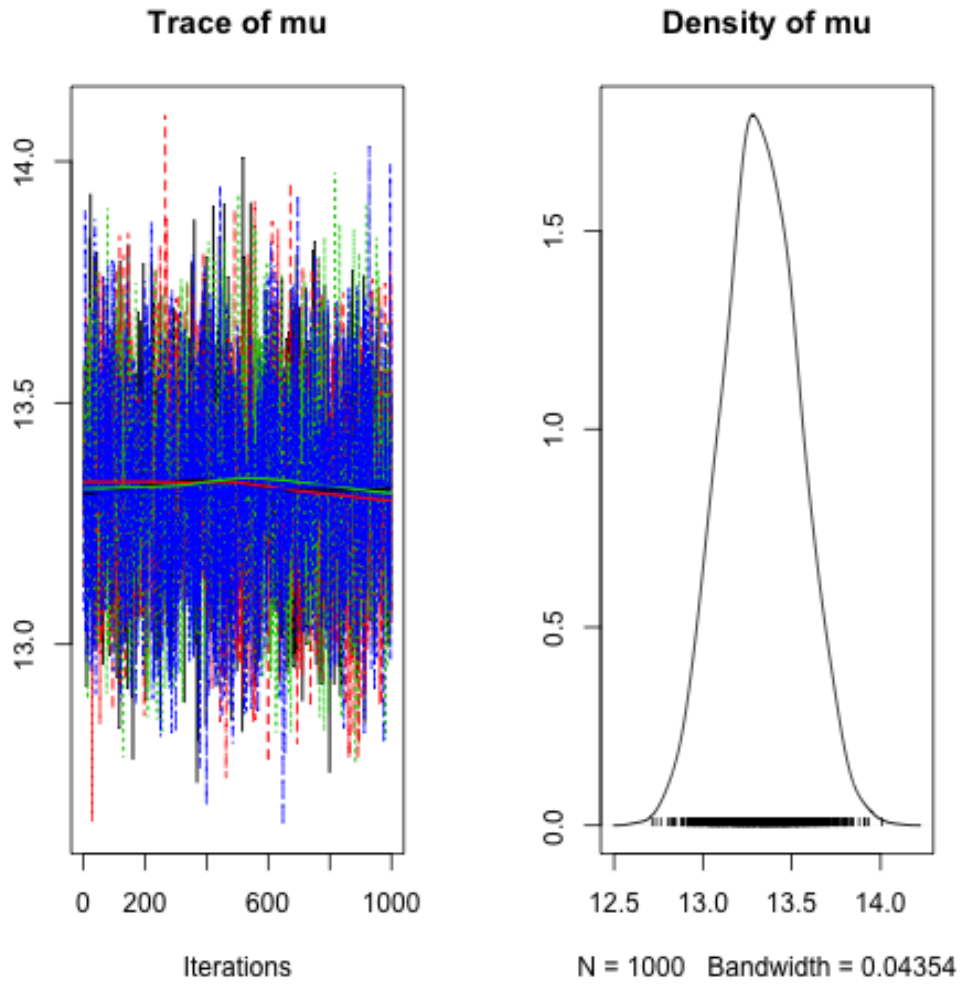
- As in the binomial example, we have a conjugate prior here
- Posterior has closed form solution, which could be used to assess quality of MCMC
- But we see that MCMC solution is the MLE so we skip that analysis

- Let's show that inference can be very bad if the wrong prior is used

```
model
{
  for (i in 1:N)
  {
    x[i] ~ dnorm(mu, tau)
  }

  mu ~ dnorm(0, 10)

  sigma <- 3
  tau <- pow(sigma, -2)
}
```

- Prior has mean 0
- Prior has variance $\frac{1}{10}$
- With so little variance, the prior pulls the posterior towards itself

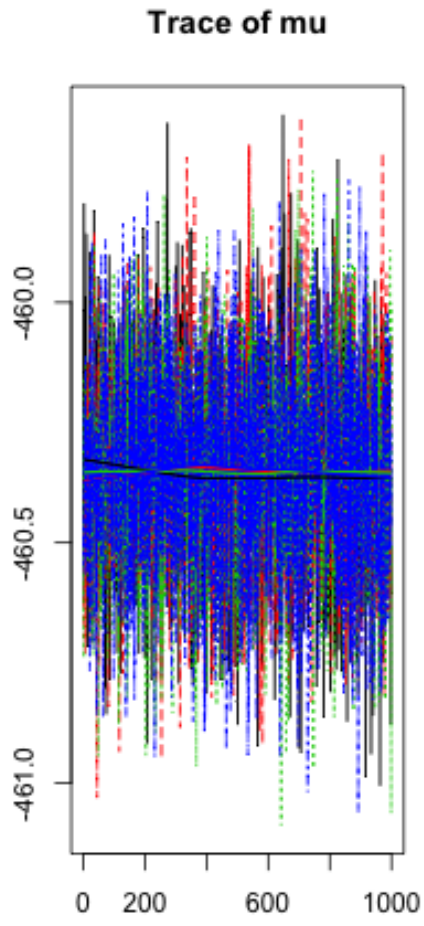
```
Iterations = 1:1000
Thinning interval = 1
Number of chains = 4
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

          Mean             SD       Naive SE Time-series SE
     13.327539       0.215767       0.003412       0.003343

2. Quantiles for each variable:

 2.5%   25%   50%   75% 97.5%
12.92 13.18 13.32 13.47 13.75
```

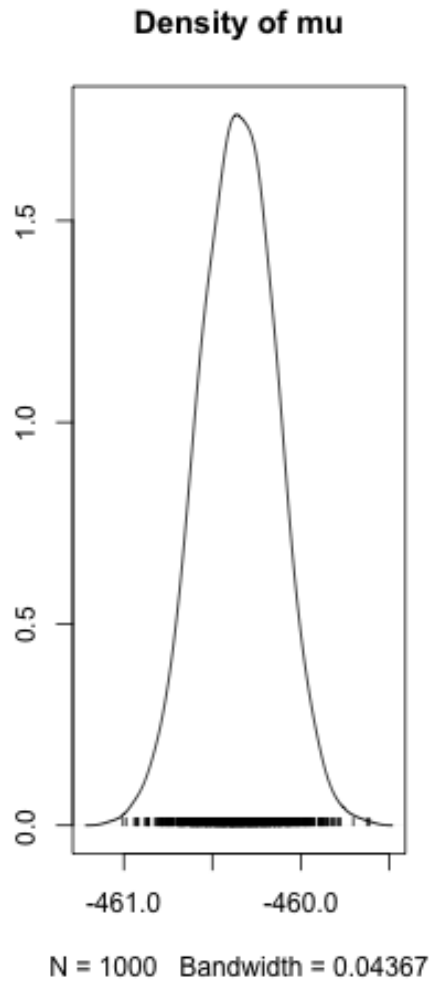

Trace of mu
14.0
13.5
13.0
0
200
600
1000
Iterations
Density of mu
1.5
1.0
0.5
0.0
12.5
13.0
13.5
14.0
N = 1000 Bandwidth = 0.04354

- It can easily get worse

```
model
{
  for (i in 1:N)
  {
    x[i] ~ dnorm(mu, tau)
  }

  mu ~ dnorm(-1000, 10)

  sigma <- 3
  tau <- pow(sigma, -2)
}
```

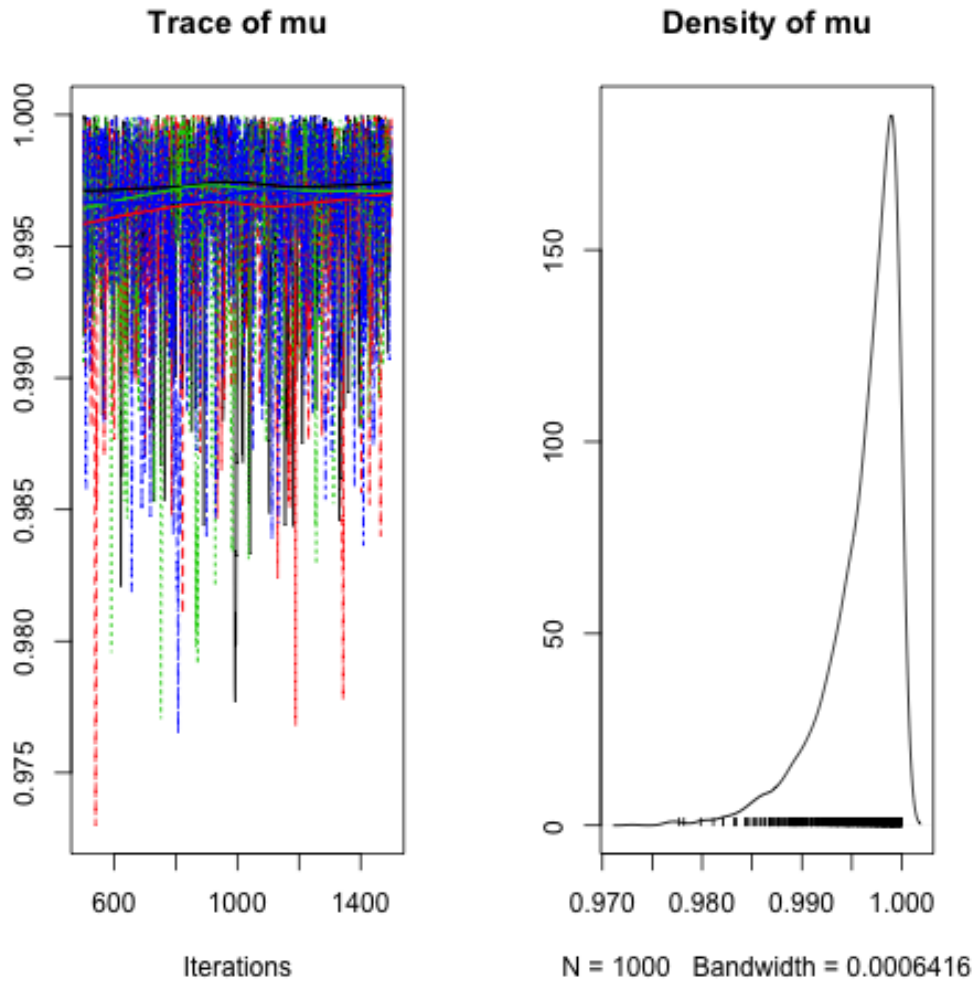
```
Iterations = 1:1000
Thinning interval = 1
Number of chains = 4
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

          Mean             SD       Naive SE Time-series SE
    -4.604e+02      2.164e-01      3.422e-03      3.507e-03

2. Quantiles for each variable:

  2.5%    25%    50%    75%  97.5%
-460.8 -460.5 -460.4 -460.2 -459.9
```


Trace of mu
-460.0
-460.5
-461.0
0
200
600
1000
Iterations


Density of mu
1.5
1.0
0.5
0.0
-461.0
-460.0
N = 1000 Bandwidth = 0.04367

- Using the wrong prior variance causes trouble
- Using the wrong prior mean causes more trouble
- Using the wrong prior functional form can be still worse

```
model
{
  for (i in 1:N)
  {
    x[i] ~ dnorm(mu, tau)
  }

  mu ~ dunif(0, 1)

  sigma <- 3
  tau <- pow(sigma, -2)
}
```


Trace of mu
1.000
0.995
0.990
0.985
0.980
0.975
600
1000
1400
Iterations
Density of mu
150
100
50
0
0.970
0.980
0.990
1.000
N = 1000 Bandwidth = 0.0006416

```
Iterations = 501:1500
Thinning interval = 1
Number of chains = 4
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

          Mean             SD       Naive SE Time-series SE
     9.962e-01      3.691e-03      5.836e-05      1.361e-04

2. Quantiles for each variable:

  2.5%    25%    50%    75%  97.5%
0.9861 0.9946 0.9973 0.9989 0.9999
```

- Because our prior assigns 0 probability to most values of μ, it can't reach them even with infinite data
- Lindley refers to the requirement that priors not assign 0 probability as Cromwell's Rule:

> *I beseech you, in the bowels of Christ, think it possible that you may be mistaken.*

- When you violate Cromwell's Rule, you can get extremely tight posteriors around very wrong values
- In this case, you can discover your mistake because of the truncated posterior

- But take away this lesson:
  - If you have valid prior information, put it in the prior
  - Otherwise, give the prior very high variance

- Let's leave single parameter inference behind
- We'll implement a Bayesian linear regression

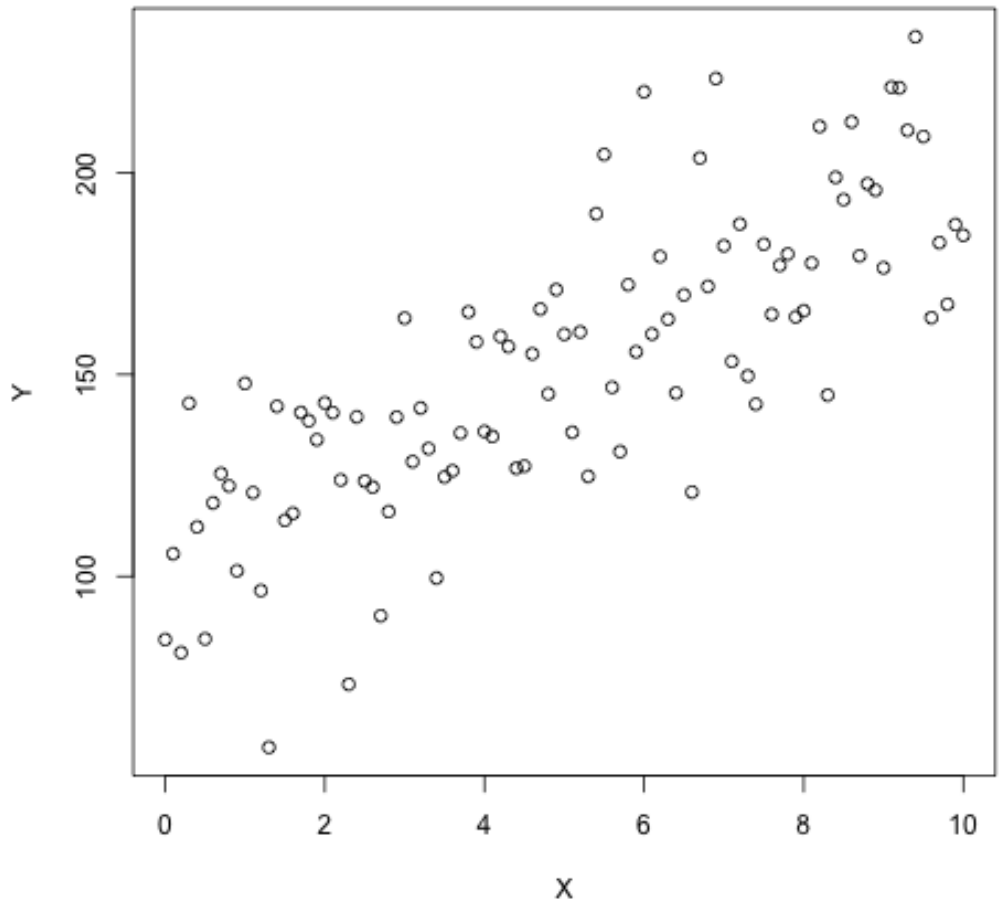
```
model
{
  for (i in 1:N)
  {
    y[i] ~ dnorm(mu[i], tau)
    mu[i] <- a * x[i] + b
  }

  a ~ dnorm(0, 0.0001)
  b ~ dnorm(0, 0.0001)

  tau <- pow(sigma, -2)
  sigma ~ dunif(0, 10000)
}
```

```
"X","Y"
0,84.3386547314417
0.1,105.591083105552
0.2,81.1092846897488
0.3,142.882020053445
...
9.7,182.668364644078
9.8,167.384684627541
9.9,187.164984089017
10,184.490833069397
```

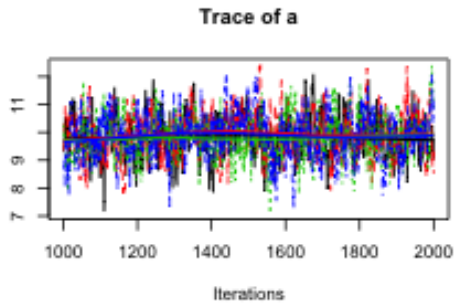
For the sample data:

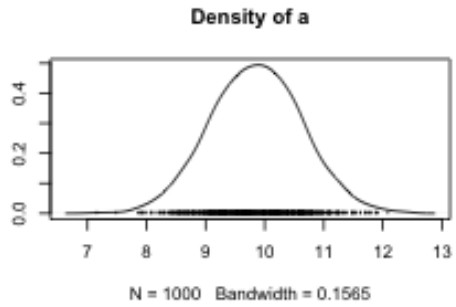
- $a = 10$
- $b = 100$
- $\sigma = 25$

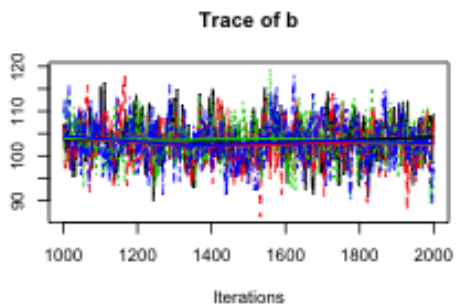
```
library('rjags')

df <- read.csv(file.path('data',
                         'ols',
                         'ols_regression.csv'))

with(df, plot(X, Y))
```

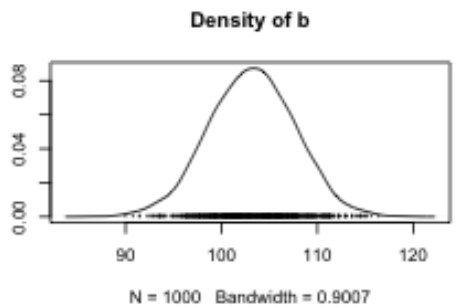

Y
100
150
200
0
2
4
6
8
10
X

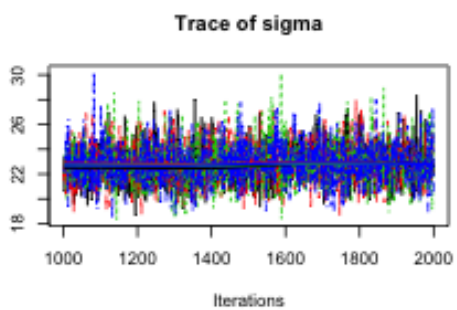
```
jags <- jags.model(file.path('bugs',
                             'ols',
                             'ols_regression.bugs'),
                   data = list('x' = with(df, X),
                               'y' = with(df, Y),
                               'N' = nrow(df)),
                   n.chains = 4,
                   n.adapt = 1000)

mcmc.samples <- coda.samples(jags,
                             c('a', 'b', 'sigma'),
                             1000)

plot(mcmc.samples)

summary(mcmc.samples)
```

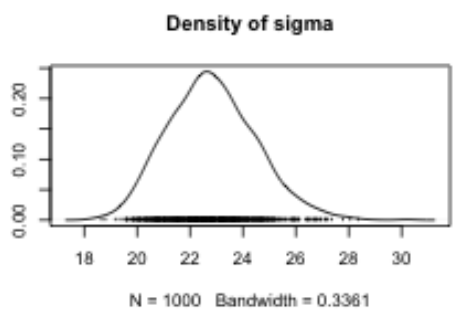

Trace of a
7
8
9
11
1000
1200
1400
1600
1800
2000
Iterations


Density of a
0.0
0.2
0.4
7
8
9
10
11
12
13
N = 1000 Bandwidth = 0.1565


Trace of b
90
100
110
120
1000
1200
1400
1600
1800
2000
Iterations


Density of b
0.00
0.04
0.08
90
100
110
120
N = 1000 Bandwidth = 0.9007


Trace of sigma
18
22
26
30
1000
1200
1400
1600
1800
2000
Iterations


Density of sigma
0.00
0.10
0.20
18
20
22
24
26
28
30
N = 1000 Bandwidth = 0.3361

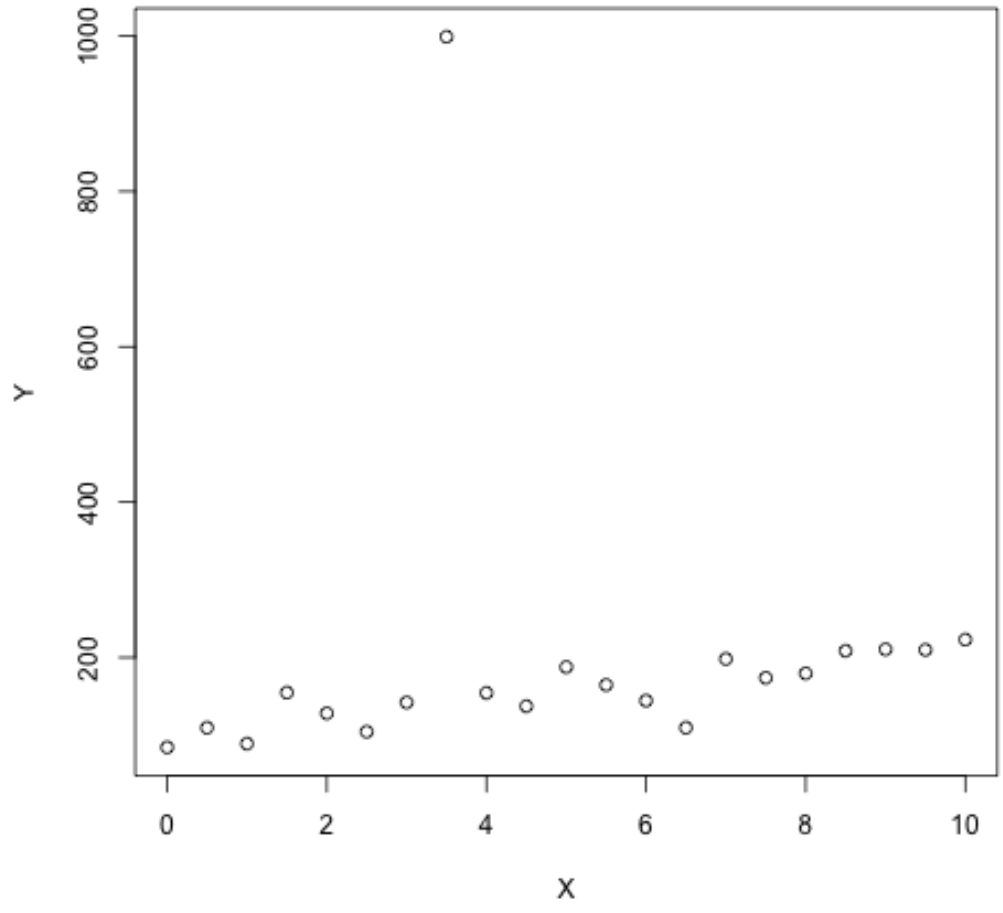
```
Iterations = 1001:2000
Thinning interval = 1
Number of chains = 4
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

          Mean     SD Naive SE Time-series SE
a        9.875 0.8035  0.01270         0.03743
b      103.023 4.6591  0.07367         0.22097
sigma   22.805 1.6429  0.02598         0.03003

2. Quantiles for each variable:

         2.5%     25%     50%    75%  97.5%
a       8.239   9.349   9.887  10.40  11.45
b      93.962  99.996 103.088 105.97 112.60
sigma 19.895  21.640  22.687  23.83  26.32
```

```
Call:
lm(formula = Y ~ X, data = df)

Coefficients:
(Intercept)            X
    103.620        9.784
```

- Implementing simple linear regression is easy
- BUGS's virtue is that alternatives are just as easy to implement

- Consider a case where the Gaussian noise assumption is wrong
- One solution is to replace the OLS objective with the LAD objective
- For a Bayesian this amounts to assuming Laplace noise

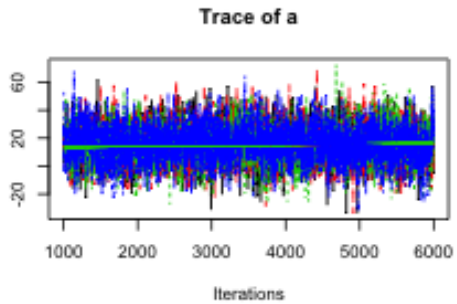
```
library('rjags')

df <- read.csv(file.path('data',
                         'ols',
                         'ols_regression_outlier.csv'))

with(df, plot(X, Y))
```

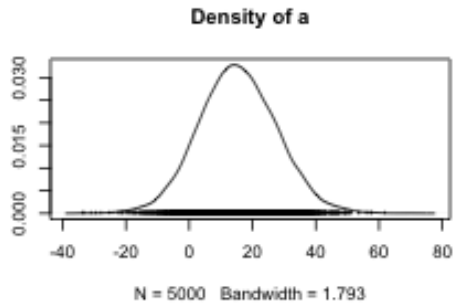

Y
1000
800
600
400
200
0
2
4
6
8
10
X

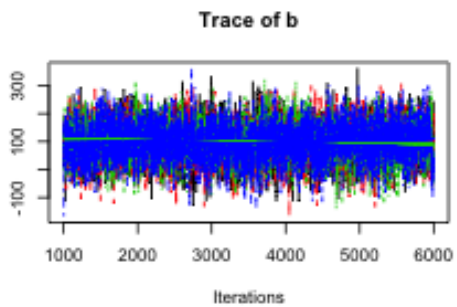
For the sample data:

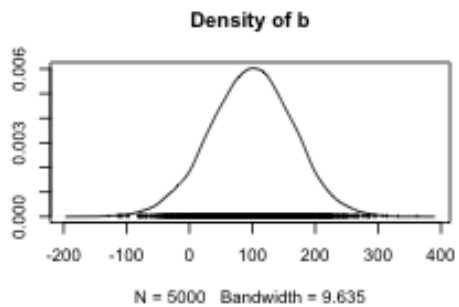
- $a = 10$
- $b = 100$
- $\sigma = 25$
- One outlier was added post hoc

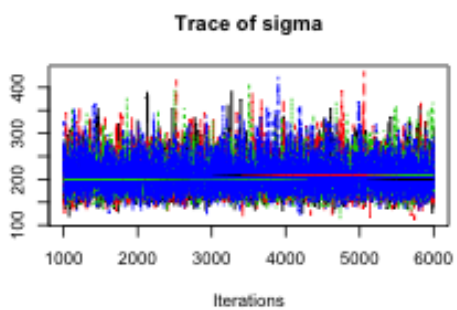
```
jags <- jags.model(file.path('bugs',
                             'ols',
                             'ols_regression_outlier.bugs'),
                   data = list('x' = with(df, X),
                               'y' = with(df, Y),
                               'N' = nrow(df)),
                   n.chains = 4,
                   n.adapt = 1000)

mcmc.samples <- coda.samples(jags,
                             c('a', 'b', 'sigma'),
                             5000)

plot(mcmc.samples)

summary(mcmc.samples)
```

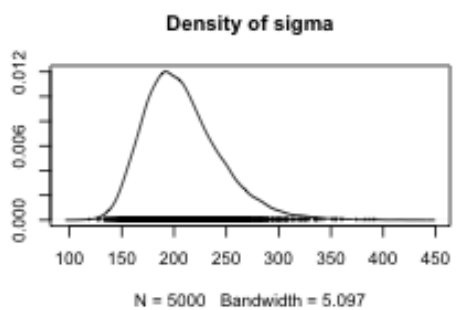

Trace of a
60
20
-20
1000
2000
3000
4000
5000
6000
Iterations


Density of a
0.030
0.015
0.000
-40
-20
0
20
40
60
80
N = 5000 Bandwidth = 1.793


Trace of b
300
100
-100
1000
2000
3000
4000
5000
6000
Iterations


Density of b
0.006
0.003
0.000
-200
-100
0
100
200
300
400
N = 5000 Bandwidth = 9.635


Trace of sigma
400
300
200
100
1000
2000
3000
4000
5000
6000
Iterations


Density of sigma
0.012
0.006
0.000
100
150
200
250
300
350
400
450
N = 5000 Bandwidth = 5.097

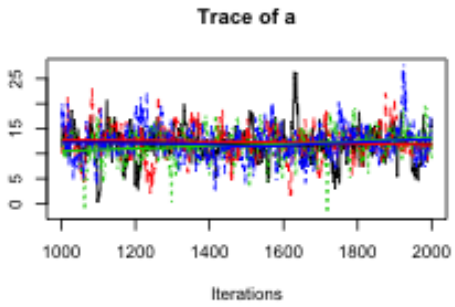
```
Iterations = 1001:6000
Thinning interval = 1
Number of chains = 4
Sample size per chain = 5000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

          Mean    SD Naive SE Time-series SE
a        15.41 12.27  0.08675          0.1764
b        98.72 65.88  0.46585          0.9934
sigma   208.10 36.85  0.26056          0.4147

2. Quantiles for each variable:

           2.5%     25%    50%    75%  97.5%
a        -8.068   7.127  15.16  23.55  39.64
b      -33.903  54.731  99.57 143.41 225.82
sigma  150.876 181.921 203.17 228.62 293.77
```

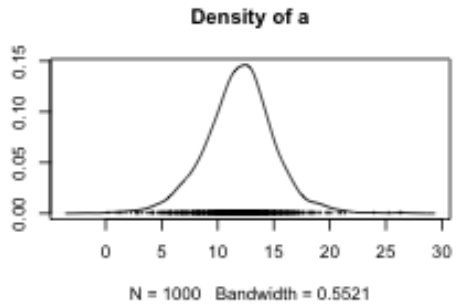
- Using a heavier-tailed error distribution gives the outlier less influence
- We use Laplace errors, but we could use other distributions

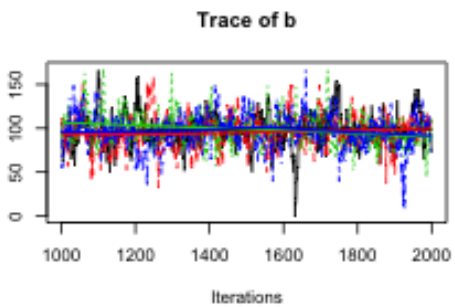
```
model
{
  for (i in 1:N)
  {
    y[i] ~ ddexp(mu[i], tau)
    mu[i] <- a * x[i] + b
  }

  a ~ dnorm(0, 0.0001)
  b ~ dnorm(0, 0.0001)

  tau <- pow(sigma, -2)
  sigma ~ dunif(0, 100)
}
```

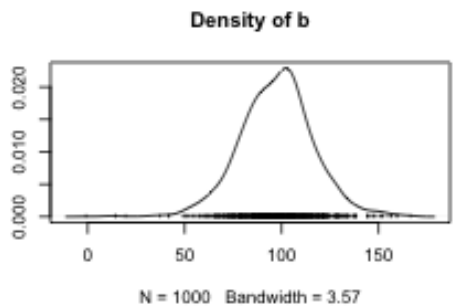
```
library('rjags')

df <- read.csv(file.path('data',
                         'lad',
                         'lad_regression.csv'))

with(df, plot(X, Y))
```

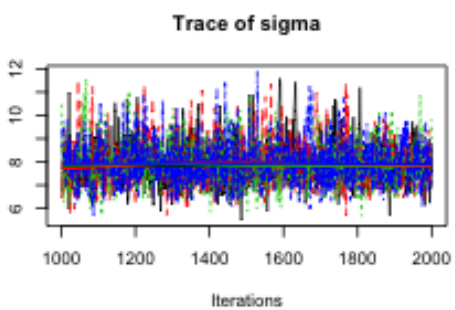
```
jags <- jags.model(file.path('bugs',
                             'lad',
                             'lad_regression.bugs'),
                   data = list('x' = with(df, X),
                               'y' = with(df, Y),
                               'N' = nrow(df)),
                   n.chains = 4,
                   n.adapt = 1000)

mcmc.samples <- coda.samples(jags,
                             c('a', 'b', 'sigma'),
                             1000)

plot(mcmc.samples)

summary(mcmc.samples)
```

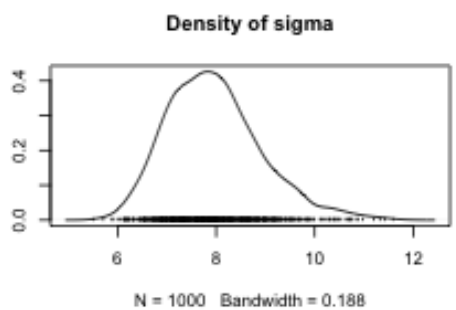

Trace of a
0
5
15
25
1000
1200
1400
1600
1800
2000
Iterations


Density of a
0.00
0.05
0.10
0.15
0
5
10
15
20
25
30
N = 1000 Bandwidth = 0.5521


Trace of b
0
50
100
150
1000
1200
1400
1600
1800
2000
Iterations


Density of b
0.000
0.010
0.020
0
50
100
150
N = 1000 Bandwidth = 3.57

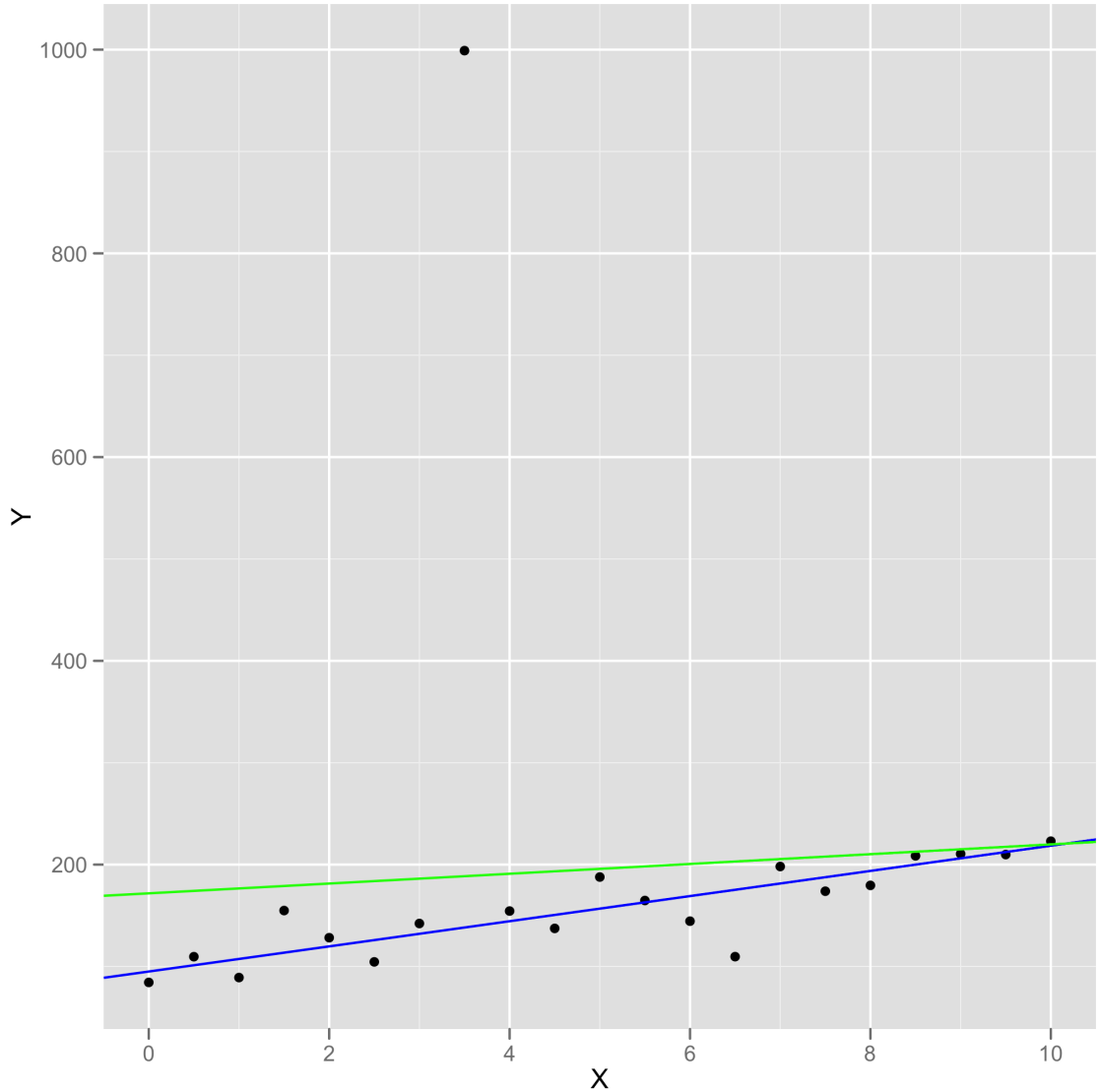

Trace of sigma
6
8
10
12
1000
1200
1400
1600
1800
2000
Iterations


Density of sigma
0.0
0.2
0.4
6
8
10
12
N = 1000 Bandwidth = 0.188

```
Iterations = 1001:2000
Thinning interval = 1
Number of chains = 4
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

         Mean      SD Naive SE Time-series SE
a      11.956  3.1146  0.04925        0.18855
b      97.419 19.0487  0.30119        1.10237
sigma   7.959  0.9604  0.01519        0.02498

2. Quantiles for each variable:

         2.5%    25%    50%     75%  97.5%
a       5.654 10.144 12.038  13.811  18.28
b      59.353 85.228 98.091 108.933 135.82
sigma   6.361  7.264  7.869   8.513  10.22
```

- Our inferences for a and b are much better
- σ is no longer meaningful since we have a different error distribution

- Visualizing the OLS and LAD lines is even more compelling


1000
800
600
400
200
Y
0
2
4
6
8
10
X

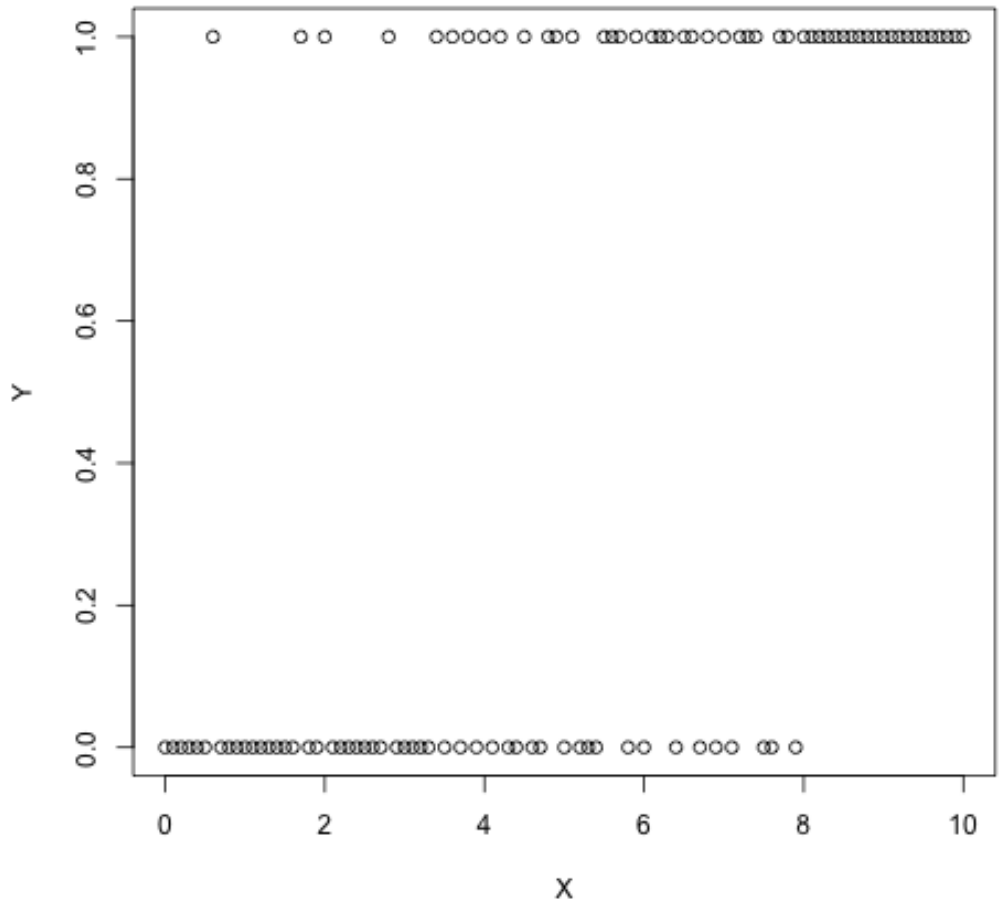
Instead of modeling continuous data, we can model 0/1 data:

- Logit regression
- Probit regression
- Robit regression

```
model
{
  for (i in 1:N)
  {
    y[i] ~ dbern(p[i])
    logit(p[i]) <- a * x[i] + b
  }

  a ~ dnorm(0, 0.0001)
  b ~ dnorm(0, 0.0001)
}
```

```
library('rjags')

df <- read.csv(file.path('data',
                         'logit',
                         'logit_regression.csv'))

with(df, plot(X, Y))
```

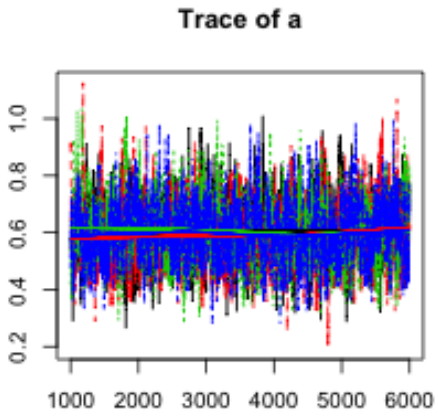
```
"X","Y"
3.1,0
3.2,0
3.3,0
3.4,1
...
7.1,0
7.2,1
7.3,1
7.4,1
```

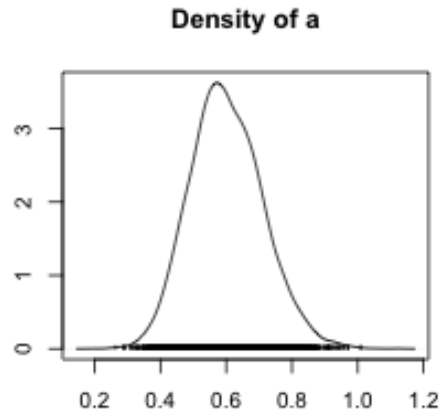

Y
X
0.0
0.2
0.4
0.6
0.8
1.0
0
2
4
6
8
10

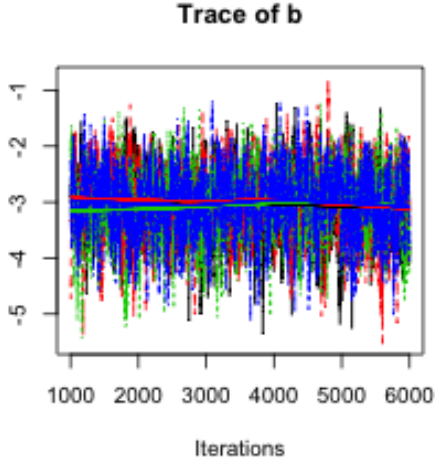
For the sample data:

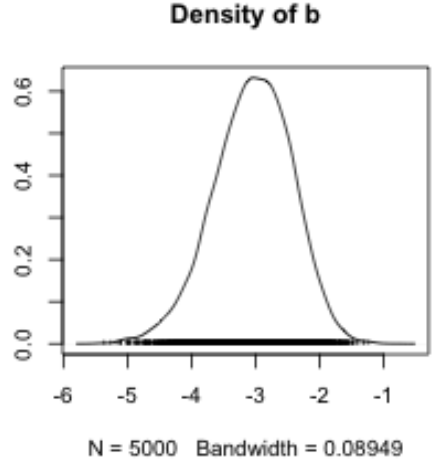
- $y \sim f(ax + b)$
- $a = 0.55$
- $b = -3$

```
jags <- jags.model(file.path('bugs',
                             'logit',
                             'logit.bugs'),
                   data = list('x' = with(df, X),
                               'y' = with(df, Y),
                               'N' = nrow(df)),
                   n.chains = 4,
                   n.adapt = 1000)

mcmc.samples <- coda.samples(jags,
                             c('a', 'b'),
                             5000)

plot(mcmc.samples)

summary(mcmc.samples)
```


Trace of a
0.2
0.4
0.6
0.8
1.0
1000
2000
3000
4000
5000
6000
Iterations


Density of a
0
1
2
3
0.2
0.4
0.6
0.8
1.0
1.2
N = 5000 Bandwidth = 0.01617


Trace of b
-1
-2
-3
-4
-5
1000
2000
3000
4000
5000
6000
Iterations


Density of b
0.0
0.2
0.4
0.6
-6
-5
-4
-3
-2
-1
N = 5000 Bandwidth = 0.08949

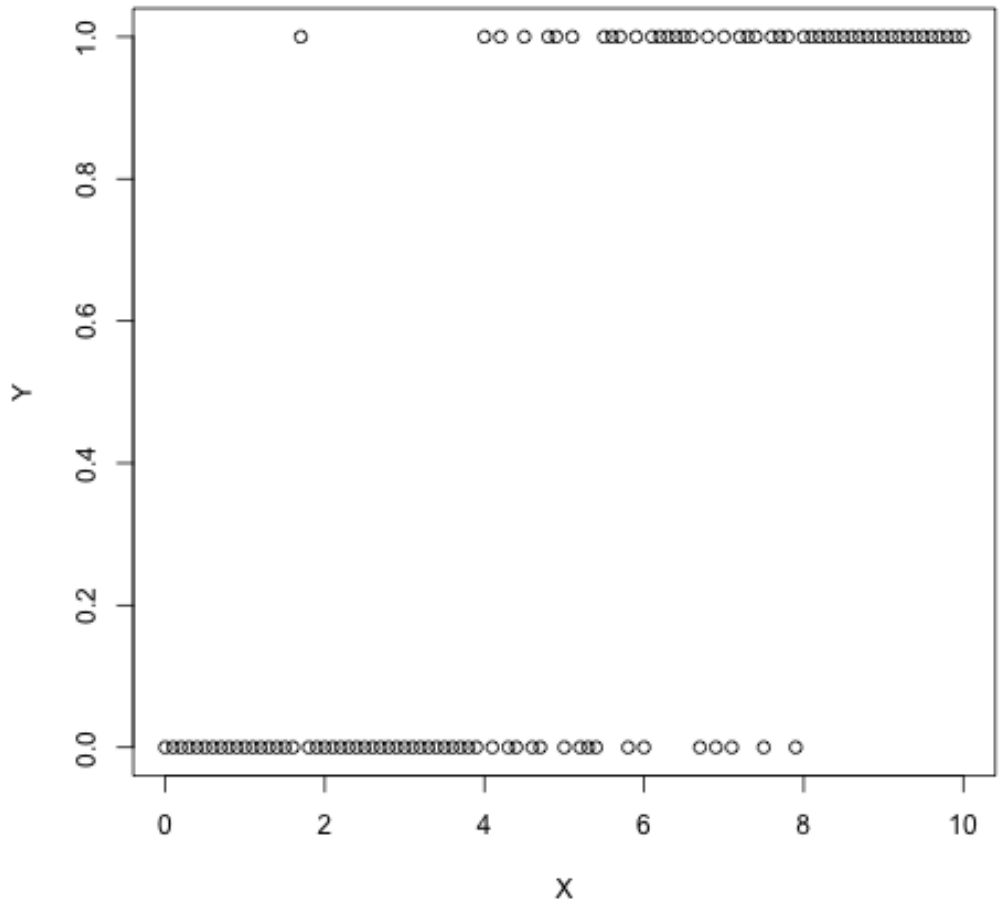
```
Iterations = 1001:6000
Thinning interval = 1
Number of chains = 4
Sample size per chain = 5000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

     Mean     SD  Naive SE Time-series SE
a  0.6012 0.1105 0.0007816       0.003321
b -3.0437 0.6119 0.0043267       0.018217

2. Quantiles for each variable:

     2.5%     25%     50%     75%   97.5%
a  0.4002  0.5246  0.5956  0.6738  0.8313
b -4.3329 -3.4444 -3.0180 -2.6117 -1.9305
```

- The probit model, popular in econometrics, is largely equivalent to the logit model
- The probit link function is used instead of the logit link function

```
model
{
  for (i in 1:N)
  {
    y[i] ~ dbern(p[i])
    probit(p[i]) <- a * x[i] + b
  }

  a ~ dnorm(0, 0.0001)
  b ~ dnorm(0, 0.0001)
}
```

```
library('rjags')

df <- read.csv(file.path('data',
                         'probit',
                         'probit_regression.csv'))

with(df, plot(X, Y))
```

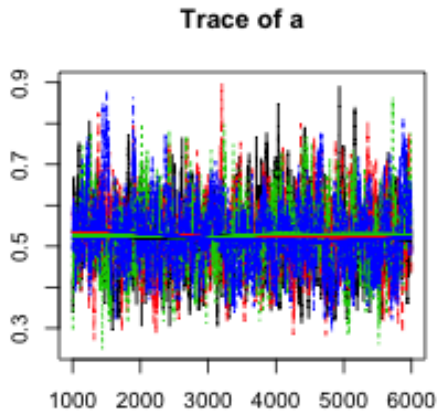
```
"X","Y"
3.1,0
3.2,0
3.3,0
3.4,0
...
7.1,0
7.2,1
7.3,1
7.4,1
```

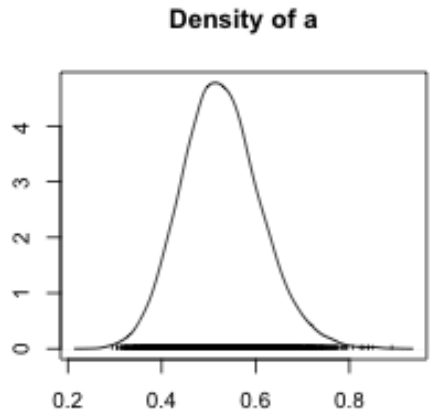

Y
X
0.0
0.2
0.4
0.6
0.8
1.0
0
2
4
6
8
10

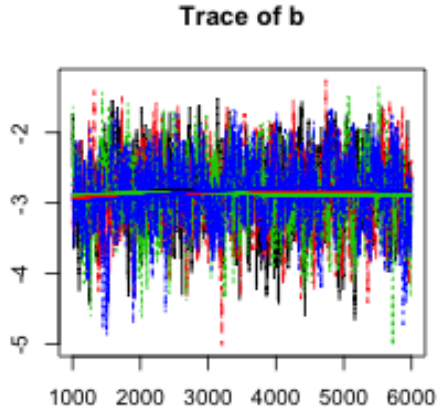
For the sample data:

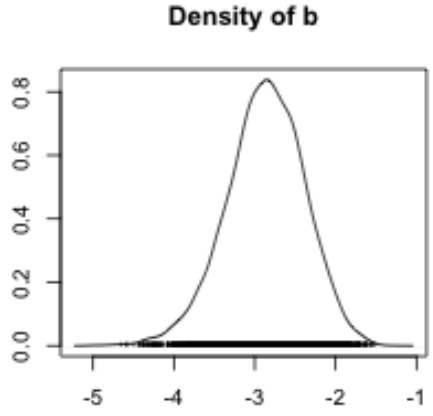
- $y \sim f(ax + b)$
- $a = 0.55$
- $b = -3$

```
jags <- jags.model(file.path('bugs',
                             'probit',
                             'probit.bugs'),
                   data = list('x' = with(df, X),
                               'y' = with(df, Y),
                               'N' = nrow(df)),
                   n.chains = 4,
                   n.adapt = 1000)

mcmc.samples <- coda.samples(jags,
                             c('a', 'b'),
                             5000)

plot(mcmc.samples)

summary(mcmc.samples)
```


Trace of a
0.3
0.5
0.7
0.9
1000
2000
3000
4000
5000
6000
Iterations


Density of a
0
1
2
3
4
0.2
0.4
0.6
0.8
N = 5000 Bandwidth = 0.01212


Trace of b
-5
-4
-3
-2
1000
2000
3000
4000
5000
6000
Iterations


Density of b
0.0
0.2
0.4
0.6
0.8
-5
-4
-3
-2
-1
N = 5000 Bandwidth = 0.06943

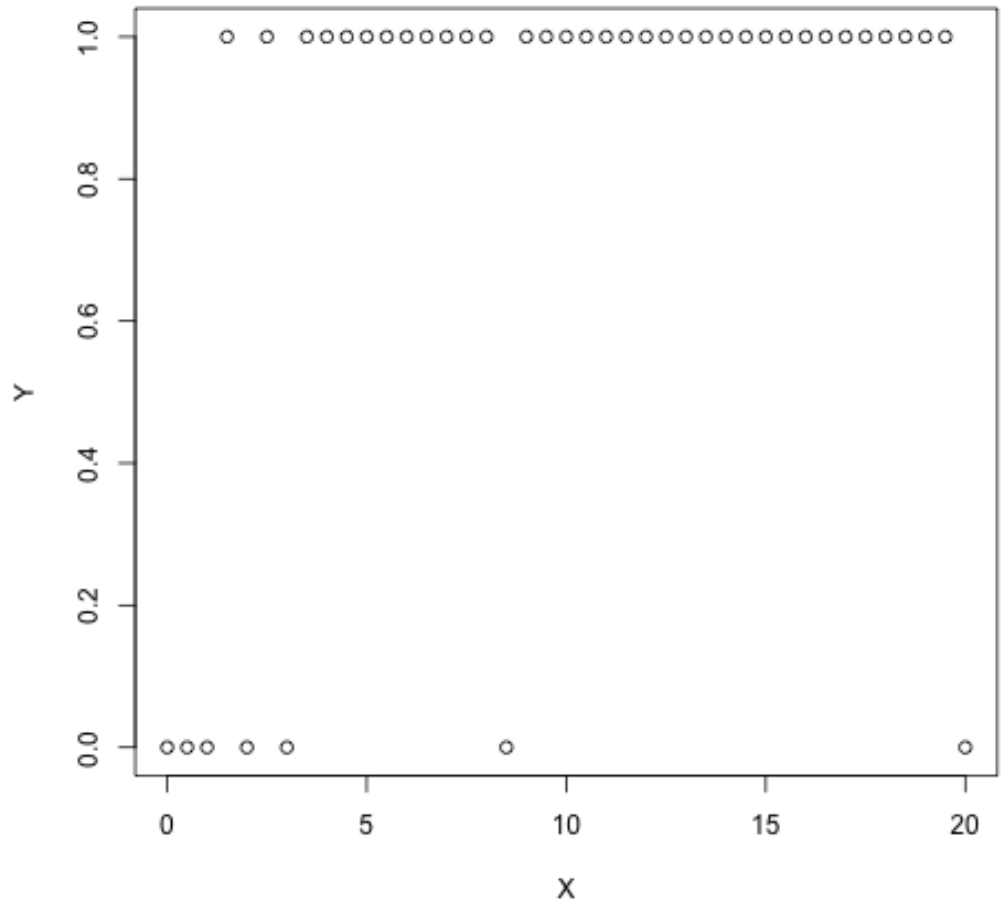
```
Iterations = 1001:6000
Thinning interval = 1
Number of chains = 4
Sample size per chain = 5000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

     Mean      SD  Naive SE Time-series SE
a  0.5267 0.08412 0.0005948       0.003186
b -2.8686 0.48380 0.0034210       0.018409

2. Quantiles for each variable:

     2.5%     25%     50%     75%  97.5%
a  0.3721  0.4688  0.5231  0.5799  0.703
b -3.8845 -3.1716 -2.8515 -2.5355 -1.972
```

- As with the OLS model, outliers can cause trouble for the logit/probit models
- Like the LAD model, the robit model attempts to be more robust to outliers

```
model
{
  for (i in 1:N)
  {
    y[i] ~ dbern(p[i])
    p[i] <- pt(z[i], 0, 1, 1)
    z[i] <- a * x[i] + b
  }

  a ~ dnorm(0, 0.0001)
  b ~ dnorm(0, 0.0001)
}
```

```
library('rjags')

df <- read.csv(file.path('data',
                         'robit',
                         'robit_regression.csv'))

with(df, plot(X, Y))
```

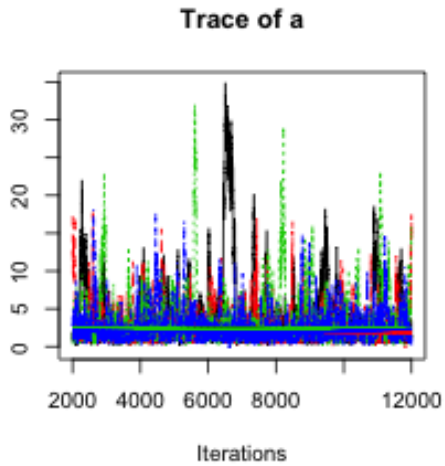
```
"X","Y"
0,0
0.5,0
1,0
1.5,1
...
18.5,1
19,1
19.5,1
20,0
```

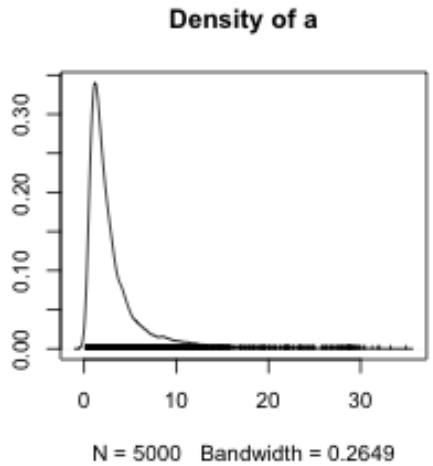

Y
X
0.0
0.2
0.4
0.6
0.8
1.0
0
5
10
15
20

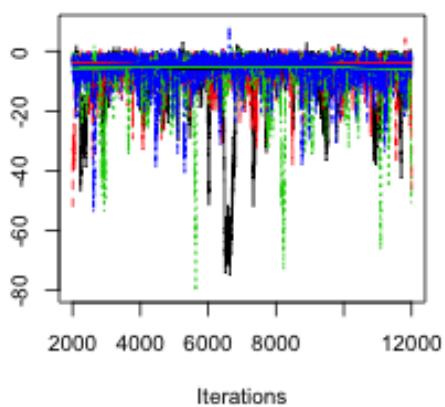
For the sample data:

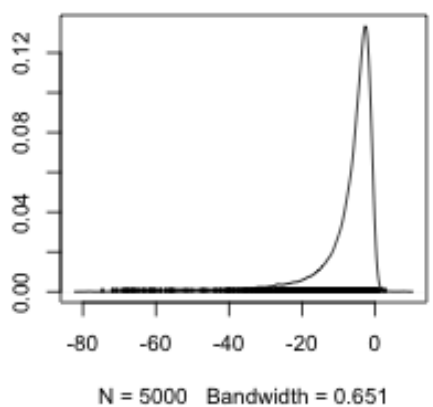
- $y \sim f(ax + b)$
- $a = 2$
- $b = -5$

```
jags <- jags.model(file.path('bugs',
                             'probit',
                             'probit.bugs'),
                   data = list('x' = with(df, X),
                               'y' = with(df, Y),
                               'N' = nrow(df)),
                   n.chains = 4,
                   n.adapt = 1000)

mcmc.samples <- coda.samples(jags,
                             c('a', 'b'),
                             5000)

plot(mcmc.samples)

summary(mcmc.samples)
```


Trace of a
0
5
10
20
30
2000
4000
6000
8000
12000
Iterations


Density of a
0.00
0.10
0.20
0.30
0
10
20
30
N = 5000 Bandwidth = 0.2649


Trace of b
-80
-60
-40
-20
0
2000
4000
6000
8000
12000
Iterations


Density of b
0.00
0.04
0.08
0.12
-80
-60
-40
-20
0
N = 5000 Bandwidth = 0.651

- Because our posteriors are very skewed, we take medians rather than means

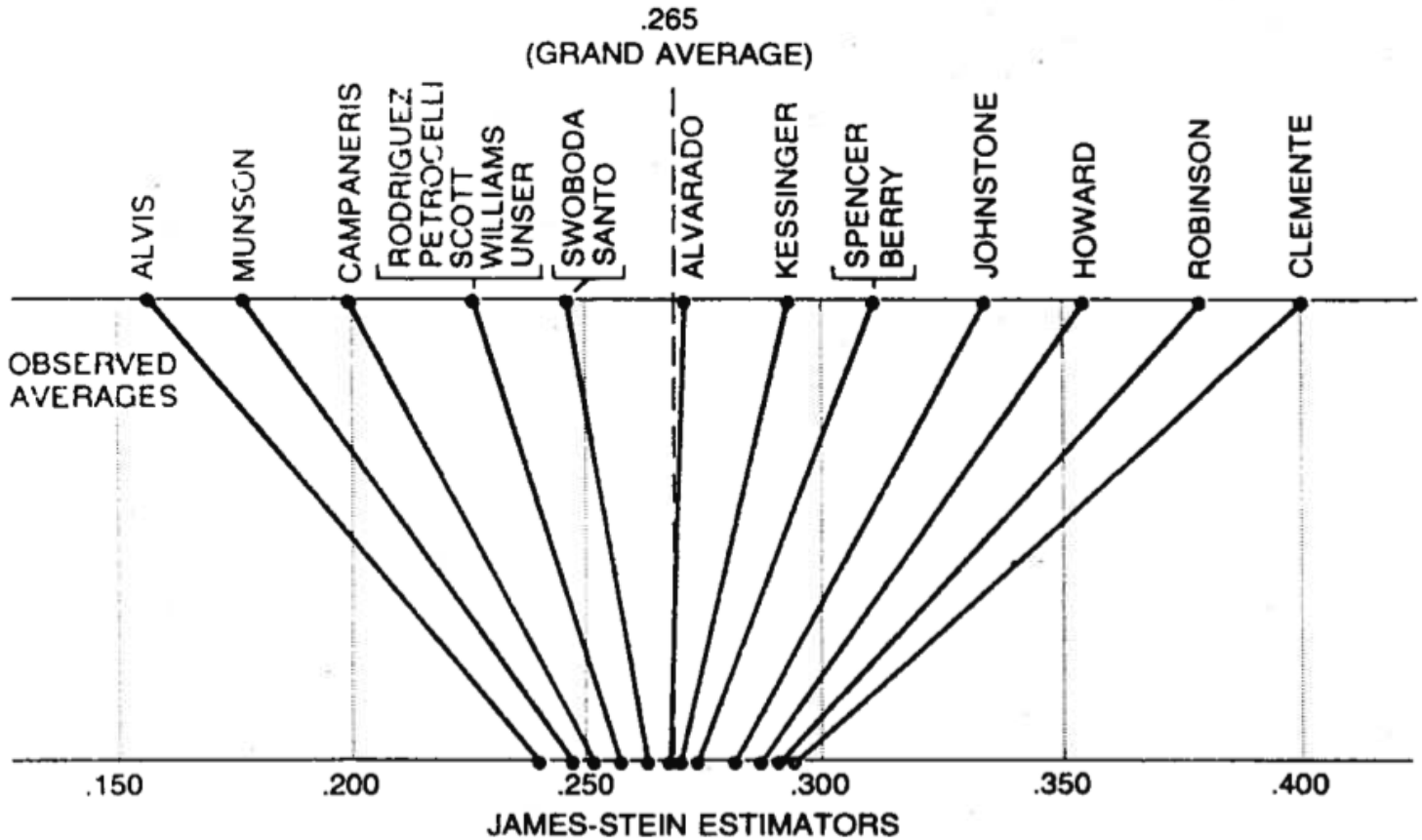
```
apply(as.matrix(mcmc.samples), 2, median)
#         a         b
# 2.031132 -4.533720
```

- So far these models aren't outperforming classical procedures
- The only virtue has been the simplicity of implementing new models in BUGS

- Bayesian methods start to shine for more complex models
  - Models with many parameters
  - Models using missing data
  - Models that require label imputation

Let's go through three such problems:

- Hierarchical OLS regression
- Hierarchical logistic regression
- The ideal points model


.265
(GRAND AVERAGE)
ALVIS
MUNSON
CAMPANERIS
RODRIGUEZ
PETROCELLI
SCOTT
WILLIAMS
UNSER
SWOBODA
SANTO
ALVARADO
KESSINGER
SPENCER
BERRY
JOHNSTONE
HOWARD
ROBINSON
CLEMENTE
OBSERVED
AVERAGES
.150
.200
.250
.300
.350
.400
JAMES-STEIN ESTIMATORS

- In a hierarchical model, we have groups of parameters
- We believe parameters within a group should be similar
- We induce this by adding a layer of adjustable priors to our model

- We start with hierarchical linear regression
- We assume that we have K groups

```
model
{
  for (i in 1:N)
  {
    y[i] ~ dnorm(mu[i], tau)
    mu[i] <- a[g[i]] * x[i] + b[g[i]]
  }

  for (j in 1:K)
  {
    a[j] ~ dnorm(mu.a, tau.a)
    b[j] ~ dnorm(mu.b, tau.b)
  }
```

```
  mu.a ~ dnorm(0, 0.0001)
  mu.b ~ dnorm(0, 0.0001)

  tau <- pow(sigma, -2)
  sigma ~ dunif(0, 1000)

  tau.a <- pow(sigma.a, -2)
  tau.b <- pow(sigma.b, -2)
  sigma.a ~ dunif(0, 1000)
  sigma.b ~ dunif(0, 1000)
}
```

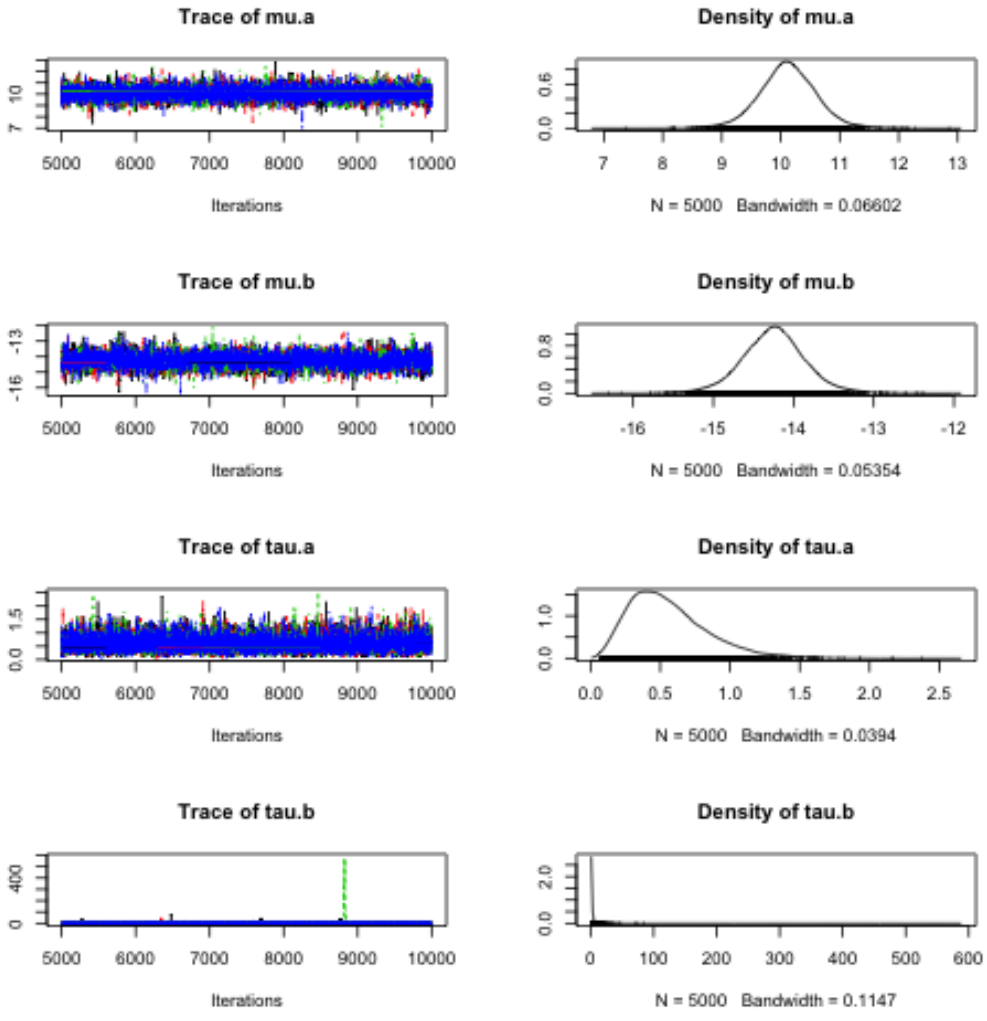
```
library('rjags')

df <- read.csv(file.path('data',
                         'hierarchical',
                         'hierarchical_linear.csv'))
```

```
"g","t","x","y"
1,1,2.01681931037456,8.90568024969301
1,2,6.60797792486846,49.1123529360177
1,3,2.05974574899301,2.70506413639457
...
10,98,2.81181986443698,12.7356528582657
10,99,8.29269654583186,66.2010735394361
10,100,0.0725971511565149,-8.11623818910855
```

For the sample data:

- $y \sim a_{g(i)}x + b_{g(i)}$
- $\mu_a = 10$
- $\mu_b = -15$

```
jags <- jags.model(file.path('bugs',
                             'hierarchical',
                             'hierarchical_linear.bugs'),
                   data = list('x' = with(df, X),
                               'y' = with(df, Y),
                               'N' = nrow(df)),
                   n.chains = 4,
                   n.adapt = 1000)

mcmc.samples <- coda.samples(jags,
                             c('mu.a',
                               'mu.b',
                               'tau.a',
                               'tau.b'),
                             5000)

plot(mcmc.samples)

summary(mcmc.samples)
```


Trace of mu.a
Density of mu.a
Iterations
N = 5000 Bandwidth = 0.06602
Trace of mu.b
Density of mu.b
Iterations
N = 5000 Bandwidth = 0.05354
Trace of tau.a
Density of tau.a
Iterations
N = 5000 Bandwidth = 0.0394
Trace of tau.b
Density of tau.b
Iterations
N = 5000 Bandwidth = 0.1147

```
Iterations = 5001:10000
Thinning interval = 1
Number of chains = 4
Sample size per chain = 5000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

          Mean      SD Naive SE Time-series SE
mu.a   10.1173  0.4890 0.003458      0.003566
mu.b  -14.2479  0.3997 0.002826      0.005236
tau.a   0.5579  0.2833 0.002004      0.002953
tau.b   1.8164 10.0432 0.071016      0.350492
```

- Let's also implement a hierarchical logit model

```
model
{
  for (i in 1:N)
  {
    y[i] ~ dbern(p[i])
    logit(p[i]) <- a[g[i]] * x[i] + b[g[i]]
  }

  for (j in 1:K)
  {
    a[j] ~ dnorm(mu.a, tau.a)
    b[j] ~ dnorm(mu.b, tau.b)
  }
```

```
  mu.a ~ dnorm(0, 0.0001)
  mu.b ~ dnorm(0, 0.0001)

  tau.a <- pow(sigma.a, -2)
  tau.b <- pow(sigma.b, -2)
  sigma.a ~ dunif(0, 1000)
  sigma.b ~ dunif(0, 1000)
}
```

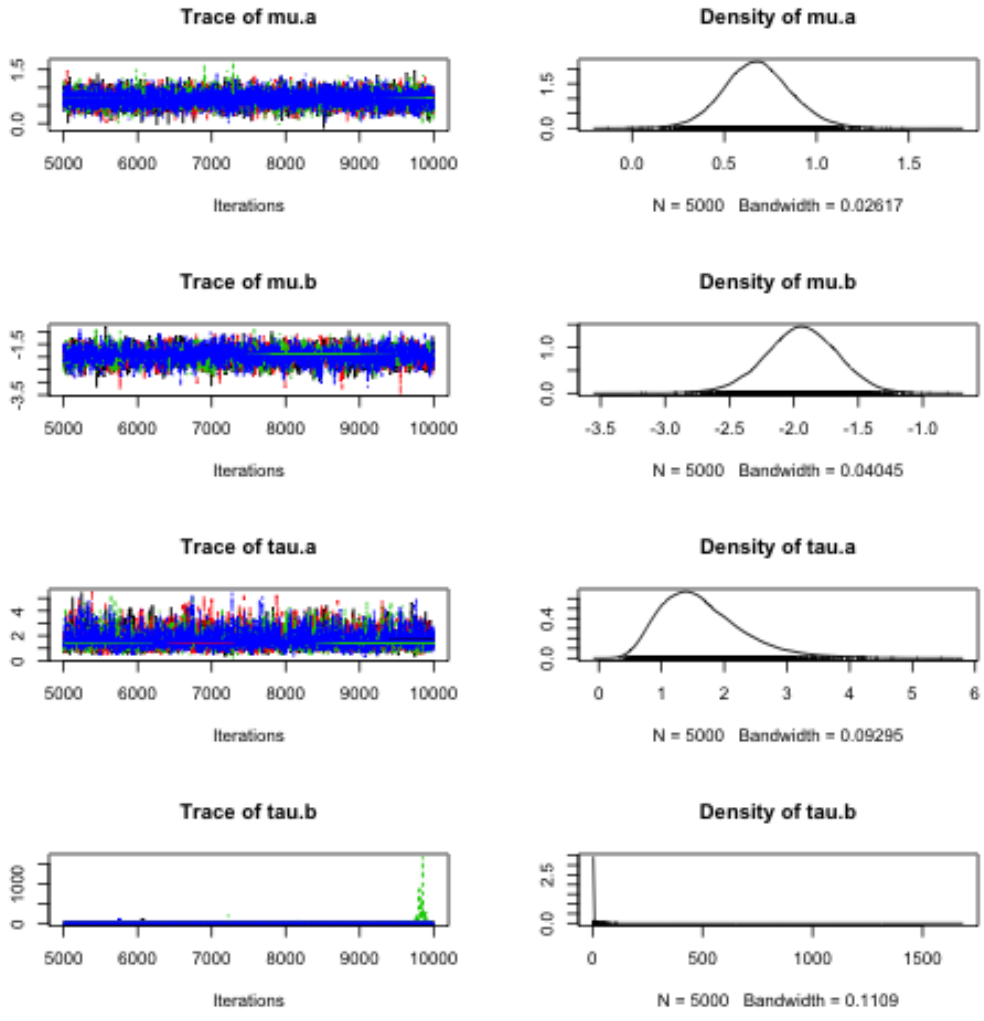
```
library('rjags')

df <- read.csv(file.path('data',
                         'hierarchical',
                         'hierarchical_logit.csv'))
```

```
"g","t","x","y"
1,1,2.01681931037456,1
1,2,9.44675268605351,0
1,3,6.2911404389888,0
...
25,48,6.72132012201473,0
25,49,3.42435503611341,0
25,50,7.37378113903105,0
```

For the sample data:

- $y \sim f(a_{g(i)}x + b_{g(i)})$
- $\mu_a = 0.5$
- $\mu_b = -2$

```
jags <- jags.model(file.path('bugs',
                             'hierarchical',
                             'hierarchical_logit.bugs'),
                   data = list('x' = with(df, x),
                               'y' = with(df, y),
                               'g' = with(df, g),
                               'N' = nrow(df),
                               'K' = with(df, max(g))),
                   n.chains = 4,
                   n.adapt = 5000)

mcmc.samples <- coda.samples(jags,
                             c('mu.a',
                             'mu.b',
                             'tau.a',
                             'tau.b'),
                             5000)

plot(mcmc.samples)
```


Trace of mu.a
Iterations
Density of mu.a
N = 5000 Bandwidth = 0.02617
Trace of mu.b
Iterations
Density of mu.b
N = 5000 Bandwidth = 0.04045
Trace of tau.a
Iterations
Density of tau.a
N = 5000 Bandwidth = 0.09295
Trace of tau.b
Iterations
Density of tau.b
N = 5000 Bandwidth = 0.1109

```
Iterations = 5001:10000
Thinning interval = 1
Number of chains = 4
Sample size per chain = 5000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

          Mean      SD Naive SE Time-series SE
mu.a    0.6795  0.1854 0.001311       0.002471
mu.b   -1.9432  0.2827 0.001999       0.006487
tau.a   1.6534  0.6791 0.004802       0.013086
tau.b   3.8376 31.0577 0.219611       1.581173
```

- Both of these hierarchical models are very powerful in practice
- Try them out on your data and see if they make better predictions on held out data

- As one of two closing models, let's implement the ideal points model
- This model is quite complex to implement without Bayesian methods
- It also produces beautiful results

```
Senator,Bill,Vote
BYRD (D WV),2,0
ENZI (R WY),2,1
```

```
model
{
  for (i in 1:M)
  {
    for (j in 1:N)
    {
      votes[i, j] ~ dbern(p[i, j])
      logit(p[i, j]) <- g[j] * (a[i] - b[j])
    }
  }
```

```
for (i in 1:M)
{
  a[i] ~ dnorm(0, tau.a)
}

tau.a <- pow(sigma.a, -2)
sigma.a ~ dunif(0, 100)
```

```
  for (j in 1:N)
  {
    b[j] ~ dnorm(mu.b, tau.b)
    g[j] ~ dnorm(0, tau.g)
   }

  mu.b ~ dnorm(0, .0001)

  tau.b <- pow(sigma.b, -2)
  sigma.b ~ dunif(0, 100)

  tau.g <- pow(sigma.g, -2)
  sigma.g ~ dunif(0, 100)
}
```

```
library('rjags')

binary.votes <- read.table(file.path('data',
                                     'ideal_points',
                                     'ideal_points.txt'))
binary.votes <- as.matrix(binary.votes)
```

```
a <- rep(NA, nrow(binary.votes))
a[which(row.names(binary.votes) == "COBURN (R OK)")] <- 2

jags <- jags.model(file.path('bugs',
                             'ideal_points',
                             'ideal_points.bugs'),
                   data = list('votes' = binary.votes,
                               'M' = nrow(binary.votes),
                               'N' = ncol(binary.votes),
                               'a' = a),
                   n.chains = 4,
                   n.adapt = 500)
```

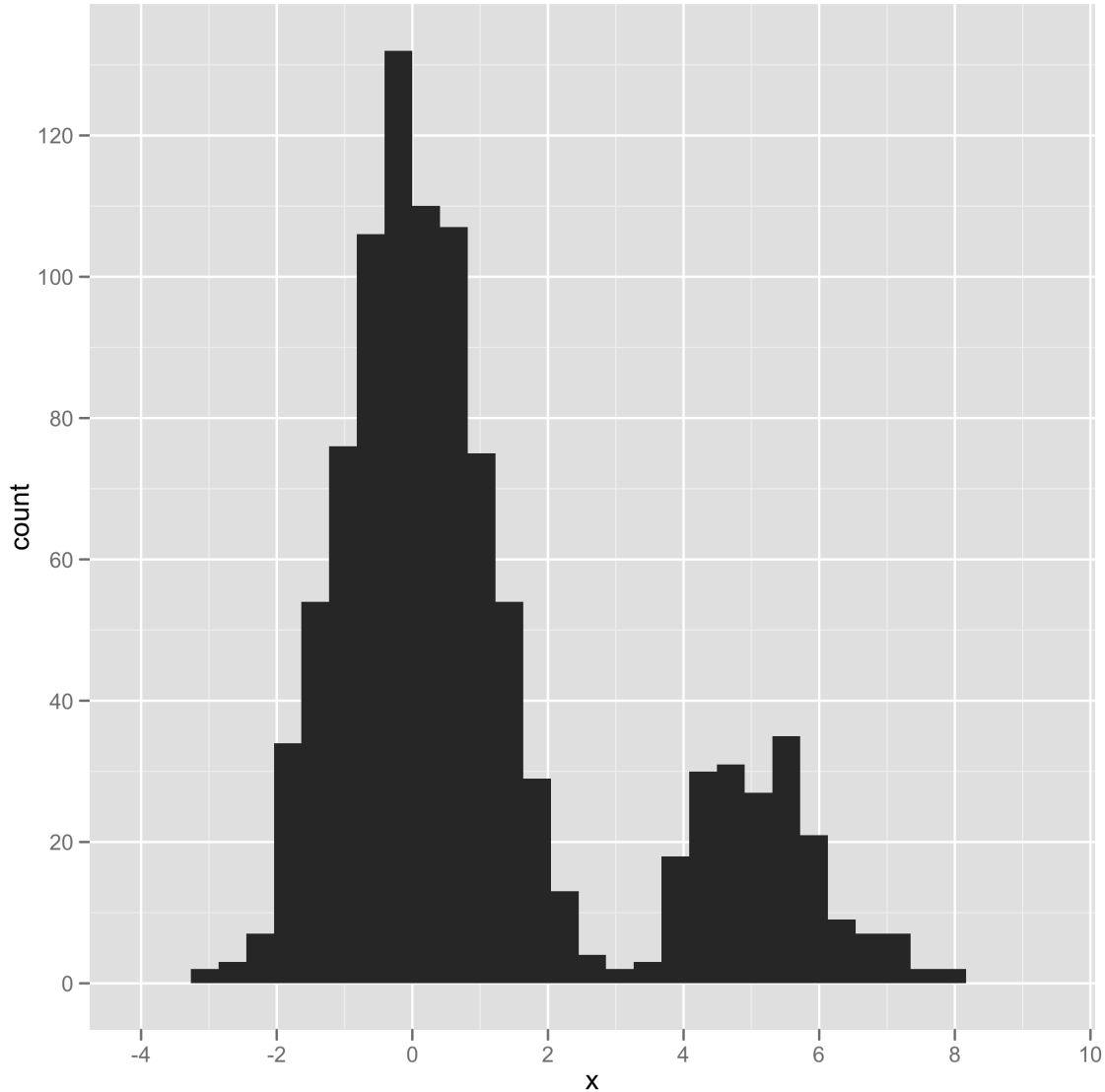
```
j.samples <- jags.samples(jags,
                          c('a', 'b', 'g'),
                          250)

estimated.a <- apply(j.samples$a, 1, mean)

df <- data.frame(Senator = row.names(binary.votes),
                 IdealPoint = estimated.a)
head(df)
tail(df)
```

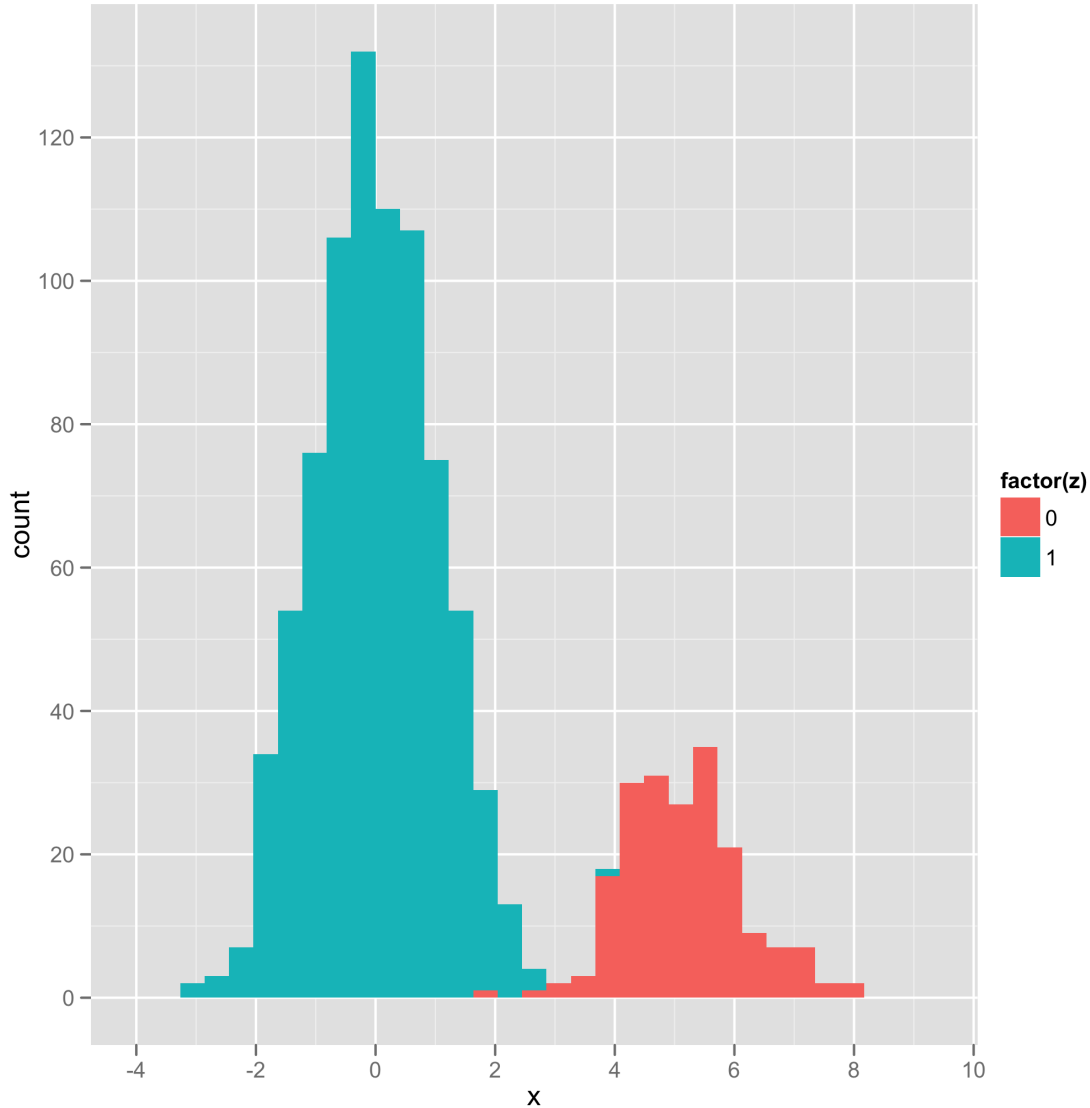
```
           Senator IdealPoint
1     BUSH (R USA)   1.321483
2  SESSIONS (R AL)   2.042710
3    SHELBY (R AL)   1.346424
4 MURKOWSKI (R AK)   1.000675
5   STEVENS (R AK)   1.069571
6       KYL (R AZ)   1.757788
               Senator IdealPoint
97         BYRD (D WV) -0.7941595
98  ROCKEFELLER (D WV) -1.1672899
99     FEINGOLD (D WI) -1.5509000
100        KOHL (D WI) -1.0407957
101        ENZI (R WY)  1.8374551
102      THOMAS (R WY)  1.8247487
```

- As a last model, we'll implement a mixture of two Gaussians

```
model
{
  for (i in 1:N)
  {
    z[i] ~ dbern(p)
    mu[i] <- z[i] * mu1 + (1 - z[i]) * mu2
    x[i] ~ dnorm(mu[i], tau)
  }

  p ~ dbeta(1, 1)

  mu1 ~ dnorm(0, 0.0001)
  mu2 ~ dnorm(1, 0.0001)

  tau <- pow(sigma, -2)
  sigma ~ dunif(0, 100)
}
```

```
library('rjags')

df <- read.csv(file.path('data',
                         'mixture_models',
                         'two_normals.csv'))
```

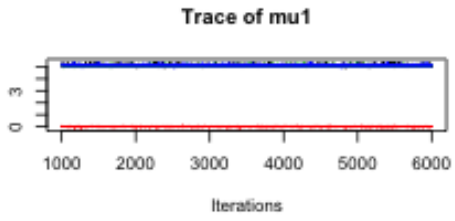

count
120
100
80
60
40
20
0
-4
-2
0
2
4
6
8
10
x

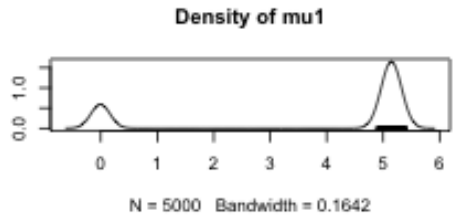

count
120
100
80
60
40
20
0
-4
-2
0
2
4
6
8
10
x
factor(z)
0
1

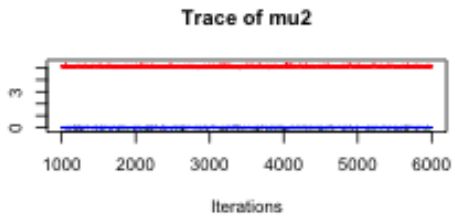
For the sample data:

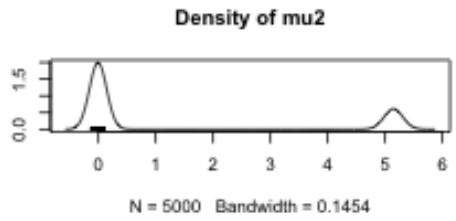
- $p = 0.8$
- $\mu_1 = 0$
- $\mu_2 = 5$
- $\sigma = 1$

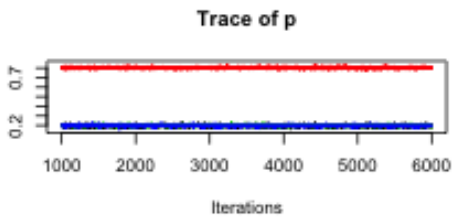
```
jags <- jags.model(file.path('bugs',
                             'mixture_models',
                             'two_normals.bugs'),
                   data = list('x' = with(df, x),
                               'N' = nrow(df)),
                   n.chains = 4,
                   n.adapt = 1000)

mcmc.samples <- coda.samples(jags,
                             c('p', 'mu1', 'mu2', 'sigma'),
                             5000)

plot(mcmc.samples)

summary(mcmc.samples)
```

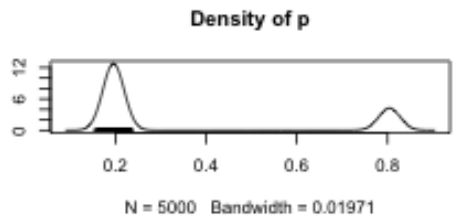

Trace of mu1
0
3
1000
2000
3000
4000
5000
6000
Iterations

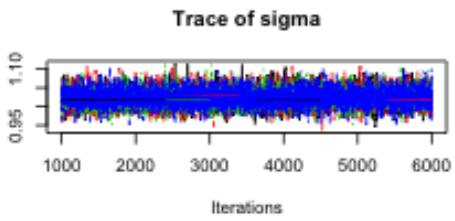

Density of mu1
0.0
1.0
0
1
2
3
4
5
6
N = 5000 Bandwidth = 0.1642

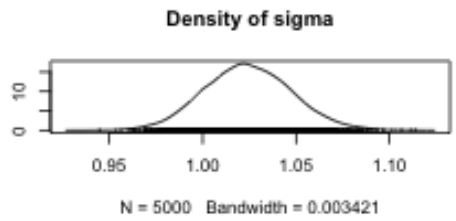

Trace of mu2
0
3
1000
2000
3000
4000
5000
6000
Iterations


Density of mu2
0.0
1.5
0
1
2
3
4
5
6
N = 5000 Bandwidth = 0.1454


Trace of p
0.2
0.7
1000
2000
3000
4000
5000
6000
Iterations


Density of p
0
6
12
0.2
0.4
0.6
0.8
N = 5000 Bandwidth = 0.01971


Trace of sigma
0.95
1.10
1000
2000
3000
4000
5000
6000
Iterations


Density of sigma
0
10
0.95
1.00
1.05
1.10
N = 5000 Bandwidth = 0.003421

```
Iterations = 1001:6000
Thinning interval = 1
Number of chains = 4
Sample size per chain = 5000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

        Mean      SD  Naive SE Time-series SE
mu1    3.858 2.23225 0.0157844      5.426e-04
mu2    1.281 2.23140 0.0157784      3.988e-04
p      0.348 0.26360 0.0018640      8.817e-05
sigma  1.024 0.02339 0.0001654      2.155e-04
```

- We'll stop there, but BUGS can easily be used for other models:
  - LDA with a fixed number of topics
  - Social Network Analysis via the stochastic blockmodel
  - ...