Brigham Young University

Applied Bayesian Statistics

STAT 451

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Semester | *Teacher*
Winter 2013 | Dr. Gil Fellingham

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Contents

1 **Class Introduction** 1

2 **Bayesian Methodology** 2
- 2.1 Metropolis Sampler 2
  - 2.1.1 Metropolis Sampler Steps 2
  - 2.1.2 Metropolis Code 2

3 **Two Sample t test** 4

4 **Diagnostics** 6

5 **Posterior Predictives** 11

6 **Linear Regression** 13

7 **Multiple Linear Regression** 17

8 **ANOVA** 21
- 8.1 Compare Means 25
- 8.2 ANOVA Marginal Means 26
- 8.3 ANOVA Interactions 27
- 8.4 Linear Algebra Solution 27

9 **Analysis of Covariance ANCOVA** 28

10 **Multiple Sources of Variation** 33

11 **Random Coefficients Model** 36

12 **Hierarchical Models** 40

13 **Exam Debriefing** 43

14 **Logistic Regression** 44

* * January 8, 2013 * *

1 Class Introduction

Office Hours Monday

Keep a copy of the code

Preliminary assignment email now.

2 Bayesian Methodology

Parameterize state of knowledge

Estimate parameters

$$f(\underline{\theta}|\underline{x}) = \frac{L(\underline{x}|\underline{\theta})\prod(\underline{\theta})}{\int\int_{\underline{\theta}} L(\underline{x}|\underline{\theta})\prod(\underline{\theta})\mathrm{d}\underline{\theta}} \propto L(\underline{x}|\underline{\theta})\prod(\underline{\theta})$$

2.1 Metropolis Sampler

$$\begin{aligned} \pi\left[\frac{1}{\Gamma(\alpha)\beta^\alpha}x^{\alpha-1}\exp\left(-\frac{x}{\beta}\right)\right] + (\pi-1)\left[\frac{1}{\Gamma(\alpha)\beta^\alpha}x^{\alpha-1}\exp\left(-\frac{x}{\beta}\right)\right] \\ \frac{1}{4}\left[\frac{1}{\Gamma(2)3^2}x^{2-1}\exp\left(-\frac{x}{3}\right)\right] + \frac{3}{4}\left[\frac{1}{\Gamma(4)3^4}x^{4-1}\exp\left(-\frac{x}{3}\right)\right] \\ k = 4\Gamma(4)3^3 \end{aligned}$$

$$g(x) = k \cdot f(x) = 18x\exp\left(-\frac{x}{3}\right) + x^3\exp\left(-\frac{x}{3}\right)$$

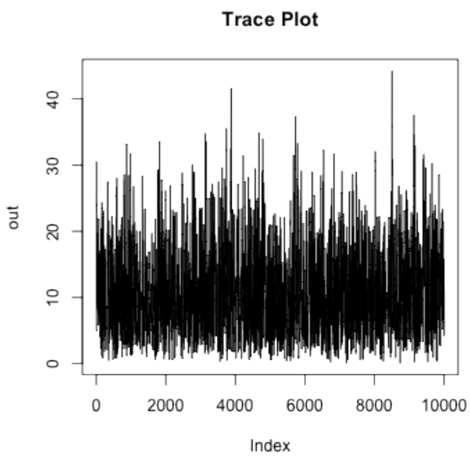
2.1.1 Metropolis Sampler Steps

- Initial $x = x_0$
- for $i = 1$ to n
  - generate candidate c
  - $\frac{g(c)}{g(x_{i-1}} = r$
  - let $x_i = c$ with $\mathrm{P} = \min(1, r)$

2.1.2 Metropolis Code

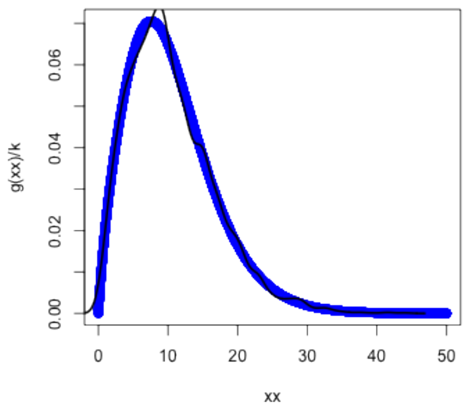
```
# Define g function
g <- function(x) {
    18 * x * exp(-x/3) + x^3 * exp(-x/3)
}

# Write Sampler
out <- NULL
out[1] <- 5
candidate.sigma <- 20
counter <- 0
samples <- 10^4
for (i in 2:samples) {
```

```r
    out[i] <- out[i - 1]
    candidate <- rnorm(1, out[i - 1], candidate.sigma)
    if (candidate > 0) {
        r <- g(candidate)/g(out[i - 1])
        if (r > runif(1, 0, 1)) {
            out[i] <- candidate
            counter <- counter + 1
        }
    }
}
message(counter/samples)  # should be about 24-40

## 0.3285

plot(out, type = "l", main = "Trace Plot")
```



Trace Plot looks good

```r
xx <- seq(0, 50, length = 1e+05)
k <- 4 * gamma(4) * 3^3
# Plot the exact distribution
plot(xx, g(xx)/k, lwd = 2, col = "blue")
# curve(.25*dgamma(x, shape=2, scale=3)+.75*dgamma(x, shape=4, scale=3),
# add=TRUE, col='blue') Both of these should produce the same line

lines(density(out), lwd = 2)

# Exact Mean
0.25 * (2 * 3) + 0.75 * (4 * 3)

## [1] 10.5


# Approximate Mean
mean(out)

## [1] 10.35
```



* * January 10, 2013 * *

Paul Sabin — Stat 451 TA
Tuesday 2:30-4:00
Friday: 9:30-11:00
Office: 233
Email:r.paul.sabin@gmail.com

```
# For Winbugs
install.packages("ARM", "R2WinBUGS")

# For jags
install.packages("R2jags")
```

3 Two Sample t test

$$y \sim \mathcal{N}(\mu, \sigma^2) \quad i = 1, 2$$
$$f(\mu_1) = \mathcal{N}(\mu = 0, \sigma^2 = 1000) f(\sigma^2) = \text{Unif}(0, 5000)$$

PROC MCMC two group t test

```
data examp2;
infile dataset;
input tmt response;
run;

/*
nmc: Number of Marcov Chains
nbi: Number Burn in

dic: information criteria
*/
proc mcmc data=examp2 outpost=post2 seed=1234 nmc=100000 nbi=5000
                        statistics(alpha=.05)=(summary interval) thin=10
```

```
                        moniter=( parms mudif varratio) propcov=quannew
                        diagnostics=(all) dic ;
array mu[2] mu1-mu2;
arra sig2[2] sig21-sig22;
prams: mu: sig2:;
prior mu: ~ normal(0, sd=10000);
prior sig21 ~ unif(9, 5000); /* gamma(shape=30, scale=50) */
prior sig22 ~ unif(9, 5000);
mudif = mu1 - mu2;
varratio = sig21/sig22;
mm = mu[tmt];
vv = sig2[tmt];
model response ~ normal(mm, var=vv);
run;

proc export data=post2 outfile='twogroups.csv' dbms=csv replace;
run;
```

HPD — Highest Posterior Density the smallest interval

Fischer variance problem — a two sample t test with unequal variances

Check the posterior autocorolations

* * January 15, 2013 * *

```
library(rjags)
library(R2jags)
```

JAGS uses precisions, not variances. Precisions are $\frac{1}{\sigma^2}$

```
library(R2jags)
mdl <- "
    model {
        for (i in 1:33) {
            y[i] ~ dnorm(mu[tmt[i]], prec[tmt[i]])
        }

        for (i in 1:2) {
            mu[i] ~ dnorm(0,0.000001)
            vr[i] ~ dunif(0,5000)
            prec[i] <- 1/vr[i]
        }
    }
"
mdl <- "
    model {
        for (i in 1:33) {
            y[i] ~ dnorm(mu[tmt[i]], prec[tmt[i]])
        }

        for (i in 1:2) {
            mu[i] ~ dnorm(100,0.01)
            vr[i] ~ dgamma(20,.05)
            prec[i] <- 1/vr[i]
```

```
        }
    }
"
mdl <- "
    model {
        for (i in 1:33) {
            y[i] ~ dnorm(mu[tmt[i]], prec[tmt[i]])
        }

        for (i in 1:2) {
            mu[i] ~ dnorm(100,0.01)
            vr[i] ~ dgamma(10,200)
            prec[i] <- 1/vr[i]
        }
    }
"
groups <- read.table("../data/01twogroups.dat", col.names=c("tmt", "y"))
writeLines(mdl, "twogroups.jags")
tmt <- groups$tmt
y <- groups$y
# Data to go into jags
data.jags <- c('tmt','y')
# what parameters to keep track of
parms <- c('mu','vr')
# Initial Values
innts <- function() {list('mu' = rnorm(2,125,5), 'vr' = runif(2,0,5000))}
twogroups.sim <- jags(data=data.jags, parameters.to.save=parms, inits=innts,
   model.file="twogroups.jags",
    n.iter=11000, n.burnin=1000, n.chains=1, n.thin=1)

twogroups.sim

sims <- as.mcmc(twogroups.sim)
plot(sims)

plot(sims[,2], type='l')
```

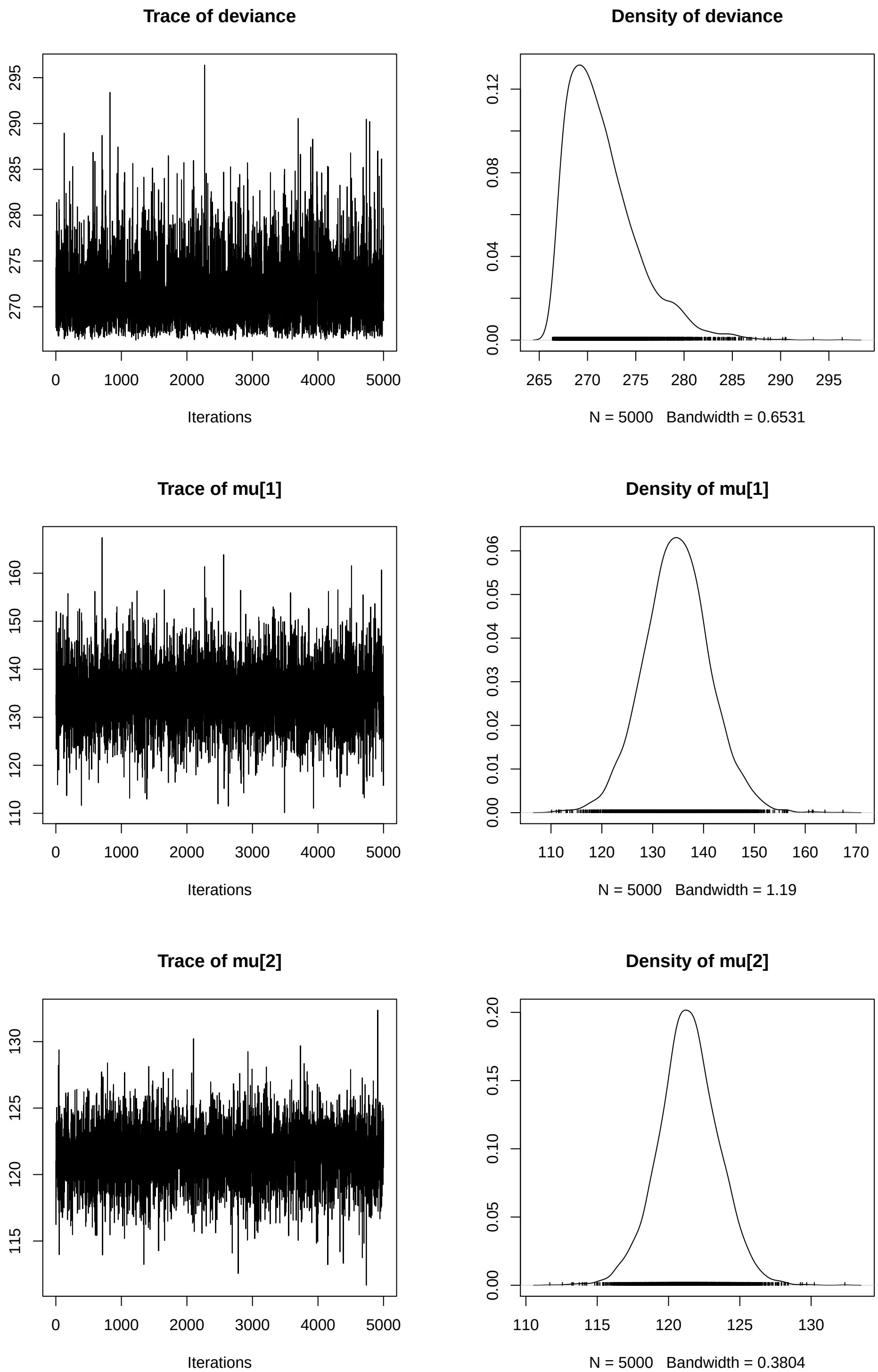
* * January 17, 2013 * *

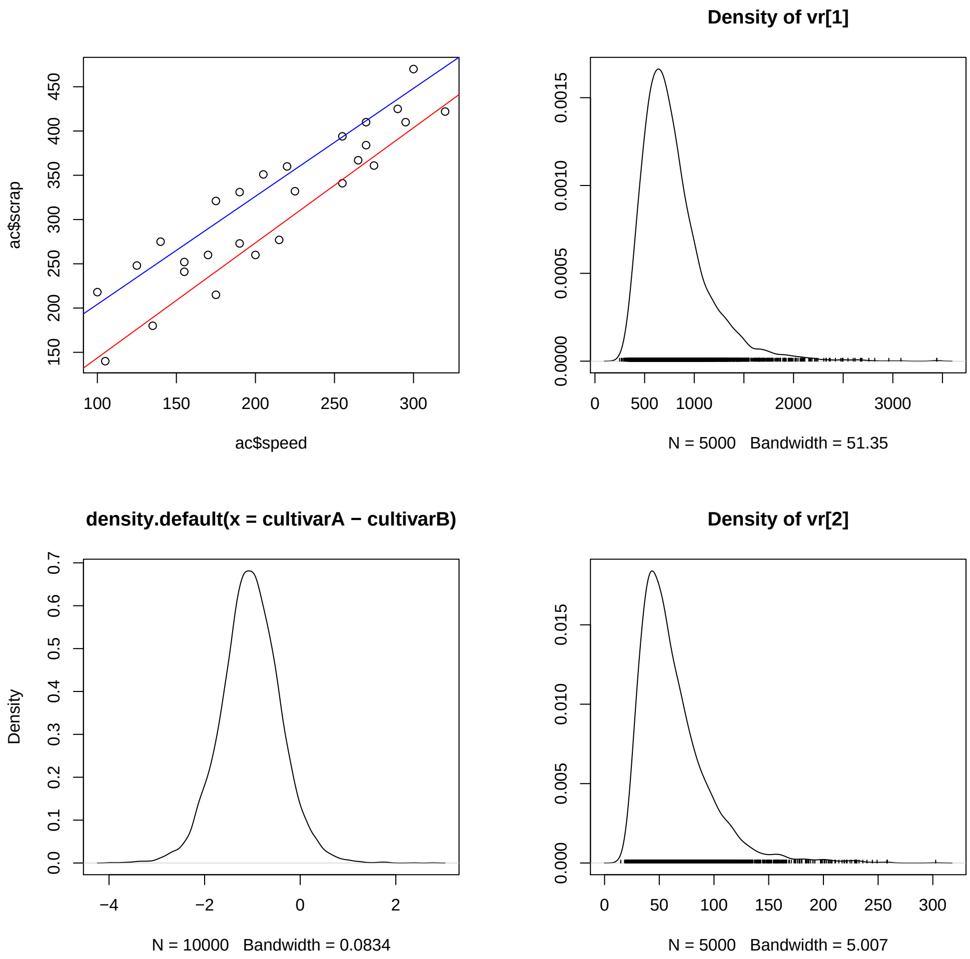
You need to think about priors

4 Diagnostics

```
library(R2jags)
mdl <- "
    model {
        for (i in 1:33) {
            y[i] ~ dnorm(mu[tmt[i]], prec[tmt[i]])
        }

        for (i in 1:2) {
            mu[i] ~ dnorm(0,0.000001)
            vr[i] ~ dunif(0,5000)
```

```
            prec[i] <- 1/vr[i]
        }
    }
"
groups <- read.table("data/01twogroups.dat", col.names=c("tmt", "y"))
writeLines(mdl, "code/twogroups.jags")
tmt <- groups$tmt
y <- groups$y
# Data to go into jags
data.jags <- c('tmt','y')
# what parameters to keep track of
parms <- c('mu','vr')
# Initial Values
innts <- function() {list('mu' = rnorm(2,125,5), 'vr' = runif(2,0,5000))}
twogroups.sim <- jags(data=data.jags, parameters.to.save=parms, inits=innts, model.file="code/twogroups.jags",
    n.iter=6000, n.burnin=1000, n.chains=1, n.thin=1)

## module glm loaded

## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 76
##
## Initializing model


twogroups.sim

## Inference for Bugs model at "code/twogroups.jags", fit using jags,
##  1 chains, each with 6000 iterations (first 1000 discarded)
##  n.sims = 5000 iterations saved
##          mu.vect sd.vect   2.5%    25%    50%    75%  97.5%
## mu[1]     134.75   6.499 122.11 130.61 134.70 138.87  147.8
## mu[2]     121.40   2.110 117.16 120.09 121.38 122.73  125.6
## vr[1]     797.45 333.228 381.36 573.92 723.20 930.48 1659.5
## vr[2]      63.12  31.741  26.22  41.34  55.22  76.11  146.2
## deviance  271.55   3.652 266.96 268.84 270.74 273.37  280.5
##
## DIC info (using the rule, pD = var(deviance)/2)
## pD = 6.7 and DIC = 278.2
## DIC is an estimate of expected predictive error (lower deviance is better).


sims <- as.mcmc(twogroups.sim)
plot(sims, auto.layout=FALSE, ask=FALSE)

# plot(sims[,2], type='l')
```


Trace of deviance
Iterations
Density of deviance
N = 5000 Bandwidth = 0.6531
Trace of mu[1]
Iterations
Density of mu[1]
N = 5000 Bandwidth = 1.19
Trace of mu[2]
Iterations
Density of mu[2]
N = 5000 Bandwidth = 0.3804

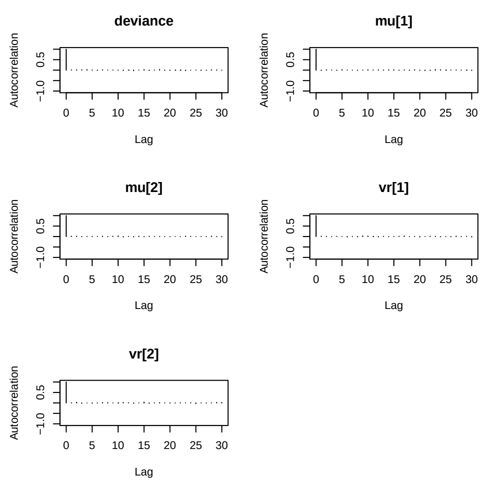


First diagnostic: Look at your trace plot

Second diagnostic: look at auto corilation

```
autocorr(sims)

## , , deviance
##
##          deviance       mu[1]     mu[2]      vr[1]      vr[2]
## Lag 0    1.000000  0.0397216 -0.025591  0.5294713  0.5567647
## Lag 1    0.009287  0.0178228 -0.001470 -0.0079258  0.0045190
## Lag 5    0.008346  0.0222125 -0.004006  0.0258781  0.0005049
## Lag 10  -0.003025  0.0082836 -0.023008  0.0244412 -0.0188622
## Lag 50  -0.004687 -0.0007478 -0.009660 -0.0006706  0.0165176
##
## , , mu[1]
##
##         deviance       mu[1]     mu[2]      vr[1]     vr[2]
## Lag 0   0.039722  1.0000000 -0.019048  0.0242092  0.013122
## Lag 1   0.010297 -0.0176032 -0.018843 -0.0115282 -0.001713
## Lag 5   0.009260  0.0203083 -0.010197  0.0290402 -0.001748
## Lag 10  0.002206  0.0183513  0.048567 -0.0005999  0.015041
## Lag 50  0.001726 -0.0001966  0.002256  0.0190355 -0.014390
##
## , , mu[2]
##
##          deviance       mu[1]     mu[2]     vr[1]     vr[2]
## Lag 0   -0.025591 -0.0190482  1.000000 -0.002025 -0.017025
```

```
## Lag 1  -0.007725 -0.0083044  0.016805 -0.021768  0.005684
## Lag 5   0.030497 -0.0280916 -0.008886  0.010412  0.008702
## Lag 10  0.015048 -0.0139730  0.026550  0.019316 -0.003001
## Lag 50  0.010831  0.0004535 -0.001931 -0.006375  0.012813
##
## , , vr[1]
##
##         deviance     mu[1]     mu[2]     vr[1]     vr[2]
## Lag 0   0.529471  0.024209 -0.002025  1.000000  0.006924
## Lag 1   0.012432  0.008644  0.003187  0.013754  0.002647
## Lag 5  -0.006325 -0.007802 -0.013119 -0.001014  0.001037
## Lag 10 -0.001276 -0.022398 -0.016429  0.018451 -0.021251
## Lag 50  0.020901 -0.010891 -0.008754  0.011124  0.031264
##
## , , vr[2]
##
##         deviance    mu[1]    mu[2]    vr[1]      vr[2]
## Lag 0   0.556765 0.013122 -0.01702 0.006924  1.0000000
## Lag 1  -0.002083 0.002571 -0.00108 0.004606  0.0085805
## Lag 5   0.007769 0.018526 -0.01204 0.033278 -0.0131159
## Lag 10  0.020122 0.035722 -0.01813 0.019459 -0.0003303
## Lag 50 -0.019064 0.023849 -0.01956 0.001463 -0.0069104

autocorr.plot(sims)
```



A good autocorrelation plot shows the first bar being tall, but the rest being relatively small.

Fourth diagnostic: Effective Sample size

```
effectiveSize(sims)

## deviance    mu[1]    mu[2]    vr[1]    vr[2]
##     5000     5000     5000     5000     4840
```

these should be relatively close to the actual sample size

fifth diagnostic: Raftery Lewis Diagnostic

```
raftery.diag(sims)

##
## Quantile (q) = 0.025
## Accuracy (r) = +/- 0.005
## Probability (s) = 0.95
##
##           Burn-in  Total Lower bound  Dependence
##           (M)      (N)   (Nmin)       factor (I)
```

```
##  deviance 2        3741  3746         0.999
##  mu[1]    2        3741  3746         0.999
##  mu[2]    2        3930  3746         1.050
##  vr[1]    2        3803  3746         1.020
##  vr[2]    2        3561  3746         0.951
```

Check if you are within .005 (in the tails) with high probability

Dependence Factor should be less than 5

These five are the most commonly used, but there are others

```
geweke.diag(sims)

##
## Fraction in 1st window = 0.1
## Fraction in 2nd window = 0.5
##
## deviance    mu[1]    mu[2]    vr[1]    vr[2]
##  -0.6146  -1.7786  -0.8627   0.7567   0.1023
```

Tests for drift in the samples. does something like a t test on the first 10% and the last 50% of the chain.

Heild

```
heidel.diag(sims)

##
##          Stationarity start     p-value
##          test         iteration
## deviance passed       1         0.822
## mu[1]    passed       1         0.140
## mu[2]    passed       1         0.398
## vr[1]    passed       1         0.684
## vr[2]    passed       1         0.636
##
##          Halfwidth Mean  Halfwidth
##          test
## deviance passed    271.5 0.1012
## mu[1]    passed    134.7 0.1802
## mu[2]    passed    121.4 0.0585
## vr[1]    passed    797.5 9.2366
## vr[2]    passed     63.1 0.8942
```

test of stationarity, or convergence

both the stationarity and half width mean test should pass.

Gelmen needs chains started at different points

* * January 22, 2013 * *

5 Posterior Predictives

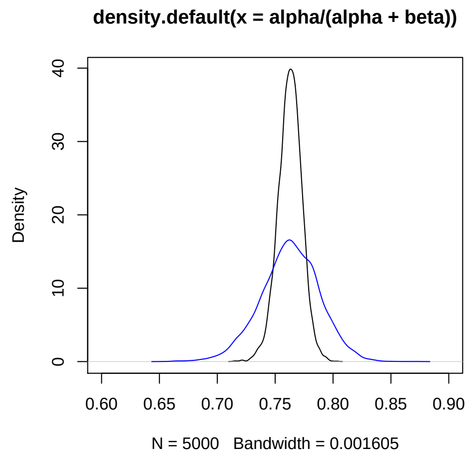
Liklihood $g_{i1} \sim \mathcal{N}(\mu_1, \sigma_1^2,\ g_{i2} \sim \mathcal{N}(\mu_2, \sigma_2^2$

Get a new y by plugging the sampled values of the parameters into a random sampler for the likelihood

```
ynew_1 <- rnorm(1,mu1[1],sigma1[1])
```

$$\begin{array}{ccccc} \mu_1 & \sigma_1^2 & \mu_2 & \sigma_2^2 & y_{\text{new1}} \\ \vdots & \vdots & \vdots & \vdots & \vdots \end{array}$$

```
ratios <- read.table("../Homework/01/monkeyratio.dat")[,1]
library(R2jags)
N <- length(ratios)

mdl <- "
    model {
        for (i in 1:N) {
            ratios[i] ~ dbeta(alpha, beta)
        }

        alpha ~ dgamma(5, .025)
        beta ~ dgamma(5, .025)
    }
"
writeLines(mdl, "code/hw1.jags")

jags.data <- c("ratios", "N")
jags.params <- c("alpha", "beta")
jags.inits <- function() {
    list('alpha' <- rgamma(5,.025), 'beta' <- rgamma(5,.025))
}
set.seed(5487)

ratios.sim <- jags(data=jags.data,
                   parameters.to.save=jags.params,
                   # inits=jags.inits,
                   model.file="code/hw1.jags",
                   n.iter=6000, n.burnin=1000, n.chains=1, n.thin=1)

## module glm loaded

## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 10
##
## Initializing model


sims <- as.mcmc(ratios.sim)

# autocorr.plot(sims)
alpha <- sims[,1]
beta <- sims[,2]
ynew <- rbeta(10000,alpha,beta)

# Plot of the density of the mean and the posterior predictive
plot(density(alpha/(alpha+beta)), xlim=c(.6,.9))
lines(density(ynew), col='blue') # Plot of the posterior predictive
```



We don't make up data we get it from "Pedagogically flexible data acquisition."—Dr Tolly.

You can use other priors, they just may not be as easy for example:

6 Linear Regression

Likelihood

$$y_i \; \mathcal{N}(\mu_i, \sigma^2)$$

The mean is different for every data point, but the variance is constant.

$$\begin{aligned} \mu_1 &\leftarrow \beta_0 + \beta_1 x \\ \beta_0 &\sim \mathcal{N}(, \tau = .001) \\ \beta_1 &\sim \mathcal{N}(\mu = 0, \tau = .001) \\ \sigma^2 &\sim \end{aligned}$$

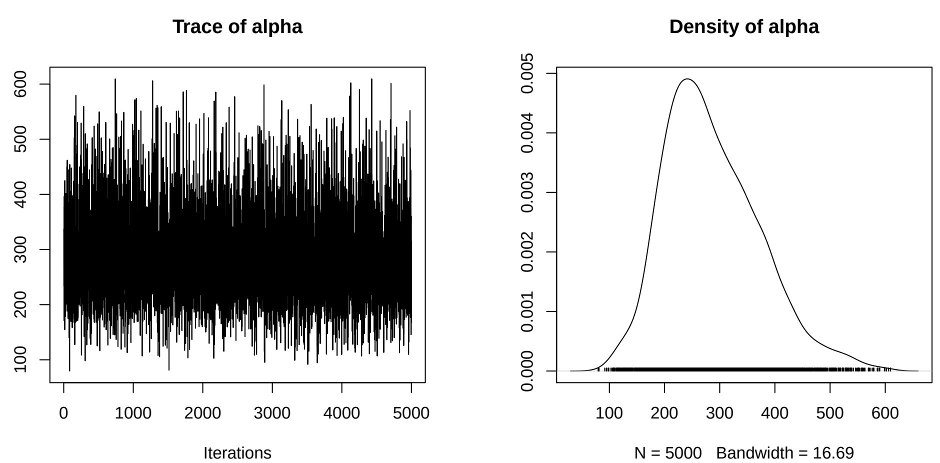
* * January 24, 2013 * *

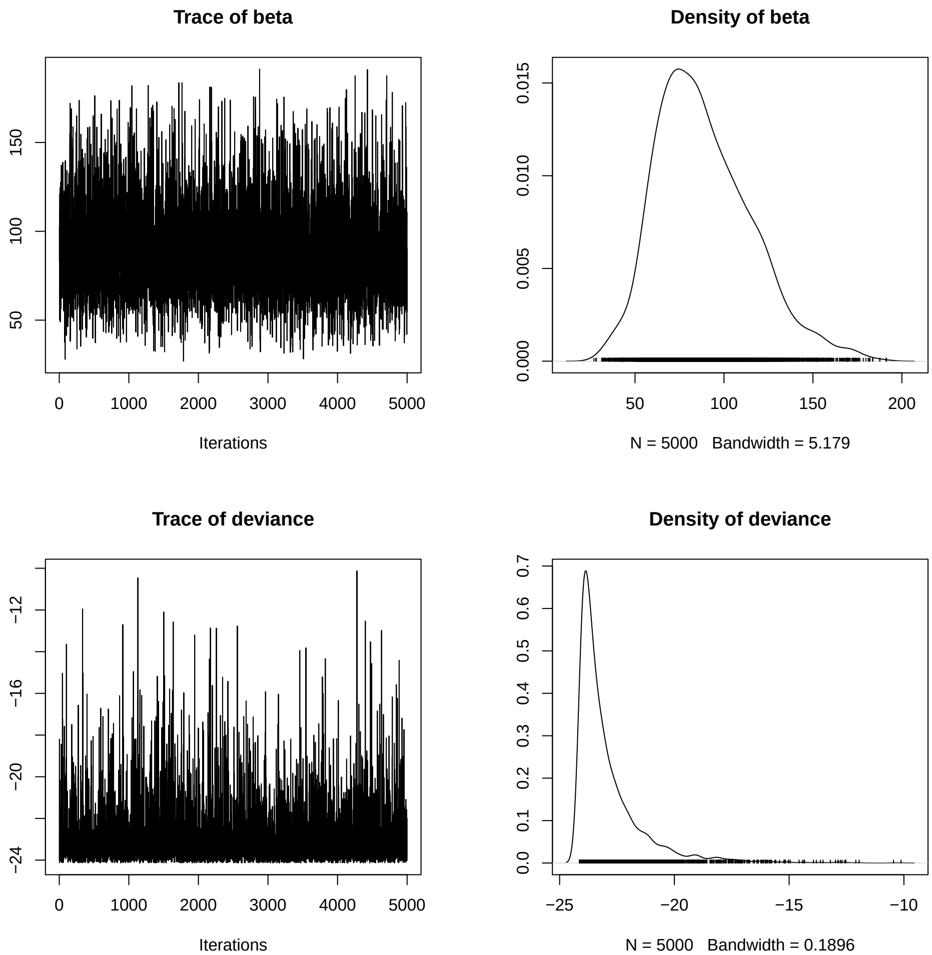
```
jags.modelfile <- "code/linreg.jags"
mdl <- "\nmodel {\nfor (i in 1:N) {\ny[i] ~ dnorm(mu[i], prec)\nmu[i] <- beta_0 + beta_1 * x[i]\n}\ninvisible(\".BeGiN_TiDy_IdEr
writeLines(mdl, "code/linreg.jags")


linregdata <- read.table("data/02linreg.dat", col.names = c("lotsize", "manhours"))
N <- nrow(linregdata)
y <- linregdata[, 2]
x <- linregdata[, 1]
jags.data <- c("y", "x", "N")
jags.params <- c("beta_0", "beta_1", "sigma2")


set.seed(5487)
linreg.sim <- jags(data = jags.data, parameters.to.save = jags.params, model.file = "code/linreg.jags",
    n.iter = 10000, n.burnin = 5000, n.chains = 1, n.thin = 1)
```

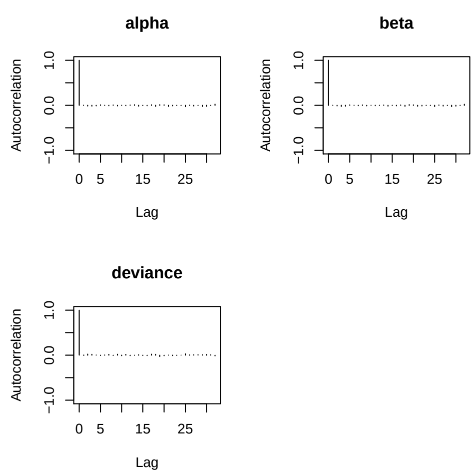
```
## module glm loaded

## Error:
## Error parsing model file:
## syntax error on line 7 near """

linreg.sim

## Error:  object 'linreg.sim' not found
```

Let's check for convergence

```
sims <- as.mcmc(linreg.sim)

## Error:  object 'linreg.sim' not found

# Trace Plots
plot(sims, auto.layout = FALSE, ask = FALSE)
# Autocorrelation plots
autocorr.plot(sims, ask = FALSE)
effectiveSize(sims)

##    alpha     beta deviance
##     5000     5000     5000

raftery.diag(sims)

##
## Quantile (q) = 0.025
## Accuracy (r) = +/- 0.005
## Probability (s) = 0.95
##
##            Burn-in  Total Lower bound  Dependence
##            (M)      (N)   (Nmin)       factor (I)
##  alpha     2        3741  3746         0.999
##  beta      2        3680  3746         0.982
##  deviance 2         3680  3746         0.982
```







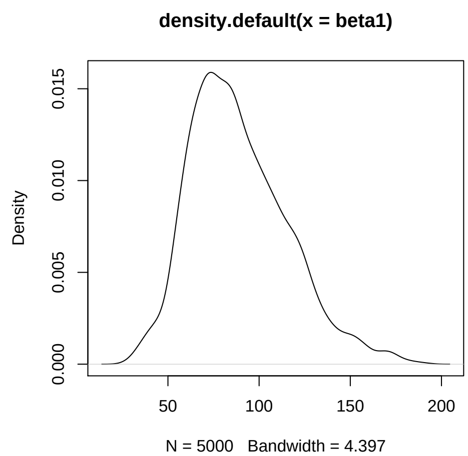
Here's the frequentest method for an ANOVA

```
fit.1 <- lm(y ~ x)
anova(fit.1)

## Analysis of Variance Table
##
## Response: y
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## x          1  13600   13600    1813  1e-10 ***
## Residuals  8     60       7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

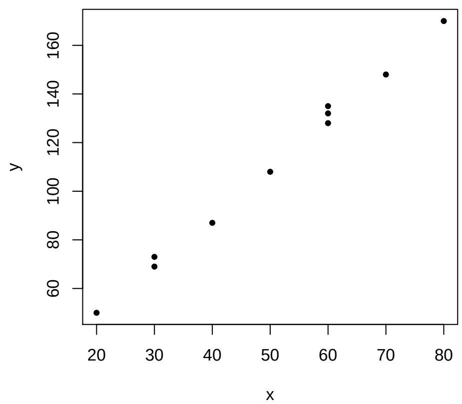
to check the value of the slope

```
beta0 <- sims[, 1]
beta1 <- sims[, 2]
sigma2 <- sims[, 4]

## Error:  subscript out of bounds


# Probability slope is greater than 0
mean(beta1 > 0)

## [1] 1


# Plot the density of the slope of the line
plot(density(beta1))
```



Plot of regression

```
plot(x, y, pch = 20)
abline(mean(beta0), mean(beta1))
xx <- seq(min(x), max(x), by = 0.01)

ans <- beta0 + outer(beta1, xx, "*")
lines(xx, apply(ans, 2, quantile, 0.025), col = "blue")
lines(xx, apply(ans, 2, quantile, 0.975), col = "blue")

# generate a new data set with the first set of
points(xx, beta0[1] + beta1[1] * xx + rnorm(length(xx), 0, sqrt(sigma2[1])), pch = 20)

## Error:  object 'sigma2' not found
```



Homework Plot the prediction interval from the problem in class

generate a normal using ans each ans and sigma

* * January 29, 2013 * *

7 Multiple Linear Regression

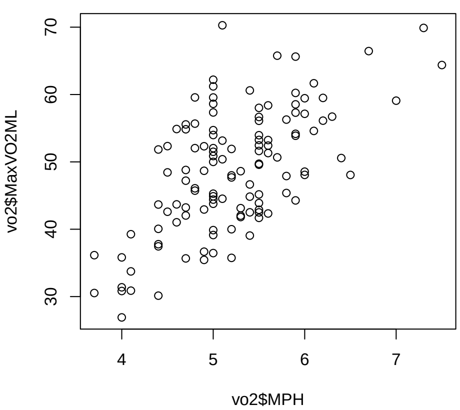
```
%let datadir = Z:\Dropbox\Active\STAT451\Notes\data;
data vo2;
    infile "&datadir.\03vo2.dat" firstobs=2;
    input id gender age bmi mph hr rpe maxvo2;
run;

ods _all_ close;
ods html;

proc mcmc data=vo2 outpost=vo2out seed=1234
          nmc=300000
          nbi=60000
          thin=30
          statistics=(summary interval)
          diagnostics=(rl ess)
          dic
          propcov=quanew
          monitor=(_parms_);

    parms b1 50 b2 10 b3 0 b4 0 b5 0 b6 0 s2f 20 s2m 30;

    prior b1 ~ normal(50, var=1000);
    prior b2 ~ normal(10, var=1000);
    prior b3 ~ normal(0, var=1000);
    prior b4 ~ normal(0, var=1000);
    prior b5 ~ normal(0, var=1000);
    prior b6 ~ normal(0, var=1000);
```

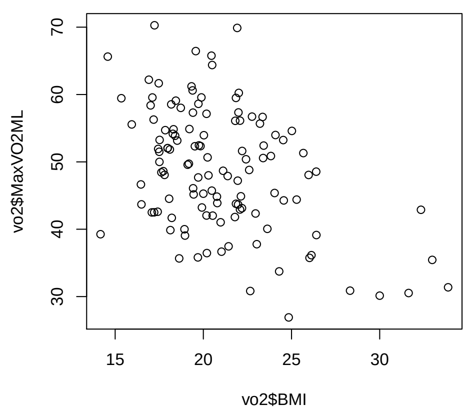
```
    prior s2f ~ gamma(2, scale=20);
    prior s2m ~ gamma(2, scale=30);

    mu= b1 + b2*gender + b3*bmi + b4*mph + b5*hr + b6*rpe;
    if gender=0 then vv=s2f;
    else vv=s2m;

    model maxvo2 ~ normal(mu, var=vv);
run;
```

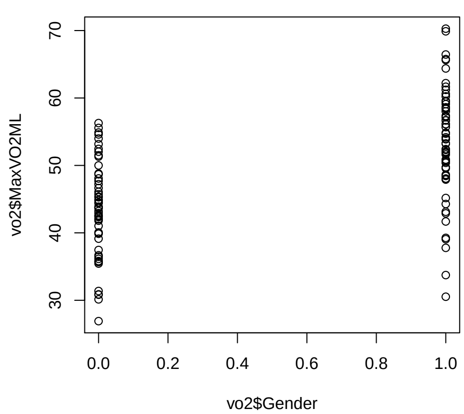
Raftery-lewis diagnostics should be less than 5.

Let the variance increase proportionaly with the xs

```r
vo2 <- read.table("data/03vo2.dat", skip = 1, col.names = c("ID", "Gender", "Age1",
    "BMI", "MPH", "HR", "RPE", "MaxVO2ML"))
plot(vo2$MPH, vo2$MaxVO2ML)
plot(vo2$BMI, vo2$MaxVO2ML)
plot(vo2$Gender, vo2$MaxVO2ML)
```







DIC Deviance information criteria (calculated in formula 1)

$$\text{deviance} = -2\log(\mathcal{L}) \tag{1}$$

* * January 31, 2013 * *

```
# Using the VO2 Data
N <- nrow(vo2)
mdl <- '
model {
    for( i in 1:N){
        y[i] ~ dnorm(mu[i], prec)
        mu[i] <- b_0 +
                 b_gen*gender[i] +
                 b_bmi*bmi[i] +
                 b_mph*mph[i] +
                 b_hr*hr[i] +
                 b_rpe*rpe[i] +
                 # b_gen_bmi*gen_bmi[i] +
                 # b_gen_mph*gen_mph[i] +
                 # b_gen_hr*gen_hr[i] +
                 # b_gen_rpe*gen_rpe[i] +
                 # b_bmi_mph*bmi_mph[i] +
                 # b_bmi_hr*bmi_hr[i] +
                 # b_bmi_rpe*bmi_rpe[i] +
                 b_mph_hr*mph_hr[i] # +
                 # b_mph_rpe*mph_rpe[i] +
                 # b_hr_rpe*hr_rpe[i]
    }

    b_0   ~ dnorm(0, .00001);
    b_gen ~ dnorm(0, .001);
    b_bmi ~ dnorm(0, .001);
    b_mph ~ dnorm(0, .001);
    b_hr  ~ dnorm(0, .001);
    b_rpe ~ dnorm(0, .001);

    # b_gen_bmi ~ dnorm(0, .001);
    # b_gen_mph ~ dnorm(0, .001);
    # b_gen_hr  ~ dnorm(0, .001);
    # b_gen_rpe ~ dnorm(0, .001);
    # b_bmi_mph ~ dnorm(0, .001);
    # b_bmi_hr  ~ dnorm(0, .001);
    # b_bmi_rpe ~ dnorm(0, .001);
    b_mph_hr  ~ dnorm(0, .001);
    # b_mph_rpe ~ dnorm(0, .001);
    # b_hr_rpe  ~ dnorm(0, .001);

    vr ~ dgamma(2, .05)
    prec <- 1/vr
}
'
writeLines(mdl, "code/multipleRegression.jags")

y <- vo2[,8]
gender <- vo2[,2]
bmi <- vo2[,4]
hr <- vo2[,6]
mph <- vo2[,5]
rpe <- vo2[,7]

# gen_bmi <- gender*bmi
# gen_hr <- gender*hr
# gen_mph <- gender*mph
# gen_rpe <- gender*rpe
# bmi_mph <- bmi*mph
# bmi_hr <- bmi*hr
# bmi_rpe <- bmi*rpe
mph_hr <- mph*hr
# mph_rpe <- mph*rpe
# hr_rpe <- hr*rpe
```

```
jags.data <- c(
"N",
"y",
"gender",
"bmi",
"hr",
"mph",
"rpe",
# "gen_bmi",
# "gen_hr",
# "gen_mph",
# "gen_rpe",
# "bmi_mph",
# "bmi_hr" #,
# "bmi_rpe",
"mph_hr" #,
# "mph_rpe",
# "hr_rpe",
)
jags.params <- c(
"b_0",
"b_gen",
"b_bmi",
"b_hr",
"b_mph",
"b_rpe",
# "b_gen_bmi",
# "b_gen_hr",
# "b_gen_mph",
# "b_gen_rpe",
# "b_bmi_mph",
# "b_bmi_hr",
# "b_bmi_rpe",
"b_mph_hr",
# "b_mph_rpe",
"vr"
)

set.seed(1234)
multr.sim <- jags(data=jags.data,
                  parameters.to.save=jags.params,
                  model.file="code/multipleRegression.jags",
                  n.iter=10000, n.burnin=5000, n.chains=1, n.thin=1)

## module glm loaded

## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 1294
##
## Initializing model
```

Full	756.4
-hr	764.4
-rpe	759.2
+ all two way interactions	766.7

$$\begin{aligned} IC &= -2\log(\mathcal{L}) + \text{penalty}(\text{parameters}) \\ \text{Deviance} &= -2\log(\mathcal{L}) \\ DIC &= -2\log(\mathcal{L}) + pD \\ pD &= \frac{\text{VAR}(\text{deviance})}{2} \end{aligned}$$

8 ANOVA

Cell means model of ANOVA

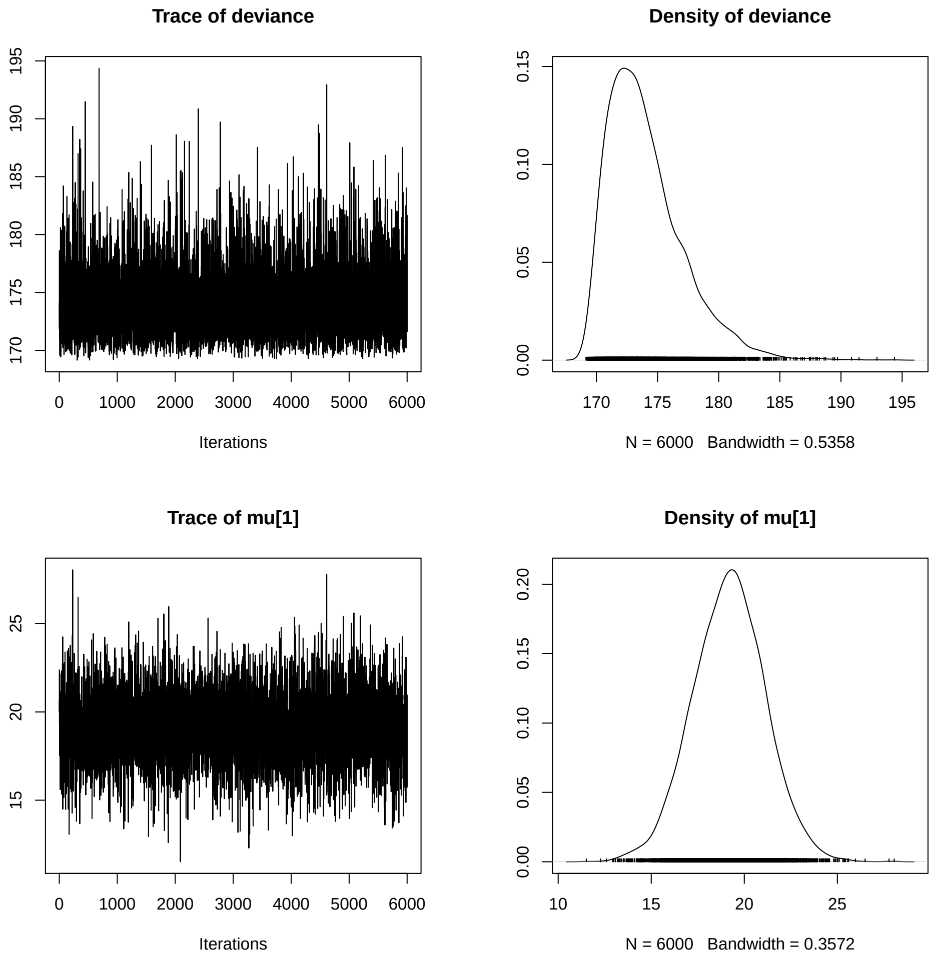
Treatement 1	Treatement 2	Treatement 3	Treatement 4
y_{11}	y_{21}	y_{31}	y_{41}
y_{12}	y_{22}	y_{32}	y_{42}
y_{13}	y_{23}	y_{33}	y_{43}
y_{14}	y_{24}	y_{34}	y_{44}

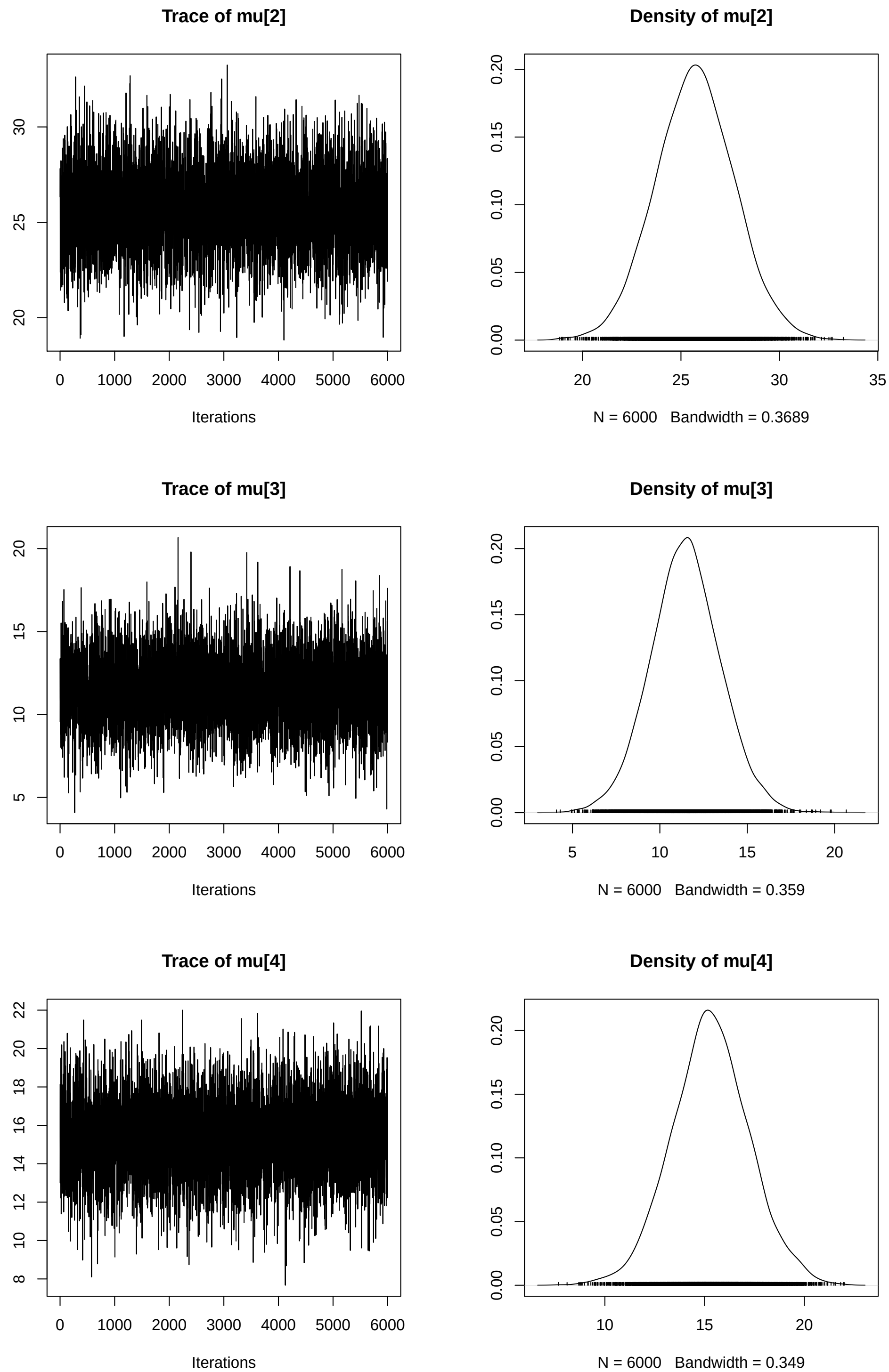
so given this data we say that $y_1 \sim \text{N}(\mu, \sigma^2)$

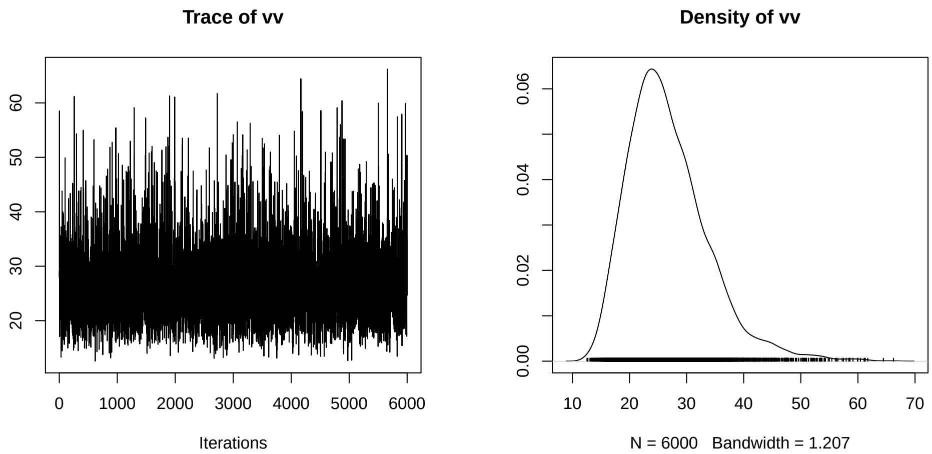
```
anova <- read.table("data/04anova.dat" ,col.names=c("tmt","response","tmt1"))
N <- nrow(anova)
mdl <- 'model {
    # Likelihood
    for (i in 1:N){
        response[i] ~ dnorm(mu[tmt[i]], prec)
    }

    # Create priors for each treatment
    for(i in 1:4){
        mu[i] ~ dnorm(15,.0001)
    }
    prec <- 1/vv
    vv ~ dgamma(1.1,.1)
}
'
writeLines(mdl, "code/ANOVAmodel.jags")
response <- anova$response
tmt <- anova$tmt
```

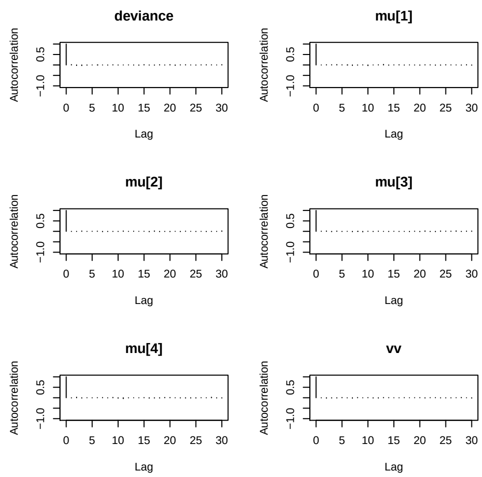
```
jags.data <- c("N", "response", "tmt")
jags.params <- c("mu", "vv")
anova.sim <- jags(data = jags.data, parameters.to.save = jags.params, model.file = "code/ANOVAmodel.jags",
    n.iter = 12000, n.chains = 1, n.thin = 1)

## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 68
##
## Initializing model

sims <- as.mcmc(anova.sim)
plot(sims, auto.layout = FALSE, ask = FALSE)
autocorr.plot(sims)
raftery.diag(sims)

##
## Quantile (q) = 0.025
```

```
## Accuracy (r) = +/- 0.005
## Probability (s) = 0.95
##
##           Burn-in  Total Lower bound  Dependence
##           (M)      (N)   (Nmin)       factor (I)
##  deviance 2        3761  3746         1.00
##  mu[1]    2        3710  3746         0.99
##  mu[2]    2        3761  3746         1.00
##  mu[3]    2        3761  3746         1.00
##  mu[4]    2        3813  3746         1.02
##  vv       3        4028  3746         1.08

effectiveSize(sims)

## deviance    mu[1]    mu[2]    mu[3]    mu[4]       vv
##     6448     6000     6000     6000     5800     6000
```




Trace of mu[2]
Iterations
Density of mu[2]
N = 6000 Bandwidth = 0.3689
Trace of mu[3]
Iterations
Density of mu[3]
N = 6000 Bandwidth = 0.359
Trace of mu[4]
Iterations
Density of mu[4]
N = 6000 Bandwidth = 0.349






```
mdl <- 'model {
    # Likelihood
    for (i in 1:N){
        response[i] ~ dnorm(mu[tmt[i]], prec[tmt[i]])
    }

    # Create priors for each treatment
    for(i in 1:4){
        mu[i] ~ dnorm(15,.0001)
        prec[i] <- 1/vv[i]
        vv[i] ~ dgamma(1.1,.1)
    }
}
'
writeLines(mdl, "code/ANOVAmodelNCvariance.jags")
```

```
si

## Error:  object 'si' not found
```

Devience is the -2*log likelihood

8.1 Compare Means

We don't care about multiple test becasue we are not under the constraint of a null hypothisis

```
diff12 <- sims[, 2] - sims[, 3]
mean(dif12 > 0)

## Error:  object 'dif12' not found

dif13 <- sims[, 2] - sims[, 4]
dif14 <- sims[, 2] - sims[, 5]
dif23 <- sims[, 3] - sims[, 4]
dif24 <- sims[, 3] - sims[, 5]
dif34 <- sims[, 4] - sims[, 5]
mean(dif13 > 0)

## [1] 0.9958

mean(dif14 > 0)

## [1] 0.9277

mean(dif23 > 0)

## [1] 1

mean(dif24 > 0)

## [1] 0.9995

mean(dif34 > 0)

## [1] 0.08267
```

Two by three factorial design.

```
twoway <- read.table("data/05twoway.dat", col.names = c("block", "seedType", "inoculate",
    "yield"))
```

Using cell means method

Table should be rotated

	a	b	
dea	μ_{11}	μ_{12}	$\mu_{1\cdot}$
con	μ_{21}	μ_{22}	$\mu_{2\cdot}$
liv	μ_{31}	μ_{22}	$\mu_{3\cdot}$
	$\mu_{\cdot 1}$	$\mu_{\cdot 2}$	

Degrees of freedom is 5, one for type, two for inoculate, and two for interaction

```
y <- as.numeric(twoway$seedType)

mdl <- '
model {
    for (i in 1:24) {
        yield[i] ~ dnorm(mu[ncult[i],ninoc[i]], 1/vv)
    }

    for (i in 1:2) {
        for (j in 1:3) {
            mu[i,j] ~ dnorm(0, .000001)
        }
    }

    vv ~ dgamma(1.5, .1)
}
'
```

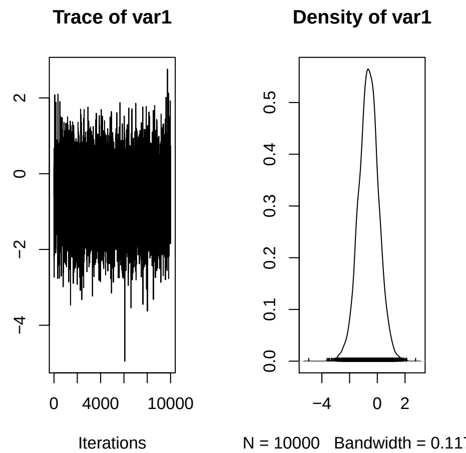
```
writeLines(mdl, 'code/CultModel.jags')

yield <- twoway$yield
ncult <- as.numeric(twoway$seedType)
ninoc <- as.numeric(twoway$inoculate)

jags.data <- c('yield', 'ncult', 'ninoc')
jags.params <- c('mu','vv')

innits <- function(){list('mu'= matrix(0,2,3), 'vv', 15)}

cult1.jags <- jags( data=jags.data,
                    # inits=innits,
                    parameters.to.save=jags.params,
                    model.file='code/CultModel.jags',
                    n.iter=12000, n.burnin=2000,
                    n.chains=1, n.thin=1)

## module glm loaded

## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 85
##
## Initializing model

cult1.sim <- as.mcmc(cult1.jags)
```

Effects model and cell means model are two different ways to do analysis of variance. BYU was a pioneer of the cell means model.

8.2 ANOVA Marginal Means

marginals are calculated as $\mu_{1\cdot} = \frac{\mu_{11}+\mu_{12}+\mu_{13}}{3}$ its just a mean of the means

```
mu1dot <- (cult1.sim[, 2] + cult1.sim[, 4] + cult1.sim[, 6])/3
mu2dot <- (cult1.sim[, 3] + cult1.sim[, 5] + cult1.sim[, 7])/3

plot(mu1dot - mu2dot)
mean(mu2dot - mu1dot > 0)

## [1] 0.8171


mudot1 <- (cult1.sim[, 2] + cult1.sim[, 3])/2
mudot2 <- (cult1.sim[, 4] + cult1.sim[, 5])/2
mudot3 <- (cult1.sim[, 6] + cult1.sim[, 7])/2

mean(mudot1 - mudot2 < 0)  # Probability mu_dot2 is bigger than mu_dot1

## [1] 0.9858

mean(mudot3 - mudot2 > 0)  # Probability mu_dot3 is bigger than mu_dot2

## [1] 0.9991
```



8.3 ANOVA Interactions

interactions are tested in four cell groups the formula is

$$\mu_{11} - \mu_{21} = \mu_{12} - \mu_{22}$$
$$\mu_{11} - \mu_{21} - \mu_{12} + \mu_{22} = 0$$

```
int1 <- cult1.sim[, 2] - cult1.sim[, 4] - cult1.sim[, 3] - cult1.sim[, 4]
int2 <- cult1.sim[, 4] - cult1.sim[, 6] - cult1.sim[, 5] + cult1.sim[, 7]
```

Finally, compare to seed types that with the best inoculate, does it make sense to pay for the better seed or does the $\mu_{11} - \mu_{21} = \mu_{12} - \mu_{22}$ come from the inoculate

```
se1 <- cult1.sim[, 6] - cult1.sim[, 7]
mean(se1 < 0)

## [1] 0.6194
```

8.4 Linear Algebra Solution

$$\underline{\hat{\mu}} = (W'W)^{-1}W'\underline{y}$$

Least Squares Solution

```
w <- rbind(diag(1, 6), diag(1, 6), diag(1, 6), diag(1, 6))
muhat <- solve(t(w) %*% w) %*% t(w) %*% twoway$yield
```

$$y = W\mu$$
$$y = WI\mu$$
$$y = \underbrace{WA^{-1}}_{X}\underbrace{A\mu}_{\beta}$$

$$\begin{bmatrix} \frac{1}{6} & \frac{1}{6} & \frac{1}{6} & \frac{1}{6} & \frac{1}{6} & \frac{1}{6} \\ \frac{1}{6} & \frac{1}{6} & \frac{1}{6} & \frac{1}{6} & \frac{1}{6} & \frac{1}{6} \\ \frac{1}{2} & -\frac{1}{2} & 0 & \frac{1}{2} & -\frac{1}{2} & 0 \\ 0 & \frac{1}{2} & -\frac{1}{2} & 0 & \frac{1}{2} & -\frac{1}{2} \\ 1 & -1 & 0 & -1 & 1 & 0 \\ 0 & 1 & -1 & 0 & -1 & 1 \end{bmatrix} \begin{bmatrix} \mu_{11} \\ \mu_{12} \\ \mu_{13} \\ \mu_{21} \\ \mu_{22} \\ \mu_{23} \end{bmatrix} = \begin{bmatrix} \mu_{\cdot\cdot} \\ \mu_{1\cdot} - \mu_{2\cdot} \\ \mu_{\cdot 1} - \mu_{\cdot 2} \\ \mu_{\cdot 2} - \mu_{\cdot 3} \\ \mu_{11} - \mu_{12} - \mu_{21} + \mu_{22} \\ \mu_{12} - \mu_{13} - \mu_{22} + \mu_{23} \end{bmatrix}$$

* * February 12, 2013 * *

```
dev <- function(x) {
    fp <- length(y) * log(2* pi)
    sp <-
}
```

* * February 14, 2013 * *

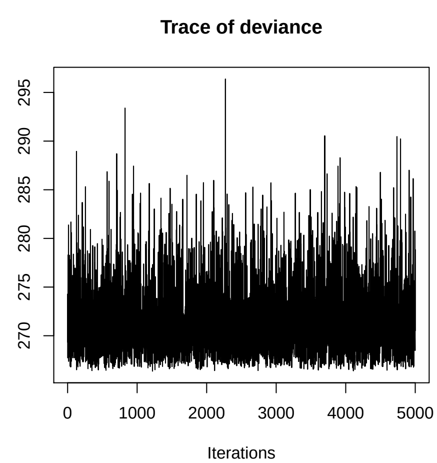
9 Analysis of Covariance ANCOVA

Join Me 777-129-200

```
ac <- read.table("data/06ancova.dat", header = TRUE)
```

First thing you do for analysis is plot the data

```
plot(ac$speed, ac$scrap, pch = ac$lines)
```



Let's try and come up with a model

$$y_{ij} = \beta_0 + \beta_1 \cdot \text{Line} + \beta_2 \cdot \text{Speed} + \beta_3 \cdot \text{Line} \cdot \text{Speed} \tag{2}$$

Or we could do this

$$y_{ij} = \beta_{0i} + \beta_{1i} \cdot \text{Speed}$$

```
mdl <- 'model {
    for(i in 1:27) {
        scrap[i] ~ dnorm(mu[i], prec);
        mu[i] <- b_0[line[i]] + b_1[line[i]]*speed[i];
    }

    for (i in 1:2) {
        b_0[i] ~ dnorm(30, .001);
        b_1[i] ~ dnorm(0, .01);
    }

    vr ~ dgamma(1.5, .0125);
    prec <- 1/vr;
}
'
writeLines(mdl, 'code/ANCOVAModel.jags')
```

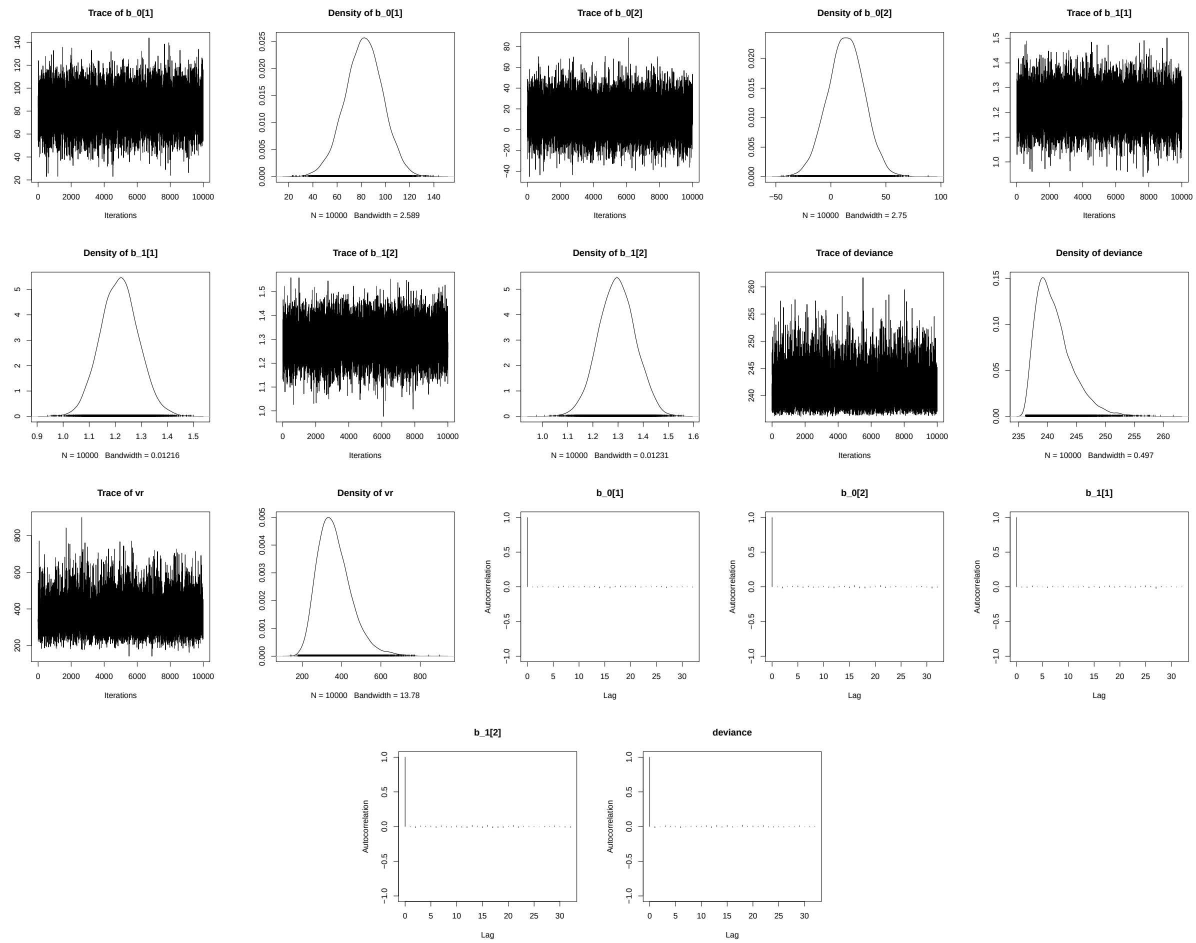
prior for beta not covers 30*100

```
speed <- ac$speed
line <- ac$line
scrap <- ac$scrap
jags.data <- c('speed', 'line', 'scrap')
jags.params <- c('b_0','b_1', 'vr')
ancova.jags <- jags( data=jags.data,
                    # inits=innits,
                    parameters.to.save=jags.params,
                    model.file='code/ANCOVAModel.jags',
                    n.iter=12000, n.burnin=2000,
                    n.chains=1, n.thin=1)

## module glm loaded

## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 148
##
## Initializing model

ancova.jags

## Inference for Bugs model at "code/ANCOVAModel.jags", fit using jags,
##  1 chains, each with 12000 iterations (first 2000 discarded)
##  n.sims = 10000 iterations saved
##          mu.vect sd.vect    2.5%     25%     50%     75%   97.5%
## b_0[1]    81.738  15.570  50.441  71.518  81.938  92.185 111.585
## b_0[2]    13.553  16.417 -18.292   2.490  13.616  24.485  45.839
## b_1[1]     1.218   0.074   1.079   1.168   1.217   1.266   1.365
## b_1[2]     1.297   0.074   1.149   1.248   1.297   1.347   1.440
## vr       363.557  85.792 229.893 302.708 351.820 411.422 569.708
## deviance 241.252   3.179 236.996 238.870 240.626 242.949 249.002
##
## DIC info (using the rule, pD = var(deviance)/2)
## pD = 5.1 and DIC = 246.3
## DIC is an estimate of expected predictive error (lower deviance is better).
```

Diagnostics

```
ancova.sim <- as.mcmc(ancova.jags)
plot(ancova.sim, auto.layout = FALSE, ask = FALSE)
autocorr.plot(ancova.sim, auto.layout = FALSE, ask = FALSE)
raftery.diag(ancova.sim)

##
## Quantile (q) = 0.025
## Accuracy (r) = +/- 0.005
## Probability (s) = 0.95
##
```

```
##           Burn-in  Total Lower bound  Dependence
##           (M)      (N)   (Nmin)       factor (I)
##  b_0[1]   2        3650  3746         0.974
##  b_0[2]   2        3680  3746         0.982
##  b_1[1]   2        3680  3746         0.982
##  b_1[2]   2        3834  3746         1.020
##  deviance 2        3680  3746         0.982
##  vr       2        3620  3746         0.966
```



Test the probability that the β_1. are different

```
b11 <- ancova.sim[, 3]
b12 <- ancova.sim[, 4]
slopdif <- b11 - b12
mean(slopdif < 0)

## [1] 0.7814

mean(slopdif > 0)

## [1] 0.2186
```

Try a new model without the different β_1 then compare the DIC

```
mdl <- 'model {
    for(i in 1:27) {
        scrap[i] ~ dnorm(mu[i], prec);
        mu[i] <- b_0[line[i]] + b_1*speed[i];
    }
```

```
    b_1 ~ dnorm(0, .01);
    for (i in 1:2) {
        b_0[i] ~ dnorm(30, .001);
    }

    vr ~ dgamma(1.5, .0125);
    prec <- 1/vr;
}
'
writeLines(mdl, 'code/ANCOVAModel_1.jags')
```

prior for beta not covers

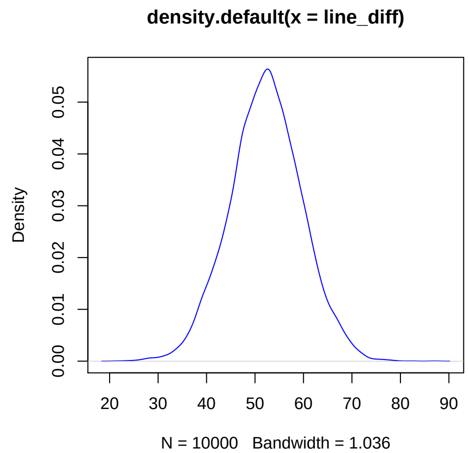
```
speed <- ac$speed
line <- ac$line
scrap <- ac$scrap
jags.data <- c('speed', 'line', 'scrap')
jags.params <- c('b_0','b_1', 'vr')
ancova1.jags <- jags( data=jags.data,
                    # inits=innits,
                    parameters.to.save=jags.params,
                    model.file='code/ANCOVAModel_1.jags',
                    n.iter=12000, n.burnin=2000,
                    n.chains=1, n.thin=1)

## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 142
##
## Initializing model

ancova1.jags

## Inference for Bugs model at "code/ANCOVAModel_1.jags", fit using jags,
##  1 chains, each with 12000 iterations (first 2000 discarded)
##  n.sims = 10000 iterations saved
##          mu.vect sd.vect    2.5%     25%     50%     75%  97.5%
## b_0[1]    74.154  11.580  50.987  66.643  74.236  81.949  96.90
## b_0[2]    21.933  12.213  -2.044  13.621  22.005  30.055  45.95
## b_1        1.257   0.052   1.156   1.222   1.256   1.291   1.36
## vr       369.910  85.910 233.121 308.243 359.554 419.347 564.88
## deviance 242.053   2.761 238.636 240.016 241.464 243.406 248.97
##
## DIC info (using the rule, pD = var(deviance)/2)
## pD = 3.8 and DIC = 245.9
## DIC is an estimate of expected predictive error (lower deviance is better).
```

Diagnostics

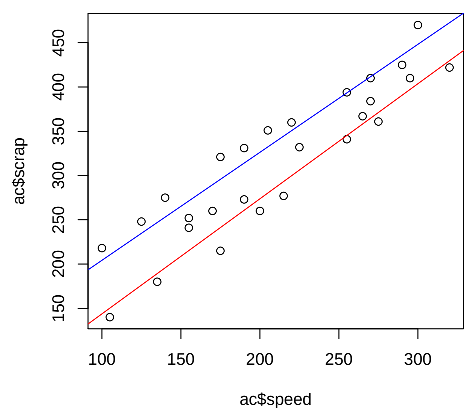
```
ancova1.sim <- as.mcmc(ancova1.jags)
# plot(ancova.sim, auto.layout=FALSE, ask=FALSE) autocorr.plot(ancova.sim,
# auto.layout=FALSE, ask=FALSE) raftery.diag(ancova.sim)
```

Lets test differences in line by testing difference in intercept

```
b_0_1 <- ancova1.sim[, 1]
b_0_2 <- ancova1.sim[, 2]
line_diff <- b_0_1 - b_0_2
mean(line_diff < 0)

## [1] 0

mean(line_diff > 0)

## [1] 1

plot(density(line_diff), col = "blue")
```




```r
plot(ac$speed, ac$scrap, pch = ac$lines)
abline(82.2, 1.22, col = "blue")
abline(13.7, 1.3, col = "red")

b_0_1 <- ancova.sim[, 1]
b_0_2 <- ancova.sim[, 2]
b_1_1 <- ancova.sim[, 3]
b_1_2 <- ancova.sim[, 4]

y1_300 <- 300 * b_1_1 + b_0_1
y2_300 <- 300 * b_1_2 + b_0_2
diff_300 <- y1_300 - y2_300
mean(diff_300 > 0)

## [1] 1
```



* * February 21, 2013 * *

$$
\begin{array}{cc|ccccc}
 & & & \text{B} & & & \\
 & & 1 & 2 & 3 & 4 & \\
 & 1 & \mu_{11} & \mu_{12} & \mu_{13} & mu_{14} & \mu_{1\bullet} \\
\text{A} & 2 & \mu_{21} & \mu_{22} & \mu_{23} & mu_{24} & \mu_{2\bullet} \\
 & 3 & \mu_{31} & \mu_{32} & \mu_{33} & mu_{34} & \mu_{3\bullet} \\
 & 4 & \mu_{41} & \mu_{42} & \mu_{43} & mu_{44} & \mu_{4\bullet}
\end{array}
$$

10 Multiple Sources of Variation

$$
\begin{aligned}
\underline{y} &= X\underline{\beta} + \underline{\varepsilon} \\
\varepsilon &\sim \mathcal{N}(\underline{0}, \sigma^{2\underline{T}}) \\
\underline{y} &= X\underline{\beta} + Z\underline{u} + e \\
e &\sim \mathcal{N}(\underline{0}, R) \\
\underline{u} &\sim \mathcal{N}(\underline{0}, G)
\end{aligned}
$$

$$
\begin{aligned}
\mathrm{E}(Y) = \mathrm{E}(X\beta + Zu + e) &= \mathrm{E}(X\beta) + \mathrm{E}(Zu) + \mathrm{E}(e) = X\beta \\
\mathrm{Var}(Y) &= \mathrm{Var}(X\beta + Zu + e) = \mathrm{Var}(Zu + e)
\end{aligned}
$$

If we assume that u and e are independent then we can move forward easily

$V(A\underline{z}) = AV(z)A'$ $AV(z)A'$ is a $p \times p$ matrix

$$
\mathrm{Var}(Zu + e) = V(Z\underline{u}) + \mathrm{Var}(\underline{e}) = Z\mathrm{Var}(\underline{u})Z' + V(\underline{e} = ZGZ' + R
$$

* * February 26, 2013 * *

	Block 1	Block 2
Treatments:	I (y_{11})	I (y_{12})
	II (y_{21})	II (y_{22})

Model in matrix form (Equation 3)

$$
\begin{bmatrix} y_{11} \\ y_{12} \\ y_{21} \\ y_{22} \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ 1 & 0 \\ 0 & 1 \\ 0 & 1 \end{bmatrix} \begin{pmatrix} \mu_1 \\ \mu_2 \end{pmatrix} + \begin{bmatrix} 1 & 0 \\ 0 & 1 \\ 1 & 0 \\ 0 & 1 \end{bmatrix} \begin{pmatrix} u_1 \\ u_2 \end{pmatrix} + \begin{bmatrix} e_{11} \\ e_{12} \\ e_{21} \\ e_{22} \end{bmatrix} \tag{3}
$$

$$
\begin{aligned}
e_{ij} &\sim^{iid} N(0, \sigma_e^2) \\
u_j &\sim^{iid} N(0, \sigma_b^2)
\end{aligned}
$$

$$
\begin{aligned}
R &= \begin{bmatrix} \sigma_e^2 & 0 & 0 & 0 \\ 0 & \sigma_e^2 & 0 & 0 \\ 0 & 0 & \sigma_e^2 & 0 \\ 0 & 0 & 0 & \sigma_e^2 \end{bmatrix} \\
G &= \begin{pmatrix} \sigma_b^2 & 0 \\ 0 & \sigma_b^2 \end{pmatrix}
\end{aligned}
$$

$$\begin{bmatrix} 1 & 0 \\ 1 & 0 \\ 0 & 1 \\ 0 & 1 \end{bmatrix} \begin{pmatrix} \sigma_b^2 & 0 \\ 0 & \sigma_b^2 \end{pmatrix} \begin{bmatrix} 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 \end{bmatrix} + \begin{bmatrix} \sigma_e^2 & 0 & 0 & 0 \\ 0 & \sigma_e^2 & 0 & 0 \\ 0 & 0 & \sigma_e^2 & 0 \\ 0 & 0 & 0 & \sigma_e^2 \end{bmatrix}$$

$$ZGZ' + R = \begin{bmatrix} \sigma_e^2 + \sigma_b^2 & 0 & \sigma_b^2 & 0 \\ 0 & \sigma_e^2 + \sigma_b^2 & 0 & \sigma_b^2 \\ \sigma_b^2 & 0 & \sigma_e^2 + \sigma_b^2 & 0 \\ 0 & \sigma_b^2 & 0 & \sigma_e^2 + \sigma_b^2 \end{bmatrix}$$

$$\rho_{y_{11}y_{21}} = \frac{\sigma_b^2}{\sqrt{\sigma_3^2 + \sigma_b^2}\sqrt{\sigma_3^2 + \sigma_b^2}} = \frac{\sigma_b^2}{\sigma_3^2 + \sigma_b^2}$$

```
twoway <- read.table("data/05twoway.dat", col.names = c("block", "seedType", "inoculate",
    "yield"))
```

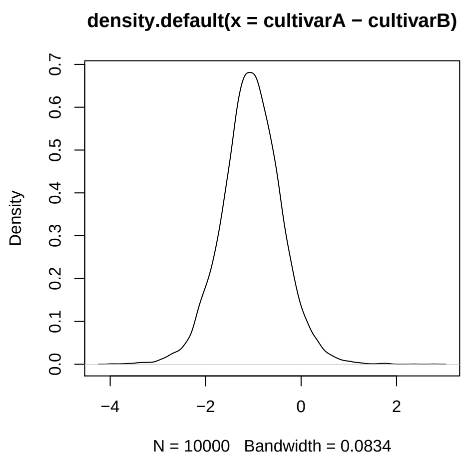
First model with multiple souces of variance, s2blk is a hyper-prior, or a prior on a prior

```
mdl <- ' model {
    for (i in 1:21) {
        yield[i] ~ dnorm(mu[i], 1/s2e)
        mu[i] <- aaron[cultn[i], inocn[i]] + u[block[i]]
    }

    for (i in 1:2){
        for (j in 1:3) {
            aaron[i,j] ~ dnorm(30, .001);

        }
    }

    for (i in 1:4) {
        u[i] ~ dnorm(0, 1/s2blk)
    }

    s2e ~ dgamma(1.5, .1);
    s2blk ~ dgamma(1.5, .1);
}
'
writeLines(mdl, 'code/MixedModels.jags')
```

```
yield <- twoway[, 4]
cultn <- as.numeric(twoway$seedType)
inocn <- as.numeric(twoway$inoculate)
block <- twoway[, 1]

jags.data <- c("yield", "cultn", "inocn", "block")
jags.params <- c("aaron", "s2e", "s2blk")
set.seed(343)
mixedm.jags <- jags(data = jags.data, parameters.to.save = jags.params, model.file = "code/MixedModels.jags",
    n.iter = 12000, n.burnin = 2000, n.chains = 1, n.thin = 1)

## module glm loaded

## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 137
##
## Initializing model
```

Difference between 1 and 2

```
mixedm.sim <- as.mcmc(mixedm.jags)
cultivarA <- (mixedm.sim[, 1] + mixedm.sim[, 3] + mixedm.sim[, 5])/3
cultivarB <- (mixedm.sim[, 2] + mixedm.sim[, 4] + mixedm.sim[, 6])/3

mean(cultivarA)

## [1] 30.09

mean(cultivarB)

## [1] 31.13

plot(density(cultivarA - cultivarB))
```



* * February 28, 2013 * *

Simpler Mixed Model

```
bond <- read.table("data/07mixedmods.dat", header = TRUE)
metn <- rep(1:3, 21/3)
bond <- cbind(bond, metn)
```

```
mdl <- " model{\nfor (i in 1:21){\npressure[i] ~ dnorm(mu[i], 1/s2error);\nmu[i] <- gamma[metn[i]] + u[ingot[i]]\n}\ninvisible(\
writeLines(mdl, "code/SimpleMixedModel.jags")
```

```
metn <- bond[, 4]
ingot <- bond[, 1]
pressure <- bond[, 3]

jags.data <- c("metn", "ingot", "pressure")
jags.params <- c("gamma", "s2error", "s2ing")

bond.jags <- jags(data = jags.data, parameters.to.save = jags.params, model.file = "code/SimpleMixedModel.jags",
    n.iter = 12000, n.burnin = 2000, n.chains = 1, n.thin = 1)

## module glm loaded

## Error:
## Error parsing model file:
## syntax error on line 6 near """

bond.sim <- as.mcmc(bond.jags)

## Error:  object 'bond.jags' not found
```

ICC or interclass corelation is a measure of reliability of messurements

$$ICC = \frac{\sigma_i^2}{\sigma_e^2 + \sigma_i^2} \tag{4}$$

```
icc <- bond.sim[, 5]/(bond.sim[, 6] + bond.sim[, 5])

## Error:  object 'bond.sim' not found

plot(density(icc))

## Error:  object 'icc' not found
```

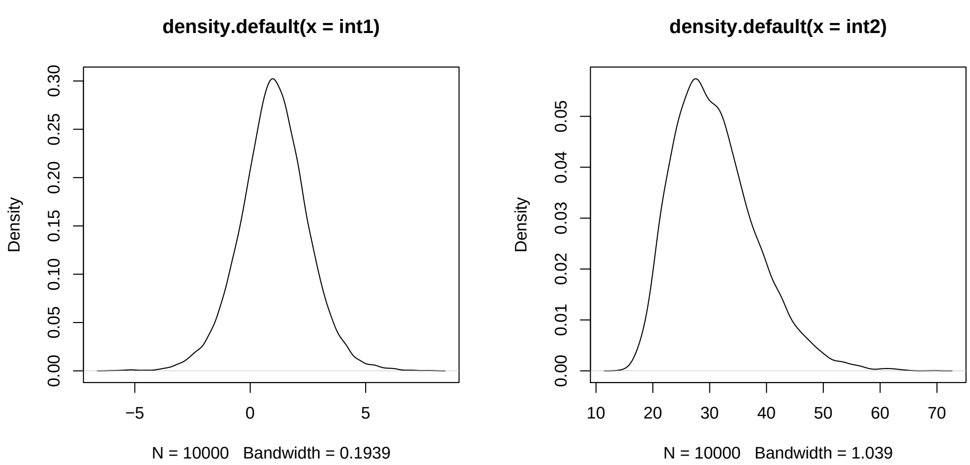
plot something

```
indif <- bond.sim[, 3] - bond.sim[, 2]

## Error:  object 'bond.sim' not found

icdif <- bond.sim[, 3] - bond.sim[, 4]

## Error:  object 'bond.sim' not found
```

Back to Complex

		inoc		
		con	dea	liv
cult	a	α_{11}	α_{12}	α_{13}
	b	α_{21}	α_{22}	α_{23}

```
int1 <- mixedm.sim[, 2] - mixedm.sim[, 4] - mixedm.sim[, 3] + mixedm.sim[, 5]
int2 <- mixedm.sim[, 4] - mixedm.sim[, 6] - mixedm.sim[, 5] + mixedm.sim[, 7]
plot(density(int1))
plot(density(int2))
```



Let's say that there's no interaction, because

* * March 5, 2013 * *

11 Random Coefficients Model

Genetically identical seeds we treat as subjects

Sixty observations, but only ten wheat types, so there are really somewhere in the middle

$$\text{yield}_{ij} = \beta_0 + \beta_1 \cdot \text{moisture}_j + u1_i + u2_i \cdot \text{moisture}_j + \text{error}_{ij}$$

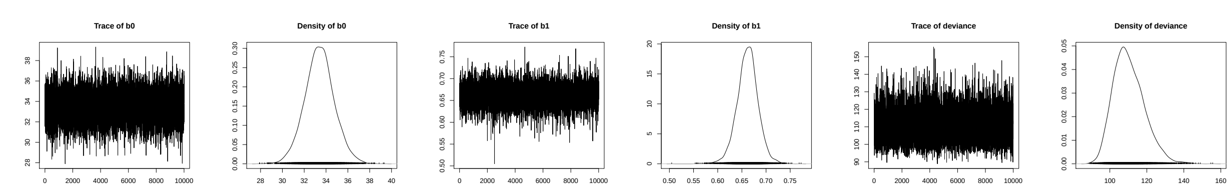
so the deviation u has both a slope and an intercept.

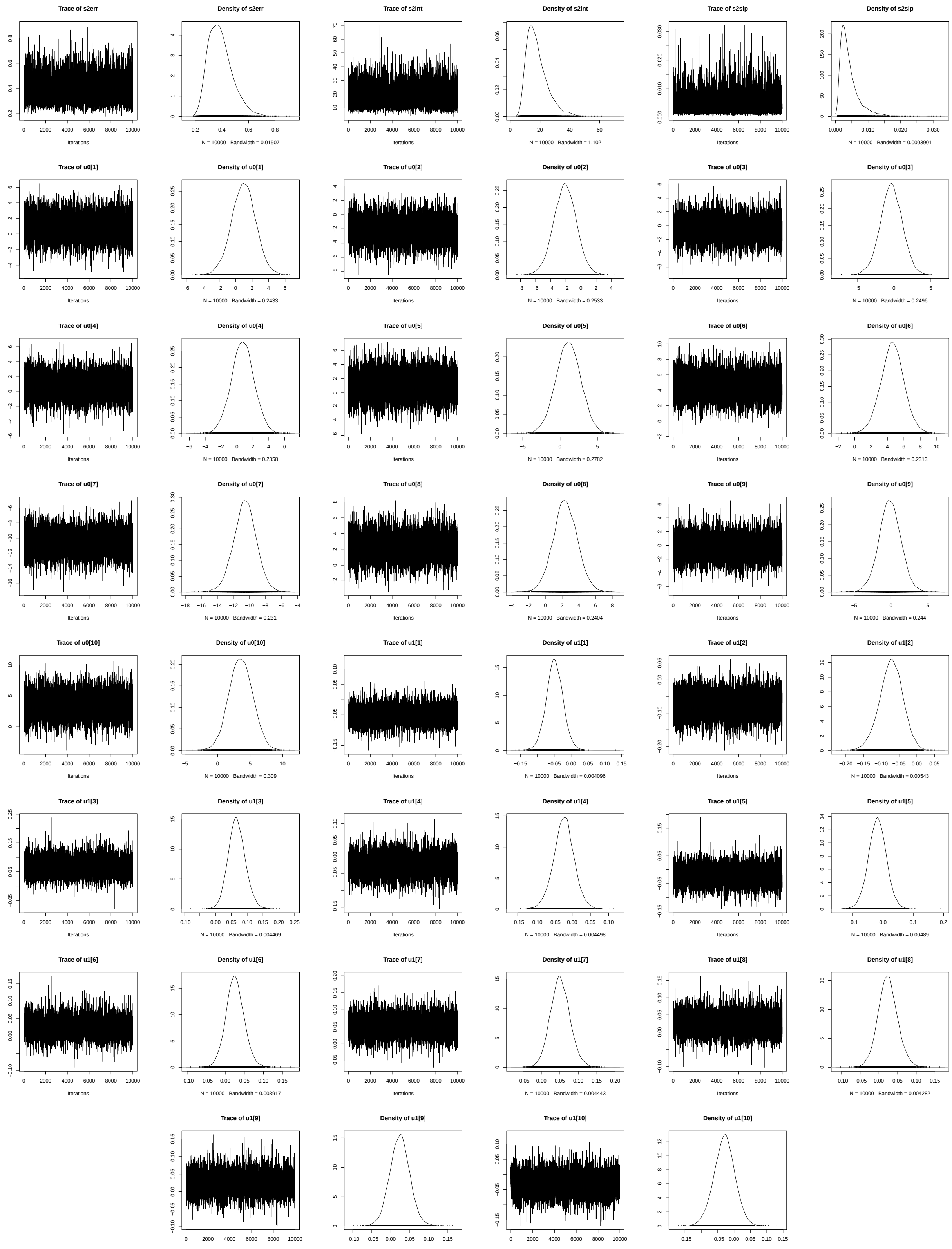
$$y = \begin{bmatrix} 1 & 10 \\ 1 & 17 \\ 1 & \vdots \\ \vdots & \ddots \end{bmatrix} \begin{pmatrix} \beta_0 \\ \beta_1 \end{pmatrix} \begin{bmatrix} 1 & 10 & 0 & 0 & 0 & 0 & \dots \\ 1 & 57 & 0 & 0 & 0 & 0 & \dots \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \dots \\ 1 & 40 & 0 & 0 & 0 & 0 & \dots \\ 0 & 0 & 1 & 16 & 0 & 0 & \dots \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \dots \\ 0 & 0 & 0 & 0 & 1 & 39 & \dots \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \ddots \end{bmatrix} \begin{pmatrix} u0_1 \\ u1_1 \\ u0_2 \\ u1_2 \\ u0_3 \\ u1_3 \\ u0_4 \\ u1_4 \\ u0_5 \\ u1_5 \\ u0_6 \\ u1_6 \end{pmatrix}$$

$$G = \begin{bmatrix} \sigma^2_{int} & 0 & 0 & 0 & \dots \\ 0 & \sigma^2_{slp} & 0 & 0 & \dots \\ 0 & 0 & \sigma^2_{int} & 0 & \dots \\ 0 & 0 & 0 & \sigma^2_{slp} & \dots \\ \vdots & \vdots & \vdots & \vdots & \ddots \end{bmatrix}$$

```
wheat <- read.table("data/10randomcoef.dat", header=TRUE)
yield <- wheat$yield
variety <- wheat$variety
moisture <- wheat$moisture
mdl <- ' model {
    for (i in 1:60) {
        yield[i] ~ dnorm(mu[i], 1/s2err)
        mu[i] <- b0 + b1 * moisture[i] + u0[variety[i]] + u1[variety[i]] * moisture[i]
    }

    b0 ~ dnorm(30, 0.001)
    b1 ~ dnorm(0, 0.1)

    for (i in 1:10) {
        u0[i] ~ dnorm(0, 1/s2int)
        u1[i] ~ dnorm(0, 1/s2slp)
    }

    s2err ~ dgamma(1.1, .5)
    s2int ~ dgamma(1.1, .1)
    s2slp ~ dgamma(1.1, 2)
}
'
writeLines(mdl, 'code/RandomCoeff.jags')
```

```
jags.data <- c("yield", "variety", "moisture")
jags.params <- c("b0", "b1", "u0", "u1", "s2err", "s2int", "s2slp")

rc1.jags <- jags(data = jags.data, parameters.to.save = jags.params, model.file = "code/RandomCoeff.jags",
    n.iter = 12000, n.burnin = 2000, n.chains = 1, n.thin = 1)

## module glm loaded

## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 366
##
## Initializing model

rc1.jags

## Inference for Bugs model at "code/RandomCoeff.jags", fit using jags,
##  1 chains, each with 12000 iterations (first 2000 discarded)
##  n.sims = 10000 iterations saved
##          mu.vect sd.vect    2.5%     25%     50%     75%   97.5%
## b0        33.406   1.355  30.710  32.525  33.397  34.263  36.139
## b1         0.662   0.022   0.617   0.648   0.662   0.675   0.704
## s2err      0.389   0.092   0.248   0.322   0.378   0.442   0.603
## s2int     17.953   7.124   8.213  12.823  16.548  21.613  36.010
## s2slp      0.004   0.003   0.001   0.002   0.003   0.005   0.013
## u0[1]      0.958   1.472  -1.995  -0.016   0.964   1.925   3.839
## u0[2]     -2.114   1.518  -5.174  -3.128  -2.109  -1.107   0.894
## u0[3]     -0.371   1.501  -3.410  -1.352  -0.376   0.639   2.534
## u0[4]      0.716   1.447  -2.145  -0.225   0.713   1.656   3.551
## u0[5]      1.097   1.664  -2.225  -0.001   1.102   2.217   4.370
## u0[6]      4.602   1.434   1.760   3.684   4.604   5.529   7.451
## u0[7]    -10.563   1.420 -13.406 -11.479 -10.560  -9.637  -7.808
## u0[8]      2.380   1.449  -0.466   1.433   2.365   3.350   5.277
## u0[9]     -0.162   1.492  -3.148  -1.131  -0.170   0.815   2.783
## u0[10]     3.573   1.840  -0.041   2.339   3.551   4.809   7.153
## u1[1]     -0.049   0.026  -0.099  -0.065  -0.049  -0.032   0.002
## u1[2]     -0.072   0.033  -0.141  -0.093  -0.071  -0.050  -0.009
## u1[3]      0.067   0.028   0.016   0.049   0.066   0.085   0.124
## u1[4]     -0.023   0.028  -0.080  -0.041  -0.023  -0.005   0.033
## u1[5]     -0.019   0.030  -0.079  -0.038  -0.019   0.001   0.040
## u1[6]      0.026   0.025  -0.022   0.010   0.025   0.041   0.075
## u1[7]      0.051   0.027  -0.001   0.033   0.050   0.068   0.107
## u1[8]      0.024   0.027  -0.028   0.007   0.023   0.041   0.079
## u1[9]      0.024   0.027  -0.028   0.006   0.024   0.041   0.077
## u1[10]    -0.029   0.033  -0.095  -0.050  -0.029  -0.008   0.034
## deviance 110.389   8.401  96.576 104.372 109.459 115.604 128.815
##
## DIC info (using the rule, pD = var(deviance)/2)
## pD = 35.3 and DIC = 145.7
## DIC is an estimate of expected predictive error (lower deviance is better).

rc1.sim <- as.mcmc(rc1.jags)
plot(rc1.sim, auto.layout = FALSE, ask = FALSE)
```





Find the variance of the y

```
g <- rbind(cbind(18.645, 0), cbind(0, 0.005))
r <- diag(0.392, 60)
z <- model.matrix(~-1 + as.factor(variety) + as.factor(variety):moisture, wheat)
Z <- z[, c(1, 11, 2, 12, 3, 13, 4, 14, 5, 15, 6, 16, 7, 17, 8, 18, 9, 19, 10, 20)]  # need to rearrange so that the intercepts a
G <- kronecker(diag(1, 10), g)
V <- Z %*% G %*% t(Z) + r
```

* * March 7, 2013 * *

To get the slope or intercept for the particular variety, add the fixed effect and the random effect for the variety.

12 Hierarchical Models

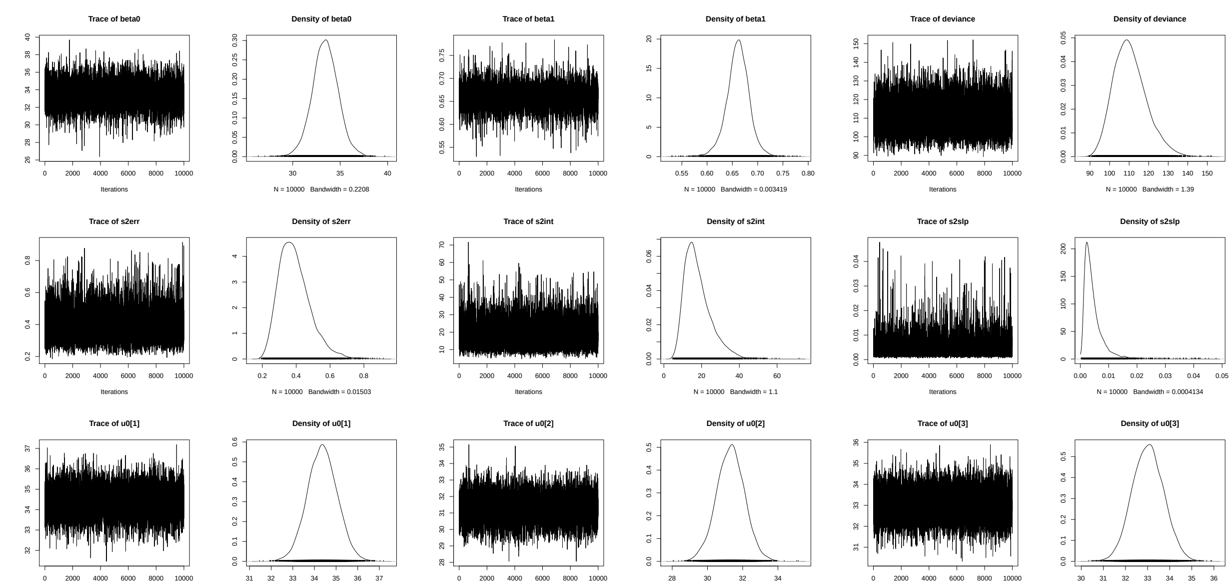
$y = \mu_0 + \mu_s \text{moisture} + e$

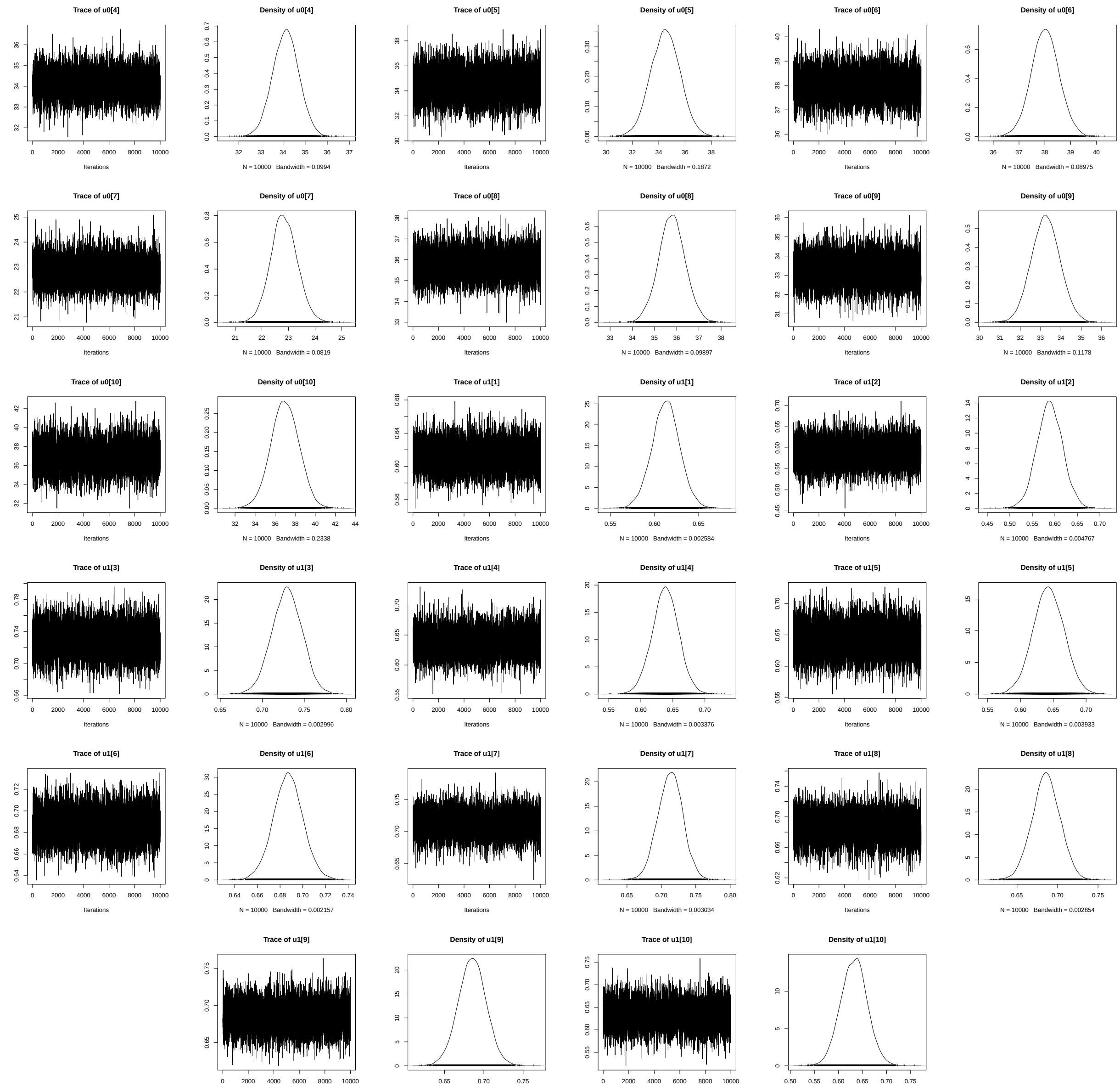
$\mu_0 \, \mathcal{N}(\mu_0, \sigma_0^2)$, $\mu_s \sim \mathcal{N}(\mu, \sigma_s^2)$, $e \sim (0, \sigma_e^2$

```
wheat <- read.table("data/10randomcoef.dat", header=TRUE)
yield <- wheat$yield
variety <- wheat$variety
moisture <- wheat$moisture
mdl <- ' model {
    for (i in 1:60) {
        yield[i] ~ dnorm(mu[i], 1/s2err)
        mu[i] <- u0[variety[i]] + u1[variety[i]] * moisture[i]
    }

    b0 ~ dnorm(30, 0.001)
    b1 ~ dnorm(0, 0.1)

    for (i in 1:10) {
        u0[i] ~ dnorm(beta0, 1/s2int)
        u1[i] ~ dnorm(beta1, 1/s2slp)
    }

    beta0 ~ dnorm(30, 0.001)
    beta1 ~ dnorm(0, 0.1)

    s2err ~ dgamma(1.1, .5)
    s2int ~ dgamma(1.1, .1)
    s2slp ~ dgamma(1.1, 2)
}
'
writeLines(mdl, 'code/Hierarchical.jags')
```

```
jags.data <- c("yield", "variety", "moisture")
jags.params <- c("beta0", "beta1", "u0", "u1", "s2err", "s2int", "s2slp")

hier.jags <- jags(data = jags.data, parameters.to.save = jags.params, model.file = "code/Hierarchical.jags",
    n.iter = 12000, n.burnin = 2000, n.chains = 1, n.thin = 1)

## module glm loaded

## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 334
##
## Initializing model

hier.jags
```

```
## Inference for Bugs model at "code/Hierarchical.jags", fit using jags,
##  1 chains, each with 12000 iterations (first 2000 discarded)
##  n.sims = 10000 iterations saved
##          mu.vect sd.vect   2.5%     25%     50%     75%   97.5%
## beta0     33.422   1.366 30.708  32.548  33.423  34.308  36.162
## beta1      0.661   0.023  0.613   0.648   0.662   0.675   0.706
## s2err      0.391   0.094  0.247   0.324   0.379   0.444   0.613
## s2int     18.019   7.236  8.118  12.861  16.541  21.633  35.702
## s2slp      0.005   0.004  0.001   0.002   0.004   0.006   0.015
## u0[1]     34.367   0.689 33.034  33.905  34.362  34.826  35.724
## u0[2]     31.309   0.794 29.711  30.783  31.322  31.840  32.870
## u0[3]     33.022   0.706 31.659  32.538  33.019  33.497  34.405
## u0[4]     34.126   0.592 32.972  33.725  34.129  34.518  35.286
## u0[5]     34.508   1.114 32.321  33.749  34.511  35.256  36.712
## u0[6]     38.019   0.539 36.958  37.661  38.017  38.376  39.098
## u0[7]     22.834   0.499 21.876  22.506  22.821  23.160  23.828
## u0[8]     35.783   0.599 34.601  35.388  35.780  36.178  36.983
## u0[9]     33.254   0.704 31.901  32.778  33.251  33.717  34.645
## u0[10]    36.978   1.391 34.238  36.047  36.969  37.916  39.672
## u1[1]      0.613   0.016  0.581   0.603   0.613   0.623   0.644
## u1[2]      0.589   0.028  0.533   0.570   0.589   0.608   0.645
## u1[3]      0.729   0.018  0.694   0.717   0.729   0.741   0.764
## u1[4]      0.638   0.021  0.598   0.625   0.638   0.652   0.679
## u1[5]      0.643   0.023  0.596   0.627   0.642   0.659   0.688
## u1[6]      0.687   0.013  0.661   0.678   0.687   0.696   0.713
## u1[7]      0.713   0.018  0.678   0.701   0.713   0.725   0.748
## u1[8]      0.686   0.017  0.652   0.675   0.686   0.697   0.719
## u1[9]      0.685   0.018  0.650   0.674   0.685   0.697   0.720
## u1[10]     0.632   0.027  0.579   0.614   0.633   0.650   0.686
## deviance 110.551   8.430 96.364 104.516 109.746 115.607 129.397
##
## DIC info (using the rule, pD = var(deviance)/2)
## pD = 35.5 and DIC = 146.1
## DIC is an estimate of expected predictive error (lower deviance is better).

hier.sim <- as.mcmc(hier.jags)
plot(hier.sim, auto.layout = inter_plots, ask = inter_plots)
```





Hierarchical models are virtually identical as random coefficients models, but are more pure Bayesian in thought process and methodology.

```
%let notedir = Z:\Dropbox\Active\STAT451\Notes\data;
filename data "&notedir./data/10randomcoef.dat";
filename outfile "&notedir./output/2013-03-07.html";
ods listing close;

data monkeyRatio;
    infile data;
    input obs variety yield moisture;
run;

ODS GRAPHICS on / imagename="2013-03-07-Plots";
ods html body=outfile (url=none)
```

```
        GPATH="&notedir.\figures\";

proc mcmc data=wheat output=wheat_chains nmc=100000 nbi=20000 thin=10
    seed=1234 monitor=(_parms_);
     diag(ess autocorr rl) propcov=quanew;
     parms mu0 30 mu1 0 s2 1;
     parms s2int 30 s2slp .1;
     random int ~ normal(mu0,var=s2int) subject=variety monitor=(int_1 int_2);
     random slp ~ normal(mu1,var=s2slp) subject=variety;
     prior mu0 ~ normal(30, var=100);
     prior mu1 ~ normal(0, var=0.1);
     prior s2 ~ dunif(0,3);
     prior s2int ~ dunif(0,50);
     prior s2slp ~ dunif(0,.2);
     mu = int + slp*moisture;
     model yield ~ normal(mu,var=s2);
run;
ods html close;
```

* * March 12, 2013 * *

13 Exam Debriefing

Covergence Diagnostics should have included:

- Traceplots
- Autocorrelation
- Effective sample size
- Raftery-lewis

Model should have been a model with six means and six variances

		Gain			
		1	2	3	
Duration	1	μ_1	μ_2	μ_3	$\frac{\mu_1+\mu_2+\mu_3}{3}$
	2	μ_4	μ_5	μ_6	$\frac{\mu_4+\mu_5+\mu_6}{3}$
		$\frac{\mu_1+\mu 4}{2}$	$\frac{\mu_2+\mu 5}{2}$	$\frac{\mu_3+\mu 6}{2}$	

Next exam will probably have

- a random effects and or hierarchal model
- Non-normal likelihood

14 Logistic Regression

What we have done so far:

- ANOVA
- Regression
- ANCOVA — Both Categorical and Continuous predictors
- Mixed — More than one source of variability

		Response Categorical	Continuous
Predictors	Categorical		ANOVA
	Continuous		Regression

$y = \text{Binomial}(n, \pi)$, with $0 \leq \pi \leq 1$

Odds: $\frac{\pi}{1-\pi}$

Sports "3 to 1" is 3 failures for every one success or $\pi = .25$

$Odds > 0$, 1 should be the midpoint

odds have a skewed distribution

probability π	Odds Success-Failure	log(Odds) $\log(S/F)$
$\frac{1}{5}$	1 - 1	0
$\frac{1}{5}$	1 - 4	-1.39
$\frac{4}{5}$	4 - 1	1.39

```
chd <- rbind(c(17, 274, 0, 0, 0), c(15, 122, 0, 1, 0), c(7, 59, 0, 0, 1), c(5, 32,
    0, 1, 1), c(1, 8, 1, 9, 9), c(9, 39, 1, 1, 0), c(3, 17, 1, 0, 1), c(14, 58, 1,
    1, 1))
colnames(chd) <- c("CHD", "nRisk", "Cat", "agegrp", "abECG")
tmt <- seq(8)
chd <- cbind(chd, tmt)
CHD <- chd[, 1]
nRisk <- chd[, 2]
tmt <- chd[, 6]
```

Cell means model

```
mdl <- ' model {
    for (i in 1:8) {
        CHD[i] ~ dbin(p[i], nRisk[i]);
            logit(p[i]) <- b[tmt[i]];
            b[i] ~ dnorm(0, .1);
    }
}
'
writeLines(mdl,'code/LogitBinomial.jags')
```

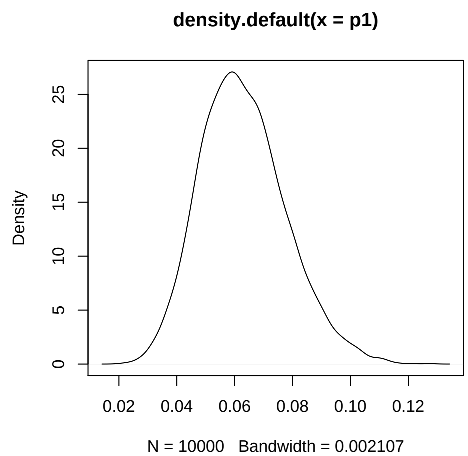
```
jags.data <- c("CHD", "nRisk", "tmt")
jags.params <- c("b")

# innits <- list(list('p' <- runif(8,0,1)))

logit.jags <- jags(data = jags.data, parameters.to.save = jags.params, model.file = "code/LogitBinomial.jags",
```

```
    n.iter = 12000, n.burnin = 2000, n.chains = 1, n.thin = 1)

## module glm loaded

## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
##    Graph Size: 42
##
## Initializing model
```

* * March 14, 2013 * *

$$
\begin{aligned}
\text{logit}(p_i) &= b_i \\
\log(\frac{p_i}{1-p_i}) &= b_i \\
\frac{p_i}{1-p_i} &= e^{b_i} \\
p_i &= e^{b_i} - pe^{b_i} \\
p_i + p_i e^{b_i} &= e^{b_i} \\
p_i &= \frac{e^{b_i}}{1+e^{b_i}} \frac{e^{-b_i}}{e^{-b_i}} \\
p_i &= \frac{1}{e^{-b_i+1}}
\end{aligned}
$$

```
logit.sim <- as.mcmc(logit.jags)
p1 <- 1/(exp(-logit.sim[, 1]) + 1)
plot(density(p1))
```




```
jags.params <- c("b", "p")
logit.jags <- jags(data = jags.data, parameters.to.save = jags.params, model.file = "code/LogitBinomial.jags",
    n.iter = 12000, n.burnin = 2000, n.chains = 1, n.thin = 1)

## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
```

```
##    Graph Size: 42
##
## Initializing model

logit.sim <- as.mcmc(logit.jags)
```

factorial design

			abEUG	
			Y	O
Cat-N	abECG	N	μ_1	μ_2
		Y	μ_3	μ_4

			abEUG	
			Y	O
Cat-Y	abECG	N	μ_5	μ_6
		Y	μ_7	μ_8

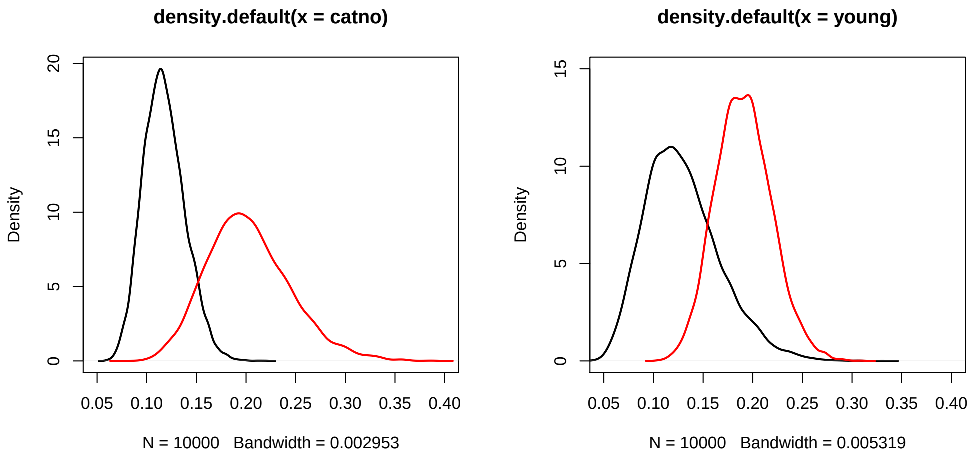
To find the marginals for cat

$$\text{Cat-n} = \frac{\mu_1 + \mu_2 + \mu_3 + \mu_4}{4} \text{Cat-y} = \frac{\mu_1 + \mu_2 + \mu_3 + \mu_4}{4} \tag{5}$$

```
p1 <- logit.sim[, 10]
p2 <- logit.sim[, 11]
p3 <- logit.sim[, 12]
p4 <- logit.sim[, 13]
p5 <- logit.sim[, 14]
p6 <- logit.sim[, 15]
p7 <- logit.sim[, 16]
p8 <- logit.sim[, 17]
```

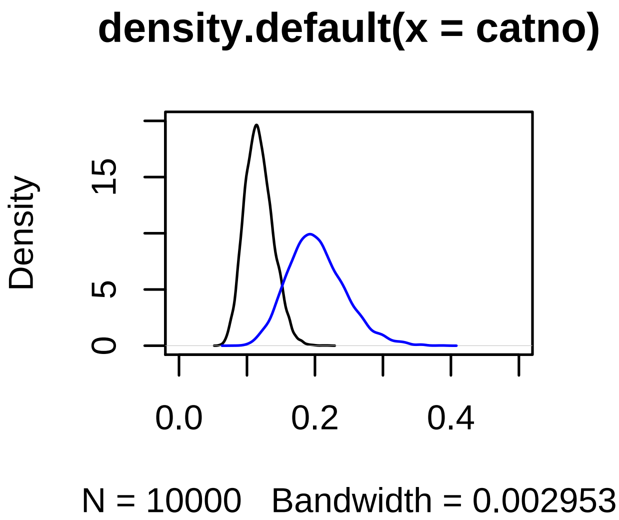
Find the marginals

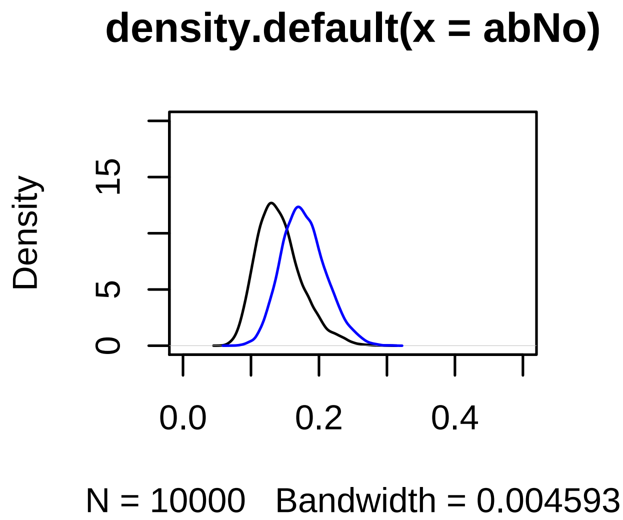
```
catno <- (p1 + p2 + p3 + p4)/4
catyes <- (p5 + p6 + p7 + p8)/4
plot(density(catno), xlim = c(0.05, 0.4), lwd = 2)
lines(density(catyes), lwd = 2, col = "red")

young <- (p1 + p3 + p5 + p7)/4
old <- (p2 + p4 + p6 + p8)/4
plot(density(young), xlim = c(0.05, 0.4), ylim = c(0, 15), lwd = 2)
lines(density(old), lwd = 2, col = "red")

abNo <- (p1 + p2 + p5 + p6)/4
abYes <- (p3 + p4 + p7 + p8)/4
```

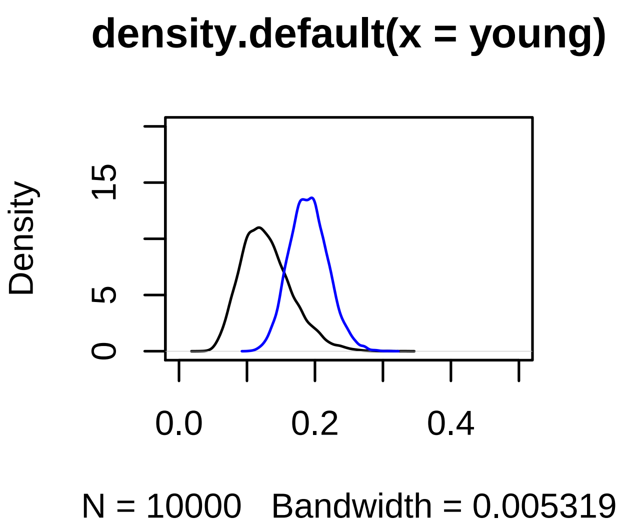


To compare old to young we use an odds ratio or a risk ratio

```
ORage <- (old/(1 - old))/(young/(1 - young))
mean(ORage > 1)

## [1] 0.9027


RRage <- old/young
mean(RRage > 1)

## [1] 0.9027


ORab <- (abYes/(1 - abYes))/(abNo/(1 - abNo))
ORCat <- (catyes/(1 - catyes))/(catno/(1 - catno))

mean(ORab)

## [1] 1.402

mean(ORCat)

## [1] 2.001

par(mfrow = c(2, 2))
xlims <- c(0, 0.5)
ylims <- c(0, 20)
plot(density(catno), xlim = xlims, ylim = ylims)
lines(density(catyes), col = "blue")
plot(density(abNo), xlim = xlims, ylim = ylims)
lines(density(abYes), col = "blue")
plot(density(young), xlim = xlims, ylim = ylims)
lines(density(old), col = "blue")
par(mfrow = c(1, 1))
```







two way interaction for abnormal ECG and age averaged over catacolamines

$$\mu_1 + \mu_5 - \mu_2 - \mu_6 - \mu_3 - \mu_7 + \mu_4 + \mu_8 = 0$$

to average across abnormal ECG, rewrite the tables abECG-N

		abEUG	
		Y	O
Cat	N	μ_1	μ_2
	Y	μ_5	μ_6

			abEUG	
			Y	O
abECG-Y	Cat	N	μ_3	μ_4
		Y	μ_7	μ_8

$$\mu_1 + \mu_3 - \mu_2 - \mu_4 - \mu_5 - \mu_7 + \mu_6 + \mu_8 = 0$$

```r
intageab <- p1 + p5 - p2 - p6 - p3 - p7 + p4 + p8
plot(density(intageab))
```