

STA 360: Homework 10c

Samuel Eure

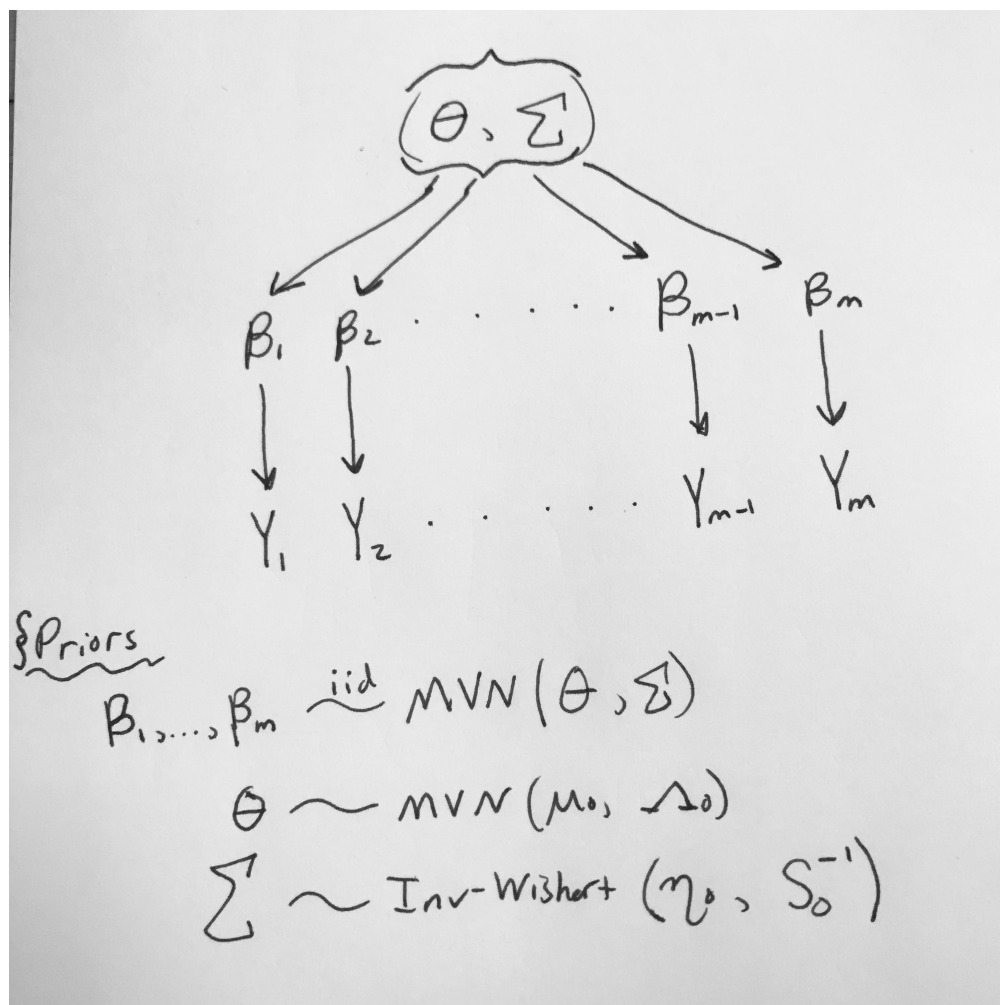
12/2/2018

Problem 11.4

The Data

```
data <- read.csv("mathstandard.txt", header = T)
counties <- unique(data$county)
Y <- data$metstandard;
X <- matrix(c(data$percentms), ncol = 1);
```

Part a



Part b

Logistic

```
BetaEstimate <- matrix(0,nrow = length(counties), ncol = 3);
colnames(BetaEstimate)<- c('intercept', 'percentMasters', 'samples');
rownames(BetaEstimate)<- counties;
plotXValues <- c();
countyToX    <- list();
countyToY    <- list();
countyToProbs <- list();
for(j in 1:length(counties)){
  countyX1      <- X[data$county == counties[j]];
  countyY      <- Y[data$county == counties[j]];
  model.j      <- glm(countyY ~ 1+ countyX1, family = binomial);
  beta.j       <- model.j$coef;
  BetaEstimate[j,c(1,2)] <- beta.j;
  if(length(countyY) == 1){BetaEstimate[j,2] <-0; beta.j[2]<-0}
  countyToX[[j]] <- countyX1; #This will be used in the MH step
  countyToY[[j]] <- countyY; #This will be used in the MH step
  BetaEstimate[j,3] <- length(countyY)
  z <-countyX1*beta.j[2]+beta.j[1];
  countyToProbs[[j]] <- exp(z)/(1+exp(z));
}
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
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## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
BetaEstimate
```

	intercept	percentMasters	samples
## Adams	931.2082644	-2.178458e+01	3
## Asotin	-1376.5980410	1.938916e+01	3
## Benton	-17.8895771	2.735615e-01	8

## Chelan	-13.8759019	1.928240e-01	7
## Clallam	-1.3131724	7.395515e-03	7
## Clark	-0.9551942	1.877388e-02	19
## Columbia	22.5660686	0.000000e+00	1
## Cowlitz	-0.3564859	-2.238540e-03	8
## Douglas	-23.5660685	1.698666e-16	3
## Ferry	-23.5660685	4.511809e-16	3
## Franklin	-2094.1646233	3.221858e+01	4
## Garfield	-22.5660685	0.000000e+00	1
## Grant	-1.7867982	3.004804e-03	12
## Grays Harbor	-8.4978525	1.174606e-01	10
## Island	-5398.6556245	8.886664e+01	3
## Jefferson	23.5660689	-6.671826e-12	3
## King	-2.8641607	5.537192e-02	64
## Kitsap	-3.4675513	5.926339e-02	10
## Kittitas	-3110.1242439	5.053044e+01	3
## Klickitat	-2.0628118	3.566456e-02	4
## Lewis	-3.5101909	3.372968e-02	12
## Lincoln	-233.7985949	3.054159e+00	5
## Mason	-153.9108965	2.600869e+00	5
## Okanogan	-14.3877504	2.177999e-01	7
## Pacific	-629.3599478	9.538342e+00	4
## Pend Oreille	-801.7189011	1.334867e+01	3
## Pierce	-7.3545109	1.064683e-01	27
## San Juan	23.5660689	-1.358459e-11	3
## Skagit	-2.3920152	4.282731e-02	7
## Skamania	-22.5660685	0.000000e+00	1
## Snohomish	-1.2003330	1.495265e-02	30
## Spokane	2.3035123	-3.555875e-02	27
## Stevens	-2.2734717	4.176312e-02	7
## Thurston	-1.5709685	3.233877e-02	13
## Wahkiakum	-22.5660685	0.000000e+00	1
## Walla Walla	-3.8581685	2.878328e-02	7
## Whatcom	-8.5641958	1.818284e-01	10
## Whitman	885.2327349	-1.007939e+01	9
## Yakima	-4.0847169	2.081292e-02	20

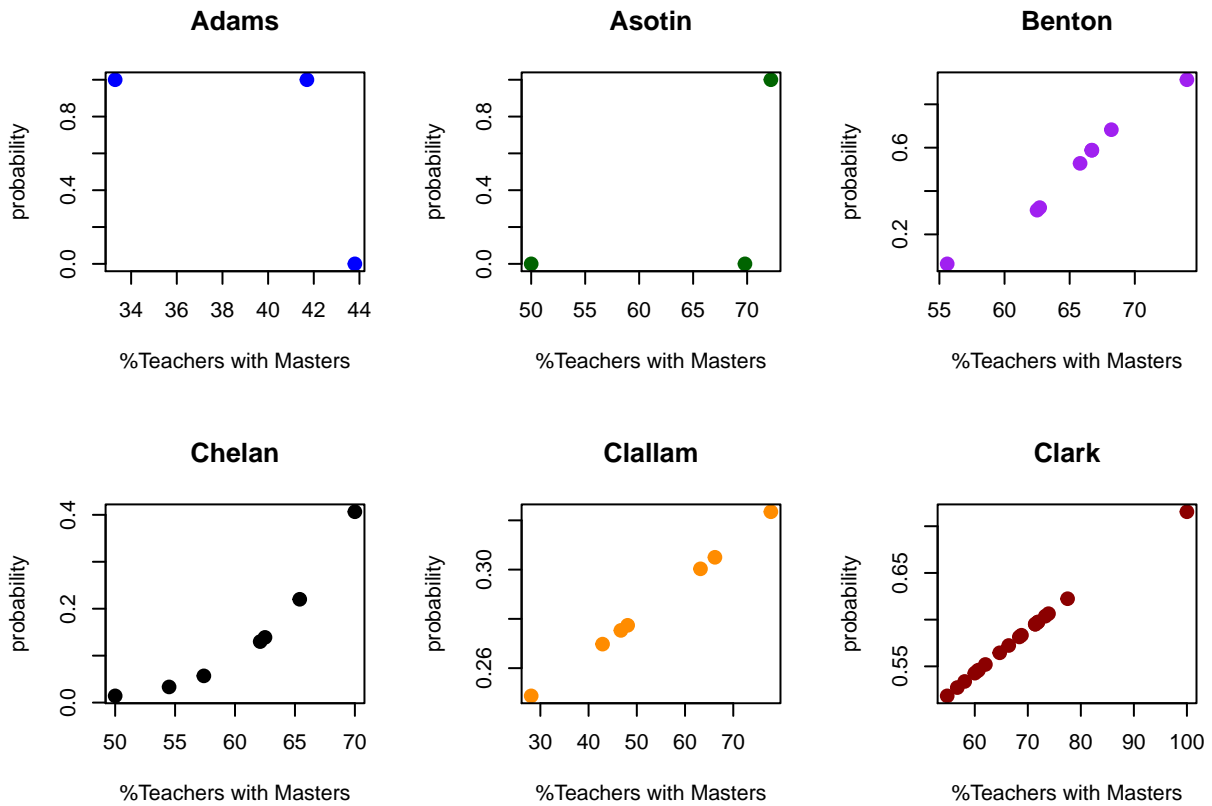
The table above shows my initial estimates of the values of β_j for each county j . As shown, some of these values are 0.0000, which may look like a computation error or data entry error. However, these values were initially *NA*, I simply changed them to zero for an important reason. First, notice that all the counties j which have a *NA* value for $x_{1,j}$ also only have one sample (or school) which represents them in the data set. Thus, a regression line can only be a constant (the intercept) value since one must have two data points to calculate slope.

```
i=1
C <- c('darkred', 'blue', 'darkgreen','purple','black','darkorange')
while(i < length(counties)){
  par(mfrow = c(2,3))
  top <- min((i+5),length(counties))
  for(j in i:top){
    countyX1 <- X[data$county == counties[j]];
    plot(countyX1, countyToProbs[[j]], main = counties[j],
         xlab = '%Teachers with Masters', ylab = 'probability',
```

```

    col = C[j%%6+1], pch = 20, cex = 2)
  }
  i <- i + 6;
}

```

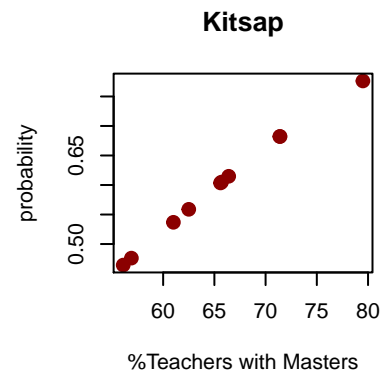
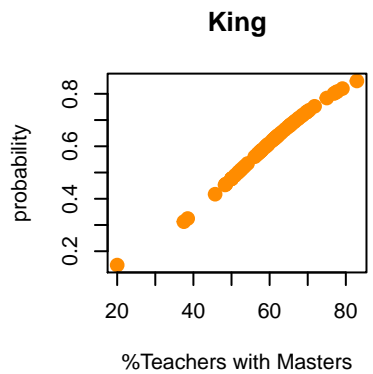
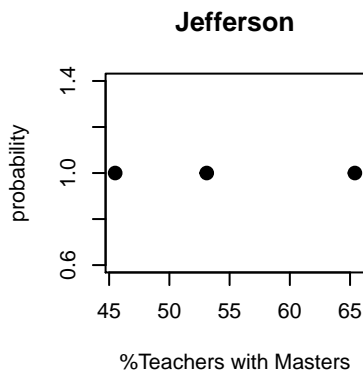
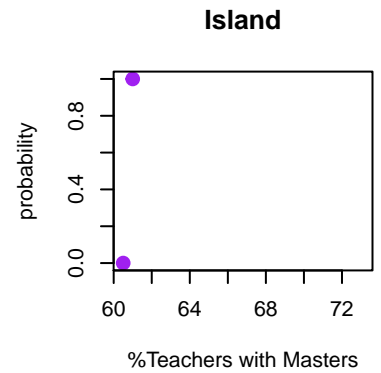
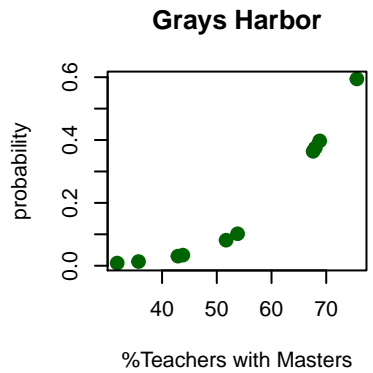
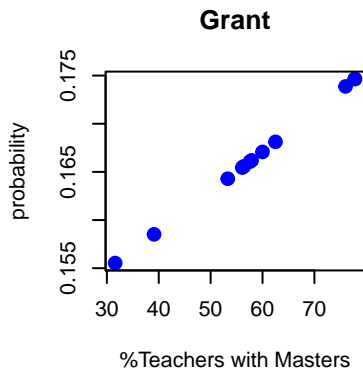
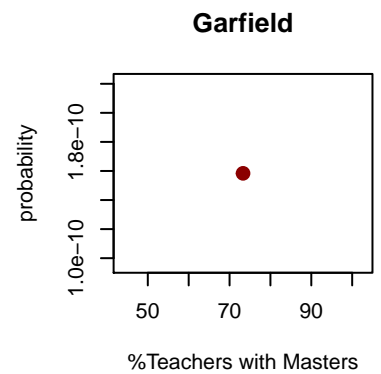
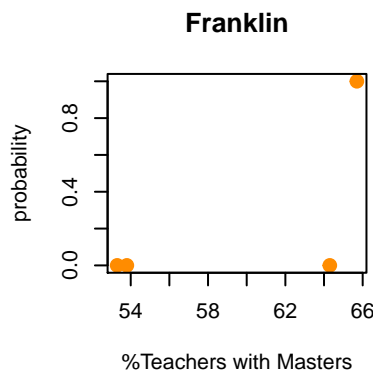
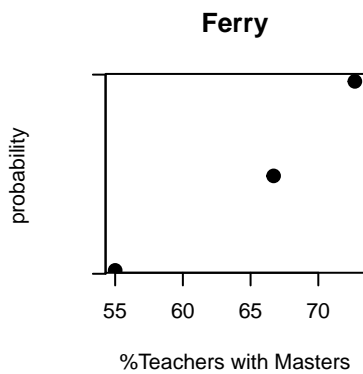
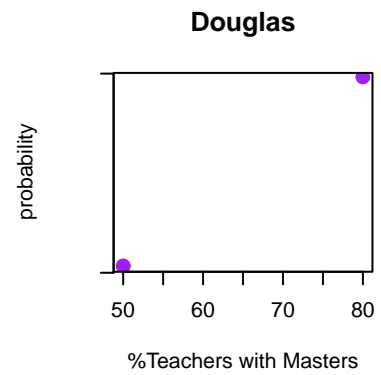
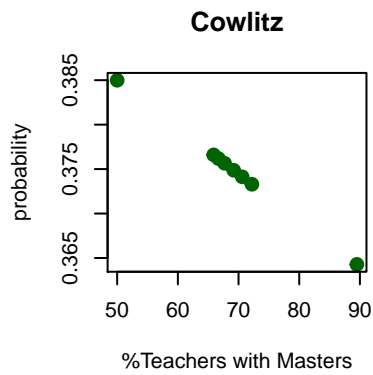
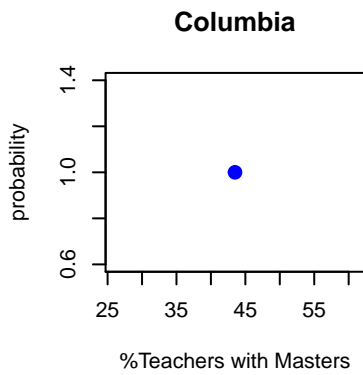


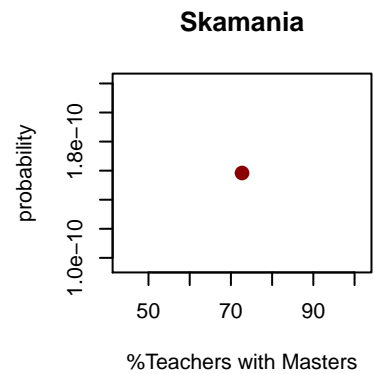
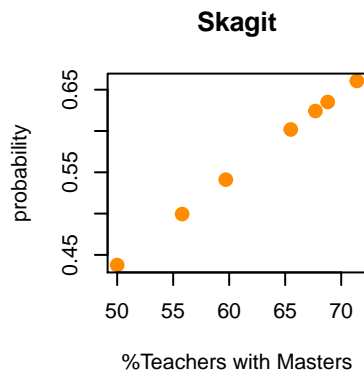
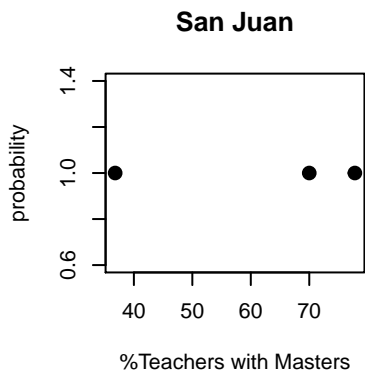
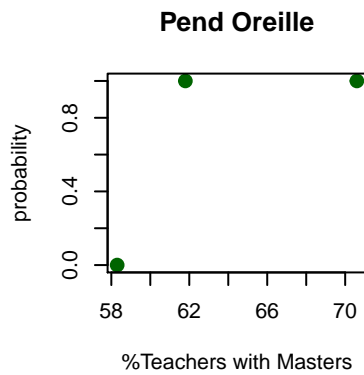
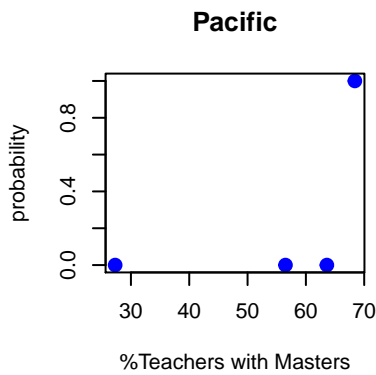
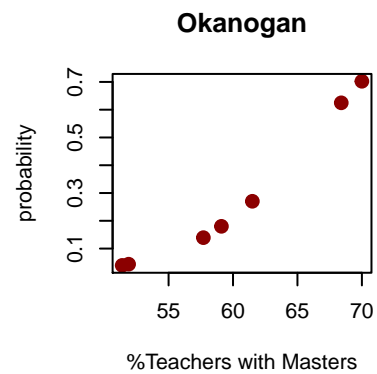
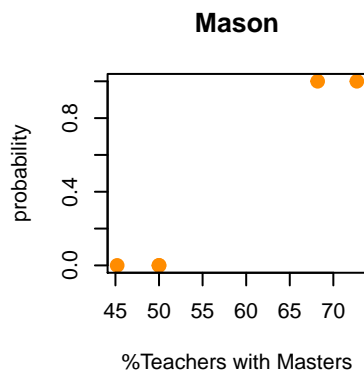
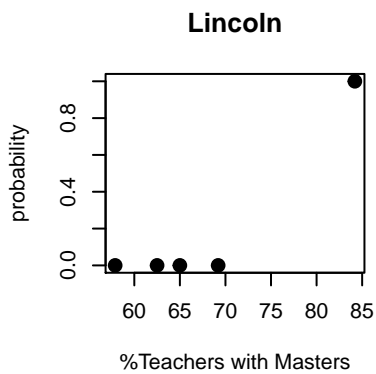
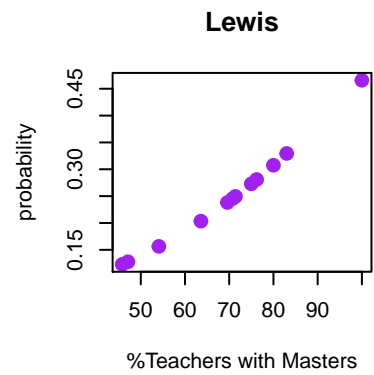
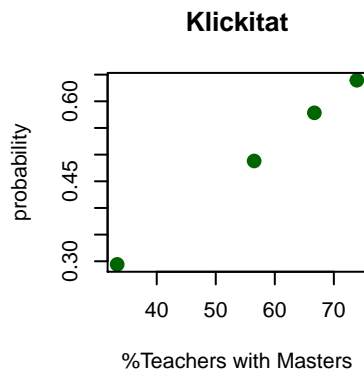
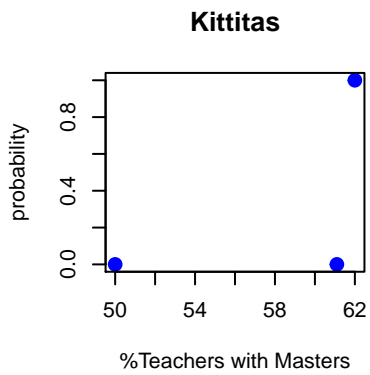
```

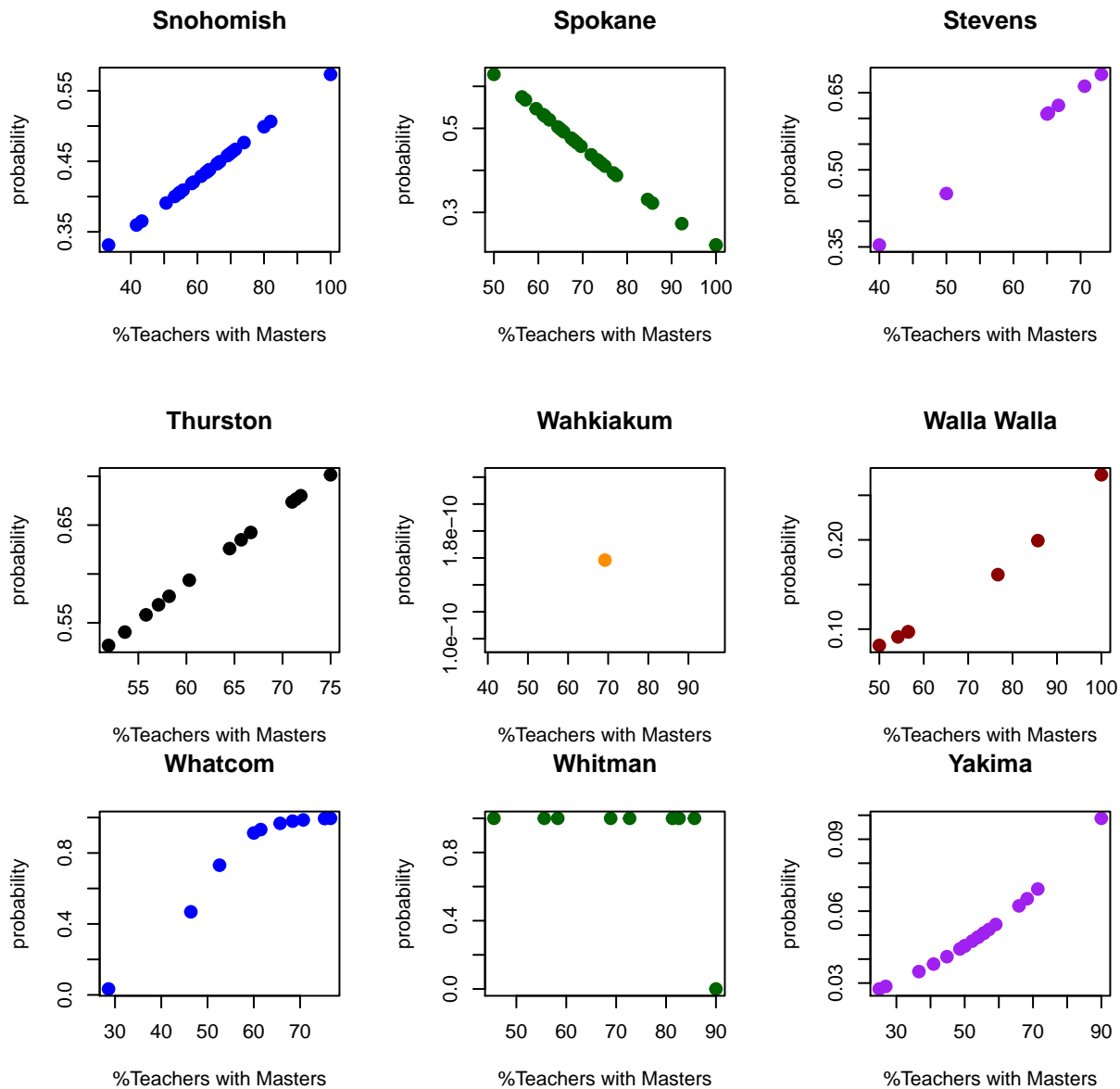
## Warning in plot.window(...): relative range of values = 30 * EPS, is small
## (axis 2)

## Warning in plot.window(...): relative range of values = 23 * EPS, is small
## (axis 2)

```







Probit

```
pro.BetaEstimate <- matrix(0,nrow = length(counties), ncol = 3);
colnames(pro.BetaEstimate)<- c('intercept', 'percentMasters', 'samples');
rownames(pro.BetaEstimate)<- counties;
plotXValues <- c();
pro.countyToProbs <- list();
for(j in 1:length(counties)){
  countyX1      <- X[data$county == counties[j]];
  countyY       <- Y[data$county == counties[j]];
  model.j      <- glm(countyY ~ 1+ countyX1, family = binomial(link = "probit"));
  beta.j       <- model.j$coef;
  pro.BetaEstimate[j,c(1,2)] <- beta.j;
  if(length(countyY) == 1){pro.BetaEstimate[j,2] <-0; beta.j[2]<-0}
  pro.BetaEstimate[j,3] <- length(countyY)
```

```

z <-countyX1*beta.j[2]+beta.j[1];
pro.countyToProbs[[j]] <- pnorm(z);
}

```

```

## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
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## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

```

```
pro.BetaEstimate
```

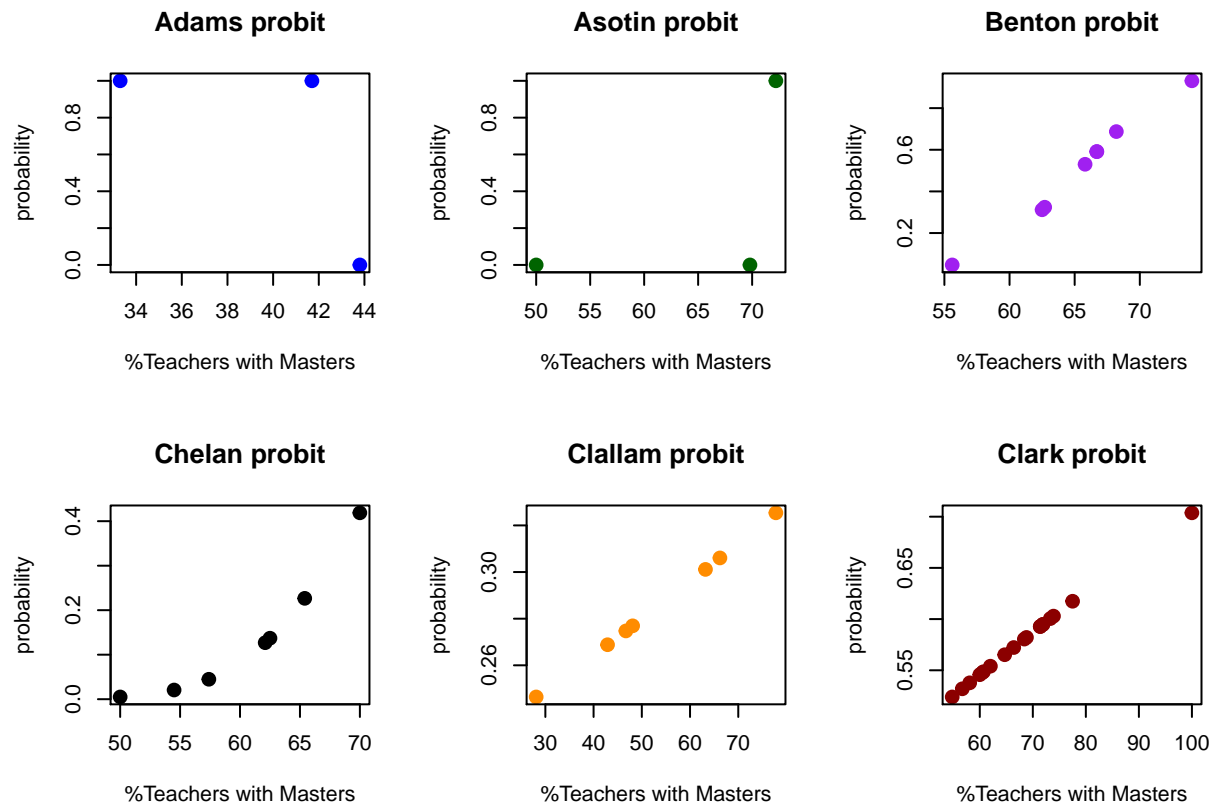
##	intercept	percentMasters	samples
## Adams	261.1533328	-6.109142e+00	3
## Asotin	-375.2196571	5.284843e+00	3
## Benton	-11.2237251	1.717281e-01	8
## Chelan	-8.4979976	1.184708e-01	7
## Clallam	-0.8175796	4.690423e-03	7
## Clark	-0.5159491	1.051194e-02	19
## Columbia	6.2437504	0.000000e+00	1
## Cowlitz	-0.2146536	-1.508529e-03	8
## Douglas	-6.4000838	4.573291e-17	3
## Ferry	-6.4000838	1.644081e-16	3
## Franklin	-591.3443818	9.097686e+00	4
## Garfield	-6.2437504	0.000000e+00	1
## Grant	-1.0827330	1.953467e-03	12
## Grays Harbor	-5.1217816	7.069872e-02	10
## Island	-1537.3016492	2.530536e+01	3
## Jefferson	6.4000838	-8.374934e-12	3
## King	-1.7068805	3.304999e-02	64
## Kitsap	-2.2073879	3.764587e-02	10
## Kittitas	-872.4594319	1.417487e+01	3
## Klickitat	-1.3208736	2.261177e-02	4
## Lewis	-2.2577675	2.209851e-02	12
## Lincoln	-65.6033716	8.563292e-01	5
## Mason	-41.6017930	7.033422e-01	5
## Okanogan	-8.9446635	1.356044e-01	7
## Pacific	-176.1340078	2.669124e+00	4
## Pend Oreille	-217.7896667	3.626472e+00	3
## Pierce	-4.4015101	6.368808e-02	27

## San Juan	6.4000838	-1.177615e-11	3
## Skagit	-1.5076571	2.693985e-02	7
## Skamania	-6.2437504	0.000000e+00	1
## Snohomish	-0.7545658	9.399968e-03	30
## Spokane	1.4811569	-2.288736e-02	27
## Stevens	-1.4429036	2.639003e-02	7
## Thurston	-0.9102153	1.903244e-02	13
## Wahkiakum	-6.2437504	0.000000e+00	1
## Walla Walla	-2.4057579	1.861378e-02	7
## Whatcom	-5.1055123	1.081552e-01	10
## Whitman	252.1465727	-2.870719e+00	9
## Yakima	-2.2740561	1.148984e-02	20

```

i=1
while(i < length(counties)){
  par(mfrow = c(2,3))
  top <- min((i+5),length(counties))
  for(j in i:top){
    countyX1 <- X[data$county == counties[j]];
    plot(countyX1, pro.countyToProbs[[j]], main = paste(counties[j], 'probit'),
         xlab = '%Teachers with Masters', ylab = 'probability',
         col = C[j%6+1], pch = 20, cex = 2)
  }
  i <- i + 6;
}

```



```

## Warning in plot.window(...): relative range of values = 23 * EPS, is small
## (axis 2)

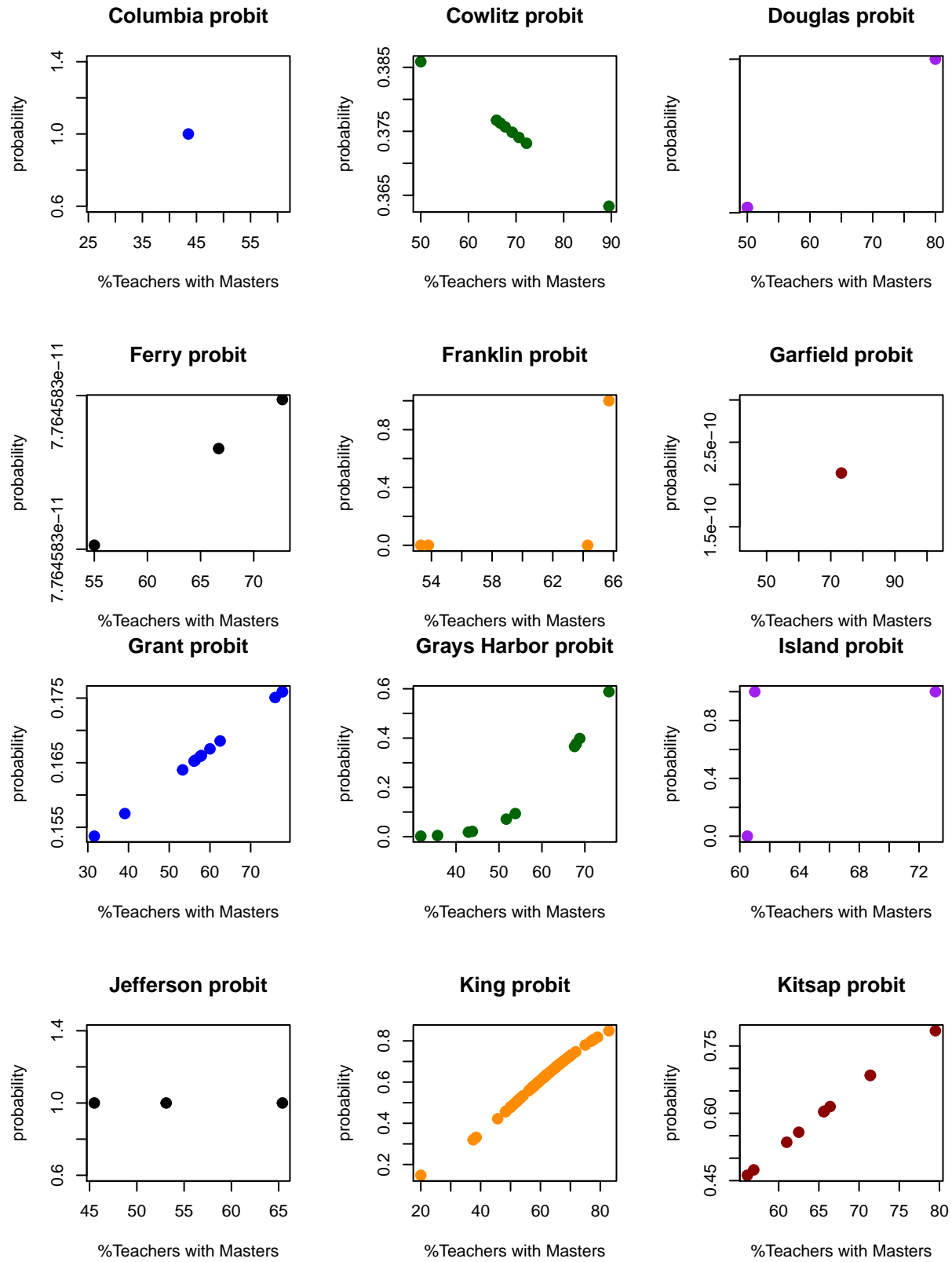
```

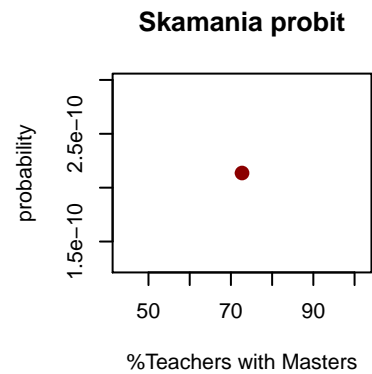
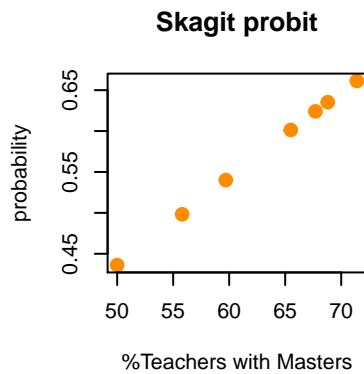
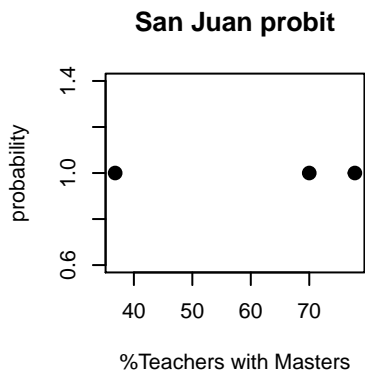
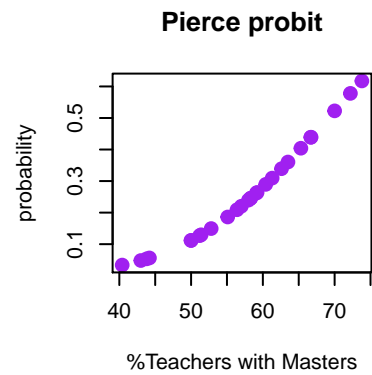
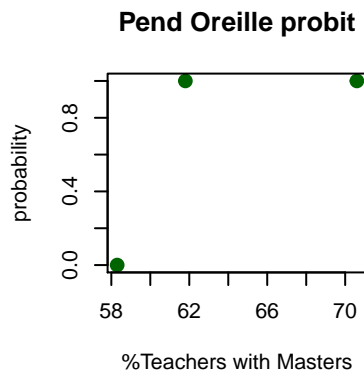
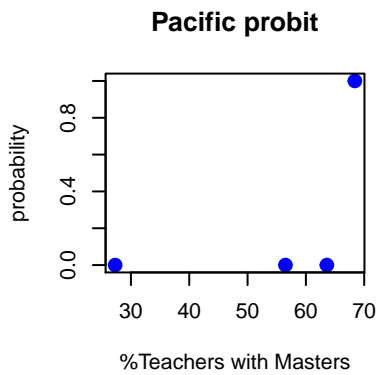
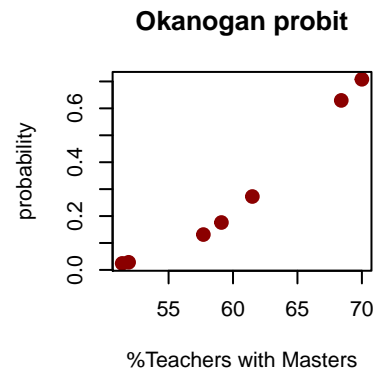
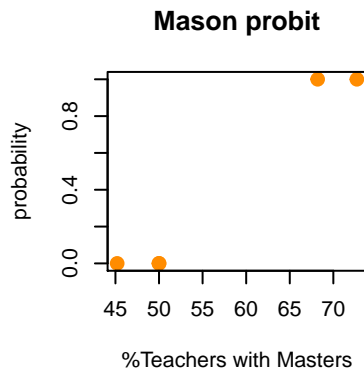
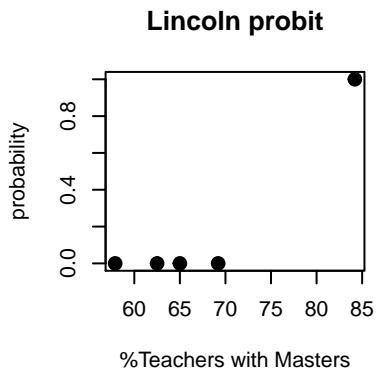
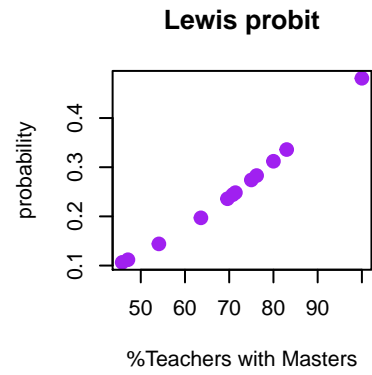
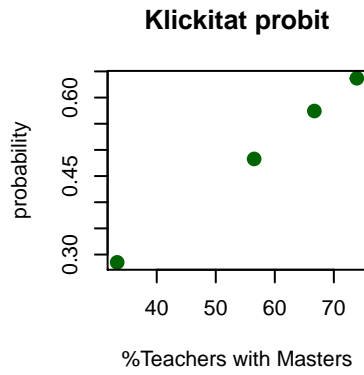
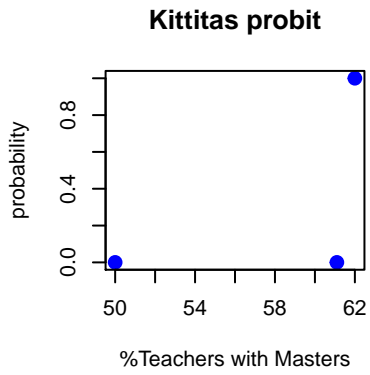
```

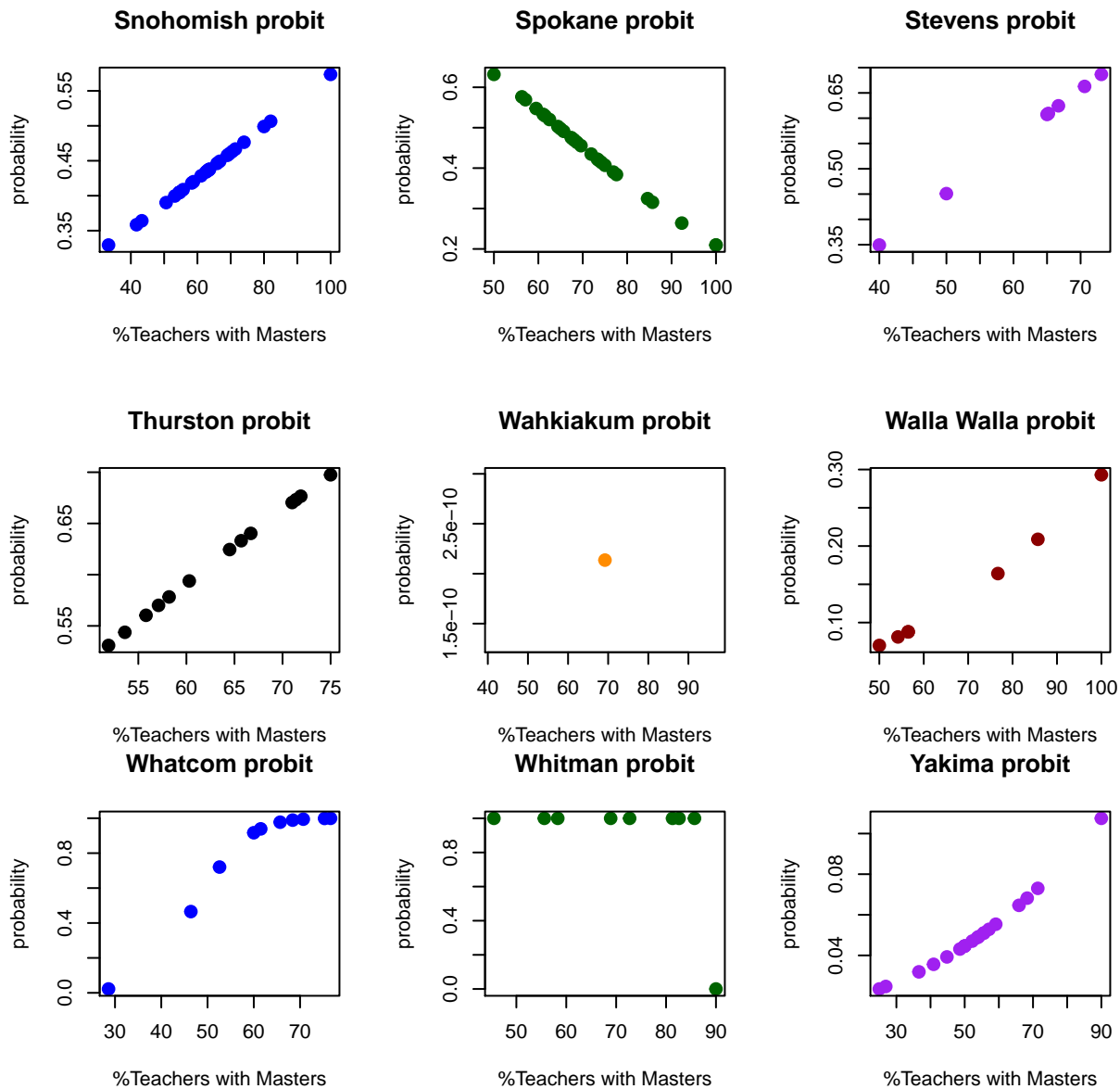
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```

(axis 2)





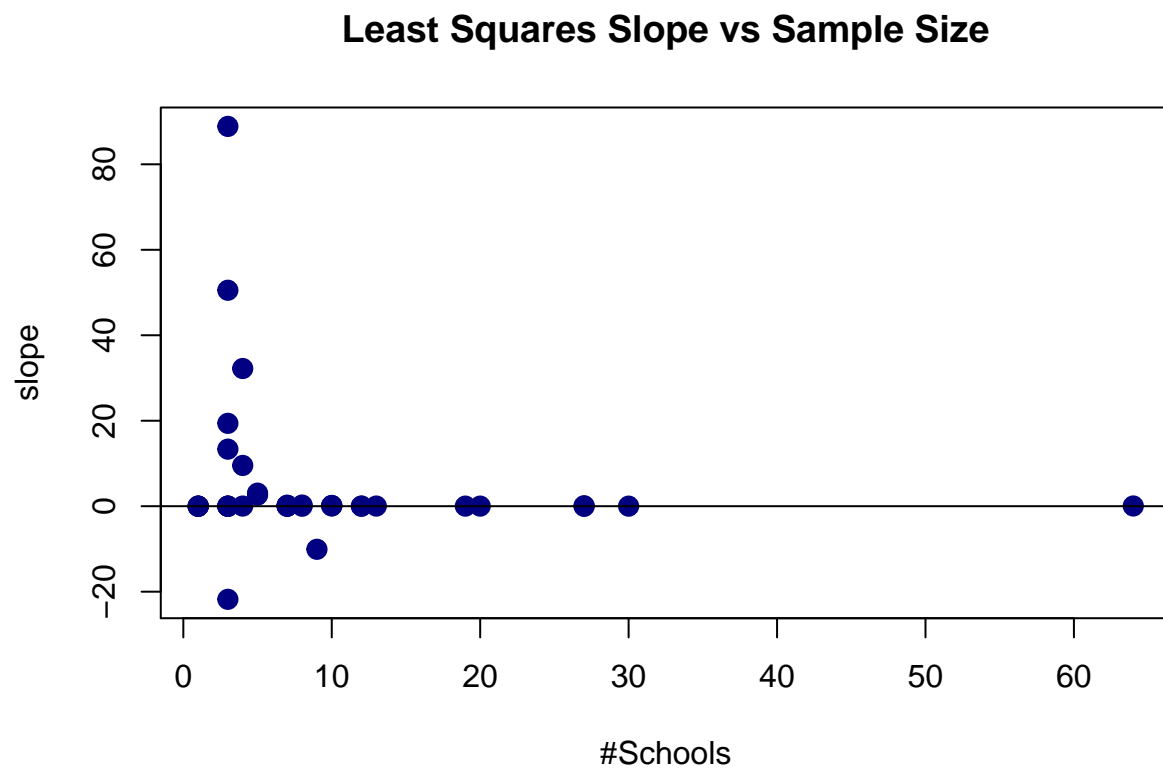


Comments

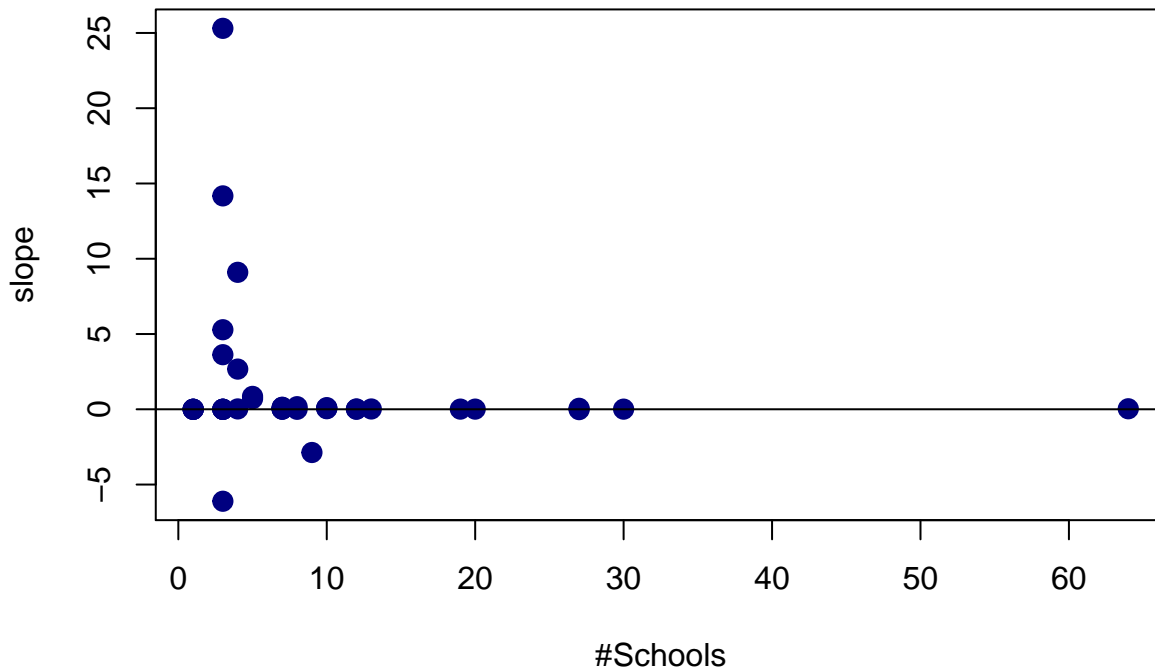
It appears that some of the counties (Yakima and Clark for example) show positive linear trends between the probability and X_1 , while others (Spokane and Cowlitz for example) show negative linear trends, while others (San Juan and Whitman for example) don't show any evident trends in the data. This supports the idea that the relationship between the predictor X_1 (percent of teachers with a master's degree) and Y (if more than 50 percent of students passed the test) differ from county to county. The probit regression method and the default method yield similar in terms of the shape of the plots, however the probit regression method yields less extreme coefficients. Note the differences in the y axis in the two plots below.

Logistic

```
plot(BetaEstimate[,3], BetaEstimate[,2], pch = 20, cex = 2, col = 'navy',
     main = "Least Squares Slope vs Sample Size", xlab = '#Schools', ylab = 'slope')
abline(0,0)
```



Least Squares Slope vs Sample Size



As can be seen above, schools with more extreme slope value have small sample sizes.

Ad hoc estimates $\hat{\theta}, \hat{\Sigma}$ for θ, Σ can be obtained by taking the average and covariance of $\beta_{j,MLE}$ values which have samples ≥ 10 , which is performed below.

Logistic

I'll use this subset

```
moreThan10 <- BetaEstimate[BetaEstimate[,3]>9,]
moreThan10
```

```
##           intercept percentMasters samples
## Clark      -0.9551942      0.018773879      19
## Grant      -1.7867982      0.003004804      12
## Grays Harbor -8.4978525      0.117460555      10
## King       -2.8641607      0.055371915      64
## Kitsap     -3.4675513      0.059263387      10
## Lewis      -3.5101909      0.033729679      12
## Pierce     -7.3545109      0.106468262      27
## Snohomish  -1.2003330      0.014952651      30
## Spokane     2.3035123     -0.035558754      27
## Thurston   -1.5709685      0.032338772      13
## Whatcom    -8.5641958      0.181828364      10
## Yakima     -4.0847169      0.020812918      20
```

```
theta0.hat <- mean(moreThan10[,1]);
theta1.hat <- mean(moreThan10[,2]);
```

```

theta.hat <- c(theta0.hat, theta1.hat);
print("Theta.hat")

## [1] "Theta.hat"
theta.hat

## [1] -3.46274671  0.05070387
Sigma.hat <- var(moreThan10[,c(1,2)])
print("Sigma.hat")

## [1] "Sigma.hat"
print(Sigma.hat)

##               intercept percentMasters
## intercept      10.755821      -0.1793610
## percentMasters -0.179361       0.0034898

```

Thus with logistic regression

$$\hat{\theta} = [-3.46275, 0.05070] \text{ and } \hat{\Sigma} = \begin{bmatrix} 10.755821 & -0.1793610 \\ -0.179361 & 0.0034898 \end{bmatrix}$$

Probit

```

pro.moreThan10 <- pro.BetaEstimate[pro.BetaEstimate[,3]>9,]
pro.moreThan10

```

```

##               intercept percentMasters samples
## Clark          -0.5159491      0.010511938      19
## Grant          -1.0827330      0.001953467      12
## Grays Harbor   -5.1217816      0.070698724      10
## King           -1.7068805      0.033049985      64
## Kitsap         -2.2073879      0.037645873      10
## Lewis          -2.2577675      0.022098506      12
## Pierce         -4.4015101      0.063688080      27
## Snohomish      -0.7545658      0.009399968      30
## Spokane         1.4811569     -0.022887357      27
## Thurston       -0.9102153      0.019032443      13
## Whatcom        -5.1055123      0.108155224      10
## Yakima         -2.2740561      0.011489838      20

```

```

theta0.hat <- mean(pro.moreThan10[,1]);
theta1.hat <- mean(pro.moreThan10[,2]);
pro.theta.hat <- c(theta0.hat, theta1.hat);
print("Pro.Theta.hat")

```

```

## [1] "Pro.Theta.hat"
pro.theta.hat

```

```

## [1] -2.07143352  0.03040306

```

```

pro.Sigma.hat <- var(pro.moreThan10[,c(1,2)])
print("pro.Sigma.hat")

## [1] "pro.Sigma.hat"

print(pro.Sigma.hat)

##               intercept percentMasters
## intercept      3.93338187    -0.065478933
## percentMasters -0.06547893     0.001261682

```

Part c

With priors of

$$\theta \sim MVN(\hat{\theta}, \hat{\Sigma}), \quad \Sigma^{-1} \sim Wishart(4, \hat{\Sigma}^{-1})$$

their full conditional distributions are simply

$$\begin{aligned}
(\theta \mid \dots) &\sim MVN\left((\hat{\Sigma}^{-1} + m\Sigma^{-1})^{-1}(\hat{\Sigma}^{-1}\hat{\theta} + m\Sigma^{-1}\bar{\beta}), (\hat{\Sigma}^{-1} + m\Sigma^{-1})^{-1}\right), \quad \bar{\beta} := \frac{1}{m} \sum_j^m \beta_j \\
\Sigma &\sim Wishart\left(4 + m, [\hat{\Sigma} + S_\theta]^{-1}\right), \quad S_\theta := \sum_j^m (\beta_j - \theta)(\beta_j - \theta)^T
\end{aligned}$$

and for each $\beta_j, \beta_j^{(s+1)}$ can be obtained from $\beta_j^{(s)}$ and $\Sigma^{(s+1)}$ through proposing new values with

$$\beta_j^* \sim MVN(\beta_j^{(s)}, \Sigma^{(s+1)})$$

which makes the proposals symmetric, while

$$p(y_j \mid \beta_j^{(s)}, x_j) = \prod_i^{n_j} p_{i,j,(s)}^{y_{i,j}} (1 - p_{i,j,(s)})^{1-y_{i,j}}$$

where

$$p_{i,j,s} = \frac{e^{\beta_j^{(s)T} x_{i,j}}}{1 + e^{\beta_j^{(s)T} x_{i,j}}}$$

Thus, the acceptance probability r can be calculated as

$$\begin{aligned}
p_{j,*} &= \frac{\exp\{\beta_{i,j}^{(*)T} x_{i,j}\}}{1 + \exp\{\beta_{i,j}^{(*)T} x_{i,j}\}} \\
p_{j,s} &= \frac{\exp\{\beta_j^{(s)T} x_{i,j}\}}{1 + \exp\{\beta_j^{(s)T} x_{i,j}\}}
\end{aligned}$$

$$r = \min \left(1, \frac{\prod_i^{n_j} \text{dbern}(y_{i,j}, p_{i,j,*})}{\prod_i^{n_j} \text{dbern}(y_{i,j}, p_{i,j,(s)})} \right), \quad \log(r) = \min \left(0, \sum_i^{n_j} \log(\text{dbern}(y_{i,j}, p_{i,j,*})) - \sum_i^{n_j} \log(\text{dbern}(y_{i,j}, p_{i,j,(s)})) \right)$$

since

$$\log(\text{dbern}(y, p)) = \log(p^y (1-p)^{1-y}) = y \log(p) + (1-y) \log(1-p) = y \log\left(\frac{e^{\beta^T x}}{1 + e^{\beta^T x}}\right) + (1-y) \log\left(\frac{1}{1 + e^{\beta^T x}}\right)$$

$$\begin{aligned} &= y \log\left(e^{\beta^T x}\right) - y \log\left(1 + e^{\beta^T x}\right) + (1-y) \log(1) - (1-y) \log\left(1 + e^{\beta^T x}\right) \\ &= y\beta^T x - y \log(1 + e^{\beta^T x}) - \log(1 + e^{\beta^T x}) + y \log(1 + e^{\beta^T x}) = y\beta^T x - \log(1 + e^{\beta^T x}) \end{aligned}$$

$$\Rightarrow r = \min \left(0, \sum_i^{n_j} \left(y_{i,j} \beta_{j,*}^T x_{i,j} - \log(1 + e^{\beta_{j,*}^T x_{i,j}}) + \log \text{dMVN}(\beta_{j,*}, \theta^{(s+1)}, \Sigma^{(s+1)}) \right) - \sum_i^{n_j} \left(y_{i,j} \beta_{j,(s)}^T x_{i,j} - \log(1 + e^{\beta_{j,(s)}^T x_{i,j}}) + \log \text{dMVN}(\beta_{j,(s)}, \theta^{(s)}, \Sigma^{(s)}) \right) \right)$$

The Metropolis-Hastings Algorithm

Functions

```
logLikeBeta <- function(Betas, x, y) {
  z <- x*(Betas[2]) + Betas[1]
  p <- exp(z)/(1+exp(z))
  probs<- dbinom(y,1,p)
  return (sum(log(probs)))
}

logLikeProbit <- function(Betas, x, y) {
  z <- x*(Betas[2]) + Betas[1]
  p <- pnorm(z)
  probs<- dbinom(y,1,p)
  return (sum(log(probs)))
}

sigmaToVec <- function(Sigma){
  a <- Sigma[1,1];
  b <- Sigma[1,2];
  c <- Sigma[2,2];
  return(c(a,b,c));
}

vecToSigma <- function(sigmaVec){
  Sigma <- matrix(c(sigmaVec[1],sigmaVec[2],
                    sigmaVec[2],sigmaVec[3]),
                 nrow = 2, ncol = 2, byrow = T)
  return(Sigma);
}
```

```
library(MASS)
library(mvtnorm)
library(coda)
```

```

ARBetas <- rep(0,length(counties));
set.seed(1)
#Data Structures
Samples <- 5000; m <- length(counties); thinning <- 1;
SAMPLES <- Samples*thinning;
BETAS <- list();
SIGMA <- matrix(0, nrow = 1, ncol = 3);
THETA <- matrix(0, nrow = 1, ncol = 2);
#Initial Values
for(j in 1:m){
  BETAS[[j]] <- matrix(0, nrow = 1, ncol = 2);
}
currentBetas <- BetaEstimate[,c(1,2)]*0;
currentBetas[,1] <- theta.hat[1]
currentBetas[,2] <- theta.hat[2]
SIGMA[1,] <- sigmaToVec(Sigma.hat);
currentSigma <- Sigma.hat;
THETA[1,] <- theta.hat;
currentTheta <- theta.hat;
Sigma.hat.inv <- solve(Sigma.hat)

pro.BETAS <- list();
pro.SIGMA <- matrix(0, nrow = 1, ncol = 3);
pro.THETA <- matrix(0, nrow = 1, ncol = 2);
#Initial Values
for(j in 1:m){
  pro.BETAS[[j]] <- matrix(0, nrow = 1, ncol = 2);
}
pro.currentBetas <- pro.BetaEstimate[,c(1,2)]*0;
pro.currentBetas[,1] <- pro.theta.hat[1]
pro.currentBetas[,2] <- pro.theta.hat[2]
pro.SIGMA[1,] <- sigmaToVec(pro.Sigma.hat);
pro.currentSigma <- pro.Sigma.hat;
pro.THETA[1,] <- pro.theta.hat;
pro.currentTheta <- pro.theta.hat;
pro.Sigma.hat.inv <- solve(pro.Sigma.hat)

for(i in 2:SAMPLES){
  #Update theta
  sigma.s.inv <- solve(currentSigma);
  #pro.sigma.s.inv <- solve(pro.currentSigma);
  beta.mean <- colSums(currentBetas)/m;
  #pro.beta.mean <- colSums(pro.currentBetas)/m;
  t.var <- solve(Sigma.hat.inv + m*sigma.s.inv);
  #pro.t.var <- solve(pro.Sigma.hat.inv + m*pro.sigma.s.inv);
  t.mean <- t.var%*(Sigma.hat.inv%*theta.hat + m*sigma.s.inv%*beta.mean);
  #pro.t.mean <- pro.t.var%*(pro.Sigma.hat.inv%*pro.theta.hat + m*pro.sigma.s.inv%*pro.beta.mean);
  theta.new <- mvnrm(1, t.mean, t.var);
  #pro.theta.new <- mvnrm(1, pro.t.mean, pro.t.var);
  currentTheta<- theta.new;
  #pro.currentTheta<- pro.theta.new;
  #Update Sigma

```

```

S.theta <- matrix(0, nrow = 2, ncol =2)
#pro.S.theta <- matrix(0, nrow = 2, ncol =2)
for(k in 1:length(counties)){
  S.theta <- S.theta + (currentBetas[k,]-currentTheta)%*%t(currentBetas[k,]-currentTheta);
  #pro.S.theta <- pro.S.theta + (pro.currentBetas[k,]-pro.currentTheta)%*%t(pro.currentBetas[k,]-pro
}
Sigma.new.inv <- rWishart(1, 4+m, solve(Sigma.hat + S.theta))[,1];
#pro.Sigma.new.inv <- rWishart(1, 4+m, solve(pro.Sigma.hat + pro.S.theta))[,1];
Sigma.new <- solve(Sigma.new.inv);
#pro.Sigma.new <- solve(pro.Sigma.new.inv);
currentSigma <- Sigma.new;
#pro.currentSigma <- pro.Sigma.new;
for(j in 1:m){ #We can iterate through these individually.
  countyX <- countyToX[[j]];
  countyY <- countyToY[[j]];
  beta.s <- currentBetas[j,];
  beta.pro <- mvrnorm(1, beta.s, 2*currentSigma);
  logP.s <- logLikeBeta(beta.s, countyX, countyY);
  logP.pro <- logLikeBeta(beta.pro, countyX, countyY);
  prior.pro<- log(dmvnorm(beta.pro,currentTheta, currentSigma));
  prior.s <- log(dmvnorm(beta.s,currentTheta, currentSigma));
  logDiff <- logP.pro - logP.s + prior.pro - prior.s;
  logU <- log(runif(1,0,1));
  accept <- (logDiff >= logU);
  if(accept){ARBetas[j] <- ARBetas[j]+1};
  currentBetas[j,] <- beta.pro*as.vector(accept) + beta.s*as.vector(!accept)
}
#for(j in 1:m){ #We can iterate through these individually.
# countyX <- countyToX[[j]];
# countyY <- countyToY[[j]];
# pro.beta.s <- pro.currentBetas[j,];
# pro.beta.pro <- mvrnorm(1, pro.beta.s, pro.currentSigma);
# pro.logP.s <- logLikeProbit(pro.beta.s, countyX, countyY);
# pro.logP.pro <- logLikeProbit(pro.beta.pro, countyX, countyY);
# pro.prior.pro<- log(dmvnorm(pro.beta.pro, pro.currentTheta, pro.currentSigma));
# pro.prior.s <- log(dmvnorm(pro.beta.s, pro.currentTheta, pro.currentSigma));
# pro.logDiff <- logP.pro - pro.logP.s + pro.prior.pro - pro.prior.s;
# pro.logU <- log(runif(1,0,1));
# pro.accept <- (pro.logDiff >= pro.logU);
# pro.currentBetas[j,] <- pro.beta.pro*as.vector(pro.accept) + pro.beta.s*as.vector(!pro.accept))
#}
SIGMA <- rbind(SIGMA,sigmaToVec(Sigma.new));
THETA <- rbind(THETA,theta.new);
for(j in 1:m){
  BETAS[[j]] <- rbind(BETAS[[j]],currentBetas[j,]);
}
#pro.SIGMA <- rbind(pro.SIGMA,sigmaToVec(pro.Sigma.new));
#pro.THETA <- rbind(pro.THETA, pro.theta.new);
#for(j in 1:m){
# pro.BETAS[[j]] <- rbind(pro.BETAS[[j]],pro.currentBetas[j,]);
#}
}
print("done")

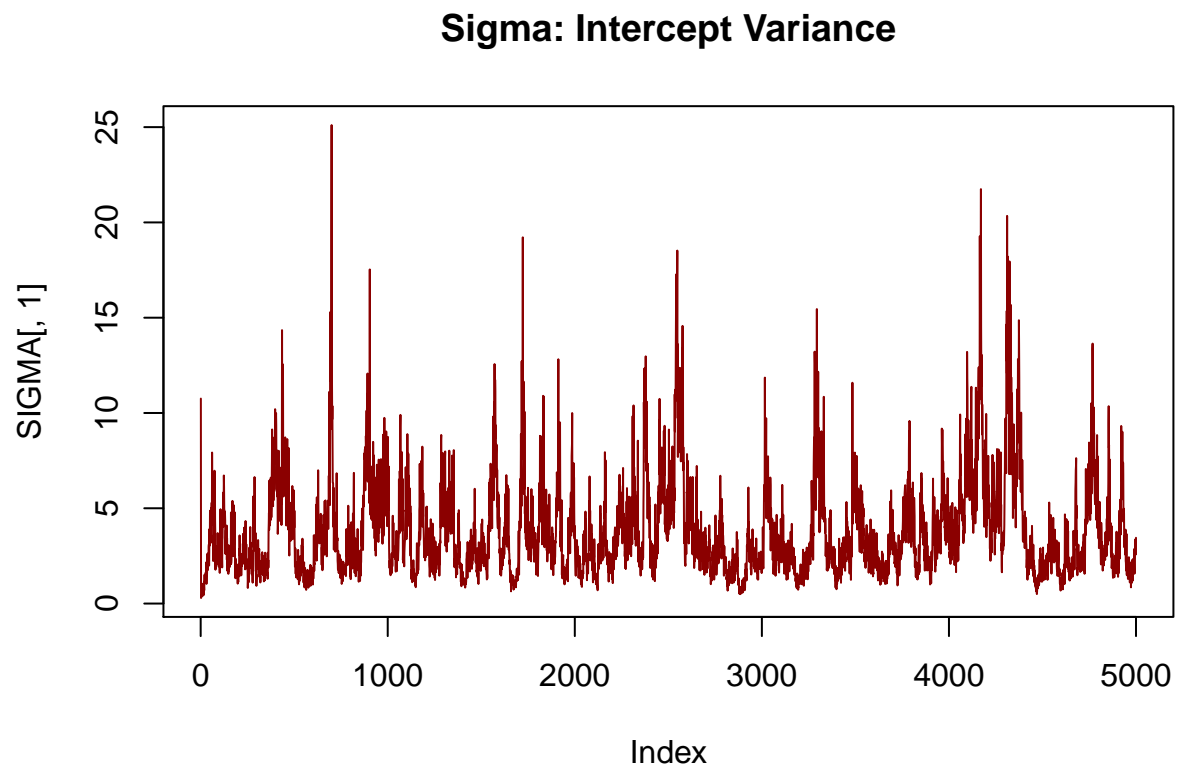
```

```
## [1] "done"
```

Part d

Logistic

```
plot(SIGMA[,1], type = 'l', col = C[1], main = 'Sigma: Intercept Variance')
```

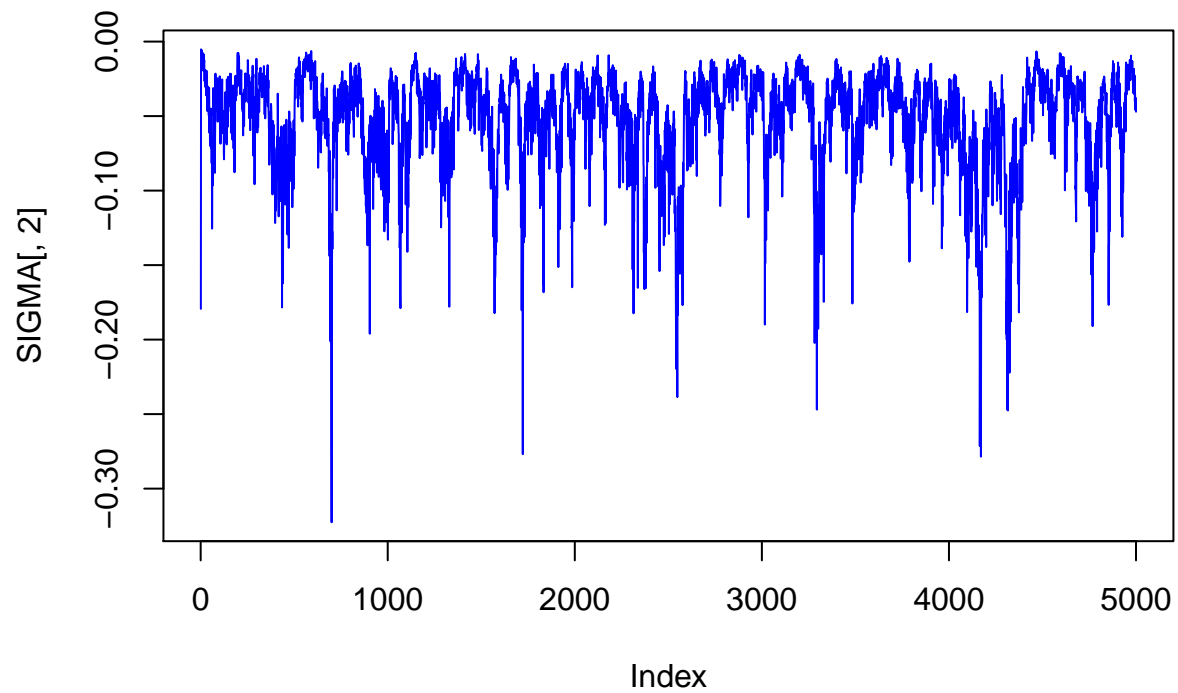


```
effectiveSize(SIGMA[,1])
```

```
##      var1  
## 118.8534
```

```
plot(SIGMA[,2], type = 'l', col = C[2], main = 'Sigma: Covariance')
```

Sigma: Covariance

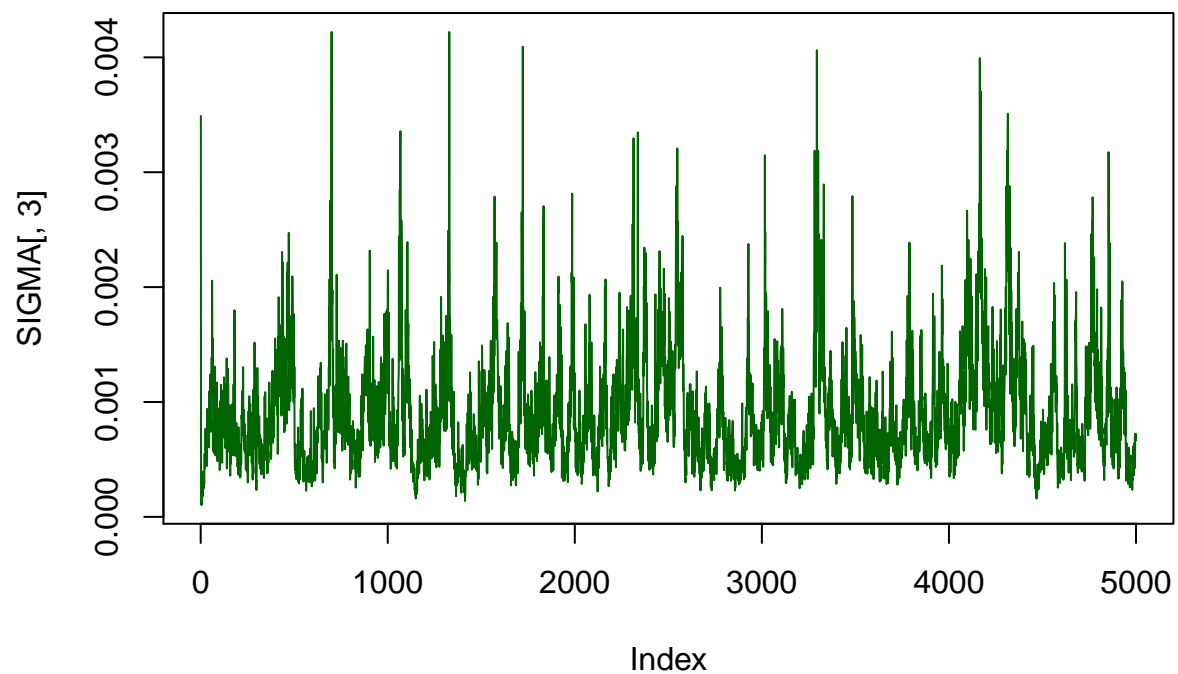


```
effectiveSize(SIGMA[,2])
```

```
##      var1  
## 147.0702
```

```
plot(SIGMA[,3], type = 'l', col = C[3], main = 'Sigma: Slope Variance')
```

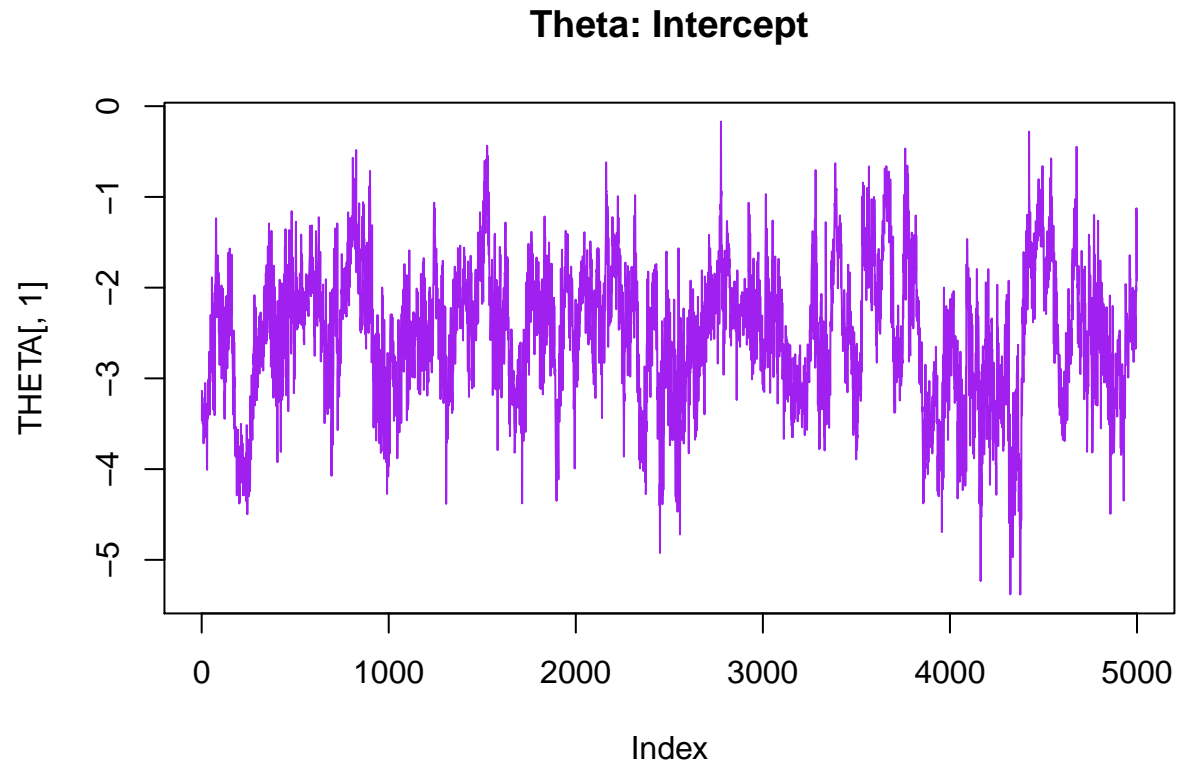
Sigma: Slope Variance



```
effectiveSize(SIGMA[,3])
```

```
##      var1  
## 179.2111
```

```
plot(THETA[,1], type = 'l', col = C[4], main = 'Theta: Intercept')
```

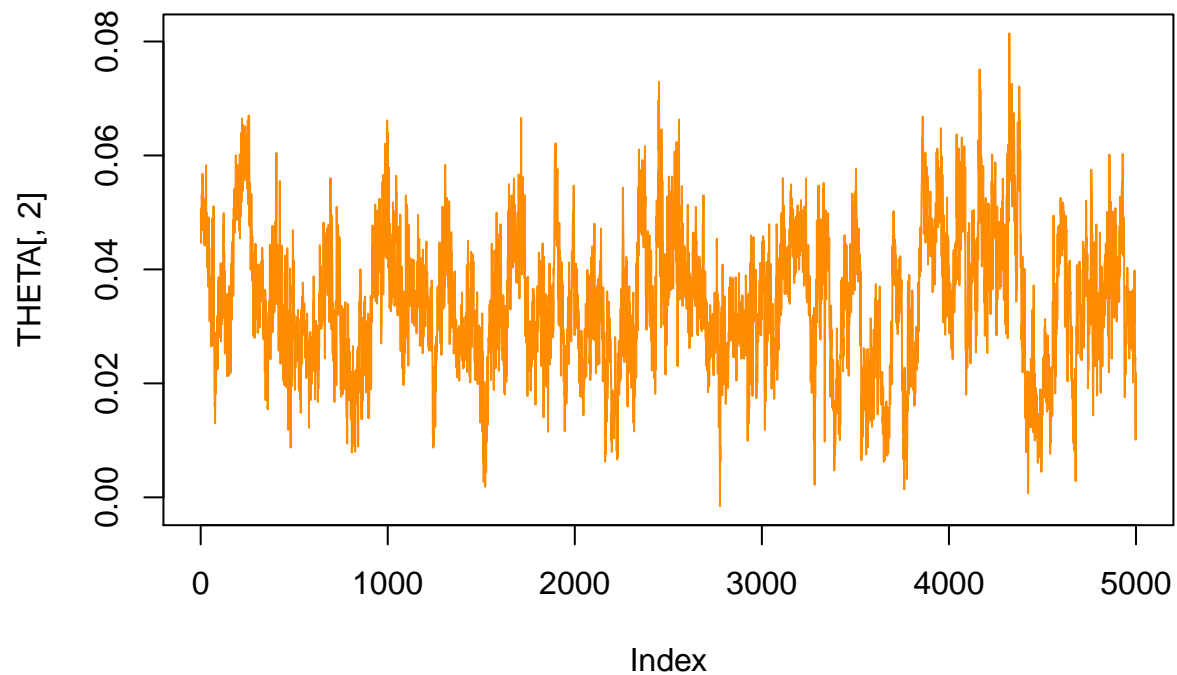


```
effectiveSize(THETA[,1])
```

```
##      var1  
## 78.23242
```

```
plot(THETA[,2], type = 'l', col = C[6], main = 'Theta: Slope')
```

Theta: Slope



```
effectiveSize(THETA[,2])
```

```
##      var1
## 79.27545
```

Part e

Posterior expectation of β

```
postBeta <- matrix(0, nrow = length(counties), ncol = 2)
colnames(postBeta) <- c("Beta_0,j", "Beta_1,j")
colN <- c();
for(j in 1:length(counties)){
  countyB <- BETAS[[j]];
  b0 <- countyB[,1]; b1 <- countyB[,2];
  postBeta[j,1] <- mean(b0); postBeta[j,2] <- mean(b1);
  colN <- c(colN, paste("Beta_", j, sep = " "));
}
rownames(postBeta) <- colN;
postBeta
```

```
##      Beta_0,j  Beta_1,j
## Beta_1 -1.0484037 0.016926857
## Beta_2 -2.9074281 0.038735088
## Beta_3 -3.0102136 0.044392673
## Beta_4 -3.3422520 0.038031387
## Beta_5 -2.3078772 0.027276412
## Beta_6 -2.2636841 0.036215773
```

```
## Beta_7  -1.5791156 0.025518948
## Beta_8  -2.2242517 0.026635791
## Beta_9  -2.7643559 0.028749876
## Beta_10 -2.7874777 0.028414655
## Beta_11 -2.9538822 0.037688558
## Beta_12 -2.4574342 0.028188769
## Beta_13 -2.7425245 0.026750786
## Beta_14 -3.6129112 0.045513634
## Beta_15 -2.5265783 0.039782341
## Beta_16 -1.3100116 0.028870461
## Beta_17 -2.3736204 0.045862134
## Beta_18 -2.3442052 0.038229892
## Beta_19 -2.8292338 0.038602909
## Beta_20 -2.3325947 0.035034805
## Beta_21 -2.8530271 0.029836748
## Beta_22 -3.3942032 0.039658661
## Beta_23 -3.3930415 0.050240687
## Beta_24 -3.0642483 0.039623537
## Beta_25 -3.1601721 0.041968792
## Beta_26 -2.5949183 0.041021131
## Beta_27 -3.6628984 0.046423184
## Beta_28 -1.5925618 0.032224107
## Beta_29 -2.2757931 0.036158095
## Beta_30 -2.6288759 0.030252155
## Beta_31 -2.0230707 0.027712427
## Beta_32 -0.7788214 0.006995258
## Beta_33 -2.3404848 0.037412155
## Beta_34 -2.3391851 0.040412685
## Beta_35 -2.5841489 0.030790579
## Beta_36 -2.5524771 0.023082119
## Beta_37 -2.5256009 0.052572245
## Beta_38 -1.0116718 0.028004027
## Beta_39 -3.4545094 0.029324757
```

Regression Plot Comparisons

In the plots below, the red line represents the value of $\beta_{0,j} + \beta_{1,j}$ from the estimates found in part b, while the blue line represents the posterior estimates of these values. Plotted in black also is my value of $\hat{\theta}$, which was used as the prior mean of each θ . The lines are plotted over the range of 20 to 100, which is the range of values observed in the dataset. Plotted in the titles of each of these plots is an number which represents the number of schools sampled in this county.

```
i=1
while(i < length(counties)){
  par(mfrow = c(1,2))
  top <- min((i+5),length(counties))
  for(j in i:top){
    countyX1 <- 20:100
    plot(countyX1, countyX1*postBeta[j,2]+postBeta[j,1], main = paste(counties[j], "Posterior", BetaEst.
      xlab = 'x = %Teachers with Masters', ylab = 'B0+xB1',
      col = 'blue', type = 'l', ylim = c(-5,5), lwd = 2)
    abline(BetaEstimate[j,1], BetaEstimate[j,2], col = 'red')
```

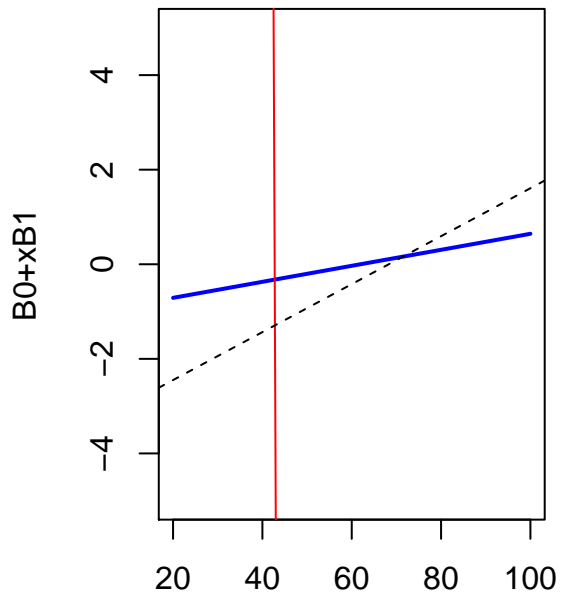


```

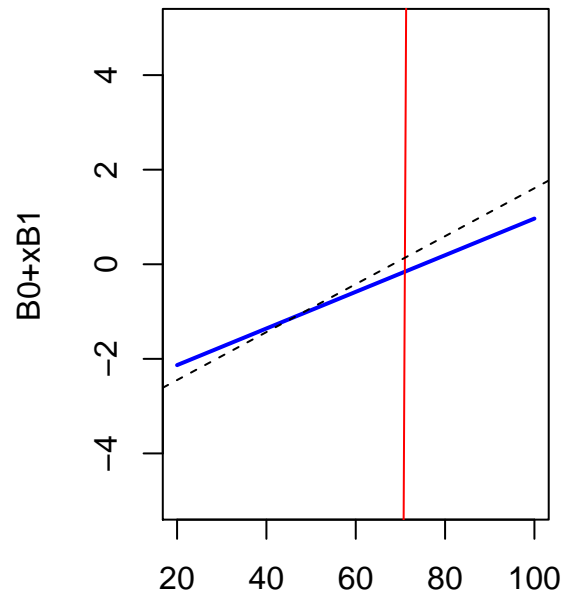
abline(theta.hat[1], theta.hat[2], lty =2)
}
i <- i + 6;
}

```

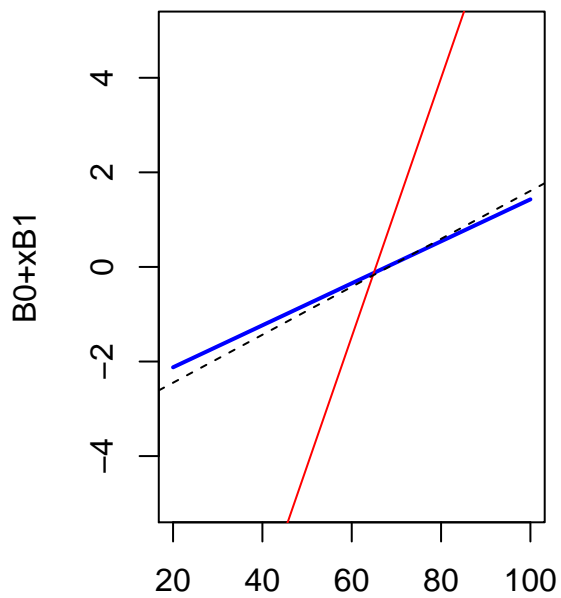
Adams Posterior 3



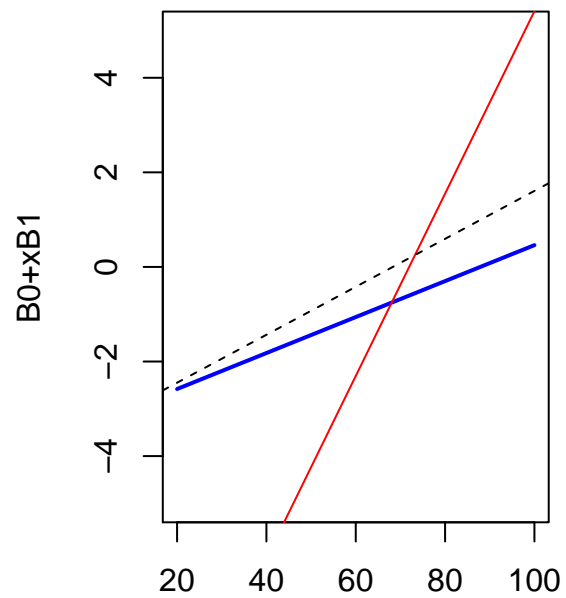
Asotin Posterior 3



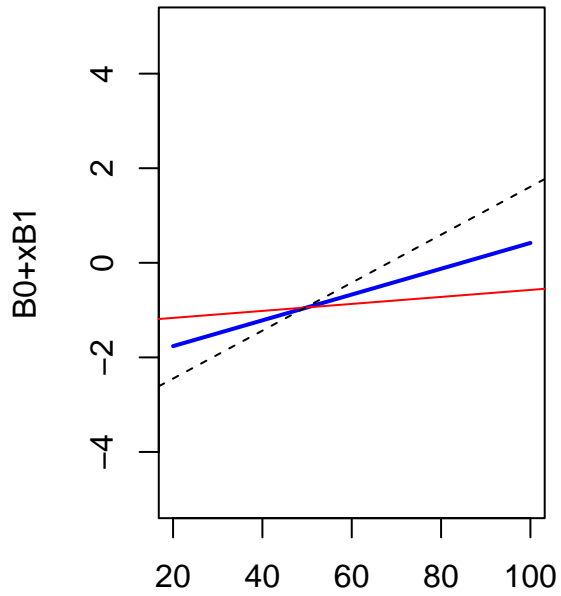
Benton Posterior 8



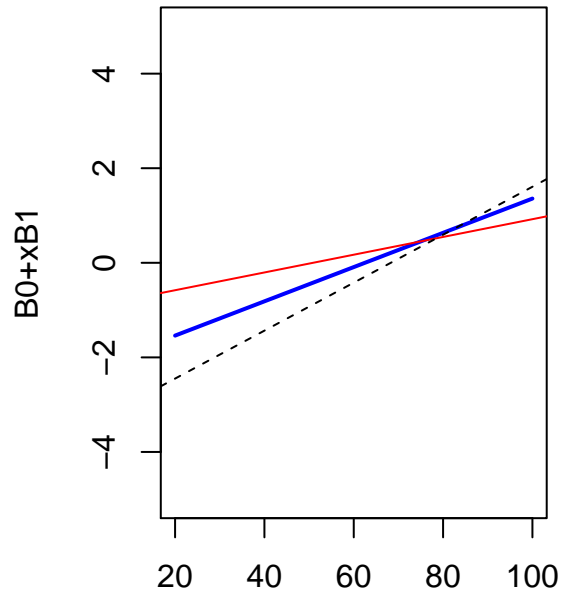
Chelan Posterior 7



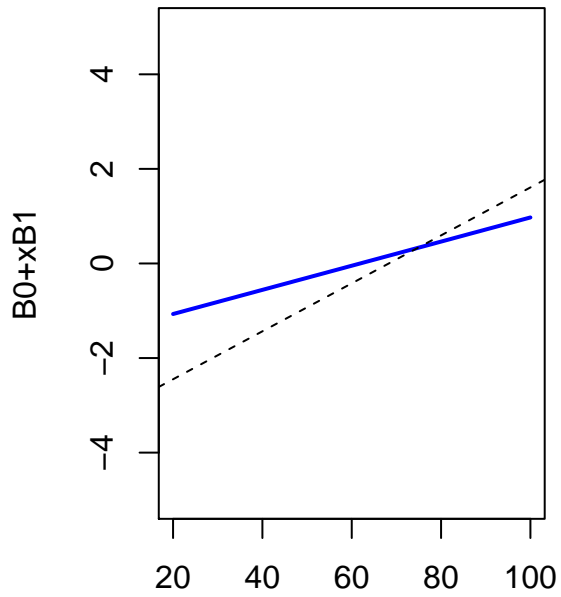
Clallam Posterior 7



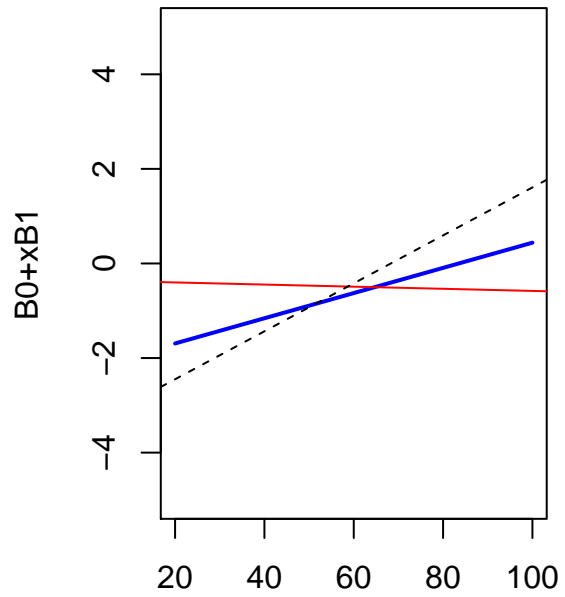
Clark Posterior 19



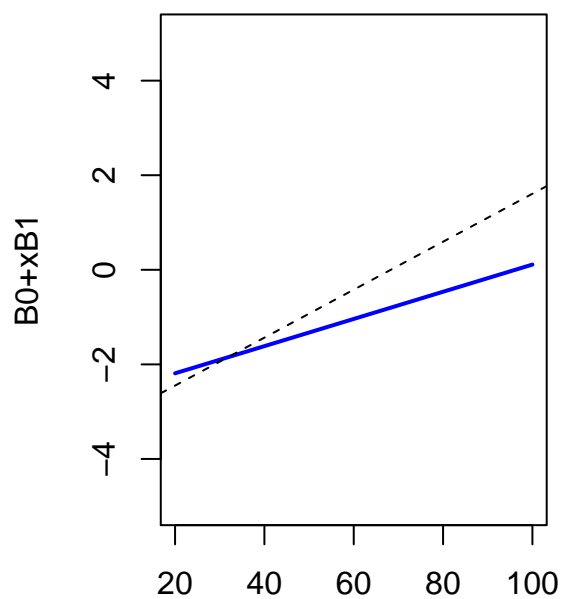
$x = \% \text{Teachers with Masters}$
Columbia Posterior 1



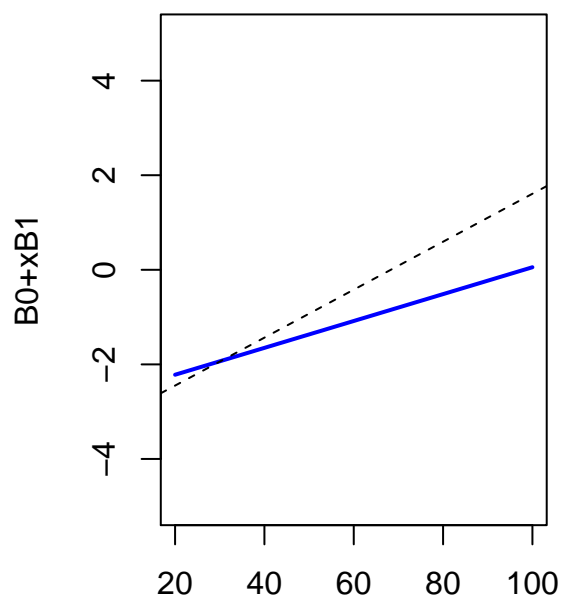
$x = \% \text{Teachers with Masters}$
Cowlitz Posterior 8



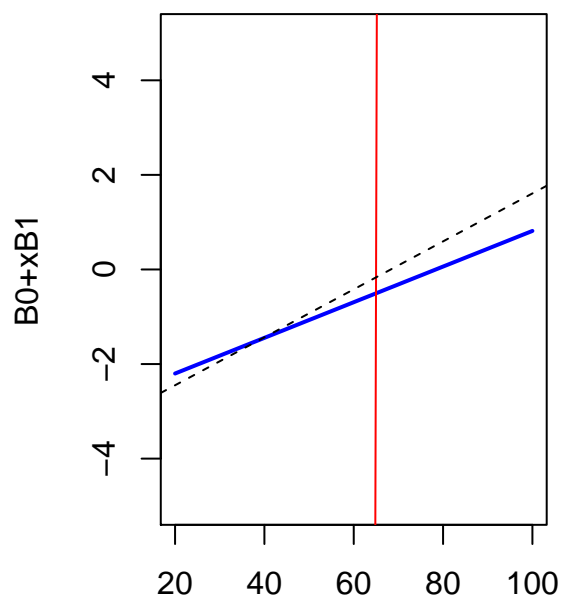
Douglas Posterior 3



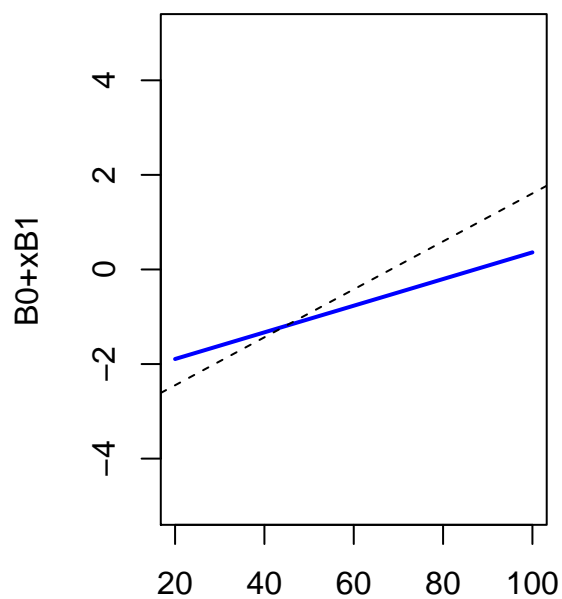
Ferry Posterior 3



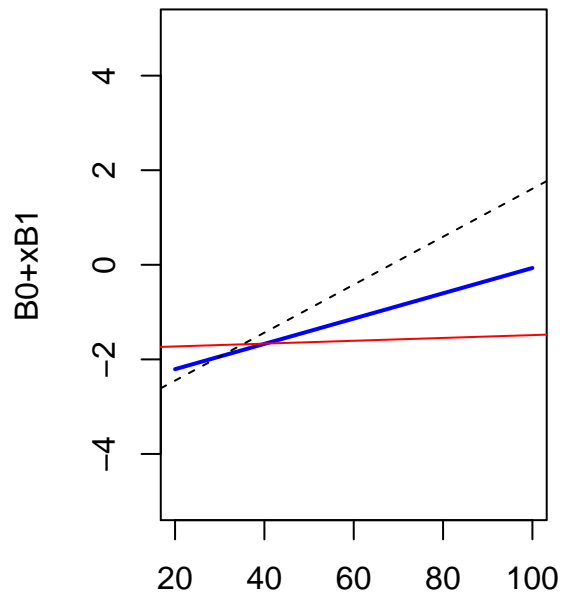
$x = \% \text{Teachers with Masters}$
Franklin Posterior 4



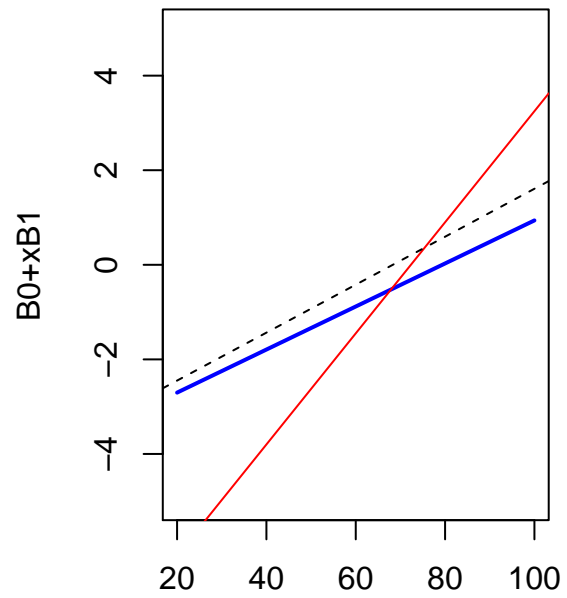
$x = \% \text{Teachers with Masters}$
Garfield Posterior 1



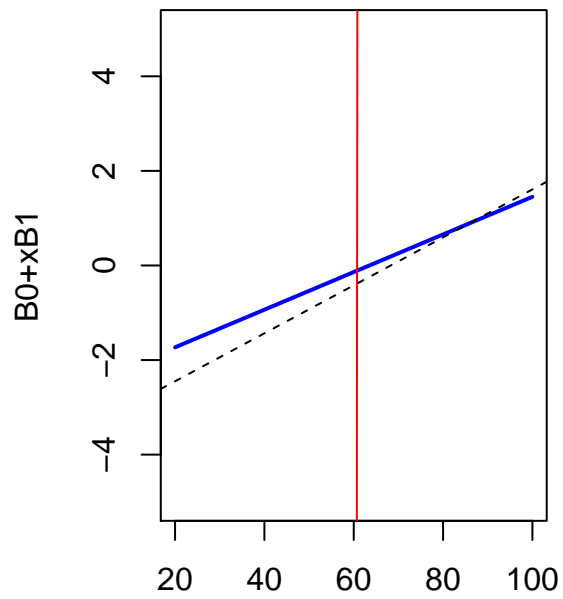
Grant Posterior 12



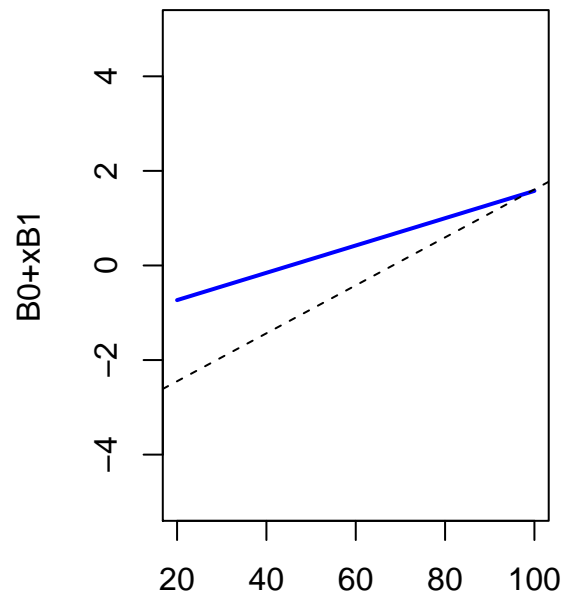
Grays Harbor Posterior 10



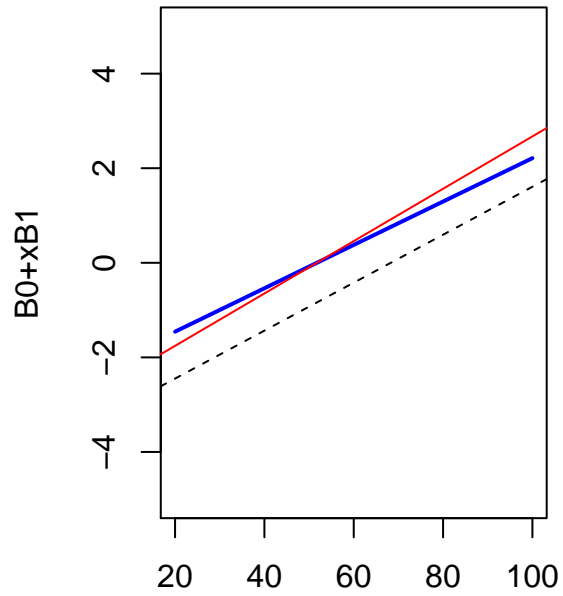
Island Posterior 3



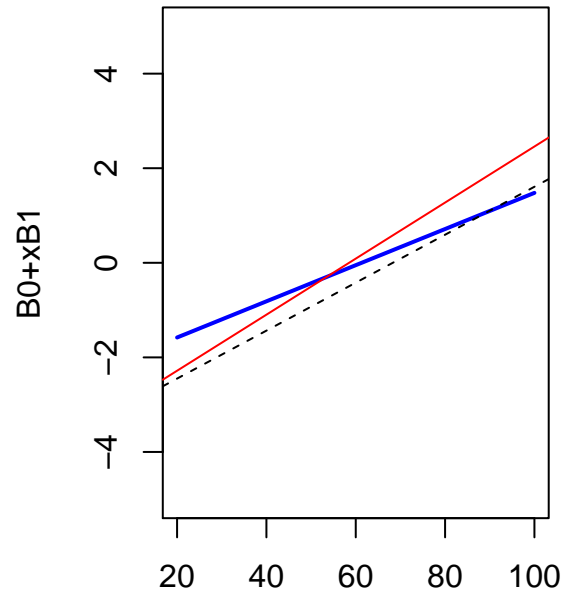
Jefferson Posterior 3



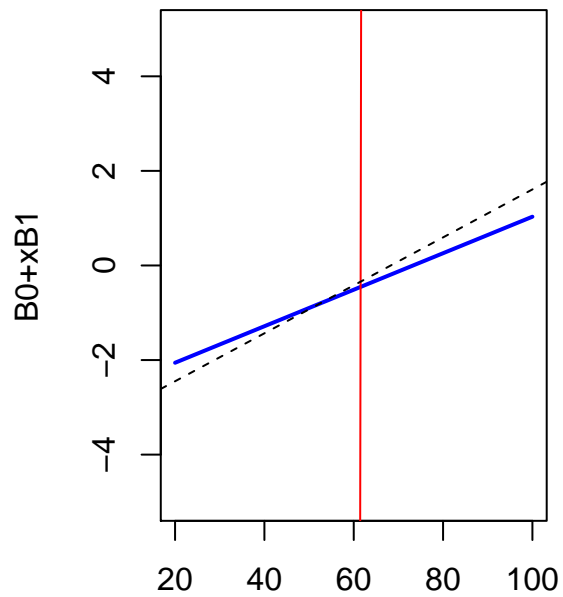
King Posterior 64



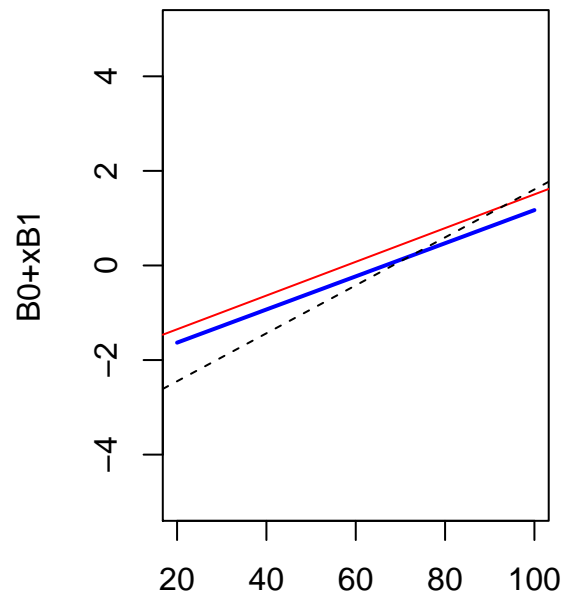
Kitsap Posterior 10



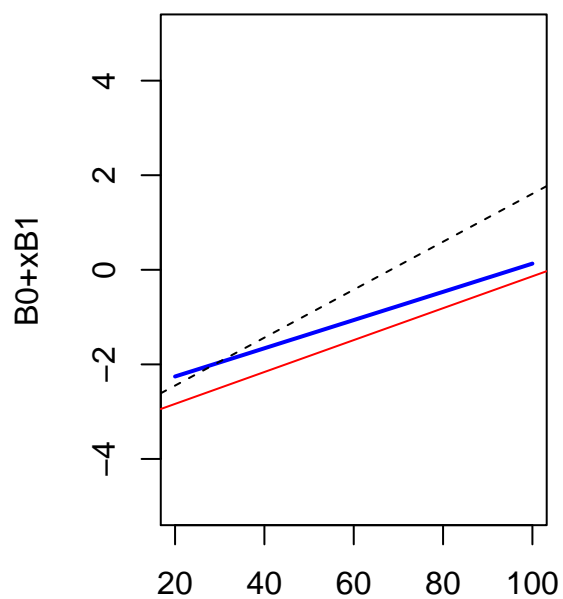
Kittitas Posterior 3



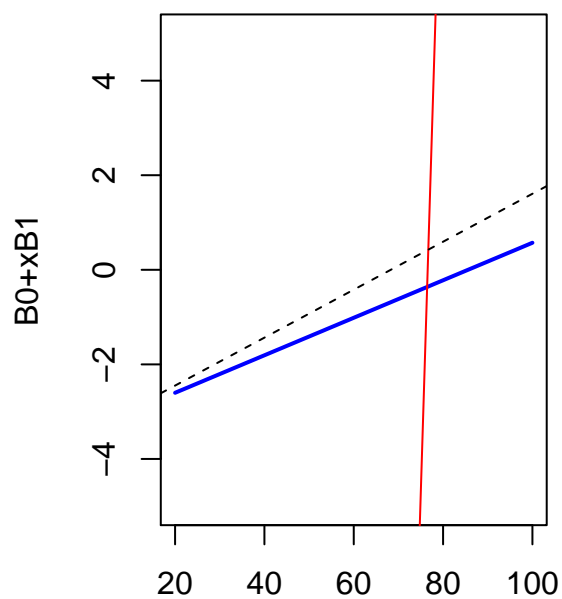
Klickitat Posterior 4



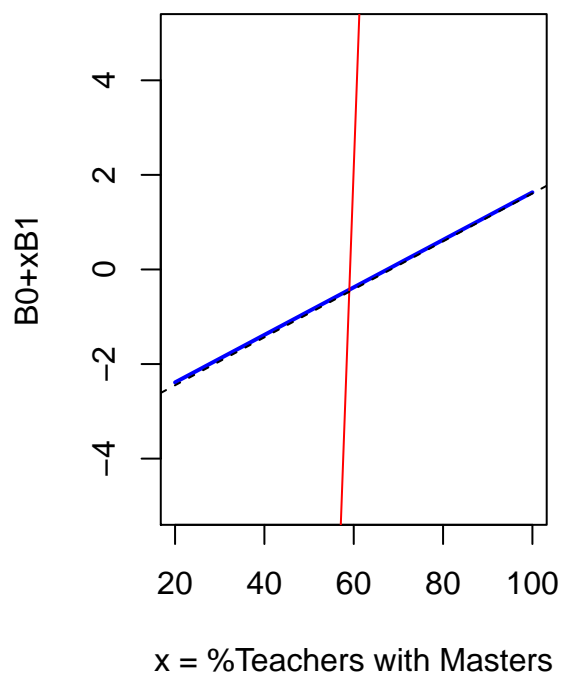
Lewis Posterior 12



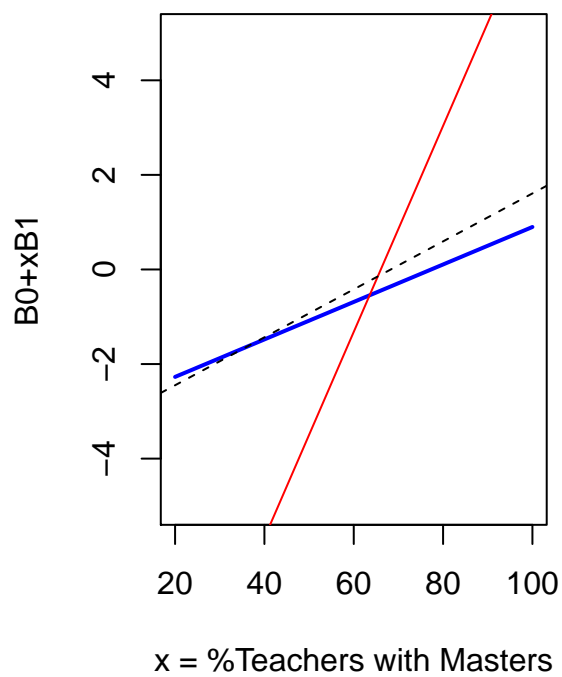
Lincoln Posterior 5



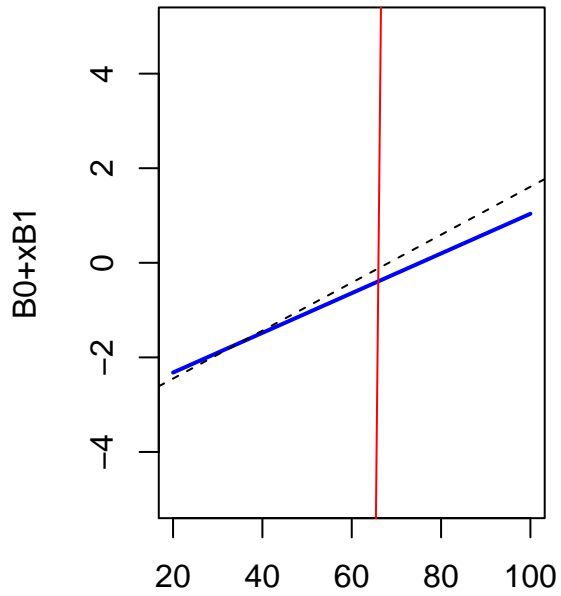
Mason Posterior 5



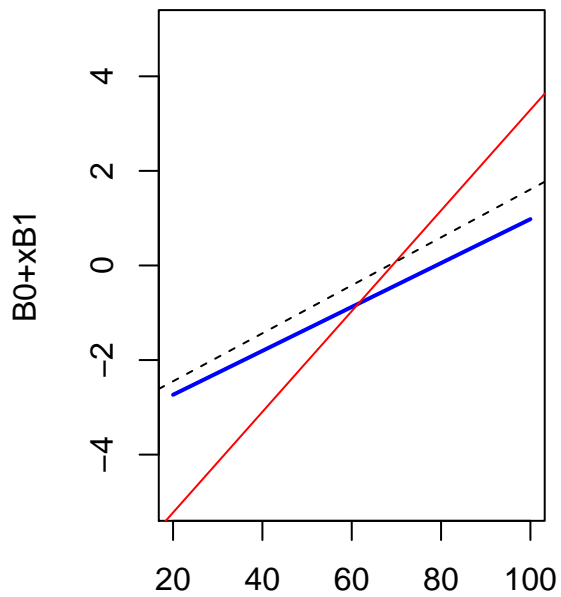
Okanogan Posterior 7



Pacific Posterior 4

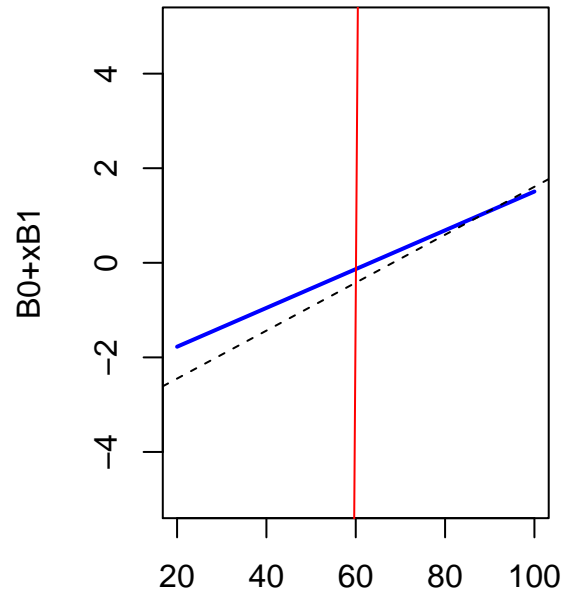


x = %Teachers with Masters
Pierce Posterior 27

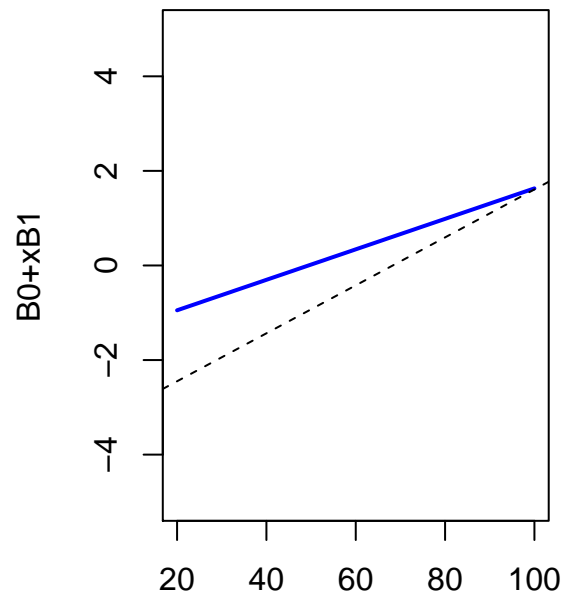


x = %Teachers with Masters

Pend Oreille Posterior 3

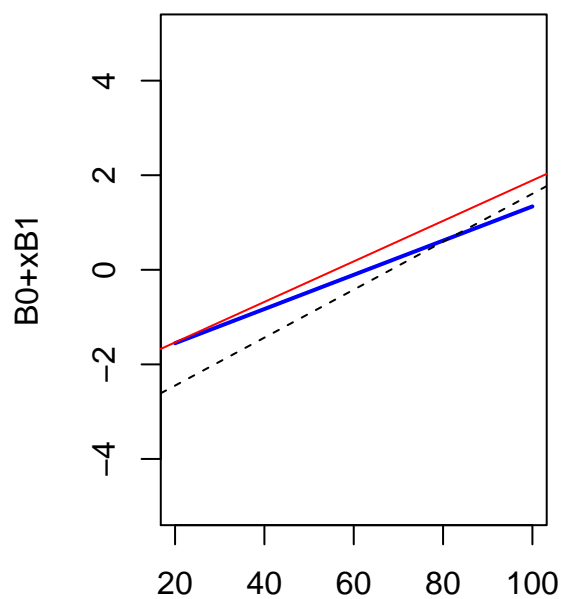


x = %Teachers with Masters
San Juan Posterior 3

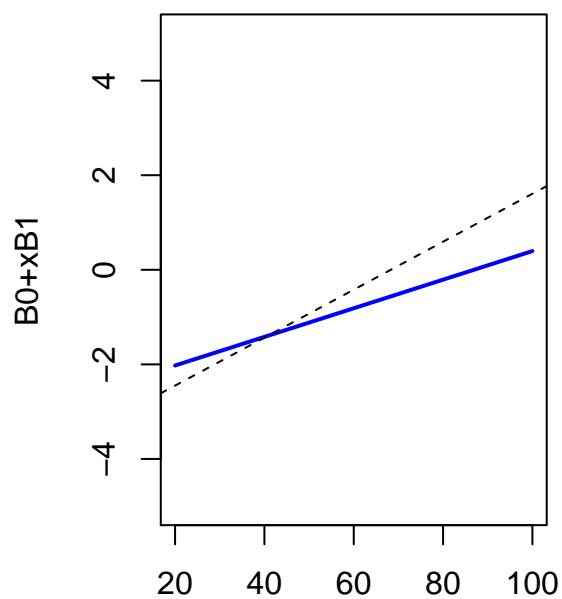


x = %Teachers with Masters

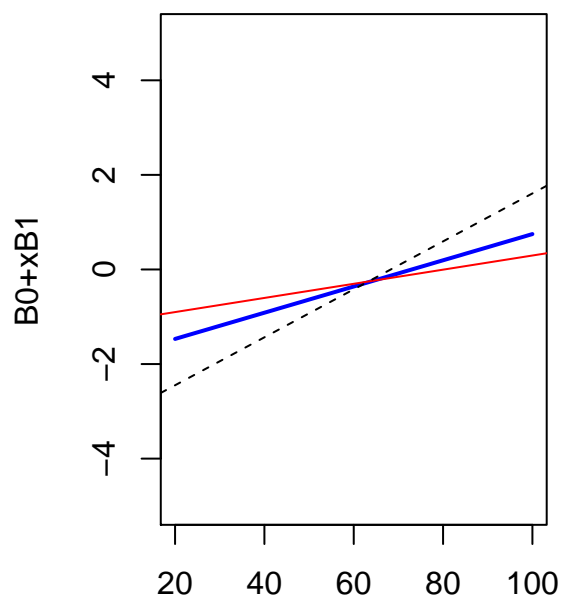
Skagit Posterior 7



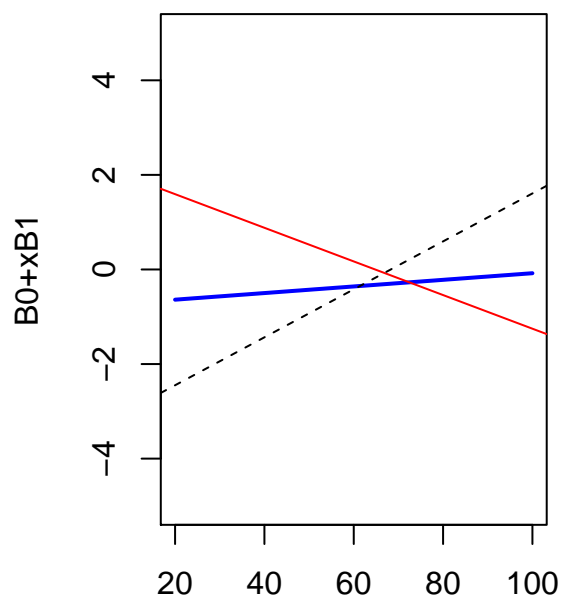
Skamania Posterior 1



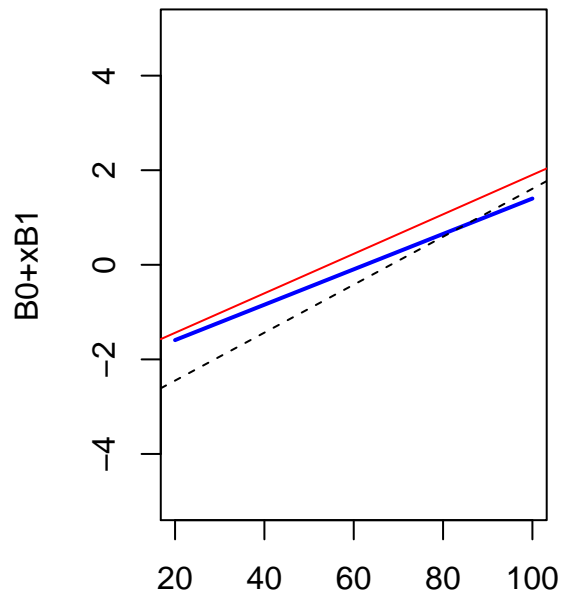
$x = \% \text{Teachers with Masters}$
Snohomish Posterior 30



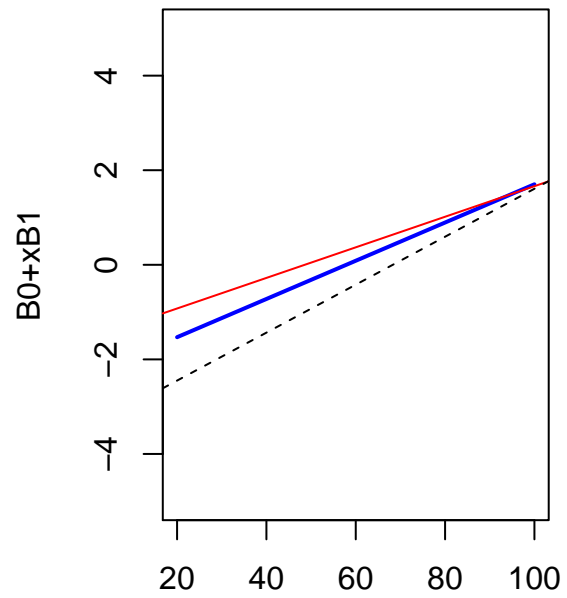
$x = \% \text{Teachers with Masters}$
Spokane Posterior 27



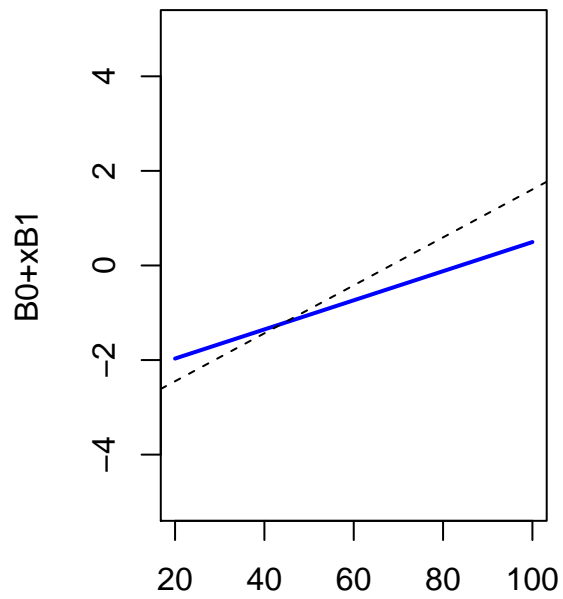
Stevens Posterior 7



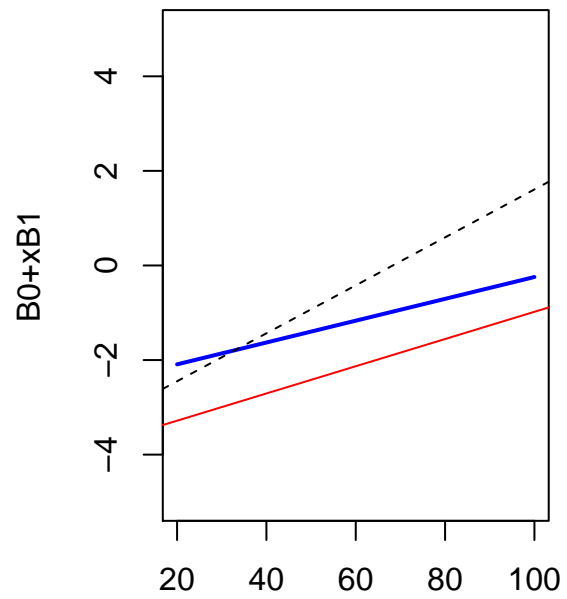
Thurston Posterior 13



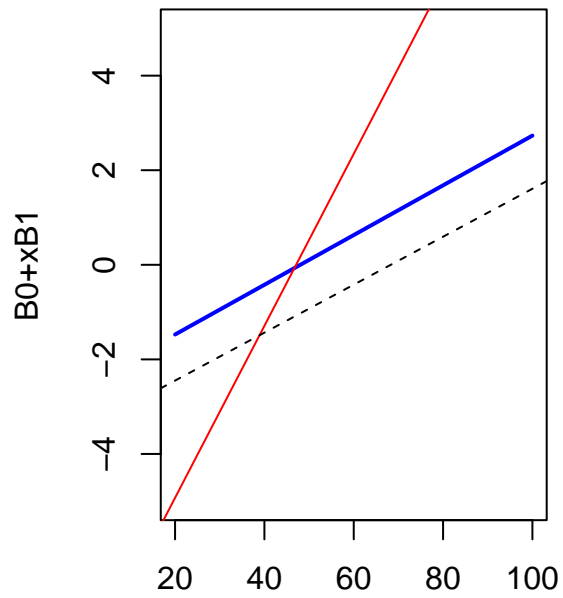
$x = \% \text{Teachers with Masters}$
Wahkiakum Posterior 1



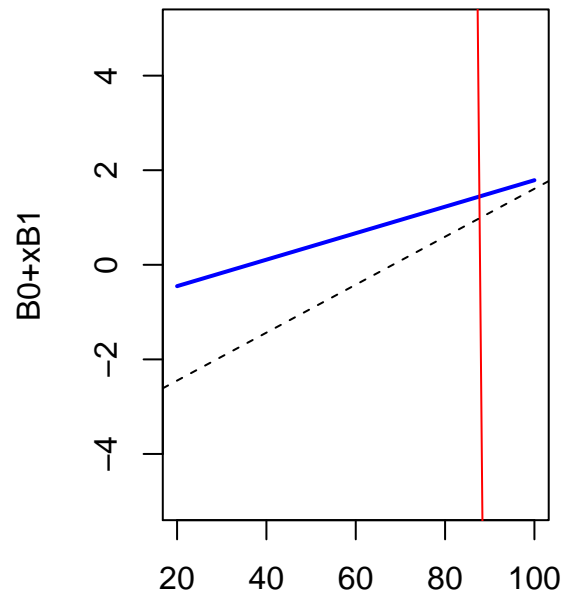
$x = \% \text{Teachers with Masters}$
Walla Walla Posterior 7



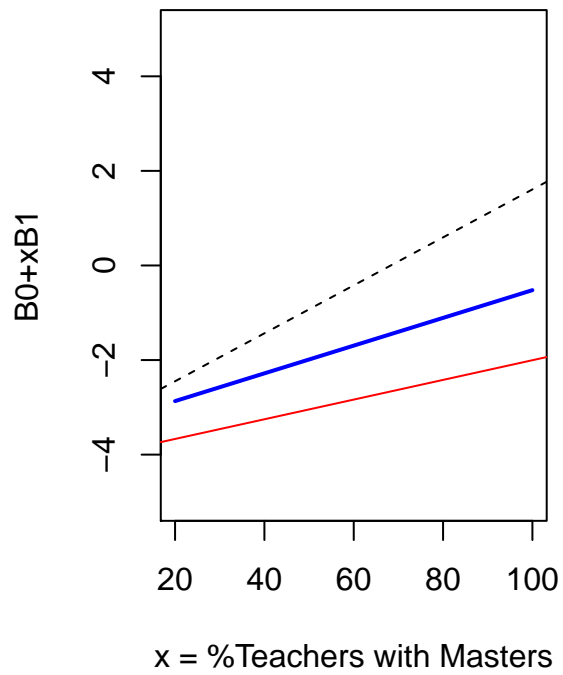
Whatcom Posterior 10



Whitman Posterior 9



Yakima Posterior 20



Comments

In the plots above, some counties have red (old) and blue (new) lines which look quite similar, some have lines that are different but only slightly so, and some have lines which are extremely different (in some cases, the red line is not even visible on the plot. This is due to the extreme intercept values $\beta_{0,j}$ for these estimates). One may notice that for plots with lines which are very different from each other, the sample sizes tend to be quite small, while those with large sample sizes tend to have similar lines. Also note that for values with small sample sizes, the blue lines and the black dashed line tend to look quite similar. This is due to shrinkage.

Part f

Below, the black dashed line represents my ad hoc estimates calculated in part b for these values.

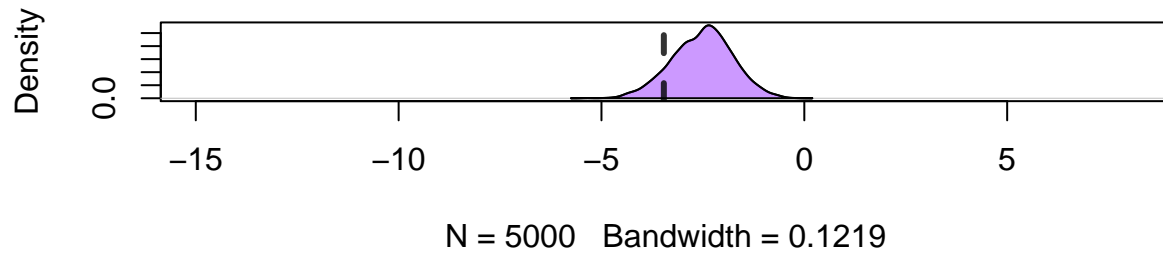
```
library(MCMCpack)

## ##
## ## Markov Chain Monte Carlo Package (MCMCpack)
## ## Copyright (C) 2003-2018 Andrew D. Martin, Kevin M. Quinn, and Jong Hee Park
## ##
## ## Support provided by the U.S. National Science Foundation
## ## (Grants SES-0350646 and SES-0350613)
## ##

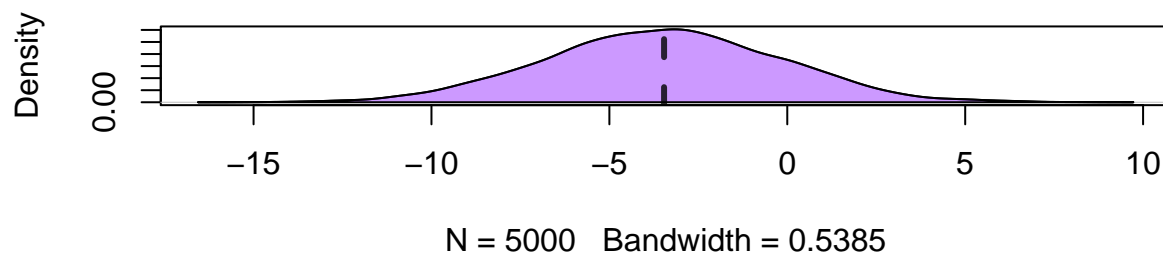
set.seed(10)
priorTheta <- rmvnorm(Samples, theta.hat, Sigma.hat)
priorSigma <- matrix(0, nrow = Samples, ncol = 3);
priorMean <- solve(Sigma.hat);
for(i in 1:Samples){
  priorSigma[i,]<- sigmaToVec(solve(rWishart(1, 4, priorMean)[,1]));
}

for(i in 1:2){
  par(mfrow = c(2,1))
  plot(density(THETA[,i]), main = paste('Posterior Theta', i-1),
       xlim =c(min(priorTheta[,i]),max(priorTheta[,i])))
  polygon(density(THETA[,i]), col=rgb(.5*i,0,1,.4), border="black")
  abline(v=theta.hat[i], lwd = 3, col = rgb(0,0,0,.8), lty = 2)
  plot(density(priorTheta[,i]), main = paste('Prior Theta', i-1))
  polygon(density(priorTheta[,i]), col=rgb(.5*i,0,1,.4), border="black")
  abline(v=theta.hat[i], lwd = 3, col = rgb(0,0,0,.8), lty = 2)
}
```

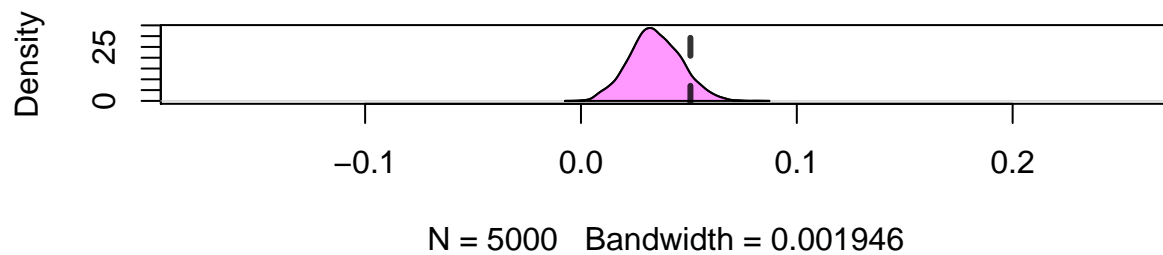
Posterior Theta 0



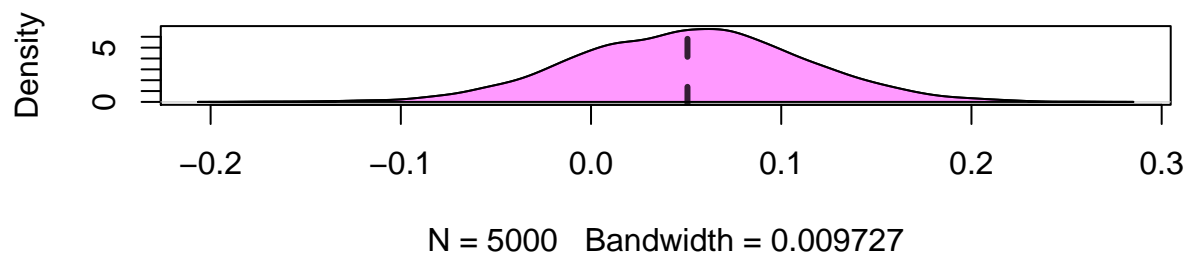
Prior Theta 0



Posterior Theta 1



Prior Theta 1



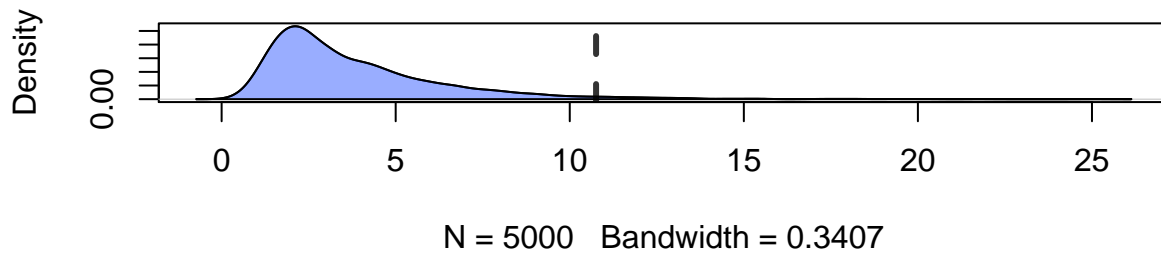
```
a1 <- quantile(priorSigma[,1], c(.05, .95))
a2 <- quantile(priorSigma[,2], c(.05, .95))
a3 <- quantile(priorSigma[,3], c(.05, .95))
par(mfrow = c(2,1))
plot(density(SIGMA[,1]), main = paste('Posterior Intercept Var'))
```

```

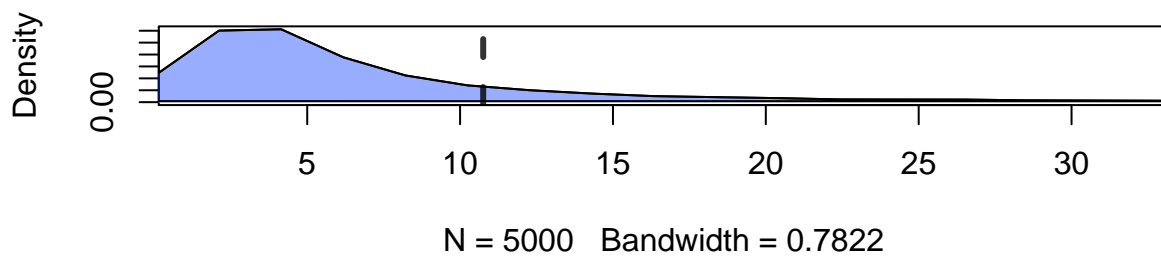
polygon(density(SIGMA[,1]), col=rgb(0,.2,1,.4), border="black")
abline(v=Sigma.hat[1,1], lwd = 3, col = rgb(0,0,0,.8), lty = 2)
plot(density(priorSigma[,1]), main = paste('Prior Intercept Var'),
     xlim=c(a1[1], a1[2]))
polygon(density(priorSigma[,1]), col=rgb(0,.2,1,.4), border="black")
abline(v=Sigma.hat[1,1], lwd = 3, col = rgb(0,0,0,.8), lty = 2)

```

Posterior Intercept Var



Prior Intercept Var

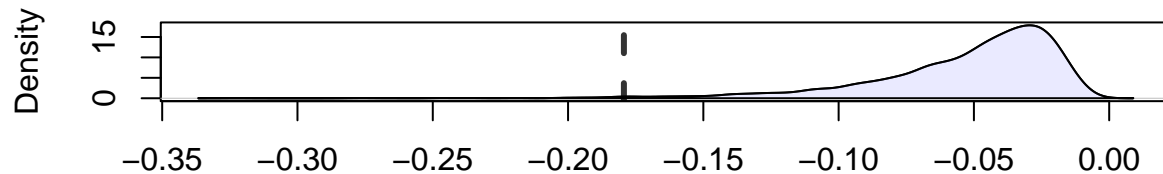


```

par(mfrow = c(2,1))
plot(density(SIGMA[,2]), main = paste('Posterior Covariance'))
polygon(density(SIGMA[,2]), col=rgb(.8,.8,1,.4), border="black")
abline(v=Sigma.hat[1,2], lwd = 3, col = rgb(0,0,0,.8), lty = 2)
plot(density(priorSigma[,2]), main = paste('Prior Covariance'),
     xlim=c(a2[1], a2[2]))
polygon(density(priorSigma[,2]), col=rgb(.8,.8,1,.4), border="black")
abline(v=Sigma.hat[1,2], lwd = 3, col = rgb(0,0,0,.8), lty = 2)

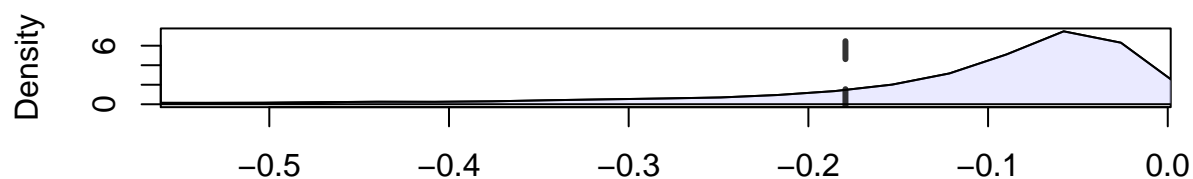
```

Posterior Covariance



N = 5000 Bandwidth = 0.004706

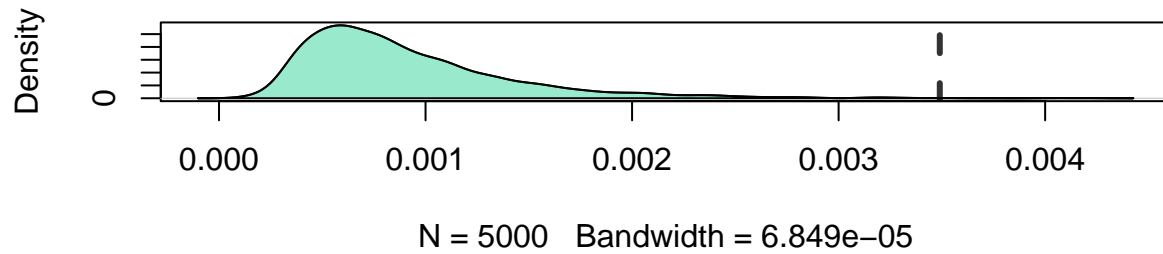
Prior Covariance



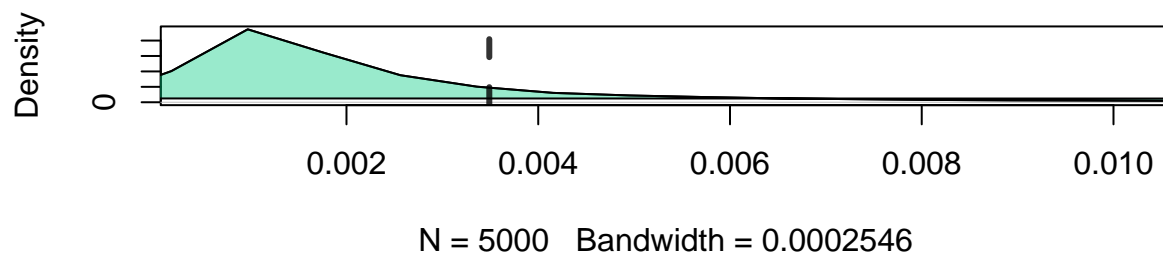
N = 5000 Bandwidth = 0.01321

```
par(mfrow = c(2,1))
plot(density(SIGMA[,3]), main = paste('Posterior Slope Var'))
polygon(density(SIGMA[,3]), col=rgb(0,.8,.5,.4), border="black")
abline(v=Sigma.hat[2,2], lwd = 3, col = rgb(0,0,0,.8), lty = 2)
plot(density(priorSigma[,3]), main = paste('Prior Slope Var'),
      xlim=c(a3[1], a3[2]))
polygon(density(priorSigma[,3]), col=rgb(0,.8,.5,.4), border="black")
abline(v=Sigma.hat[2,2], lwd = 3, col = rgb(0,0,0,.8), lty = 2)
```

Posterior Slope Var



Prior Slope Var



Given the size of the spread of my variences of my Σ values, I conclude that there is reasonable evidence to believe that there are differences between the slopes and intercepts across groups.