#1

a) According to piss of the textbook, 
$$\beta = (x^{T}x)^{-1}x^{T}y$$

$$VE\beta_{0}[\beta,\sigma'] = VE(x^{T}x)^{-1}x^{T}y]$$

$$= (x^{T}x)^{-1}x^{T}VEY] \times (x^{T}x)^{-1}$$

$$=\frac{(\chi_1\chi_1)}{2} Q_1 \sum_{i=1}^{n} \chi_{i,i}$$

$$=\frac{(\chi_1\chi_1)}{2} \chi_{i,i} \chi_{i,i} \chi_{i,i}$$

$$=\frac{\sigma^{2}}{\left(\sum_{i=1}^{n}\chi_{i}^{2}\right)^{2}}\cdot\sum_{i=1}^{n}\frac{\chi_{i}^{2}}{w_{i}^{2}}$$

In to: 
$$\frac{dL}{dp} = 0$$
  $\Rightarrow \frac{\sum_{i=1}^{n} w_i x_i y_i - \sum_{i=1}^{n} w_i x_i \beta_{x_i} = 0}{\sum_{i=1}^{n} w_i x_i y_i}$ 

VE 
$$\beta_{n}[\beta,\sigma^{2}] = \left(\frac{1}{\sum_{i=1}^{N} w_{i}x_{i}}\right)^{2} V\left[\sum_{j=1}^{N} w_{j}x_{j}y_{j}\right]$$

$$= \left(\frac{1}{\sum_{i=1}^{N} w_{i}x_{i}}\right)^{2} \sum_{i=1}^{N} w_{i}x_{i}^{2} V\left[y_{j}\right]$$

$$= \frac{1}{\sum_{i=1}^{N} w_{i}x_{i}^{2}} \sum_{i=1}^{N} w_{i}^{2}x_{i}^{2} V\left[y_{j}\right]$$

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$$= \frac{1}{\sum_{i=1}^{N} w_{i}^{2}} \sum_{i=1}^{N} w_{i}x_{i}^{2} V\left[y_{j}\right] \sum_{i=1}^{N} w_{i}$$

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() 
$$P(\beta | y, ... y_{n}, \sigma^{i}) = P(y, ... y_{n} | P, \sigma^{i}) \cdot P(\beta | \sigma^{i}) / P(y, ... y_{n})$$

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$$= \exp \left\{ -\frac{1}{2} \left( \frac{\sum_{i=1}^{n} v_{i}(y_{i})}{\sigma^{i}} + \frac{1}{\sigma^{i}} \right) - P(\beta | \sigma^{i}) \right\}$$

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$$= \frac{\sum_{i=1}^{n} v_{i}(y_{i$$

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# 1

a) 
$$P(P|Y,\sigma') \propto P(P,Y,\sigma')$$

=  $P(Y,P|\sigma')P(\sigma')$ 
 $\varphi = P(Y,P|\sigma')P(\sigma')$ 
 $\varphi =$ 

$$\begin{array}{lll}
\rho_{0}e & 5 \\
b) & \chi^{7}\chi = \begin{bmatrix} \chi_{1}^{7}\chi_{1} & 0 \\ 0 & \chi_{p}^{7}\chi_{p} \end{bmatrix}, \quad \hat{\rho}_{0} = (\chi^{7}\chi)^{-1} \chi^{7}\chi, \quad \hat{\rho}_{0} = (\chi^{1}\chi^{1})^{-1} \chi^{1}\chi^{1}y \\
\chi^{7}\chi + 1\chi = \begin{bmatrix} \chi_{1}^{7}\chi_{1} + \lambda & 0 \\ 0 & \chi_{p}^{7}\chi_{p} + \lambda \end{bmatrix}, \quad \hat{\beta}_{\chi} = (\chi^{1}\chi^{1}+1\chi)^{-1}\chi^{1}\chi, \quad \hat{\beta}_{\chi} = (\chi^{1}\chi^{1}+1\chi)^{-1}\chi^{1}\chi^{1}y \\
& \frac{\hat{\beta}_{\lambda_{1}}}{\hat{\beta}_{0_{1}}} = \frac{(\chi^{1}\chi^{1}+1\chi)^{-1}\chi^{1}\chi^{1}y}{(\chi^{1}\chi^{1})^{-1}\chi^{1}\chi^{1}y} = \frac{\chi_{1}^{7}\chi_{1} + \lambda}{\chi_{1}^{7}\chi_{1}} \\
& \hat{\beta}_{\lambda_{1}} = \frac{\chi_{1}^{7}\chi_{1} + \lambda}{\chi_{1}^{7}\chi_{1}} \quad \hat{\beta}_{0_{1}} \\
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Efter at 
$$\chi$$
: As  $\chi \to 0$ ,  $\beta_{\chi_i} = \beta_0$ , thus two regresses are similar.

As  $\chi \to \infty$ ,  $\beta_{\chi_i} = \frac{\chi_i \tau_y}{\chi_i \tau_{\chi_i} + \infty} = 0$ , the regresser gives on as coefficients for  $\chi_i$ .

Meaning  $V[\beta]$  is very small and  $\tau_i$ 0

# STA360 Homework 8 (Ken Ye)

```
library(latex2exp)
library(ggplot2)
library(MASS)
library(ggrepel)
library(mvtnorm)
set.seed(0)
```

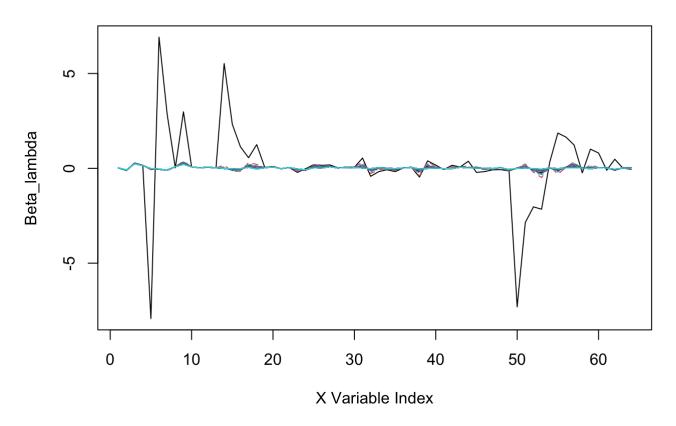
## **Question 3**

```
# load diabetes data
yX <- dget(url("https://www2.stat.duke.edu/~pdh10/FCBS/Inline/yX.diabetes.train"))
y <- yX[,1]
X <- yX[,-1]</pre>
```

#### Part a

```
# compute beta_lambda hat for each lambda in {0, ..., 100}
lambdas <- seq(0, 100, by = 1)
beta_lambdas <- matrix(0, nrow = 64, ncol = 101)
for (lam in lambdas){
   beta_lambda <- solve(t(X) %*% X + lam * diag(rep(1, 64))) %*% t(X) %*% y
   beta_lambdas[,lam+1] <- beta_lambda
}</pre>
```

#### Beta\_lambda vs X Under Different Lambdas



There are 101 lines representing 101 beta\_lambda vectors (each 64 by 1) and their respective value for each X variable. It's hard to discern a single beta\_lambda vector in the graph because there are so many of them, but this graph shows the beta\_lambda estimate for each lambda in {0, 1, ..., 99, 100}, and for each beta\_lambda, how its beta\_lambda\_i varies for each X\_i, for i from 1 to 64 (there are 64 x variables in total).

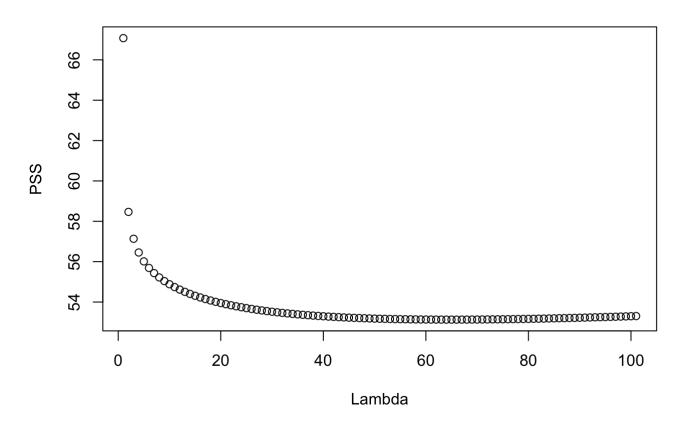
#### Part b

```
# load diabetes data, test set
yX.test <- dget(url("https://www2.stat.duke.edu/~pdh10/FCBS/Inline/yX.diabetes.test"))
y.test <- yX.test[,1]
X.test <- yX.test[,-1]</pre>
```

```
# calculate predictive error sum of squares
PSS <- rep(0,101)
for (i in 1:101){
   PSS[i] <- sum((y.test - (X.test %*% beta_lambdas[,i]))^2)
}</pre>
```

```
# plot
plot(PSS,
    main = 'Predictive Error Sum of Squares For Each Lambda',
    ylab = 'PSS',
    xlab = 'Lambda')
```

#### **Predictive Error Sum of Squares For Each Lambda**



 $\ensuremath{\textit{\# OLS}}$  estimate predictive error sum of squares  $\ensuremath{\mathsf{PSS[1]}}$ 

## [1] 67.07489

We know that beta\_OLS = beta\_lambda when lambda = 0. The unbiased OLS estimate for prediction has a predictive error sum of squares of 67.07, which is the highest among all beta estimates (which can be told from the graph). Beta\_OLS doesn't perform well.

### Part c

```
# identify the value of lambda that has the best predictive performance
index <- which.min(PSS)
# this is the index, the value of lambda = index - 1 since lambda starts from 0
index</pre>
```

## [1] 65

The value of lambda that has the best predictive performance is lambda = 64.

```
# find x-variables that have the largest effects
beta_lambda.best <- array(beta_lambdas[,65])
names(beta_lambda.best) <- colnames(X.test)
sort(beta_lambda.best, decreasing = TRUE)</pre>
```

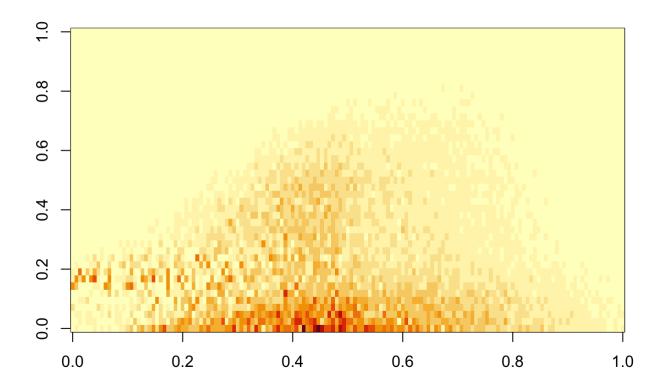
,,,		<u>.</u> .		<u>.</u> .		_
##	bmi	ltg	map	, ,		glu
##	0.252909731	0.228397916	0.147254764	0.087941087	0.087934685	0.077338474
##	age:sex	bmi^2	tch^2	bmi:glu	bmi:map	sex:hdl
##	0.076324787	0.071152071	0.058732597	0.058276976	0.049170486	0.043500542
##	sex:bmi	sex:map	age:map	ldl:ltg	map:ltg	hdl:ltg
##	0.043490113	0.041124402	0.040800031	0.038342222	0.035184329	0.034370233
##	age:hdl	glu^2	age^2	ldl:tch	map^2	tc:hdl
##	0.033915390	0.031990446	0.028071754	0.026620010	0.024993749	0.024568090
##	map:ldl	sex:glu	ldl:glu	age	map:tc	hdl:glu
##	0.023869197	0.022266772	0.022153006	0.021963242	0.021280595	0.019970286
##	bmi:hdl	sex:tc	ltg:glu	age:tch	tc:glu	age:glu
##	0.018778877	0.018338931	0.017996024	0.017610083	0.017397253	0.016284681
##	tch:glu	map:hdl	sex:tch	tc:ldl	bmi:ldl	tc^2
##	0.014990058	0.009804745	0.009214922	-0.001376226	-0.003008950	-0.007634208
##	map:tch	bmi:ltg	bmi:tch	sex:ltg	age:bmi	ldl:hdl
##	-0.011186191	-0.011266451	-0.014018574	-0.014901732	-0.015406394	-0.016465109
##	tc	sex:ldl	hdl^2	ld1^2	hdl:tch	tc:tch
##	-0.017435685	-0.017546233	-0.018174450	-0.024323567	-0.025176356	-0.025552851
##	age:tc	ltg^2	bmi:tc	ldl	tc:ltg	tch:ltg
##	-0.031782045	-0.034849965	-0.035749440	-0.040005158	-0.047686902	-0.052317906
##	map:glu	age:ldl	sex	hdl		
##	-0.073321473	-0.080450910	-0.091657677	-0.109873439		

The x-variables that have the largest effects (top 5) are bmi, ltg, map, age:ltg, and tch. The rest are printed above in decreasing effect order.

# **Question 4**

```
# load water data
yX <- readRDS("yXSS.rds")
y <- yX[,1]
X <- yX[,-1]</pre>
```

```
# view image
y <- yX[,1]
image(matrix(y,151,43))</pre>
```



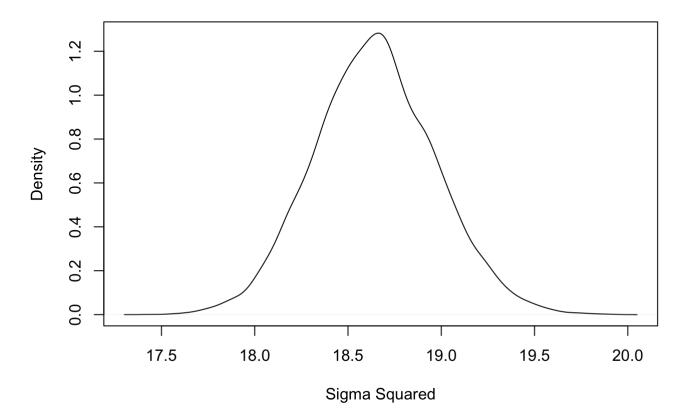
#### Part a

```
# obtain posterior distribution of beta and sigma2 given y with MCMC
n <- dim(X)[1]
p <- dim(X)[2]
# priors
nu.0 < -1
beta.0 <- rep(1/9, p)
sigma.0 <- matrix(0, p, p)
diag(sigma.0) <- 1 # sigma.0 = I 9
sigma2.0 <- diag(p)
sample.size <- 10000
BETA <- matrix(nrow = sample.size, ncol = p) # posterior storage
SIGMA2 <- rep(NA, sample.size) # posterior storage</pre>
# common quantities
X <- as.matrix(X)</pre>
y <- as.matrix(y)</pre>
isigma.0 <- solve(sigma.0)</pre>
XtX <- t(X) %*% X
Xty < - t(X) % % y
# start values
sigma2 <- var(residuals(lm(y ~ 0 + X)))
# Gibbs sampling
for (s in 1 : sample.size) {
  # update beta
  beta.V <- solve(isigma.0 + XtX / sigma2)</pre>
  beta.E <- beta.V %*% (isigma.0 %*% beta.0 + Xty / sigma2)
  beta <- mvrnorm(1, beta.E, beta.V)</pre>
  # update sigma2
  nu.n <- nu.0 + n
  ss.n <- nu.0 * sigma2.0 + sum((y - X %*% beta)^2)
  sigma2 <- 1/rgamma(1, nu.n / 2, ss.n / 2)
```

```
# store sample
BETA[s,] <- beta
SIGMA2[s] <- sigma2
}</pre>
```

```
# posterior distribution of sigma2
plot(density(SIGMA2),
    main = 'Posterior Distribution of Sigma Squared',
    xlab = 'Sigma Squared')
```

## Posterior Distribution of Sigma Squared



```
# 95% confidence intervals for each element of beta
CI <- NULL
for (i in 1: dim(BETA)[2]){
  print(paste('The 95% CI for Beta', i, "is: "))
  print(quantile(BETA[,i], c(0.0025, 0.975)))
  CI <- c(CI, quantile(BETA[,i], c(0.0025, 0.975)))
}</pre>
```

```
## [1] "The 95% CI for Beta 1 is: "
       0.25%
                 97.5%
##
## 0.3794342 0.6672999
## [1] "The 95% CI for Beta 2 is: "
##
         0.25%
                     97.5%
## -0.07597283 0.02150432
## [1] "The 95% CI for Beta 3 is: "
##
         0.25%
                     97.5%
## -0.02184565 0.01643633
## [1] "The 95% CI for Beta 4 is: "
         0.25%
##
                     97.5%
## -0.01622588 0.09902869
## [1] "The 95% CI for Beta 5 is: "
##
           0.25%
                         97.5%
## -0.0315009542 0.0009156621
## [1] "The 95% CI for Beta 6 is: "
       0.25%
                 97.5%
##
## 0.1707828 0.3449928
## [1] "The 95% CI for Beta 7 is: "
##
        0.25%
                   97.5%
## 0.09072786 0.20750827
## [1] "The 95% CI for Beta 8 is: "
         0.25%
##
                     97.5%
## 0.002263687 0.006809795
## [1] "The 95% CI for Beta 9 is: "
##
         0.25%
                     97.5%
## -0.30283697 0.06189633
```

Effluent, soil, street (weak, very small coefficient), and swine are the main sources of the water sample as their 95% CI do not contain 0.

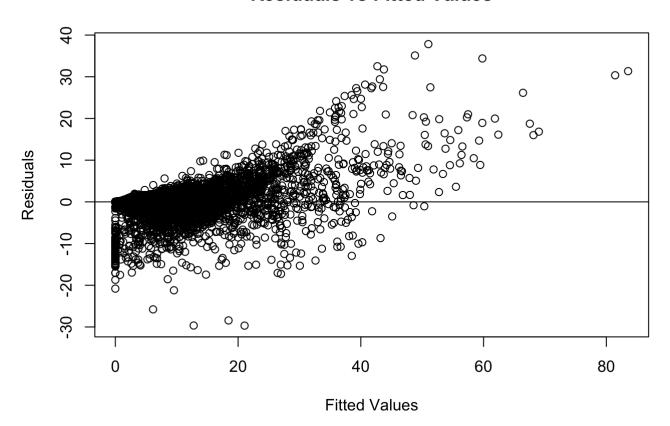
## Part b

```
# check constant variance condition

# obtain residual
beta.mean <- apply(BETA, 2, mean)
y.pred <- X %*% beta.mean
residual <- y - y.pred

# residual plot
plot(y, residual,
    main = 'Residuals vs Fitted Values',
    ylab = 'Residuals',
    xlab = 'Fitted Values')
abline(0,0)</pre>
```

#### Residuals vs Fitted Values



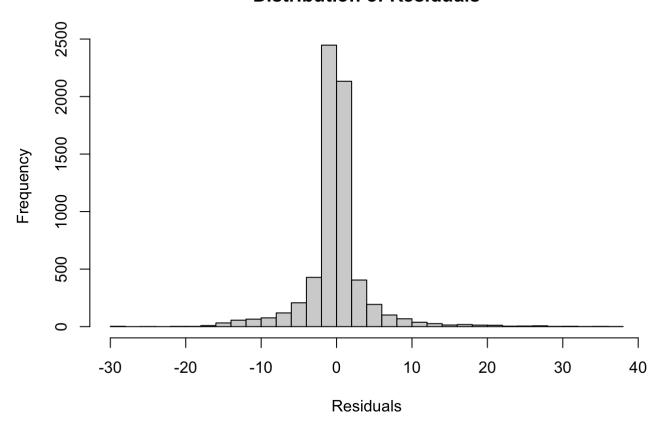
The constant variance condition seems to be violated as the residuals are not randomly spread across all fitted values of y. In fact, as the fitted value increases, the residual increases.

#### **Check Independence Condition**

The independence condition seems to be satisfied since y is the vectorization of a spectroscopy image of a water sample taken from the Neuse River in North Carolina. It is reasonable to assume the entries of the vectors are uncorrelated.

```
# check normal condition
# distribution of y
hist(residual,
    main = 'Distribution of Residuals',
    xlab = 'Residuals',
    breaks = 30)
```

#### **Distribution of Residuals**



The distribution of the residuals approximately normal, and the sample size is larger than 30, thus the normal condition is satisfied.

### Part c

Since it doesn't make sense for the coefficients of beta to be negative, a modification to the prior distribution for beta could be picking a distribution with a positive support, such as beta or gamma.

Suppose we use beta distribution as the prior distribution for beta. We first need to derive the posterior distribution of beta. For the Gibbs sampler, with starting values for sigma2 and beta, in each iteration we update and get a new beta from the posterior calculation formula, and get a new sigma2 (just as we did in part a). In the end, we would get a storage vector BETA of all positive values, since beta distribution lies in the first quadrant.