

# MIDTERM EXAM

p.1

1.  $Y = X\beta + \epsilon$ ,  $\forall \epsilon \in \mathbb{R}^n$ ,  $X \in \mathbb{R}^{n \times p}$

$E(\epsilon) = 0$ ,  $\text{var}(\epsilon) = \sigma^2 I_n$ ,  $q \in \{1, \dots, p\} = \text{rank}(X)$

① Show that  $H$  for  $X$  can be  $H = X(X^T X)^+ X^T$ . Let  $h_i$  be  $i^{\text{th}}$  leverage score ( $i^{\text{th}}$  diag. of  $H$ ). Show  $0 \leq h_i \leq 1$ .

① From Moore-Penrose we have

①  $AA^+A = A$

②  $A^+AA^+ = A^+$

and for nonsingular  $A$ ,  $A^+ = A^{-1}$

③  $(AA^+)^T = AA^+$

④  $(A^+A)^T = A^+A$

In HW7 we showed that

$H = XX^+$

$= (XX^+)^T$  by ③

$= (X^+)^T X^T$

$= [(X^T X)^+ X^T]^T X^T$  by ②

$= X [(X^T X)^+]^T X^T$

$= X (X^T X)^+ X^T$  by ④

which, when  $X$  is singular and when

$(X^T X)$  is invertible,  $= X(X^T X)^{-1} X^T$

and is the hat matrix of  $X$ .

② If  $h_i$  is the  $i^{\text{th}}$  leverage score,

$h_i = x_i^T (X^T X)^{-1} x_i$ , distance from  $x_i$  to  $X$

Since  $H$  and  $(I - H)$  are psd and  $(X^T X)^{-1}$  is pd, without

$h_i = 0$  only when  $x_i = 0$

If  $X \in \mathbb{R}^{n \times p}$ , say  $x_i$  is the last row of  $X \rightarrow X^T = [X_{(i)}^T, x_i]$

when  $h_i = 1$ ,  $H$  is now  $= \begin{bmatrix} X_{(i)} (X^T X)^{-1} X_{(i)}^T & 0 \\ 0 & 1 \end{bmatrix}$

and since  $H$  is idempotent,

$\text{rank}(X_{(i)}) = \text{rank}[X_{(i)} (X^T X)^{-1} X_{(i)}^T] = \text{trace}[X_{(i)} (X^T X)^{-1} X_{(i)}^T]$

$= p-1$  and  $\text{rank}(X^T) = p$ , when  $h_i = 1$ .

So,  $h_i$  is 0 or 1  $\rightarrow 0 \leq h_i \leq 1$

1. continued

p.2

(b) Let  $\hat{\epsilon} = (I_n - H)Y = QY$  be residuals for linreg model

(i) Derive an expression for  $E(\hat{\epsilon}^T \hat{\epsilon})$ , use to find unbiased estimator for  $\sigma^2$

know:  $E(\epsilon) = 0$ ,  $\text{var}(\epsilon) = \sigma^2 I_n$ ,  $\hat{\epsilon} = Y - X\hat{\beta}$   
 $\hat{\epsilon} = Y - X\hat{\beta} = Y - X(X^T X)^{-1} X^T Y = [I - X(X^T X)^{-1} X^T] Y$   
 $= (I - H)Y = QY = Q(X\beta + \epsilon) = QX\beta + Q\epsilon = Q\hat{\epsilon}$

because  $QX\beta$  goes to zero

Now,  $E(\hat{\epsilon}^T \hat{\epsilon}) = E(\hat{\epsilon}^T Q\epsilon)$   
 $= E[\text{trace}(\hat{\epsilon}^T Q\epsilon)] = E[\text{trace}(Q\epsilon\hat{\epsilon}^T)]$   
 $= \text{trace}[E(Q\epsilon\hat{\epsilon}^T)] = \text{trace}[QE(\hat{\epsilon}\hat{\epsilon}^T)]$   
 $= \text{trace}(Q\sigma^2 I_n) = \sigma^2 \text{trace}(Q)$   
 $= \sigma^2 \text{trace}(I - H) = \sigma^2 \text{trace}[I - X(X^T X)^{-1} X^T]$   
 $= \sigma^2 [\text{trace}(I) - \text{trace}(X(X^T X)^{-1} X^T)]$   
 $= \sigma^2 [n - \text{trace}(X(X^T X)^{-1} X^T)]$   
 $= \sigma^2 (n - p)$

making an unbiased estimator for  $\sigma^2$   
to be  $s^2 = \frac{\hat{\epsilon}^T \hat{\epsilon}}{n - p}$

(ii)  $\hat{\epsilon}_i$  is  $i^{\text{th}}$  element of  $\hat{\epsilon}$ , derive  $\text{var}(\hat{\epsilon}_i)$  in terms of  $\sigma^2$  and leverage scores  $h_1, \dots, h_n$ .

If  $s^2 = \frac{\hat{\epsilon}^T \hat{\epsilon}}{n - p}$ ,  $s^2 = \frac{\sum_{i=1}^n \hat{\epsilon}_i^2}{n - p}$

If  $\hat{\epsilon} = (I - H)Y$ , then  $\hat{\epsilon}_i = (I - h_i)Y$

$$\begin{aligned}\text{var}(\hat{\epsilon}) &= \text{var}[(I - H)Y] = \text{var}[(I - H)(X\beta + \epsilon)] \\ &= \text{var}[(I - H)\epsilon] = (I - H) \text{var}(\epsilon) (I - H)^T \\ &= \sigma^2 (I - H)(I - H)^T = \sigma^2 (I - H)\end{aligned}$$

And for  $\hat{\epsilon}_i$  where the associated leverage score is  $h_i$ ,  $\text{var}(\hat{\epsilon}_i) = \sigma^2 (1 - h_i)$

(iii)  $x_i$  is  $i^{\text{th}}$  row of  $X$ , find expression for magnitude of difference between  $y_i$  and line at  $x_i$

observation at  $x_i \rightarrow \hat{y}_i = h_i y$

error at  $x_i \rightarrow \hat{\epsilon}_i = (I - h_i) y_i$

distance:  $d_i = \frac{\hat{\epsilon}_i}{1 - h_{ii}}$  (the larger  $h_{ii}$  is, the further away  $X$  is from  $x_i$ )

2.  $y_i = f(x_i) + \epsilon_i$ ,  $x_i \in \mathbb{R}^p$ ,  $\epsilon_1, \dots, \epsilon_n$  satisfy  $E(\epsilon_i) = 0$ ,  $\text{cov}(\epsilon_i, \epsilon_j) = \sigma^2 \mathbb{1}\{i=j\}$ .  $\hat{f}(x)$  is estimate for  $f(x)$ .

$$df = \frac{1}{\sigma^2} \sum_{i=1}^n \text{cov}\{\hat{f}(x_i), y_i\}$$

- ① If  $\hat{f}(x_i) = \frac{1}{n} \sum_{j=1}^n y_j$ , show  $df = 1$  and if  $\hat{f}(x_i) = y_i$ , show  $df = n$ .

Let's call  $\hat{f}(x_i) = \hat{y}_i$

For  $\hat{y}_i = \frac{1}{n} \sum_{j=1}^n y_j$ ,  $\hat{y}_i = \bar{y}_{\text{avg}}$  where  $\bar{y}_{\text{avg}} = \{\bar{y}, \dots, \bar{y}\}$  and  $\bar{y} = \frac{1}{n} \sum_{j=1}^n y_j$

$$df(\hat{y}_i) = df(\bar{y}_{\text{avg}}) = \frac{1}{\sigma^2} \sum_{j=1}^n \text{cov}(\bar{y}, y_j) = \frac{1}{\sigma^2} \sum_{j=1}^n \sigma^2 \cdot \frac{1}{n} = \frac{\sigma^2}{\sigma^2} \cdot n \cdot \frac{1}{n} = 1$$

For  $\hat{y}_i = y_i$ , (and since  $x_i \in \mathbb{R}^p$ ,  $y \in \mathbb{R}^{n \times p}$ )

$$df(y_i) = \frac{1}{\sigma^2} \sum_{j=1}^n \text{cov}(y_i, y_j) = \frac{1}{\sigma^2} \sum_{j=1}^n \text{var}(y_i) = \frac{1}{\sigma^2} \cdot \sigma^2 \cdot n = n$$

- ②  $Y = (y_1, \dots, y_n)^T$ ,  $\hat{Y} = (\hat{y}_1, \dots, \hat{y}_n)^T \in \mathbb{R}^n$

$\hat{Y} = LY$  for some  $L \in \mathbb{R}^{n \times n}$ , depends only on  $x_1, \dots, x_n$

Show that  $df = \text{trace}(L)$

If  $\hat{Y} = LY$ , we already know  $\hat{Y} = HY$  so  $L$  is our hat matrix for  $X$

$$\begin{aligned} df &= \frac{1}{\sigma^2} \sum_{i=1}^n \text{cov}(\hat{y}_i, y_i) = \frac{1}{\sigma^2} \text{trace}[\text{cov}(LY, Y)] \\ &= \frac{1}{\sigma^2} \text{trace}[X(X^T X)^{-1} X^T \text{cov}(Y, Y)] \quad \text{since } L \text{ only depends on } X \\ &= \frac{1}{\sigma^2} \cdot \sigma^2 \cdot \text{trace}[X(X^T X)^{-1} X^T] \\ &= \text{trace}[X(X^T X)^{-1} X^T] \\ &= \text{trace}[X^T X (X^T X)^{-1}] = \text{trace}(I_n) = n = \text{tr}(L) \end{aligned}$$

- ③  $X \in \mathbb{R}^{n \times p}$ , full-rank design, rows  $x_i$ .

Show if  $\hat{f}(x_i) = x_i^T (X^T X)^{-1} X^T Y$  is OLS estimate for  $f(x_i)$ ,

then  $df = p$  we know:  $h_{ij} = x_i^T (X^T X)^{-1} x_j^T$

$$df(\hat{f}(x_i)) = \frac{1}{\sigma^2} \text{trace}[\text{cov}(x_i^T (X^T X)^{-1} X^T Y, Y)]$$

$$= \frac{1}{\sigma^2} \cdot \text{trace}(x_i^T (X^T X)^{-1} X^T) \cdot \text{cov}(Y, Y)$$

$$= \text{trace}(x_i^T (X^T X)^{-1} X^T) = \text{trace}(X^T x_i^T (X^T X)^{-1})$$

$$= \text{trace}(I_p) = p \quad \text{when } x_i \text{ are rows}$$

of  $X \in \mathbb{R}^{n \times p}$

2, continued

p.4

① For  $x \in \mathbb{R}^p$ ,  $K \geq 1$ ,  $N_K(x) = \{i_1, \dots, i_K\} \subseteq \{1, \dots, n\}$  be

$K$ -nearest neighboring indices of  $x$ , i.e.

$$\|x - x_{i_1}\|_2 \leq \dots \leq \|x - x_{i_K}\|_2, \|x - x_{i_K}\|_2 \leq \|x - x_j\|_2 \text{ for } j \notin \{i_1, \dots, i_K\}$$

Define KNN estimate for  $f(x_i)$  to be

$$\hat{f}(x_i) = K^{-1} \sum_{j \in N_K(x_i)} y_j$$

① Find  $L \in \mathbb{R}^{n \times n}$  such that  $\hat{Y} = LY$ .

$$\text{If } Y = X\beta, \quad \hat{Y} = X\hat{\beta} \quad \text{and} \quad \hat{\beta} = (X^T X)^{-1} X^T Y$$

From ①,  $L$  is our hat matrix,

$$\text{so } \hat{Y} = X\hat{\beta} = X(X^T X)^{-1} X^T Y$$

Hat matrix

$$= LY, \text{ when } L \in \mathbb{R}^{n \times n}$$

② Derive df for KNN regression. ( $\hat{f}(x_i) = K^{-1} \sum_{j \in N_K(x_i)} y_j$ )

$$df = \frac{1}{\sigma^2} \sum_{i=1}^n \text{cov} \{ \hat{f}(x_i), y_i \}$$

$$= \frac{1}{\sigma^2} \sum_{i=1}^n \text{cov} \left\{ K^{-1} \sum_{j \in N_K(x_i)} y_j, y_i \right\}$$

→ make  $j \in N_K(x_i) = x_i \in N_K(x_i)$

$$= \frac{1}{\sigma^2} \sum_{i=1}^n \text{cov} \left\{ K^{-1} \sum_{x_i \in N_K(x_i)} y_i, y_i \right\}$$

$$= \frac{1}{\sigma^2} \text{trace} \left\{ \text{cov} \left( K^{-1} \sum_{x_i \in N_K(x_i)} y_i, y_i \right) \right\}$$

$$= \frac{1}{\sigma^2} \cdot \frac{1}{K^2} \text{trace} \left\{ \text{cov} \left( \sum_{x_i \in N_K(x_i)} y_i, y_i \right) \right\}$$

$\sum_{x_i \in N_K(x_i)} y_i$  is the average responses of

$K$ -nearest  $x_i$  to  $x$ , and we minimize

that distance  $\rightarrow \|x - x_{i_k}\|_2$  for  $k=1, \dots, K$ .

So we take  $n$  out and calculate

$$= \frac{1}{\sigma^2} \cdot \frac{1}{K^2} \cdot \text{trace}(\|x - x_i\|_2) \cdot \text{cov}(y_i, y_i) \cdot n$$

$$= \frac{1}{\sigma^2} \cdot \frac{1}{K^2} \cdot n \cdot \text{trace}(\|x - x_i\|_2)$$

$$= \frac{n}{K^2} \cdot \text{trace}(\|x - x_i\|_2)$$

↳ which is minimized at

$i=K$

$$= \frac{n}{K^2} \cdot K = \frac{n}{K} \text{ degrees of freedom}$$

$$\text{Simplified: } df = \frac{1}{\sigma^2} \sum_{i=1}^n \text{cov}(y_i, y_i) = \frac{1}{\sigma^2} \sum_{i=1}^n \sigma^2 \cdot K^{-1} = \frac{n}{K}$$

3. Experiment run  $m$  times, parameter  $\theta \in \mathbb{R}$

For experiment  $j$ ,  $\hat{\theta}_j \sim N(\theta, v_j)$ ,  $\hat{\theta}_1, \dots, \hat{\theta}_m$  are independent

ⓐ Find BLUE for  $\theta$  using summary-level data

$\hat{\theta}_1, \dots, \hat{\theta}_m$ . Find variance of estimator. (HW7 92ⓐ)

While normal data is sometimes estimated

(its parameters, that is) using the

Gaussian pdf:  $p(x) = \frac{1}{\sqrt{2\pi}\sigma^2} \exp(-\frac{(x-\mu)^2}{2\sigma^2})$ ,

with several unbiased estimators from an

independent set of data, we can better

estimate the parameter by averaging.

We have  $\{\hat{\theta}_1, \dots, \hat{\theta}_m\}$ ,  $\hat{\theta}_j \sim N(\theta, v_j)$  for  $j=1, \dots, m$

and  $\hat{\theta}_j$  are independent.

Estimator:  $\hat{\theta} = \frac{1}{m} \sum_{j=1}^m \hat{\theta}_j = \frac{1}{m} \cdot m \cdot \theta = \theta$

Variance:  $\text{var}(\hat{\theta}) = \text{var}(\frac{1}{m} \sum_{j=1}^m \hat{\theta}_j)$

$$= \frac{1}{m^2} \sum_{j=1}^m \text{var}(\hat{\theta}_j) = \frac{1}{m^2} \cdot m \cdot v = \frac{1}{m} v$$

$\hat{\theta}$  is BLUE because the data is linearly estimated (multiple experiments of the same parameter, is it a normal approx for binomial?), the mean shows that it's unbiased, and it minimizes the variance.

ⓑ Suppose  $\hat{\theta}_j \sim N(\theta_j, v_j)$ ,  $\theta_j \sim N(\theta_0, V_0)$ ,  $V_0 > 0$ . Is  $\hat{\theta}$  still unbiased estimate of  $\theta_0$ ? Is it BLUE for  $\theta_0$ ?

$$E(\hat{\theta}_j) = \theta_j, \text{ and } E(\theta_j) = \theta_0$$

Now we have intermediate steps:

$$\text{Estimator: } \hat{\theta} = \frac{1}{m} \sum_{j=1}^m \hat{\theta}_j = \frac{1}{m} \sum_{j=1}^m \left[ \frac{1}{m} \sum_{j=1}^m \theta_j \right] = \frac{1}{m} \sum_{j=1}^m \theta_0 = \frac{1}{m} \cdot m \cdot \theta_0 = \theta_0$$

$$\text{Variance: } \text{var}(\hat{\theta}) = \text{var}\left(\frac{1}{m} \sum_{j=1}^m \left[ \frac{1}{m} \sum_{j=1}^m \theta_j \right]\right) = \frac{1}{m^2} \sum_{j=1}^m \text{var}\left(\frac{1}{m} \sum_{j=1}^m \theta_j\right)$$

$$= \frac{1}{m^2} \sum_{j=1}^m \frac{1}{m^2} \text{var}(\theta_j) = \frac{1}{m^2} \sum_{j=1}^m \frac{1}{m^2} V_0 \cdot m = \frac{1}{m^2} \cdot \frac{1}{m^2} \cdot m \cdot m \cdot V_0 = \frac{1}{m^2} V_0$$

Since the estimator is no longer linear and the variance weight has changed,  $\hat{\theta}$  is no longer BLUE.

4.  $Y$ :  $46 \times 10$  matrix with log-transformed expression of  $m=10$  genes from  $n=46$  unrelated people  
 Data:  $46 \times 1$  data frame of conc (drug A concentration in  $\mu\text{mol}$ )

①  $Y^{(i)} \in \mathbb{R}^{n \times 1}$  is gene  $i$  expression. conc is a factor variable with 5 levels. Model  $Y^{(i)}$  as a function of conc. state any assumptions, define parameters.

Assumptions:

- $E(Y^{(i)})$  is linear in factor (conc)
- residuals are independent, identically distributed (constant variance)

Parameters:

- $Y_i^{(i)}$ : gene  $i$  expression
- $X_i$ : concentration as factor, levels of drug A  
 $\text{levels} = \{0, 0.625, 1.25, 2.5, 5\}$
- $\epsilon_i$ : errors, normally distributed under assumptions above
- $\beta_i$ : coefficient by  $X_i$  level,  $\beta_0 = \text{intercept}$

Model:

$$Y_i^{(i)} = \beta_0 + \beta_i X_i + \epsilon_i$$

② 95% CI for

$$E\{Y_i^{(i)} | \text{conc} = 1.25\} - E\{Y_i^{(i)} | \text{conc} = 0\}$$

To assess the difference, we treat conc as 4 different indicators (when each of these is 0, we are left with the lowest level (0)).

The levels of  $X_i$ :

$$X_{i1} = 1 \text{ for } \text{conc} = 0.625, \quad 0 \text{ for ow}$$

$$X_{i2} = 1 \text{ for } \text{conc} = 1.25, \quad 0 \text{ for ow}$$

$$X_{i3} = 1 \text{ for } \text{conc} = 2.5, \quad 0 \text{ for ow}$$

$$X_{i4} = 1 \text{ for } \text{conc} = 5, \quad 0 \text{ for ow} \rightarrow$$

46, continued

p.7

when all  $X_i$  are zero, we're left with  $\beta_0$  which indicates gene expression for no administration of drug A.

$$E(Y_i | X_i = 1.25) - E(Y_i | X_i = 0)$$

$$= (\beta_0 + \beta_2) - (\beta_0) = \beta_2$$

From R,  $\hat{\beta}_2 = .3319$

$$CI: \hat{\beta}_2 \pm t(\alpha/2, n-p) \cdot SE(\hat{\beta}_2)$$

$$\text{at } 41 \text{ df, } 95\%, t = 2.018$$

$$SE(\hat{\beta}_2) = .6649$$

$$CI \Rightarrow (-1.010, 1.674)$$

47<sup>th</sup> patient  $\rightarrow .625 \mu\text{mol}$  ( $X_i = 1$ )

Find 95% CI (see next page for q-q plot)

Assumptions:

- value is within scope of the model (satisfied, new  $X_i$  is at a level we know)
- linearity, independence, normal, constant variance (q-q plot shows almost a trend, so we may suspect no linearity?)

Defining  $X_i$  "as.factor" in R, we can estimate the gene expression of the new patient using  $\hat{\beta}_1$ .

$$\hat{Y}_i(.625) = \hat{\beta}_0 + \hat{\beta}_1 X_i + \epsilon_i \rightarrow = \hat{\beta}_1(1) = 3.4473$$

( $X_i$  still as.factor (conc))

$$t(\alpha/2, df=41) = 2.018$$

$$SE(\hat{\beta}_1) = .6862$$

$$CI: (2.062, 4.833)$$

d) Hypothesis:  $E(Y_i)$  is linear in drug Administration

Model: To make  $Y_i$  estimable / testable, we remove the intercept

$$Y_i = \beta_j X_{ij} + \epsilon_i$$

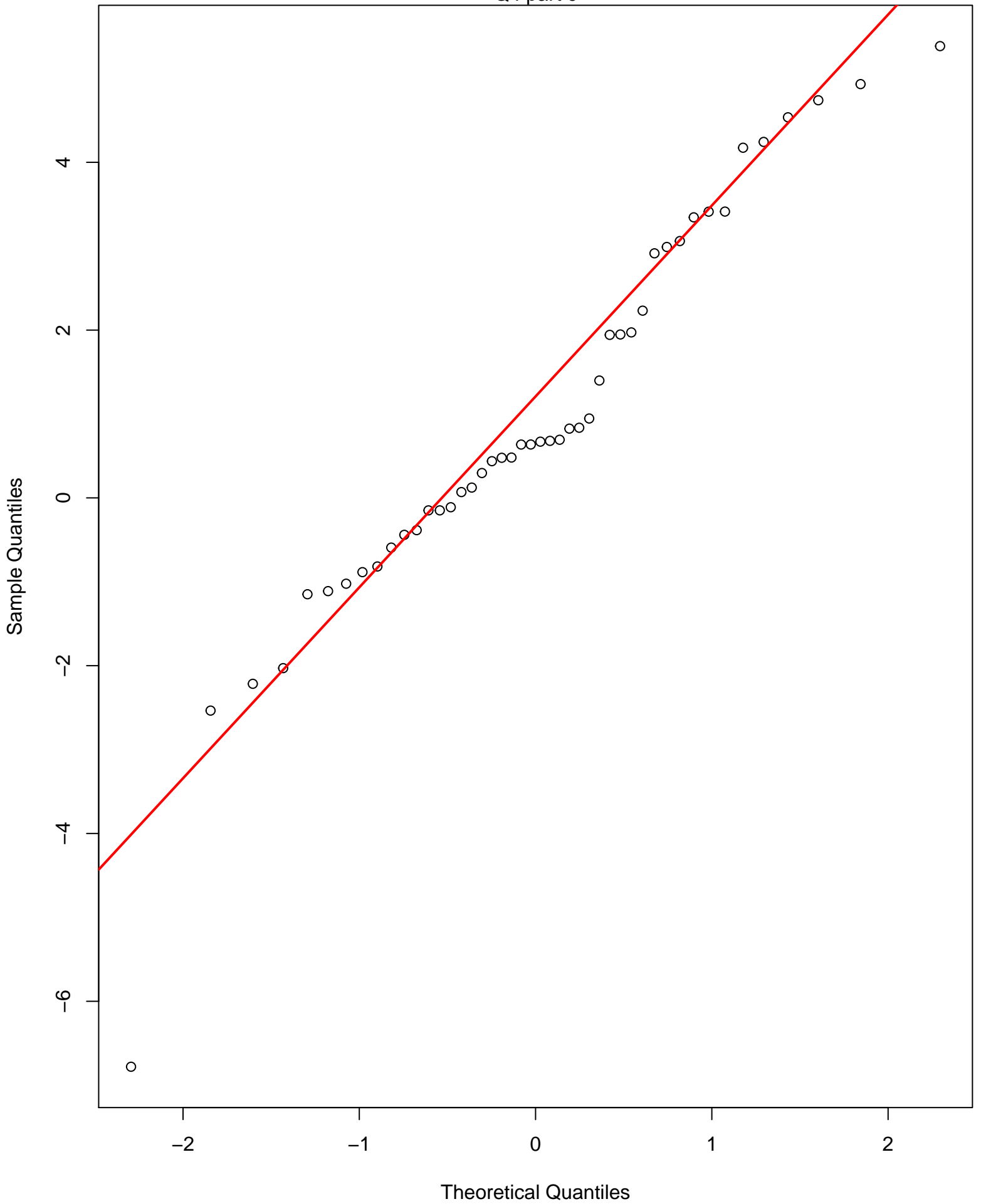
$\beta_j$  is matrix of coefficients for each level of  $X_i$

$X_{ij}$  is factor (as.factor), levels =  $\{0, .625, 1.25, 2.5, 5\}$

# Normal Q-Q Plot

p.8

Q4 part c





4(d), continued (i)

p.9

$\epsilon_i$  are errors,  $\sim N(0, \sigma^2)$  iid

$Y_i^{(j)}$  is gene  $j$  expression as a function of drug A administration

(ii) show (i) is a sub-model of (a)

In (a), the model  $\rightarrow Y_i^{(j)} = \beta_0 + \beta_{1j}X_{ij} + \epsilon_i$

In (i), model  $\rightarrow Y_i^{(j)} = \beta_{1j}X_{ij} + \epsilon_i$

Because (a) is not full rank, in (i) where the sum of  $X_i$ 's = 1, we do have a

full-rank model, making (i) a sub-model of (a).

(iii) Test null ( $H_0$ ) that  $E(Y_i^{(j)})$  is linear,  $\alpha = 0.05$

$H_0: E(Y_i^{(j)})$  is linear in drug A ad. ( $X_{ij}$ )

$H_A: E(Y_i^{(j)})$  is not linear in  $X_{ij}$

With 41 degrees of freedom (46 observations, predictor of 5 levels,  $46 - 5 = 41$ ) and  $\alpha = 0.05$ ,

R tells us that this model has an F-stat of 13.82 ( $F(\alpha, 5, 41)$ ) and p-value =  $6.36 \times 10^{-6}$

We can reject the null and conclude that a linear model is likely not the appropriate model for relationship between drug A administration (as a factor variable) and gene  $j$  expression.

(c)  $Y_i^{(j)}$  is gene  $j$  expression

$H_0: E(Y_i^{(j)})$  is linear vs.  $H_A: E(Y_i^{(j)})$  not linear

Use FWER,  $\alpha = 0.05$ , to determine which

of  $m = 10$  genes are not linear in drug A administration.

FWER lowers the "cutoff" from  $\alpha$  to  $\frac{\alpha}{H}$  ( $H \rightarrow$  estimators)

for model:  $Y_i^{(j)} = \beta_{1k}X_{ik} + \epsilon_i$

$$= \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \beta_4 X_{i4} + \epsilon_i$$

when all are 0, drug A = 0  $\mu$ mol  $\rightarrow$

40, continued

p.10

Using the no-intercept models for each of the  $m=10$  gene expressions  $Y^{(i)}$ , I modeled drug A administration as a factor variable. The models including the intercept would tell us that genes 3,4,5,6 should be modeled linearly (by FWER), but since these models are not full rank, we use the no-intercept models. With a cutoff of  $\frac{\alpha}{4}$ , we find that all of the adjusted p-values fall under the cutoff, leading us to conclude that none of the  $m=10$  gene expressions should be modeled as linear functions of administration of drug A.

#### R Code for Problem 4

```
load(file = "Genes.RData")

# (a)
Y_1 = Y[,1]
conc.f = as.factor(Data$conc)
model1 = lm(Y_1 ~ conc.f)

# (b)
summary(model1)
confint(model1)

# (c)
confint(model1)

qqnorm(Y_1, pch = 1, frame = TRUE)
qqline(Y_1, col = "red", lwd = 2)
mtext("Q4 part c", side = 3)

# (d)
model2 = lm(Y_1 ~ conc.f + 0)
summary(model2)

# (e)
Y_1 = Y[,1] ; Y_2 = Y[,2] ; Y_3 = Y[,3] ; Y_4 = Y[,4] ; Y_5 = Y[,5] ;
Y_6 = Y[,6] ; Y_7 = Y[,7] ; Y_8 = Y[,8] ; Y_9 = Y[,9] ; Y_10 = Y[,10]

model_1 = lm(Y_1 ~ conc.f + 0); model_2 = lm(Y_2 ~ conc.f + 0); model_3 = lm(Y_3 ~ conc.f + 0)
model_4 = lm(Y_4 ~ conc.f + 0); model_5 = lm(Y_5 ~ conc.f + 0); model_6 = lm(Y_6 ~ conc.f + 0)
model_7 = lm(Y_7 ~ conc.f + 0); model_8 = lm(Y_8 ~ conc.f + 0); model_9 = lm(Y_9 ~ conc.f + 0)
model_10 = lm(Y_10 ~ conc.f + 0)

Regressionp <- function (x) {
  if (class(x) != "lm") stop("Not an object of class 'lm' ")
  f <- summary(x)$fstatistic
  p <- pf(f[1], f[2], f[3], lower.tail = F)
  attributes(p) <- NULL
  return(p)
}

p = c(Regressionp(model_1), Regressionp(model_2), Regressionp(model_3), Regressionp(model_4),
      Regressionp(model_5), Regressionp(model_6), Regressionp(model_7), Regressionp(model_8),
      Regressionp(model_9), Regressionp(model_10))
p

p.ad = p.adjust(p, method = "bonferroni")
p.ad > .05/4
```