

STAT 511 FINAL EXAM SOLUTIONS
SPRING 2010

a) $1 + 6 + 2.5 = 9.5$

b) $t = 0.602 \quad d.f. = 60 - 4 = 56$

p-value ≈ 0.55

The mean response for Treatment 1 was not significantly different from 0.

<u>EFFECT DIFF</u>	<u>ESTIMATE</u>	<u>SE</u>	<u>t-stat</u>	<u>P < 0.05</u>
1 - 2	-4	2.036	-1.965	No
1 - 3	-6	2.036	-2.948	Yes
2 - 3	-2	2.036	-3/ 2.036	No

d) $\hat{y}_{\text{drug}2} = \bar{y}_{.2.} - \bar{y}_{.1.}$

$$\hat{\text{Var}}(\hat{y}_{\text{drug}2}) = \frac{\hat{\sigma}^2}{30} + \frac{\hat{\sigma}^2}{30} = \frac{\hat{\sigma}^2}{15}$$

1 d) (continued)

$$SE(\hat{\sigma}^2) = \hat{\sigma} / \sqrt{15}$$

From the R output,

$$SE(\hat{\sigma}^2) = 1.662$$

$$\begin{aligned} \text{Thus, } \hat{\sigma}^2 &= (1.662 \sqrt{15})^2 \\ &= 1.662^2 * 15 \end{aligned}$$

1 e) d.f. = 60 - 4 = 56

2 a) $\begin{array}{cccccc} 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 1 & 0 & 1 \end{array}$

b) $\begin{array}{cccccc|c} 1 & 0 & 0 & 0 & 0 & 0 & 1 \\ & & & & & & \underbrace{0 \ 0 \ 0 \ 0 \ldots 0}_{11 \text{ zeros}} \\ 0 & 0 & 0 & 0 & 0 & 1 & \underbrace{0 \ 0 \ 0 \ldots 0}_{11 \text{ zeros}} \end{array}$

c) $\left[I_{6 \times 6} \otimes \frac{1}{4 \times 1}, I_{12 \times 12} \otimes \frac{1}{2 \times 1} \right]$

d) σ_s^2 = Variance of subject random effects
 σ_r^2 = Variance of ear random effects

σ_e^2 = Error Variance.

e) $\sigma_s^2 + \sigma_r^2 + \sigma_e^2$

f)
$$\frac{\sigma_s^2 + \sigma_r^2}{\sigma_s^2 + \sigma_r^2 + \sigma_e^2}$$

$$2 \text{ g) } \frac{\sigma_s^2}{\sigma_s^2 + \sigma_r^2 + \sigma_e^2}$$

2 h) There is a mean for each combination of hearing aid and test. We should expect the pre-test means to be identical across hearing aid types because the pretest data is collected before the hearing aids are placed. Thus, rather than 6 means, we should have only 4 (pretest and posttest for each of the 3 hearing aid types).

3. a) Model 2

b) $128.10 - 2(11) + \log(20)(11)$

c) i. $42.834 - 14.397$

ii. $11 - 1 = 10$

iii. Model 2 does fit significantly better. The test stat is far bigger than $18.307 = \chi^2_{10}(.95)$.

d) i. $38.69 - 14.397$

ii. $11 - 2 = 9$

iii. Again Model 2 fits significantly better.

3e) The mean number of infected cells for plants of Genotype 2 was estimated to be $\exp\{0.22450\}$ times the mean number of infected cells for plants of genotype 1.

$$3f) \exp\{2.68785 + 0.22450\}$$

$$4. (X'X + \lambda^2 D)^{-1} X'Y \text{ where } D = \begin{bmatrix} 0 & 0 \\ 0 & 1 \end{bmatrix}$$

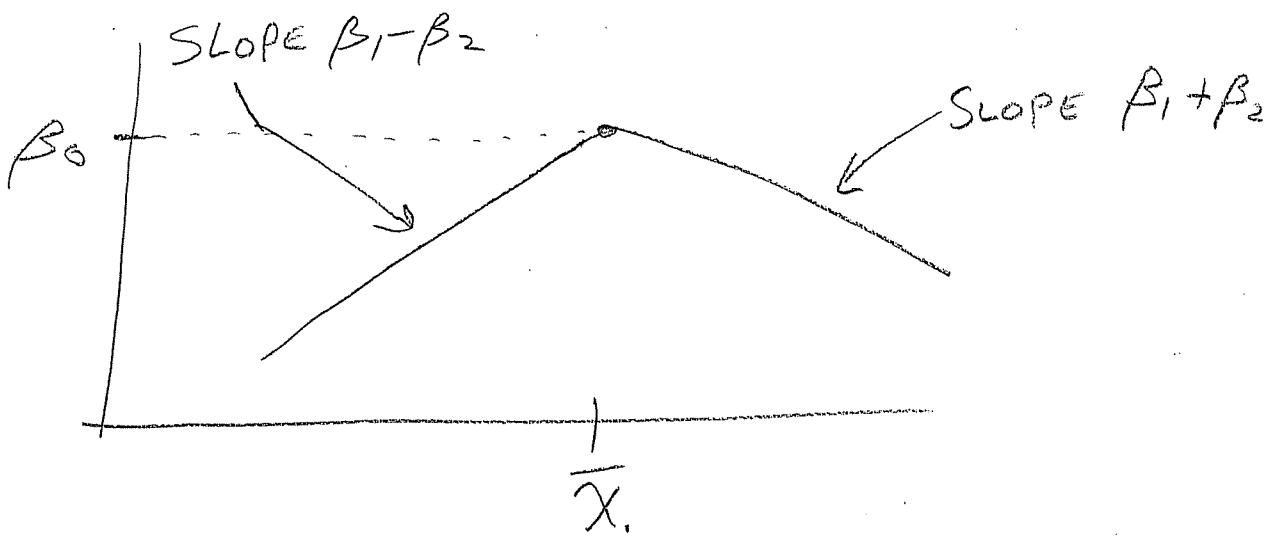
$$X'X = \begin{bmatrix} n & 0 \\ 0 & \sum_{i=1}^n (x_i - \bar{x}_.)^2 \end{bmatrix}$$

$$X'Y = \sum_{i=1}^n y_i \\ \sum_{i=1}^n (x_i - \bar{x}_.) y_i$$

$$\hat{\beta}_{\lambda^2} = \frac{\begin{bmatrix} \bar{y}_. \\ \sum_{i=1}^n (x_i - \bar{x}_.) y_i \end{bmatrix}}{\sum_{i=1}^n (x_i - \bar{x}_.)^2 + \lambda^2}$$

$$5. \beta_0 + \beta_1 (x_i - \bar{x}_.) + \beta_2 |x_i - \bar{x}_.|$$

$$= \begin{cases} \beta_0 + (\beta_1 - \beta_2) (x_i - \bar{x}_.) & \text{if } x_i \leq \bar{x}_. \\ \beta_0 + (\beta_1 + \beta_2) (x_i - \bar{x}_.) & \text{if } x_i > \bar{x}_. \end{cases}$$



This is a continuous, piecewise linear spline function with a knot at $\bar{x}_.$

$$6 \text{ a) } 0.1142$$

$$\text{b) } 0.0128$$

$$\text{c) } 0.1113 - 0.1142$$

$$\text{d) } 0.1142 - (0.1113 - 0.1142)$$

$$= 2(0.1142) - 0.1113$$

$$\text{e) } 0.0898 \rightarrow 0.1323$$