Biometry Quiz #3 R Handout Results #1

**> library(NCStats)**

**> ff <- read.table("http://www.ncfaculty.net/dogle/R/Data\_Master/R/FlyingFox1.txt",header=TRUE)**

**> str(ff)**

'data.frame': 223 obs. of 3 variables:

$ forearm.len: num 152 154 157 157 158 ...

$ body.mass : num 779 788 839 761 763 ...

$ sex : Factor w/ 3 levels "female","male",..: 2 2 2 2 2 2 2 2 2 2 ...

**> ff$sex <- factor(ff$sex,levels=c("young","male","female"))**

**> table(ff$sex)**

young male female

79 75 69

**> lm1 <- lm(body.mass~forearm.len\*sex,data=ff)**

**> transChooser(lm1,show.stats=TRUE)**

** **

**> anova(lm1)**

Response: body.mass

Df Sum Sq Mean Sq F value Pr(>F)

forearm.len 1 9051340 9051340 1792.2167 < 2e-16 \*\*\*

sex 2 987212 493606 97.7368 < 2e-16 \*\*\*

forearm.len:sex 2 30210 15105 2.9908 0.05232 .

Residuals 217 1095928 5050

**> compSlopes(lm1)**

Multiple Slope Comparisons

comparison diff lwr upr raw.p adj.p

1 male-young 5.67494 0.80082 10.54905 0.02270 0.06178

2 female-young -0.08093 -4.76632 4.60445 0.97287 0.97287

3 female-male -5.75587 -11.27945 -0.23228 0.04119 0.06178

Slope Information

level slopes lwr upr raw.p adj.p

3 female 7.2419 3.4534 11.030 0.00021 0.00021

1 young 7.3229 4.5661 10.080 0.00000 0.00000

2 male 12.9978 8.9782 17.017 0.00000 0.00000

**> compIntercepts(lm1)**

Tukey HSD on adjusted means assuming parallel lines.

comparison diff lwr upr p.adj

1 male-young 274.22 247.00 301.44 0

2 female-young 117.43 89.61 145.25 0

3 female-male -156.79 -184.95 -128.63 0

Mean adjusted values at a covariate value of 154.9

young male female

490.56 764.78 607.99

**> fitPlot(lm1,legend="topleft",col="gray")**

****

**> predict(lm1,data.frame(forearm.len=c(155,155,155),sex=c("young","male","female")))**

1 2 3

471.0677 723.9145 619.1563

**> ff$log.bm <- log(ff$body.mass)**

**> ff$log.fl <- log(ff$forearm.len)**

**> lm2 <- lm(log.bm~log.fl\*sex,data=ff)**

**> anova(lm2)**

Response: log.bm

Df Sum Sq Mean Sq F value Pr(>F)

log.fl 1 31.4080 31.4080 2588.8126 < 2e-16 \*\*\*

sex 2 1.8891 0.9445 77.8534 < 2e-16 \*\*\*

log.fl:sex 2 0.0606 0.0303 2.4973 0.08467 .

Residuals 217 2.6327 0.0121

**> compSlopes(lm2)**

Multiple Slope Comparisons

comparison diff lwr upr raw.p adj.p

1 male-young -0.43715 -1.6134 0.73908 0.46465 0.46465

2 female-young -1.26771 -2.3880 -0.14740 0.02675 0.08025

3 female-male -0.83056 -2.2220 0.56091 0.24070 0.36105

Slope Information

level slopes lwr upr raw.p adj.p

3 female 1.7103 0.75957 2.6610 0.00048 0.00048

2 male 2.5409 1.52483 3.5569 0.00000 0.00000

1 young 2.9780 2.38538 3.5706 0.00000 0.00000

**> compIntercepts(lm2)**

Tukey HSD on adjusted means assuming parallel lines.

comparison diff lwr upr p.adj

1 male-young 0.43712 0.39502 0.47921 0

2 female-young 0.24246 0.19944 0.28548 0

3 female-male -0.19465 -0.23821 -0.15110 0

Mean adjusted values at a covariate value of 5.039

young male female

6.1314 6.5685 6.3739

**> fitPlot(lm2,legend="topleft",col="gray")**

****

**> predict(lm2,data.frame(log.fl=c(5.04,5.04,5.04),sex=c("young","male","female")))**

1 2 3

6.172781 6.575204 6.419336

Biometry Quiz #3 R Handout Results #2

**> library(NCStats)**

**> d <- readData("C:/aaaWork/Consulting/Kennedy (Tony) -- 50maturity/NewData.csv")**

**> str(d)**

'data.frame': 735 obs. of 6 variables:

$ Year : int 2011 2011 2011 2011 2011 2011 2011 2011 2011 2011 ...

$ Maturity: int 0 0 0 0 0 0 0 0 0 0 ...

$ Sex : logi FALSE FALSE FALSE FALSE FALSE FALSE ...

$ TL : int 405 397 395 322 295 305 278 314 351 300 ...

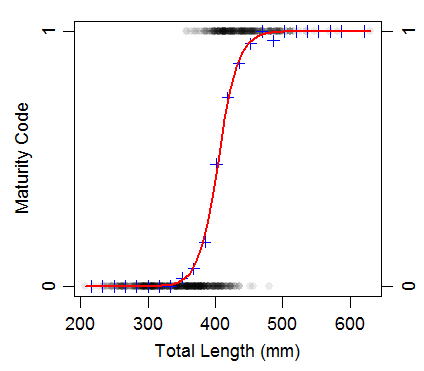
$ Weight : int 592 524 554 294 208 232 188 240 394 240 ...

$ Age : int 4 3 4 2 2 2 2 2 3 2 ...

**> d$Maturity <- factor(d$Maturity)**

**> glm1 <- glm(Maturity~TL,data=d,family=binomial)**

**> fitPlot(glm1,main="",xlab="Total Length (mm)",ylab="Maturity Code")**



**> summary(glm1)**

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) -27.619919 2.314125 -11.94 <2e-16 \*\*\*

TL 0.068230 0.005738 11.89 <2e-16 \*\*\*

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 948.93 on 734 degrees of freedom

Residual deviance: 355.00 on 733 degrees of freedom

AIC: 359