

HW_3

2a

```
## 2
data("Prostate")

prostate.lm = lm(lcavol~., data = Prostate)
summary.pros = summary(prostate.lm)
pros.coefs = summary.pros$coefficients
# log
log = cbind(pros.coefs[, "Estimate"], confint(prostate.lm))
# Normal Scale
cbind(exp(pros.coefs[, "Estimate"]), exp(confint(prostate.lm)))

##              2.5 %    97.5 %
## (Intercept) 0.1043400 0.008536064 1.275392
## lweight     0.9294461 0.657145428 1.314580
## age         1.0229965 1.000948079 1.045531
## lbph        0.9162654 0.816377603 1.028375
## svi         0.8576225 0.517768270 1.420551
## lcp         1.4438310 1.227477507 1.698319
## gleason     1.2101672 0.890611734 1.644381
## pgg45       0.9928680 0.984368001 1.001441
## lpsa        1.7732205 1.495272134 2.102835

1.1^confint(prostate.lm)["lweight",]

##      2.5 %    97.5 %
## 0.9607741 1.0264117

1.1^confint(prostate.lm)["lbph",]

##      2.5 %    97.5 %
## 0.9808494 1.0026703

1.1^confint(prostate.lm)["lcp",]

##      2.5 %    97.5 %
## 1.019727 1.051776

1.1^confint(prostate.lm)["lpsa",]

##      2.5 %    97.5 %
## 1.039089 1.073412

(exp(confint(prostate.lm)["age",]) - 1) * 100

##      2.5 %    97.5 %
## 0.0948079 4.5530562

(exp(confint(prostate.lm)["svi",]) - 1) * 100

##      2.5 %    97.5 %
## -48.22317 42.05511
```

```
(exp(confint(prostate.lm)["gleason",])-1) * 100
```

```
##      2.5 %      97.5 %
## -10.93883  64.43805
```

```
(exp(confint(prostate.lm)["pgg45",])-1) * 100
```

```
##      2.5 %      97.5 %
## -1.5631999  0.1441355
```

Interpretations

While holding everything else constant, for a 10% increase in prostate weight, we are 95% confident that cancer volume will increase by -4 to 2.6%.

While holding everything else constant, we are 95% confident that for every increase of 1 year of patient, the cancer volume will increase by .09 to 4.5% cc.

While holding everything else constant, for a 10% increase in the amount of benign hyperplasia(cm^2), we are 95% confident that cancer volume will change by -1.9 to .2 percent.

While holding everything else constant, we are 95% confident that for every patient with seminal vesicle invasion, the cancer volume will change by -48.22 to 42.05% cc.

While holding everything else constant, for a 10% increase in the amount of capsular penetration(cm), we are 95% confident that cancer volume will increase by 1.97 to 5.2 percent.

While holding everything else constant, we are 95% confident that for every increase of 1 in the Gleason score, the cancer volume will change by -10.94 to 64.44% cc.

While holding everything else constant, we are 95% confident that for every increase of 1 in percentage of gleason scores that are 4 or 5, the cancer volume will change by -1.56 to .144% cc.

While holding everything else constant, for a 10% increase in the amount of prostate specific antigen, we are 95% confident that cancer volume will increase by 3.9 to 7.3%.

2b

```
prostate.sv = lm(lcavol ~ svi + lpsa, data = Prostate)
summary.sv = summary(prostate.sv)
coefs = summary.sv$coefficients
cbind(coefs[, "Estimate"], confint(prostate.sv))
```

```
##              2.5 %      97.5 %
## (Intercept) -0.3607832 -0.76206250 0.04049613
## svi          0.5153381  0.04704349 0.98363261
## lpsa         0.6452684  0.47731669 0.81322011
```

```
exp(cbind(coefs[, "Estimate"], confint(prostate.sv)))
```

```
##              2.5 %      97.5 %
## (Intercept) 0.6971301 0.4667029 1.041327
## svi         1.6742044 1.0481676 2.674153
## lpsa        1.9064987 1.6117438 2.255158
```

```
coefs.est = coefs[, "Estimate"]
```

```

lpsa = Prostate$lpsa
data1 <- data.frame(cbind(seq(min(lpsa)-1,max(lpsa)+1,
                             length.out=100),rep(0,100)))
colnames(data1) <- c("lpsa","svi")

data2 <- data1
data2$svi <- rep(1,100)

pred.svi.not = predict.lm(prostate.sv,newdata = data1, interval = "c", level = .95 )
pred.svi = predict.lm(prostate.sv,newdata = data2,interval = "c", level = .95)

data.svi.not = cbind(data1,pred.svi.not)
data.svi = cbind(data2, pred.svi)

prostate.plot = ggplot(data = Prostate, aes(x = lpsa, y = lcavol, color = factor(svi))) + geom_point()
prostate.plot + geom_abline(intercept = coefs.est[1] + coefs.est[2], slope = coefs.est[3], color = "red",
                             geom_abline(intercept = coefs.est[1], slope = coefs.est[3], color = "blue") +
                             geom_line(data = data.svi, aes(x = lpsa, y = lwr), color = "red", linetype = "dashed") +
                             geom_line(data = data.svi, aes(x = lpsa, y = upr), color = "red", linetype = "dashed") +
                             geom_line(data = data.svi.not, aes(x = lpsa, y = lwr), color = "blue", linetype = "dashed") +
                             geom_line(data = data.svi.not, aes(x = lpsa, y = upr), color = "blue", linetype = "dashed"))

```

