Homework 4

Zach White

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data(Prostate)
prostate.sv = lm(lcavol ~ svi + lpsa, data = Prostate)
summary.sv = summary(prostate.sv)
coefs = summary.sv$coefficients
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")

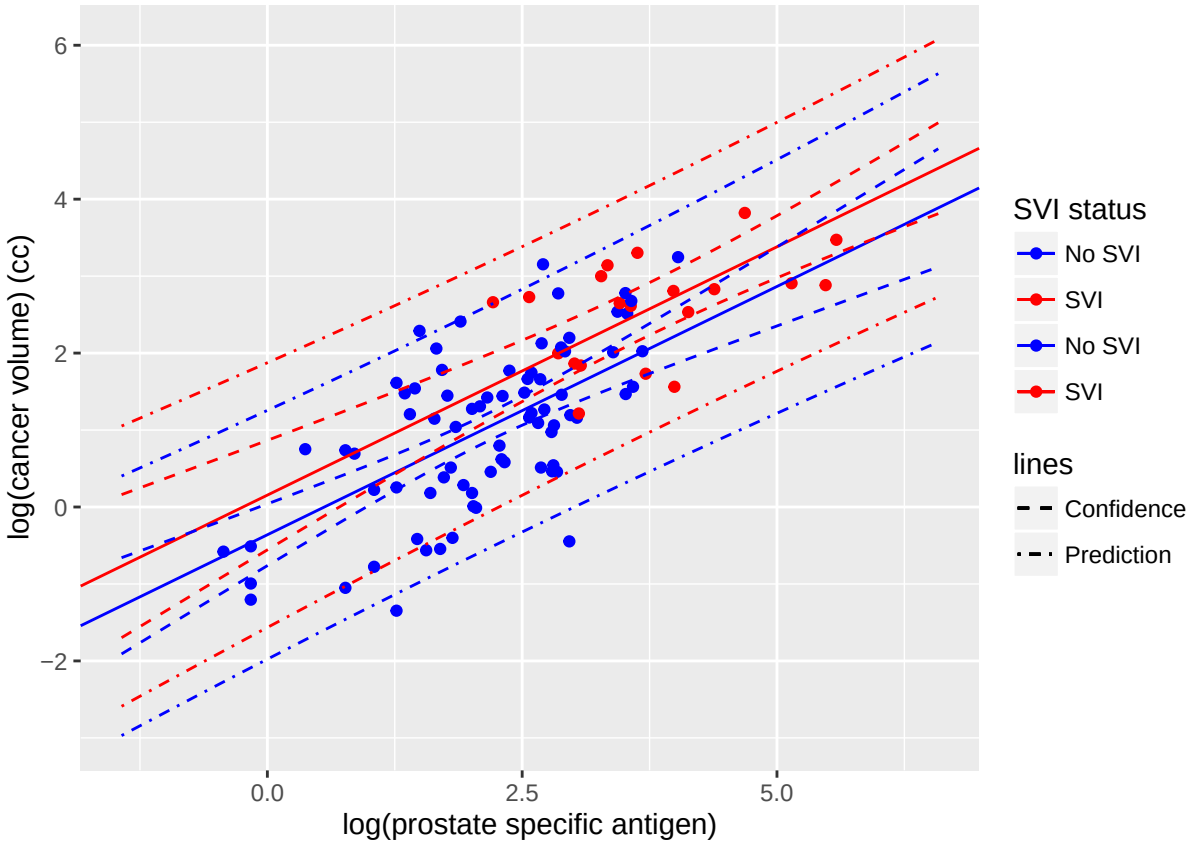
data2 <- data1
data2$svi <- rep(1,100)

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

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

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

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")) +
  geom_line(data = pi.data.svi, aes(x = lpsa, y = lwr, color = "red", linetype = "dotdash")) +
  geom_line(data = pi.data.svi, aes(x = lpsa, y = upr, color = "red", linetype = "dotdash")) +
  geom_line(data = pi.data.svi.not, aes(x = lpsa, y = lwr, color = "blue", linetype = "dotdash")) +
  geom_line(data = pi.data.svi.not, aes(x = lpsa, y = upr, color = "blue", linetype = "dotdash")) +
  labs(x = "log(prostate specific antigen)" , y = "log(cancer volume) (cc)"  ) +
  scale_colour_manual(name = "SVI status",values=c("blue","red","blue","red"), labels = c("No SVI", "SVI
  scale_linetype_manual(name = "lines",values = c("dashed", "dotdash"), labels = c("Confidence", "Predi
```


6
4
2
0
−2
log(cancer volume) (cc)
0.0
2.5
5.0
log(prostate specific antigen)
SVI status
No SVI
SVI
No SVI
SVI
lines
Confidence
Prediction