Case-study-hypertension

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```
rhc <- read.csv("http://biostat.mc.vanderbilt.edu/wiki
/pub/Main/DataSets/rhc.csv")
rhc <- rhc[,-1]</pre>
```

Data preparation

```
data <- rhc[,c("t3d30", "dth30", "swang1", "age", "cat1",</pre>
"ca", "sex", "race", "edu", "income", "ninsclas", "res
p", "card", "neuro", "gastr", "renal", "meta", "hema",
       "seps", "trauma", "ortho", "temp1", "meanbp1",
"resp1", "hrt1", "pafi1", "paco21", "ph1", "wblc1", "h
emal", "sod1", "pot1", "crea1", "bili1", "alb1", "scom
a1",
       "aps1", "dnr1", "das2d3pc", "cardiohx", "chfhx"
, "dementhx", "chrpulhx" , "renalhx" , "liverhx" , "gi
bledhx" , "malighx" , "immunhx" , "transhx" , "amihx")
1
dd <- rhc[,c("t3d30", "dth30", "swang1", "age", "cat1", "</pre>
ca", "sex", "race", "edu", "income", "ninsclas", "resp
", "card", "neuro", "gastr", "renal", "meta", "hema",
       "seps", "trauma", "ortho", "temp1", "meanbp1",
"resp1", "hrt1", "pafi1", "paco21", "ph1", "wblc1", "h
ema1", "sod1", "pot1", "crea1", "bili1", "alb1", "scom
a1",
       "aps1", "dnr1", "das2d3pc", "cardiohx", "chfhx"
 "dementhx", "chrpulhx", "renalhx", "liverhx", "gi
bledhx" , "malighx" , "immunhx" , "transhx" , "amihx")
1
for (i in names(data)) {
  data[,i] <- as.numeric((data[,i]))</pre>
  if(mean(data[,i], na.rm = T) < 5){
    data[,i] <- as.factor((dd[,i]))</pre>
  }else{
    data[,i] <- ((dd[,i]))
  }
}
data$dth30 <- as.numeric(data$dth30) - 1</pre>
index <- sample(nrow(data), 0.6*nrow(data), replace =</pre>
T)
train <- data[index,]</pre>
```

Data preparation

Cox Regression

valid <- data[-index,]</pre>

Cox Regression

fit3 <- coxph(Surv(t3d30,dth30) ~ swang1 + age + sex +
race + edu + income + ninsclas + resp + card + neuro +
gastr + renal + meta + hema + seps + trauma + ortho +
temp1 + meanbp1 + resp1 + hrt1 + pafi1 + paco21 + ph1
+ wblc1 + hema1 + sod1 + pot1 + creal + bili1 + alb1 +
scoma1 + aps1 + dnr1 + das2d3pc + cardiohx + chfhx + d
ementhx + chrpulhx + renalhx + liverhx + gibledhx + ma
lighx + immunhx + transhx + amihx, data = train, metho
d="breslow")</pre>

```
## Warning in fitter(X, Y, strats, offset, init, contr
ol,
## weights = weights, : Loglik converged before variab
## 36,38,43,88,94,98,102,103,106,109,111,113,114,115,1
16,117,118,119,120,121,122,123,124,125,126,127,128,129
,130,131,132,133,134,135,136,137,138,139,140,141,142,1
43,144,145,146,147,148,149,150,151,152,153,154,155,156
,157,158,159,160,161,162,163,164,165,166,167,168,169,1
70,171,172,173,174,175,176,178,179,180,181,183,184,185
,186,187,188,189,190,191,192,193,194,196,197,199,200,2
02,203,204,205,207,208,209,210,212,213,214,215,216,217
,218,221,222,223,224,225,226,229,230,242,243,246,252,2
53,254,260,301,309,312,320,321,326,327,329,330,333,335
,337,338,339,341,355,356,361,381,383,386,389,391,394,3
98,407,423,433,438,440,451,452,465,475,481,505,514,530
,531,532,533,534,535,536,537,538,539,540,541,542,543,5
44,545,546,547,548,550,551,552,553,554,555,556,557,558
,559,560,561,562,563,564,565,566,567,568,569,570,571,5
73,576,578;
## beta may be infinite.
```

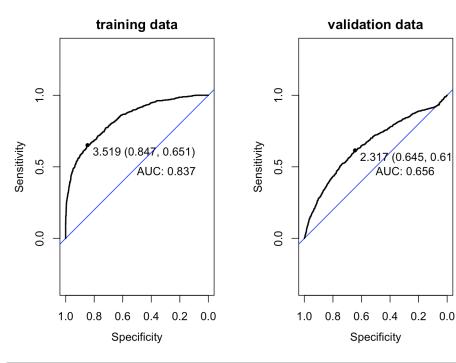
```
pred1.1 <- predict(fit3, newdata = valid, type = "risk</pre>
")
pred2.2 <- predict(fit3, newdata = train, type = "risk</pre>
")
r1.1 <- roc(valid$dth30~pred1.1)
r2.1 <- roc(train$dth30~pred2.2)
par(mfrow = c(1,2))
plot(r2.1, print.auc = T, print.thres = T, identity.co
l="blue", main = "training data")
plot(r1.1, print.auc = T, print.thres = T, identity.co
l="blue", main = "validation data")
```

validation data

Specificity

2.317 (0.645, 0.61

AUC: 0.656



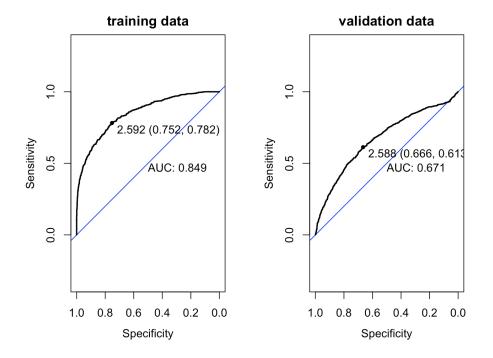
fit1 <- coxph(Surv(t3d30,dth30) ~ swang1 + age*cat1 + age*ca + age + sex + race + edu + income + ninsclas + resp + card + neuro + gastr + renal + meta + hema + se ps + trauma + ortho + temp1 + meanbp1 + resp1 + hrt1 + pafi1 + paco21 + ph1 + wblc1 + hema1 + sod1 + pot1 + c real + bili1 + alb1 + scoma1 + aps1 + dnr1 + das2d3pc + cardiohx + chfhx + dementhx + chrpulhx + renalhx + 1 iverhx + gibledhx + malighx + immunhx + transhx + amih x, data = train, method="breslow")

Warning in fitter(X, Y, strats, offset, init, contr ol, ## weights = weights, : Loglik converged before variab ## 5,46,48,53,98,104,108,112,113,119,121,123,124,125,1 26, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139 ,140,141,142,143,144,145,146,147,148,149,150,151,152,1 53, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166 ,167,168,169,170,171,172,173,174,175,176,177,178,179,1 80,181,182,183,184,185,186,188,189,190,191,193,194,195 ,196,197,198,199,200,201,202,203,204,206,207,209,210,2 12,213,214,215,217,218,219,220,222,223,224,225,226,227 ,228,231,232,233,234,235,236,239,240,252,253,256,263,2 64,269,270,271,311,319,322,330,331,336,337,339,340,343 ,345,347,348,349,351,365,366,371,391,393,396,399,401,4 04,408,417,433,443,448,450,461,462,475,485,491,515,524 ,540,541,542,543,544,545,546,547,548,549,550,551,552,5 53,554,555,556,557,558,560,561,562,563,564,565,566,567 ,568,569,570,571,572,573,574,575,576,577,579,580,581,5 83,586,588; ## beta may be infinite.

```
pred1 <- predict(fit1, newdata = valid, type = "risk")
pred2 <- predict(fit1, newdata = train, type = "risk")

r1 <- roc(valid$dth30~pred1)
r2 <- roc(train$dth30~pred2)

par(mfrow = c(1,2))
plot(r2, print.auc = T, print.thres = T, identity.col=
"blue", main = "training data")
plot(r1, print.auc = T, print.thres = T, identity.col=
"blue", main = "validation data")</pre>
```



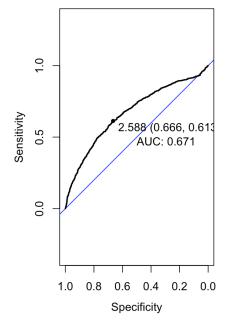
```
par(mfrow = c(1,2))
plot(r1.1, print.auc = T, print.thres = T, identity.co
l="blue", main = "validation data without interaction"
)

plot(r1, print.auc = T, print.thres = "best", identity
.col="blue", main = "validation data with interaction"
)
```



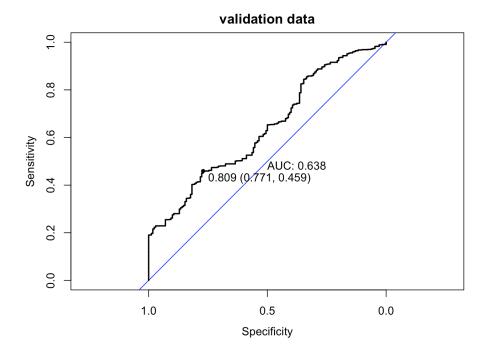
0: - 2.317 (0.645, 0.61 AUC: 0.656 AUC: 0.656 1.0 0.8 0.6 0.4 0.2 0.0 Specificity

validation data with interaction

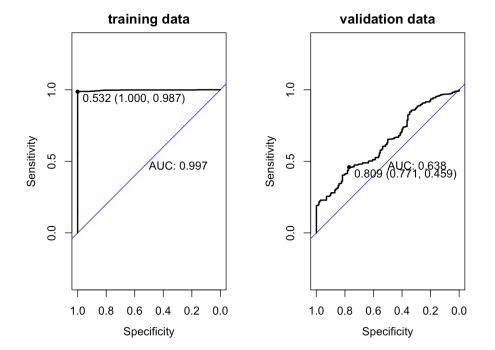


```
fit2 <- rfsrc(Surv(t3d30,dth30) ~ ., data = train, nsp
lit = 10, importance = TRUE, ntree = 100)</pre>
```

```
p1 <- predict(fit2, newdata = valid)</pre>
Fsurv <- data.frame(p1$survival)</pre>
Rsurv <- matrix(NA, nrow = nrow(Fsurv), ncol = 30)</pre>
for (i in 1:30) {
  Rsurv[i,valid$t3d30[i]:30] <- 0</pre>
Rsurv <- data.frame(Rsurv)</pre>
Rsurv[is.na(Rsurv)] <- 1</pre>
Fsurv <- data.frame(t(Fsurv))</pre>
Rsurv <- data.frame(t(Rsurv[,1:29]))</pre>
fsurv <- gather(Fsurv, key = "time", value = "status",</pre>
index = 1:ncol(Fsurv))
rsurv <- gather(Rsurv, key = "time", value = "status",</pre>
index = 1:ncol(Rsurv))
r2 <- roc(rsurv$status ~fsurv$status)</pre>
plot(r2, print.auc = T, print.thres = T, identity.col=
"blue", main = "validation data")
```



```
p2 <- predict(fit2, newdata = train)</pre>
Fsurv2 <- data.frame(p2$survival)
Rsurv2 <- matrix(NA, nrow = nrow(Fsurv2), ncol = 30)</pre>
for (i in 1:30) {
  Rsurv2[i,train$t3d30[i]:30] <- 0</pre>
Rsurv2 <- data.frame(Rsurv2)</pre>
Rsurv2[is.na(Rsurv2)] <- 1</pre>
Fsurv2 <- data.frame(t(Fsurv2))</pre>
Rsurv2 <- data.frame(t(Rsurv2[,1:29]))</pre>
fsurv2 <- gather(Fsurv2, key = "time", value = "status</pre>
", index = 1:nrow(Fsurv2))
rsurv2 <- gather(Rsurv2, key = "time", value = "status</pre>
", index = 1:nrow(Rsurv2))
r3 <- roc(rsurv2$status ~fsurv2$status)
par(mfrow = c(1,2))
plot(r3, print.auc = T, print.thres = T, identity.col=
"blue", main = "training data")
plot(r2, print.auc = T, print.thres = T, identity.col=
"blue", main = "validation data")
```



```
data1 <- data0 <- data
data1$swang1 <- data$swang1[2]
data0$swang1 <- data$swang1[1]

fit1pred1 <- survfit(fit1, newdata = data1)
fit1pred2 <- survfit(fit1, newdata = data0)</pre>
```