# $MetBiost\_HW2$

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### Part I: Prediction models for having a major smoking caused disease

#### Problem 1.

##

##

0 5898 3126 3017

1 657 639 311

```
load(here("data", "nmes.rdata"))
nmes[nmes == "."] <- NA
nmes <- mutate(nmes, mscd = ifelse((lc5==1)|(chd5==1), 1, 0))
Create variable smkstatus to distinguish people who never smoked, former smokers and current smokers:
nmes <- mutate(nmes, smkstatus = case_when(</pre>
  eversmk==0 ~ 0, #0 stands for never smoked
  (eversmk==1) & (current==0) ~ 1, #1 stands for former smokers
  (eversmk==1) & (current==1) ~ 2 #2 stands for current smokers
 ))
Select a subset of features as predictors for statistical prediction models:
d <- data.frame(</pre>
  mscd = factor(nmes$mscd),
  age = nmes$lastage,
 male = factor(nmes$male),
  smkstatus = factor(nmes$smkstatus),
  packyears = as.numeric(nmes$packyears),
 marital = factor(nmes$marital)
set.seed(1234)
if(!file.exists(here("data", "imp_d.RData"))){
  imp.d \leftarrow rfImpute(x = d[,2:6], y = d[,1])
  save(imp.d, file = "imp_d.RData")
  load(here("data", "imp d.RData"))
  imp.d \leftarrow rename(imp.d, mscd = `d[, 1]`)
}
summary(imp.d)
##
   mscd
                              male
                                       smkstatus packyears
                                                                   marital
                   age
                                               Min. : 0.00
  0:12041
              Min. :40.0
                              0:7760
                                       0:6555
                                                                   1:8869
   1: 1607
              1st Qu.:49.0
                              1:5888
                                       1:3765
                                                  1st Qu.: 0.00
                                                                   2:2557
##
##
              Median:61.0
                                       2:3328
                                                 Median: 3.86
                                                                   3:1205
              Mean :60.6
                                                  Mean : 17.00
##
                                                                   4: 355
              3rd Qu.:71.0
                                                  3rd Qu.: 28.00
                                                                   5: 662
##
              Max.
                                                         :216.00
table(MSCD = imp.d$mscd, Smoking_Status = imp.d$smkstatus)
##
       Smoking_Status
## MSCD
         0 1
                     2
```

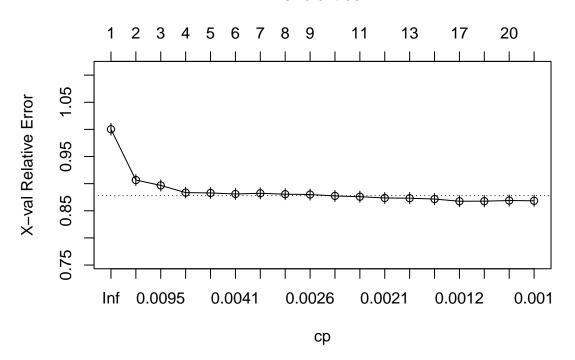
Among the 13648 people in the imputed data set, 1607 of them have major smoking-caused disease(MSCD) and 12041 of them don't. Among people who don't have MSCD, 5898 of them never smoked, 3126 are former smokers, and 3017 are current smokers. Among people who have MSCD, 657 of them never smoked, 639 are former smokers, and 311 are current smokers.

### Problem 2.

```
set.seed(1234)
# Create indicators for the cases and controls
orig0 <- which(d$mscd == 0)</pre>
orig1 <- which(d$mscd == 1)</pre>
# Create an upweighted sample of cases
orig1up <- sample(orig1, ceiling(length(orig1)*2.5), replace = TRUE)</pre>
# Create a new upweighted dataset
updat <- rbind(imp.d[orig0, ], imp.d[orig1up, ])</pre>
set.seed(1234)
# From the new upweighted dataset, create a training and validation sample
controls <- which(updat$mscd == 0)</pre>
cases <- which(updat$mscd == 1)</pre>
train0 <- sample(controls, floor(length(controls)*0.7))</pre>
train1 <- sample(cases, floor(length(cases)*0.7))</pre>
# Name the training and validation samples
d.train <- rbind(updat[train0, ], updat[train1, ])</pre>
d.test <- rbind(updat[-train0, ], updat[-train1, ])</pre>
```

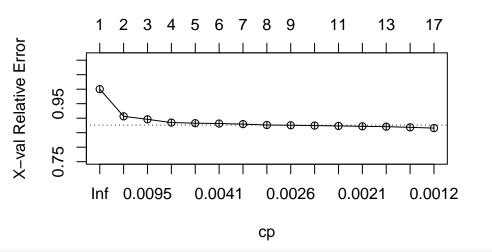
### Problem 3.

size of tree



Find the optimal value of cp that yields the smallest cross-validation error. Then prune the tree using this optimal cp value:

### size of tree



fancyRpartPlot(tree.p3, sub = "", palettes = "OrRd")

