STATS 101C - Statistical Models and Data Mining - Homework $\boldsymbol{6}$

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Question 1 (Exercise 2 from Section 5.4)

Part A

The probability that the first bootstrap observation is not the jth observation from the original sample is $1-\frac{1}{n}$. The probability that it is the jth observation is $\frac{1}{n}$ because each element is equally as likely to be chosen. Thus, we just do $1-\frac{1}{n}$ to obtain the probability that is is not.

Part B

The same answer and reasoning as seen in Part A since the position in the bootstrap sample does not affect the probability of which observation is chosen.

Part C

We know that the probability that the jth observation is not in the first, second, etc bootstrap observation is $1 - \frac{1}{n}$. Thus, if there are n spots, the probability that the jth observation is not in any of the spots (so the jth observation isn't in the bootstrap sample at all) is just $(1 - \frac{1}{n})^n$.

Part D

$$1 - (1 - 1/5)^5 = .67232$$

Part E

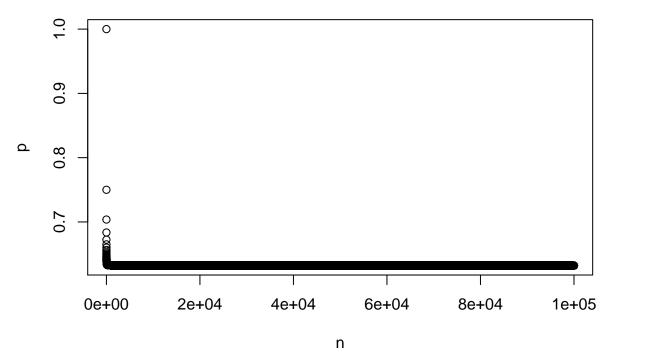
$$1 - (1 - 1/100)^{100} = .63397$$

Part F

$$1 - (1 - 1/10000)^{10000} = .63214$$

Part G

```
n <- 1:100000
p <- 1 - (1 - 1/(n))^(n)
plot(p, xlab = 'n')</pre>
```



```
min(p)
```

[1] 0.6321224

We notice that the probability drops really quickly and begins to stabilize around .63.

Part H

```
set.seed(999)
store <- rep(NA, 10000)
for (i in 1:10000) {
   store[i] <- sum(sample(1:100, rep=TRUE) == 4) > 0
}
mean(store)

## [1] 0.6376

1 - (1 - 1/(100))^(100)
```

[1] 0.6339677

We see that the empirical rate is slightly higher than the actual rate (0.6376 vs 0.6339677).

Question 2 (Exercise 10 from Section 8.4)

```
library(ISLR)
library(gbm)
library(glmnet)
library(randomForest)
library(caret)
```

Part A

```
Hitters <- Hitters[!is.na(Hitters$Salary),]
Hitters$Salary <- log(Hitters$Salary)</pre>
```

Part B

```
hitters.training <- Hitters[1:200, ]
hitters.testing <- Hitters[-(1:200), ]

dim(hitters.training)

## [1] 200 20

dim(hitters.testing)

## [1] 63 20</pre>
```

Part C

```
set.seed(999)
alpha.grid \leftarrow seq(.000001, 1, by = .01)
train.mse <- rep(NA, length(alpha.grid))</pre>
test.mse <- rep(NA, length(alpha.grid))</pre>
for (i in seq(1, length(alpha.grid))){
  boost.temp <- gbm(Salary ~ .,</pre>
                        data = hitters.training,
                        distribution = "gaussian",
                        n.trees = 1000,
                        shrinkage = alpha.grid[i])
  train.predicted <- predict(boost.temp, hitters.training, n.trees = 1000)</pre>
  test.predicted <- predict(boost.temp, hitters.testing, n.trees = 1000)</pre>
  train.mse[i] <- mean((train.predicted - hitters.training$Salary)^2)</pre>
  test.mse[i] <- mean((test.predicted - hitters.testing$Salary)^2)</pre>
}
plot(alpha.grid, train.mse,
     xlab = "Shrinkage Parameter",
     ylab = "Training MSE")
      0.8
      9.0
      0.4
```

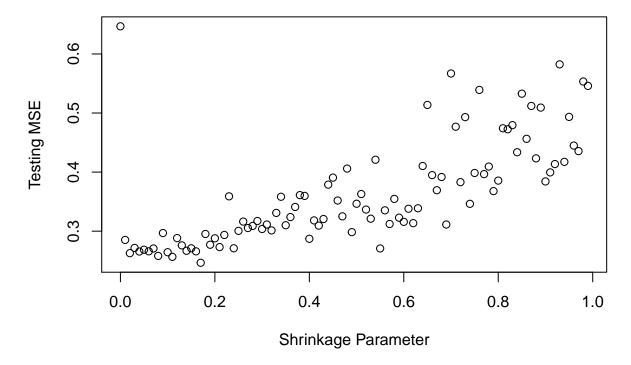
```
min(train.mse)

## [1] 0.0004535139

alpha.grid[which.min(train.mse)]
```

[1] 0.960001

Part D



min(test.mse)

[1] 0.2465204

```
alpha.grid[which.min(test.mse)]
```

[1] 0.170001

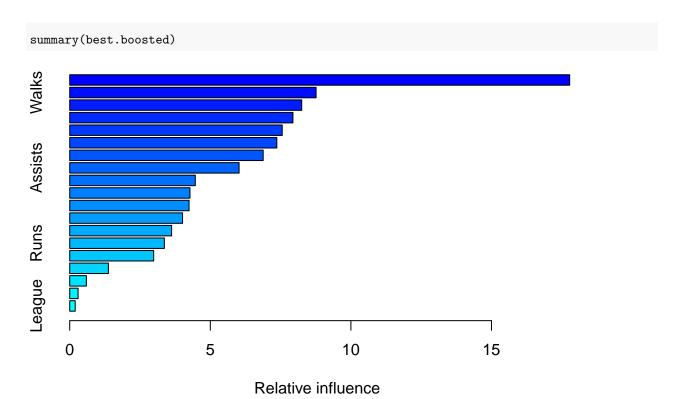
Part E

```
lm.model <- lm(Salary ~ ., data = hitters.training)</pre>
lm.predictions <- predict(lm.model, newdata = hitters.testing)</pre>
lm.test.mse <- mean((lm.predictions - hitters.testing$Salary)^2)</pre>
lm.test.mse
## [1] 0.4917959
grid <- 10^seq(10, -2, length = 100)
x <- model.matrix(Salary ~ ., hitters.training)[, -1]
y <- hitters.training$Salary
ridge.model <- glmnet(x, y,</pre>
                       family = "gaussian",
                       alpha = 0,
                       lambda = grid,
                       standardize = TRUE)
set.seed(999)
ridge.cv.output <- cv.glmnet(x, y, family = "gaussian", alpha = 0,</pre>
                               lambda = grid, standardize = TRUE,
                               nfolds = 10)
ridge.best.lambda.cv <- ridge.cv.output$lambda.min</pre>
ridge.predictions <- predict(ridge.model,</pre>
                               s = ridge.best.lambda.cv,
                               newx = model.matrix(Salary ~ ., hitters.testing)[,-1])
ridge.test.mse <- mean((ridge.predictions - hitters.testing$Salary)^2)</pre>
ridge.test.mse
```

[1] 0.4645472

The test MSE for boosting, linear regression, and ridge regression are 0.2465204, 0.4917959, and 0.4645472, respectively. We can see that using boosting yielded us the lowest test MSE out of all three methods.

Part F

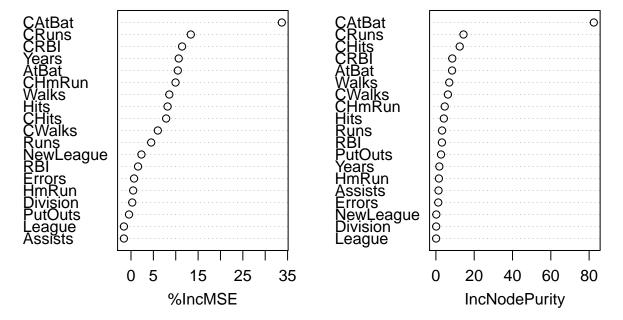


##		var	rel.inf
##	CAtBat	\mathtt{CAtBat}	17.7814528
##	Walks	Walks	8.7623928
##	CWalks	CWalks	8.2509715
##	PutOuts	PutOuts	7.9388886
##	CRuns	CRuns	7.5583932
##	CRBI	CRBI	7.3659814
##	Years	Years	6.8809469
##	Assists	Assists	6.0240156
##	CHmRun	$\tt CHmRun$	4.4665944
##	HmRun	HmRun	4.2757269
##	RBI	RBI	4.2446482
##	Hits	Hits	4.0136771
##	AtBat	AtBat	3.6233743
##	Runs	Runs	3.3658857
##	Errors	Errors	2.9860672
##	CHits	CHits	1.3760289
##	Division	Division	0.5921576
##	${\tt NewLeague}$	NewLeague	0.2975151
##	League	League	0.1952818

The most important variables in the boosted model are 'CAtBat', 'Walks', 'CWalks', 'PutOuts', and 'CRuns'.

Part G

bagged.tree



```
bagged.tree.predictions <- predict(bagged.tree, hitters.testing)
bagged.tree.mse <- mean((bagged.tree.predictions - hitters.testing$Salary)^2)
bagged.tree.mse</pre>
```

[1] 0.2323669

Using bagging, the test MSE is 0.2323669, which is not better than boosting. The most important predictors when using bagging are 'CAtBat', 'CRuns', 'CRBI', 'Years', and 'AtBat'. It is interesting to note that just cause a variable is important for bagging, that does not mean that variable will be important for boosting. For example, 'AtBat' is important for bagging, but not so important for boosting.