Model Fitting II

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Slide Code

```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.0 --

## v ggplot2 3.3.3     v purrr   0.3.4
## v tibble  3.0.6     v dplyr   1.0.4
## v tidyr   1.1.2     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.1

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(caret)
```

```
## Loading required package: lattice

##
## Attaching package: 'caret'

## The following object is masked from 'package:purrr':
##
##     lift
```

```
insurance <- read_csv("insurance.csv")
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   age = col_double(),
##   sex = col_character(),
##   bmi = col_double(),
##   children = col_double(),
##   smoker = col_character(),
##   region = col_character(),
##   charges = col_double()
## )
```

```
insurance
```

```
## # A tibble: 1,338 x 7
##      age sex      bmi children smoker region    charges
##    <dbl> <chr>  <dbl>    <dbl> <chr>  <chr>       <dbl>
##  1    19 female  27.9        0 yes    southwest  16885.
##  2    18 male    33.8        1 no     southeast   1726.
##  3    28 male    33          3 no     southeast   4449.
##  4    33 male    22.7        0 no     northwest  21984.
##  5    32 male    28.9        0 no     northwest   3867.
##  6    31 female  25.7        0 no     southeast   3757.
##  7    46 female  33.4        1 no     southeast   8241.
##  8    37 female  27.7        3 no     northwest   7282.
##  9    37 male    29.8        2 no     northeast   6406.
## 10    60 female  25.8        0 no     northwest  28923.
## # ... with 1,328 more rows
```

```
# transform categories to numbers
insurance <- insurance %>%
  mutate(sexN = case_when(
    sex == "male" ~ 1,
    sex == "female" ~ 0
    )) %>%
  mutate(smokerN = case_when(
    smoker == "yes" ~ 1,
    smoker == "no" ~ 0
    )) %>%
  mutate(regionN = case_when(
    region == "southwest" ~ 1,
    region == "southeast" ~ 2,
    region == "northwest" ~ 3,
    region == "northeast" ~ 4
    ))

# only select numeric variables
df <- insurance %>%
  dplyr::select(charges, age, sexN, bmi, children, smokerN, regionN)

# drop missing values NAs
df1 <- drop_na(df)

# compute correlation between predictos
cor(df1[,2:7])
```

```
##                   age         sexN          bmi    children      smokerN
## age       1.000000000 -0.020855872  0.109271882  0.04246900 -0.025018752
## sexN     -0.020855872  1.000000000  0.046371151  0.01716298  0.076184817
## bmi       0.109271882  0.046371151  1.000000000  0.01275890  0.003750426
## children  0.042468999  0.017162978  0.012758901  1.00000000  0.007673120
## smokerN  -0.025018752  0.076184817  0.003750426  0.00767312  1.000000000
## regionN  -0.002127313 -0.004588385 -0.157565849 -0.01656945  0.002180682
##               regionN
## age      -0.002127313
```

```
## sexN     -0.004588385
## bmi      -0.157565849
## children -0.016569446
## smokerN   0.002180682
## regionN   1.000000000
```

```
# compute correlation between predictos and the target
cor(df1[,1:7])
```

```
##              charges          age         sexN          bmi    children
## charges   1.000000000  0.299008193  0.057292062  0.198340969  0.06799823
## age       0.299008193  1.000000000 -0.020855872  0.109271882  0.04246900
## sexN      0.057292062 -0.020855872  1.000000000  0.046371151  0.01716298
## bmi       0.198340969  0.109271882  0.046371151  1.000000000  0.01275890
## children  0.067998227  0.042468999  0.017162978  0.012758901  1.00000000
## smokerN   0.787251430 -0.025018752  0.076184817  0.003750426  0.00767312
## regionN   0.006208235 -0.002127313 -0.004588385 -0.157565849 -0.01656945
##               smokerN      regionN
## charges    0.787251430  0.006208235
## age       -0.025018752 -0.002127313
## sexN       0.076184817 -0.004588385
## bmi        0.003750426 -0.157565849
## children   0.007673120 -0.016569446
## smokerN    1.000000000  0.002180682
## regionN    0.002180682  1.000000000
```

```
# age, bmi, and smoking are highly correlated with health costs

set.seed(12L) # set a starting seed to be able to get reproducible results

# partition data
trainIndex <- createDataPartition(df1$charges, # target variable
                                  p = 0.8, # percentage that goes to training
                                  list = FALSE, # results will not be in a list
                                  times = 1) # number of partitions to create

charges_train <- df1[trainIndex, ] # data frame for training
```

```
## Warning: The ‘i‘ argument of ‘‘[‘()‘ can’t be a matrix as of tibble 3.0.0.
## Convert to a vector.
## This warning is displayed once every 8 hours.
## Call ‘lifecycle::last_warnings()‘ to see where this warning was generated.
```

```
charges_test <- df1[-trainIndex, ] # data frame for testing

# use training set to build model
model <- train(charges ~ age + bmi + smokerN,
               data = charges_train, # use training set
               method = "lm") # linear regression

# now predict outcomes in test set
p <- predict(model, charges_test)
```

```r
# how did we do? calculate performance across resamples
# RMSE and R-squared
postResample(pred = p, obs = charges_test$charges)
```

```
##         RMSE     Rsquared          MAE
## 5808.0045894    0.7989742 4184.9721150
```

```r
# on average, our prediction is off by $5,808.00

# how can we improve performance? Try a different method!
model2 <- train(charges ~ age + bmi + smokerN,
                data = charges_train, # use training set
                method = "ranger") # random forest
```

```
## note: only 2 unique complexity parameters in default grid. Truncating the grid to 2 .
```

```r
# now predict outcomes in test set
p1 <- predict(model2, charges_test)

# how did we do? calculate performance across resamples
# RMSE and R-squared
postResample(pred = p1, obs = charges_test$charges)
```

```
##         RMSE     Rsquared          MAE
## 4205.4282707    0.8933816 2436.1432025
```

```r
# on average, our prediction is off by $4,632.99

# first collect the resampling results of each model
resamps <- resamples(list(LM = model,
                          RF = model2))
resamps
```

```
##
## Call:
## resamples.default(x = list(LM = model, RF = model2))
##
## Models: LM, RF
## Number of resamples: 25
## Performance metrics: MAE, RMSE, Rsquared
## Time estimates for: everything, final model fit
```

```r
# then use a simple t-test to evaluate the null hypothesis that there is no difference
summary(diff(resamps))
```

```
##
## Call:
## summary.diff.resamples(object = diff(resamps))
##
## p-value adjustment: bonferroni
```

```
## Upper diagonal: estimates of the difference
## Lower diagonal: p-value for H0: difference = 0
##
## MAE
##    LM        RF
## LM           1403
## RF < 2.2e-16
##
## RMSE
##    LM        RF
## LM           1156
## RF 2.139e-15
##
## Rsquared
##    LM       RF
## LM          -0.09466
## RF 1.17e-14
```