5. Problem Statement

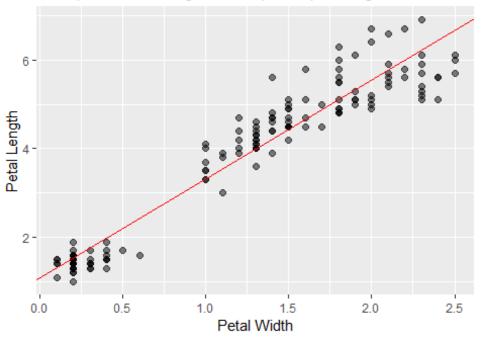
- 1. Perform the below given activities:
- a. Take a sample data set of your choice
- b. Apply random forest, logistic regression using Spark R
- c. Predict for new dataset

```
library(sparklyr)
library(ggplot2)
library(dplyr)
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
##
       intersect, setdiff, setequal, union
sc <- spark connect(master = "local")</pre>
iris_tbl <- copy_to(sc, iris, "iris", overwrite = TRUE)</pre>
iris_tbl
## # Source:
               table<iris> [?? x 5]
## # Database: spark_shell_connection
##
      Sepal_Length Sepal_Width Petal_Length Petal_Width Species
##
             <dbl>
                          <dbl>
                                        <dbl>
                                                    <dbl> <chr>
## 1
               5.1
                            3.5
                                          1.4
                                                      0.2 setosa
               4.9
                            3
## 2
                                          1.4
                                                      0.2 setosa
               4.7
## 3
                            3.2
                                          1.3
                                                      0.2 setosa
## 4
               4.6
                            3.1
                                          1.5
                                                      0.2 setosa
## 5
               5
                            3.6
                                          1.4
                                                      0.2 setosa
               5.4
## 6
                            3.9
                                          1.7
                                                      0.4 setosa
## 7
                                                      0.3 setosa
               4.6
                            3.4
                                          1.4
## 8
               5
                            3.4
                                          1.5
                                                      0.2 setosa
                            2.9
                                                      0.2 setosa
## 9
               4.4
                                          1.4
```

```
## 10
               4.9
                           3.1
                                        1.5
                                                     0.1 setosa
## # ... with more rows
lm_model <- iris_tbl %>%
  select(Petal Width, Petal Length) %>%
  ml linear regression(Petal Length ~ Petal Width)
iris tbl %>%
  select(Petal_Width, Petal_Length) %>%
  collect %>%
  ggplot(aes(Petal_Length, Petal_Width)) +
  geom_point(aes(Petal_Width, Petal_Length), size = 2, alpha = 0.5) +
  geom_abline(aes(slope = coef(lm_model)[["Petal_Width"]],
                  intercept = coef(lm_model)[["(Intercept)"]]),
              color = "red") +
  labs(
    x = "Petal Width",
    y = "Petal Length",
    title = "Linear Regression: Petal Length ~ Petal Width",
    subtitle = "Use Spark.ML linear regression to predict petal length as a f
unction of petal width."
```

Linear Regression: Petal Length ~ Petal Width

Use Spark.ML linear regression to predict petal length as a function of



```
pca_model <- tbl(sc, "iris") %>%
   select(-Species) %>%
   ml_pca()
print(pca_model)
```

```
## Explained variance:
##
##
           PC1
                       PC2
                                   PC3
                                               PC4
## 0.924618723 0.053066483 0.017102610 0.005212184
##
## Rotation:
##
                        PC1
                                    PC2
                                                PC3
                                                           PC4
## Sepal Length -0.36138659 -0.65658877 0.58202985 0.3154872
## Sepal Width
               0.08452251 -0.73016143 -0.59791083 -0.3197231
## Petal Length -0.85667061 0.17337266 -0.07623608 -0.4798390
## Petal Width -0.35828920 0.07548102 -0.54583143 0.7536574
```

b. Apply random forest, logistic regression using Spark R

c. Predict for new dataset

```
#Random Forest
#Use Spark's Random Forest to perform regression or multicla
ss classification.
rf_model <- iris_tbl %>%
  ml random forest(Species ~ Petal Length + Petal Width, type = "classificati
on")
rf predict <- sdf predict(rf model, iris tbl) %>%
  ft_string_indexer("Species", "Species_idx") %>%
  collect
## Warning in sdf_predict.ml_model(rf_model, iris_tbl): The signature
## sdf predict(model, dataset) is deprecated and will be removed in a future
## version. Use sdf predict(dataset, model) or ml predict(model, dataset)
## instead.
table
## function (..., exclude = if (useNA == "no") c(NA, NaN), useNA = c("no",
       "ifany", "always"), dnn = list.names(...), deparse.level = 1)
##
## {
##
       list.names <- function(...) {</pre>
           1 <- as.list(substitute(list(...)))[-1L]</pre>
##
##
           nm < - names(1)
##
           fixup <- if (is.null(nm))</pre>
##
               seq_along(1)
           else nm == ""
##
           dep <- vapply(l[fixup], function(x) switch(deparse.level +</pre>
##
               1, "", if (is.symbol(x)) as.character(x) else "",
##
               deparse(x, nlines = 1)[1L]), "")
##
           if (is.null(nm))
##
```

```
##
                dep
##
            else {
##
                nm[fixup] <- dep
##
##
            }
##
##
       miss.use <- missing(useNA)</pre>
##
       miss.exc <- missing(exclude)</pre>
##
       useNA <- if (miss.use && !miss.exc && !match(NA, exclude,
##
            nomatch = 0L)
##
            "ifany"
##
       else match.arg(useNA)
##
       doNA <- useNA != "no"
##
       if (!miss.use && !miss.exc && doNA && match(NA, exclude,
##
            nomatch = 0L)
            warning("'exclude' containing NA and 'useNA' != \"no\"' are a bit
##
contradicting")
##
       args <- list(...)</pre>
##
       if (!length(args))
##
            stop("nothing to tabulate")
##
       if (length(args) == 1L && is.list(args[[1L]])) {
##
            args <- args[[1L]]
##
            if (length(dnn) != length(args))
##
                dnn <- if (!is.null(argn <- names(args)))</pre>
##
##
                else paste(dnn[1L], seq_along(args), sep = ".")
##
##
       bin <- 0L
##
       lens <- NULL
##
       dims <- integer()</pre>
##
       pd <- 1L
##
       dn <- NULL
##
       for (a in args) {
##
            if (is.null(lens))
##
                lens <- length(a)</pre>
##
            else if (length(a) != lens)
                stop("all arguments must have the same length")
##
##
            fact.a <- is.factor(a)</pre>
##
            if (doNA)
##
                aNA \leftarrow anyNA(a)
##
            if (!fact.a) {
##
##
                a <- factor(a, exclude = exclude)</pre>
##
            }
            add.na <- doNA
##
##
            if (add.na) {
##
                ifany <- (useNA == "ifany")</pre>
##
                anNAc <- anyNA(a)
##
                add.na <- if (!ifany || anNAc) {
##
                     11 <- levels(a)</pre>
```

```
##
                     if (add.ll <- !anyNA(ll)) {
##
                       11 < -c(11, NA)
##
                       TRUE
                     }
##
##
                     else if (!ifany && !anNAc)
##
                       FALSE
                     else TRUE
##
##
                else FALSE
##
##
##
            if (add.na)
                 a <- factor(a, levels = 11, exclude = NULL)
##
##
            else ll <- levels(a)
##
            a <- as.integer(a)</pre>
            if (fact.a && !miss.exc) {
##
                 11 <- 11[keep <- which(match(11, exclude, nomatch = 0L) ==</pre>
##
##
##
                a <- match(a, keep)</pre>
##
##
            else if (!fact.a && add.na) {
##
                 if (ifany && !aNA && add.ll) {
##
                     11 <- 11[!is.na(11)]</pre>
                     is.na(a) <- match(a0, c(exclude, NA), nomatch = 0L) >
##
##
                }
##
##
                else {
                     is.na(a) <- match(a0, exclude, nomatch = 0L) >
##
                       0L
##
##
                 }
            }
##
            nl <- length(ll)</pre>
##
            dims <- c(dims, n1)</pre>
##
##
            if (prod(dims) > .Machine$integer.max)
##
                 stop("attempt to make a table with >= 2^31 elements")
##
            dn <- c(dn, list(ll))</pre>
##
            bin \leftarrow bin + pd * (a - 1L)
##
            pd <- pd * nl
##
        }
##
       names(dn) <- dnn
##
       bin <- bin[!is.na(bin)]</pre>
##
        if (length(bin))
##
            bin <- bin + 1L
       y <- array(tabulate(bin, pd), dims, dimnames = dn)</pre>
##
       class(y) <- "table"</pre>
##
##
       У
## }
## <bytecode: 0x000000019782370>
## <environment: namespace:base>
```

```
partitions <- tbl(sc, "iris") %>%
  sdf partition(training = 0.75, test = 0.25, seed = 1099)
fit <- partitions$training %>%
  ml linear regression(Petal Length ~ Petal Width)
estimate mse <- function(df){</pre>
  sdf predict(fit, df) %>%
    mutate(resid = Petal_Length - prediction) %>%
    summarize(mse = mean(resid ^ 2)) %>%
    collect
}
sapply(partitions, estimate mse)
## Warning in sdf_predict.ml_model(fit, df): The signature sdf_predict(model,
## dataset) is deprecated and will be removed in a future version. Use
## sdf predict(dataset, model) or ml_predict(model, dataset) instead.
## Warning: Missing values are always removed in SQL.
## Use `AVG(x, na.rm = TRUE)` to silence this warning
## Warning in sdf_predict.ml_model(fit, df): The signature sdf_predict(model,
## dataset) is deprecated and will be removed in a future version. Use
## sdf predict(dataset, model) or ml predict(model, dataset) instead.
## Warning: Missing values are always removed in SQL.
## Use `AVG(x, na.rm = TRUE)` to silence this warning
## $training.mse
## [1] 0.2374596
##
## $test.mse
## [1] 0.1898848
#Use ft_string_indexer and ft_index_to_string to convert a character column i
nto a numeric column and back again.
ft string2idx <- iris tbl %>%
  ft_string_indexer("Species", "Species_idx") %>%
  ft_index_to_string("Species_idx", "Species_remap") %>%
  collect
table(ft_string2idx$Species, ft_string2idx$Species_remap)
##
##
                setosa versicolor virginica
##
                    50
                                0
     setosa
                     0
                               50
                                          0
##
     versicolor
                                          50
##
    virginica
```

```
ft string2idx <- iris tbl %>%
 sdf mutate(Species idx = ft string indexer(Species)) %>%
 sdf_mutate(Species_remap = ft_index_to_string(Species_idx)) %>%
 collect
ft string2idx %>%
 select(Species, Species_idx, Species_remap) %>%
 distinct
## # A tibble: 3 x 3
##
    Species Species_idx Species_remap
                <dbl> <chr>
##
    <chr>
## 1 setosa
                         2 setosa
## 2 versicolor
                         0 versicolor
## 3 virginica
                         1 virginica
#Use Spark's Logistic regression to perform Logistic regression, modeling a b
inary outcome as a function of one or more explanatory variables.
# Prepare beaver dataset
beaver <- beaver2
beaver$activ <- factor(beaver$activ, labels = c("Non-Active", "Active"))</pre>
copy_to(sc, beaver, "beaver")
## # Source:
              ## # Database: spark shell connection
##
       day time temp activ
     <dbl> <dbl> <dbl> <chr>
##
            930 36.6 Non-Active
## 1
       307
## 2
       307
             940 36.7 Non-Active
           950 36.9 Non-Active
## 3
       307
## 4
       307 1000 37.2 Non-Active
## 5
      307 1010 37.2 Non-Active
       307 1020 37.2 Non-Active
## 6
## 7
      307 1030 37.2 Non-Active
## 8
       307 1040 36.9 Non-Active
## 9
       307 1050 37.0 Non-Active
## 10
       307 1100 36.9 Non-Active
## # ... with more rows
beaver tbl <- tbl(sc, "beaver")</pre>
glm model <- beaver tbl %>%
mutate(binary response = as.numeric(activ == "Active")) %>%
ml_logistic_regression(binary_response ~ temp)
glm model
## Formula: binary_response ~ temp
##
## Coefficients:
```

```
## (Intercept)
                     temp
   550.52331 -14.69184
##
#First, we will copy the mtcars dataset into Spark.
mtcars_tbl <- copy_to(sc, mtcars, "mtcars")</pre>
# transform our data set, and then partition into 'training', 'test'
partitions <- mtcars_tbl %>%
  filter(hp >= 100) %>%
  sdf_mutate(cyl8 = ft_bucketizer(cyl, c(0,8,12))) %>%
  sdf_partition(training = 0.5, test = 0.5, seed = 888)
# fit a linear mdoel to the training dataset
fit <- partitions$training %>%
 ml_linear_regression(mpg ~ wt + cyl)
# summarize the model
summary(fit)
## Deviance Residuals:
      Min
           10 Median
                               3Q
                                      Max
## -2.0947 -1.2747 -0.1129 1.0876 2.2185
##
## Coefficients:
## (Intercept)
                       wt
                                  cyl
##
    33.795576 -1.596247 -1.580360
##
## R-Squared: 0.8267
## Root Mean Squared Error: 1.437
```