# Enzyme Classifier - SparkML

July 26, 2019

## **Team Members**

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#### ReadMe:

- Data Preparation through python script
- Convert raw data csv and then to libsvm in R
- Run spark ML algos in jupyter notebook

```
In [1]: import pandas as pd
    import glob
    from pyspark.ml.classification import LogisticRegression
    from pyspark.ml import Pipeline
    from pyspark.ml.classification import DecisionTreeClassifier
    from pyspark.ml.classification import RandomForestClassifier
    from pyspark.ml.classification import MultilayerPerceptronClassifier, OneVsRest
    from pyspark.ml.feature import IndexToString, StringIndexer, VectorIndexer
    from pyspark.ml.evaluation import MulticlassClassificationEvaluator
    from pyspark.sql import SparkSession
```

### Read data

Read cleaned and processed data for enzymes from data directory

```
In [2]: data = pd.DataFrame()
    files = glob.glob("data/*.csv")
    for file in files :
        print("Processing File :", file)
        df = pd.read_csv(file)
        print(df.shape)
        data = data.append(df, ignore_index=True)

def type_to_numeric(x):
    if x=='uniprot-Isomerase':
```

```
return 0
           if x=='uniprot-Lyase':
               return 1
           if x=='uniprot-ligase':
               return 2
           if x=='uniprot-Transferases' :
               return 3
           if x=='uiprot-Hydrolases' :
               return 4
           if x=='uniprot-Oxidoreductases' :
               return 5
       data['type_numeric'] = data['Type'].apply(type_to_numeric)
        #Final csv to work upon and run spark ML algorithms
       #Taking 100000 records of each enzyme
       data.to_csv("final_data/protien-sequences.csv", index=False)
       data.sample(5)
Processing File : data/uniprot-Oxidoreductases.csv
(89604, 24)
Processing File : data/uniprot-Isomerase.csv
(100001, 24)
Processing File : data/uniprot-Hydrolases.csv
(100001, 24)
Processing File : data/uniprot-ligase.csv
(100001, 24)
Processing File : data/uniprot-Lyase.csv
(100001, 24)
Processing File : data/uniprot-Transferases.csv
(100001, 24)
Out[2]:
                       С
                           D
                                  Ε
                                       F
                                              G
                                                   Η
                                                         Ι
                                                              K
                                                                    L ...
                                                                               S\
                  Α
       334374
                2.0 0.0
                           5.0 12.0
                                      2.0
                                           7.0 1.0 10.0
                                                            7.0 10.0 ...
                                                                             7.0
                          7.0
                                7.0
                                      6.0 14.0 8.0 10.0
                                                           0.0 14.0 ...
       447198 22.0 1.0
                                                                             6.0
       329103 18.0 3.0 12.0 15.0 11.0 21.0 5.0 19.0 16.0 33.0 ...
                                                                            24.0
       215190 31.0 7.0
                          11.0 19.0 10.0 14.0 8.0 11.0
                                                             5.0 35.0
                                                                      ... 14.0
               22.0 4.0 19.0 20.0 10.0 20.0 8.0 15.0 22.0 25.0 ...
       92571
                                                                            17.0
                                                       Sequence
                                                                   T \
       334374 MGRTDDMLIIRGVNVFPSQIESVLLENGDTTPHYQLIVNRKGNLDD...
                                                                 5.0
       447198 MPHRILVLHGPNLNLLGTREPEVYGRTTLADIDAALTAQAQTAGAE...
                                                                 9.0
       329103 MVHELLQQAKWRIIDQSHFGPMFDAKQSFAIDDTLCTSVGKGLSDP...
                                                                13.0
       215190 MFDIGVNLTSTQFAKDRDKVVKRAREAGISGMLITGTNALESQQAL...
                                                                14.0
       92571
               MKLSFNTWVYNSFPSMLPFYPLEEVISRIAAFGYDGIEIGCASPHA...
                            Type
                                               Y
                                                     gravy
                                                               weight type_numeric
```

```
      334374
      uniprot-ligase
      10.0
      0.0
      1.0
      -0.410577
      11844.5304
      2

      447198
      uniprot-Lyase
      11.0
      1.0
      5.0
      0.094595
      15959.8291
      1

      329103
      uniprot-ligase
      21.0
      4.0
      13.0
      -0.012950
      31174.5785
      2

      215190
      uiprot-Hydrolases
      13.0
      5.0
      2.0
      -0.122394
      28765.5914
      4

      92571
      uniprot-Isomerase
      15.0
      8.0
      14.0
      -0.422857
      31818.8477
      0
```

[5 rows x 25 columns]

#### R Code

Convert csv data to libsvm for sparkML

```
In [3]: %load_ext rpy2.ipython
In [4]: %%R
        # Ref : https://vatsalbits.wordpress.com/2016/01/13/csv-to-libsvm/
        # download e1071 library if not available
        if (!require(e1071)) {install.packages("e1071")}
        # download sparseM library if not available
        if (!require(SparseM)) {install.packages("SparseM")}
        # load the libraries
        library(e1071)
        library(SparseM)
        # load the csv dataset into memory
        data <- read.csv('final data/protien-sequences.csv')</pre>
        # take the numeric columns are format as matrix
        x <- as.matrix(data[,c('A', 'C', 'D', 'E', 'F', 'G', 'H', 'I', 'K', 'L', 'M',
                                'N', 'P', 'Q', 'R', 'S', 'T', 'V', 'W', 'Y',
                                'gravy', 'weight')])
        # assign labels to vector y
        y <- data[,'type_numeric']</pre>
        # convert input columns to sparse matrix
        x_matrix <- as.matrix.csr(x)</pre>
        # write output to libsum format
        write.matrix.csr(x_matrix, y=y, file="final_data/protien-sequences-libsvm.txt")
R[write to console]: Loading required package: e1071
R[write to console]: Loading required package: SparseM
R[write to console]:
Attaching package: SparseM
```

```
backsolve
In [5]: #create a new spark session
       MAX\_MEMORY = "5g"
        spark = SparkSession.builder.appName('protien-classifier').
        config("spark.executor.memory", MAX_MEMORY).
        config("spark.driver.memory", MAX_MEMORY).getOrCreate()
In [6]: # Load training data
        data = spark.read.format("libsvm").load("final_data/protien-sequences-libsvm.txt")
  Run Spark-MLlib Algorithms
  Logistic Regression Classifier
  Code chunks are directly taken from official spark-ml documentation.
  Ref - https://spark.apache.org/docs/latest/ml-classification-regression.html
In [7]: %%time
        #split dataset in test and training sets
        (train, test) = data.randomSplit([0.7, 0.3])
        #use max iteration of 10, and few default parameters
        logistic_reg = LogisticRegression(maxIter=20, regParam=0.005,
                                           elasticNetParam=0.005)
        # Fit the model
        logic_reg_model = logistic_reg.fit(train)
        # coefficients and intercept for multi class logistic regression
        print("Logistic Reg Coefficients: " + str(logic_reg_model.coefficientMatrix))
        print("Logistic Reg Intercept: " + str(logic_reg_model.interceptVector))
        # Print model summary
        model_summary = logic_reg_model.summary
        accuracy = str(model_summary.accuracy)
        false_positive_rate = str(model_summary.weightedFalsePositiveRate)
        true_positive_rate = str(model_summary.weightedTruePositiveRate)
        f_measure = str(model_summary.weightedFMeasure())
        precision = str(model_summary.weightedPrecision)
        recall = str(model_summary.weightedRecall)
        print("Model accuracy : " + accuracy +
              "\nFalse positive rate : " + false_positive_rate +
```

R[write to console]: The following object is masked from package:base:

```
"\nTrue positive rate : " + true_positive_rate +
              "\nF-measure : " + f_measure +
              "\nPrecision : " + precision +
              "\nRecall : " + recall)
Logistic Reg Coefficients: DenseMatrix([[ 5.45202991e-03, -8.41721306e-02, 1.47792590e-02,
               3.31893586e-03, -3.73312494e-04, -9.73336894e-04,
              -1.93253095e-02, -5.61266461e-03, 2.89474262e-02,
               3.58842586e-03, 6.87395544e-04, -1.34753590e-03,
              -2.70238535e-03, 1.24997026e-02, 3.13580444e-04,
              -6.59144958e-03, 1.79010417e-03, -1.75218553e-03,
              -1.02059722e-01, -1.99632503e-02, -8.86660848e-01,
               8.33571514e-07],
             [8.85022716e-03, -1.18602161e-02, 2.83949155e-03,
              -4.75651902e-03, -1.67761010e-02, 3.44992374e-03,
              -2.00237860e-02, -3.42373036e-03, -1.04233788e-02,
               1.00570350e-03, 9.45213109e-03, 2.87557424e-02,
              -0.00000000e+00, 4.38811521e-03, -3.17804872e-03,
               7.87092740e-03, 1.46965982e-02, -3.95256967e-03,
              -3.74618000e-02, -7.53803470e-03, 1.78657822e-01,
               1.01338335e-06],
             [-5.44382414e-04, -3.65995056e-02, 1.58249042e-02,
               2.90505556e-02, 1.97166963e-02, -2.58209170e-03,
              -2.72139077e-02, -3.92640394e-03, 1.39468558e-02,
               6.41660339e-03, -4.90823743e-03, -1.22397775e-02,
              -2.10386699e-03, -2.55006639e-03, 3.58658471e-04,
              -9.47427993e-03, -3.44740078e-03, -1.08598272e-03,
               2.32355489e-02, 1.23598495e-02, -1.95403376e-01,
              -1.24076148e-06],
             [-2.03297917e-02, 1.21864343e-02, -1.58565824e-02,
              -2.09937573e-02, -1.88554774e-02, 6.02781399e-03,
               2.04237107e-02, 8.34704605e-02, 2.49272055e-03,
              -3.20490486e-02, -6.43147253e-02, 7.89723454e-03,
              -7.28943716e-03, -9.92204577e-03, 2.17382198e-03,
              -7.46535750e-04, -1.25944695e-02, 2.74750585e-02,
               1.58983343e-02, -0.00000000e+00, 1.12359426e+00,
              -3.18344785e-07],
             [-2.45574514e-03, 2.79102499e-02, 1.62842341e-03,
              -4.20275874e-03, 3.90743498e-03, -2.62320748e-03,
               6.86609432e-02, -6.35138103e-03, -4.75216675e-03,
               1.00420738e-03, 1.78526063e-02, -2.75581708e-03,
               7.65353346e-04, -5.89824624e-03, -3.73230530e-04,
               1.84585536e-02, 1.37432514e-03, -7.31473093e-03,
              -4.08326154e-03, 1.26975951e-02, -5.71198888e-02,
               4.24723852e-07],
             [-7.61661945e-04, 1.22353827e-01, -1.39996583e-02,
              -9.55126011e-03, 8.01425588e-03, -3.50855993e-03,
               8.79739093e-03, -1.08732097e-02, -9.43516283e-03,
```

```
7.07526911e-03, 6.41561717e-03, -7.95823268e-04,
               2.42710127e-04, -4.77668365e-03, -6.11424855e-03,
               3.65983003e-02, 6.71549501e-04, -3.34873437e-01,
              -6.77072976e-0711)
Logistic Reg Intercept: [0.17462809241234534,0.010481053067311924,-0.6559807909752295,0.535728
Model accuracy: 0.36205831255588106
False positive rate : 0.12731148458569602
True positive rate: 0.36205831255588106
F-measure: 0.3611527231912624
Precision: 0.3628963004678636
Recall: 0.36205831255588106
CPU times: user 21.3 ms, sys: 6.57 ms, total: 27.8 ms
Wall time: 12.6 s
  Decision Tree Classifier
In [8]: %%time
        #mark labels as index of libsvm data
        label_index = StringIndexer(inputCol="label", outputCol="index_label").fit(data)
        # Mark all input columns as features
        feature_index = VectorIndexer(inputCol="features",
                                      outputCol="index_features",
                                      maxCategories=2).fit(data)
        # Lets do 60:40 ratio for training and test data
        (train, test) = data.randomSplit([0.6, 0.4])
        # Make a decision tree model
        decision_tree_classifier = DecisionTreeClassifier(labelCol="index_label",
                                                          featuresCol="index_features")
        # Create a pipeline of decision tree model
        pipeline = Pipeline(stages=[label_index, feature_index, decision_tree_classifier])
        # train our decision tree using input columns
        decision_tree_model = pipeline.fit(train)
       model_summary = decision_tree_model.stages[2]
        # summary only
        print("Created decision tree classifier with : \n")
       print(model_summary)
        # Get predictions for test set
        predictions_test = decision_tree_model.transform(test)
```

0.00000000e+00, 1.20510455e-03, -7.56656920e-03,

```
# Look at top 10 predictions, 9/10 predictions seems correct
predictions_test.select("prediction", "index_label", "features").show(10)

# calculate accurancy on test set
multi_class_classification_evaluator = MulticlassClassificationEvaluator(
    labelCol="index_label", predictionCol="prediction", metricName="accuracy")
accuracy_percentage = multi_class_classification_evaluator.evaluate(predictions_test)
print("Test set error = %f " % (1.0 - accuracy_percentage))
```

Created decision tree classifier with :

DecisionTreeClassificationModel (uid=DecisionTreeClassifier\_62c948558ae8) of depth 5 with 51 new part of the second secon

prediction	index_label	features
++   5.0    5.0    0.0    3.0    5.0    5.0    5.0    3.0	5.0  5.0  5.0  5.0  5.0  5.0	(22, [0,1,2,3,4,5,] (22, [0,1,2,3,4,5,] (22, [0,1,2,3,4,5,] (22, [0,1,2,3,4,5,] (22, [0,1,2,3,4,5,] (22, [0,1,2,3,4,5,] (22, [0,1,2,3,4,5,] (22, [0,1,2,3,4,5,] (22, [0,1,2,3,4,5,]
3.0	5.0	(22,[0,1,2,3,4,5,

only showing top 10 rows

Test set error = 0.651715 CPU times: user 41.3 ms, sys: 9.75 ms, total: 51.1 ms

Wall time: 13.2 s

Random Forest Classifier

As per our evaluation, this gives us best result with accuracy of 57% with 30 trees. We can further work on this to increase number of trees, max depth and other hyper parameter tunings

```
(train, test) = data.randomSplit([0.7, 0.3])
       # Create a random forest classifier with 20 trees
       random_forest_classifier = RandomForestClassifier(labelCol="index_label",
                                                         featuresCol="index features",
                                                         numTrees=30, maxDepth=10)
       # label converter to convert indexed labels
       label_converter = IndexToString(inputCol="prediction", outputCol="predicted_label",
                                      labels=label_index.labels)
       # Create a pipeline of random forest model
       pipeline = Pipeline(stages=[label_index, feature_index,
                                   random_forest_classifier, label_converter])
       # Train random forest classifier
       random_forest_model = pipeline.fit(train)
       model_summary = random_forest_model.stages[2]
       # summary only
       print("Created random forest classifier with : \n")
       print(model_summary)
       # Get predictions for test set
       predictions_test = random_forest_model.transform(test)
       # see few of our predictions
       predictions_test.select("predicted_label", "label", "features").show(10)
       # Calculate test set error
       multi_class_classification_evaluator = MulticlassClassificationEvaluator(
            labelCol="index_label", predictionCol="prediction", metricName="accuracy")
       accuracy_percentage = multi_class_classification_evaluator.evaluate(predictions_test)
       print("Test set error = %f " % (1.0 - accuracy_percentage))
Created random forest classifier with :
RandomForestClassificationModel (uid=RandomForestClassifier_5f69f240db35) with 30 trees
+----+
|predicted_label|label|
+----+
            5.0| 5.0| (22,[0,1,2,3,4,5,...]
            5.0| 5.0| (22,[0,1,2,3,4,5,...]
            5.0| 5.0| (22,[0,1,2,3,4,5,...]
            5.0| 5.0| (22,[0,1,2,3,4,5,...]
            5.0 \mid 5.0 \mid (22, [0, 1, 2, 3, 4, 5, \ldots)
            5.0 \mid 5.0 \mid (22, [0, 1, 2, 3, 4, 5, \ldots)
```

```
5.0| 5.0| (22,[0,1,2,3,4,5,...]
             5.0| 5.0|(22,[0,1,2,3,4,5,...|
             5.0 \mid 5.0 \mid (22, [0, 1, 2, 3, 4, 5, \ldots)
    -----+
only showing top 10 rows
Test set error = 0.436635
CPU times: user 46 ms, sys: 11 ms, total: 57 ms
Wall time: 35.3 s
  One-vs-Rest classifier (a.k.a. One-vs-All)
  Create classifier with multiple binary classifiers and combine
  Increasing number of iterations in this case doesn't affects accuracy beyond 39%
In [10]: %%time
         #split train and test set in 80:20 ratio
         (train, test) = data.randomSplit([0.8, 0.2])
         # instantiate logistic regression classifier
         logistic_regression_classifier = LogisticRegression(maxIter=30,
                                                              tol=1E-7, fitIntercept=True)
         # initializer our one vs rest classifier
         one_vs_rest = OneVsRest(classifier=logistic_regression_classifier)
         # train model on training data
         one_vs_rest_model = one_vs_rest.fit(train)
         # get predictions on test data
         test_predictions = one_vs_rest_model.transform(test)
         # Test accuracy using multi class evaluator
         multi_class_evaluator = MulticlassClassificationEvaluator(metricName="accuracy")
         accuracy_percentage = multi_class_evaluator.evaluate(test_predictions)
         print("Test set error = %f " % (1.0 - accuracy_percentage))
Test set error = 0.614291
CPU times: user 256 ms, sys: 58 ms, total: 314 ms
Wall time: 43.2 s
```

## Feedforward Artificial Neural Network Classifier

 $5.0 \mid 5.0 \mid (22, [0, 1, 2, 3, 4, 5, \ldots)$ 

- References:
- https://dzone.com/articles/deep-learning-via-multilayer-perceptron-classifier
- https://spark.apache.org/docs/2.2.1/api/java/index.html?org/apache/spark/ml/classification/Randor

Neural network test test accuracy calculation has some issues with library

```
In [12]: %%time
         #split data in 60:40 ratio
         random_split = data.randomSplit([0.6, 0.4])
         train = random_split[0]
         test = random_split[1]
         # specify input, middle, output layers
         # No of input layers - 20
         # intermediate layers - 15, 10, 8
         # output layers - 3
         layers = [20, 15, 10, 8, 6]
         # create multilayer neural network classifier
         nn_model = MultilayerPerceptronClassifier(maxIter=100,
                                                   layers=layers, blockSize=128)
         # train our neural network
         model = nn_model.fit(train)
         # compute accuracy on the test set
         test_predictions = model.transform(test)
         predictionAndLabels = test_predictions.select("prediction", "label")
CPU times: user 31.3 ms, sys: 6.53 ms, total: 37.9 ms
Wall time: 28.7 s
```

/Users/anmol/OneDrive - Indian S.../.../genomics/Protien\_File\_Processor.py Page 1/2 Printed: 26/07/19, 8:49:24 PM Printed for: Anmol

```
# Team Members
  # - Shubhendu Vimal - 11915067
2
  # - Dharani Kiran Kavuri - 11915033
3
  # - Anmol More - 11915043
5
  #Data Preparation in plain Python
6
7
8
  #Read raw fasta protien sequence files and convert it to parsable CSV files
  using biopython
9
  #Embedded block of code for converting to pdf only, run separately (time
10
  taking)
11
  import sys
12
  import pandas as pd
13
  from Bio.SeqUtils.ProtParam import ProteinAnalysis
14
15
  #arg 1 - fasta file name
16
17 #arg 2 - no of records to process
18 | file = str(sys.argv[1])
  limit = int(sys.argv[2])
19
  print("Processing file : ", file)
20
21
  df = pd.DataFrame()
22
  enzyme\_type = file[:-6]
23
24
  # read fasta files, line by line and process enzyme sequence
25
  print("Group all as : ", enzyme_type)
26
  with open(file) as fileobject:
27
       start = True
28
       row = ""
29
       for line in fileobject:
30
           if("sp|" in line or "tr|" in line) :
31
               start = True
32
               if(row != "") :
33
                    row dict = {}
34
                   row_dict["Sequence"] = row
35
                    row dict["Type"] = enzyme type
36
37
                   try:
38
                        #use biopython library to process enzyme sequence
39
                        analysed_seq = ProteinAnalysis(row)
40
                        #print(analysed seg)
41
                        amino_acid_counts = analysed_seq.count_amino_acids()
42
                        row_dict.update(amino_acid_counts)
43
                        analysed_seq = ProteinAnalysis(row)
44
                        row_dict["weight"] = analysed_seq.molecular_weight()
45
                        row dict["gravy"] = analysed seq.gravy()
46
                        df = df.append(row_dict, ignore_index=True)
47
                        print(df.shape)
48
                        if(df.shape[0] > limit) :
49
                            break
50
```

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