```
In [1]: from pyspark.sql.types import BooleanType
        from pyspark.ml.feature import StringIndexer, VectorAssembler
        from pyspark.ml.classification import LinearSVC
        from pyspark.sql.session import SparkSession
        from pyspark.sql.functions import expr
        from pyspark.ml.evaluation import BinaryClassificationEvaluator
        from helpers.helper_functions import translate_to_file_string
        from pvspark.sql import DataFrameReader
        from pyspark.sql import SparkSession
        from pyspark.ml.feature import IndexToString, Normalizer, StringInd
        from pyspark.ml.evaluation import BinaryClassificationEvaluator
        from pyspark.ml.classification import DecisionTreeClassifier
        from pyspark.ml.tuning import CrossValidator, ParamGridBuilder
        from pyspark.ml import Pipeline
        from helpers.helper_functions import translate_to_file_string
        from sklearn.metrics import roc_curve, auc
        from sklearn.tree import plot_tree
        import seaborn as sns
        import pandas as pd
        import os
        import warnings
        import matplotlib.pyplot as plt
        warnings.filterwarnings('ignore')
In [2]: inputFile = translate to file string("../data/heart val.csv")
In [3]: spark = (SparkSession
               .builder
               appName("HeartDiseaseAnalDT")
               .getOrCreate())
In [4]: # load data file.
        # create a DataFrame using an ifered Schema
        df = spark.read.option("header", "true") \
               option("inferSchema", "true") \
               .option("delimiter", ";") \
               .csv(inputFile)
In [5]: #remove the outliner
        df_filtered=df.filter(df.age > 30)
In [6]: #transform labels to number values
        labelIndexer = StringIndexer().setInputCol("target").setOutputCol("
        sexIndexer = StringIndexer().setInputCol("sex").setOutputCol("sex n
```

```
In [7]: #feature columns
         featureCols = df.columns.copy()
         featureCols.remove("target")
         featureCols.remove("sex")
         featureCols = featureCols + ["sex num"]
 In [8]: #vector assembler
         assembler = VectorAssembler(outputCol="features", inputCols=list(f
 In [9]: #Build feauture Indexer
         featureIndexer = VectorIndexer(inputCol="features",outputCol="index
In [10]: #Convert Indexed labels back to original labels
         predConverter = IndexToString(inputCol="prediction",outputCol="pred
In [11]: |#Build decistion tree model
         dt = DecisionTreeClassifier(labelCol="label", featuresCol="features")
In [12]: # build a parameter grid for different values
         paramGrid = ParamGridBuilder().addGrid(dt.maxDepth, [ 5, 10 ]) \
                                        .addGrid(dt.minInfoGain, [0.05, 0.025
                                        .addGrid(dt.minInstancesPerNode, [5,
                                        .addGrid(dt.maxBins, [5, 6, 9]) \
                                        .build()
In [13]: #split data for testing
         splits = df.randomSplit([0.6, 0.4], 3455)
         train = splits[0]
         test = splits[1]
In [14]: #Pipelining of all steps
         pipeline = Pipeline(stages= [labelIndexer,sexIndexer, assembler, f
In [15]: #build evaluator
         evaluator = BinaryClassificationEvaluator(labelCol="label", rawPred
In [16]: #Cross validator
         cv = CrossValidator(estimator=pipeline, evaluator=evaluator,estimat
In [17]: #train model
         cvModel = cv.fit(train)
In [18]: #Find out the best model
         treeModel = cvModel.bestModel.stages[4]
         print("Learned classification tree model:\n",treeModel)
         print("Best Params: \n", treeModel.explainParams())
```

Learned classification tree model:

DecisionTreeClassificationModel: uid=DecisionTreeClassifier_6d1df 8416897, depth=4, numNodes=13, numClasses=2, numFeatures=13 Best Params:

cacheNodeIds: If false, the algorithm will pass trees to executor s to match instances with nodes. If true, the algorithm will cache node IDs for each instance. Caching can speed up training of deepe r trees. Users can set how often should the cache be checkpointed or disable it by setting checkpointInterval. (default: False) checkpointInterval: set checkpoint interval (>= 1) or disable checkpoint (-1). E.g. 10 means that the cache will get checkpointed every 10 iterations. Note: this setting will be ignored if the check point directory is not set in the SparkContext. (default: 10) featuresCol: features column name. (default: features, current: features)

impurity: Criterion used for information gain calculation (case-in sensitive). Supported options: entropy, gini (default: gini)

labelCol: label column name. (default: label, current: label)

leafCol: Leaf indices column name. Predicted leaf index of each in stance in each tree by preorder. (default:)

maxBins: Max number of bins for discretizing continuous features.
Must be >=2 and >= number of categories for any categorical featur
e. (default: 32, current: 5)

maxDepth: Maximum depth of the tree. (>= 0) E.g., depth 0 means 1
leaf node; depth 1 means 1 internal node + 2 leaf nodes. (default:
5, current: 5)

maxMemoryInMB: Maximum memory in MB allocated to histogram aggregation. If too small, then 1 node will be split per iteration, and its aggregates may exceed this size. (default: 256)

minInfoGain: Minimum information gain for a split to be considered at a tree node. (default: 0.0, current: 0.025)

minInstancesPerNode: Minimum number of instances each child must have after split. If a split causes the left or right child to have fewer than minInstancesPerNode, the split will be discarded as invalid. Should be >= 1. (default: 1, current: 10)

minWeightFractionPerNode: Minimum fraction of the weighted sample count that each child must have after split. If a split causes the fraction of the total weight in the left or right child to be less than minWeightFractionPerNode, the split will be discarded as invalid. Should be in interval [0.0, 0.5). (default: 0.0)

predictionCol: prediction column name. (default: prediction)

probabilityCol: Column name for predicted class conditional probabilities. Note: Not all models output well-calibrated probability e stimates! These probabilities should be treated as confidences, not precise probabilities. (default: probability)

rawPredictionCol: raw prediction (a.k.a. confidence) column name.
(default: rawPrediction)

seed: random seed. (default: 52393225941365585)

thresholds: Thresholds in multi-class classification to adjust the probability of predicting each class. Array must have length equal to the number of classes, with values > 0, excepting that at most one value may be 0. The class with largest value p/t is predicted, where p is the original probability of that class and t is the class's threshold. (undefined)

weightCol: weight column name. If this is not set or empty, we tre at all instance weights as 1.0. (undefined)

```
In [19]: #show tree
plt.figure(figsize=(20,20))
features = df.columns

classes = ["No Disease", "Diasease"]

#plot_tree(treeModel, feature_names=features, class_names=classes, fil
#plt.show()
```

<Figure size 1440x1440 with 0 Axes>

```
In [20]: #test model
predictions = cvModel.transform(test)
predictions.select("prediction", "label", "target", "features").sho
```

```
|prediction|label|target|
                                          features |
        0.01
               0.01
                          y | [34.0, 1.0, 118.0, 2...]
                          y|(13,[0,1,2,3,6,9,...]
        0.01
               0.01
        1.0
               1.0|
                          n \mid [39.0, 0.0, 118.0, 2...]
        0.0
               0.0
                          y | (13, [0,1,2,3,6,9,...]
        1.0|
               1.0
                          n \mid [40.0, 0.0, 110.0, 1...]
                          y | [41.0, 1.0, 105.0, 1...]
        0.0
               0.0
        0.01
               0.01
                          y | [41.0, 1.0, 130.0, 2... |
        0.01
               0.0
                          y | [41.0, 1.0, 110.0, 2...]
        0.0
               0.0
                          y | [41.0, 2.0, 112.0, 2...]
                          y | [41.0, 2.0, 130.0, 2...]
        1.0
               0.0
        0.0
               0.0
                          y | [42.0,0.0,102.0,2...|
        0.0
               0.0
                          y | [42.0,2.0,120.0,2...|
        0.0
               1.0|
                          n | [42.0, 0.0, 136.0, 3...]
        0.01
               0.0
                          y | (13, [0,2,3,5,6,9,...]
        0.01
               0.0
                          y | [42.0, 2.0, 130.0, 1...]
                          y | [42.0,3.0,148.0,2...|
        0.0
               0.0
        1.0|
               1.0|
                          n \mid [43.0, 0.0, 132.0, 3...]
        0.0
               0.0
                          y | [43.0, 0.0, 115.0, 3...]
                          n | [43.0, 0.0, 120.0, 1...]
        1.0
               1.0
                          n | (13, [0,2,3,6,9,10...]
        1.0
               1.0
```

only showing top 20 rows

```
In [21]: accuracy = evaluator.evaluate(predictions)
print("Test Error = " ,(1.0 - accuracy))
```

Test Error = 0.1752653301886793

In [22]: spark.stop()