Q3-Python

August 15, 2024

1 NAFLD detection using RNA-Seq data

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In this part, we need to split the classifiers from Part 1 into two connected machines and evaluate how the overall performance of the task changes.

2 Q3 - Python section

For the first machine, we need to classify normal samples versus any type of fibrosis samples.

[1]:
```
# Import needed libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.metrics import precision_score, recall_score
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
from sklearn.linear_model import LassoCV
from sklearn.decomposition import PCA
from sklearn.manifold import TSNE
import warnings
warnings.filterwarnings("ignore")
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
from sklearn.ensemble import RandomForestClassifier
from sklearn.neural_network import MLPClassifier
```

[2]:
```
# Load Data
normal_counts = pd.read_csv('Normal.counts.voom.csv')
meta_data = pd.read_csv('meta_data.csv')
```

[3]:
```
def determine_class(row):
    if row['Simplified_class'] == 'Normal':
        return "Normal"
    else:
```

```
        return "Fibrosis"
```

[4]:
```
meta_data['class'] = meta_data.apply(determine_class, axis=1)
meta_data = pd.DataFrame(meta_data)
```

[5]:
```
meta_data
```

[5]:
```
    Patient_ID     SEX    BMI_surg  Age         Run        Diabet  \
0    DLDR_0001  Female   35.214555   55  SRR8378590  Non Diabetic
1    DLDR_0002  Female   39.421748   47  SRR8378589      Diabetic
2    DLDR_0003    Male   48.758108   46  SRR8378432  Non Diabetic
3    DLDR_0004  Female   41.822607   36  SRR8378431  Non Diabetic
4    DLDR_0005  Female   53.582192   54  SRR8378434  Non Diabetic
..         …       …          …   …          …             …
187  DLDR_0188    Male   40.216173   59  SRR8378532      Diabetic
188  DLDR_0189  Female   50.077601   52  SRR8378525  Non Diabetic
189  DLDR_0190    Male  104.921344   28  SRR8378526      Diabetic
190  DLDR_0191  Female   47.495069   36  SRR8378566  Non Diabetic
191  DLDR_0192  Female   45.418221   53  SRR8378565  Non Diabetic

    Simplified_class   class
0             Normal  Normal
1             Normal  Normal
2             Normal  Normal
3             Normal  Normal
4             Normal  Normal
..               …       …
187           Normal  Normal
188           Normal  Normal
189           Normal  Normal
190           Normal  Normal
191           Normal  Normal

[192 rows x 8 columns]
```

Let's split our data and labels to train and test sets

[6]:
```
X_train, X_test, y_train, y_test = train_test_split(normal_counts.iloc[0:,1:].
↪T, meta_data[['Simplified_class', 'class']], test_size=0.3, random_state =␣
↪10101)
```

Now, let's save the training set data to use in the R Jupyter Notebook for feature selection

[7]:
```
X_train.T.to_csv('train_normal_counts.csv', index=False)
y_train.to_csv('train_meta_data.csv', index=False)
```

Run R Jupyter Notebook Let's load the output of R to continue the task for the first machine classification

2.1 First Machine

[9]:
```
subset_data1 = pd.read_csv('subset_data1.csv')
```

[10]:
```
subset_data1.head()
```

[10]:
```
   Unnamed: 0  DLDR_0036  DLDR_0081  DLDR_0191  DLDR_0188  DLDR_0130  \
0          10   4.589555   5.482169   5.013154   5.066071   4.655817
1          17   5.449846   5.626559   5.668470   5.824931   5.645748
2          67   5.513839   6.027475   6.073207   5.862186   5.755947
3         278   5.529902   5.846272   5.553583   5.359267   5.774549
4         301   5.713408   6.171415   5.919896   6.081949   5.670238

   DLDR_0013  DLDR_0079  DLDR_0131  DLDR_0135  …  DLDR_0175  DLDR_0052  \
0   4.299078   4.752957   5.409514   4.993777  …   4.853565   4.567173
1   5.172477   5.550495   5.445684   5.825299  …   5.574066   5.250757
2   4.997887   5.706940   5.780650   6.019866  …   5.756585   5.475180
3   4.962662   5.201300   5.500205   5.782051  …   5.862067   5.038603
4   5.175044   5.884826   5.889699   6.276855  …   5.934795   5.737267

   DLDR_0087  DLDR_0155  DLDR_0092  DLDR_0187  DLDR_0186  DLDR_0179  \
0   4.985158   5.234776   4.900754   4.923087   5.004500   5.058062
1   6.008989   6.014251   5.971633   5.707487   5.784668   5.655138
2   5.981856   5.873197   5.862836   5.832565   5.770585   5.658351
3   5.665231   5.781140   5.745159   5.438062   5.570169   5.558701
4   6.233433   6.223520   5.936271   6.109439   5.724249   6.160191

   DLDR_0182  DLDR_0001
0   5.002454   4.221450
1   5.919827   5.086468
2   6.017044   5.071807
3   5.733822   5.220121
4   6.032172   5.201384

[5 rows x 135 columns]
```

[11]:
```
subset_data1.shape
```

[11]:
```
(300, 135)
```

[12]:
```
meta_data1 = pd.read_csv('meta_data1.csv')
```

[13]:
```
meta_data1.head()
```

[13]:
```
   Unnamed: 0    Simplified_class     class
0           1              Normal    Normal
1           2   Advanced_fibrosis  Fibrosis
2           3              Normal    Normal
```

```
3           4                 Normal    Normal
4           5  Non_advanced_Fibrosis  Fibrosis
```

[14]:
```
meta_data1.shape
```

[14]:
```
(134, 3)
```

[16]:
```
print("Number of Normal samples: ",meta_data1['class'].to_list().
 ↪count("Normal"))
print("Number of Fibrosis samples: ",meta_data1['class'].to_list().
 ↪count("Fibrosis"))
```

```
Number of Normal samples:  44
Number of Fibrosis samples:  90
```

We need to extract the same features for the X test dataset as well. To do this, we must identify the indices of our selected DEGs and apply the same subsetting to the test data.

[17]:
```
selected_genes_R = subset_data1.T.iloc[0,:].to_list()
```

[18]:
```
selected_genes_Python = [int(i-1) for i in selected_genes_R ]
```

[19]:
```
selected_genes_Python[:10]
```

[19]:
```
[9, 16, 66, 277, 300, 309, 340, 351, 406, 469]
```

[20]:
```
len(selected_genes_Python)
```

[20]:
```
300
```

[21]:
```
df_deg = subset_data1.iloc[0:,1:].T
df_deg_test = X_test[selected_genes_Python]
```

[22]:
```
df_deg.head()
```

[22]:
```
                 0         1         2         3         4         5    \
DLDR_0036  4.589555  5.449846  5.513839  5.529902  5.713408  0.318451
DLDR_0081  5.482169  5.626559  6.027475  5.846272  6.171415  0.096738
DLDR_0191  5.013154  5.668470  6.073207  5.553583  5.919896  1.033084
DLDR_0188  5.066071  5.824931  5.862186  5.359267  6.081949  0.356896
DLDR_0130  4.655817  5.645748  5.755947  5.774549  5.670238  0.362589

                 6         7         8         9    …       290       291  \
DLDR_0036  6.089009  5.898008  5.466634  7.043227  …  3.701934 -0.719024
DLDR_0081  6.539682  6.101239  5.802716  6.942228  …  4.184201 -2.225190
DLDR_0191  6.434588  6.098648  5.685361  7.127258  …  3.703438 -0.624028
DLDR_0188  6.476384  6.118797  5.751021  7.095522  …  3.731021 -0.190591
DLDR_0130  6.486240  6.239292  5.826980  7.227713  …  3.965653 -3.096843
```

```
                292       293       294       295       296       297  \
DLDR_0036  7.142553 -2.645023  1.442439 -1.797026  0.318451  3.496573
DLDR_0081  7.531366 -2.225190  0.582165 -2.225190 -2.225190  2.984263
DLDR_0191  7.789600 -4.324468  0.884985 -1.154543  0.199094  2.333744
DLDR_0188  7.891558 -3.891031  2.131337  1.238252  2.086249  2.518360
DLDR_0130  7.909951 -4.681805  1.248932 -3.096843 -0.774915  2.925525

                298       299
DLDR_0036  6.925971  4.440316
DLDR_0081  7.323632  5.032198
DLDR_0191  7.411511  4.749674
DLDR_0188  7.189120  5.276387
DLDR_0130  7.519400  5.094628

[5 rows x 300 columns]
```

[23]:
```
df_deg_test.head()
```

[23]:
```
                  9        16        66       277       300       309  \
DLDR_0022  3.967031  4.998491  5.013351  5.101756  4.988498  2.077214
DLDR_0016  4.603126  5.185253  5.176144  5.079298  5.421363  2.274384
DLDR_0004  4.003661  5.030589  4.919722  5.125878  5.200742  2.538993
DLDR_0165  5.286333  5.689689  5.901682  5.827910  5.834420  1.225221
DLDR_0127  5.118729  5.592257  5.464008  5.446251  5.955723  0.897457

                340       351       406       469  …     15501     15828  \
DLDR_0022  5.845657  5.444621  5.221772  6.469531  …  3.735705  1.561293
DLDR_0016  5.735367  5.394124  5.403911  6.502406  …  3.078076  1.531716
DLDR_0004  6.049955  5.583037  5.306224  6.467268  …  3.697330  2.231420
DLDR_0165  6.994423  6.261908  6.098429  7.503492  …  4.231154 -3.697611
DLDR_0127  6.472366  5.832644  5.859725  7.239886  …  3.857711  0.766213

              15857     15977     16049     16112     16277     16419  \
DLDR_0022  6.821586 -0.425287  3.172973  1.999735  2.186148  3.883221
DLDR_0016  7.132365 -0.172299  2.725254  2.389205  2.373351  3.416537
DLDR_0004  6.847587  0.328096  3.209833  2.468026  2.921937  3.697330
DLDR_0165  8.110147 -5.282573  0.907251 -1.582134 -1.582134  2.543975
DLDR_0127  7.988758 -1.510628  1.231876  0.146485  1.777617  2.816839

              17074     17347
DLDR_0022  6.646771  3.811348
DLDR_0016  6.739625  3.447152
DLDR_0004  6.827647  3.707635
DLDR_0165  7.434889  5.282529
DLDR_0127  7.391864  4.626561

[5 rows x 300 columns]
```

It's time for classification. I have used four types of classifiers to classify Fibrosis samples from Normal samples

Logistic Regression

[24]:
```
# Logistic Regression
LR_model = LogisticRegression(solver='saga')
LR_model.fit(df_deg, y_train['class'])
y_pred_LR = LR_model.predict(df_deg_test)
LR_precision = precision_score(y_test['class'], y_pred_LR, average='macro')
LR_recall = recall_score(y_test['class'], y_pred_LR, average='macro')
print(LR_precision)
print(LR_recall)
```

```
0.8273809523809523
0.8273809523809523
```

Support Vector Machine

[25]:
```
# Support Vector Machine
SVM_model = SVC(kernel='linear', C=1)
SVM_model.fit(df_deg, y_train['class'])
y_pred_SVM = SVM_model.predict(df_deg_test)
SVM_precision = precision_score(y_test['class'], y_pred_SVM, average='macro')
SVM_recall = recall_score(y_test['class'], y_pred_SVM, average='macro')
print(SVM_precision)
print(SVM_recall)
```

```
0.8490909090909091
0.8428571428571429
```

Random Forest

[26]:
```
# Random Forest
RF_model = RandomForestClassifier(random_state=10101)
RF_model.fit(df_deg, y_train['class'])
y_pred_RF = RF_model.predict(df_deg_test)
RF_precision = precision_score(y_test['class'], y_pred_RF, average='macro')
RF_recall = recall_score(y_test['class'], y_pred_RF, average='macro')
print(RF_precision)
print(RF_recall)
```

```
0.8799283154121864
0.8785714285714286
```

Multi Layer Perceptron

[27]:
```
# Multi Layer Perceptron
MLP_model = MLPClassifier(hidden_layer_sizes=(100,), max_iter=300,␣
 ↪activation='relu', solver='adam',random_state=10101)
MLP_model.fit(df_deg, y_train['class'])
y_pred_MLP = MLP_model.predict(df_deg_test)
```

```
MLP_precision = precision_score(y_test['class'], y_pred_MLP, average='macro')
MLP_recall = recall_score(y_test['class'], y_pred_MLP, average='macro')
print(MLP_precision)
print(MLP_recall)
```

```
0.7138888888888889
0.6833333333333333
```

2.2 Second Machine

For the second machine, we need to classify Fibrosis samples to 2 type of Advanced and Non-Advanced.

To accomplish this task, we need to pass the outputs from the first machine that were predicted as "Fibrosis" to the second machine. The second machine will then classify these samples to determine their specific type of fibrosis (Advanced or Non-Advanced).

We can then evaluate the performance of the second machine on its own, as well as the overall performance of the two-machine system.

[28]:
```
subset_data2 = pd.read_csv('subset_data2.csv')
```

[29]:
```
subset_data2.head()
```

[29]:
```
   Unnamed: 0  DLDR_0081  DLDR_0130  DLDR_0079  DLDR_0131  DLDR_0135  \
0          57   0.582165  -0.289488  -1.138550  -4.060128  -2.104255
1         209   7.001222   7.205796   6.750193   7.459017   7.379157
2         232   7.169273   6.998994   7.278919   7.887874   7.723881
3         275   2.529697   1.467942   2.031375   2.048397   0.528013
4         297   7.759228   7.439405   7.481170   7.556880   8.322219

   DLDR_0095  DLDR_0097  DLDR_0086  DLDR_0149  …  DLDR_0166  DLDR_0089  \
0   0.018120  -0.056554  -1.903604  -1.742234  …  -1.954119  -0.631565
1   7.114793   7.020261   7.433126   7.577028  …   7.233940   7.386481
2   7.414587   7.020261   7.363651   7.612316  …   7.585871   6.621626
3   1.130013   1.708980   0.418324   0.775615  …   1.777685   1.926431
4   8.616473   8.950753   8.212480   7.661166  …   7.898745   7.797958

   DLDR_0141  DLDR_0111  DLDR_0136  DLDR_0134  DLDR_0175  DLDR_0087  \
0  -4.286453   0.493507  -2.021838  -2.650924  -2.285986  -0.385647
1   7.616299   6.879088   7.280747   7.098946   7.339114   7.366168
2   7.817818   7.058071   7.793088   7.454723   7.755217   7.485884
3   1.644284   1.992313   0.504708   0.755069   1.083248   2.055951
4   7.851498   8.601349   7.190977   7.577174   7.462766   8.581307

   DLDR_0155  DLDR_0092
0  -3.580073   0.317259
1   7.612425   7.340979
2   7.339038   6.906979
```

```
3   1.374123   1.902221
4   7.940709   8.730887

[5 rows x 91 columns]
```

[30]:
```
subset_data2.shape
```

[30]:
```
(300, 91)
```

[31]:
```
meta_data2 = pd.read_csv('meta_data2.csv')
```

[32]:
```
meta_data2.head()
```

[32]:
```
   Unnamed: 0       Simplified_class     class
0           2      Advanced_fibrosis  Fibrosis
1           5  Non_advanced_Fibrosis  Fibrosis
2           7      Advanced_fibrosis  Fibrosis
3           8  Non_advanced_Fibrosis  Fibrosis
4           9  Non_advanced_Fibrosis  Fibrosis
```

[33]:
```
meta_data2.shape
```

[33]:
```
(90, 3)
```

[34]:
```
print("Number of Advanced fibrosis samples: ", meta_data2['Simplified_class'].
 ↪to_list().count("Advanced_fibrosis"))
print("Number of Non advanced Fibrosis samples: ",␣
 ↪meta_data2['Simplified_class'].to_list().count("Non_advanced_Fibrosis"))
```

```
Number of Advanced fibrosis samples:  52
Number of Non advanced Fibrosis samples:  38
```

We need to extract the same features for the X test dataset as well. To do this, we must identify the indices of our selected DEGs and apply the same subsetting to the test data.

[35]:
```
selected_genes_R = subset_data2.T.iloc[0,:].to_list()
```

[36]:
```
selected_genes_Python = [int(i-1) for i in selected_genes_R ]
```

[37]:
```
selected_genes_Python[:10]
```

[37]:
```
[56, 208, 231, 274, 296, 389, 445, 447, 503, 524]
```

[38]:
```
len(selected_genes_Python)
```

[38]:
```
300
```

Logistic Regression Let's just pass the outputs from the first machine that were predicted as "Fibrosis" to the second machine.

[39]:
```
X_test_reset = X_test.reset_index(drop=True)
y_test_reset = y_test.reset_index(drop=True)
X_not_normal = X_test_reset[y_pred_LR != 'Normal']
y_not_normal = y_test_reset[y_pred_LR != 'Normal']
```

[40]:
```
df_deg = subset_data2.iloc[0:,1:].T
df_deg_test = X_not_normal[selected_genes_Python]
```

[41]:
```
y_train2 = y_train[y_train['Simplified_class'] != 'Normal']
```

Second machine performance :

[43]:
```
# Logistic Regression
LR_model = LogisticRegression(solver='saga')
LR_model.fit(df_deg, y_train2['Simplified_class'])
y_pred_LR2 = LR_model.predict(df_deg_test)
LR_precision = precision_score(y_not_normal['Simplified_class'], y_pred_LR2,␣
 ↪average='macro')
LR_recall = recall_score(y_not_normal['Simplified_class'], y_pred_LR2,␣
 ↪average='macro')
print(LR_precision)
print(LR_recall)
```

```
0.5
0.6058201058201058
```

The overall performance :

[45]:
```
y_pred_LR[y_pred_LR == 'Fibrosis'] = y_pred_LR2
```

[47]:
```
LR_precision = precision_score(y_test['Simplified_class'], y_pred_LR,␣
 ↪average='macro')
LR_recall = recall_score(y_test['Simplified_class'], y_pred_LR, average='macro')
print(LR_precision)
print(LR_recall)
```

```
0.7777777777777778
0.7717948717948718
```

Support Vector Machine Let's just pass the outputs from the first machine that were predicted as "Fibrosis" to the second machine.

[48]:
```
X_test_reset = X_test.reset_index(drop=True)
y_test_reset = y_test.reset_index(drop=True)
X_not_normal = X_test_reset[y_pred_SVM != 'Normal']
y_not_normal = y_test_reset[y_pred_SVM != 'Normal']
```

```
df_deg = subset_data2.iloc[0:,1:].T
df_deg_test = X_not_normal[selected_genes_Python]
y_train2 = y_train[y_train['Simplified_class'] != 'Normal']
```

Second machine performance :

[49]:
```
# Support Vector Machine
SVM_model = SVC(kernel='linear', C=1)
SVM_model.fit(df_deg, y_train2['Simplified_class'])
y_pred_SVM2 = SVM_model.predict(df_deg_test)
SVM_precision = precision_score(y_not_normal['Simplified_class'], y_pred_SVM2,␣
 ↪average='macro')
SVM_recall = recall_score(y_not_normal['Simplified_class'], y_pred_SVM2,␣
 ↪average='macro')
print(SVM_precision)
print(SVM_recall)
```

```
0.4632034632034632
0.527065527065527
```

The overall performance :

[50]:
```
y_pred_SVM[y_pred_SVM == 'Fibrosis'] = y_pred_SVM2
```

[51]:
```
SVM_precision = precision_score(y_test['Simplified_class'], y_pred_SVM,␣
 ↪average='macro')
SVM_recall = recall_score(y_test['Simplified_class'], y_pred_SVM,␣
 ↪average='macro')
print(SVM_precision)
print(SVM_recall)
```

```
0.735930735930736
0.7051282051282052
```

Random Forest Let's just pass the outputs from the first machine that were predicted as "Fibrosis" to the second machine.

[52]:
```
X_test_reset = X_test.reset_index(drop=True)
y_test_reset = y_test.reset_index(drop=True)
X_not_normal = X_test_reset[y_pred_RF != 'Normal']
y_not_normal = y_test_reset[y_pred_RF != 'Normal']
df_deg = subset_data2.iloc[0:,1:].T
df_deg_test = X_not_normal[selected_genes_Python]
y_train2 = y_train[y_train['Simplified_class'] != 'Normal']
```

Second machine performance :

[53]:
```
# Random Forest
RF_model = RandomForestClassifier(random_state=10101)
```

```
RF_model.fit(df_deg, y_train2['Simplified_class'])
y_pred_RF2 = RF_model.predict(df_deg_test)
RF_precision = precision_score(y_not_normal['Simplified_class'], y_pred_RF2,␣
↪average='macro')
RF_recall = recall_score(y_not_normal['Simplified_class'], y_pred_RF2,␣
↪average='macro')
print(RF_precision)
print(RF_recall)
```

```
0.5146520146520147
0.5851851851851851
```

The overall performance :

[54]:
```
y_pred_RF[y_pred_RF == 'Fibrosis'] = y_pred_RF2
```

[55]:
```
RF_precision = precision_score(y_test['Simplified_class'], y_pred_RF,␣
↪average='macro')
RF_recall = recall_score(y_test['Simplified_class'], y_pred_RF, average='macro')
print(RF_precision)
print(RF_recall)
```

```
0.804974595297176
0.794017094017094
```

Multi Layer Perceptron Let's just pass the outputs from the first machine that were predicted as "Fibrosis" to the second machine.

[56]:
```
X_test_reset = X_test.reset_index(drop=True)
y_test_reset = y_test.reset_index(drop=True)
X_not_normal = X_test_reset[y_pred_MLP != 'Normal']
y_not_normal = y_test_reset[y_pred_MLP != 'Normal']
df_deg = subset_data2.iloc[0:,1:].T
df_deg_test = X_not_normal[selected_genes_Python]
y_train2 = y_train[y_train['Simplified_class'] != 'Normal']
```

Second machine performance :

[57]:
```
# Multi Layer Perceptron
MLP_model = MLPClassifier(hidden_layer_sizes=(100,), max_iter=300,␣
↪activation='relu', solver='adam', random_state=10101)
MLP_model.fit(df_deg, y_train2['Simplified_class'])
y_pred_MLP2 = MLP_model.predict(df_deg_test)
MLP_precision = precision_score(y_not_normal['Simplified_class'], y_pred_MLP2,␣
↪average='macro')
MLP_recall = recall_score(y_not_normal['Simplified_class'], y_pred_MLP2,␣
↪average='macro')
print(MLP_precision)
print(MLP_recall)
```

```
0.45
0.5714285714285714
```

The overall performance :

[58]:
```
y_pred_MLP[y_pred_MLP == 'Fibrosis'] = y_pred_MLP2
```

[59]:
```
MLP_precision = precision_score(y_test['Simplified_class'], y_pred_MLP,␣
↪average='macro')
MLP_recall = recall_score(y_test['Simplified_class'], y_pred_MLP,␣
↪average='macro')
print(MLP_precision)
print(MLP_recall)
```

```
0.13
0.17333333333333334
```

So far, we have obtained only a single result for each classifier, but these results are not statistically valid. To test for reproducibility, we have put the entire process into a loop to run it 100 times. Additionally, we created an R script to perform DE analysis automatically using subprocess. Let's run this cell and save the results for statistical analysis.

[60]:
```
import subprocess

# Load Data
normal_counts = pd.read_csv('Normal.counts.voom.csv')
meta_data = pd.read_csv('meta_data.csv')

def determine_class(row):
    if row['Simplified_class'] == 'Normal':
        return "Normal"
    else:
        return "Fibrosis"
meta_data['class'] = meta_data.apply(determine_class, axis=1)
meta_data = pd.DataFrame(meta_data)


n_iterations = 300
test_size = 0.3

LR_precisions = []
LR_recalls = []
LR_precisions2 = []
LR_recalls2 = []
LR_precisions3 = []
LR_recalls3 = []

SVM_precisions = []
SVM_recalls = []
```

```
SVM_precisions2 = []
SVM_recalls2 = []
SVM_precisions3 = []
SVM_recalls3 = []

RF_precisions = []
RF_recalls = []
RF_precisions2 = []
RF_recalls2 = []
RF_precisions3 = []
RF_recalls3 = []

MLP_precisions = []
MLP_recalls = []
MLP_precisions2 = []
MLP_recalls2 = []
MLP_precisions3 = []
MLP_recalls3 = []

for i in range(100):
    print('iteration',i)
    X_train, X_test, y_train, y_test = train_test_split(normal_counts.iloc[0:,1:
 ↪].T, meta_data[['Simplified_class', 'class']], test_size=0.3, random_state =␣
 ↪i)
    X_train.T.to_csv('train_normal_counts.csv', index=False)
    y_train.to_csv('train_meta_data.csv', index=False)

    r_script_path = r"q3r.R"
    rscript_path = r"C:\Program Files\R\R-4.2.1\bin\Rscript.exe"
    # Execute the R script
    try:
            subprocess.run([rscript_path, r_script_path], capture_output=True,␣
 ↪text=True)
    except subprocess.CalledProcessError as e:
            print(f"Error executing R script: {e}")


    # Machine 1
    subset_data1 = pd.read_csv('subset_data1.csv')
    meta_data1 = pd.read_csv('meta_data1.csv')
    selected_genes_R = subset_data1.T.iloc[0,:].to_list()
    selected_genes_Python = [int(i-1) for i in selected_genes_R ]
    df_deg = subset_data1.iloc[0:,1:].T
    df_deg_test = X_test[selected_genes_Python]

    # Logistic Regression
    LR_model = LogisticRegression(solver='saga')
```

```python
    LR_model.fit(df_deg, y_train['class'])
    y_pred_LR = LR_model.predict(df_deg_test)
    LR_precision = precision_score(y_test['class'], y_pred_LR, average='macro')
    LR_recall = recall_score(y_test['class'], y_pred_LR, average='macro')
    LR_precisions.append(LR_precision)
    LR_recalls.append(LR_recall)

    # Support Vector Machine
    SVM_model = SVC(kernel='linear', C=1)
    SVM_model.fit(df_deg, y_train['class'])
    y_pred_SVM = SVM_model.predict(df_deg_test)
    SVM_precision = precision_score(y_test['class'], y_pred_SVM,␣
↪average='macro')
    SVM_recall = recall_score(y_test['class'], y_pred_SVM, average='macro')
    SVM_precisions.append(SVM_precision)
    SVM_recalls.append(SVM_recall)

    # Random Forest
    RF_model = RandomForestClassifier(random_state=i)
    RF_model.fit(df_deg, y_train['class'])
    y_pred_RF = RF_model.predict(df_deg_test)
    RF_precision = precision_score(y_test['class'], y_pred_RF, average='macro')
    RF_recall = recall_score(y_test['class'], y_pred_RF, average='macro')
    RF_precisions.append(RF_precision)
    RF_recalls.append(RF_recall)

    # Multi Layer Perceptron
    MLP_model = MLPClassifier(hidden_layer_sizes=(100,), max_iter=300,␣
↪activation='relu', solver='adam',random_state=i)
    MLP_model.fit(df_deg, y_train['class'])
    y_pred_MLP = MLP_model.predict(df_deg_test)
    MLP_precision = precision_score(y_test['class'], y_pred_MLP,␣
↪average='macro')
    MLP_recall = recall_score(y_test['class'], y_pred_MLP, average='macro')
    MLP_precisions.append(MLP_precision)
    MLP_recalls.append(MLP_recall)



    # Machine 2
    subset_data2 = pd.read_csv('subset_data2.csv')
    meta_data2 = pd.read_csv('meta_data2.csv')

    selected_genes_R = subset_data2.T.iloc[0,:].to_list()
    selected_genes_Python = [int(i-1) for i in selected_genes_R ]
```

```
    X_test_reset = X_test.reset_index(drop=True)
    y_test_reset = y_test.reset_index(drop=True)
    X_not_normal = X_test_reset[y_pred_LR != 'Normal']
    y_not_normal = y_test_reset[y_pred_LR != 'Normal']
    df_deg = subset_data2.iloc[0:,1:].T
    df_deg_test = X_not_normal[selected_genes_Python]
    y_train2 = y_train[y_train['Simplified_class'] != 'Normal']

    # Logistic Regression
    LR_model = LogisticRegression(solver='saga')
    LR_model.fit(df_deg, y_train2['Simplified_class'])
    y_pred_LR2 = LR_model.predict(df_deg_test)
    LR_precision = precision_score(y_not_normal['Simplified_class'],␣
↪y_pred_LR2, average='macro')
    LR_recall = recall_score(y_not_normal['Simplified_class'], y_pred_LR2,␣
↪average='macro')
    LR_precisions2.append(LR_precision)
    LR_recalls2.append(LR_recall)

    y_pred_LR[y_pred_LR == 'Fibrosis'] = y_pred_LR2
    LR_precision = precision_score(y_test['Simplified_class'], y_pred_LR,␣
↪average='macro')
    LR_recall = recall_score(y_test['Simplified_class'], y_pred_LR,␣
↪average='macro')
    LR_precisions3.append(LR_precision)
    LR_recalls3.append(LR_recall)



    X_test_reset = X_test.reset_index(drop=True)
    y_test_reset = y_test.reset_index(drop=True)
    X_not_normal = X_test_reset[y_pred_SVM != 'Normal']
    y_not_normal = y_test_reset[y_pred_SVM != 'Normal']
    df_deg = subset_data2.iloc[0:,1:].T
    df_deg_test = X_not_normal[selected_genes_Python]
    y_train2 = y_train[y_train['Simplified_class'] != 'Normal']

    # Support Vector Machine
    SVM_model = SVC(kernel='linear', C=1)
    SVM_model.fit(df_deg, y_train2['Simplified_class'])
    y_pred_SVM2 = SVM_model.predict(df_deg_test)
    SVM_precision = precision_score(y_not_normal['Simplified_class'],␣
↪y_pred_SVM2, average='macro')
    SVM_recall = recall_score(y_not_normal['Simplified_class'], y_pred_SVM2,␣
↪average='macro')
    SVM_precisions2.append(SVM_precision)
```

```
    SVM_recalls2.append(SVM_recall)

    y_pred_SVM[y_pred_SVM == 'Fibrosis'] = y_pred_SVM2
    SVM_precision = precision_score(y_test['Simplified_class'], y_pred_SVM,␣
↪average='macro')
    SVM_recall = recall_score(y_test['Simplified_class'], y_pred_SVM,␣
↪average='macro')
    SVM_precisions3.append(SVM_precision)
    SVM_recalls3.append(SVM_recall)




    X_test_reset = X_test.reset_index(drop=True)
    y_test_reset = y_test.reset_index(drop=True)
    X_not_normal = X_test_reset[y_pred_RF != 'Normal']
    y_not_normal = y_test_reset[y_pred_RF != 'Normal']
    df_deg = subset_data2.iloc[0:,1:].T
    df_deg_test = X_not_normal[selected_genes_Python]
    y_train2 = y_train[y_train['Simplified_class'] != 'Normal']

    # Random Forest
    RF_model = RandomForestClassifier(random_state=i)
    RF_model.fit(df_deg, y_train2['Simplified_class'])
    y_pred_RF2 = RF_model.predict(df_deg_test)
    RF_precision = precision_score(y_not_normal['Simplified_class'],␣
↪y_pred_RF2, average='macro')
    RF_recall = recall_score(y_not_normal['Simplified_class'], y_pred_RF2,␣
↪average='macro')
    RF_precisions2.append(RF_precision)
    RF_recalls2.append(RF_recall)

    y_pred_RF[y_pred_RF == 'Fibrosis'] = y_pred_RF2
    RF_precision = precision_score(y_test['Simplified_class'], y_pred_RF,␣
↪average='macro')
    RF_recall = recall_score(y_test['Simplified_class'], y_pred_RF,␣
↪average='macro')
    RF_precisions3.append(RF_precision)
    RF_recalls3.append(RF_recall)




    X_test_reset = X_test.reset_index(drop=True)
    y_test_reset = y_test.reset_index(drop=True)
```

```
    X_not_normal = X_test_reset[y_pred_MLP != 'Normal']
    y_not_normal = y_test_reset[y_pred_MLP != 'Normal']
    df_deg = subset_data2.iloc[0:,1:].T
    df_deg_test = X_not_normal[selected_genes_Python]
    y_train2 = y_train[y_train['Simplified_class'] != 'Normal']

    # Multi Layer Perceptron
    MLP_model = MLPClassifier(hidden_layer_sizes=(100,), max_iter=300,␣
↪activation='relu', solver='adam', random_state=i)
    MLP_model.fit(df_deg, y_train2['Simplified_class'])
    y_pred_MLP2 = MLP_model.predict(df_deg_test)
    MLP_precision = precision_score(y_not_normal['Simplified_class'],␣
↪y_pred_MLP2, average='macro')
    MLP_recall = recall_score(y_not_normal['Simplified_class'], y_pred_MLP2,␣
↪average='macro')
    MLP_precisions2.append(MLP_precision)
    MLP_recalls2.append(MLP_recall)

    y_pred_MLP[y_pred_MLP == 'Fibrosis'] = y_pred_MLP2
    MLP_precision = precision_score(y_test['Simplified_class'], y_pred_MLP,␣
↪average='macro')
    MLP_recall = recall_score(y_test['Simplified_class'], y_pred_MLP,␣
↪average='macro')
    MLP_precisions3.append(MLP_precision)
    MLP_recalls3.append(MLP_recall)
```

```
iteration 0
iteration 1
iteration 2
iteration 3
iteration 4
iteration 5
iteration 6
iteration 7
iteration 8
iteration 9
iteration 10
iteration 11
iteration 12
iteration 13
iteration 14
iteration 15
iteration 16
iteration 17
iteration 18
iteration 19
iteration 20
```

```
iteration 21
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iteration 67
iteration 68
```

```
iteration 69
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iteration 87
iteration 88
iteration 89
iteration 90
iteration 91
iteration 92
iteration 93
iteration 94
iteration 95
iteration 96
iteration 97
iteration 98
iteration 99
```

Last but not least, we need to report the average and confidence interval for the results of each classifier. We will also create a bar plot to visually compare the results of the classifiers. We need to compare the results of the two machines and also compare the overall performance with the performance of part 1.

[61]:
```
def␣
↪Evaluation(LR_precisions,LR_recalls,SVM_precisions,SVM_recalls,RF_precisions,RF_recalls,MLP
↪

  LR_mean_precision = np.mean(LR_precisions)
  LR_mean_recall = np.mean(LR_recalls)
  LR_precision_conf_interval = np.percentile(LR_precisions, [2.5, 97.5])
  LR_recall_conf_interval = np.percentile(LR_recalls, [2.5, 97.5])
  print(f'Mean Precision for Logistic Regression: {LR_mean_precision}, 95% CI:␣
↪{LR_precision_conf_interval}')
```

```
print(f'Mean Recall for Logistic Regression: {LR_mean_recall}, 95% CI:␣
↪{LR_recall_conf_interval}')
␣
↪print("-----------------------------------------------------------------------------------------

SVM_mean_precision = np.mean(SVM_precisions)
SVM_mean_recall = np.mean(SVM_recalls)
SVM_precision_conf_interval = np.percentile(SVM_precisions, [2.5, 97.5])
SVM_recall_conf_interval = np.percentile(SVM_recalls, [2.5, 97.5])
print(f'Mean Precision for Support Vector Machine: {SVM_mean_precision}, 95%␣
↪CI: {SVM_precision_conf_interval}')
print(f'Mean Recall for Support Vector Machine: {SVM_mean_recall}, 95% CI:␣
↪{SVM_recall_conf_interval}')
␣
↪print("-----------------------------------------------------------------------------------------

RF_mean_precision = np.mean(RF_precisions)
RF_mean_recall = np.mean(RF_recalls)
RF_precision_conf_interval = np.percentile(RF_precisions, [2.5, 97.5])
RF_recall_conf_interval = np.percentile(RF_recalls, [2.5, 97.5])
print(f'Mean Precision for Random Forest: {RF_mean_precision}, 95% CI:␣
↪{RF_precision_conf_interval}')
print(f'Mean Recall for Random Forest: {RF_mean_recall}, 95% CI:␣
↪{RF_recall_conf_interval}')
␣
↪print("-----------------------------------------------------------------------------------------

MLP_mean_precision = np.mean(MLP_precisions)
MLP_mean_recall = np.mean(MLP_recalls)
MLP_precision_conf_interval = np.percentile(MLP_precisions, [2.5, 97.5])
MLP_recall_conf_interval = np.percentile(MLP_recalls, [2.5, 97.5])
print(f'Mean Precision for Multi Layer Perceptron: {MLP_mean_precision}, 95%␣
↪CI: {MLP_precision_conf_interval}')
print(f'Mean Recall for Multi Layer Perceptron: {MLP_mean_recall}, 95% CI:␣
↪{MLP_recall_conf_interval}')

model_results = {
    'RandomForest': {
        'mean_precision': RF_mean_precision,
        'precision_ci': RF_precision_conf_interval,
        'mean_recall': RF_mean_recall,
        'recall_ci': RF_precision_conf_interval
    },
    'SVM': {
        'mean_precision': SVM_mean_precision,
        'precision_ci': SVM_precision_conf_interval,
```

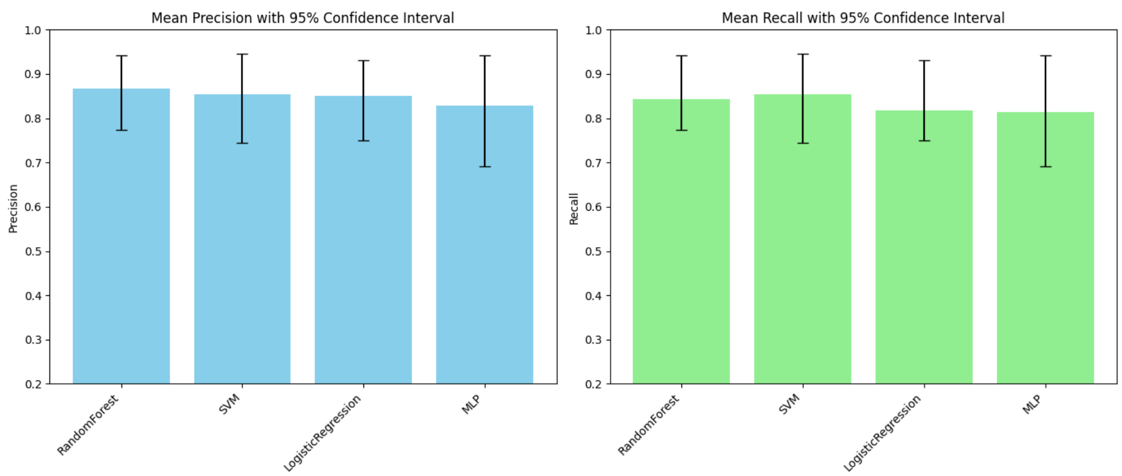
```
        'mean_recall': SVM_mean_recall,
        'recall_ci': SVM_precision_conf_interval
    },
        'LogisticRegression': {
        'mean_precision': LR_mean_precision,
        'precision_ci': LR_precision_conf_interval,
        'mean_recall': LR_mean_recall,
        'recall_ci': LR_precision_conf_interval
    },
    'MLP': {
        'mean_precision': MLP_mean_precision,
        'precision_ci': MLP_precision_conf_interval,
        'mean_recall': MLP_mean_recall,
        'recall_ci': MLP_precision_conf_interval
    }
}

models = list(model_results.keys())
mean_precisions = [model_results[model]['mean_precision'] for model in models]
precision_cis = [model_results[model]['precision_ci'] for model in models]
mean_recalls = [model_results[model]['mean_recall'] for model in models]
recall_cis = [model_results[model]['recall_ci'] for model in models]
precision_errors = np.array([[mean - ci[0], ci[1] - mean] for mean, ci in zip(mean_precisions, precision_cis)]).T
recall_errors = np.array([[mean - ci[0], ci[1] - mean] for mean, ci in zip(mean_recalls, recall_cis)]).T


fig, ax = plt.subplots(1, 2, figsize=(14, 6))

# Plot precision
ax[0].bar(models, mean_precisions, yerr=precision_errors, capsize=5, color='skyblue')
ax[0].set_title('Mean Precision with 95% Confidence Interval')
ax[0].set_ylabel('Precision')
ax[0].set_ylim([0.2, 1])
ax[0].set_xticklabels(models, rotation=45, ha="right")

# Plot recall
recall_errors = np.abs(recall_errors)
ax[1].bar(models, mean_recalls, yerr=recall_errors, capsize=5, color='lightgreen')
ax[1].set_title('Mean Recall with 95% Confidence Interval')
ax[1].set_ylabel('Recall')
ax[1].set_ylim([0.2, 1])
ax[1].set_xticklabels(models, rotation=45, ha="right")
```

```
plt.tight_layout()
plt.show()
```

First machine performance

[62]:
```
Evaluation(LR_precisions,LR_recalls,SVM_precisions,SVM_recalls,RF_precisions,RF_recalls,MLP_pr
```

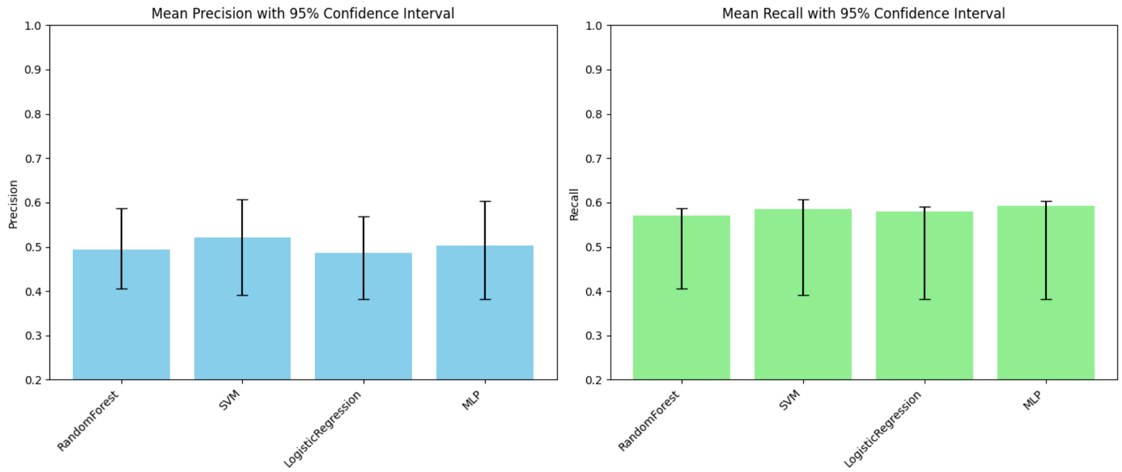
```
Mean Precision for Logistic Regression: 0.8507986028117874, 95% CI: [0.74906143
0.93196691]
Mean Recall for Logistic Regression: 0.8184382226583906, 95% CI: [0.71882411
0.91247283]
--------------------------------------------------------------------------------
-----------------
Mean Precision for Support Vector Machine: 0.8541628167891444, 95% CI:
[0.7451173  0.94618344]
Mean Recall for Support Vector Machine: 0.8532791569141659, 95% CI: [0.72634525
0.94728788]
--------------------------------------------------------------------------------
-----------------
Mean Precision for Random Forest: 0.8662842019770599, 95% CI: [0.77367045
0.94186992]
Mean Recall for Random Forest: 0.8423994128996357, 95% CI: [0.7519177
0.92569103]
--------------------------------------------------------------------------------
-----------------
Mean Precision for Multi Layer Perceptron: 0.8294359560661213, 95% CI:
[0.69210366 0.94205763]
Mean Recall for Multi Layer Perceptron: 0.8138548946171023, 95% CI: [0.67534091
0.93615888]
```



Second machine performance

[63]:
```
Evaluation(LR_precisions2,LR_recalls2,SVM_precisions2,SVM_recalls2,RF_precisions2,RF_recalls2,
```

```
Mean Precision for Logistic Regression: 0.48567706681064426, 95% CI: [0.38149909
0.56918895]
Mean Recall for Logistic Regression: 0.5799392318276589, 95% CI: [0.48022813
0.65833333]
--------------------------------------------------------------------------------
-----------------
Mean Precision for Support Vector Machine: 0.521669299221665, 95% CI:
[0.39196682 0.60654762]
Mean Recall for Support Vector Machine: 0.5853675838091306, 95% CI: [0.49366987
0.65041667]
--------------------------------------------------------------------------------
-----------------
Mean Precision for Random Forest: 0.4932939914363126, 95% CI: [0.40565889
0.58737179]
Mean Recall for Random Forest: 0.5710494493927324, 95% CI: [0.48637821
0.64583333]
--------------------------------------------------------------------------------
-----------------
Mean Precision for Multi Layer Perceptron: 0.5019645664243881, 95% CI:
[0.3821875  0.60328982]
Mean Recall for Multi Layer Perceptron: 0.5924393001225852, 95% CI: [0.5
0.66666667]
```

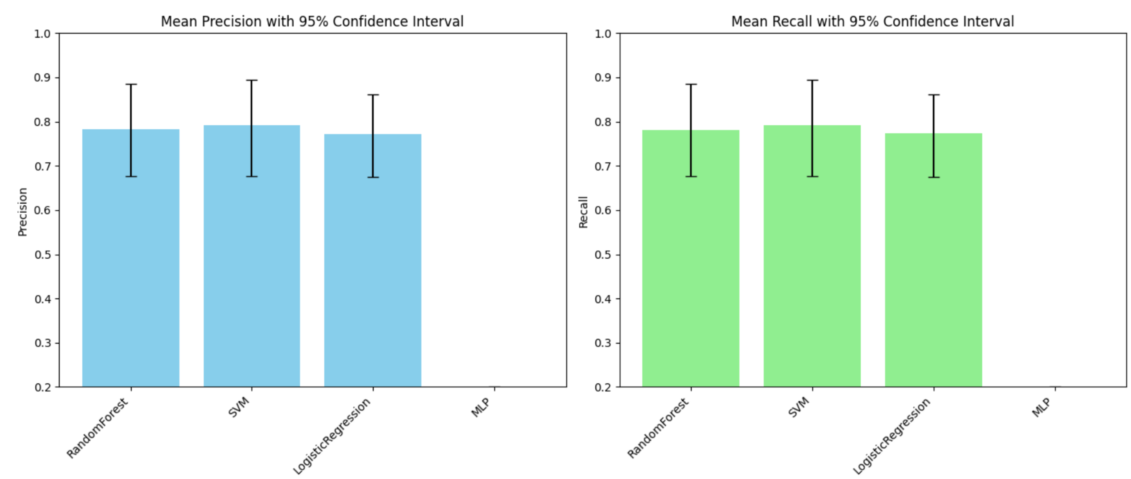


Two machines overall performance

[64]:
```
Evaluation(LR_precisions3,LR_recalls3,SVM_precisions3,SVM_recalls3,RF_precisions3,RF_recalls3,
```

```
Mean Precision for Logistic Regression: 0.7721431738642025, 95% CI: [0.67519751
0.86124603]
Mean Recall for Logistic Regression: 0.7728212040224424, 95% CI: [0.67362676
```

```
0.87607026]
--------------------------------------------------------------------------------
-----------------
Mean Precision for Support Vector Machine: 0.792152196918704, 95% CI:
[0.67607911 0.89426533]
Mean Recall for Support Vector Machine: 0.7915281309131815, 95% CI: [0.67922436
0.8902451 ]
--------------------------------------------------------------------------------
-----------------
Mean Precision for Random Forest: 0.7823179426077859, 95% CI: [0.676875
0.88465385]
Mean Recall for Random Forest: 0.7810645743189738, 95% CI: [0.64808837
0.88498188]
--------------------------------------------------------------------------------
-----------------
Mean Precision for Multi Layer Perceptron: 0.16327626954906724, 95% CI:
[0.11730603 0.2       ]
Mean Recall for Multi Layer Perceptron: 0.1476318812325906, 95% CI: [0.09738426
0.1911166 ]
```



As you can see, the results from the first machine are significantly better than those from the second machine, and the different classifiers performed mostly similar.

In comparison with the overall performance and the performance in Part 1, we can conclude that there is no significant change in results, except for the MLP model, which performs poorly in this task. This could be due to its sensitivity to the distribution of the data or its complexity in handling the hierarchical classification process.