Q2-Python

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1 NAFLD detection using RNA-Seq data

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In this part, we need to assess whether clinical data such as BMI, age, sex, and diabetes are important enough to be included in our feature selection. Additionally, we will evaluate whether their inclusion improves upon our previous results. Let's proceed and find out.

2 Q2 - Python section

[39]:
```
# 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]:
```
normal_counts.head()
```

[3]:
```
              gene  DLDR_0001  DLDR_0002  DLDR_0003  DLDR_0004  DLDR_0005  \
0  ENSG00000000003   5.965571   5.741587   5.996891   5.551919   6.430237
```

```
1  ENSG00000000005   1.612375   2.147793   0.418542   0.702492   1.215978
2  ENSG00000000419   4.133821   4.120969   4.086129   4.116240   4.393797
3  ENSG00000000457   4.111056   3.922234   3.964871   3.978350   4.018235
4  ENSG00000000460   4.150662   3.732756   3.634637   3.853979   3.614220

   DLDR_0006  DLDR_0007  DLDR_0008  DLDR_0009  …  DLDR_0183  DLDR_0184  \
0   6.234619   6.071503   6.441882   5.752712  …   6.304802   6.576246
1   0.920810   0.458163   0.927224   1.089389  …  -0.031596  -1.091275
2   4.390909   4.148242   4.554655   4.203819  …   4.176599   4.244459
3   3.864521   4.263119   3.896271   4.139546  …   4.378342   4.453838
4   3.500857   4.000565   4.016287   3.904500  …   2.974209   3.720038

   DLDR_0185  DLDR_0186  DLDR_0187  DLDR_0188  DLDR_0189  DLDR_0190  \
0   6.735760   6.344234   6.608924   6.480745   6.360397   6.367705
1  -0.942637  -0.026585  -0.757399  -1.083676   0.886550  -0.902201
2   4.342765   4.179319   4.274450   4.361634   4.093280   4.148010
3   4.685598   4.438796   4.042577   4.313540   4.205119   4.506058
4   4.640011   3.814717   2.126408   3.120196   3.336802   3.982071

   DLDR_0191  DLDR_0192
0   6.604050   6.514539
1  -0.865036  -1.588749
2   4.351489   3.859711
3   4.072137   4.341988
4   3.143138   2.741172

[5 rows x 193 columns]
```

[4]:
```
normal_counts.shape
```

[4]:
```
(17396, 193)
```

[5]:
```
meta_data.head()
```

[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

  Simplified_class
0           Normal
1           Normal
2           Normal
3           Normal
4           Normal
```

[6]:
```
meta_data.shape
```

[6]:
```
(192, 7)
```

[7]:
```
print("Number of Normal samples: ", meta_data['Simplified_class'].to_list().
 ↪count("Normal"))
print("Number of Non_advanced_Fibrosis samples: ",␣
 ↪meta_data['Simplified_class'].to_list().count("Non_advanced_Fibrosis"))
print("Number of Advanced_fibrosis: ", meta_data['Simplified_class'].to_list().
 ↪count("Advanced_fibrosis"))
```

```
Number of Normal samples:  74
Number of Non_advanced_Fibrosis samples:  53
Number of Advanced_fibrosis:  65
```

To include our clinical data, we need to perform some preprocessing steps. For categorical data, we will use one-hot encoding, and for continuous data, we will apply normalization.

[8]:
```
# One-Hot Encoding for categorical features
categorical_features = ['SEX', 'Diabet']
ohe = OneHotEncoder()
# Standardize continuous variables
numerical_features = ['BMI_surg', 'Age']
scaler = StandardScaler()
# Preprocess clinical data
preprocessor = ColumnTransformer(
    transformers=[
        ('num', scaler, numerical_features),
        ('cat', ohe, categorical_features)])
```

[9]:
```
clinical_data = preprocessor.fit_transform(meta_data)
```

[10]:
```
clinical_data = pd.DataFrame(clinical_data).iloc[:, [0, 1, 2, 4]]
clinical_data.columns = ['BMI_surg', 'Age', 'Sex', 'Diabet']
```

[11]:
```
clinical_data
```

[11]:

	BMI_surg	Age	Sex	Diabet
0	-1.308155	0.855160	1.0	0.0
1	-0.857325	0.145913	1.0	1.0
2	0.143131	0.057257	0.0	0.0
3	-0.600056	-0.829302	1.0	0.0
4	0.660065	0.766504	1.0	0.0
..	…	…	…	…
187	-0.772196	1.209783	0.0	1.0
188	0.284524	0.589192	1.0	0.0
189	6.161411	-1.538548	0.0	1.0
190	0.007788	-0.829302	1.0	0.0

```
191 -0.214761  0.677848  1.0      0.0

[192 rows x 4 columns]
```

[12]:
```
print(clinical_data.shape)
print(normal_counts.shape)
```

```
(192, 4)
(17396, 193)
```

[13]:
```
gene_names = normal_counts.iloc[:,0]
gene_names.at[17396] = 'BMI_surg'
gene_names.at[17397] = 'Age'
gene_names.at[17398] = 'SEX'
gene_names.at[17399] = 'Diabet'
```

[14]:
```
gene_names
```

[14]:
```
0        ENSG00000000003
1        ENSG00000000005
2        ENSG00000000419
3        ENSG00000000457
4        ENSG00000000460
              …
17395    ENSG00000273294
17396           BMI_surg
17397                Age
17398                SEX
17399             Diabet
Name: gene, Length: 17400, dtype: object
```

Now, let's combine our gene expression data with clinical data

[15]:
```
combined_data = np.hstack((normal_counts.iloc[0:,1:].T, clinical_data))
combined_data = pd.DataFrame(combined_data)
```

[16]:
```
combined_data
```

[16]:
```
           0         1         2         3         4         5          6     \
0    5.965571  1.612375  4.133821  4.111056  4.150662  2.975845  11.005488
1    5.741587  2.147793  4.120969  3.922234  3.732756  3.199989  10.860700
2    5.996891  0.418542  4.086129  3.964871  3.634637  2.949733  10.934025
3    5.551919  0.702492  4.116240  3.978350  3.853979  2.991061  10.760445
4    6.430237  1.215978  4.393797  4.018235  3.614220  2.836130  11.491427
..        …         …         …         …         …         …          …
187  6.480745 -1.083676  4.361634  4.313540  3.120196  1.941859  11.451981
188  6.360397  0.886550  4.093280  4.205119  3.336802  2.911496  11.658711
189  6.367705 -0.902201  4.148010  4.506058  3.982071  2.202136  11.864397
```

```
190  6.604050 -0.865036  4.351489  4.072137  3.143138  4.037476  11.782524
191  6.514539 -1.588749  3.859711  4.341988  2.741172  2.803568  11.474777

            7         8         9    …     17390     17391     17392  \
0    4.405768  6.825329  4.221450  …  0.691230  5.637483 -0.005377
1    3.895350  6.453687  4.218183  …  1.004202  5.975612  0.532134
2    4.282577  6.437658  3.736947  …  0.943633  5.531648 -0.184123
3    4.297722  6.710840  4.003661  …  0.431190  5.571799 -0.034474
4    4.405558  7.437655  4.377965  …  0.085581  5.636848 -1.216981
..        …         …         …  …       …         …         …
187  4.556052  7.183779  5.066071  … -0.431600  2.616763  1.063165
188  4.315153  7.384726  4.627703  … -1.080284  2.975985  0.589568
189  4.348255  7.326297  4.528530  … -1.108652  3.218814 -0.416774
190  4.358527  8.468526  5.013154  … -0.624028  2.050571 -1.517113
191  3.895962  7.617180  4.778544  … -0.510747  2.572243  0.667591

        17393     17394     17395     17396     17397  17398  17399
0    1.675800  2.683536 -0.339797 -1.308155  0.855160    1.0    0.0
1    1.555218  2.926666  0.435919 -0.857325  0.145913    1.0    1.0
2    2.391906  2.260662 -0.691083  0.143131  0.057257    0.0    0.0
3    1.639298  2.341393  0.096771 -0.600056 -0.829302    1.0    0.0
4    1.974160  1.351861 -0.079478  0.660065  0.766504    1.0    0.0
..        …         …         …         …         …      …      …
187  1.941859 -2.306069  0.632531 -0.772196  1.209783    0.0    1.0
188  2.754906 -0.839275 -0.016153  0.284524  0.589192    1.0    0.0
189  2.246191 -1.639167  0.145105  6.161411 -1.538548    0.0    1.0
190  2.084923 -4.324468  0.067849  0.007788 -0.829302    1.0    0.0
191  2.160189 -3.173712  1.218606 -0.214761  0.677848    1.0    0.0

[192 rows x 17400 columns]
```

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

[17]:
```
X_train, X_test, y_train, y_test = train_test_split(combined_data,
    meta_data['Simplified_class'], test_size=0.3, random_state = 10101)
```

[18]:
```
X_train.head()
```

[18]:
```
            0         1         2         3         4         5          6  \
35   5.820135 -1.060061  4.388400  4.080172  2.564430  3.552685  11.011379
80   6.546299  0.582165  3.752090  4.645175  3.840899  3.201075  11.433579
190  6.604050 -0.865036  4.351489  4.072137  3.143138  4.037476  11.782524
187  6.480745 -1.083676  4.361634  4.313540  3.120196  1.941859  11.451981
129  6.550016 -1.222374  4.534941  4.370763  3.512952  2.517867  12.041229

            7         8         9    …     17390     17391     17392  \
35   4.682305  6.951539  4.589555  … -0.323095  3.157170  0.459313
80   3.705547  7.143316  5.482169  …  0.582165  4.041596  0.096738
```

```
190  4.358527  8.468526  5.013154  … -0.624028  2.050571 -1.517113
187  4.556052  7.183779  5.066071  … -0.431600  2.616763  1.063165
129  4.315374  7.485927  4.655817  … -0.981365  2.594319  0.447478

        17393     17394     17395     17396     17397  17398  17399
35   3.115198 -2.645023  0.760969 -0.001936 -0.120055    1.0    0.0
80   2.418666 -2.225190  0.582165 -0.661021 -1.361237    1.0    1.0
190  2.084923 -4.324468  0.067849  0.007788 -0.829302    1.0    0.0
187  1.941859 -2.306069  0.632531 -0.772196  1.209783    0.0    1.0
129  2.556600 -2.359877  0.932905  0.932361 -1.627204    1.0    0.0

[5 rows x 17400 columns]
```

[19]:
```
X_train.shape
```

[19]:
```
(134, 17400)
```

[20]:
```
y_train.head()
```

[20]:
```
35                     Normal
80          Advanced_fibrosis
190                    Normal
187                    Normal
129    Non_advanced_Fibrosis
Name: Simplified_class, dtype: object
```

[21]:
```
y_train.shape
```

[21]:
```
(134,)
```

[22]:
```
print("Number of Normal samples: ", y_train.to_list().count("Normal"))
print("Number of Non_advanced_Fibrosis samples: ", y_train.to_list().
 ↪count("Non_advanced_Fibrosis"))
print("Number of Advanced_fibrosis samples: ", y_train.to_list().
 ↪count("Advanced_fibrosis"))
```

```
Number of Normal samples:  44
Number of Non_advanced_Fibrosis samples:  38
Number of Advanced_fibrosis samples:  52
```

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

[23]:
```
X_train.T.to_csv('train_normal_counts.csv', index=False)
y_train.T.to_csv('train_meta_data.csv', index=False)
```

Run R Jupyter Notebook Let's load the output of R to continue the task and check if any clinical data have been selected or not

[24]:
```
subset_data = pd.read_csv('subset_data.csv')
```

[25]:
```
subset_data
```

[25]:
```
     Unnamed: 0       X35       X80      X190      X187      X129       X12  \
0            10  4.589555  5.482169  5.013154  5.066071  4.655817  4.299078
1            57 -0.719024  0.582165 -1.154543 -1.083676 -0.289488 -0.006469
2           265  0.587637 -2.225190 -0.076540  0.196432  0.272391  2.523150
3           275  1.662405  2.529697  1.508422  1.991612  1.467942  1.934152
4           278  5.529902  5.846272  5.553583  5.359267  5.774549  4.962662
..          …         …         …         …         …         …         …
522       16863  3.811126  3.329399  2.183327  2.412750  3.323819  2.690386
523       16887  3.576080  2.418666  3.355012  3.288878  3.231084  3.757011
524       16892  4.007463  3.060212  2.951656  3.366357  2.649112  2.774044
525       17075  6.925971  7.323632  7.411511  7.189120  7.519400  6.661844
526       17187 -2.645023 -2.225190 -4.324468 -3.891031 -4.681805  0.820694

          X78      X130      X134  …      X174       X51       X86  \
0    4.752957  5.409514  4.993777  …  4.853565  4.567173  4.985158
1   -1.138550 -4.060128 -2.104255  … -2.285986 -0.110595 -0.385647
2    1.424386  0.332190  0.217673  …  1.083248  0.352377 -0.309698
3    2.031375  2.048397  0.528013  …  1.083248  2.556469  2.055951
4    5.201300  5.500205  5.782051  …  5.862067  5.038603  5.665231
..        …         …         …  …       …         …         …
522  3.515760  3.197260  2.112975  …  1.555316  3.901539  3.344479
523  2.435441  3.079423  2.393996  …  2.974541  3.737944  2.476362
524  3.123117  2.951099  2.974696  …  2.604785  3.934981  3.001089
525  7.087205  7.366661  7.586092  …  7.491543  6.721953  7.511299
526 -3.013019 -4.060128 -4.426183  … -3.870949 -3.735085 -4.010138

         X154       X91      X186      X185      X178      X181        X0
0    5.234776  4.900754  4.923087  5.004500  5.058062  5.002454  4.221450
1   -3.580073  0.317259 -0.757399 -3.486017 -1.346471 -1.103280 -0.005377
2    0.120366  0.890444 -0.291735  0.811664 -0.246936  0.416094  2.729099
3    1.374123  1.902221  1.838969  1.643266  1.272439  1.932344  2.467558
4    5.781140  5.745159  5.438062  5.570169  5.558701  5.733822  5.220121
..        …         …         …         …         …         …         …
522  1.911780  3.763838  3.667268  2.742802  2.446087  3.857108  2.844001
523  2.817958  2.596331  3.203431  3.162640  2.353968  3.445156  3.271068
524  2.596515  3.945549  4.002569  3.359473  3.497226  3.563476  2.830128
525  7.684565  7.620817  7.419428  7.417614  7.354464  7.633460  6.752731
526 -5.165036 -2.718365 -5.149716 -5.070979 -2.568864 -3.425208  1.202731

[527 rows x 135 columns]
```

[26]:
```
subset_data.shape
```

[26]: (527, 135)

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.

[27]:
```
selected_genes_R = subset_data.T.iloc[0,:].to_list()
```

[28]:
```
selected_genes_Python = [int(i-1) for i in selected_genes_R ]
```

[29]:
```
selected_genes_Python[:10]
```

[29]: [9, 56, 264, 274, 277, 296, 309, 340, 351, 389]

[30]:
```
len(selected_genes_Python)
```

[30]: 527

[31]:
```
clinical_indices =[17396,17397,17398,17399]
common_members = set(selected_genes_Python).intersection(set(clinical_indices))
if common_members:
    print("Some clinical data is identified among DEGs")
else:
    print("No clinical data is identified among DEGs")
```

```
No clinical data is identified among DEGs
```

So in this case, no clinical data have been selected

2.0.1 Classification

Now, we need to determine whether adding clinical data improves the performance of our classification models compared to the previous results. To evaluate this, we will perform classification under three conditions: 1- using only DEGs, 2- combining DEGs and clinical data, and 3- using only clinical data. This process will help us assess the impact of clinical data on classification, both with and without the presence of DEGs.

1- Using only DEGs

[32]:
```
df_deg = subset_data.iloc[0:,1:].T
df_deg_test = X_test[selected_genes_Python]
```

[33]:
```
df_deg.head()
```

[33]:

```
             0         1         2         3         4         5         6  \
X35   4.589555 -0.719024  0.587637  1.662405  5.529902  7.549487  0.318451
X80   5.482169  0.582165 -2.225190  2.529697  5.846272  7.759228  0.096738
X190  5.013154 -1.154543 -0.076540  1.508422  5.553583  7.612538  1.033084
X187  5.066071 -1.083676  0.196432  1.991612  5.359267  8.070057  0.356896
X129  4.655817 -0.289488  0.272391  1.467942  5.774549  7.439405  0.362589
```

```
            7         8         9  …       517       518       519  \
X35  6.089009  5.898008  9.044188  …  3.104511  1.602904  0.915692
X80  6.539682  6.101239  8.633568  …  2.819204  1.234242 -0.640228
X190 6.434588  6.098648  8.244201  …  2.275445  0.884985  0.067849
X187 6.476384  6.118797  7.951712  …  2.708882  0.356896 -0.431600
X129 6.486240  6.239292  8.248378  …  2.969247  1.248932 -1.222374

          520       521       522       523       524       525       526
X35  7.886943  5.319606  3.811126  3.576080  4.007463  6.925971 -2.645023
X80  6.310085  3.797178  3.329399  2.418666  3.060212  7.323632 -2.225190
X190 7.139567  3.909152  2.183327  3.355012  2.951656  7.411511 -4.324468
X187 7.167637  4.021858  2.412750  3.288878  3.366357  7.189120 -3.891031
X129 6.106913  3.570860  3.323819  3.231084  2.649112  7.519400 -4.681805

[5 rows x 527 columns]
```

[34]:

```python
df_deg_test.head()
```

[34]:

```
           9        56       264       274       277       296       309  \
21   3.967031  0.177378  2.880522  2.254454  5.101756  7.696151  2.077214
15   4.603126  0.002788  2.608214  1.992446  5.079298  7.453528  2.274384
3    4.003661 -0.178864  2.418699  2.287454  5.125878  6.943351  2.538993
164  5.286333  0.143691  0.332137  1.587791  5.827910  7.489948  1.225221
126  5.118729 -0.818750  0.897457  1.530400  5.446251  7.622416  0.897457

          340       351       389  …     16641     16686     16715  \
21   5.845657  5.444621  8.076772  …  2.825450  0.246091  0.928350
15   5.735367  5.394124  9.027927  …  2.934201  0.299770  0.488215
3    6.049955  5.583037  8.243201  …  2.418699  0.217065 -0.519901
164  6.994423  6.261908  8.733452  …  2.368478  0.143691  0.389852
126  6.472366  5.832644  8.246698  …  2.137661  0.811301  1.128783

        16731     16762     16862     16886     16891     17074     17186
21   7.735892  4.644785  2.335526  3.460071  3.723708  6.646771  0.246091
15   7.956485  5.527246  2.274384  3.722128  3.226652  6.739625  0.545930
3    7.122512  3.978350  2.974088  3.280568  2.418699  6.827647  0.999473
164  6.695064  3.291074  1.485611  2.862085  2.892352  7.434889 -3.697611
126  6.668899  3.631283  3.308569  2.881690  2.101816  7.391864  0.215197

[5 rows x 527 columns]
```

Logistic Regression

[40]:

```python
# Logistic Regression
LR_model = LogisticRegression(solver='saga')
LR_model.fit(df_deg, y_train)
y_pred_LR = LR_model.predict(df_deg_test)
LR_precision = precision_score(y_test, y_pred_LR, average='macro')
```

```
LR_recall = recall_score(y_test, y_pred_LR, average='macro')
print(LR_precision)
print(LR_recall)
```

```
0.7842803030303029
0.752991452991453
```

Support Vector Machine

[41]:
```
# Support Vector Machine
SVM_model = SVC(kernel='linear', C=1)
SVM_model.fit(df_deg, y_train)
y_pred_SVM = SVM_model.predict(df_deg_test)
SVM_precision = precision_score(y_test, y_pred_SVM, average='macro')
SVM_recall = recall_score(y_test, y_pred_SVM, average='macro')
print(SVM_precision)
print(SVM_recall)
```

```
0.8441558441558442
0.8008547008547008
```

Random Forest

[42]:
```
# Random Forest
RF_model = RandomForestClassifier(random_state = 10101)
RF_model.fit(df_deg, y_train)
y_pred_RF = RF_model.predict(df_deg_test)
RF_precision = precision_score(y_test, y_pred_RF, average='macro')
RF_recall = recall_score(y_test, y_pred_RF, average='macro')
print(RF_precision)
print(RF_recall)
```

```
0.7743589743589744
0.7606837606837606
```

Multi Layer Perceptron

[43]:
```
# 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)
y_pred_MLP = MLP_model.predict(df_deg_test)
MLP_precision = precision_score(y_test, y_pred_MLP, average='macro')
MLP_recall = recall_score(y_test, y_pred_MLP, average='macro')
print(MLP_precision)
print(MLP_recall)
```

```
0.7317550505050505
0.7051282051282052
```

2- Combining DEGs and clinical data

[44]:
```
clinical_df_deg = np.hstack((df_deg,X_train[clinical_indices]))
```

[45]:
```
clinical_df_deg = pd.DataFrame(clinical_df_deg)
clinical_df_deg.head()
```

[45]:
```
          0         1         2         3         4         5         6    \
0  4.589555 -0.719024  0.587637  1.662405  5.529902  7.549487  0.318451
1  5.482169  0.582165 -2.225190  2.529697  5.846272  7.759228  0.096738
2  5.013154 -1.154543 -0.076540  1.508422  5.553583  7.612538  1.033084
3  5.066071 -1.083676  0.196432  1.991612  5.359267  8.070057  0.356896
4  4.655817 -0.289488  0.272391  1.467942  5.774549  7.439405  0.362589

          7         8         9    …       521       522       523       524  \
0  6.089009  5.898008  9.044188  …  5.319606  3.811126  3.576080  4.007463
1  6.539682  6.101239  8.633568  …  3.797178  3.329399  2.418666  3.060212
2  6.434588  6.098648  8.244201  …  3.909152  2.183327  3.355012  2.951656
3  6.476384  6.118797  7.951712  …  4.021858  2.412750  3.288878  3.366357
4  6.486240  6.239292  8.248378  …  3.570860  3.323819  3.231084  2.649112

        525       526       527       528  529  530
0  6.925971 -2.645023 -0.001936 -0.120055  1.0  0.0
1  7.323632 -2.225190 -0.661021 -1.361237  1.0  1.0
2  7.411511 -4.324468  0.007788 -0.829302  1.0  0.0
3  7.189120 -3.891031 -0.772196  1.209783  0.0  1.0
4  7.519400 -4.681805  0.932361 -1.627204  1.0  0.0

[5 rows x 531 columns]
```

[46]:
```
clinical_df_deg_test = np.hstack((df_deg_test,X_test[clinical_indices]))
```

[47]:
```
clinical_df_deg_test = pd.DataFrame(clinical_df_deg_test)
clinical_df_deg_test.head()
```

[47]:
```
          0         1         2         3         4         5         6    \
0  3.967031  0.177378  2.880522  2.254454  5.101756  7.696151  2.077214
1  4.603126  0.002788  2.608214  1.992446  5.079298  7.453528  2.274384
2  4.003661 -0.178864  2.418699  2.287454  5.125878  6.943351  2.538993
3  5.286333  0.143691  0.332137  1.587791  5.827910  7.489948  1.225221
4  5.118729 -0.818750  0.897457  1.530400  5.446251  7.622416  0.897457

          7         8         9    …       521       522       523       524  \
0  5.845657  5.444621  8.076772  …  4.644785  2.335526  3.460071  3.723708
1  5.735367  5.394124  9.027927  …  5.527246  2.274384  3.722128  3.226652
2  6.049955  5.583037  8.243201  …  3.978350  2.974088  3.280568  2.418699
3  6.994423  6.261908  8.733452  …  3.291074  1.485611  2.862085  2.892352
4  6.472366  5.832644  8.246698  …  3.631283  3.308569  2.881690  2.101816
```

```
        525       526       527       528  529  530
0  6.646771  0.246091 -0.082413  1.298439  1.0  0.0
1  6.739625  0.545930 -0.446496 -0.474678  1.0  0.0
2  6.827647  0.999473 -0.600056 -0.829302  1.0  0.0
3  7.434889 -3.697611  0.875886 -1.183925  1.0  0.0
4  7.391864  0.215197 -0.699417 -0.208711  1.0  1.0

[5 rows x 531 columns]
```

Logistic Regression

[48]:
```python
# Logistic Regression
LR_model = LogisticRegression(solver='saga')
LR_model.fit(clinical_df_deg, y_train)
y_pred_LR = LR_model.predict(clinical_df_deg_test)
LR_precision = precision_score(y_test, y_pred_LR, average='macro')
LR_recall = recall_score(y_test, y_pred_LR, average='macro')
print(LR_precision)
print(LR_recall)
```

```
0.8010912698412698
0.7752136752136751
```

Support Vector Machine

[49]:
```python
# Support Vector Machine
SVM_model = SVC(kernel='linear', C=1)
SVM_model.fit(clinical_df_deg, y_train)
y_pred_SVM = SVM_model.predict(clinical_df_deg_test)
SVM_precision = precision_score(y_test, y_pred_SVM, average='macro')
SVM_recall = recall_score(y_test, y_pred_SVM, average='macro')
print(SVM_precision)
print(SVM_recall)
```

```
0.8288084464555053
0.7752136752136751
```

Random Forest

[50]:
```python
# Random Forest
RF_model = RandomForestClassifier(random_state = 10101)
RF_model.fit(clinical_df_deg, y_train)
y_pred_RF = RF_model.predict(clinical_df_deg_test)
RF_precision = precision_score(y_test, y_pred_RF, average='macro')
RF_recall = recall_score(y_test, y_pred_RF, average='macro')
print(RF_precision)
print(RF_recall)
```

```
0.753968253968254
0.7461538461538462
```

Multi Layer Perceptron

[51]:
```
# Multi Layer Perceptron
MLP_model = MLPClassifier(hidden_layer_sizes=(100,), max_iter=300,␣
↪activation='relu', solver='adam',random_state = 10101)
MLP_model.fit(clinical_df_deg, y_train)
y_pred_MLP = MLP_model.predict(clinical_df_deg_test)
MLP_precision = precision_score(y_test, y_pred_MLP, average='macro')
MLP_recall = recall_score(y_test, y_pred_MLP, average='macro')
print(MLP_precision)
print(MLP_recall)
```

```
0.7662337662337663
0.7273504273504273
```

3- using only clinical data

Logistic Regression

[53]:
```
# Logistic Regression
LR_model = LogisticRegression(solver='saga')
LR_model.fit(X_train[clinical_indices], y_train)
y_pred_LR = LR_model.predict(X_test[clinical_indices])
LR_precision = precision_score(y_test, y_pred_LR, average='macro')
LR_recall = recall_score(y_test, y_pred_LR, average='macro')
print(LR_precision)
print(LR_recall)
```

```
0.49887766554433216
0.511965811965812
```

Support Vector Machine

[158]:
```
# Support Vector Machine
SVM_model = SVC(kernel='linear', C=1)
SVM_model.fit(X_train[clinical_indices], y_train)

y_pred_SVM = SVM_model.predict(X_test[clinical_indices])
SVM_precision = precision_score(y_test, y_pred_SVM, average='macro')
SVM_recall = recall_score(y_test, y_pred_SVM, average='macro')
print(SVM_precision)
print(SVM_recall)
```

```
0.47980407944176057
0.511965811965812
```

Random Forest

[54]:
```
# Random Forest
RF_model = RandomForestClassifier(random_state = 10101)
RF_model.fit(X_train[clinical_indices], y_train)
y_pred_RF = RF_model.predict(X_test[clinical_indices])
```

```
RF_precision = precision_score(y_test, y_pred_RF, average='macro')
RF_recall = recall_score(y_test, y_pred_RF, average='macro')
print(RF_precision)
print(RF_recall)
```

```
0.5344751866490997
0.5418803418803418
```

Multi Layer Perceptron

[55]:
```
# Multi Layer Perceptron
MLP_model = MLPClassifier(hidden_layer_sizes=(100,), max_iter=300,␣
 ↪activation='relu', solver='adam',random_state = 10101)
MLP_model.fit(X_train[clinical_indices], y_train)
y_pred_MLP = MLP_model.predict(X_test[clinical_indices])
MLP_precision = precision_score(y_test, y_pred_MLP, average='macro')
MLP_recall = recall_score(y_test, y_pred_MLP, average='macro')
print(MLP_precision)
print(MLP_recall)
```

```
0.5412962962962963
0.5307692307692308
```

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.

For each iteration, in addition to saving precision and recall for statistical validation, we need to check whether the clinical data have been included in our feature selection.

[57]:
```
import subprocess

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

categorical_features = ['SEX', 'Diabet']
ohe = OneHotEncoder()
numerical_features = ['BMI_surg', 'Age']
scaler = StandardScaler()
preprocessor = ColumnTransformer(
    transformers=[
        ('num', scaler, numerical_features),
        ('cat', ohe, categorical_features)])
clinical_data = preprocessor.fit_transform(meta_data)
clinical_data = pd.DataFrame(clinical_data).iloc[:, [0, 1, 2, 4]]
clinical_data.columns = ['BMI_surg', 'Age', 'Sex', 'Diabet']
gene_names = normal_counts.iloc[:,0]
gene_names.at[17396] = 'BMI_surg'
```

```
gene_names.at[17397] = 'Age'
gene_names.at[17398] = 'SEX'
gene_names.at[17399] = 'Diabet'

combined_data = np.hstack((normal_counts.iloc[0:,1:].T, clinical_data))
combined_data = pd.DataFrame(combined_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(combined_data,
 ↪meta_data['Simplified_class'], test_size=0.3, random_state = i)
    X_train.T.to_csv('train_normal_counts.csv', index=False)
    y_train.T.to_csv('train_meta_data.csv', index=False)

    r_script_path = r"q2r.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}")

    #
    subset_data = pd.read_csv('subset_data.csv')
    selected_genes_R = subset_data.T.iloc[0,:].to_list()
    selected_genes_Python = [int(i-1) for i in selected_genes_R ]

    clinical_indices =[17396,17397,17398,17399]
    common_members = set(selected_genes_Python).
↪intersection(set(clinical_indices))
    if common_members:
        print("Some clinical data is identified among DEGs")
    else:
        print("No clinical data is identified among DEGs")

    df_deg = subset_data.iloc[0:,1:].T
    df_deg_test = X_test[selected_genes_Python]

    # Logistic Regression
    LR_model = LogisticRegression(solver='saga')
    LR_model.fit(df_deg, y_train)
    y_pred_LR = LR_model.predict(df_deg_test)
    LR_precision = precision_score(y_test, y_pred_LR, average='macro')
    LR_recall = recall_score(y_test, 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)
    y_pred_SVM = SVM_model.predict(df_deg_test)
    SVM_precision = precision_score(y_test, y_pred_SVM, average='macro')
    SVM_recall = recall_score(y_test, 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)
    y_pred_RF = RF_model.predict(df_deg_test)
    RF_precision = precision_score(y_test, y_pred_RF, average='macro')
    RF_recall = recall_score(y_test, 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)
    y_pred_MLP = MLP_model.predict(df_deg_test)
    MLP_precision = precision_score(y_test, y_pred_MLP, average='macro')
    MLP_recall = recall_score(y_test, y_pred_MLP, average='macro')
    MLP_precisions.append(MLP_precision)
    MLP_recalls.append(MLP_recall)


    clinical_df_deg = np.hstack((df_deg,X_train[clinical_indices]))
    clinical_df_deg = pd.DataFrame(clinical_df_deg)
    clinical_df_deg_test = np.hstack((df_deg_test,X_test[clinical_indices]))
    clinical_df_deg_test = pd.DataFrame(clinical_df_deg_test)

    # Logistic Regression
    LR_model = LogisticRegression(solver='saga')
    LR_model.fit(clinical_df_deg, y_train)
    y_pred_LR = LR_model.predict(clinical_df_deg_test)
    LR_precision = precision_score(y_test, y_pred_LR, average='macro')
    LR_recall = recall_score(y_test, y_pred_LR, average='macro')
    LR_precisions2.append(LR_precision)
    LR_recalls2.append(LR_recall)

    # Support Vector Machine
    SVM_model = SVC(kernel='linear', C=1)
    SVM_model.fit(clinical_df_deg, y_train)
    y_pred_SVM = SVM_model.predict(clinical_df_deg_test)
    SVM_precision = precision_score(y_test, y_pred_SVM, average='macro')
    SVM_recall = recall_score(y_test, y_pred_SVM, average='macro')
    SVM_precisions2.append(SVM_precision)
    SVM_recalls2.append(SVM_recall)

    # Random Forest
    RF_model = RandomForestClassifier(random_state = i)
    RF_model.fit(clinical_df_deg, y_train)
    y_pred_RF = RF_model.predict(clinical_df_deg_test)
    RF_precision = precision_score(y_test, y_pred_RF, average='macro')
    RF_recall = recall_score(y_test, y_pred_RF, average='macro')
    RF_precisions2.append(RF_precision)
    RF_recalls2.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(clinical_df_deg, y_train)
    y_pred_MLP = MLP_model.predict(clinical_df_deg_test)
    MLP_precision = precision_score(y_test, y_pred_MLP, average='macro')
    MLP_recall = recall_score(y_test, y_pred_MLP, average='macro')
    MLP_precisions2.append(MLP_precision)
    MLP_recalls2.append(MLP_recall)



    # Logistic Regression
    LR_model = LogisticRegression(solver='saga')
    LR_model.fit(X_train[clinical_indices], y_train)
    y_pred_LR = LR_model.predict(X_test[clinical_indices])
    LR_precision = precision_score(y_test, y_pred_LR, average='macro')
    LR_recall = recall_score(y_test, y_pred_LR, average='macro')
    LR_precisions3.append(LR_precision)
    LR_recalls3.append(LR_recall)

    # Support Vector Machine
    SVM_model = SVC(kernel='linear', C=1)
    SVM_model.fit(X_train[clinical_indices], y_train)
    y_pred_SVM = SVM_model.predict(X_test[clinical_indices])
    SVM_precision = precision_score(y_test, y_pred_SVM, average='macro')
    SVM_recall = recall_score(y_test, y_pred_SVM, average='macro')
    SVM_precisions3.append(SVM_precision)
    SVM_recalls3.append(SVM_recall)

    # Random Forest
    RF_model = RandomForestClassifier(random_state = i)
    RF_model.fit(X_train[clinical_indices], y_train)
    y_pred_RF = RF_model.predict(X_test[clinical_indices])
    RF_precision = precision_score(y_test, y_pred_RF, average='macro')
    RF_recall = recall_score(y_test, y_pred_RF, average='macro')
    RF_precisions3.append(RF_precision)
    RF_recalls3.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(X_train[clinical_indices], y_train)
    y_pred_MLP = MLP_model.predict(X_test[clinical_indices])
    MLP_precision = precision_score(y_test, y_pred_MLP, average='macro')
    MLP_recall = recall_score(y_test, y_pred_MLP, average='macro')
    MLP_precisions3.append(MLP_precision)
    MLP_recalls3.append(MLP_recall)
```

```
iteration 0
No clinical data is identified among DEGs
iteration 1
No clinical data is identified among DEGs
iteration 2
No clinical data is identified among DEGs
iteration 3
No clinical data is identified among DEGs
iteration 4
No clinical data is identified among DEGs
iteration 5
No clinical data is identified among DEGs
iteration 6
No clinical data is identified among DEGs
iteration 7
No clinical data is identified among DEGs
iteration 8
No clinical data is identified among DEGs
iteration 9
No clinical data is identified among DEGs
iteration 10
No clinical data is identified among DEGs
iteration 11
No clinical data is identified among DEGs
iteration 12
No clinical data is identified among DEGs
iteration 13
No clinical data is identified among DEGs
iteration 14
No clinical data is identified among DEGs
iteration 15
No clinical data is identified among DEGs
iteration 16
No clinical data is identified among DEGs
iteration 17
No clinical data is identified among DEGs
iteration 18
No clinical data is identified among DEGs
iteration 19
No clinical data is identified among DEGs
iteration 20
No clinical data is identified among DEGs
iteration 21
No clinical data is identified among DEGs
iteration 22
No clinical data is identified among DEGs
iteration 23
No clinical data is identified among DEGs
```

```
iteration 24
No clinical data is identified among DEGs
iteration 25
No clinical data is identified among DEGs
iteration 26
No clinical data is identified among DEGs
iteration 27
No clinical data is identified among DEGs
iteration 28
No clinical data is identified among DEGs
iteration 29
No clinical data is identified among DEGs
iteration 30
No clinical data is identified among DEGs
iteration 31
No clinical data is identified among DEGs
iteration 32
No clinical data is identified among DEGs
iteration 33
No clinical data is identified among DEGs
iteration 34
No clinical data is identified among DEGs
iteration 35
No clinical data is identified among DEGs
iteration 36
No clinical data is identified among DEGs
iteration 37
No clinical data is identified among DEGs
iteration 38
No clinical data is identified among DEGs
iteration 39
No clinical data is identified among DEGs
iteration 40
No clinical data is identified among DEGs
iteration 41
No clinical data is identified among DEGs
iteration 42
No clinical data is identified among DEGs
iteration 43
No clinical data is identified among DEGs
iteration 44
No clinical data is identified among DEGs
iteration 45
No clinical data is identified among DEGs
iteration 46
No clinical data is identified among DEGs
iteration 47
No clinical data is identified among DEGs
```

```
iteration 48
No clinical data is identified among DEGs
iteration 49
No clinical data is identified among DEGs
iteration 50
No clinical data is identified among DEGs
iteration 51
No clinical data is identified among DEGs
iteration 52
No clinical data is identified among DEGs
iteration 53
No clinical data is identified among DEGs
iteration 54
No clinical data is identified among DEGs
iteration 55
No clinical data is identified among DEGs
iteration 56
No clinical data is identified among DEGs
iteration 57
No clinical data is identified among DEGs
iteration 58
No clinical data is identified among DEGs
iteration 59
No clinical data is identified among DEGs
iteration 60
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iteration 93
No clinical data is identified among DEGs
iteration 94
No clinical data is identified among DEGs
iteration 95
No clinical data is identified among DEGs
```

```
iteration 96
No clinical data is identified among DEGs
iteration 97
No clinical data is identified among DEGs
iteration 98
No clinical data is identified among DEGs
iteration 99
No clinical data is identified among DEGs
```

As you can see, clinical data were not selected in any of the iterations.

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 also need to compare the results of the three conditions to determine whether adding clinical data has a significant effect on performance or not.

[58]:
```
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]
```

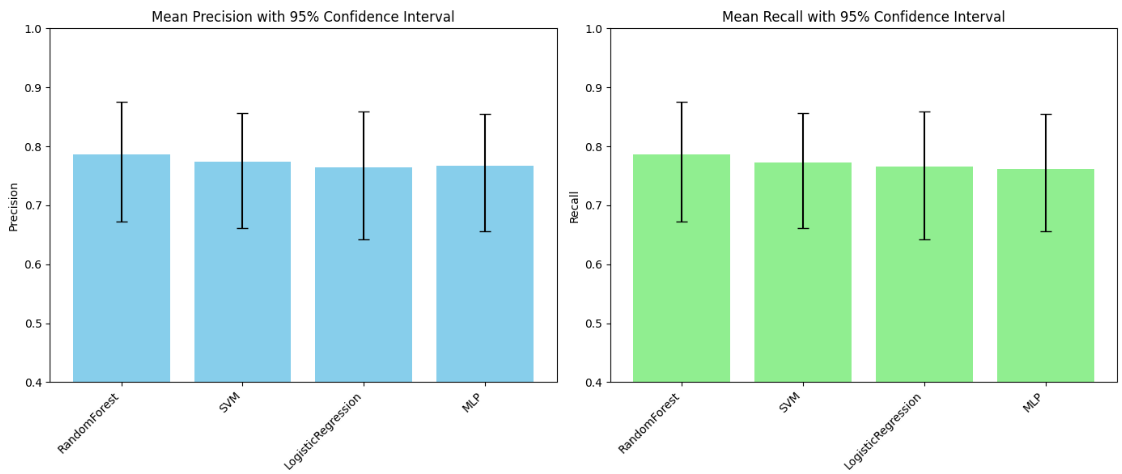
```python
precision_errors = np.array([[mean - ci[0], ci[1] - mean] for mean, ci in␣
↪zip(mean_precisions, precision_cis)]).T
recall_errors = np.array([[mean - ci[0], ci[1] - mean] for mean, ci in␣
↪zip(mean_recalls, recall_cis)]).T


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([0.4, 1])
ax[0].set_xticklabels(models, rotation=45, ha="right")

# Plot recall
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([0.4, 1])
ax[1].set_xticklabels(models, rotation=45, ha="right")

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

1- Using only DEGs

[59]:
```python
Evaluation(LR_precisions,LR_recalls,SVM_precisions,SVM_recalls,RF_precisions,RF_recalls,MLP_pr
```

```
Mean Precision for Logistic Regression: 0.7640169927513462, 95% CI: [0.64210043
0.85890152]
Mean Recall for Logistic Regression: 0.7651338428612129, 95% CI: [0.63696044
0.87401786]
--------------------------------------------------------------------------------
-----------------
Mean Precision for Support Vector Machine: 0.7743040927880918, 95% CI:
[0.66116453 0.85674319]
Mean Recall for Support Vector Machine: 0.7723320280185707, 95% CI: [0.65753472
0.86513971]
--------------------------------------------------------------------------------
-----------------
Mean Precision for Random Forest: 0.7860810773240244, 95% CI: [0.6725455
0.87525208]
Mean Recall for Random Forest: 0.7867412414621653, 95% CI: [0.65607372
0.88233974]
--------------------------------------------------------------------------------
```

Mean Precision for Multi Layer Perceptron: 0.7677514303520464, 95% CI:
[0.65656233 0.85438582]
Mean Recall for Multi Layer Perceptron: 0.7618658834643532, 95% CI: [0.6144042
0.8572071]



2- Combining DEGs and clinical data

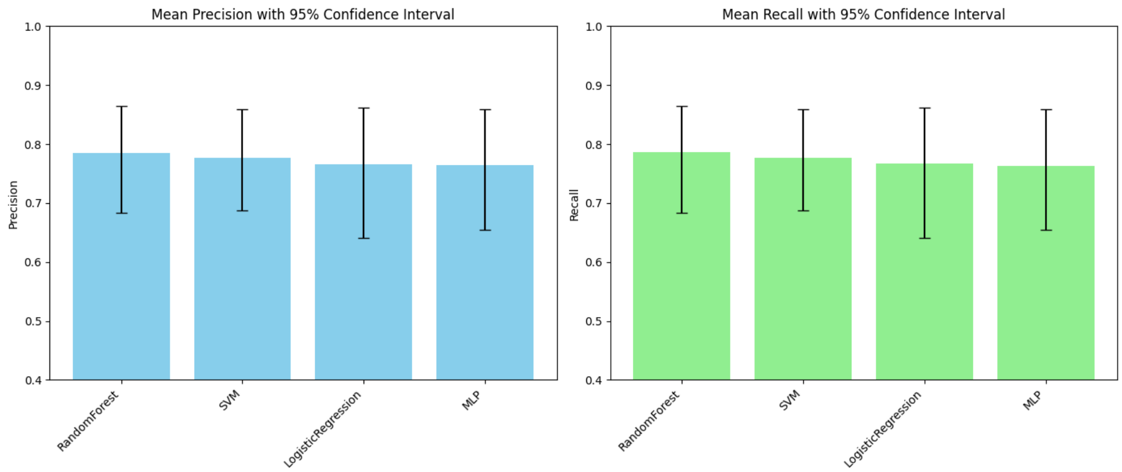
[60]:
```
Evaluation(LR_precisions2,LR_recalls2,SVM_precisions2,SVM_recalls2,RF_precisions2,RF_recalls2,
```

Mean Precision for Logistic Regression: 0.7657572934644726, 95% CI: [0.64076229
0.86249775]
Mean Recall for Logistic Regression: 0.766437798402862, 95% CI: [0.63156272
0.87401786]

Mean Precision for Support Vector Machine: 0.7773571309688684, 95% CI:
[0.68729898 0.85893579]
Mean Recall for Support Vector Machine: 0.7760440256206106, 95% CI: [0.67974551
0.85704685]

Mean Precision for Random Forest: 0.7853592442842011, 95% CI: [0.6831345
0.86472959]
Mean Recall for Random Forest: 0.7858822709176627, 95% CI: [0.68036487
0.86493412]

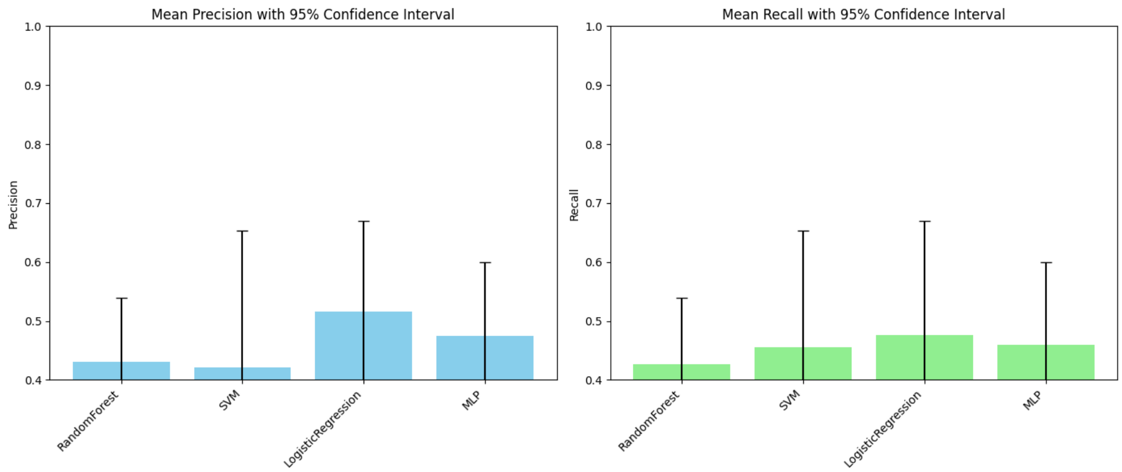
Mean Precision for Multi Layer Perceptron: 0.7649651583043456, 95% CI:
[0.65414083 0.85956706]
Mean Recall for Multi Layer Perceptron: 0.7626787599565183, 95% CI: [0.65620388
0.86896226]



3- using only clinical data

[61]:
```
Evaluation(LR_precisions3,LR_recalls3,SVM_precisions3,SVM_recalls3,RF_precisions3,RF_recalls3,
```

```
Mean Precision for Logistic Regression: 0.515218903229282, 95% CI: [0.31170101
0.66907334]
Mean Recall for Logistic Regression: 0.47621360370841015, 95% CI: [0.36085483
0.59306812]
--------------------------------------------------------------------------------
-----------------
Mean Precision for Support Vector Machine: 0.4216381464824728, 95% CI:
[0.25569444 0.65331303]
Mean Recall for Support Vector Machine: 0.45489894310748175, 95% CI: [0.36710967
0.55240385]
--------------------------------------------------------------------------------
-----------------
Mean Precision for Random Forest: 0.4311592063399727, 95% CI: [0.33722599
0.53896528]
Mean Recall for Random Forest: 0.4260025261322037, 95% CI: [0.33441138
0.52781951]
--------------------------------------------------------------------------------
-----------------
Mean Precision for Multi Layer Perceptron: 0.4748118320079058, 95% CI:
[0.33603222 0.59929803]
Mean Recall for Multi Layer Perceptron: 0.4600780548510615, 95% CI: [0.33597553
0.57160134]
```



As you can see, adding clinical data to DEGs does not have a significant effect on model performance, and the clinical data alone are not strong features for this classification task.