BENG203_Prj.0.3

June 8, 2022

1 BENG 203

2 Course project

2.1 Dependencies

[1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
%matplotlib inline
import pickle
import os
# Silence warnings to avoid multiple messages from a foreseen error.
import warnings
warnings.filterwarnings('ignore')
plt.rcParams['figure.dpi'] = 300
```

2.2 General arguments

[2]:
```
# ---> Paths.
course_path = '/Users/vfajardo/iCloud_Drive/UCSD_classes/year-1_spring-quarter/
 ↪BENG_203'
prj_path = course_path + '/project'
data_path = prj_path + '/data'
results_path = prj_path + '/results'
feats_path = results_path + '/feature_engineering'
# ---> File definitions.
# @ Expression data.
cancer_train_tpm_file = data_path + '/MergedTPMData.csv'
cancer_test_tpm_file = data_path + '/validation_exon_tpm.tsv'
# @ Metadata.
cancer_train_meta_file = data_path + '/MergedMetadata.csv'
cancer_test_meta_file = data_path + '/ValidationSamplesMetadata.csv'
gene_types_file = data_path + '/EnsemblGeneBiotypes_GRCh38.csv'
# @ Feature-related data.
# Cancer-related features.
```

```
cancer_feats_file = feats_path + '/DEA-Cancer_C-vs-N.csv'
# Recurrence-related features.
rec_feats_file = feats_path + '/DEA-Recurrence_R-vs-N.csv'
```

2.3 General functions

A function to save objects

[3]:
```
def SaveObj(this_object, file_pfx):
    # Save assessment dictionary
    tmp_file_name = file_pfx + '.pickle'
    tmp_file_name = os.path.join(results_path, tmp_file_name)
    file_to_store = open(tmp_file_name, "wb")
    pickle.dump(this_object, file_to_store)
    file_to_store.close()
```

2.4 Load data

[13]:
```
# ---> Expression data.
# cancer_train_tpm = pd.read_csv(cancer_train_tpm_file, header=None,␣
 ↪index_col=0, sep='\t')
cancer_train_tpm = pd.read_csv(cancer_train_tpm_file, index_col='geneid')
cancer_test_tpm = pd.read_csv(cancer_test_tpm_file, sep='\t')
# ---> Meta data
# cancer_train_meta = pd.read_csv(cancer_train_meta_file, index_col='sample_id')
cancer_train_meta = pd.read_csv(cancer_train_meta_file, index_col='sample.id')
cancer_test_meta = pd.read_csv(cancer_test_meta_file, index_col='sample_id')
gene_types = pd.read_csv(gene_types_file)
# ---> Condition-related features.
cancer_feats = pd.read_csv(cancer_feats_file, index_col='gene.id')
rec_feats = pd.read_csv(rec_feats_file, index_col='gene.id')
```

2.5 Preprocess data

[14]:
```
# ---> Expression data.
# Set unique sample IDs.
cancer_train_tpm.columns = cancer_train_meta.index
# Uniquely valid features will be those present in both training and test␣
 ↪datasets.
train_genes, test_genes = set(cancer_train_tpm.index.values),␣
 ↪set(cancer_test_tpm.index.values)
print(len(train_genes) == len(train_genes.intersection(test_genes)))
# Set predictor variables.
X_train = cancer_train_tpm.T
```

```
X_test = cancer_test_tpm.T.loc[:, X_train.columns]
# X_test = cancer_test_tpm.T.loc[:, X_train.columns].values
# X_train = X_train.values
# Lucky us, both have been mapped to the exact same reference.
# ---> Metadata (target variable to be taken for either dataset)
# Of interest is the breast cancer status of each sample.
if all(cancer_train_meta.isin(cancer_train_tpm.columns)):
    cancer_train_tpm = cancer_train_tpm.loc[:, cancer_train_meta.index.values]
    y_train = cancer_train_meta.loc[:, ['disease.status']]
    y_train = cancer_train_meta.loc[:, ['disease.status']].values
    y_train = (y_train=='cancer')*1
else:
    raise ValueError('Training data misaligned.\n')
if all(cancer_test_meta.isin(cancer_test_tpm.columns)):
    cancer_test_tpm = cancer_test_tpm.loc[:, cancer_test_meta.index.values]
    y_test = cancer_test_meta.loc[:, ['cancer_status']].values
    y_test = (y_test=='cancer')*1
else:
    raise ValueError('Test data misaligned.\n')
# Gene biotypes.
gene_types.columns = ['gene_id', 'biotype']

# ---> Condition-related features
# Subset info to keep info relevant to rank the features.
cancer_feats['abs_lfc'] = np.abs(cancer_feats['lfc..minimum'])
cancer_feats['adj_p'] = cancer_feats['p.adj..maximum']
cancer_rank = cancer_feats.loc[:, ['abs_lfc', 'adj_p']]
# Include non-assessed features.
eng_feats = set(cancer_rank.index.values)
all_feats = set(cancer_train_tpm.index.values)
left_feats = all_feats.difference(eng_feats)
left_feats = {'gene.id':list(left_feats), 'abs_lfc':np.repeat(None,␣
 ↪len(left_feats)), 'adj_p':np.repeat(None, len(left_feats))}
left_feats = pd.DataFrame.from_dict(left_feats)
left_feats = left_feats.set_index('gene.id')
cancer_rank = pd.concat([cancer_rank, left_feats])
# Rank features and set cummulative percentage.
cancer_rank = cancer_rank.sort_values(by=['abs_lfc', 'adj_p'], ascending=[True,␣
 ↪False])
cancer_rank['rank'] = np.arange(1, cancer_rank.shape[0]+1)
cancer_rank['cumm_percent'] = (cancer_rank['rank']*100)/cancer_rank.shape[0]
```

```
True
```

2.6 Further data exploration

snoRNAs that are differentially expressed between cancer and non-cancer samples

[21]:
```
feat_subset = gene_types.loc[gene_types['biotype']=='snoRNA', 'gene_id']
feat_subset = feat_subset[feat_subset.isin(X_test.columns.values)].values
len(feat_subset)
```

[21]: 939

[20]:
```
feat_subset = gene_types.loc[gene_types['biotype']=='snoRNA', 'gene_id']
feat_subset = feat_subset[feat_subset.isin(X_train.columns.values)].values
len(feat_subset)
```

[20]: 939

[25]:
```
tmp_data = cancer_feats.merge(gene_types, left_index=True, right_on='gene_id')
tmp_data
```

[25]:

	lfc..minimum	lfc.control	lfc.se.control	p.adj..maximum	\
20783	0.259479	0.259479	0.217941	0.530332	
20779	0.285348	0.285348	0.298568	0.635478	
20915	0.306443	0.306443	0.301675	0.612728	
46710	-0.172090	-0.172090	0.219941	0.707074	
45006	-0.213192	-0.213192	0.193605	0.570593	
…	…	…	…	…	
61374	0.543567	0.543567	0.344133	0.370763	
20999	-0.093806	-0.093806	0.296680	0.898512	
51979	0.235160	0.235160	0.355525	0.766215	
22532	-0.169926	-0.169926	0.260306	0.766763	
13687	-0.726819	-0.726819	0.349859	0.199799	

	p.adj.control	p.val.control	test.stat.control	mean.tpm.control	\
20783	0.530332	0.234336	1.189263	14.164084	
20779	0.635478	0.340227	0.953718	16.256396	
20915	0.612728	0.313699	1.007492	14.221749	
46710	0.707074	0.433194	-0.783737	12.161375	
45006	0.570593	0.270999	-1.100765	16.063505	
…	…	…	…	…	
61374	0.370763	0.114403	1.578706	8.978616	
20999	0.898512	0.751564	-0.316578	8.046123	
51979	0.766215	0.513355	0.653622	12.401986	
22532	0.766763	0.513920	-0.652746	10.841728	
13687	0.199799	0.035160	-2.106506	28.318337	

	mean.tpm.cancer	abs_lfc	adj_p	gene_id	biotype
20783	21.437919	0.259479	0.530332	ENSG00000000003	protein_coding

```
20779        25.824944  0.285348  0.635478  ENSG00000000005  protein_coding
20915        23.245797  0.306443  0.612728  ENSG00000000419  protein_coding
46710        13.742320  0.172090  0.707074  ENSG00000000457  protein_coding
45006        16.954631  0.213192  0.570593  ENSG00000000460  protein_coding
…                  …         …         …                …               …
61374        20.446707  0.543567  0.370763  ENSG00000283108          lncRNA
20999         9.703975  0.093806  0.898512  ENSG00000283117          lncRNA
51979        20.658275  0.235160  0.766215  ENSG00000283118          lncRNA
22532        11.762477  0.169926  0.766763  ENSG00000283122          lncRNA
13687        19.383413  0.726819  0.199799  ENSG00000283125          lncRNA

[34448 rows x 13 columns]
```

[37]:
```
tmp_data.loc[(tmp_data['adj_p']<0.05) & (tmp_data['biotype']=='snoRNA'), :]
```

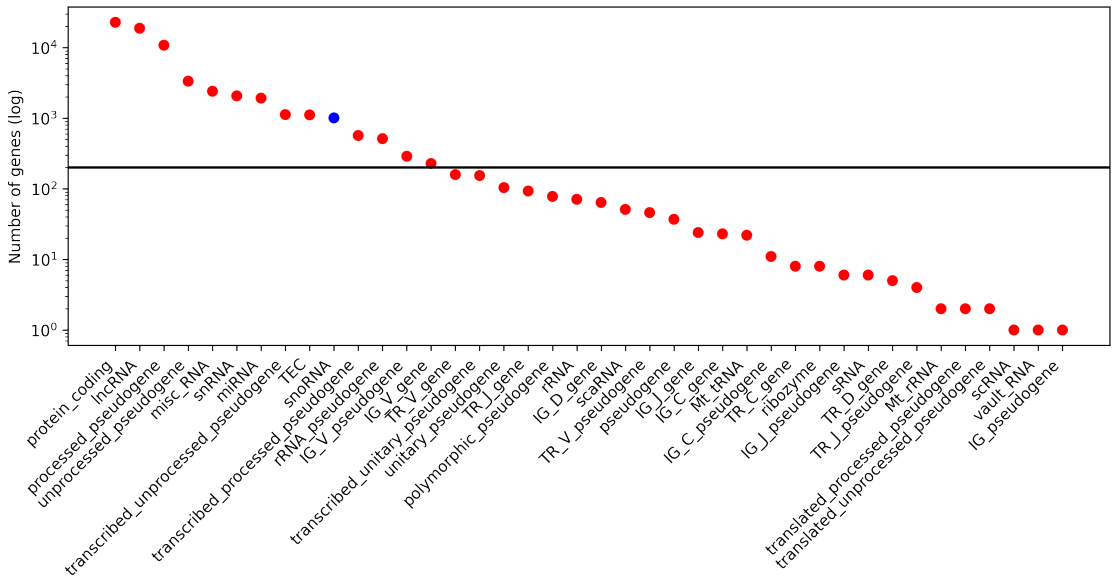
[37]:
```
       lfc..minimum  lfc.control  lfc.se.control  p.adj..maximum  \
34891     -2.272754    -2.272754        0.213187    3.323485e-23

       p.adj.control  p.val.control  test.stat.control  mean.tpm.control  \
34891   3.323485e-23   1.808311e-26           -10.64661         537.88419

       mean.tpm.cancer   abs_lfc         adj_p          gene_id biotype
34891       130.107368  2.272754  3.323485e-23  ENSG00000222604  snoRNA
```

Number of genes per biotype

[84]:
```
# Get data
tmp_data = pd.DataFrame(gene_types['biotype'].value_counts())
tmp_data.columns = ['Count']
tmp_data.sort_values('Count', ascending=False)
# tmp_data.index.values == 'snoRNA'
# tmp_data['is_snorna'] = tmp_data.index.values == 'snoRNA'
to_check = tmp_data.index.values=='snoRNA'
tmp_cols = ['blue' if i==True else 'red' for i in to_check]
# Plot.
xlabels = list(tmp_data.index)
fig, ax = plt.subplots(figsize=(12, 4))
ax.scatter(tmp_data.index.values, tmp_data.Count, c=tmp_cols)
ax.set_yscale('log')
ax.set_ylabel('Number of genes (log)')
ax.set_xticklabels(xlabels, rotation = 45, ha='right')
plt.axhline(y = 200, color = 'black', label = 'axvline - full height')
plt.show()
```



3 Cancer prediction

3.0.1 Load needed sklearn models and tools

[7]:
```
from sklearn.pipeline import Pipeline
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import GridSearchCV, RandomizedSearchCV
from sklearn.preprocessing import StandardScaler
from sklearn.metrics import confusion_matrix, classification_report
from sklearn.metrics import roc_curve
```

4 Cancer prediction according to ranked features (based on LFC)

4.0.1 Define general pipeline to train models according to ranked gene subset

[67]:
```
def GeneralClassifierPipeline(clas_model, model_lab, param_grid,␣
 ↪defined_range=None, search_scoring='accuracy', cv_no=5):
    # ---> Define objects to save the models and the reports on testing data.
    model_list = list()
    eval_list = list()
    scores_list = list()
    # ---> Apply pipeline to each subset.
```

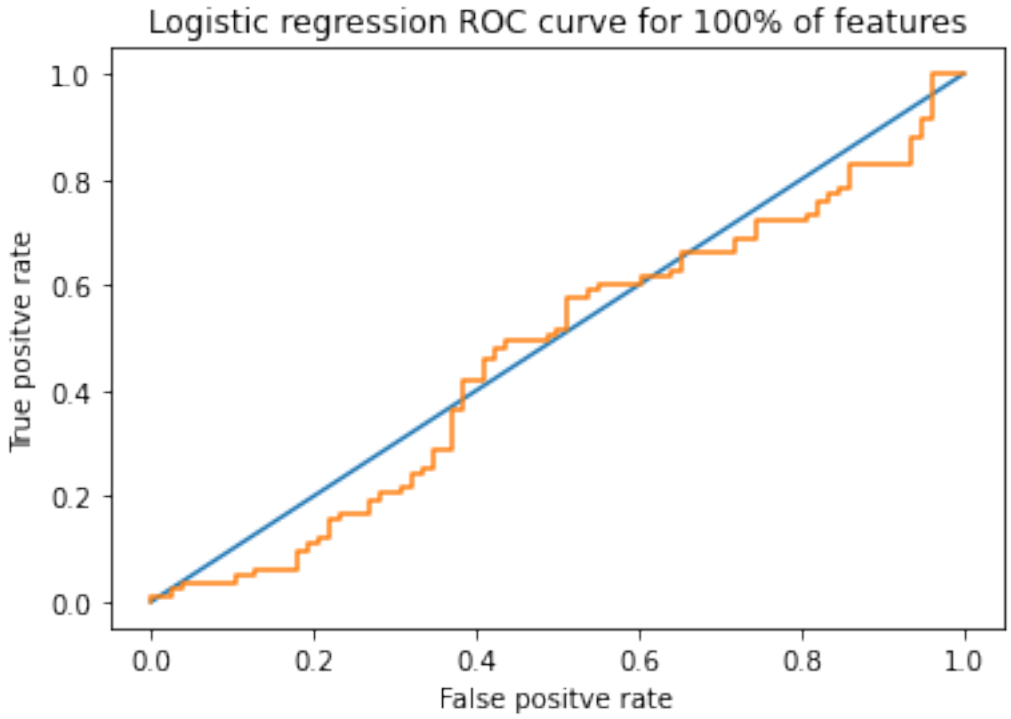
```
    print('Instancing models.')
    if defined_range is None:
        defined_range = np.arange(5, 105, 5)
    for i in defined_range:
#         print('Percent of data:' + str(i))
        # Select data subsets.
        feat_subset = cancer_rank.loc[cancer_rank['cumm_percent']<=i, :].index.
 ↪values
        X_train_subset = X_train.loc[:, feat_subset].values
        X_test_subset = X_test.loc[:, feat_subset].values
        # Set up pipeline.
        steps = [('scaler', StandardScaler()), ('model', clas_model)]
        model_pipeline = Pipeline(steps)
        # Instantiate the GridSearchCV object.
        model_cv = RandomizedSearchCV(model_pipeline, param_grid, cv=cv_no,␣
 ↪scoring=search_scoring)
        # Fit it to the training data
        model_cv.fit(X_train_subset, y_train.ravel())
        model_list.append(model_cv)
        # Print the optimal parameters and best score
        y_pred = model_cv.predict(X_test_subset)
        class_report = classification_report(y_test, y_pred, output_dict=True)
        eval_list.append(class_report)
        # Final score.
        scores_list.append(model_cv.score(X_test_subset, y_test))
    print('All models have been instanced.')
    # ---> Output ROC curve for best score.
    # Identify best score.
    best_score = max(scores_list)
    for i in range(0, len(scores_list)):
        if scores_list[i] == best_score:
            best_model_i = i
            break
    print('Best average ROC AUC is: ' + str(np.round(model_cv.best_score_, 3)))
    print('Best parameters:')
    print(model_cv.best_params_)
    print('This model\'s ROC AUC for the testing dataset is: ' + str(np.
 ↪round(best_score, 3)))
    # Get susbet accordingly.
#     feat_subset = cancer_rank.
 ↪loc[cancer_rank['cumm_percent']<=((best_model_i+1)*5), :].index.values
    feat_subset = cancer_rank.
 ↪loc[cancer_rank['cumm_percent']<=defined_range[best_model_i], :].index.values
    X_test_subset = X_test.loc[:, feat_subset].values
    # Calculate TPR and FPRs.
    y_pred_prob = model_list[best_model_i].predict_proba(X_test_subset)[:, 1]
    fpr, tpr, tholds = roc_curve(y_test, y_pred_prob)
```

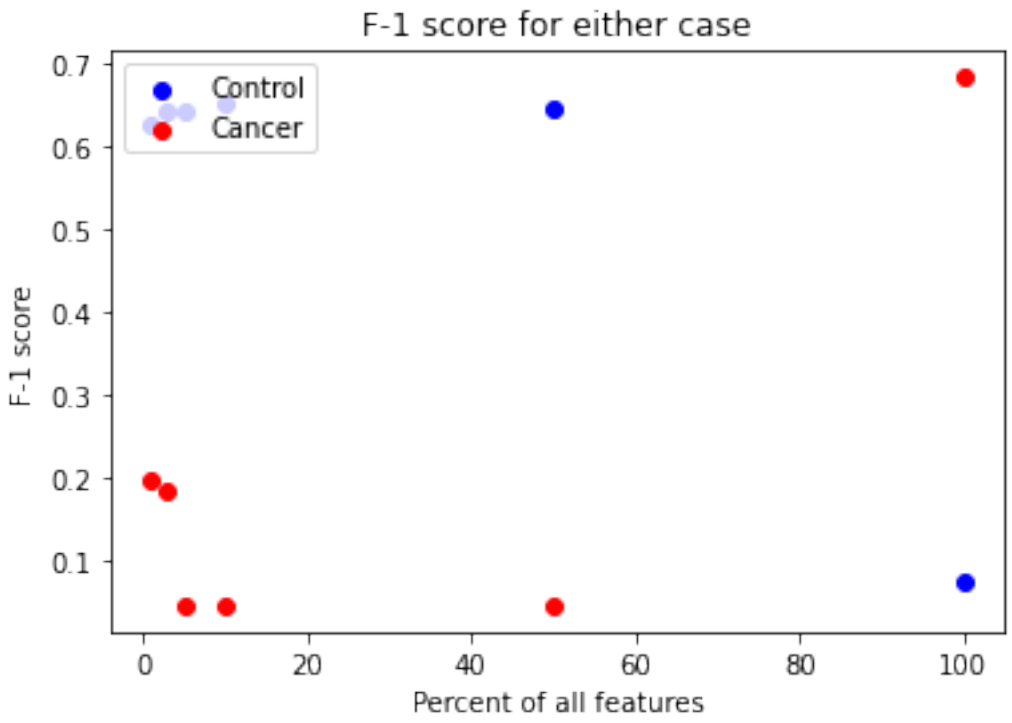
```
    # Output plot.
    plt.plot([0, 1], [0, 1])
    plt.plot(fpr, tpr, label=model_lab)
    plt.xlabel('False positve rate')
    plt.ylabel('True positve rate')
    plt.title('Logistic regression ROC curve for ' +␣
 ↪str(defined_range[best_model_i]) + '% of features')
    plt.show()
    # ---> Output F-1 scores.
    # Get F-1 scores for each class.
    ctrl_scores = [i['0']['f1-score'] for i in eval_list]
    cancer_scores = [i['1']['f1-score'] for i in eval_list]
    # Plot.
    plt.plot()
    plt.scatter(defined_range, ctrl_scores, c='blue', label='Control')
    plt.scatter(defined_range, cancer_scores, c='red', label='Cancer')
    plt.xlabel('Percent of all features')
    plt.ylabel('F-1 score')
    plt.title('F-1 score for either case')
    plt.legend(loc="upper left")
    plt.show()
    # ---> Output calculated data.
    output = {'model_lab': model_lab, 'model_list':model_list, 'eval_list':
 ↪eval_list, 'scores_list':scores_list, 'best_model_i':best_model_i}
    return output
```

4.0.2 Logistic regression

[69]:
```
tmp_file_name = os.path.join(results_path, 'CancerStatus_LogReg_RankedFeats.
 ↪pickle')
if not os.path.exists(tmp_file_name):
    # Define hyperparameter grid.
    c_space = np.logspace(-5, 8, 15)
    param_grid = {'model__C': c_space, 'model__penalty': ['l1', 'l2']}
    # Define model
    tmp_model = LogisticRegression(solver='liblinear')
    # Instance accordingly.
    logreg_instances = GeneralClassifierPipeline(tmp_model, 'Logistic␣
 ↪regression', param_grid, defined_range=[1, 3, 5, 10, 50, 100],␣
 ↪search_scoring='roc_auc', cv_no=5)
    # Save results
    SaveObj(logreg_instances, 'CancerStatus_LogReg_RankedFeats')
else:
    file = open(tmp_file_name, 'rb')
    logreg_instances = pickle.load(file)
    file.close()
```

```
Instancing models.
All models have been instanced.
Best average ROC AUC is: 1.0
Best parameters:
{'model__penalty': 'l1', 'model__C': 3.727593720314938}
This model's ROC AUC for the testing dataset is: 0.466
```

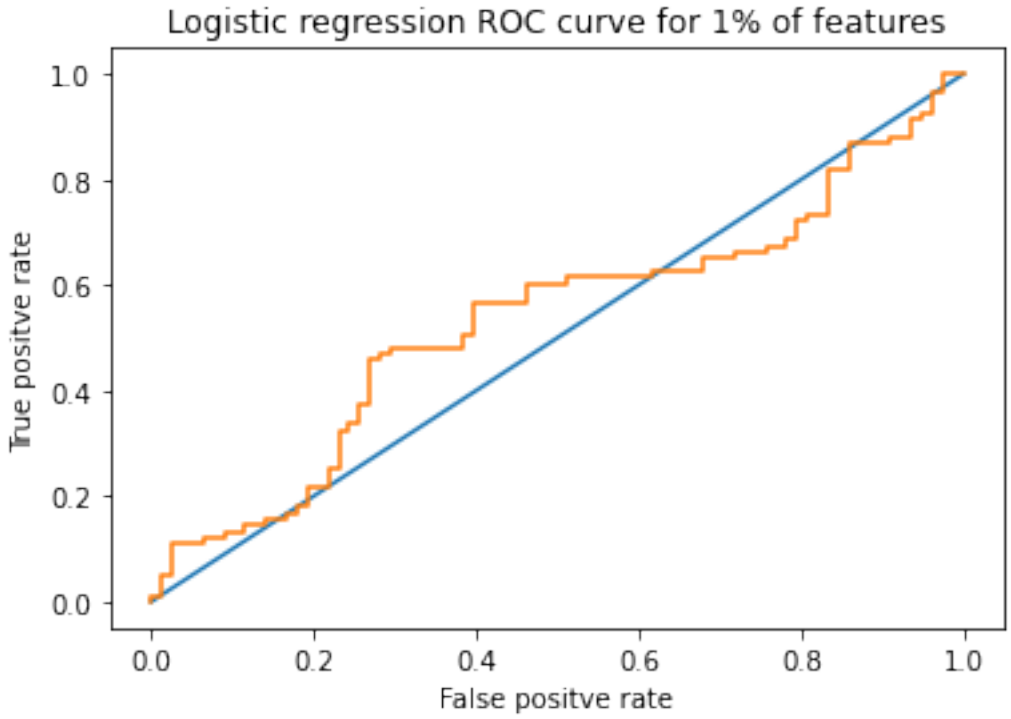


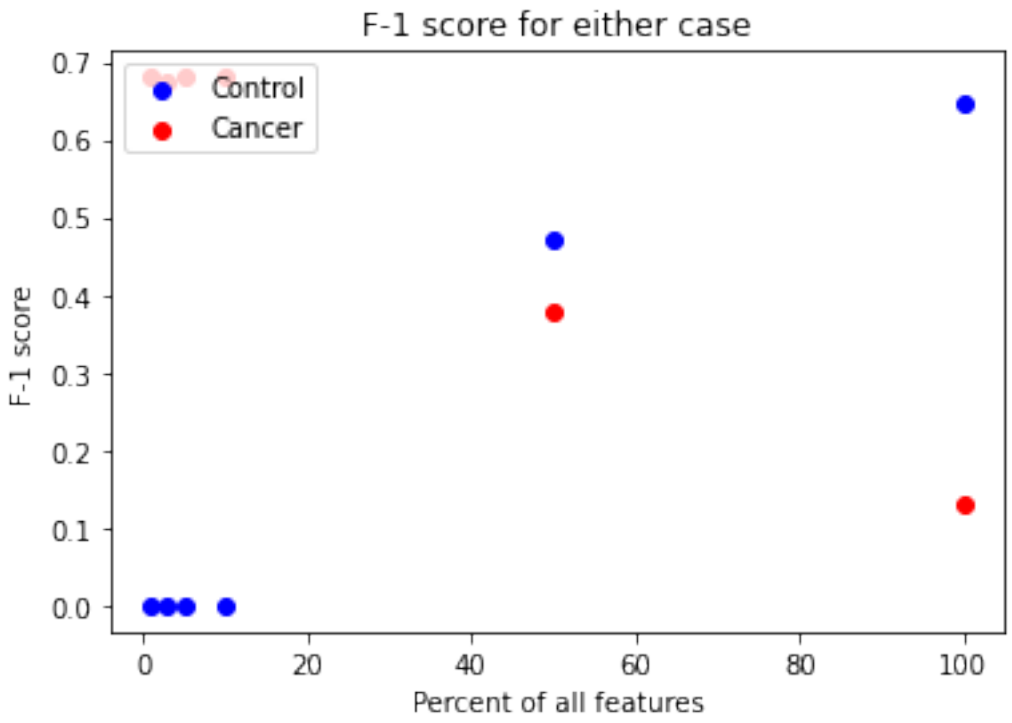


4.0.3 SVM

[70]:
```
tmp_file_name = os.path.join(results_path, 'CancerStatus_SVM_RankedFeats.
 ↪pickle')
if not os.path.exists(tmp_file_name):
    # Define hyperparameter grid.
    c_space = np.logspace(-5, 8, 15)
    kernel_space = ['linear', 'poly', 'rbf', 'sigmoid']
    gamma_space = ['scale', 'auto']
    param_grid = {'model__C': c_space, 'model__kernel': kernel_space,␣
 ↪'model__gamma': gamma_space}
    # Define model
    tmp_model = SVC(probability=True)
    # Instance accordingly.
    svm_instances = GeneralClassifierPipeline(tmp_model, 'SVM', param_grid,␣
 ↪defined_range=[1, 3, 5, 10, 50, 100], search_scoring='roc_auc', cv_no=5)
    # Save results
    SaveObj(svm_instances, 'CancerStatus_SVM_RankedFeats')
else:
    file = open(tmp_file_name, 'rb')
    svm_instances = pickle.load(file)
    file.close()
```

```
Instancing models.
All models have been instanced.
Best average ROC AUC is: 0.996
Best parameters:
{'model__kernel': 'sigmoid', 'model__gamma': 'scale', 'model__C':
163789.3706954068}
This model's ROC AUC for the testing dataset is: 0.468
```

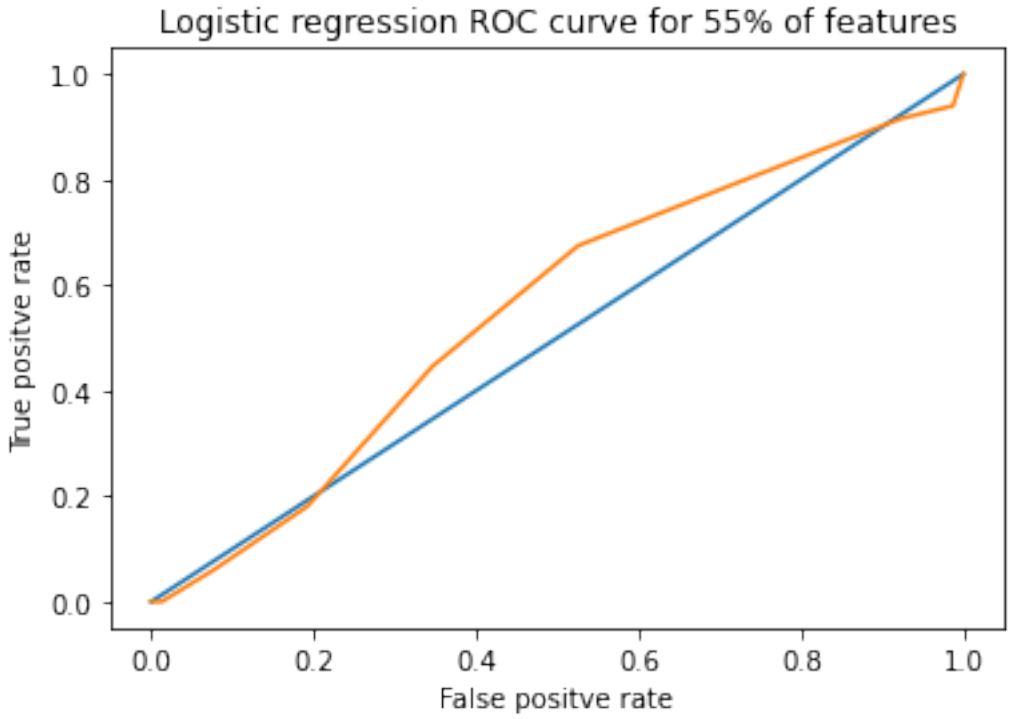


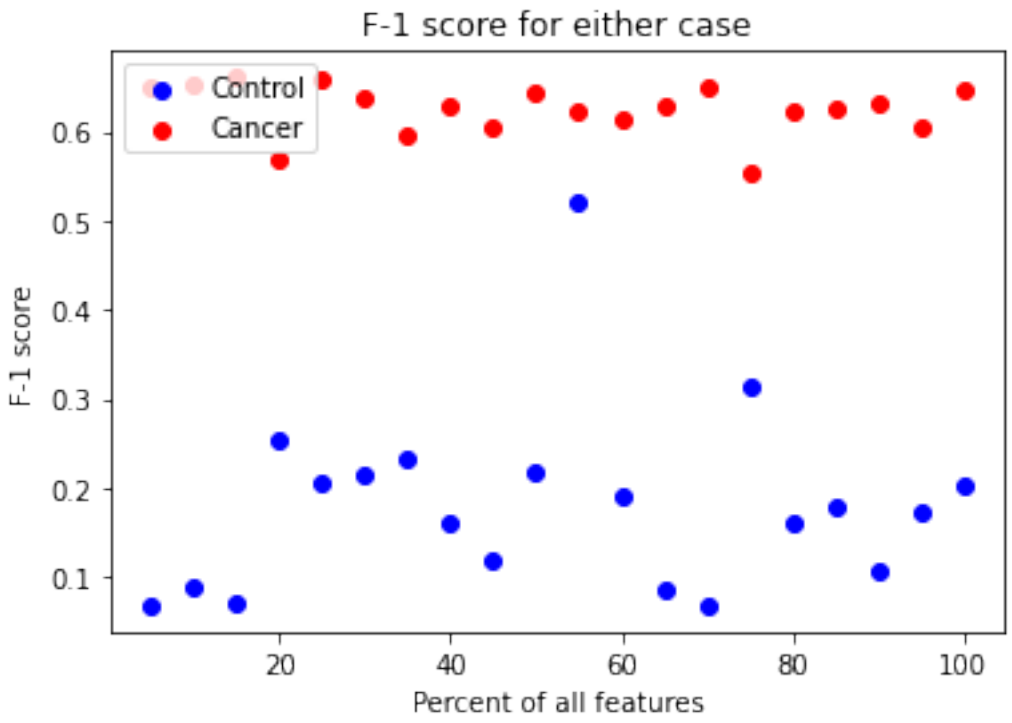


4.0.4 Random forests

[76]:
```
tmp_file_name = os.path.join(results_path,␣
 ↪'CancerStatus_RandomForests_RankedFeats.pickle')
if not os.path.exists(tmp_file_name):
    # Define hyperparameter grid.
    estimators_space = np.arange(10, 210, 10)
    # criterion_space = ['gini', 'entropy', 'log_loss']
    criterion_space = ['gini', 'entropy']
    param_grid = {'model__n_estimators': estimators_space, 'model__criterion':␣
 ↪criterion_space}
    # Define model
    tmp_model = RandomForestClassifier()
    # Instance accordingly.
    rforests_instances = GeneralClassifierPipeline(tmp_model, 'Random forests',␣
 ↪param_grid, cv_no=5)
    # Save results
    SaveObj(rforests_instances, 'CancerStatus_RandomForests_RankedFeats')
else:
    file = open(tmp_file_name, 'rb')
    rforests_instances = pickle.load(file)
    file.close()
```

```
Instancing models.
All models have been instanced.
Best average ROC AUC is: 0.906
Best parameters:
{'model__n_estimators': 170, 'model__criterion': 'gini'}
This model's ROC AUC for the testing dataset is: 0.578
```





5 Cancer prediction according to features grouped based on biotype

5.0.1 Define general pipeline to train models according to ranked gene subset

[73]:
```
def ClassifierPipelinePerBiotype(clas_model, model_lab, param_grid,␣
 ↪type_count_thold=200, search_scoring='accuracy', cv_no=5):
    # ---> Define biotypes to try.
    type_counts = gene_types['biotype'].value_counts()
    biotypes_to_try = type_counts[type_counts > type_count_thold].index.values
    # ---> Define objects to save the models and the reports on testing data.
    model_list = list()
    eval_list = list()
    scores_list = list()
    # ---> Apply pipeline to each subset.
    print('Instancing models.')
    for biotype in biotypes_to_try:
#         print('Percent of data:' + str(i))
        # Select data subsets.
        feat_subset = gene_types.loc[gene_types['biotype']==biotype, 'gene_id']
```

```
        feat_subset = feat_subset[feat_subset.isin(X_train.columns.values)].
↪values
        X_train_subset = X_train.loc[:, feat_subset].values
        X_test_subset = X_test.loc[:, feat_subset].values
        # Set up pipeline.
        steps = [('scaler', StandardScaler()), ('model', clas_model)]
        model_pipeline = Pipeline(steps)
        # Instantiate the GridSearchCV object.
        model_cv = RandomizedSearchCV(model_pipeline, param_grid, cv_no,␣
↪scoring=search_scoring)
        # Fit it to the training data
        model_cv.fit(X_train_subset, y_train.ravel())
        model_list.append(model_cv)
        # Print the optimal parameters and best score
        y_pred = model_cv.predict(X_test_subset)
        class_report = classification_report(y_test, y_pred, output_dict=True)
        eval_list.append(class_report)
        # Final score.
        scores_list.append(model_cv.score(X_test_subset, y_test))
    print('All models have been instanced.')
    # ---> Output ROC curve for best score.
    # Identify best score.
    best_score = max(scores_list)
    for i in range(0, len(scores_list)):
        if scores_list[i] == best_score:
            best_model_i = i
            break
    print('Best biotype is: ' + biotypes_to_try[best_model_i])
    print('Best average ROC AUC is: ' + str(np.round(model_cv.best_score_, 3)))
    print('Best parameters:')
    print(model_cv.best_params_)
    print('This model\'s ROC AUC for the testing dataset is: ' + str(np.
↪round(best_score, 3)))
    # Get susbet accordingly.
    feat_subset = gene_types.
↪loc[gene_types['biotype']==biotypes_to_try[best_model_i], 'gene_id']
    feat_subset = feat_subset[feat_subset.isin(X_train.columns.values)].values
    X_test_subset = X_test.loc[:, feat_subset].values
    # Calculate TPR and FPRs.
    y_pred_prob = model_list[best_model_i].predict_proba(X_test_subset)[:, 1]
    fpr, tpr, tholds = roc_curve(y_test, y_pred_prob)
    # Output plot.
    plt.plot([0, 1], [0, 1])
    plt.plot(fpr, tpr, label=model_lab)
    plt.xlabel('False positve rate')
    plt.ylabel('True positve rate')
    plt.title('ROC curve for biotype: ' + biotypes_to_try[best_model_i])
```

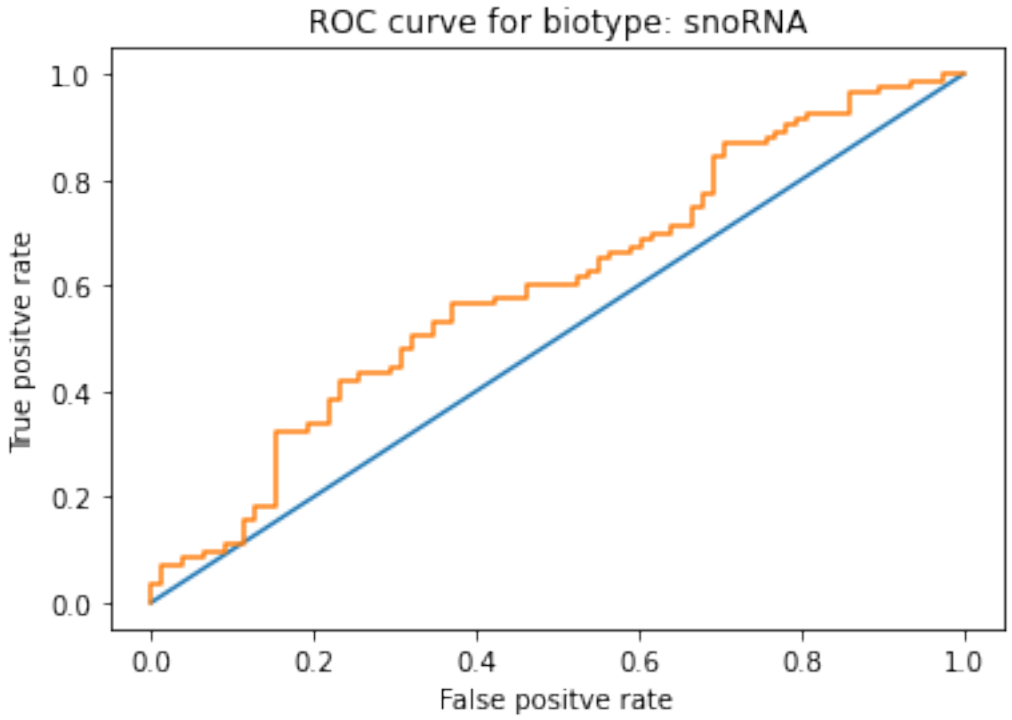
```
    plt.show()
    # ---> Output F-1 scores.
    # Get F-1 scores for each class.
    ctrl_scores = [i['0']['f1-score'] for i in eval_list]
    cancer_scores = [i['1']['f1-score'] for i in eval_list]
    # Plot.
    plt.plot()
    plt.scatter(biotypes_to_try, ctrl_scores, c='blue', label='Control')
    plt.scatter(biotypes_to_try, cancer_scores, c='red', label='Cancer')
    plt.xlabel('Percent of all features')
    plt.ylabel('F-1 score')
    plt.title('F-1 score for either case')
    plt.legend(loc="upper left")
    plt.show()
    # ---> Output calculated data.
    output = {'model_lab': model_lab, 'biotypes': biotypes_to_try, 'model_list':
 ↪model_list, 'eval_list':eval_list, 'scores_list':scores_list, 'best_model_i':
 ↪best_model_i}
    return output
```

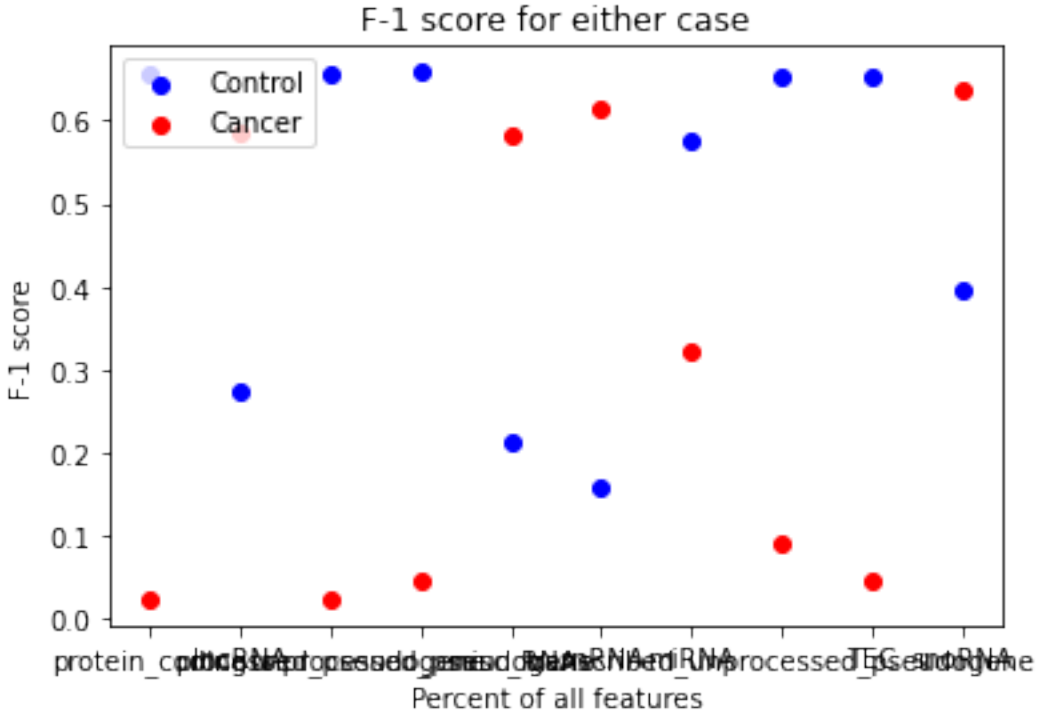
5.0.2 Logistic regression

[74]:
```
tmp_file_name = os.path.join(results_path, 'CancerStatus_LogReg_Biotypes.
 ↪pickle')
if not os.path.exists(tmp_file_name):
    # Define hyperparameter grid.
    c_space = np.logspace(-5, 8, 15)
    param_grid = {'model__C': c_space, 'model__penalty': ['l1', 'l2']}
    # Define model
    tmp_model = LogisticRegression(solver='liblinear')
    # Instance accordingly.
    logreg_btype_instances = ClassifierPipelinePerBiotype(tmp_model, 'Logistic␣
 ↪regression', param_grid, search_scoring='roc_auc', cv_no=5,␣
 ↪type_count_thold=1000)
    # Save results
    SaveObj(logreg_btype_instances, 'CancerStatus_LogReg_Biotypes')
else:
    file = open(tmp_file_name, 'rb')
    logreg_btype_instances = pickle.load(file)
    file.close()
```

```
Instancing models.
All models have been instanced.
Best biotype is: snoRNA
Best average ROC AUC is: 0.923
Best parameters:
{'model__penalty': 'l1', 'model__C': 268.2695795279727}
```

```
This model's ROC AUC for the testing dataset is: 0.6
```

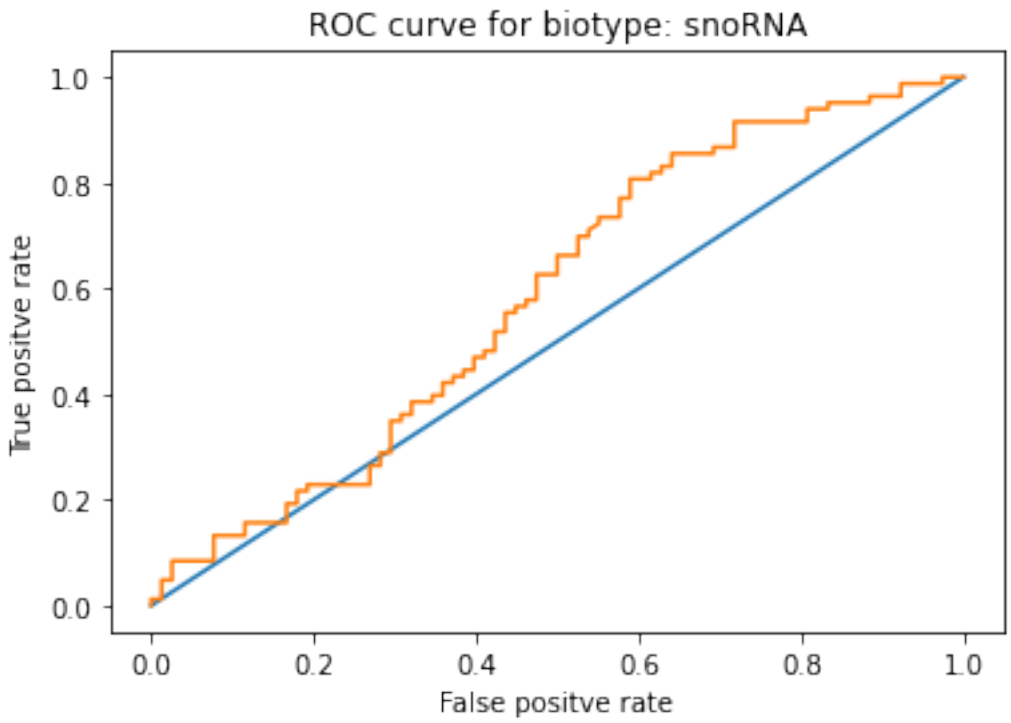


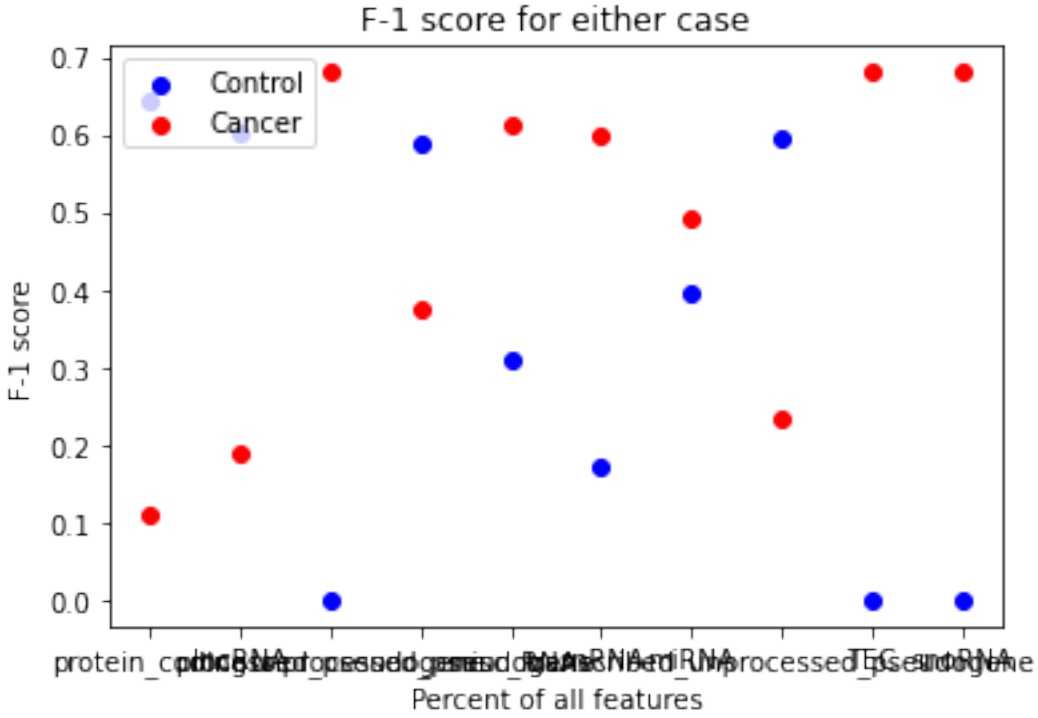


5.0.3 SVM

[78]:
```
tmp_file_name = os.path.join(results_path, 'CancerStatus_SVM_Biotypes.pickle')
if not os.path.exists(tmp_file_name):
    # Define hyperparameter grid.
    c_space = np.logspace(-5, 8, 15)
    kernel_space = ['linear', 'poly', 'rbf', 'sigmoid']
    gamma_space = ['scale', 'auto']
    param_grid = {'model__C': c_space, 'model__kernel': kernel_space,␣
 ↪'model__gamma': gamma_space}
    # Define model
    tmp_model = SVC(probability=True)
    # Instance accordingly.
    svm_btype_instances = ClassifierPipelinePerBiotype(tmp_model, 'SVM',␣
 ↪param_grid, search_scoring='roc_auc', cv_no=5, type_count_thold=1000)
    # Save results
    SaveObj(svm_btype_instances, 'CancerStatus_SVM_Biotypes')
else:
    file = open(tmp_file_name, 'rb')
    svm_btype_instances = pickle.load(file)
    file.close()
```

```
Instancing models.
All models have been instanced.
Best biotype is: snoRNA
Best average ROC AUC is: 0.714
Best parameters:
{'model__kernel': 'linear', 'model__gamma': 'auto', 'model__C': 1e-05}
This model's ROC AUC for the testing dataset is: 0.586
```

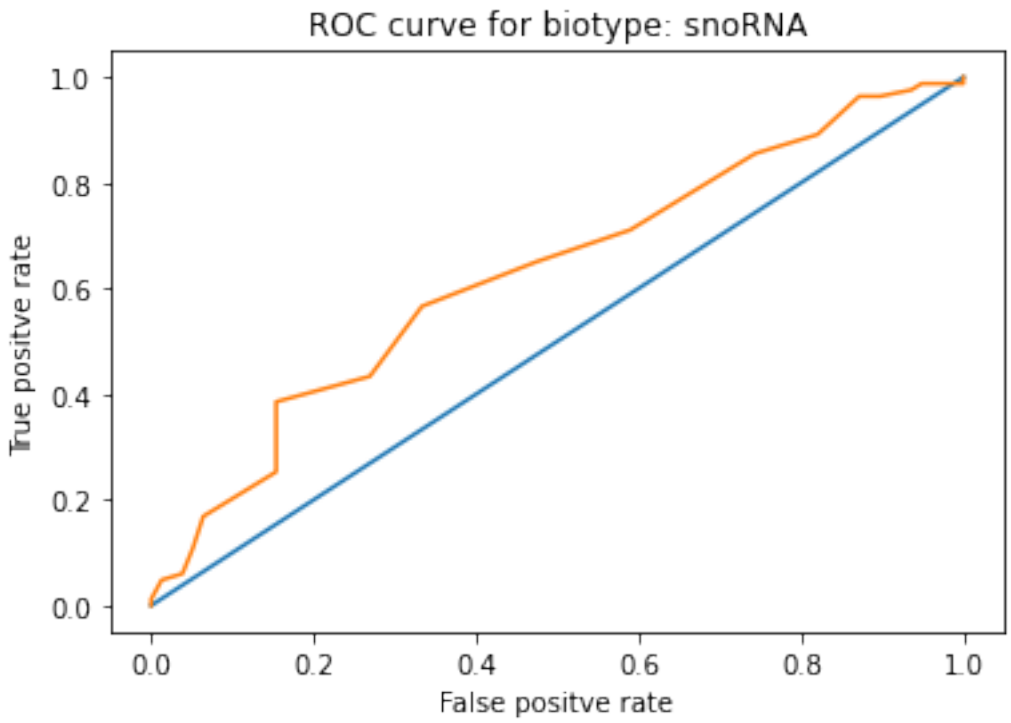

ROC curve for biotype: snoRNA
True positve rate
False positve rate
0.0
0.2
0.4
0.6
0.8
1.0

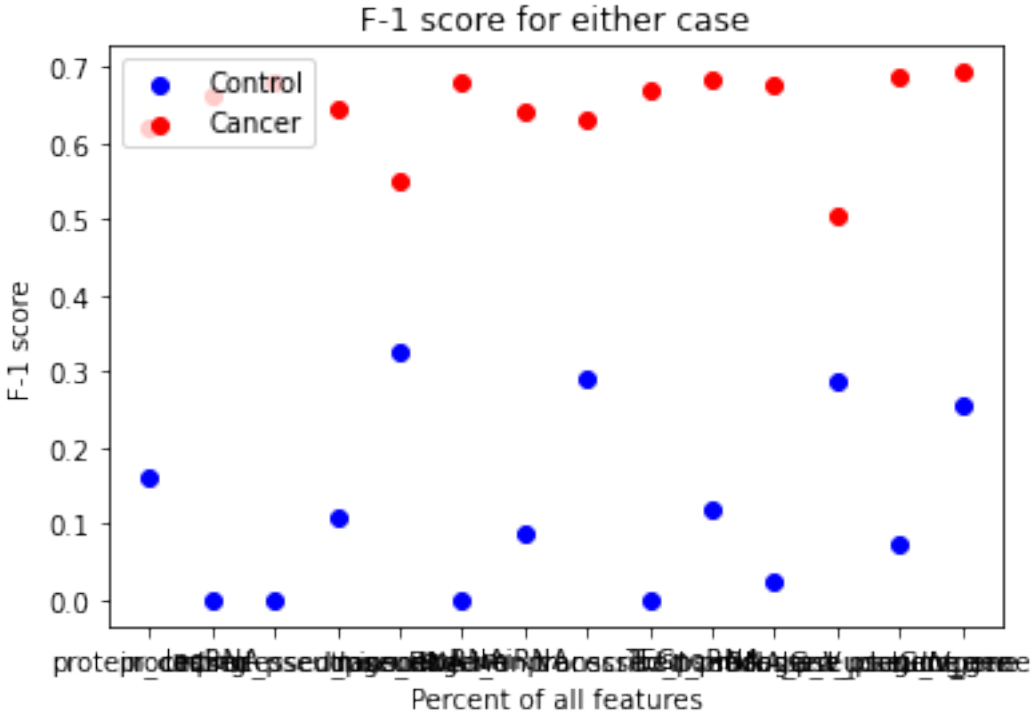

F-1 score for either case
Control
Cancer
F-1 score
Percent of all features
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7

5.0.4 Random forests

[80]:
```
tmp_file_name = os.path.join(results_path, 'CancerStatus_RandomForests_Biotypes.
↪pickle')
if not os.path.exists(tmp_file_name):
    # Define hyperparameter grid.
    estimators_space = np.arange(10, 210, 10)
    # criterion_space = ['gini', 'entropy', 'log_loss']
    criterion_space = ['gini', 'entropy']
    param_grid = {'model__n_estimators': estimators_space, 'model__criterion':␣
↪criterion_space}
    # Define model
    tmp_model = RandomForestClassifier()
    # Instance accordingly.
    rforests_btype_instances = ClassifierPipelinePerBiotype(tmp_model, 'Random␣
↪forests', param_grid, search_scoring='roc_auc', cv_no=100)
    # Save results
    SaveObj(rforests_btype_instances, 'CancerStatus_RandomForests_Biotypes')
else:
    file = open(tmp_file_name, 'rb')
    rforests_btype_instances = pickle.load(file)
    file.close()
```

```
Instancing models.
All models have been instanced.
Best biotype is: snoRNA
Best average ROC AUC is: 0.892
Best parameters:
{'model__n_estimators': 70, 'model__criterion': 'entropy'}
This model's ROC AUC for the testing dataset is: 0.628
```

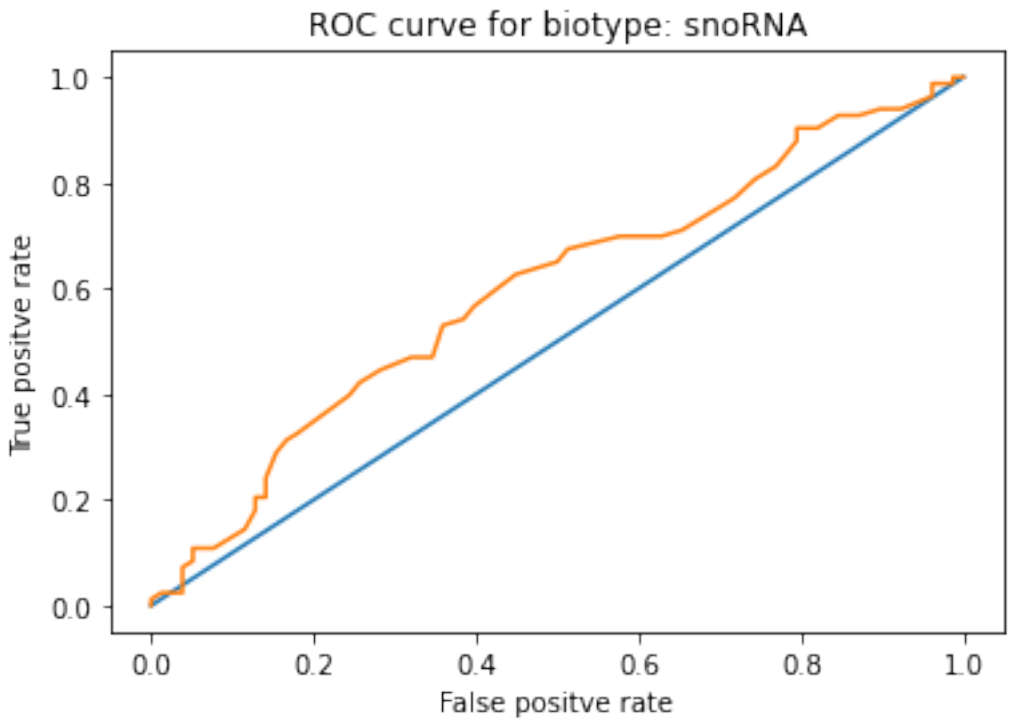

ROC curve for biotype: snoRNA
True positve rate
False positve rate
0.0
0.2
0.4
0.6
0.8
1.0

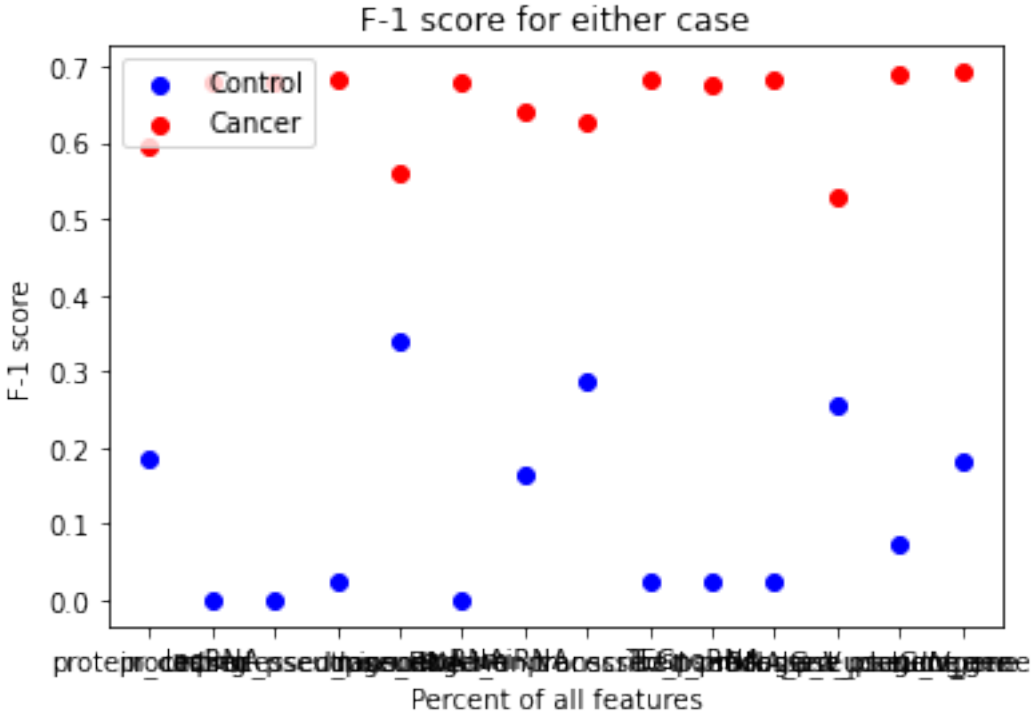

F-1 score for either case
Control
Cancer
F-1 score
Percent of all features
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7

5.0.5 Random forests 2

[82]:
```
tmp_file_name = os.path.join(results_path,␣
 ↪'CancerStatus_RandomForests_Biotypes-2.pickle')
if not os.path.exists(tmp_file_name):
    # Define hyperparameter grid.
    estimators_space = np.arange(10, 210, 10)
    # criterion_space = ['gini', 'entropy', 'log_loss']
    criterion_space = ['gini', 'entropy']
    param_grid = {'model__n_estimators': estimators_space, 'model__criterion':␣
 ↪criterion_space}
    # Define model
    tmp_model = RandomForestClassifier()
    # Instance accordingly.
    rforests_btype_instances_2 = ClassifierPipelinePerBiotype(tmp_model,␣
 ↪'Random forests', param_grid, search_scoring='roc_auc', cv_no=250)
    # Save results
    SaveObj(rforests_btype_instances_2, 'CancerStatus_RandomForests_Biotypes-2')
else:
    file = open(tmp_file_name, 'rb')
    rforests_btype_instances_2 = pickle.load(file)
    file.close()
```

```
Instancing models.
All models have been instanced.
Best biotype is: snoRNA
Best average ROC AUC is: 0.883
Best parameters:
{'model__n_estimators': 170, 'model__criterion': 'entropy'}
This model's ROC AUC for the testing dataset is: 0.596
```


ROC curve for biotype: snoRNA
True positve rate
False positve rate
0.0
0.2
0.4
0.6
0.8
1.0


F-1 score for either case
Control
Cancer
F-1 score
Percent of all features
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7

6 Cancer prediction according to features grouped based on biotype, log-transformed data

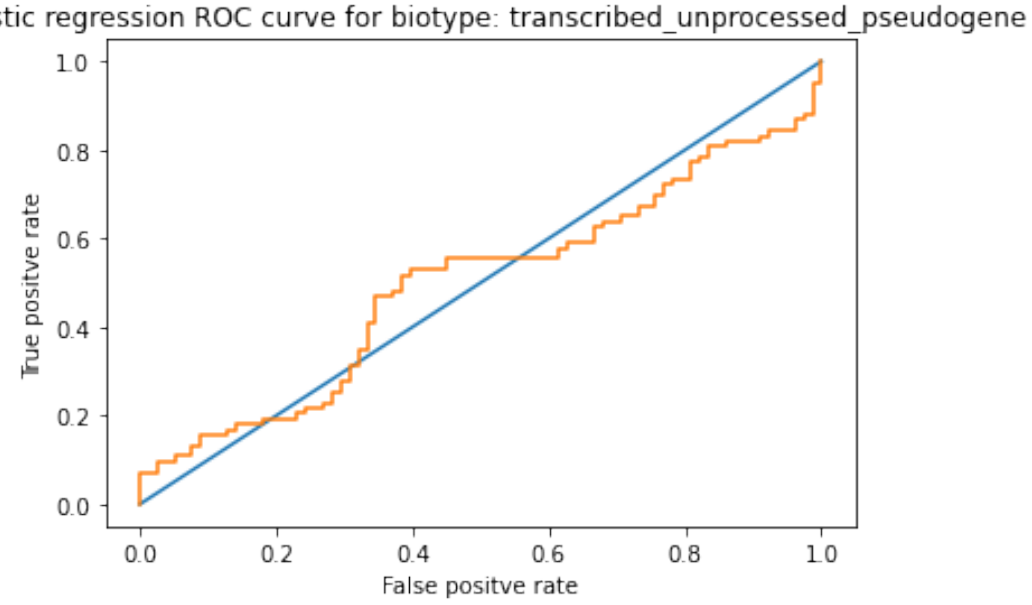
[47]:
```
def ClassifierPipelinePerBiotypeLog(clas_model, model_lab, param_grid,␣
 ↪type_count_thold=200, search_scoring='accuracy', cv_no=5):
    # ---> Define biotypes to try.
    type_counts = gene_types['biotype'].value_counts()
    biotypes_to_try = type_counts[type_counts > type_count_thold].index.values
    # ---> Define objects to save the models and the reports on testing data.
    model_list = list()
    eval_list = list()
    scores_list = list()
    # ---> Apply pipeline to each subset.
    print('Instancing models.')
    for biotype in biotypes_to_try:
#         print('Percent of data:' + str(i))
        # Select data subsets.
        feat_subset = gene_types.loc[gene_types['biotype']==biotype, 'gene_id']
        feat_subset = feat_subset[feat_subset.isin(X_train.columns.values)].
 ↪values
        X_train_subset = X_train.loc[:, feat_subset].values
        X_test_subset = X_test.loc[:, feat_subset].values
        # Set up pipeline.
        steps = [('model', clas_model)]
        model_pipeline = Pipeline(steps)
        # Instantiate the GridSearchCV object.
        model_cv = RandomizedSearchCV(model_pipeline, param_grid, cv_no,␣
 ↪scoring=search_scoring)
        # Fit it to the training data
        model_cv.fit(np.log2(X_train_subset+1), y_train.ravel())
        model_list.append(model_cv)
        # Print the optimal parameters and best score
        y_pred = model_cv.predict(np.log2(X_test_subset+1))
        class_report = classification_report(y_test, y_pred, output_dict=True)
        eval_list.append(class_report)
        # Final score.
        scores_list.append(model_cv.score(np.log2(X_test_subset+1), y_test))
    print('All models have been instanced.')
    # ---> Output ROC curve for best score.
    # Identify best score.
    best_score = max(scores_list)
    for i in range(0, len(scores_list)):
        if scores_list[i] == best_score:
            best_model_i = i
            break
```

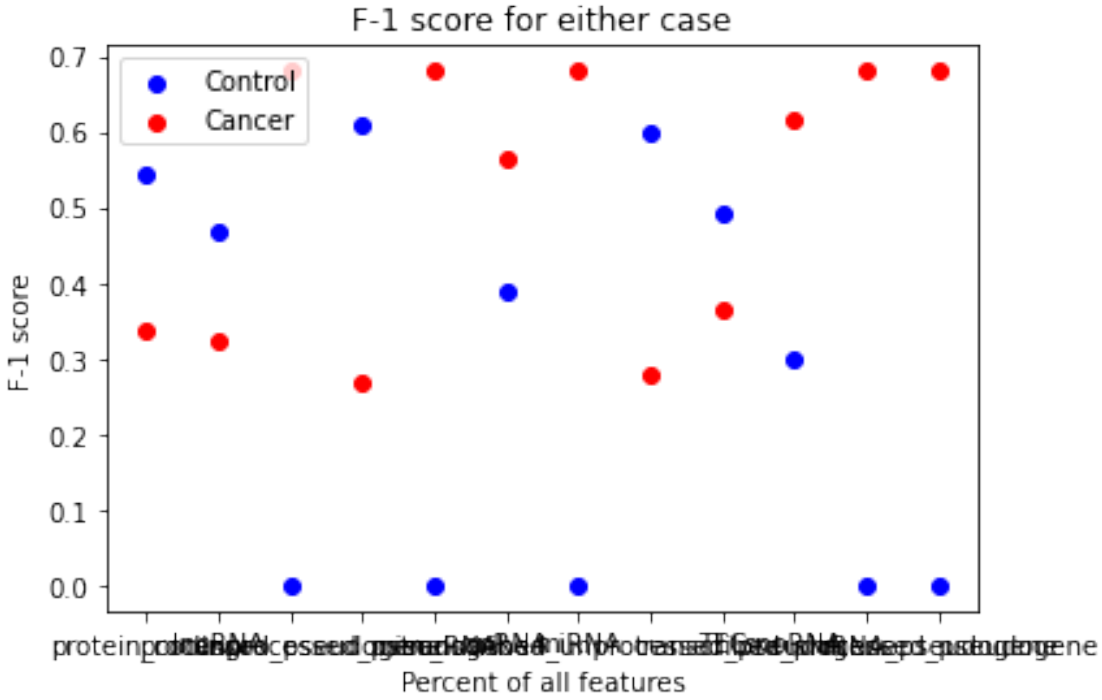
```
    print('Best biotype is: ' + biotypes_to_try[best_model_i])
    print('Best average ROC AUC is: ' + str(np.round(model_cv.best_score_, 3)))
    print('This model\'s ROC AUC for the testing dataset is: ' + str(np.
↪round(best_score, 3)))
    # Get susbet accordingly.
    feat_subset = gene_types.
↪loc[gene_types['biotype']==biotypes_to_try[best_model_i], 'gene_id']
    feat_subset = feat_subset[feat_subset.isin(X_train.columns.values)].values
    X_test_subset = X_test.loc[:, feat_subset].values
    # Calculate TPR and FPRs.
    y_pred_prob = model_list[best_model_i].predict_proba(np.
↪log2(X_test_subset+1))[:, 1]
    fpr, tpr, tholds = roc_curve(y_test, y_pred_prob)
    # Output plot.
    plt.plot([0, 1], [0, 1])
    plt.plot(fpr, tpr, label=model_lab)
    plt.xlabel('False positve rate')
    plt.ylabel('True positve rate')
    plt.title('Logistic regression ROC curve for biotype: ' +␣
↪biotypes_to_try[best_model_i])
    plt.show()
    # ---> Output F-1 scores.
    # Get F-1 scores for each class.
    ctrl_scores = [i['0']['f1-score'] for i in eval_list]
    cancer_scores = [i['1']['f1-score'] for i in eval_list]
    # Plot.
    plt.plot()
    plt.scatter(biotypes_to_try, ctrl_scores, c='blue', label='Control')
    plt.scatter(biotypes_to_try, cancer_scores, c='red', label='Cancer')
    plt.xlabel('Percent of all features')
    plt.ylabel('F-1 score')
    plt.title('F-1 score for either case')
    plt.legend(loc="upper left")
    plt.show()
    # ---> Output calculated data.
    model_list = list()
    eval_list = list()
    scores_list = list()
    output = {'model_lab': model_lab, 'biotypes': biotypes_to_try, 'model_list':
↪model_list, 'eval_list':eval_list, 'scores_list':scores_list, 'best_model_i':
↪best_model_i}
    return output
```

6.0.1 SVM

[52]:
```
tmp_file_name = os.path.join(results_path, 'CancerStatus_SVM_Biotypes-Log2-2.
 ↪pickle')
if not os.path.exists(tmp_file_name):
    # Define hyperparameter grid.
    c_space = np.logspace(-5, 8, 15)
    kernel_space = ['linear', 'poly', 'rbf', 'sigmoid']
    gamma_space = ['scale', 'auto']
    param_grid = {'model__C': c_space, 'model__kernel': kernel_space,␣
 ↪'model__gamma': gamma_space}
    # Define model
    tmp_model = SVC(probability=True)
    # Instance accordingly.
    svm_btype_log_instances = ClassifierPipelinePerBiotypeLog(tmp_model, 'SVM',␣
 ↪param_grid, search_scoring='roc_auc', cv_no=100, type_count_thold=500)
    # Save results
    SaveObj(svm_btype_log_instances, 'CancerStatus_SVM_Biotypes-Log2')
else:
    file = open(tmp_file_name, 'rb')
    svm_btype_log_instances = pickle.load(file)
    file.close()
```

```
Instancing models.
All models have been instanced.
Best biotype is: transcribed_unprocessed_pseudogene
Best average ROC AUC is: 0.998
This model's ROC AUC for the testing dataset is: 0.496
```




F-1 score for either case
Control
Cancer
F-1 score
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Percent of all features