```
→ 17 cells hidden
```

Run the Classifiers

▼ Load the data

```
def getDataAndLabels(name, features, label_encoder):
    labels_string = features.cancer_type
                   = label_encoder.fit_transform(labels_string)
    # Get rid of the cancer type and patient_barcode columns
    data = features[features.columns[3:]]
    print('Loading training data ...')
# label encoder
label_encoder = preprocessing.LabelEncoder()
# get all file names that start with features_
train_files = glob.glob("./data/features_*.train.csv")
all_train_data = {}
# load all of the files
for filename in train_files:
    name = filename[16:-10]
print(" ", name)
train_features = pd.read_csv(filename)
    all_train_data[name] = getDataAndLabels(name, train_features, label_encoder)
print("done.")
Loading training data ...
       topgenes_small
       bestfit_with_topgenes
       bestfit_med
       bestfit_large
       all
       l1reg_c0.5
       llreg_cl
       llreg_c10
       llreg_c100
       after_pca
     done.
print('Loading test data ...')
test_files = glob.glob("./data/features_*.test.csv")
all_test_data = {}
for filename in test_files:
    name = filename[16:-9]
#if (name != 'after_pca'):
print(" ", name)
    test_features = pd.read_csv(filename)
all_test_data[name] = getDataAndLabels(name, test_features, label_encoder)
print("done.")
Loading test data ...
       topgenes_small
       bestfit_with_topgenes
       hestfit med
       bestfit_large
       all
       l1reg_c0.5
       l1reg_c1
       l1reg_c10
       l1reg_c100
       after_pca
```

Functions for running different classifiers

```
classifier = LinearSVC(penalty='12')
      # Fit training data
svm.fit(train_data, train_labels)
      # Show the best C parameter to use and the expected accuracy print(' Best param:', svm.best_params_)
print(' Accuracy: ', np.round(svm.best_score_, 4) )
      return svm.best_params_
#
# Logistic regression
def run_logistic_regression(train_data, train_labels, test_data, test_labels, name, hyper_params):
      start = time.process_time()
if name in hyper_params and 'lr' in hyper_params[name]:
    best_params_logit = hyper_params[name]['lr']
             print("Running grid search on Logistic Regression...")
             best_params_logit = getBestParamsLogit(train_data, train_labels)
      # Run logistic regression with L2 regularization on reduced
      lr.fit(train_data, train_labels)
predict = lr.predict(test_data)
elapsed_time = time.process_time() - start
      # Get precision, recall, f1 scores
      logit_prf_scores = precision_recall_fscore_support(test_labels, predict, average='weighted')
logit_scores_by_label = precision_recall_fscore_support(test_labels, predict, average=None)
        Get confusion matrix
      logit_confusion
                                         = confusion matrix(test labels, predict)
      print("\nLogistic Regression", name)
print(" precision:", np.round(logit_prf_scores[0], 4))
print(" recall: ", np.round(logit_prf_scores[1], 4))
print(" f1: ", np.round(logit_prf_scores[2], 4))
print(" time: ", np.round(lelapsed_time, 2))
      return { 'scores': [
    logit_prf_scores[0],
    logit_prf_scores[1],
    logit_prf_scores[2],
    logit_scores_by_label,
    logit_confusion],
                'time': elapsed_time }
# Linear SVM
#
def run_linear_svm(train_data, train_labels, test_data, test_labels, name, hyper_params):
    print("\nLinear_SVM", name)
    start = time.process_time()
    if name in hyper_params and 'svm' in hyper_params[name]:
             best_params_svm = hyper_params[name]['svm']
             print("Running grid search on Linear SVM...")
             best_params_svm = getBestParamsSVM(train_data, train_labels)
      svm = LinearSVC(penalty='12', C=best_params_svm['C'])
      svm.fit(train_data, train_labels,)
      predict = svm.predict(test_data)
elapsed_time = time.process_time() - start
      # Get precision, recall, f1 scores
svm_prf_scores = precision_recall_fscore_support(test_labels, predict, average='weighted')
svm_scores_by_label = precision_recall_fscore_support(test_labels, predict, average=None)
      # Get confusion matrix
      svm_confusion
                                      = confusion_matrix(test_labels, predict)
      print(" precision:", np.round(svm_prf_scores[0], 4))
print(" recall: ", np.round(svm_prf_scores[1], 4))
print(" fl: ", np.round(svm_prf_scores[2], 4))
print(" time: ", np.round(elapsed_time, 2))
      return {'scores': [
    svm_prf_scores[0],
    svm_prf_scores[1],
    svm_prf_scores[2],
    svm_scores_by_label,
               svm_confusion],
'time': elapsed_time }
# Decision tree
def run_decision_tree(train_data, train_labels, test_data, test_labels, name, hyper_params):
      print("\nDecision Tree", name)
start = time.process_time()
dt = DecisionTreeClassifier()
      dt.fit(train_data, train_labels,)
      predict = dt.predict(test_data)
elapsed_time = time.process_time() - start
      # Get precision, recall, f1 scores
      dt prf_scores = precision_recall_fscore_support(test_labels, predict, average='weighted')
dt_scores_by_label = precision_recall_fscore_support(test_labels, predict, average=None)
      # Get confusion matrix
                                    = confusion_matrix(test_labels, predict)
      print(" precision:", np.round(dt_prf_scores[0], 4))
print(" recall: ", np.round(dt_prf_scores[1], 4))
print(" f1: ", np.round(dt_prf_scores[2], 4))
```

```
print(" time:
                                            ", np.round(elapsed_time, 2))
       return {'scores': [
                           dt_prf_scores[0],
dt_prf_scores[1],
dt_prf_scores[2],
                           dt scores by label,
                   dt_confusion],
'time': elapsed_time }
#
# Random forest
def run_random_forest(train_data, train_labels, test_data, test_labels, name, hyper_params):
       print("\nRandom Forest", name)
start = time.process_time()
       rf = RandomForestClassifier(n estimators=500)
       rf.fit(train_data, train_labels,)
       predict = rf.predict(test_data)
elapsed_time = time.process_time() - start
        # Get precision, recall, f1 scores
       rf_prf_scores = precision_recall_fscore_support(test_labels, predict, average='weighted')
rf_scores_by_label = precision_recall_fscore_support(test_labels, predict, average=None)
                                             = confusion_matrix(test_labels, predict)
       rf_confusion
       print(" precision:", np.round(rf_prf_scores[0], 4))
print(" recall: ", np.round(rf_prf_scores[1], 4))
print(" f1: ", np.round(rf_prf_scores[2], 4))
print(" time: ", np.round(elapsed_time, 2))
       rf_scores_by_label,
  rf_confusion],
'time': elapsed_time }
#
# Neural Net
def run_neural_net(train_data, train_labels, test_data, test_labels, name, hyper params):
       print("\nNeural Net", name)
tr_lab = to_categorical(train_labels)
        test lab = to categorical(test labels)
       start = time.process_time()
model = K.Sequential()
       model.add(Dropout(0.2))
model.add(Dense(1000, activation='relu'))
model.add(Dropout(0.2))
       model.add(Dropout(0.2))
model.add(Dense(400, activation='relu'))
model.add(Dropout(0.2))
model.add(Dense(100, activation='relu'))
       model.add(Dense(100, activation='relu'))
model.add(Dense(64, activation='relu'))
model.add(Dense(64, activation='relu'))
model.add(Dense(64, activation='sigmoid'))
model.ompile(optimizer='adam', loss='categorical_crossentropy', metrics = ["accuracy"])
#model.fit(train_data, tr_lab, epochs=1000, batch_size=100)
model.fit(train_data, tr_lab, epochs=1000, batch_size=100)
evaluate = model.evaluate(x = test_data, y = test_lab)
predict = model.predict(test_data)
elapsed_time = time.process_time() - start
# Get precision, recall, fl scores
nn prf_scores = precision_recall_fscore_support(test_labels,np.argmax(predict,l), average='weighted')
nn_scores_by_label = precision_recall_fscore_support(test_labels,np.argmax(predict,l), average=None)
       #nn_confusion
                                             = confusion_matrix(test_labels, predict)
       print(" precision:", np.round(nn_prf_scores[0], 4))
print(" recall: ", np.round(nn_prf_scores[1], 4))
print(" f1: ", np.round(nn_prf_scores[2], 4))
print(" time: ", np.round(elapsed_time, 2))
       return {'scores': [
                           nn_prf_scores[0],
nn_prf_scores[1],
                     nn_prf_scores[2],
nn_scores by label,
[]], ## TODO Jeremy: add confusion matrix
'time': elapsed_time}
#
# XGBoost
"def run_xg_boost(train_data, train_labels, test_data, test_labels, name, hyper_params):
    print("\nxG Boost", name)
    start = time.process_time()
        xgb_params =
         'max_depth': 2,
'eta': 0.3,
        'eta': 0.3,
'silent': False,
'verbose': True,
'objective': 'multi:softprob',
'num_class': 32,
'num_boost_round': 2}
       xgb_cfr = xgb.XGBClassifier(**xgb_params)
xgb_cfr.fit(train_data, train_labels)
       predict = xgb_cfr.predict(test_ata)
elapsed_time = time.process_time() - start
        # Get precision, recall, f1 scores
       xgb_prf_scores = precision_recall_fscore_support(test_labels, predict, average='weighted')
xgb_scores_by_label = precision_recall_fscore_support(test_labels, predict, average=None)
```

Get confusion matrix

```
xgb_confusion = confusion_matrix(test_labels, predict)
print(" precision:", np.round(xgb_prf_scores[0], 4))
print(" recall: ", np.round(xgb_prf_scores[1], 4))
print(" fl: ", np.round(xgb_prf_scores[2], 4))
print(" time: ", np.round(elapsed_time, 8))

return {'scores': [
    xgb_prf_scores[0],
    xgb_prf_scores[1],
    xgb_prf_scores[1],
    xgb_prf_scores[2],
    xgb_scores_y_label,
    xgb_confusion],
    'time': elapsed_time}
```

▼ Run the different classifiers

```
def get_saved_metrics():
    metrics_filename = "./data/metrics.csv"
    if os.path.isfile(metrics_filename):
        df_report_existing = pd.read_csv(metrics_filename)
             return df_report_existing
             return pd.DataFrame(columns=['name', 'classifier', 'feature_size', 'precision', 'recall', 'f1', 'time'])
def save metrics(scores, times, save=True):
      df_scores = pd.DataFrame(scores)
df_times = pd.DataFrame(times)
       rows = []
      for classifier in df scores.index:
             for name in df_scores.columns:
                   rows.append([
                                      all_train_data[name]['feature_size'],
                                      classifier,
                                      df_scores.loc[classifier][name][0],
df_scores.loc[classifier][name][1],
                                      df scores.loc[classifier][name][2],
                                      df_times.loc[classifier][name]
                                      1)
      df_report = pd.DataFrame(rows, columns=['name', 'feature_size', 'classifier', 'precision', 'recall', 'f1', 'time'])
            Write out scores as csv files
         print("\nWriting metrics ...")
df_report.to_csv("./data/metrics.csv")
print("done.")
      return df_report
hyper_params = {
   'llreg_c0.5':
       def is_existing_run(existing_runs, the_classifier, the_name):
    matches = existing_runs[(existing_runs.classifier == the_classifier) & (existing_runs.name == the_name)]
       return matches.shape[0]
def copy_metrics(existing_runs, the_classifier, the_name):
   matches = existing_runs((existing_runs.classifier == the_classifier) & (existing_runs.name == the_name)]
   scores[the_name][the_classifier] = [matches.precision.values[0], matches.recall.values[0], matches.fl.values[0]]
   times[the_name][the_classifier] = matches.time.values[0]
def run_classifiers(train_data, train_labels, test_data, test_labels, name, scores, times, existing_runs):
      scores[name] = {
times[name] = {}
      if is_existing_run(existing_runs, 'lr', name) == 0:
    lr = run_logistic_regression(train_data, train_labels, test_data, test_labels, name, hyper_params)
    scores[name]['lr'] = lr['scores']
    times[name]['lr'] = lr['time']
else.
             copy_metrics(existing_runs, 'lr', name)
      if is_existing_run(existing_runs, 'svm', name) == 0:
   svm = run_linear_svm(train_data, train_labels, test_data, test_labels, name, hyper_params)
   scores[name]['svm'] = svm['scores']
   times[name]['svm'] = svm['time']
      else:
             copy_metrics(existing_runs, 'svm', name)
      if is_existing_run(existing_runs, 'dt', name) == 0:
    dt = run_decision_tree(train_data, train_labels, test_data, test_labels,
    scores[name]['dt'] = dt['scores']
    times[name]['dt'] = dt['time']
             copy_metrics(existing_runs, 'dt', name)
      if is_existing_run(existing_runs, 'rf', name) == 0:
    rf = run_random_forest(train_data, train_labels, test_data, test_labels,
    scores[name]['rf'] = rf['scores']
    times[name]['rf'] = rf['time']
      else:
             copy_metrics(existing_runs, 'rf', name)
      if is_existing_run(existing_runs, 'nn', name) == 0:
    nn = run_neural_net(train_data, train_labels, test_data, test_labels, name, hyper_params)
    scores[name]['nn'] = nn['scores']
    times[name]['nn'] = nn['time']
      else:
```

```
copy_metrics(existing_runs, 'nn', name)
save_metrics(scores, times)

scores = {}
times = {}
existing_runs = get_saved_metrics()

for name in all_train_data.keys():
    print("********************************
    print(name)
    print("**********************************

train = all_train_data[name]
    test = all_test_data[name]
run_classifiers(train['data'], train['labels'], test['data'], test['labels'], name, scores, times, existing_runs)
```

▼ Visualize Performance across different feature sets, different classifiers

```
df_report = save_metrics(scores, times, False)
df_report
```



		name	feature_size	classifier	precision	recall	f1	time
	0	topgenes_small	8865	dt	0.355003	0.347652	0.345478	22.808223
3 bestft_large 8000 dt 0.377208 0.347652 0.347006 1971753 4 all 19198 dt 0.344090 0.346653 0.339775 12.234848 5 11reg_c.05 4697 dt 0.344179 0.331769 0.331770 12.24848 6 11reg_c.10 13680 dt 0.344436 0.341179 0.331770 20.674227 8 11reg_c.10 18680 dt 0.358837 0.359140 0.359141 0.559712 9.780744 9 offer_pca 8000 lr 0.539149 0.53960 0.519651 17.25751 10 tospenes 8000 lr 0.539149 0.53960 0.519730 7.78374 11 bestfft_large 8000 lr 0.539149 0.53960 0.519730 17.75757 14 all 119198 lr 0.549620 0.543450 0.519730 17.7371 15 lreg_c.b 4050 lr 0.54402	1	bestfit_with_topgenes	5000	dt	0.343186	0.338661	0.336160	12.592472
4 all 19198 dt 0.344909 0.346653 0.339245 46.565313 5 Hreg.c0.5 4697 dt 0.363232 0.321168 0.331770 12.234848 6 Hreg.c10 13680 dt 0.344197 0.331167 0.331707 20.674227 7 Hreg.c100 13833 dt 0.348887 0.359141 0.342122 43.72572 9 after_pca 8000 dt 0.25818 0.19130 0.19420 157.5780 10 topgenes_small 8805 lr 0.54976 0.539149 0.53990 0.51970 9.789974 11 bestiff_und 5000 lr 0.539149 0.54960 0.51970 9.78394 12 bestiff_und 5000 lr 0.539149 0.54960 0.51907 0.749381 147.7575 14 all larg.c1 3000 lr 0.539140 0.54160 0.51207 0.54973 0.51207 0.516773 14.69937	2	bestfit_med	5000	dt	0.342441	0.340160	0.336631	12.373375
Ilreg_clo.5	3	bestfit_large	8000	dt	0.357208	0.347652	0.347006	19.917533
	4	all	19198	dt	0.344909	0.346653	0.339245	46.563513
	5	l1reg_c0.5	4697	dt	0.336232	0.332168	0.330775	12.234848
	6	l1reg_c1	7430	dt	0.341197	0.331169	0.331370	20.674227
9 after_pca 8006 dt 0.205518 0.191309 0.194230 155.75809 10 topgenes_small 8865 ir 0.549762 0.53960 0.519851 17.257251 11 bestfit_med 5000 ir 0.539149 0.539861 0.51970 9.780974 12 bestfit_med 5000 ir 0.539149 0.51980 0.51970 9.74394 13 bestfit_med 5000 ir 0.539480 0.51973 0.510737 10.406144 16 Ilreg_c10 4697 ir 0.54620 0.54390 0.510737 10.406144 16 Ilreg_c10 13680 ir 0.545209 0.54390 0.512073 15.67111 17 ilreg_c10 13680 ir 0.546700 0.549700 0.523676 0.523675 0.523191 36.91981 13.91981 18 Ilreg_c10 13680 ir 0.546700 0.549700 0.523193 0.521931 36.91931 36.91931 <th>7</th> <th>l1reg_c10</th> <th>13680</th> <th>dt</th> <th>0.346436</th> <th>0.343157</th> <th>0.338764</th> <th>35.242824</th>	7	l1reg_c10	13680	dt	0.346436	0.343157	0.338764	35.242824
10 topgenes,small 8865 Ir 0.549762 0.53960 0.51987 17.257251 11 bestfit_with_topgenes 5000 Ir 0.539149 0.538961 0.51970 9.780974 12 bestfit_large 8000 Ir 0.539140 0.518970 9.743394 13 bestfit_large 8000 Ir 0.554420 0.54820 0.51973 14.775475 14 all 19198 Ir 0.544209 0.530470 0.510737 10.406144 15 Ilreg_c.05 4667 Ir 0.544209 0.530480 0.512307 15.647111 16 Ilreg_c.10 13680 Ir 0.550274 0.54420 0.52367 4.459937 18.647111 17 Ilreg_c.10 13680 Ir 0.550274 0.54451 0.52367 4.699937 18 dilreg_c.10 13680 Ir 0.52267 0.54420 0.54420 0.54360 0.49700 0.485023 0.5817843 0.52367 24947351 <th>8</th> <th>l1reg_c100</th> <th>18363</th> <th>dt</th> <th>0.358837</th> <th>0.359141</th> <th>0.352412</th> <th>43.472572</th>	8	l1reg_c100	18363	dt	0.358837	0.359141	0.352412	43.472572
	9	after_pca	8006	dt	0.205518	0.191309	0.194230	155.755809
	10	topgenes_small	8865	lr	0.549762	0.539960	0.519851	17.257251
	11	bestfit_with_topgenes	5000	lr	0.539149	0.538961	0.515970	9.780974
	12	bestfit_med	5000	lr	0.539149	0.538961	0.515970	9.743394
1	13	bestfit_large	8000	lr	0.554484	0.541459	0.519183	14.775475
	14	all	19198	lr	0.549622	0.543956	0.521253	63.787119
	15	l1reg_c0.5	4697	lr	0.536659	0.530470	0.510773	10.406144
	16	l1reg_c1	7430	lr	0.544209	0.531968	0.512307	15.647111
19 after_pca 8006 ir 0.528760 0.501998 0.485617 863.19856 20 topgenes_small 8865 nn 0.481773 0.476523 0.458466 395.713549 21 bestfit_with_topgenes 5000 nn 0.497606 0.49001 0.479298 268.178483 22 bestfit_lerge 8000 nn 0.510077 0.495504 0.480739 364.302666 24 all 19198 nn 0.512175 0.493007 0.483623 761.913399 25 I1reg_c10 4697 nn 0.00100 0.09990 0.00198 342.288193 26 I1reg_c10 13680 nn 0.00100 0.09990 0.00198 242.288193 27 I1reg_c10 13680 nn 0.00100 0.00990 0.00198 242.288193 30 topgenes_small 8865 rf 0.449816 0.457043 0.410779 178.149539 31 bestfft_with_topgenes 5000 rf </th <th>17</th> <th>l1reg_c10</th> <th>13680</th> <th>lr</th> <th>0.565763</th> <th>0.549451</th> <th>0.523657</th> <th>44.599937</th>	17	l1reg_c10	13680	lr	0.565763	0.549451	0.523657	44.599937
20 topgenes_small 8865 nn 0.481773 0.476523 0.458486 395.71354 21 bestfit_with_topgenes 5000 nn 0.497606 0.499001 0.479298 268.178483 22 bestfit_large 8000 nn 0.510077 0.495504 0.480739 364.302666 24 all 19198 nn 0.512175 0.49300 0.40323 761.913399 25 I1reg_c15 4697 nn 0.468076 0.49900 0.407255 214.016822 26 I1reg_c10 13680 nn 0.000100 0.00990 0.00198 342.288193 27 I1reg_c10 13680 nn 0.00100 0.00990 0.00198 621.967364 28 I1reg_c10 13680 nn 0.00100 0.00990 0.00198 422.288193 30 topgenes_small 8865 rf 0.449816 0.457043 0.410779 178.149539 31 bestfft_with_topgenes 5000 rf </th <th>18</th> <th>l1reg_c100</th> <th>18363</th> <th>lr</th> <th>0.550274</th> <th>0.543457</th> <th>0.521391</th> <th>63.918611</th>	18	l1reg_c100	18363	lr	0.550274	0.543457	0.521391	63.918611
21 bestfit_with_topgenes 5000 nn 0.497606 0.499001 0.497928 268.178484 22 bestfit_med 5000 nn 0.487686 0.486014 0.469875 229.497351 23 bestfit_large 8000 nn 0.510077 0.493504 0.480739 364.302666 24 all 19198 nn 0.512175 0.493007 0.483623 761.913399 25 I1reg_c0.5 4697 nn 0.468076 0.499500 0.470255 214.016822 26 I1reg_c10 13680 nn 0.000100 0.00990 0.00198 342.288193 27 I1reg_c10 13680 nn 0.000100 0.00990 0.00198 621.967364 28 I1reg_c10 18363 nn 0.51938 0.56494 0.42145 757.566261 39 after_pca 8006 nn 0.000100 0.00990 0.00198 418.716873 31 bestfit_with_topgenes 5000 rf	19	after_pca	8006	lr	0.528760	0.501998	0.485617	863.198566
22 bestfit_large 5000 nn 0.487688 0.486014 0.469875 229.49731 23 bestfit_large 8000 nn 0.510077 0.495504 0.480739 364.302666 24 all 19198 nn 0.512175 0.49307 0.483623 761.913399 25 l1reg_c0.5 4697 nn 0.468076 0.49900 0.470255 214.016822 26 l1reg_c10 13680 nn 0.000100 0.009990 0.00198 342.288193 27 l1reg_c10 13680 nn 0.000100 0.009990 0.00198 621.967364 28 l1reg_c10 18363 nn 0.519938 0.506494 0.492145 757.566261 29 after_pca 8006 nn 0.000100 0.009990 0.00198 418.716876 30 topgenes_small 8865 rf 0.449816 0.457043 0.41079 178.149539 31 bestfit_with_topgenes 5000 rf	20	topgenes_small	8865	nn	0.481773	0.476523	0.458486	395.713549
23 bestfit_large 8000 nn 0.510077 0.495504 0.480739 364.302666 24 all 19198 nn 0.512175 0.493007 0.483623 761.913399 25 l1reg_c0.5 4697 nn 0.468076 0.499500 0.470255 214.016822 26 l1reg_c10 13680 nn 0.000100 0.009990 0.00018 342.288193 27 l1reg_c100 18363 nn 0.519938 0.506494 0.492145 757.566261 29 after_pca 8006 nn 0.000100 0.009990 0.00198 418.716876 30 topgenes_small 8865 rf 0.449816 0.457043 0.410779 178.149539 31 bestfit_with_topgenes 5000 rf 0.45264 0.455540 0.41381 123.981630 32 bestfit_large 8000 rf 0.440372 0.458042 0.41381 123.981630 34 all 19198 rf	21	bestfit_with_topgenes	5000	nn	0.497606	0.499001	0.479298	268.178483
24 all 19198 nn 0.512175 0.493007 0.483623 761.913939 25 l1reg_c0.5 4697 nn 0.468076 0.499500 0.470255 214.016822 26 l1reg_c10 7430 nn 0.000100 0.009990 0.000198 342.288193 27 l1reg_c10 13680 nn 0.000100 0.009990 0.000198 621.967364 28 l1reg_c100 18363 nn 0.519938 0.506494 0.492145 757.566261 29 after_pca 8006 nn 0.000100 0.009990 0.00198 418.716876 30 topgenes_small 8865 rf 0.449816 0.457043 0.410779 178.149539 31 bestift_with_topgenes 5000 rf 0.449816 0.455544 0.41381 123.981630 32 bestift_large 8000 rf 0.440372 0.458042 0.41381 123.981630 34 all 19198 rf	22	bestfit_med	5000	nn	0.487686	0.486014	0.469875	229.497351
25 I1reg_c0.5 4697 nn 0.468076 0.499500 0.470255 214.016822 26 I1reg_c10 7430 nn 0.000100 0.009990 0.000198 342.288193 27 I1reg_c10 13680 nn 0.000100 0.009990 0.000198 621.967364 28 I1reg_c100 18363 nn 0.519938 0.506494 0.492145 757.566261 29 after_pca 8006 nn 0.000100 0.009990 0.00198 418.716876 30 topgenes_small 8865 rf 0.449816 0.457043 0.410779 178.149539 31 bestfit_with_topgenes 5000 rf 0.454264 0.455544 0.414381 123.981630 32 bestfit_large 8000 rf 0.446372 0.458042 0.415872 124.758752 33 bestfit_large 8000 rf 0.446646 0.445554 0.409261 168.571105 34 all 19198 rf <th>23</th> <th>bestfit_large</th> <th>8000</th> <th>nn</th> <th>0.510077</th> <th>0.495504</th> <th>0.480739</th> <th>364.302666</th>	23	bestfit_large	8000	nn	0.510077	0.495504	0.480739	364.302666
26 Ilreg_c1 7430 nn 0.000100 0.009990 0.000198 342,288193 27 Ilreg_c10 13680 nn 0.000100 0.009990 0.000198 621,967364 28 Ilreg_c100 18363 nn 0.519938 0.506494 0.492145 757,566261 29 after_pca 8006 nn 0.000100 0.009990 0.000198 418,716876 30 topgenes_small 8865 rf 0.449816 0.457043 0.41077 178,149539 31 bestfit_with_topgenes 5000 rf 0.454264 0.455544 0.414381 123,981630 32 bestfit_large 8000 rf 0.440372 0.458042 0.415872 124,758752 33 bestfit_large 8000 rf 0.440372 0.455346 0.409261 168,571105 34 all 19198 rf 0.446646 0.445554 0.404035 226,3347652 35 Ilreg_c10 13680 rf <th>24</th> <th>all</th> <th>19198</th> <th>nn</th> <th>0.512175</th> <th>0.493007</th> <th>0.483623</th> <th>761.913399</th>	24	all	19198	nn	0.512175	0.493007	0.483623	761.913399
27 Ilreg_c10 13680 nn 0.000100 0.009990 0.000198 621.967364 28 Ilreg_c100 18363 nn 0.519938 0.506494 0.492145 757.566261 29 after_pca 8006 nn 0.000100 0.009990 0.000198 418.716876 30 topgenes_small 8865 rf 0.449816 0.457043 0.410779 178.149539 31 bestfit_with_topgenes 5000 rf 0.430347 0.458042 0.41381 123.981630 32 bestfit_large 8000 rf 0.430347 0.458042 0.415872 124.758752 33 bestfit_large 8000 rf 0.440372 0.453546 0.409261 168.571105 34 all 19198 rf 0.446646 0.445554 0.403445 298.347052 35 Ilreg_c0.5 4697 rf 0.476551 0.46203 0.422663 166.029324 37 Ilreg_c1 7330 rf	25	l1reg_c0.5	4697	nn	0.468076	0.499500	0.470255	214.016822
28 I1reg_c100 18363 nn 0.519938 0.506494 0.492145 757.566261 29 after_pca 8006 nn 0.000100 0.00990 0.000198 418.716876 30 topgenes_small 8865 rf 0.449816 0.457043 0.410779 178.149539 31 bestfit_with_topgenes 5000 rf 0.45264 0.455544 0.414381 123.981630 32 bestfit_large 8000 rf 0.430347 0.458042 0.415872 124.758752 33 bestfit_large 8000 rf 0.446646 0.445554 0.409261 168.571105 34 all 19198 rf 0.446646 0.445554 0.403445 298.347052 35 I1reg_c0.5 4697 rf 0.476551 0.462038 0.422633 162.03234 36 I1reg_c10 13680 rf 0.47814 0.464036 0.422663 166.029324 37 I1reg_c100 18363 rf <th>26</th> <th>l1reg_c1</th> <th>7430</th> <th>nn</th> <th>0.000100</th> <th>0.009990</th> <th>0.000198</th> <th>342.288193</th>	26	l1reg_c1	7430	nn	0.000100	0.009990	0.000198	342.288193
29 after_pca 8006 nn 0.000100 0.009990 0.000198 418.716876 30 topgenes_small 8865 rf 0.449816 0.457043 0.410779 178.149539 31 bestfit_with_topgenes 5000 rf 0.454264 0.455544 0.414381 123.981630 32 bestfit_large 8000 rf 0.440372 0.453546 0.409261 168.571105 34 all 19198 rf 0.446646 0.445554 0.403445 298.347052 35 l1reg_c0.5 4697 rf 0.476551 0.462038 0.422336 122.613206 36 l1reg_c1 7430 rf 0.462523 0.453040 0.422663 160.029324 37 l1reg_c10 13680 rf 0.462523 0.453040 0.404060 290.577816 39 after_pca 8006 rf 0.13701 0.140360 0.091183 742.582230 40 topgenes_small 8865 svm <th>27</th> <th>l1reg_c10</th> <th>13680</th> <th>nn</th> <th>0.000100</th> <th>0.009990</th> <th>0.000198</th> <th>621.967364</th>	27	l1reg_c10	13680	nn	0.000100	0.009990	0.000198	621.967364
30 topgenes_small 8865 rf 0.449816 0.457043 0.410779 178.149539 31 bestfit_with_topgenes 5000 rf 0.454264 0.455544 0.414381 123.981630 32 bestfit_med 5000 rf 0.430347 0.458042 0.415872 124.758752 33 bestfit_large 8000 rf 0.440372 0.453546 0.409261 168.571105 34 all 19198 rf 0.446646 0.445554 0.403445 298.347052 35 I1reg_c0.5 4697 rf 0.476551 0.462038 0.42236 122.613206 36 l1reg_c10 13680 rf 0.474814 0.464036 0.42263 166.029324 37 l1reg_c10 13680 rf 0.441456 0.45549 0.411935 240.343188 38 l1reg_c100 18363 rf 0.441456 0.450549 0.404603 290.577816 39 after_pca 8006 rf	28	l1reg_c100	18363	nn	0.519938	0.506494	0.492145	757.566261
31 bestfit_with_topgenes 5000 rf 0.454264 0.455544 0.414381 123.981630 32 bestfit_med 5000 rf 0.430347 0.458042 0.415872 124.758752 33 bestfit_large 8000 rf 0.440372 0.453546 0.409261 168.571105 34 all 19198 rf 0.446646 0.445554 0.403445 298.347052 35 I1reg_c0.5 4697 rf 0.476551 0.462038 0.422336 122.613206 36 I1reg_c1 7430 rf 0.474814 0.46036 0.42263 166.029324 37 I1reg_c10 13680 rf 0.462523 0.45049 0.411935 240.343188 38 I1reg_c100 18363 rf 0.414356 0.450549 0.404603 290.577816 39 after_pca 8006 rf 0.137010 0.140360 0.091183 742.582230 40 topgenes_small 8865 svm	29	after_pca	8006	nn	0.000100	0.009990	0.000198	418.716876
32 bestfit_med 5000 rf 0.430347 0.458042 0.415872 124.758752 33 bestfit_large 8000 rf 0.440372 0.45346 0.409261 168.571105 34 all 19198 rf 0.446646 0.445554 0.403445 298.347052 35 I1reg_c0.5 4697 rf 0.476551 0.462038 0.422336 122.613206 36 I1reg_c10 13680 rf 0.474814 0.464036 0.42263 166.029324 37 I1reg_c100 13680 rf 0.462523 0.453047 0.411935 240.343188 38 I1reg_c100 18363 rf 0.441456 0.450549 0.404603 290.577816 39 after_pca 8006 rf 0.137010 0.140360 0.091183 742.582230 40 topgenes_small 8865 svm 0.508267 0.518981 0.497027 2.395096 42 bestfit_large 8000 svm	30	topgenes_small	8865	rf	0.449816	0.457043	0.410779	178.149539
33 bestfit_large 8000 rf 0.440372 0.453546 0.409261 168.571105 34 all 19198 rf 0.446646 0.445554 0.403445 298.347052 35 l1reg_c0.5 4697 rf 0.476551 0.462038 0.422363 122.613206 36 l1reg_c10 13680 rf 0.474814 0.464036 0.422663 166.029324 37 l1reg_c100 18363 rf 0.441456 0.450549 0.40403 290.577816 39 after_pca 8006 rf 0.137010 0.140360 0.091183 742.582230 40 topgenes_small 8865 svm 0.531526 0.532967 0.510535 3.671322 41 bestfit_with_topgenes 5000 svm 0.508267 0.518981 0.497027 2.326138 43 bestfit_large 8000 svm 0.508267 0.518981 0.497027 2.326138 44 all 19198 svm	31	bestfit_with_topgenes	5000	rf	0.454264	0.455544	0.414381	123.981630
34 all 19198 rf 0.446646 0.445554 0.403445 298.347052 35 l1reg_c0.5 4697 rf 0.476551 0.462038 0.422336 122.613206 36 l1reg_c1 7430 rf 0.474814 0.464036 0.42263 166.029324 37 l1reg_c10 13680 rf 0.462523 0.453047 0.411935 240.343188 38 l1reg_c100 18363 rf 0.441456 0.450549 0.404603 290.577816 39 after_pca 8006 rf 0.137010 0.140360 0.091183 742.582230 40 topgenes_small 8865 svm 0.531526 0.532967 0.510535 3.671322 41 bestfit_with_topgenes 5000 svm 0.508267 0.518981 0.497027 2.326138 43 bestfit_large 8000 svm 0.538267 0.518981 0.497027 2.326138 44 all 19198 svm <	32	bestfit_med	5000	rf	0.430347	0.458042	0.415872	124.758752
35 I1reg_c0.5 4697 rf 0.476551 0.462038 0.422336 122.613206 36 I1reg_c1 7430 rf 0.474814 0.464036 0.422633 166.029324 37 I1reg_c10 13680 rf 0.462523 0.453047 0.411935 240.343188 38 I1reg_c100 18363 rf 0.441456 0.450549 0.404603 290.577816 39 after_pca 8006 rf 0.137010 0.140360 0.091183 742.582230 40 topgenes_small 8865 svm 0.531526 0.532967 0.510535 3.671322 41 bestfit_with_topgenes 5000 svm 0.508267 0.518981 0.497027 2.326138 43 bestfit_large 8000 svm 0.537923 0.535964 0.517101 3.330731 44 all 19198 svm 0.538346 0.512240 0.520709 6.428361 45 I1reg_c10.5 4697 svm	33	bestfit_large	8000	rf	0.440372	0.453546	0.409261	168.571105
36 I1reg_c10 7430 rf 0.474814 0.464036 0.422663 166.029324 37 I1reg_c10 13680 rf 0.462523 0.453047 0.411935 240.343188 38 I1reg_c100 18363 rf 0.441456 0.450549 0.404603 290.577816 39 after_pca 8006 rf 0.137010 0.140360 0.091183 742.582230 40 topgenes_small 8865 svm 0.531526 0.532967 0.510535 3.671322 41 bestfit_with_topgenes 5000 svm 0.508267 0.518981 0.497027 2.395096 42 bestfit_large 8000 svm 0.537923 0.535964 0.517101 3.330731 44 all 19198 svm 0.538346 0.512405 0.520709 6.428361 45 I1reg_c0.5 4697 svm 0.526239 0.535465 0.513222 3.134554 46 I1reg_c10 13680 svm	34	all	19198	rf	0.446646	0.445554	0.403445	298.347052
37 I1reg_c10 13680 rf 0.462523 0.453047 0.411935 240.343188 38 I1reg_c100 18363 rf 0.441456 0.450549 0.404603 290.577816 39 after_pca 8006 rf 0.137010 0.140360 0.091183 742.582230 40 topgenes_small 8865 svm 0.531526 0.532967 0.510535 3.671322 41 bestfit_with_topgenes 5000 svm 0.508267 0.518981 0.497027 2.395096 42 bestfit_large 8000 svm 0.508267 0.518981 0.497027 2.326138 43 bestfit_large 8000 svm 0.538792 0.535964 0.517101 3.330731 44 all 19198 svm 0.526820 0.535465 0.512240 2.253765 45 I1reg_c10.5 4697 svm 0.526820 0.535465 0.513322 3.134554 47 I1reg_c10 13680 svm	35	l1reg_c0.5	4697	rf	0.476551	0.462038	0.422336	122.613206
38 l1reg_c100 18363 rf 0.441456 0.450549 0.404603 290.577816 39 after_pca 8006 rf 0.137010 0.140360 0.091183 742.582230 40 topgenes_small 8865 svm 0.531526 0.532967 0.510535 3.671322 41 bestfit_with_topgenes 5000 svm 0.508267 0.518981 0.497027 2.395096 42 bestfit_large 8000 svm 0.537923 0.535964 0.517101 3.330731 44 all 19198 svm 0.538346 0.520709 6.428361 45 l1reg_c0.5 4697 svm 0.526820 0.535465 0.512240 2.253765 46 l1reg_c1 7430 svm 0.526239 0.535465 0.513322 3.134554 47 l1reg_c10 13680 svm 0.538732 0.544456 0.509875 5.420964 48 l1reg_c100 18363 svm 0.538732	36	l1reg_c1	7430	rf	0.474814	0.464036	0.422663	166.029324
39 after_pca 8006 rf 0.137010 0.140360 0.091183 742.582230 40 topgenes_small 8865 svm 0.531526 0.532967 0.510535 3.671322 41 bestfit_with_topgenes 5000 svm 0.508267 0.518981 0.497027 2.395096 42 bestfit_large 8000 svm 0.508267 0.518981 0.497027 2.326138 43 bestfit_large 8000 svm 0.537923 0.535964 0.517101 3.330731 44 all 19198 svm 0.538346 0.544456 0.520709 6.428361 45 l1reg_c0.5 4697 svm 0.526820 0.535465 0.512240 2.253765 46 l1reg_c10 13680 svm 0.526239 0.534965 0.509875 5.420964 48 l1reg_c100 18363 svm 0.538732 0.544456 0.520623 6.368480	37	l1reg_c10	13680	rf	0.462523	0.453047	0.411935	240.343188
40 topgenes_small 8865 svm 0.531526 0.532967 0.510535 3.671322 41 bestfit_with_topgenes 5000 svm 0.508267 0.518981 0.497027 2.395096 42 bestfit_large 8000 svm 0.537923 0.538981 0.497027 2.326138 43 bestfit_large 8000 svm 0.537923 0.535964 0.517101 3.330731 44 all 19198 svm 0.538346 0.520709 6.428361 45 l1reg_c0.5 4697 svm 0.526820 0.535465 0.512240 2.253765 46 l1reg_c1 7430 svm 0.526239 0.535465 0.513322 3.134554 47 l1reg_c10 13680 svm 0.525074 0.534965 0.509875 5.420964 48 l1reg_c100 18363 svm 0.538732 0.544456 0.520623 6.368480	38	l1reg_c100	18363	rf	0.441456	0.450549	0.404603	290.577816
41 bestfit_with_topgenes 5000 svm 0.508267 0.518981 0.497027 2.395096 42 bestfit_med 5000 svm 0.508267 0.518981 0.497027 2.326138 43 bestfit_large 8000 svm 0.537923 0.535964 0.517101 3.330731 44 all 19198 svm 0.538346 0.520709 6.428361 45 l1reg_c0.5 4697 svm 0.526820 0.535465 0.512240 2.253765 46 l1reg_c1 7430 svm 0.526239 0.535465 0.513322 3.134554 47 l1reg_c10 13680 svm 0.525074 0.534965 0.509875 5.420964 48 l1reg_c100 18363 svm 0.538732 0.544456 0.520623 6.368480	39	after_pca	8006	rf	0.137010	0.140360	0.091183	742.582230
42 bestfit_med 5000 svm 0.508267 0.518981 0.497027 2.326138 43 bestfit_large 8000 svm 0.537923 0.535964 0.517101 3.330731 44 all 19198 svm 0.538346 0.544456 0.520709 6.428361 45 l1reg_c0.5 4697 svm 0.526820 0.535465 0.512240 2.253765 46 l1reg_c1 7430 svm 0.526239 0.535465 0.513322 3.134554 47 l1reg_c10 13680 svm 0.525074 0.534965 0.509875 5.420964 48 l1reg_c100 18363 svm 0.538732 0.544456 0.520623 6.368480	40	topgenes_small	8865	svm	0.531526	0.532967	0.510535	3.671322
43 bestfit_large 8000 svm 0.537923 0.535964 0.517101 3.330731 44 all 19198 svm 0.538346 0.544456 0.520709 6.428361 45 l1reg_c0.5 4697 svm 0.526820 0.535465 0.512240 2.253765 46 l1reg_c1 7430 svm 0.526239 0.535465 0.513322 3.134554 47 l1reg_c10 13680 svm 0.525074 0.534965 0.509875 5.420964 48 l1reg_c100 18363 svm 0.538732 0.544456 0.520623 6.368480	41	bestfit_with_topgenes	5000	svm	0.508267	0.518981	0.497027	2.395096
44 all 19198 svm 0.538346 0.544456 0.520709 6.428361 45 l1reg_c0.5 4697 svm 0.526820 0.535465 0.512240 2.253765 46 l1reg_c1 7430 svm 0.526239 0.535465 0.513322 3.134554 47 l1reg_c10 13680 svm 0.525074 0.534965 0.509875 5.420964 48 l1reg_c100 18363 svm 0.538732 0.544456 0.520623 6.368480	42	bestfit_med	5000	svm	0.508267	0.518981	0.497027	2.326138
45 l1reg_c0.5 4697 svm 0.526820 0.535465 0.512240 2.253765 46 l1reg_c1 7430 svm 0.526239 0.535465 0.513322 3.134554 47 l1reg_c10 13680 svm 0.525074 0.534965 0.509875 5.420964 48 l1reg_c100 18363 svm 0.538732 0.544456 0.520623 6.368480	43	bestfit_large	8000	svm	0.537923	0.535964	0.517101	3.330731
46 I1reg_c1 7430 svm 0.526239 0.535465 0.513322 3.134554 47 I1reg_c10 13680 svm 0.525074 0.534965 0.509875 5.420964 48 I1reg_c100 18363 svm 0.538732 0.544456 0.520623 6.368480	44	all	19198	svm	0.538346	0.544456	0.520709	6.428361
47 I1reg_c10 13680 svm 0.525074 0.534965 0.509875 5.420964 48 I1reg_c100 18363 svm 0.538732 0.544456 0.520623 6.368480	45	l1reg_c0.5	4697	svm	0.526820	0.535465	0.512240	2.253765
48	46	l1reg_c1	7430	svm	0.526239	0.535465	0.513322	3.134554
	47	l1reg_c10	13680	svm	0.525074	0.534965	0.509875	5.420964
49 after_pca 8006 svm 0.516078 0.515485 0.490608 289.964595	48	l1reg_c100	18363	svm	0.538732	0.544456	0.520623	6.368480
	49	after_pca	8006	svm	0.516078	0.515485	0.490608	289.964595

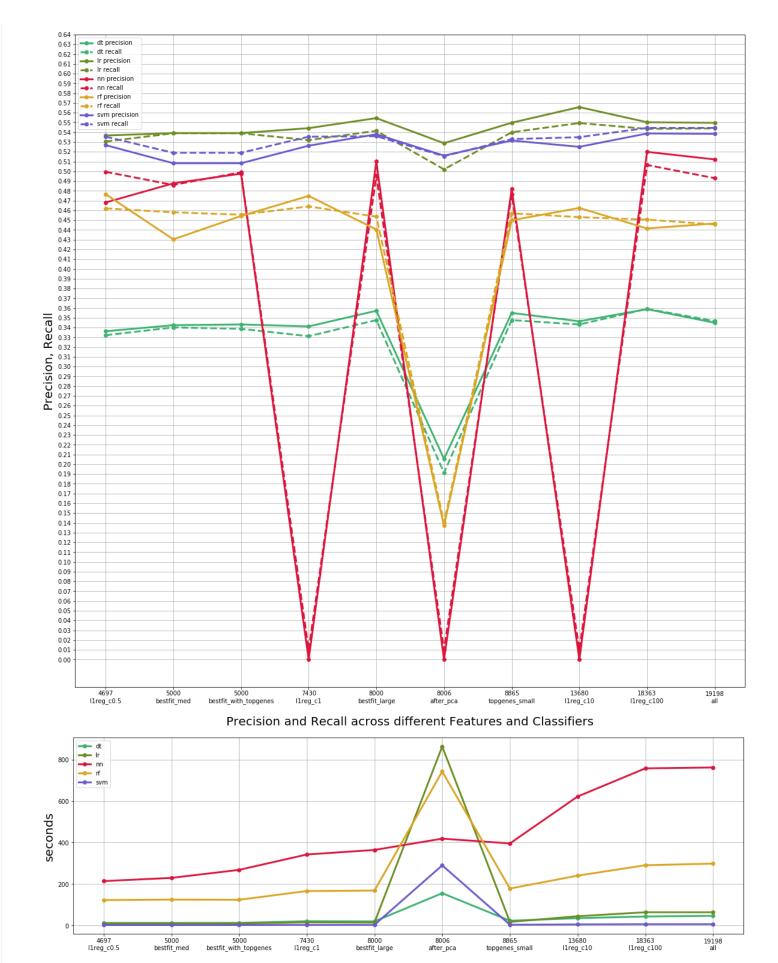
```
labels = []
      for key, group in df_report.groupby(['feature_size', 'name']):
    labels.append(str(key[0]) + '\n' + key[1])
      sorted_df_report = df_report.sort_values(by=['classifier', 'feature_size', 'iname'], ascending=[1,1,1])
      for classifier, group in sorted_df_report.groupby(['classifier']):
            plt.yticks(np.arange(0, .65, .01))
plt.ylabel('Precision, Recall', fontsize=20)
plt.xlabel('Precision and Recall across different Features and Classifiers', fontsize=20, labelpad=20)
      plt.legend()
      plt.grid()
      plt.show()
def plot_classifier_times(df_report, label_encoder):
      plt.rcParams["figure.figsize"] = (20,6)
      for key, group in df_report.groupby(['feature_size', 'name']):
    labels.append(str(key[0]) + '\n' + key[1])
      sorted_df_report = df_report.sort_values(by=['classifier', 'feature_size', 'hame'], ascending=[1,1,1])
      for classifier, group in sorted df report.groupby(['classifier']):
            plt.ylabel('seconds', fontsize=20)
plt.xlabel('Run times across different Features and Classifiers', fontsize=20, labelpad=20)
      plt.legend()
plt.grid()
      plt.show()
def show_precision_recall_by_label(precision_by_label, recall_by_label, name, classifier, label_encoder):
    plt.rcParams["figure.figsize"] = (20,20)
      factor = ...
labels = []
for i in range(len(precision_by_label)):
    label = label_encoder.inverse_transform([i])[0]
    labels.append(label)
      y pos = np.arange(len(labels))
      fig, (ax1, ax2) = plt.subplots(ncols=2, sharey=False)
      ax1.invert_xaxis()
ax1.yaxis.tick_right()
      ax1.set_yticks(y_pos)
ax1.set_yticklabels(labels)
      ax2.set_yticks(y_pos)
ax2.set_yticklabels(labels)
      ax1.barh(y_pos, precision_by_label, color=colors[classifier] , label="precision")
ax2.barh(y_pos, recall_by_label, color=colors[classifier], label='recall')
      ax1.set_title('Precision( ' + classifier + ')')
ax2.set_title('Recall (' + classifier + ')')
      plt.grid()
def coords_of_max(theArray, n):
       # Flatten the 2D array
      # Flatten the 2D array
flat = theArray.flatten()
# Partition so that the we know the sort order for
# the cells with the highest values. We just
# care about the top n highest values. So for example,
# if n = 3, get return 3 indices.
      # Reverse so that we show index of highest value first
       # (descending)
      indices = indices[np.argsort(-flat[indices])]
      indices = indices[np.argsort(-flat[indices])]
# Now return the coordinates for these indices
# for a 2D array. This will return 2 arrays,
# the first for the row index, the second for the
# column index. The row index represents the
# actual digit, the column index represents
# the confused digit
      return np.unravel_index(indices, theArray.shape)
def show_confusion matrix(conf_mx, label_encoder):
    # Determine the error rates for each misclassification pair
    row_sums = conf_mx.sum(axis=1, keepdims=True)
    norm_conf_mx = conf_mx / row_sums
    # Set the error rates for correctly classified pairs (the diagonal) to zero
      np.fill_diagonal(norm_conf_mx, 0)
      max_coords = coords_of_max(norm_conf_mx, 20)
      confusion_rows = []
for i in range(len(max_coords[0])):
             # This is the actual label
            actual_label_idx = max_coords[0][i]
actual_label = label_encoder.inverse_transform([actual_label_idx])[0]
             # This is the predicted label
            predicted_label_idx = max_coords[1][i]
predicted_label = label_encoder.inverse_transform([predicted_label_idx])[0]
```

This is the error rate

▼ Plot precision metrics across different classifiers and feature sets

```
# Plot precision and accuracy across different classifiers
plot_classifier_metrics(df_report, label_encoder)
# Plot time across different classifiers
plot_classifier_times(df_report, label_encoder)
```





Run times across different Features and Classifiers



Best precision

	name	feature_size	classifier	precision	recall	11	time
17	l1reg_c10	13680	lr	0.565763	0.549451	0.523657	44.599937

Best recall

	name	feature_size	classifier	precision	recall	f1	time
17	l1reg_c10	13680	Ir	0.565763	0.549451	0.523657	44.599937

Best fl

	name	feature_size	classifier	precision	recall	f1	time
17	l1reg_c10	13680	Ir	0.565763	0.549451	0.523657	44.599937

Precision and Recall by Label for classifier Classifier: lr Feature set: llreg_c10



	actual	predicted	actual_name	predicted_name	error_rate	error_count
0	READ	COAD	Rectum_adenocarcinoma	Colon_adenocarcinoma	0.720000	18
1	ACC	BRCA	Adrenocortical_carcinoma	Breast_invasive_carcinoma	0.500000	10
2	PCPG	PRAD	Pheochromocytoma_and_Paraganglioma	Prostate_adenocarcinoma	0.413793	12
3	TGCT	PRAD	Testicular_Germ_Cell_Tumors	Prostate_adenocarcinoma	0.380952	8
4	KICH	BRCA	Kidney_Chromophobe	Breast_invasive_carcinoma	0.352941	6
5	MESO	PRAD	Mesothelioma	Prostate_adenocarcinoma	0.333333	7
6	PCPG	THCA	Pheochromocytoma_and_Paraganglioma	Thyroid_carcinoma	0.310345	9
7	UCS	UCEC	Uterine_Carcinosarcoma	Uterine_Corpus_Endometrial_Carcinoma	0.307692	4
8	DLBC	STAD	Lymphoid_Neoplasm_Diffuse_Large_B-cell_Lymphoma	Stomach_adenocarcinoma	0.300000	3
9	CESC	BRCA	Cervical_squamous_cell_carcinoma_and_endocervi	Breast_invasive_carcinoma	0.290909	16
10	THYM	BRCA	Thymoma	Breast_invasive_carcinoma	0.280000	7
11	SARC	BRCA	Sarcoma	Breast_invasive_carcinoma	0.269231	14
12	KIRP	BRCA	Kidney_renal_papillary_cell_carcinoma	Breast_invasive_carcinoma	0.262295	16
13	MESO	KIRC	Mesothelioma	Kidney_renal_clear_cell_carcinoma	0.238095	5
14	MESO	BRCA	Mesothelioma	Breast_invasive_carcinoma	0.238095	5
15	TGCT	THCA	Testicular_Germ_Cell_Tumors	Thyroid_carcinoma	0.238095	5
16	UCS	BRCA	Uterine_Carcinosarcoma	Breast_invasive_carcinoma	0.230769	3
17	UCS	OV	Uterine_Carcinosarcoma	Ovarian_serous_cystadenocarcinoma	0.230769	3
18	OV	BRCA	Ovarian_serous_cystadenocarcinoma	Breast_invasive_carcinoma	0.223684	17
19	SARC	PRAD	Sarcoma	Prostate_adenocarcinoma	0.211538	11

▼ Write out the confusion matrix and precision/recall by label to file

8

```
df_confusion_matrix = pd.DataFrame(best_confusion_matrix)
df_precision_by_label = pd.DataFrame(precision_by_label)
df_recall_by_label = pd.DataFrame(recall_by_label)

print("\nWriting_metrics ...")
df_confusion_matrix.to_csv("./data/metrics_confusion_matrix.csv")
print("done.")

print("\nWriting_metrics ...")
df_precision_by_label.to_csv("./data/metrics_precision_by_label.csv")
print("done.")

print("\nWriting_metrics ...")
df_recall_by_label.to_csv("./data/metrics_recall_by_label.csv")
print("done.")

Writing_metrics ...
done.

Writing_metrics ...
done.

Writing_metrics ...
done.
```