# 2.0 classification models

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## 1 2.0 Classification

### 1.1 Supervised classification models for the deduplicated vectorized data

- test train split
- run model, get scores
- plot roc auc for multiple models
- pull top 5000 features based on coef or log proba from chosen model
- make matrix based on above for further feature selection

```
[]: from sklearn.model_selection import StratifiedShuffleSplit
     from sklearn.preprocessing import LabelEncoder
     from sklearn import naive_bayes
     from sklearn.neighbors import KNeighborsClassifier
     from sklearn.linear_model import LogisticRegression, SGDClassifier
     from sklearn.dummy import DummyClassifier
     from sklearn.ensemble import RandomForestClassifier
     from sklearn.metrics import confusion_matrix
     from sklearn import metrics
     from sklearn.metrics import roc_curve, auc, classification_report, u
     →make_scorer, accuracy_score
     import matplotlib
     import matplotlib.patches as mpatches
     import matplotlib.cm as cm
     import matplotlib.pyplot as plt
     %matplotlib inline
     import seaborn as sns
     import time
     import math
     import itertools
     from datetime import datetime
     import sys
     import numpy as np
```

```
import pickle
     import pandas as pd
     from scipy.sparse import csr_matrix, vstack
     from importlib_metadata import version
     libraries = ['pandas', 'numpy', 'scikit-learn', 'scipy', 'matplotlib']
     print('last ran: ',datetime.now() )
     print("Python Version:", sys.version[0:7])
     print( "operating system:", sys.platform)
     for lib in libraries:
         print(lib + ' version: ' + version(lib))
[]: def feature_unpickle(path):
         mat = \Pi
         for i in range(0,10):
             with open(path+'textfeatures_mat'+str(i+1)+'.pickle', 'rb') as f:
                 mat.append(pickle.load(f,encoding='latin1'))
         mat=vstack(mat)
         q=[mat]
         with open(path+'textfeatures_vocab.pickle', 'rb') as f:
             vocab=pickle.load(f,encoding='latin1')
             q.append(vocab)
         with open(path+'textfeatures_id.pickle', 'rb') as f:
             ids=pickle.load(f,encoding='latin1')
             q.append(ids)
         with open(path+'textfeatures_source.pickle', 'rb') as f:
             source=pickle.load(f,encoding='latin1')
             q.append(source)
         return q
[]: startTime = datetime.now()
     print (startTime)
     #load input data
     path ="./"
     path1 = "LR/"
     path2 = "NB/"
[]: r=feature_unpickle(path)
     XX = r[0]
     y = r[3]
```

```
[]: \#Stratified\ b/c\ we\ have\ unbalanced\ classes\ (more\ non-transfused\ than
     \hookrightarrow transfused),
     # and shuffle b/c the classe are grouped together in the matrix. This function
     will help us to get a balanced, random selection of each class into our test
     \rightarrow and train sections.
     rs = StratifiedShuffleSplit(n_splits=1, random_state=42, test_size=0.25,__
     →train_size=None)
     for train_index, test_index in rs.split(XX,y):
         print('TRAIN:', train_index, "TEST:", test_index)
     X train = XX[train index,:]
     X_test = XX[test_index,:]
     y_train = y[train_index]
     y_test = y[test_index]
[]: m = LabelEncoder()
     y_test1 = m.fit_transform(y_test)
     m = LabelEncoder()
     y_train1 = m.fit_transform(y_train)
[]: def plot_confusion_matrix(cm, classes,
                                normalize=False,
                                title='Confusion matrix',
                                cmap=plt.cm.summer):
         if normalize:
             cm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]
         plt.imshow(cm, interpolation='nearest', cmap=cmap)
         plt.title(title, fontsize=30)
         plt.colorbar()
         tick_marks = np.arange(len(classes))
         plt.xticks(tick_marks, classes, fontsize=20)
         plt.yticks(tick_marks, classes, fontsize=20)
         fmt = '.2f' if normalize else 'd'
         thresh = cm.max() / 2.
         for i, j in itertools.product(range(cm.shape[0]), range(cm.shape[1])):
             plt.text(j, i, format(cm[i, j], fmt), horizontalalignment="center",
                      color="white" if cm[i, j] < thresh else "black", fontsize=40)</pre>
         plt.tight_layout()
         plt.ylabel('True label', fontsize=30)
         plt.xlabel('Predicted label', fontsize=30)
         return plt
```

### 2 Models

#### 2.0.1 Naive Bayes

```
[]: NBmodel = naive_bayes.MultinomialNB()
     NBmodel.fit(X_train, y_train)
     # save model
     with open('NBmodel.pickle', 'wb') as picklefile:
         pickle.dump(NBmodel,picklefile)
     #with open('NB model.pickle', 'rb') as f:
       # NBmodel = pickle.load(f,encoding='latin1')
     print ("naive bayes Scoring on test set")
     Y_pred = NBmodel.predict(X_test)
     cr = classification report(y test, Y pred)
     print( cr)
[]: cm = confusion_matrix(y_test, Y_pred)
     fig = plt.figure(figsize=(8, 8))
     plot = plot_confusion_matrix(cm, classes=['Non','Transfused'], normalize=False)
     plt.savefig("NB_confusion_matrix.svg")
     plt.show()
     print(cm)
```

# 3 logistic regression

```
[]: LRmodel = LogisticRegression(verbose=1)
   LRmodel.fit(X_train, y_train)
#save model
with open('LRmodel.pickle', 'wb') as picklefile:
        pickle.dump(LRmodel.picklefile)
#load model
#with open('LRmodel.pickle', 'rb') as f:
# LRmodel = pickle.load(f,encoding='latin1')

print( "Logistic regression Scoring on test set")
   LR_Y_pred = LRmodel.predict(X_test)
   cr = classification_report(y_test, LR_Y_pred)
   print (cr)
```

```
[]: cm = confusion_matrix(y_test, LR_Y_pred)
  fig = plt.figure(figsize=(8, 8))
  plot = plot_confusion_matrix(cm, classes=['Non','Transfused'], normalize=False)
  plt.savefig("LR_confusion_matrix.svg")
  plt.show()
  print(cm)
```

#### 3.1 Random Forest

```
[]: r forest_model = RandomForestClassifier(n_estimators=10)
     r_forest_model.fit(X_train, y_train)
     # save model
     with open('r_forest_model.pickle', 'wb') as picklefile:
         pickle.dump(r_forest_model,picklefile)
     print ("Random Forest Scoring on test set")
     Y_pred = r_forest_model.predict(X_test)
     cr = classification_report(y_test, Y_pred)
     print (cr)
[]: feats=r[4]
     feature_names = [feats[i] for i in r_forest_model.feature_importances_]
     feature_importances = pd.DataFrame(r_forest_model.feature_importances_,
                                        index = feature_names,
                                     columns=['importance']).

→sort_values('importance', ascending=False)
[]:
[]: SGDc_model = SGDClassifier(loss='modified_huber', penalty='12',\
                           alpha=1e-3, random_state=42,\
                           max iter=100, tol=None, shuffle=True)
         #loss="modified_huber", penalty="l2", max_iter=100, shuffle=True)
     SGDc model.fit(X train, y train)
     # save model
     with open('SGDc_model.pickle', 'wb') as picklefile:
         pickle.dump(SGDc_model,picklefile)
     print ("SVM Scoring on test set")
     Y_pred = SGDc_model.predict(X_test)
     cr = classification_report(y_test, Y_pred)
     print (cr)
[]: KNNc_model = KNeighborsClassifier(n_neighbors=5)
     KNNc_model.fit(X_train, y_train)
     # save model
     with open('KNNc_model.pickle', 'wb') as picklefile:
         pickle.dump(KNNc_model,picklefile)
     print ("KNN Scoring on test set")
     Y_pred = KNNc_model.predict(X_test)
     cr = classification_report(y_test, Y_pred)
```

```
print (cr)

[]: dummy_model = DummyClassifier(strategy='constant', constant=0)
dummy_model.fit(X_train, y_train)
```

## 4 plot roc curves

```
[ ]: def roc_plot(X_test, y_test):
        def get_roc(model, X_test, y_test):
            y_pred = model.predict(X_test)
            y_pred_proba = model.predict_proba(X_test)
            score = round(model.score(X_test,y_test), 2)
            fpr, tpr, _ = roc_curve(y_test.ravel(), y_pred_proba[:,1])
            roc_auc = auc(fpr, tpr)
            return fpr, tpr, roc_auc, score
        sns.set style('white')
        sns.set_context("talk")
        fig0 = plt.figure(figsize=(15,8), dpi=100);
        plt.plot([0, 1], [0, 1], lw=2, color = 'black', linestyle='--')
        fpr1, tpr1, roc_auc1,score1 = get_roc(NBmodel, X_test, y_test)
        plt.plot(fpr1, tpr1, lw=2, color = 'brown', label='Multinomial NB area=%0.
     →2f,accuracy={}'.format(score1) % roc_auc1)
        fpr2, tpr2, roc_auc2, score2 = get_roc(LRmodel, X_test, y_test)
        plt.plot(fpr2, tpr2, lw=2, color = 'darkviolet', label='Log Reg area=%0.
     →2f,accuracy={}'.format(score2) % roc_auc2)
        fpr5, tpr5, roc_auc5,score5 = get_roc(KNNc_model, X_test, y_test)
        plt.plot(fpr5, tpr5, lw=2, color = 'darkgray', label='KNN area=%0.
     →2f,accuracy={}'.format(score5) % roc_auc5)
        fpr3, tpr3, roc_auc3,score3 = get_roc(SGDc_model, X_test, y_test)
        plt.plot(fpr3, tpr3, lw=2, color = 'green', label='SVM area=%0.
     →2f,accuracy={}'.format(score3) % roc_auc3)
        fpr4, tpr4, roc_auc4,score4 = get_roc(r_forest_model, X_test, y_test)
        plt.plot(fpr4, tpr4, lw=2, color = 'royalblue', label='Random Forest area=%0.
     →2f,accuracy={}'.format(score4)% roc_auc4)
        fpr6, tpr6, roc_auc6,score6 = get_roc(dummy_model, X_test, y_test)
        plt.plot(fpr6, tpr6, lw=2, color = 'black', label='Chance area=%0.
```

```
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
#plt.title('ROC {}'.format(model), fontsize=12)
#plt.title('ROC All Models', fontsize=12)
plt.legend(loc="lower right")
plt.savefig(path + "roc_plot.svg")
plt.show()
```

```
[]: roc_plot(X_test, y_test1, NBmodel, LRmodel, KNNc_model, SGDc_model, __ 

→r_forest_model, dummy_model)
```

## 5 Top 1000+ features (coefs)

• get coefs from the logistic regression model

```
[]: def get_most_important_features(vectorizer, model, n=5):
         index_to_word = r[1] \#\{v:k \text{ for } k,v \text{ in } r[1]\}
         # loop for each class
         classes ={}
         for class index in range(model.coef .shape[0]):
             word_importances = [(el, index_to_word[i]) for i,el in enumerate(model.
     sorted_coeff = sorted(word_importances, key = lambda x : x[0],__
      →reverse=True)
             tops = sorted(sorted_coeff[:n], key = lambda x : x[0])
             bottom = sorted_coeff[-n:]
             classes[class_index] = {
                 'tops':tops,
                 'bottom':bottom
             }
         return classes
     importance = get_most_important_features(r[0], LRmodel, 5000)
```

```
[]: def plot_important_words(top_scores, top_words, bottom_scores, bottom_words,_u
      →name):
         y_pos = np.arange(len(top_words))
         top_pairs = [(a,b) for a,b in zip(top_words, top_scores)]
         top_pairs = sorted(top_pairs, key=lambda x: x[1])
         bottom_pairs = [(a,b) for a,b in zip(bottom_words, bottom_scores)]
         bottom_pairs = sorted(bottom_pairs, key=lambda x: x[1], reverse=True)
         top_words = [a[0] for a in top_pairs]
         top_scores = [a[1] for a in top_pairs]
         bottom_words = [a[0] for a in bottom_pairs]
         bottom_scores = [a[1] for a in bottom_pairs]
         fig = plt.figure(figsize=(10, 20))
         plt.subplot(121)
         plt.barh(y_pos,bottom_scores, alpha=0.5)
         plt.title('Non-Transfused', fontsize=20)
         plt.yticks(y_pos, bottom_words, fontsize=14)
         plt.suptitle('Key words', fontsize=16)
         plt.xlabel('Importance', fontsize=20)
         plt.subplot(122)
         plt.barh(y_pos,top_scores, alpha=0.5)
         plt.title('Transfused', fontsize=20)
         plt.yticks(y_pos, top_words, fontsize=14)
         plt.suptitle(name, fontsize=16)
         plt.xlabel('Importance', fontsize=20)
         plt.subplots adjust(wspace=0.8)
         plt.savefig(path + path1 + "top_bottom_plot.svg")
         plt.show()
     top_scores_p = [a[0] for a in importance[0]['tops']][4955:-1]
     top_words_p = [a[1] for a in importance[0]['tops']][4955:-1]
     bottom_scores_p = [a[0] for a in importance[0]['bottom']][4955:-1]
     bottom_words_p = [a[1] for a in importance[0]['bottom']][4955:-1]
     plot_important_words(top_scores_p, top_words_p, bottom_scores_p,_u
      →bottom_words_p, "Most important words for relevance")
[]: bottom_coef = pd.
     →DataFrame(columns=['vocab', 'coef'])#, data=[top_words, top_scores])
     bottom_coef('vocab') = [a[1] for a in importance[0]['bottom']]
     bottom_coef['coef'] = [a[0] for a in importance[0]['bottom']]
```

```
bottom_coef.sort_values('coef',ascending=True).head(200)
[]: top_scores = [a[0] for a in importance[0]['tops']]
     top_words = [a[1] for a in importance[0]['tops']]
     top_coef = pd.DataFrame(columns=['vocab','coef'])#, data=[top_words, top_scores])
     top_coef['vocab'] = top_words
     top_coef['coef'] = top_scores
[]: print(top_coef.shape)
     top_coef.sort_values('coef').tail(200)
[]: top_coef = top_coef.sort_values(by='coef',axis=0,ascending=False)
     top_coef.to_csv(path + path1 + 'top_logit_coef_5000.csv')
     print ('create matrix for clustering')
     top_idx=[r[1].index(k) for k in top_coef['vocab'].values]
     r0= r[0].sorted_indices()
     tmat = r0.T[top idx]
     print ('done making matrix')
     #below is input for 'Remove transfusion terms, Collapse dupes into largest⊔
     \rightarrow n-gram. ipynb'
     out=[tmat,top_coef]
     with open('logits_top_5000_matrix.pickle','wb') as f:
         pickle.dump(out,f)
```

#### 5.1 TOP 5000 features according to log probability

• for the naive Bayes model

```
t=time.strftime("%Y%m%d%H%m",time.localtime())

prob = pd.DataFrame(NBmodel.feature_log_prob_)
prob=prob.transpose()
prob.columns=NBmodel.classes_
prob['vocab']=pd.Series(r[1])
prob['ratio']=prob['transfusion']/prob['control']
prob= prob.drop(['transfusion', 'control'], axis=1)

top_all = prob.sort_values(by='ratio')
top = prob.sort_values(by='ratio').head(5000)
print(top_all.shape)
```

```
top_all.head()
top1k = prob.sort_values(by='ratio').head(1000)
```

```
[]: # save terms and ratios and model

top_all.to_pickle('NB_terms_ratio_all.pkl')

with open( 'NB_model.pickle','wb') as f:
    pickle.dump(NBmodel,f)

top.to_csv('top_5000_feat_'+t+'.csv', columns=['vocab','ratio'], index=False)
top.to_pickle('top_5000_feat.pkl')
```

```
[]: print (prob.sort_values(by='ratio').head(500))
```

# 6 create matrix for modeling

• saves results into a sparse matrix for unsupervised models (LDA, etc)

```
[]: # top 5k
  top_idx=[r[1].index(k) for k in top['vocab'].values]
  r0= r[0].sorted_indices()
  tmat = r0.T[top_idx]
  tmat.size
```

```
[]: #below is input for 'Remove transfusion terms, Collapse dupes into largest

→n-gram.ipynb'

out=[tmat,top]

with open('NB_5000_matrix.pickle','wb') as f:

pickle.dump(out,f)
```