Here we look at Medical Transcriptions dataset from Kaggle https://www.kaggle.com/tboyle10/medicaltranscriptions

This data was scraped from mtsamples.com

Inspiration Can you correctly classify the medical specialties based on the transcription text?

Let us import all the necessary libraries

```
import spacy
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import string
import re
from sklearn.feature_extraction.text import TfidfVectorizer
from sklearn.decomposition import PCA
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import train_test_split

from sklearn.metrics import confusion_matrix
from sklearn.metrics import classification_report
from sklearn.manifold import TSNE

from nltk.tokenize import word_tokenize
from nltk.tokenize import sent_tokenize
from nltk.stem import WordNetLemmatizer

from imblearn.over_sampling import SMOTE
```

A method to get unique words(vocabulary) and sentence count in a list of text

```
def get_sentence_word_count(text_list):
    sent_count = 0
    word_count = 0
    vocab = {}
    for text in text_list:
        sentences=sent_tokenize(str(text).lower())
        sent_count = sent_count + len(sentences)
        for sentence in sentences:
            words=word_tokenize(sentence)
            for word in words:
                if(word in vocab.keys()):
                    vocab[word] = vocab[word] +1
                else:
                    vocab[word] =1
    word_count = len(vocab.keys())
    return sent_count,word_count
```

Lets do some exploratory analysis of data

```
clinical_text_df = pd.read_csv('mtsamples.csv')

print(clinical_text_df.columns)
clinical_text_df.head(5)
```

```
Index(['Unnamed: 0', 'description', 'medical_specialty', 'sample_name',
       'transcription', 'keywords'],
      dtype='object')
```

	Unnamed: 0	description	medical_specialty	sample_name	transcription	keywords
0	0	A 23-year-old white female presents with comp...	Allergy / Immunology	Allergic Rhinitis	SUBJECTIVE:, This 23-year-old white female pr...	allergy / immunology, allergic rhinitis, aller...
1	1	Consult for laparoscopic gastric bypass.	Bariatrics	Laparoscopic Gastric Bypass Consult - 2	PAST MEDICAL HISTORY:, He has difficulty climb...	bariatrics, laparoscopic gastric bypass, weigh...
2	2	Consult for laparoscopic gastric bypass.	Bariatrics	Laparoscopic Gastric Bypass Consult - 1	HISTORY OF PRESENT ILLNESS: , I have seen ABC ...	bariatrics, laparoscopic gastric bypass, heart...
3	3	2-D M-Mode. Doppler.	Cardiovascular / Pulmonary	2-D Echocardiogram - 1	2-D M-MODE: , ,1. Left atrial enlargement wit...	cardiovascular / pulmonary, 2-d m-mode, dopple...
4	4	2-D Echocardiogram	Cardiovascular / Pulmonary	2-D Echocardiogram - 2	1. The left ventricular cavity size and wall ...	cardiovascular / pulmonary, 2-d, doppler, echo...

```
clinical_text_df = clinical_text_df[clinical_text_df['transcription'].notna()]
sent_count,word_count= get_sentence_word_count(clinical_text_df['transcription'].tolist())
print("Number of sentences in transcriptions column: "+ str(sent_count))
print("Number of unique words in transcriptions column: "+str(word_count))
```

```
data_categories  = clinical_text_df.groupby(clinical_text_df['medical_specialty'])
i = 1
print('===========Original Categories =======================')
for catName,dataCategory in data_categories:
    print('Cat:'+str(i)+' '+catName + ' : '+ str(len(dataCategory)) )
    i = i+1
print('==================================')
```

```
Number of sentences in transcriptions column: 140214
Number of unique words in transcriptions column: 35822
===========Original Categories =======================
Cat:1  Allergy / Immunology : 7
Cat:2  Autopsy : 8
Cat:3  Bariatrics : 18
Cat:4  Cardiovascular / Pulmonary : 371
Cat:5  Chiropractic : 14
Cat:6  Consult - History and Phy. : 516
Cat:7  Cosmetic / Plastic Surgery : 27
Cat:8  Dentistry : 27
Cat:9  Dermatology : 29
Cat:10  Diets and Nutritions : 10
Cat:11  Discharge Summary : 108
Cat:12  ENT - Otolaryngology : 96
Cat:13  Emergency Room Reports : 75
Cat:14  Endocrinology : 19
Cat:15  Gastroenterology : 224
Cat:16  General Medicine : 259
Cat:17  Hematology - Oncology : 90
Cat:18  Hospice - Palliative Care : 6
Cat:19  IME-QME-Work Comp etc. : 16
Cat:20  Lab Medicine - Pathology : 8
Cat:21  Letters : 23
Cat:22  Nephrology : 81
Cat:23  Neurology : 223
Cat:24  Neurosurgery : 94
Cat:25  Obstetrics / Gynecology : 155
Cat:26  Office Notes : 50
Cat:27  Ophthalmology : 83
Cat:28  Orthopedic : 355
Cat:29  Pain Management : 61
Cat:30  Pediatrics - Neonatal : 70
```

```
Cat:31  Physical Medicine - Rehab : 21
Cat:32  Podiatry : 47
Cat:33  Psychiatry / Psychology : 53
Cat:34  Radiology : 273
Cat:35  Rheumatology : 10
Cat:36  SOAP / Chart / Progress Notes : 166
Cat:37  Sleep Medicine : 20
Cat:38  Speech - Language : 9
Cat:39  Surgery : 1088
Cat:40  Urology : 156
==================================
```

```
filtered_data_categories = data_categories.filter(lambda x:x.shape[0] > 50)
final_data_categories = filtered_data_categories.groupby(filtered_data_categories['medical_specialty'])
i=1
print('============Reduced Categories ======================')
for catName,dataCategory in final_data_categories:
    print('Cat:'+str(i)+' '+catName + ' : '+ str(len(dataCategory)) )
    i = i+1

print('============ Reduced Categories ======================')
```

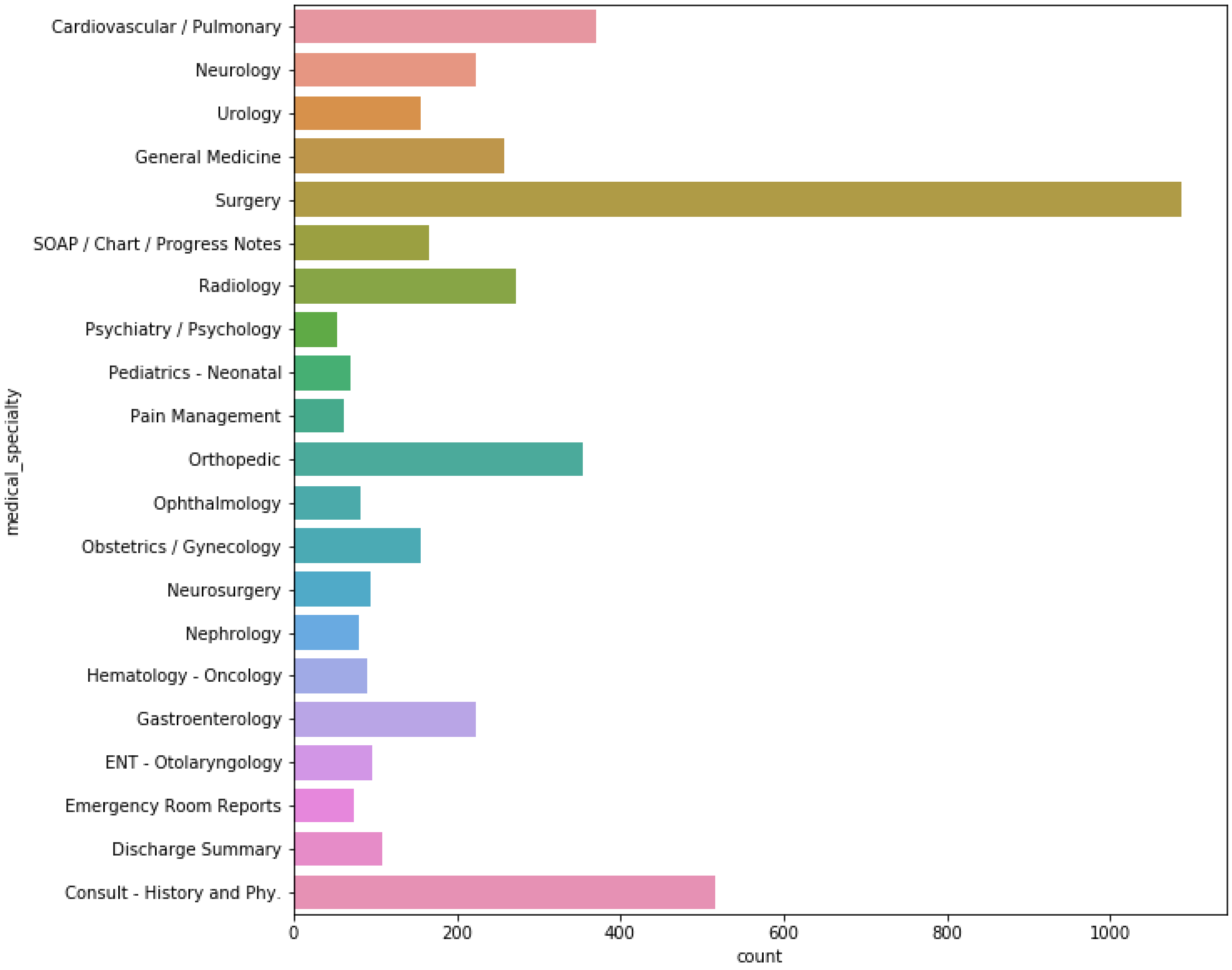
```
============Reduced Categories ======================
Cat:1  Cardiovascular / Pulmonary : 371
Cat:2  Consult - History and Phy. : 516
Cat:3  Discharge Summary : 108
Cat:4  ENT - Otolaryngology : 96
Cat:5  Emergency Room Reports : 75
Cat:6  Gastroenterology : 224
Cat:7  General Medicine : 259
Cat:8  Hematology - Oncology : 90
Cat:9  Nephrology : 81
Cat:10  Neurology : 223
Cat:11  Neurosurgery : 94
Cat:12  Obstetrics / Gynecology : 155
Cat:13  Ophthalmology : 83
Cat:14  Orthopedic : 355
Cat:15  Pain Management : 61
```

```
Cat:16  Pediatrics - Neonatal : 70
Cat:17  Psychiatry / Psychology : 53
Cat:18  Radiology : 273
Cat:19  SOAP / Chart / Progress Notes : 166
Cat:20  Surgery : 1088
Cat:21  Urology : 156
============ Reduced Categories ======================
```

```
print('============Reduced Categories Transcription example======================')
i=1
for catName,dataCategory in final_data_categories:
    print('Cat:'+str(i)+' '+catName + ' : '+ str(len(dataCategory)) )
    dataList = dataCategory['transcription'].tolist()
    print('====================================================')
    print('Sample Transcription:'+str(dataList[10]))
    print('====================================================')
    i = i+1

print('============ Reduced Categories Transcription example======================')
```

```
============Reduced Categories Transcription example======================
Cat:1  Cardiovascular / Pulmonary : 371
====================================================
Sample Transcription:PREOPERATIVE DIAGNOSIS: , Need for intravenous access.,POSTOPERATIVE DIAGNOSIS: , Need for int
====================================================
Cat:2  Consult - History and Phy. : 516
====================================================
Sample Transcription:CHIEF COMPLAINT:,  Well-child check.,HISTORY OF PRESENT ILLNESS:,  This is a 12-month-old fema
====================================================
Cat:3  Discharge Summary : 108
====================================================
Sample Transcription:ADMITTING DIAGNOSES,1. Prematurity.,2. Appropriate for gestational age.,3. Maternal group B st
====================================================
Cat:4  ENT - Otolaryngology : 96
====================================================
Sample Transcription:POSTOPERATIVE DIAGNOSIS:,  Chronic adenotonsillitis.,PROCEDURE PERFORMED: , Tonsillectomy and
====================================================
Cat:5  Emergency Room Reports : 75
====================================================
Sample Transcription:CHIEF COMPLAINT: , Nausea and feeling faint.,HPI:  ,The patient is a 74-year-old white female
====================================================
Cat:6  Gastroenterology : 224
====================================================
Sample Transcription:PREOPERATIVE DIAGNOSIS: , Gastrostomy (gastrocutaneous fistula).,POSTOPERATIVE DIAGNOSIS: , Ga
====================================================
Cat:7  General Medicine : 259
====================================================
Sample Transcription:REASON FOR ADMISSION: , Sepsis.,HISTORY OF PRESENT ILLNESS:  ,The patient is a pleasant but de
====================================================
Cat:8  Hematology - Oncology : 90
====================================================
Sample Transcription:HISTORY OF PRESENT ILLNESS: , This is a 19-year-old known male with sickle cell anemia.  He co
====================================================
Cat:9  Nephrology : 81
====================================================
Sample Transcription:REASON FOR CONSULTATION:,  Renal failure evaluation for possible dialysis therapy.,HISTORY OF
====================================================
Cat:10  Neurology : 223
====================================================
Sample Transcription:PREOPERATIVE DIAGNOSIS:,  Headaches, question of temporal arteritis.,POSTOPERATIVE DIAGNOSIS:,
====================================================
Cat:11  Neurosurgery : 94
====================================================
Sample Transcription:PREOPERATIVE DIAGNOSIS:,  Squamous cell carcinoma of right temporal bone/middle ear space.,POS
====================================================
Cat:12  Obstetrics / Gynecology : 155
====================================================
Sample Transcription:FINDINGS:,By dates the patient is 8 weeks, 2 days.,There is a gestational sac within the endom
====================================================
Cat:13  Ophthalmology : 83
====================================================
Sample Transcription:PROCEDURE IN DETAIL:,  After appropriate operative consent was obtained, the patient was broug
====================================================
Cat:14  Orthopedic : 355
====================================================
Sample Transcription:PROCEDURES: , Total knee replacement.,PROCEDURE DESCRIPTION:,  The patient was bought to the o
====================================================
plt.figure(figsize=(10,10))
sns.countplot(y='medical_specialty', data = filtered_data_categories )
plt.show()
```



We are interested only in the 'transcription' and 'medical_specialty' columns in the dataset

```
data = filtered_data_categories[['transcription', 'medical_specialty']]
data = data.drop(data[data['transcription'].isna()].index)
data.shape
```

```
(4597, 2)
```

```
print('Sample Transcription 1:'+data.iloc[5]['transcription']+'\n')
print('Sample Transcription 2:'+data.iloc[125]['transcription']+'\n')
print('Sample Transcription 3:'+data.iloc[1000]['transcription'])
```

```
Sample Transcription 1:CC:, Confusion and slurred speech.,HX , (primarily obtained from boyfriend): This 31 y/o RHF

Sample Transcription 2:ADMITTING DIAGNOSES:,1. Hematuria.,2. Benign prostatic hyperplasia.,3. Osteoarthritis.,DISCHAR

Sample Transcription 3:PREOPERATIVE DIAGNOSES: , Phimosis and adhesions.,POSTOPERATIVE DIAGNOSES:  ,Phimosis and adhe
```

Lets define soome methods for cleaning the data

```
def clean_text(text ):
    text = text.translate(str.maketrans('', '', string.punctuation))
    text1 = ''.join([w for w in text if not w.isdigit()])
    REPLACE_BY_SPACE_RE = re.compile('[/(){}\[\]\|@,;]')
    #BAD_SYMBOLS_RE = re.compile('[^0-9a-z #+_]')

    text2 = text1.lower()
    text2 = REPLACE_BY_SPACE_RE.sub('', text2) # replace REPLACE_BY_SPACE_RE symbols by space in text
    #text2 = BAD_SYMBOLS_RE.sub('', text2)
    return text2

def lemmatize_text(text):
    wordlist=[]
    lemmatizer = WordNetLemmatizer()
    sentences=sent_tokenize(text)

    intial_sentences= sentences[0:1]
    final_sentences = sentences[len(sentences)-2: len(sentences)-1]

    for sentence in intial_sentences:
        words=word_tokenize(sentence)
        for word in words:
            wordlist.append(lemmatizer.lemmatize(word))
    for sentence in final_sentences:
        words=word_tokenize(sentence)
        for word in words:
            wordlist.append(lemmatizer.lemmatize(word))
    return ' '.join(wordlist)
```

Lets clean the data

```
data['transcription'] = data['transcription'].apply(lemmatize_text)
data['transcription'] = data['transcription'].apply(clean_text)
```

```
print('Sample Transcription 1:'+data.iloc[5]['transcription']+'\n')
print('Sample Transcription 2:'+data.iloc[125]['transcription']+'\n')
print('Sample Transcription 3:'+data.iloc[1000]['transcription'])
```

```
Sample Transcription 1:cc confusion and slurred speech hx primarily obtained from boyfriend this yo rhf experienced a

Sample Transcription 2:admitting diagnosis hematuria he is to follow up with dr g of urology in the next week by phon

Sample Transcription 3:preoperative diagnosis phimosis and adhesion postoperative diagnosis phimosis and adhesion pro
```

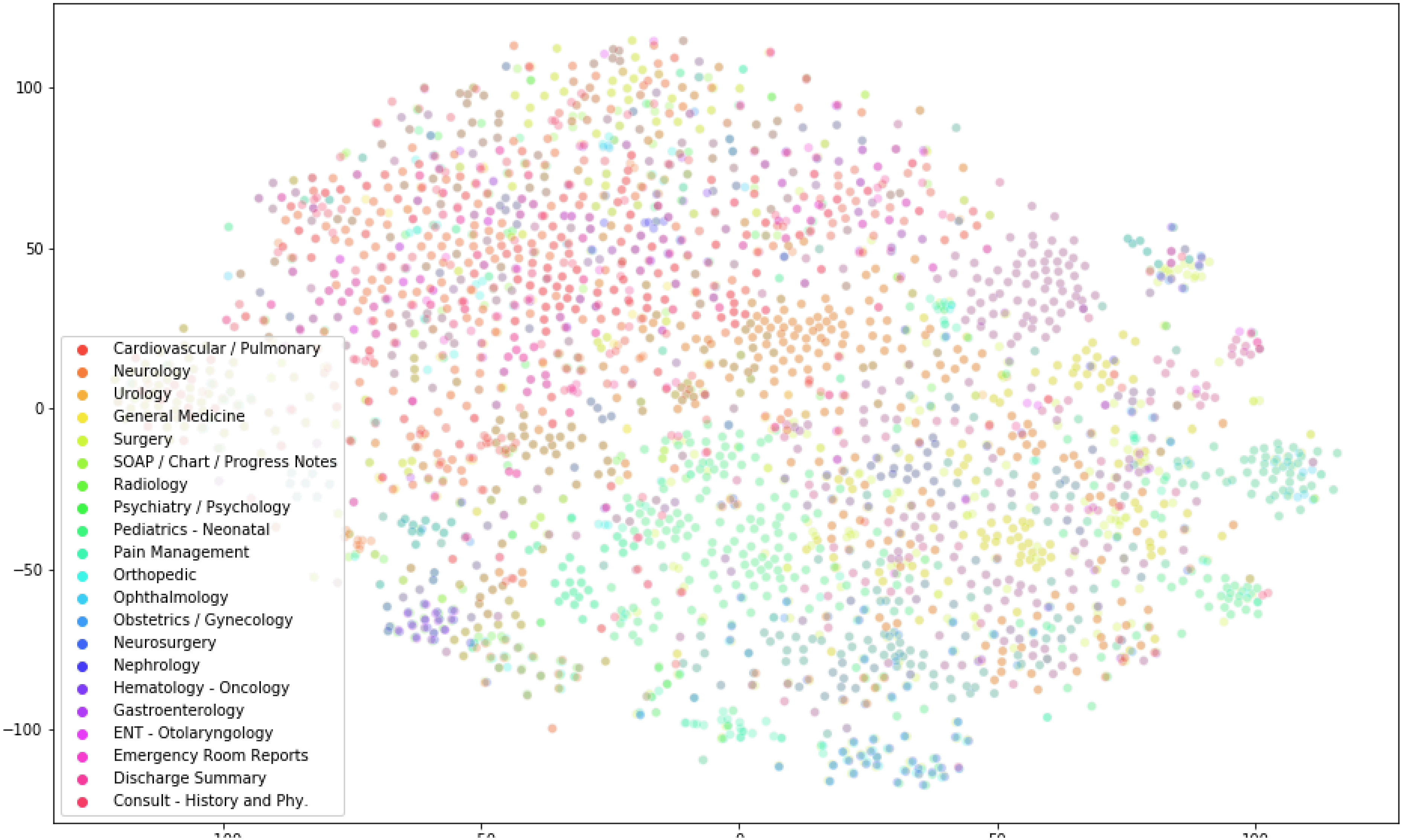
Lets us peform feature extraction using TfidfVectorizer to generate tf-idf features. For more on tf-idf check here: https://en.wikipedia.org/wiki/Tf%E2%80%93idf In information retrieval, tf–idf or TFIDF, short for term frequency–inverse document frequency, is a numerical statistic that is intended to reflect how important a word is to a document in a collection or corpus.[1] It is often used as a weighting factor in searches of information retrieval, text mining, and user modeling. The tf–idf value increases proportionally to the number of times a word appears in the document and is offset by the number of documents in the corpus that contain the word, which helps to adjust for the fact that some words appear more frequently in general.

```
vectorizer = TfidfVectorizer(analyzer='word', stop_words='english',ngram_range=(1,3), max_df=0.75, use_idf=True, smooth_
tfIdfMat  = vectorizer.fit_transform(data['transcription'].tolist() )
feature_names = sorted(vectorizer.get_feature_names())
print(feature_names)
```

```
['abc', 'abcd', 'abdomen', 'abdomen pelvis', 'abdominal', 'abdominal pain', 'abnormal', 'abnormality', 'abscess', 'ac
```

Lets visualize the tf-idf features using t-sne plot. For more on t-sne check here: https://en.wikipedia.org/wiki/T-distributed_stochastic_neighbor_embedding T-distributed Stochastic Neighbor Embedding (t-SNE) is a machine learning algorithm for visualization developed by Laurens van der Maaten and Geoffrey Hinton.[1] It is a nonlinear dimensionality reduction technique well-suited for embedding high-dimensional data for visualization in a low-dimensional space of two or three dimensions. Specifically, it models each high-dimensional object by a two- or three-dimensional point in such a way that similar objects are modeled by nearby points and dissimilar objects are modeled by distant points with high probability.

```
import gc
gc.collect()
tfIdfMatrix = tfIdfMat.todense()
labels = data['medical_specialty'].tolist()
tsne_results = TSNE(n_components=2,init='random',random_state=0, perplexity=40).fit_transform(tfIdfMatrix)
plt.figure(figsize=(16,10))
palette = sns.hls_palette(21, l=.6, s=.9)
sns.scatterplot(
    x=tsne_results[:,0], y=tsne_results[:,1],
    hue=labels,
    palette= palette,
    legend="full",
    alpha=0.3
)
plt.show()
```



Let us do PCA to reduce dimensionality of features. https://en.wikipedia.org/wiki/Principal_component_analysis PCA is defined as an orthogonal linear transformation that transforms the data to a new coordinate system such that the greatest variance by some scalar projection of the data comes to lie on the first coordinate (called the first principal component), the second greatest variance on the second coordinate, and so on

```
gc.collect()
pca = PCA(n_components=0.95)
tfIdfMat_reduced = pca.fit_transform(tfIdfMat.toarray())
labels = data['medical_specialty'].tolist()
category_list = data.medical_specialty.unique()
X_train, X_test, y_train, y_test = train_test_split(tfIdfMat_reduced, labels, stratify=labels,random_state=1)
```

```
print('Train_Set_Size:'+str(X_train.shape))
print('Test_Set_Size:'+str(X_test.shape))
```

```
Train_Set_Size:(3447, 614)
Test_Set_Size:(1150, 614)
```

Let us use Logisitic Regression to learn on training data and predict on test data https://scikit-learn.org/stable/modules/generated/sklearn.linear_model.LogisticRegression.html

```
clf = LogisticRegression(penalty= 'elasticnet', solver= 'saga', l1_ratio=0.5, random_state=1).fit(X_train, y_train)
y_test_pred= clf.predict(X_test)
```

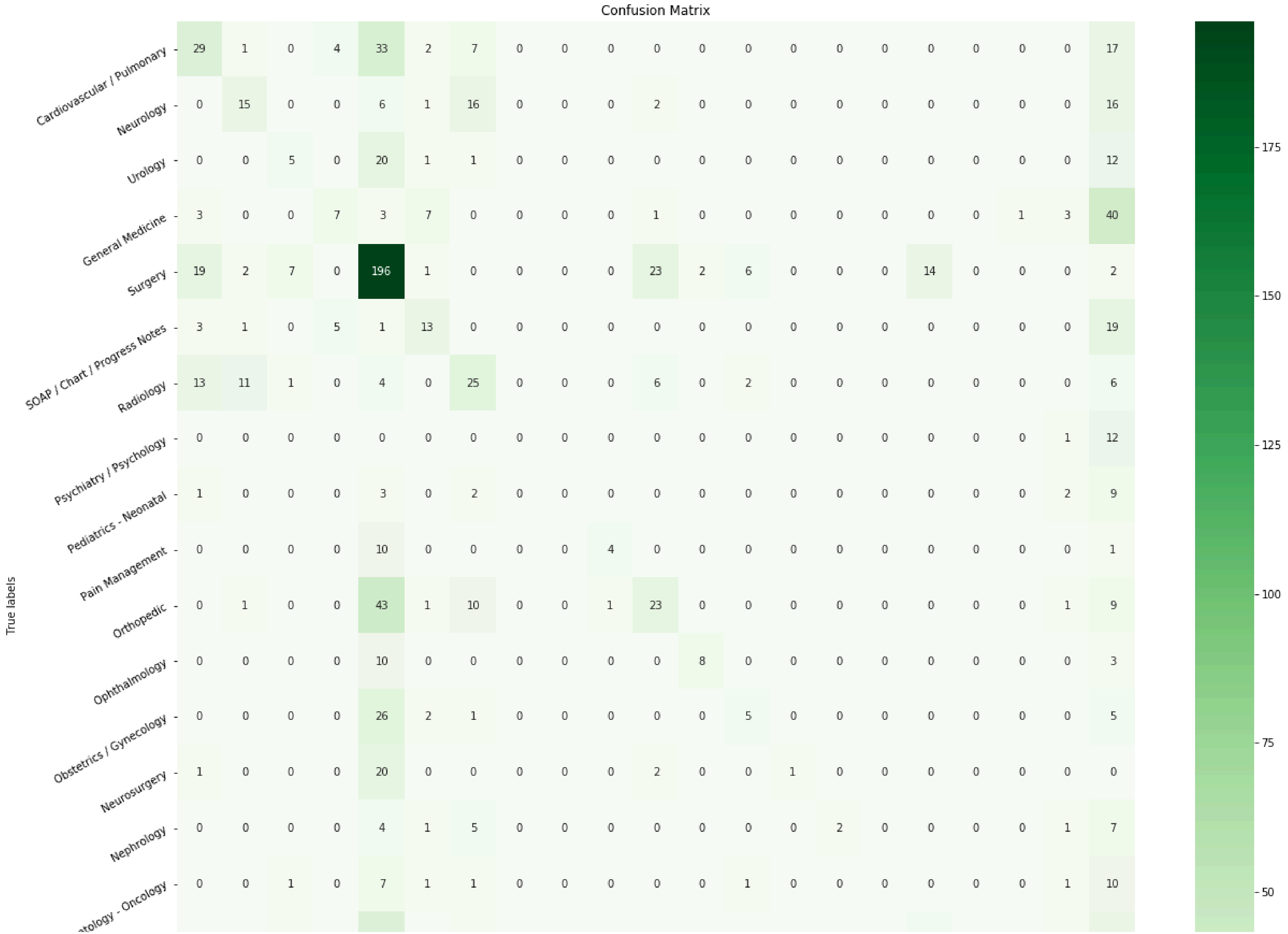
Let us visualize the confusion matrix and the classification results

```
labels = category_list
cm = confusion_matrix(y_test, y_test_pred, labels)
```

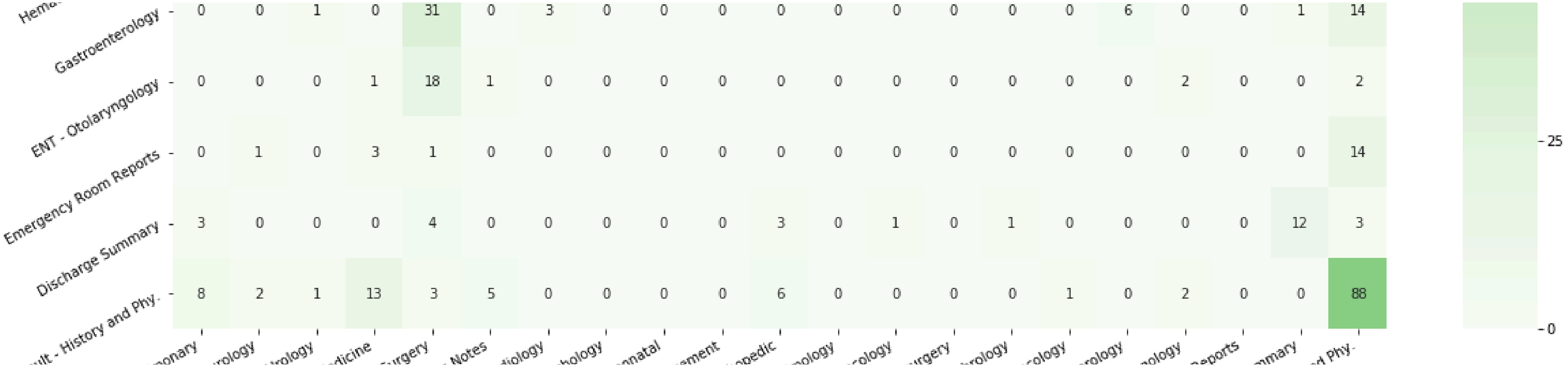
```
C:\Users\Rithesh\anaconda3\lib\site-packages\sklearn\utils\validation.py:71: FutureWarning: Pass labels=[' Cardiovasc
 ' Surgery' ' SOAP / Chart / Progress Notes' ' Radiology'
 ' Psychiatry / Psychology' ' Pediatrics - Neonatal' ' Pain Management'
 ' Orthopedic' ' Ophthalmology' ' Obstetrics / Gynecology' ' Neurosurgery'
 ' Nephrology' ' Hematology - Oncology' ' Gastroenterology'
 ' ENT - Otolaryngology' ' Emergency Room Reports' ' Discharge Summary'
 ' Consult - History and Phy.'] as keyword args. From version 0.25 passing these as positional arguments will result
  FutureWarning)
```

```
fig = plt.figure(figsize=(20,20))
ax= fig.add_subplot(1,1,1)
sns.heatmap(cm, annot=True, cmap="Greens",ax = ax,fmt='g'); #annot=True to annotate cells

# labels, title and ticks
ax.set_xlabel('Predicted labels');ax.set_ylabel('True labels');
ax.set_title('Confusion Matrix');
ax.xaxis.set_ticklabels(labels); ax.yaxis.set_ticklabels(labels);
plt.setp(ax.get_yticklabels(), rotation=30, horizontalalignment='right')
plt.setp(ax.get_xticklabels(), rotation=30, horizontalalignment='right')
plt.show()
```



Cardiovascular / Pulmonary	29	1	0	4	33	2	7	0	0	0	0	0	0	0	0	0	0	0	0	0	17
Neurology	0	15	0	0	6	1	16	0	0	0	2	0	0	0	0	0	0	0	0	0	16
Urology	0	0	5	0	20	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	12
General Medicine	3	0	0	7	3	7	0	0	0	0	1	0	0	0	0	0	0	0	1	3	40
Surgery	19	2	7	0	196	1	0	0	0	0	23	2	6	0	0	0	14	0	0	0	2
SOAP / Chart / Progress Notes	3	1	0	5	1	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	19
Radiology	13	11	1	0	4	0	25	0	0	0	6	0	2	0	0	0	0	0	0	0	6
Psychiatry / Psychology	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	12
Pediatrics - Neonatal	1	0	0	0	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	2	9
Pain Management	0	0	0	0	10	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	1
Orthopedic	0	1	0	0	43	1	10	0	0	1	23	0	0	0	0	0	0	0	0	1	9
Ophthalmology	0	0	0	0	10	0	0	0	0	0	0	8	0	0	0	0	0	0	0	0	3
Obstetrics / Gynecology	0	0	0	0	26	2	1	0	0	0	0	0	5	0	0	0	0	0	0	0	5
Neurosurgery	1	0	0	0	20	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0
Nephrology	0	0	0	0	4	1	5	0	0	0	0	0	0	0	2	0	0	0	0	1	7
atology - Oncology	0	0	1	0	7	1	1	0	0	0	0	0	1	0	0	0	0	0	0	1	10



```
print(classification_report(y_test,y_test_pred,labels=category_list))
```

```
                               precision    recall  f1-score   support

    Cardiovascular / Pulmonary       0.40      0.39      0.40        93
                     Neurology       0.40      0.41      0.41        56
                       Urology       0.22      0.13      0.16        39
              General Medicine       0.20      0.15      0.17        65
                       Surgery       0.47      0.65      0.55       272
 SOAP / Chart / Progress Notes       0.32      0.29      0.30        42
                     Radiology       0.35      0.32      0.34        68
         Psychiatry / Psychology       0.00      0.00      0.00        13
          Pediatrics - Neonatal       0.00      0.00      0.00        17
               Pain Management       0.46      0.40      0.43        15
                    Orthopedic       0.40      0.36      0.38        89
                 Ophthalmology       0.47      0.33      0.39        21
                  Office Notes       0.00      0.00      0.00        12
       Obstetrics / Gynecology       0.39      0.31      0.34        39
                  Neurosurgery       0.00      0.00      0.00        24
                    Nephrology       0.33      0.15      0.21        20
          Hematology - Oncology       0.00      0.00      0.00        22
              Gastroenterology       0.48      0.23      0.31        56
           ENT - Otolaryngology       0.56      0.21      0.30        24
        Emergency Room Reports       0.00      0.00      0.00        19
             Discharge Summary       0.41      0.52      0.46        27
    Consult - History and Phy.       0.32      0.59      0.41       129
```

```
                   accuracy                           0.39      1162
                  macro avg       0.28      0.25      0.25      1162
               weighted avg       0.36      0.39      0.36      1162

    C:\Users\Rithesh\anaconda3\lib\site-packages\sklearn\metrics\_classification.py:1221: UndefinedMetricWarning: Precis
      _warn_prf(average, modifier, msg_start, len(result))
```

Let us apply some domain knowledge and see if we can improve the results

```
filtered_data_categories['medical_specialty'] =filtered_data_categories['medical_specialty'].apply(lambda x:str.strip(x)
mask = filtered_data_categories['medical_specialty'] == 'Surgery'
filtered_data_categories = filtered_data_categories[~mask]
final_data_categories = filtered_data_categories.groupby(filtered_data_categories['medical_specialty'])
mask = filtered_data_categories['medical_specialty'] == 'SOAP / Chart / Progress Notes'
filtered_data_categories = filtered_data_categories[~mask]
mask = filtered_data_categories['medical_specialty'] == 'Office Notes'
filtered_data_categories = filtered_data_categories[~mask]
mask = filtered_data_categories['medical_specialty'] == 'Consult - History and Phy.'
filtered_data_categories = filtered_data_categories[~mask]
mask = filtered_data_categories['medical_specialty'] == 'Emergency Room Reports'
filtered_data_categories = filtered_data_categories[~mask]
mask = filtered_data_categories['medical_specialty'] == 'Discharge Summary'
filtered_data_categories = filtered_data_categories[~mask]

'''
mask = filtered_data_categories['medical_specialty'] == 'Pediatrics - Neonatal'
filtered_data_categories = filtered_data_categories[~mask]
'''
mask = filtered_data_categories['medical_specialty'] == 'Pain Management'
filtered_data_categories = filtered_data_categories[~mask]
mask = filtered_data_categories['medical_specialty'] == 'General Medicine'
filtered_data_categories = filtered_data_categories[~mask]


mask = filtered_data_categories['medical_specialty'] == 'Neurosurgery'
filtered_data_categories.loc[mask, 'medical_specialty'] = 'Neurology'
```

```
mask = filtered_data_categories['medical_specialty'] == 'Nephrology'
filtered_data_categories.loc[mask, 'medical_specialty'] = 'Urology'



i=1
print('============Reduced Categories======================')
for catName,dataCategory in final_data_categories:
    print('Cat:'+str(i)+' '+catName + ' : '+ str(len(dataCategory)) )
    i = i+1

print('============Reduced Categories======================')



data = filtered_data_categories[['transcription', 'medical_specialty']]
data = data.drop(data[data['transcription'].isna()].index)
data.shape
```

```
============Reduced Categories======================
Cat:1 Cardiovascular / Pulmonary : 371
Cat:2 ENT - Otolaryngology : 96
Cat:3 Gastroenterology : 224
Cat:4 Hematology - Oncology : 90
Cat:5 Neurology : 317
Cat:6 Obstetrics / Gynecology : 155
Cat:7 Ophthalmology : 83
Cat:8 Orthopedic : 355
Cat:9 Pediatrics - Neonatal : 70
Cat:10 Psychiatry / Psychology : 53
Cat:11 Radiology : 273
Cat:12 Urology : 237
============Reduced Categories======================
(2324, 2)
```

Let us use sciscpacy models to detect medical entities in our text scispaCy is a Python package containing spaCy models for processing biomedical, scientific or clinical text. For more on scispacy check here:https://allenai.github.io/scispacy/

```
nlp = spacy.load("en_ner_bionlp13cg_md")


def process_Text( text):
    wordlist=[]
    doc = nlp(text)
    for ent in doc.ents:
        wordlist.append(ent.text)
    return ' '.join(wordlist)


data['transcription'] = data['transcription'].apply(process_Text)
data['transcription'] = data['transcription'].apply(lemmatize_text)
data['transcription'] = data['transcription'].apply(clean_text)
```

```
print('Sample Transcription 1:'+data.iloc[5]['transcription']+'\n')
print('Sample Transcription 2:'+data.iloc[125]['transcription']+'\n')
print('Sample Transcription 3:'+data.iloc[1000]['transcription'])
```

```
Sample Transcription 1:boyfriend bed her right facial right child bp name  cn only  motor rue pronator extremity fle

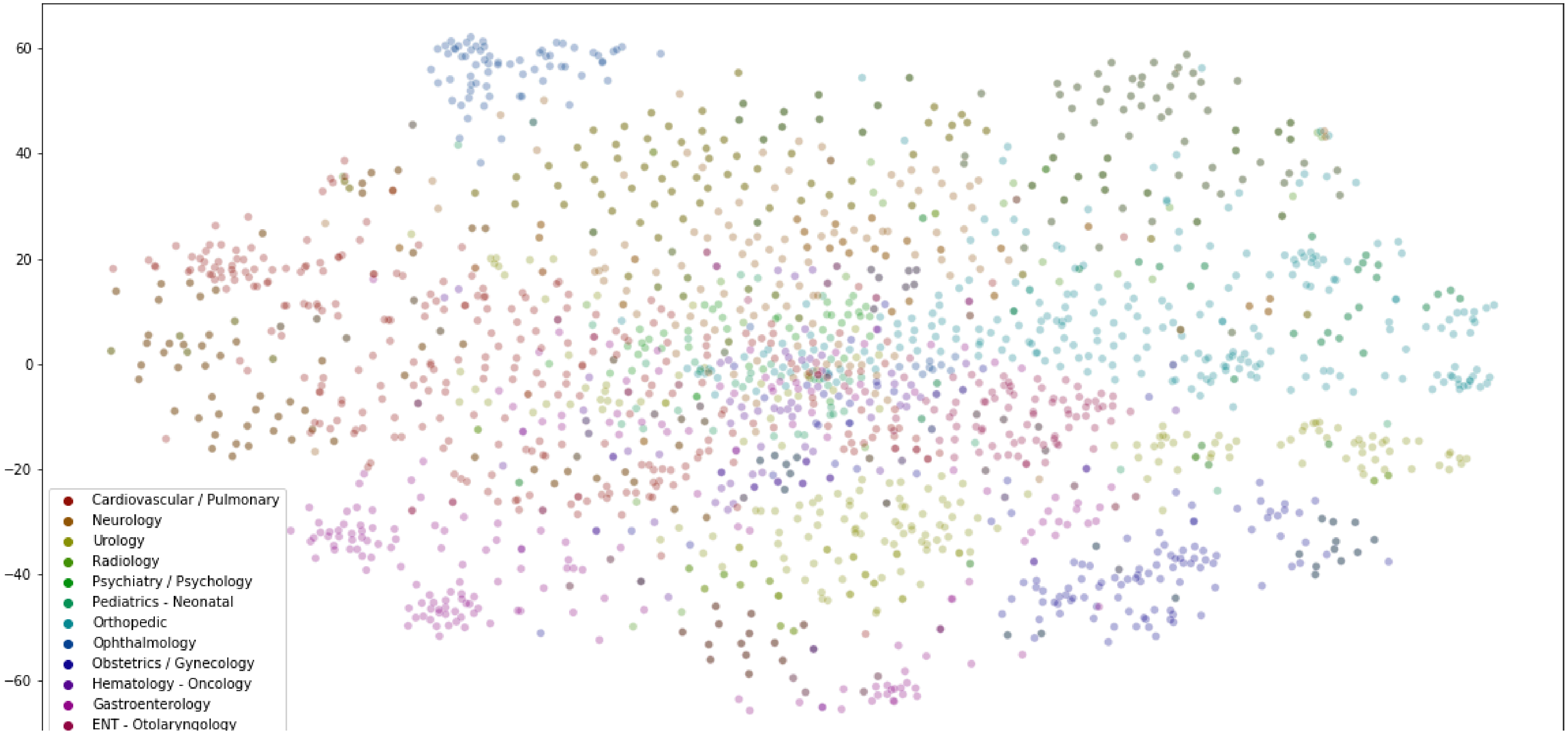
Sample Transcription 2:performed   ureteral stent right renal pelvis urine right upper pole patient right kidney pat

Sample Transcription 3:uterine bleeding uterine bleeding vaginal hysterectomy  anesthesia endotracheal endotracheal a
```

```
vectorizer = TfidfVectorizer(analyzer='word', stop_words='english',ngram_range=(1,3), max_df=0.75,min_df=5, use_idf=True
tfIdfMat  = vectorizer.fit_transform(data['transcription'].tolist() )
feature_names = sorted(vectorizer.get_feature_names())
print(feature_names)
```

```
['abc', 'abcd', 'abdomen', 'abdomen abdomen', 'abdomen bowel', 'abdomen patient', 'abdominal', 'abdominal cavity', 'a
```

```
import gc
gc.collect()
tfIdfMatrix = tfIdfMat.todense()
labels = data['medical_specialty'].tolist()
tsne_results = TSNE(n_components=2,init='random',random_state=0, perplexity=40).fit_transform(tfIdfMatrix)
plt.figure(figsize=(20,10))
palette = sns.hls_palette(12, l=.3, s=.9)
sns.scatterplot(
    x=tsne_results[:,0], y=tsne_results[:,1],
    hue=labels,
    palette= palette,
    legend="full",
    alpha=0.3
)
plt.show()
```



```
pca = PCA(n_components=0.95)
tfIdfMat_reduced = pca.fit_transform(tfIdfMat.toarray())
labels = data['medical_specialty'].tolist()
category_list = data.medical_specialty.unique()
```

Let us create train and test sets.Let us use logistic regression for developing a classification model and then visualize the results

```
X_train, X_test, y_train, y_test = train_test_split(tfIdfMat_reduced, labels, stratify=labels,random_state=1)
print('Train_Set_Size:'+str(X_train.shape))
print('Test_Set_Size:'+str(X_test.shape))
```

```
Train_Set_Size:(1743, 582)
Test_Set_Size:(581, 582)
```

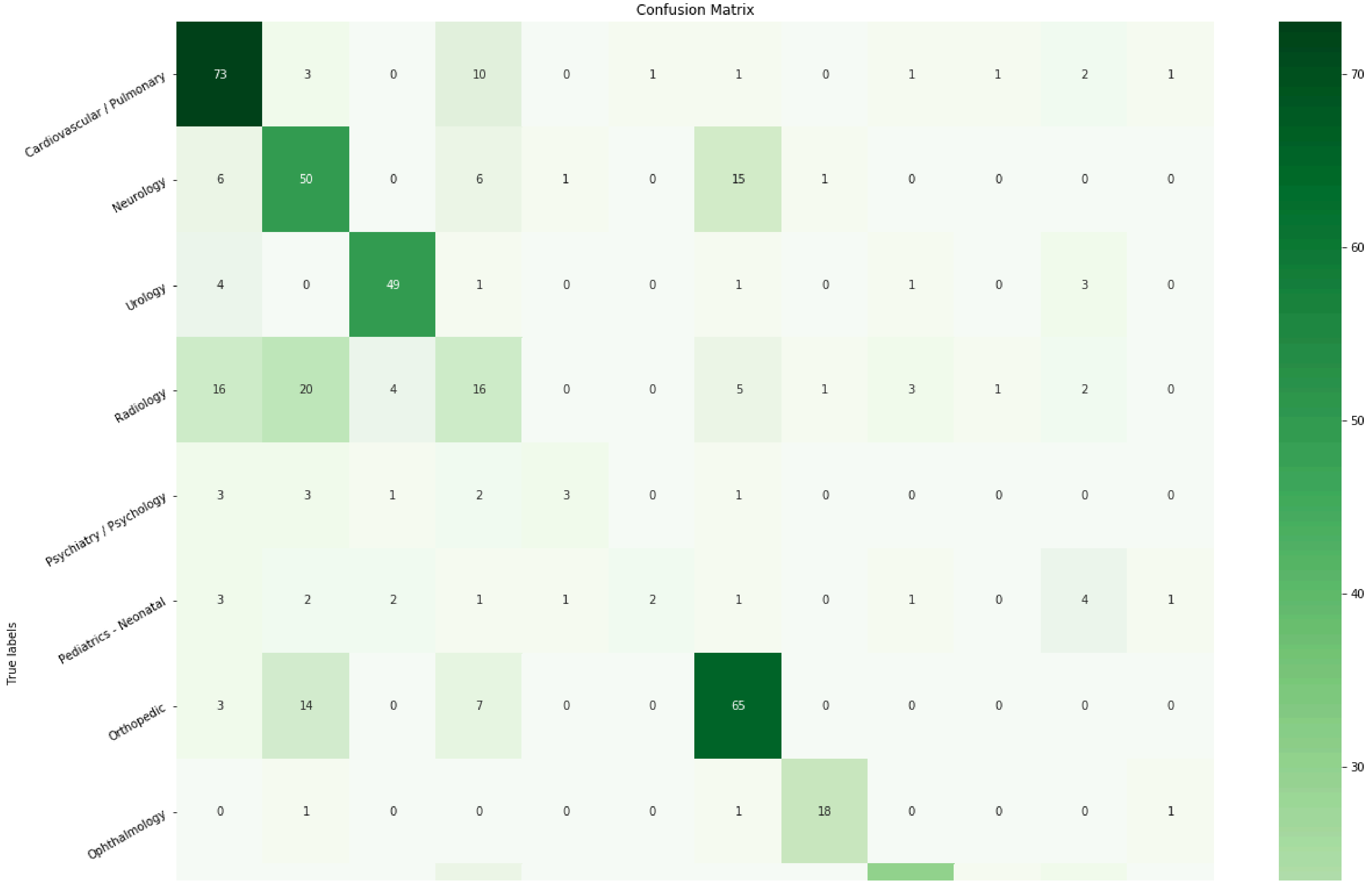
```
#clf = MLPClassifier(random_state=1, max_iter=300).fit(X_train, y_train)
clf = LogisticRegression(penalty= 'elasticnet', solver= 'saga', l1_ratio=0.5, random_state=1).fit(X_train, y_train)
y_test_pred= clf.predict(X_test)
```

```
labels = category_list
cm = confusion_matrix(y_test, y_test_pred, labels)

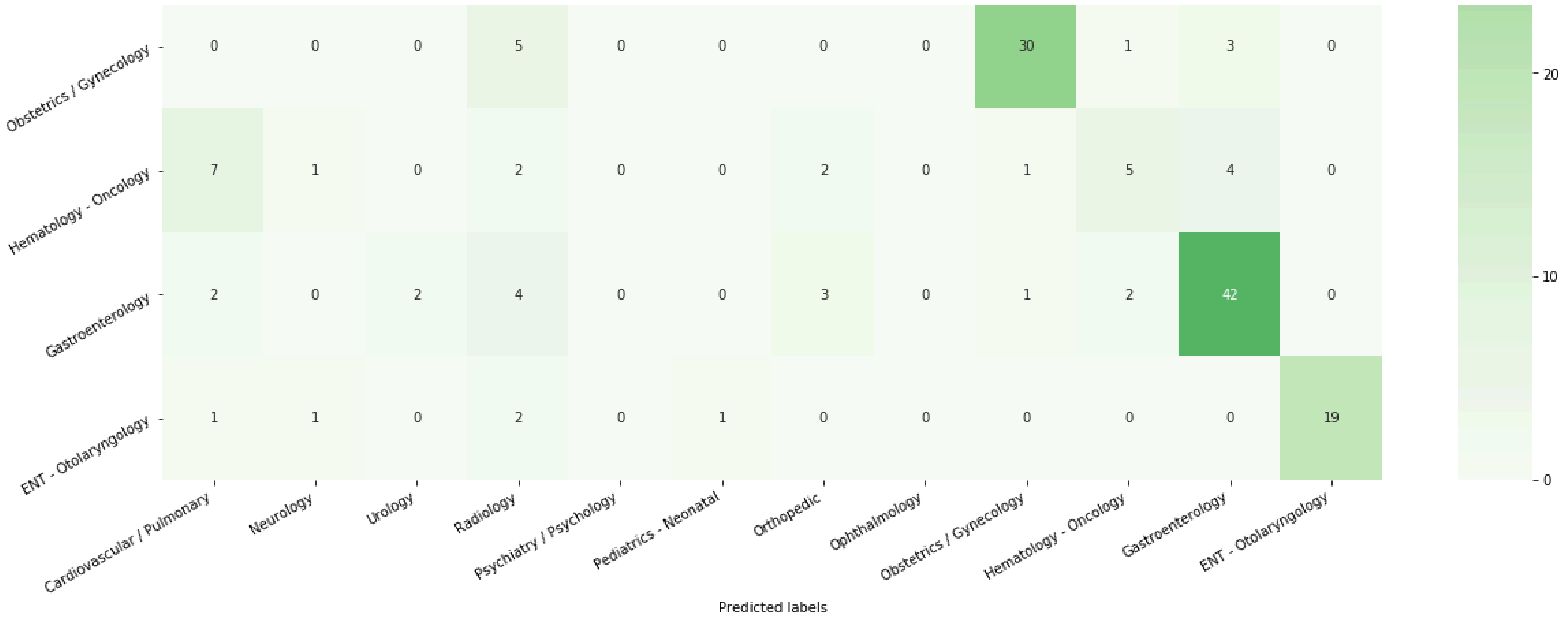
fig = plt.figure(figsize=(20,20))
ax= fig.add_subplot(1,1,1)
sns.heatmap(cm, annot=True, cmap="Greens",ax = ax,fmt='g'); #annot=True to annotate cells

# labels, title and ticks
ax.set_xlabel('Predicted labels');ax.set_ylabel('True labels');
ax.set_title('Confusion Matrix');
ax.xaxis.set_ticklabels(labels); ax.yaxis.set_ticklabels(labels);
plt.setp(ax.get_yticklabels(), rotation=30, horizontalalignment='right')
plt.setp(ax.get_xticklabels(), rotation=30, horizontalalignment='right')
plt.show()
print(classification_report(y_test,y_test_pred,labels=category_list))
```

```
C:\Users\Rithesh\anaconda3\lib\site-packages\sklearn\utils\validation.py:71: FutureWarning: Pass labels=['Cardiovas
 'Psychiatry / Psychology' 'Pediatrics - Neonatal' 'Orthopedic'
 'Ophthalmology' 'Obstetrics / Gynecology' 'Hematology - Oncology'
 'Gastroenterology' 'ENT - Otolaryngology'] as keyword args. From version 0.25 passing these as positional argument
  FutureWarning)
```



Cardiovascular / Pulmonary	73	3	0	10	0	1	1	0	1	1	2	1
Neurology	6	50	0	6	1	0	15	1	0	0	0	0
Urology	4	0	49	1	0	0	1	0	1	0	3	0
Radiology	16	20	4	16	0	0	5	1	3	1	2	0
Psychiatry / Psychology	3	3	1	2	3	0	1	0	0	0	0	0
Pediatrics - Neonatal	3	2	2	1	1	2	1	0	1	0	4	1
Orthopedic	3	14	0	7	0	0	65	0	0	0	0	0
Ophthalmology	0	1	0	0	0	0	1	18	0	0	0	1



```
                            precision    recall  f1-score   support

Cardiovascular / Pulmonary       0.62      0.78      0.69        93
                Neurology       0.53      0.63      0.57        79
                  Urology       0.84      0.83      0.84        59
                Radiology       0.29      0.24      0.26        68
   Psychiatry / Psychology       0.60      0.23      0.33        13
     Pediatrics - Neonatal       0.50      0.11      0.18        18
               Orthopedic       0.68      0.73      0.71        89
            Ophthalmology       0.90      0.86      0.88        21
   Obstetrics / Gynecology       0.79      0.77      0.78        39
     Hematology - Oncology       0.50      0.23      0.31        22
         Gastroenterology       0.70      0.75      0.72        56
      ENT - Otolaryngology       0.86      0.79      0.83        24

                 accuracy                           0.64       581
```

Since some classes are in minority we can use SMOTE(Synthetic Minority Over-sampling Technique) to generate more sample form minority class to solve the data imbalance problem. For more on SMOTE check here:https://arxiv.org/pdf/1106.1813.pdf. Let us generate new dataset using SMOTE and then perform classification on them

```
smote_over_sample = SMOTE(sampling_strategy='minority')
labels = data['medical_specialty'].tolist()
X, y = smote_over_sample.fit_resample(tfIdfMat_reduced, labels)

X_train, X_test, y_train, y_test = train_test_split(X, y, stratify=y,random_state=1)
print('Train_Set_Size:'+str(X_train.shape))
print('Test_Set_Size:'+str(X_test.shape))
```

```
Train_Set_Size:(1981, 582)
Test_Set_Size:(661, 582)
```

```
clf = LogisticRegression(penalty= 'elasticnet', solver= 'saga', l1_ratio=0.5, random_state=1).fit(X_trai
y_test_pred= clf.predict(X_test)
```

Let us visualize the data

```
labels = category_list
cm = confusion_matrix(y_test, y_test_pred, labels)

fig = plt.figure(figsize=(20,20))
ax= fig.add_subplot(1,1,1)
sns.heatmap(cm, annot=True, cmap="Greens",ax = ax,fmt='g'); #annot=True to annotate cells

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plt.setp(ax.get_yticklabels(), rotation=30, horizontalalignment='right')
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```

```
    plt.show()
    print(classification_report(y_test,y_test_pred,labels=category_list))
```

```
C:\Users\Rithesh\anaconda3\lib\site-packages\sklearn\utils\validation.py:71: FutureWarning: Pass labels=['Cardiovas
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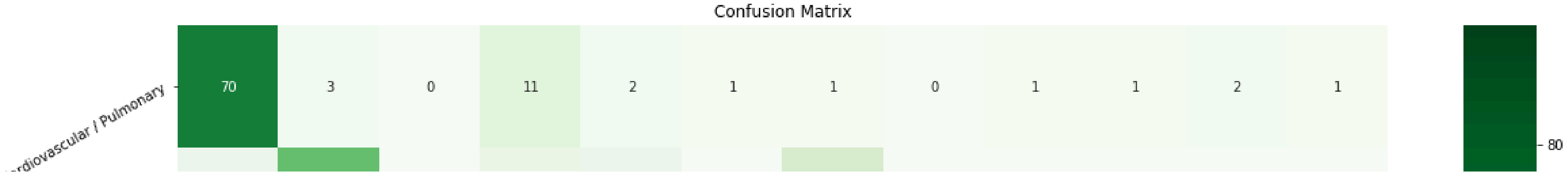
Confusion Matrix
Cardiovascular / Pulmonary