ARTChat

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1 ARTChat: Re-prescription App for HIV/ART Prescriptions

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ARTChat is an anti-retroviral therapy prescription recommendation app developed by Manan Kocher as part of a 3 week Insight Data Science Fellowship project. The three main goals of this app are to (1) streamline prescription practices to save physicians time, (2) prioritize patient safety by providing data driven recommendations, and (3) improve patient education in their own treatment through an interactive interface.

The code written out in this notebook serves as the backbone of the recommender framework. A variety of different techniques are used in creative ways to develop the app within the time constraint. If you have any questions, please do not hestitate to reach out to me at manan.kocher@gmail.com

A presentation of the project can be found at: http://bit.ly/artchat_hiv The app can be accessed at: www.manankocher.com (built using Dash)

In [1]:
```
# Import statements

import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import re #regular expression module
%matplotlib inline

import xml.etree.ElementTree as ET #XML reading and manipulation
import sqlite3

from urllib.request import urlopen
from bs4 import BeautifulSoup #Beautiful soup object is used to parse the html page in
import requests

import re #regular expression
import heapq #used in rank matrix

#Unsupervised learning:
import sklearn
from sklearn.decomposition import PCA
```

```
from sklearn.preprocessing import StandardScaler
from sklearn.cluster import KMeans

import copy
import pickle
```

1.0.1 FDA-approved list of HIV/ART drugs

Importing data manually since this is more efficient and allows me to get intimately familiar with the names.

```
In [3]: #Importing the latest approved HIV/ART drugs with Brand Name, Generic Name/Ingredients

drugs_art = pd.DataFrame(
    columns=['Brand_Names', 'Generic_Name/Other_Names', 'Drug_Class'])

drugs_art['Brand_Names'] = [
    'Ziagen', 'Emtriva', 'Epivir', 'Viread', 'Retrovir', 'Pifeltro', 'Sustiva',
    'Intelence', 'Viramune', 'Viramune XR', 'Edurant', 'Reyataz', 'Prezista',
    'Lexiva', 'Norvir', 'Invirase', 'Aptivus', 'Fuzeon', 'Selzentry',
    'Tivicay', 'Isentress', 'Isentress HD', 'Trogarzo', 'Tybost', 'Epzicom',
    'Triumeq', 'Trizivir', 'Evotaz', 'Biktarvy', 'Prezcobix', 'Symtuza',
    'Dovato', 'Juluca', 'Delstrigo', 'Atripla', 'Symfi', 'Symfi Lo', 'Genvoya',
    'Stribild', 'Odefsey', 'Complera', 'Descovy', 'Truvada', 'Cimduo',
    'Combivir', 'Kaletra'
]

drugs_art['Generic_Name/Other_Names'] = [
    ['abacavir'], ['emtricitabine'],
    ['lamivudine'],
    ['tenofovir'],
    ['zidovudine'], ['doravine'],
    ['efavirenz'], ['etravirine'], ['nevirapine'], ['nevirapine'], ['rilpivirine'],
    ['atazanavir'],
    ['darunavir'],
    ['fosamprenavir'],
    ['ritonavir'], ['saquinavir'],
    ['tipranavir'], ['enfuvirtide'], ['maraviroc'],
    ['dolutegravir'],
    ['raltegravir'],
    ['raltegravir'],
    ['ibalizumab-uiyk'],
    ['cobicistat'], ['abacavir', 'lamivudine'],
    ['abacavir','dolutegravir', 'lamivudine'],
    ['abacavir', 'lamivudine', 'zidovudine'], ['atazanavir', 'cobicistat'],
    ['bictegravir', 'emtricitabine', 'tenofovir'],
    ['darunavir', 'cobicistat'],
    ['darunavir', 'cobicistat', 'emtricitabine', 'tenofovir'],
```

```
    ['dolutegravir', 'lamivudine'], ['dolutegravir', 'rilpivirine'],
    ['doravirine', 'lamivudine', 'tenofovir'],
    ['efavirenz', 'emtricitabine', 'tenofovir'],
    ['efavirenz', 'lamivudine', 'tenofovir'],
    ['efavirenz', 'lamivudine', 'tenofovir'],
    ['elvitegravir', 'cobicistat', 'emtricitabine', 'tenofovir'],
    [
        'elvitegravir', 'cobicistat', 'emtricitabine',
        'tenofovir'
    ], ['emtricitabine', 'rilpivirine', 'tenofovir'],
    ['emtricitabine', 'rilpivirine', 'tenofovir'],
    ['emtricitabine', 'tenofovir'],
    ['emtricitabine', 'tenofovir'],
    ['lamivudine', 'tenofovir'],
    ['lamivudine', 'zidovudine'], ['lopinavir', 'ritonavir']
]

drugs_art['Drug_Class'] = [
    'NRTI', 'NRTI', 'NRTI', 'NRTI', 'NRTI', 'NNRTI', 'NNRTI', 'NNRTI', 'NNRTI',
    'NNRTI', 'NNRTI', 'PI', 'PI', 'PI', 'PI', 'PI', 'PI', 'FI', 'CCR5', 'INSTI',
    'INSTI', 'INSTI', 'PAI', 'PE', 'Comb', 'Comb', 'Comb', 'Comb', 'Comb', 'Comb',
    'Comb', 'Comb', 'Comb', 'Comb', 'Comb', 'Comb', 'Comb', 'Comb', 'Comb',
    'Comb', 'Comb', 'Comb', 'Comb', 'Comb', 'Comb', 'Comb'
]

export_csv = drugs_art.to_csv(r'/Users/mkocher/Desktop/ARTChat/HIV_ART.csv',index = No
drugs_art.to_pickle('/Users/mkocher/Desktop/ARTChat/pickled_data/drugs_art.pkl')
drugs_art.head()
```

Out[3]:

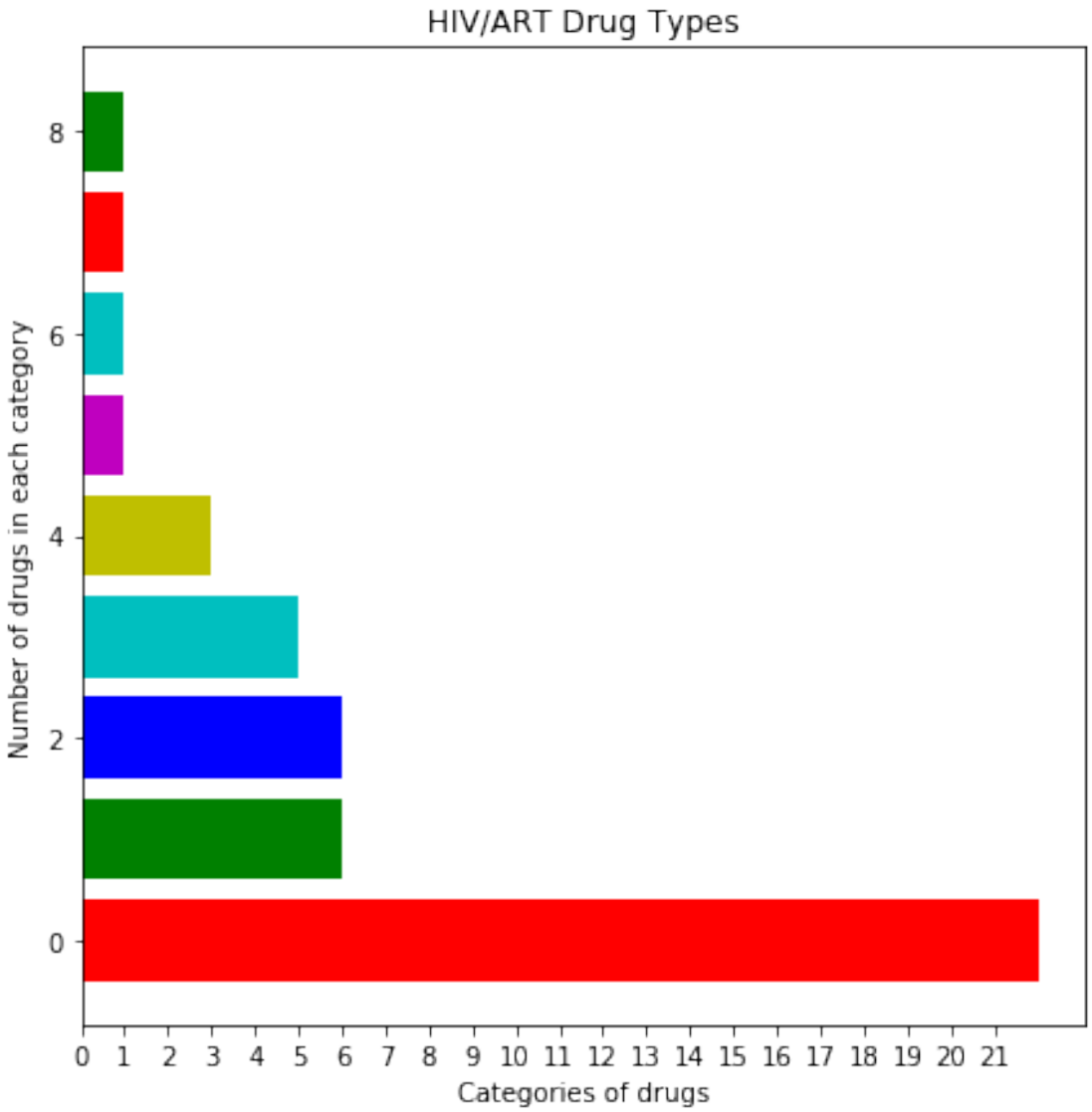
	Brand_Names	Generic_Name/Other_Names	Drug_Class
0	Ziagen	[abacavir]	NRTI
1	Emtriva	[emtricitabine]	NRTI
2	Epivir	[lamivudine]	NRTI
3	Viread	[tenofovir]	NRTI
4	Retrovir	[zidovudine]	NRTI

1.0.2 Data visualization of the breadth of HIV/ART drugs that make up combination therapies

In [4]:
```
#Histograms of different drug classes
class_count = drugs_art['Drug_Class'].value_counts()
my_colors = 'rgbcymc'
print(class_count)

plt.figure(figsize = (7,7))
plt.barh(np.arange(len(class_count.index)),class_count,color=my_colors)
plt.style.use('dark_background')
plt.xlabel('Categories of drugs')
plt.ylabel('Number of drugs in each category')
```

```
        plt.title('HIV/ART Drug Types')
        plt.savefig('/Users/mkocher/Desktop/ARTChat/figures_week2/ARTDrugs.png')
        plt.xticks(np.arange(0,22,1))
        plt.show()
```

```
Comb     22
PI        6
NNRTI     6
NRTI      5
INSTI     3
CCR5      1
PAI       1
PE        1
FI        1
Name: Drug_Class, dtype: int64
```



We have 22 combination drugs & 24 individual drugs. Drugs are administered typically as 2 NRTIs + 1 II/PI [Dr. Shihadeh]

1.0.3 Drug Side-Effect Databases : Importing, Joining, and Wrangling

In [6]:
```
#Importing tsv files of drugs and side-effects

#The following file contains the drug names + their IDs
drugs_id = pd.read_csv('drug_names.tsv',
                       sep='\t',
                       header=None,
                       error_bad_lines=False)

#The following file contains drug names and their corresponding side-effects
sideeffects = pd.read_csv(
    'meddra_freq.tsv',
    sep='\t',
    header=None)

#Cleaning up side-effect dataset
#print(drugs_id.head())  #quick view
print(sideeffects.shape)  #quick view
sideeffects.columns = [
    'CID', 'Code2', 'Code3', 'IsPlacebo', 'Freq_desc', 'freq_low', 'freq_high',
    'Labels', 'Code4', 'SideEffects'
]  #labeling columns

sideeffects = sideeffects.drop(['Code2', 'Code3', 'Code4', 'IsPlacebo'],
                               axis=1)  #dropping axes from table we don't need

#Dropping data that is uncommon, rare, postmarketing, infrequent and has a % of less t
drop_rows = sideeffects.index[(sideeffects['Labels'] == 'LLT') |
                              (sideeffects['Freq_desc'] == 'postmarketing') |
                              (sideeffects['Freq_desc'] == 'rare') | (sideeffects['Freq
                              )  #dropping rows that have LLT (only keep PT)

sideeffects = sideeffects.drop(sideeffects.index[drop_rows])

sideeffects.reset_index(inplace=True)  #reset index after row drop

sideeffects = sideeffects.drop('Labels', axis=1)  #Since the whole team is PT

#cleaning up drugs_id dataset
drugs_id.columns = ['CID', 'Drug']
```

```
        sideeffects = sideeffects.set_index('CID').join(
            drugs_id.set_index('CID'))  #combining both datasets


        #create new indices of integers
        sideeffects = sideeffects.reset_index()
        sideeffects['Freq_desc']=pd.to_numeric(sideeffects['Freq_desc'],errors='coerc') #conve
        sideeffects['Freq_desc']=sideeffects['Freq_desc'].fillna(0)
        sideeffects = sideeffects.drop('index',axis=1) #dropping the column named 'index'

        sideeffects.head()
```

```
b'Skipping line 1075: expected 2 fields, saw 3\n'


(291632, 10)
```

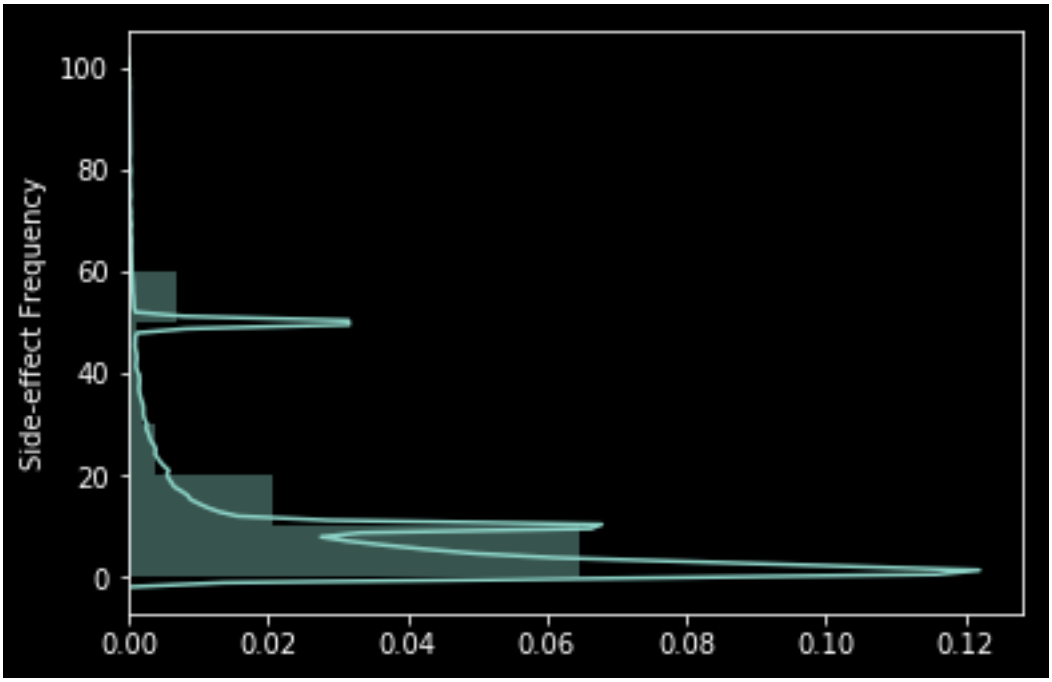
Out[6]:

	CID	Freq_desc	freq_low	freq_high	SideEffects	Drug
0	CID100000085	21.0	0.21	0.21	Abdominal pain	carnitine
1	CID100000085	21.0	0.21	0.21	Gastrointestinal pain	carnitine
2	CID100000085	5.0	0.05	0.05	Abdominal pain	carnitine
3	CID100000085	5.0	0.05	0.05	Gastrointestinal pain	carnitine
4	CID100000085	6.0	0.06	0.06	Abdominal pain	carnitine

1.0.4 Side-effects data at a glance

In [8]:
```
        #This does not contain frequencies less than a 25% - gotta reverse that.
        plt.figure()
        sns.distplot(sideeffects['Freq_desc'],bins=10,axlabel='Side-effect Frequency',vertical=
        plt.show()

        #How many unique side-effects are there in the table?
        print('The list has '+str(sideeffects['SideEffects'].nunique())+' unique sideeffects')
        print('Total number of drugs in the list are '+str(sideeffects['Drug'].nunique()))
```

```
/Users/mkocher/anaconda3/lib/python3.7/site-packages/scipy/stats/stats.py:1713: FutureWarning:
  return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval
```




```
The list has 2131 unique sideeffects
Total number of drugs in the list are 872
```

1.0.5 Clustering of drugs based on side-effect profiles

```
   Preparing the data:
   Step 1: Creating the table that contains name of drug as rows and the side-effects as colum
   Step 2: Reducing the table so it contains only HIV/ART drugs
   Step 3: Clean up the DataFrame. Ready for analysis!
```

```
In [9]: #side-effects [This part of the code takes some time to run]
        list1 = drugs_art['Generic_Name/Other_Names'].tolist() #processing out the list of gen
        cluster_drug_names = [item for sublist in list1 for item in sublist]   #flattening out

        master=pd.DataFrame()
        for rows in sideeffects.index:
            master.loc[sideeffects['Drug'][rows],sideeffects['SideEffects'][rows]] = sideeffect

        master.head() #this list contains all the drugs and their side-effects
```

```
Out[9]:                  Abdominal pain  Gastrointestinal pain  Amblyopia  Anaemia  \
        carnitine                  17.0                   17.0        2.0      3.0
        5-aminolevulinic            NaN                    NaN        NaN      NaN
        leucovorin                  NaN                    NaN        NaN      NaN
        PGE2                        NaN                    NaN        NaN      NaN
```

```
prostacyclin                5.0                    5.0        NaN      NaN

                Decreased appetite  Anxiety  Arrhythmia  Asthenia  \
carnitine                      3.0      5.0         5.0       8.0
5-aminolevulinic               NaN      NaN         NaN       NaN
leucovorin                     4.0      NaN         NaN       6.0
PGE2                           NaN      NaN         NaN       NaN
prostacyclin                  66.0      9.0         NaN       NaN

                Atrial fibrillation  Back pain  \
carnitine                       6.0       10.0
5-aminolevulinic                NaN        NaN
leucovorin                      NaN        NaN
PGE2                            NaN        NaN
prostacyclin                    NaN        2.0

                                     ...                          \
carnitine                            ...
5-aminolevulinic                     ...
leucovorin                           ...
PGE2                                 ...
prostacyclin                         ...

                Keratosis pilaris  Bowen's disease  Keratoacanthoma  \
carnitine                     NaN              NaN              NaN
5-aminolevulinic              NaN              NaN              NaN
leucovorin                    NaN              NaN              NaN
PGE2                          NaN              NaN              NaN
prostacyclin                  NaN              NaN              NaN

                Panniculitis  Papilloma  Acrochordon  Multiple sclerosis  \
carnitine                NaN        NaN          NaN                 NaN
5-aminolevulinic         NaN        NaN          NaN                 NaN
leucovorin               NaN        NaN          NaN                 NaN
PGE2                     NaN        NaN          NaN                 NaN
prostacyclin             NaN        NaN          NaN                 NaN

                Post-traumatic pain  Traumatic liver injury  \
carnitine                       NaN                     NaN
5-aminolevulinic                NaN                     NaN
leucovorin                      NaN                     NaN
PGE2                            NaN                     NaN
prostacyclin                    NaN                     NaN

                Activated partial thromboplastin time prolonged
carnitine                                                   NaN
5-aminolevulinic                                            NaN
leucovorin                                                  NaN
```

```
PGE2                                                                NaN
prostacyclin                                                        NaN

[5 rows x 2131 columns]
```

1.0.6 Step 2 and 3 of preparation for Clustering

```
In [11]: cluster_drug_names = [x.lower() for x in cluster_drug_names
                               ]  #converting all drug names to lowercase
         master.index = master.index.str.lower(
         )  #converting all indices in the master to lowercase

         master.loc[cluster_drug_names[3]]
         #reduce cluster_drug_names to an array that is within master.index
         reduced_list = master.loc[master.index.isin(cluster_drug_names) == True]
         reduced_list = reduced_list.replace(np.nan, 0)  #replacing NaNs with zeros

         nunique = reduced_list.apply(
             pd.Series.nunique
         )  #dropping all columns with only zeros since those side-effects are irrelevant here
         cols_to_drop = nunique[nunique == 1].index
         reduced_list = reduced_list.drop(cols_to_drop, axis=1)

         reduced_list.to_pickle("/Users/mkocher/Desktop/ARTChat/pickled_data/reduced_list.pkl")
         reduced_list.head()
```

Out[11]:

	Abdominal pain	Gastrointestinal pain	Anaemia	\
abacavir	0.0	0.0	0.0	
efavirenz	50.0	50.0	0.0	
lamivudine	11.0	19.0	10.0	
nevirapine	1.0	1.0	10.0	
ritonavir	5.1	5.1	4.0	

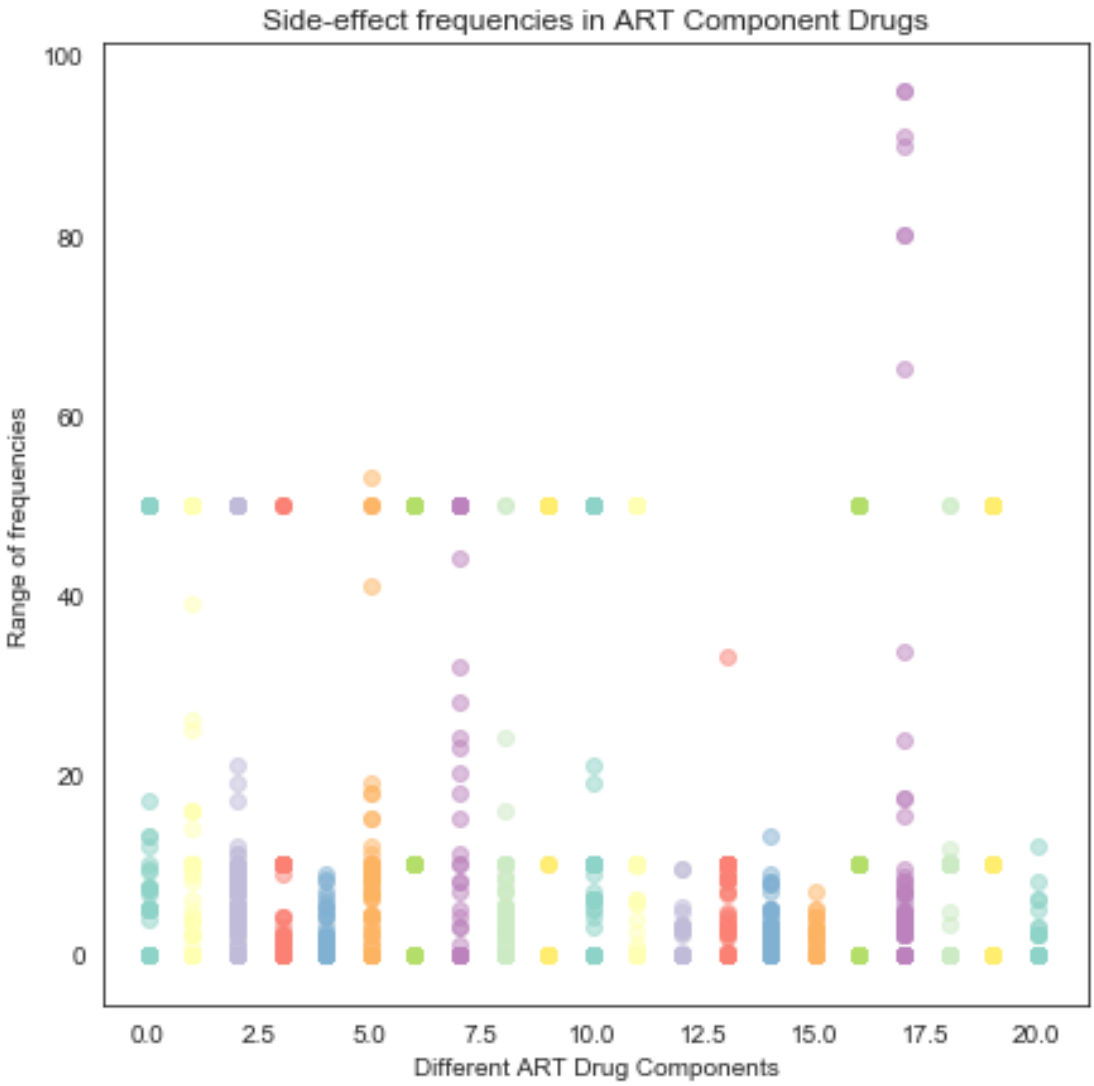
	Decreased appetite	Anxiety	Asthenia	Back pain	Bronchitis	\
abacavir	50.0	5.18	50.00	0.0	0.0	
efavirenz	2.0	50.00	50.00	0.0	0.0	
lamivudine	7.0	0.00	3.12	0.0	5.8	
nevirapine	0.0	0.00	4.00	0.0	0.0	
ritonavir	4.2	0.90	6.40	0.0	0.0	

	Chest pain	Infection	...	\
abacavir	0.0	9.88	...	
efavirenz	0.0	0.00	...	
lamivudine	0.0	21.00	...	
nevirapine	0.0	0.00	...	
ritonavir	0.0	0.00	...	

	Lymphocyte count decreased	Hepatic steatosis	Nephritis	\

```
abacavir                          0.0               0.0        0.0
efavirenz                         0.0               0.0        0.0
lamivudine                        0.0               0.0        0.0
nevirapine                        0.0               0.0        0.0
ritonavir                         0.0               0.0        0.0

            Ocular icterus  Hepatitis toxic  Rash vesicular  Anogenital warts  \
abacavir               0.0              0.0             0.0               0.0
efavirenz              0.0              0.0             0.0               0.0
lamivudine             0.0              0.0             0.0               0.0
nevirapine             0.0              0.0             0.0               0.0
ritonavir              0.0              0.0             0.0               0.0

            Apocrine and eccrine gland disorders  \
abacavir                                     0.0
efavirenz                                    0.0
lamivudine                                   0.0
nevirapine                                   0.0
ritonavir                                    0.0

            Urinary tract signs and symptoms  Vascular hypertensive disorders
abacavir                                 0.0                              0.0
efavirenz                                0.0                              0.0
lamivudine                               0.0                              0.0
nevirapine                               0.0                              0.0
ritonavir                                0.0                              0.0

[5 rows x 284 columns]
```

In [30]:
```
#Plot side-effect frequencies for the ART drugs

plt.figure(figsize=(7, 7))
sns.set_style('white')
data_to_plot = []
for i in np.arange(0, (len(reduced_list.iloc[:, 0]))):  #for each drug
    plt.scatter(np.full((1, len(reduced_list.iloc[0, :])), i),
                reduced_list.iloc[i, :],
                alpha=0.5)  #draw a categorical scatter
    #plot with no overlapping points
plt.xlabel('Different ART Drug Components')
plt.ylabel('Range of frequencies')
plt.title('Side-effect frequencies in ART Component Drugs')
plt.savefig(
    '/Users/mkocher/Desktop/ARTChat/figures_week2/ARTDrug_Frequencies.png')
plt.show()
```



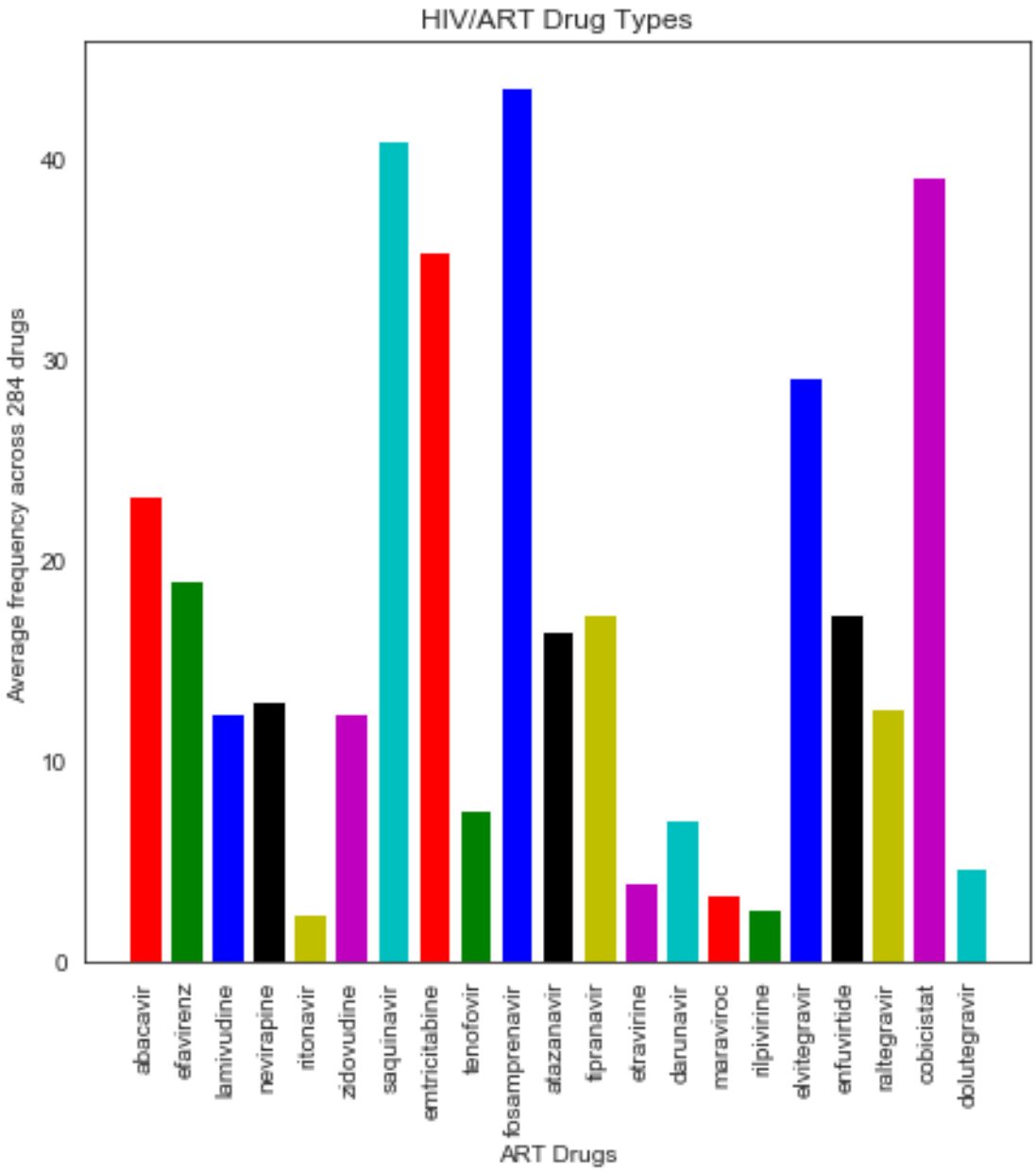

```
In [17]: #Saving the lists of side-effects as a .csv file for the Dash app
         import csv

         side_effects_dash = reduced_list.columns.tolist()
         #export_csv = side_effects_dash.save(r'/Users/mkocher/Desktop/ARTChat/data/side_effec

         with open('side_effects_dash.txt', 'w') as f:
             for item in side_effects_dash:
                 f.write("%s," % item)
```

There are a total of 21 Drugs with 284 Side-effects to consider. In the FDA drug list there are 24 individual drugs. There are some drugs missing from the list.

```
In [25]: #Side-effect visualization:
         mean_value = reduced_list[reduced_list !=0].apply(np.mean,axis=1)
```

```
my_colors = 'rgbkymc'
print(mean_value)

plt.figure(figsize = (7,7))
plt.bar(mean_value.index,mean_value,color=my_colors)
plt.xticks(rotation=90)
plt.xlabel('ART Drugs')
plt.ylabel('Average frequency across 284 drugs')
plt.title('HIV/ART Drug Types')
plt.savefig('/Users/mkocher/Desktop/ARTChat/figures_week2/Frequency_sideeffects.png')
plt.show()
```

```
abacavir         23.179394
efavirenz        18.941429
lamivudine       12.370000
nevirapine       12.954545
ritonavir         2.414286
zidovudine       12.410769
saquinavir       40.909091
emtricitabine    35.304348
tenofovir         7.514091
fosamprenavir    43.600000
atazanavir       16.434211
tipranavir       17.291429
etravirine        3.949692
darunavir         7.109123
maraviroc         3.302000
rilpivirine       2.614286
elvitegravir     29.047619
enfuvirtide      17.346000
raltegravir      12.585185
cobicistat       39.090909
dolutegravir      4.636364
dtype: float64
```



1.0.7 Principal Component Analysis for dimensionality reduction

First we reduce the number of dimensions from 284 to prepare the data for clustering

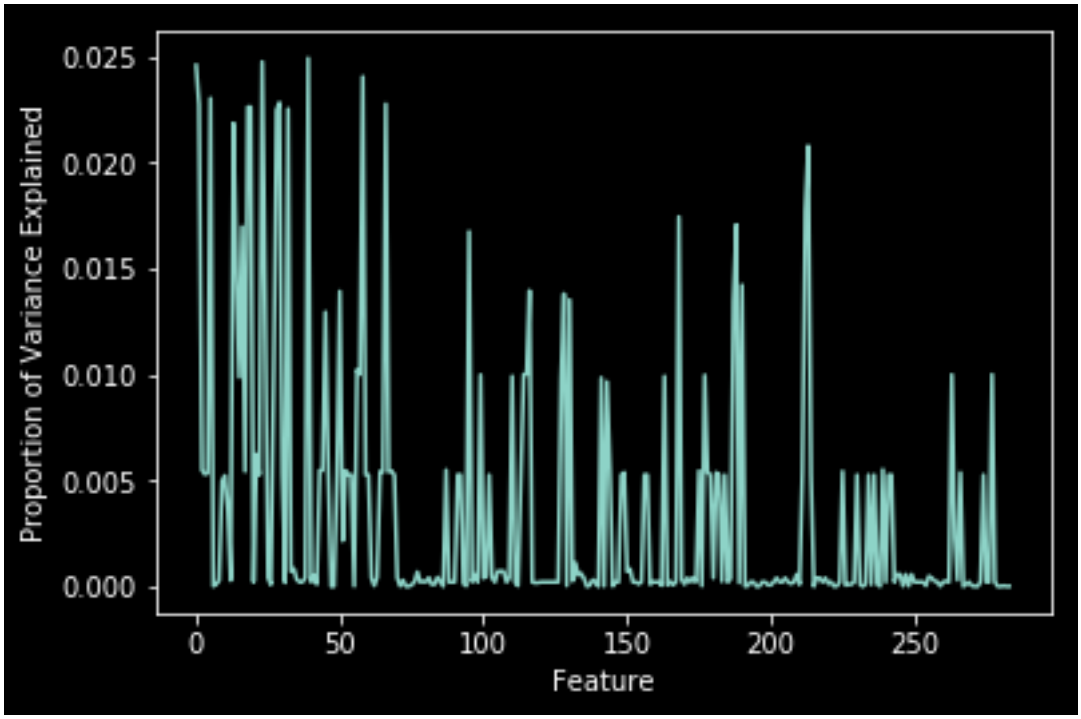
```
In [31]: stddev = np.std(reduced_list.iloc[:,0])
         reduced_list.iloc[:,0]

Out[31]: abacavir          0.0
         efavirenz        50.0
         lamivudine       11.0
```

```
nevirapine        1.0
ritonavir         5.1
zidovudine       50.0
saquinavir       50.0
emtricitabine    50.0
tenofovir         3.0
fosamprenavir    50.0
atazanavir       50.0
tipranavir       50.0
etravirine        3.0
darunavir         8.3
maraviroc         7.7
rilpivirine       2.0
elvitegravir     50.0
enfuvirtide       4.7
raltegravir       0.0
cobicistat       50.0
dolutegravir      0.0
Name: Abdominal pain, dtype: float64
```

1.0.8 Scree Plot

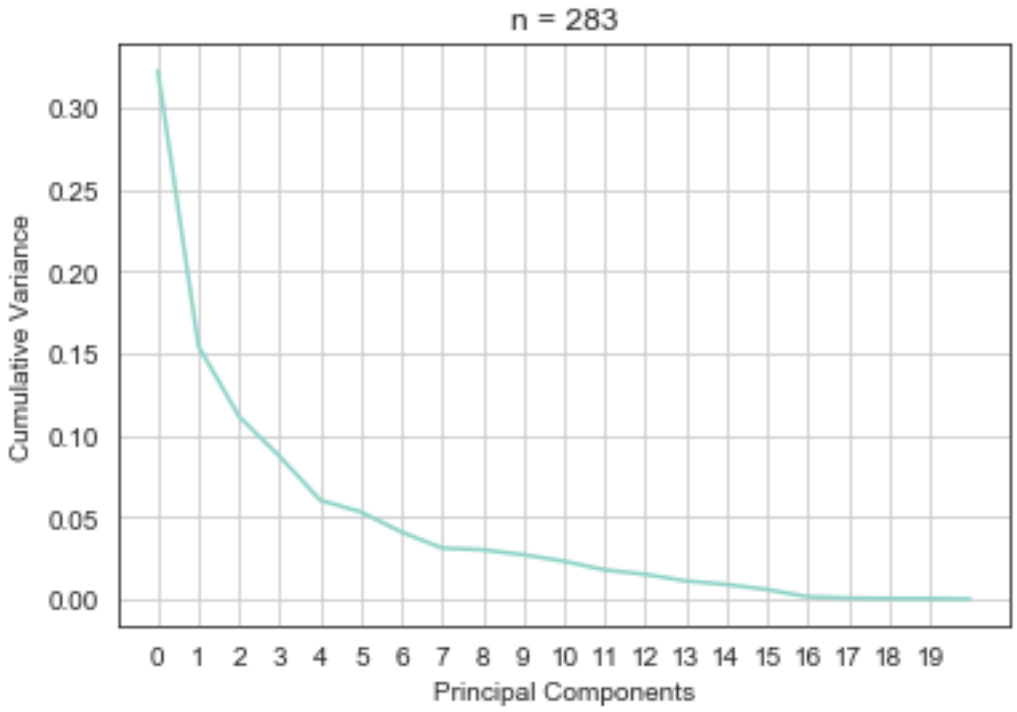
The elbow plot is used to pick number of dimensions to reduce based on variance captured

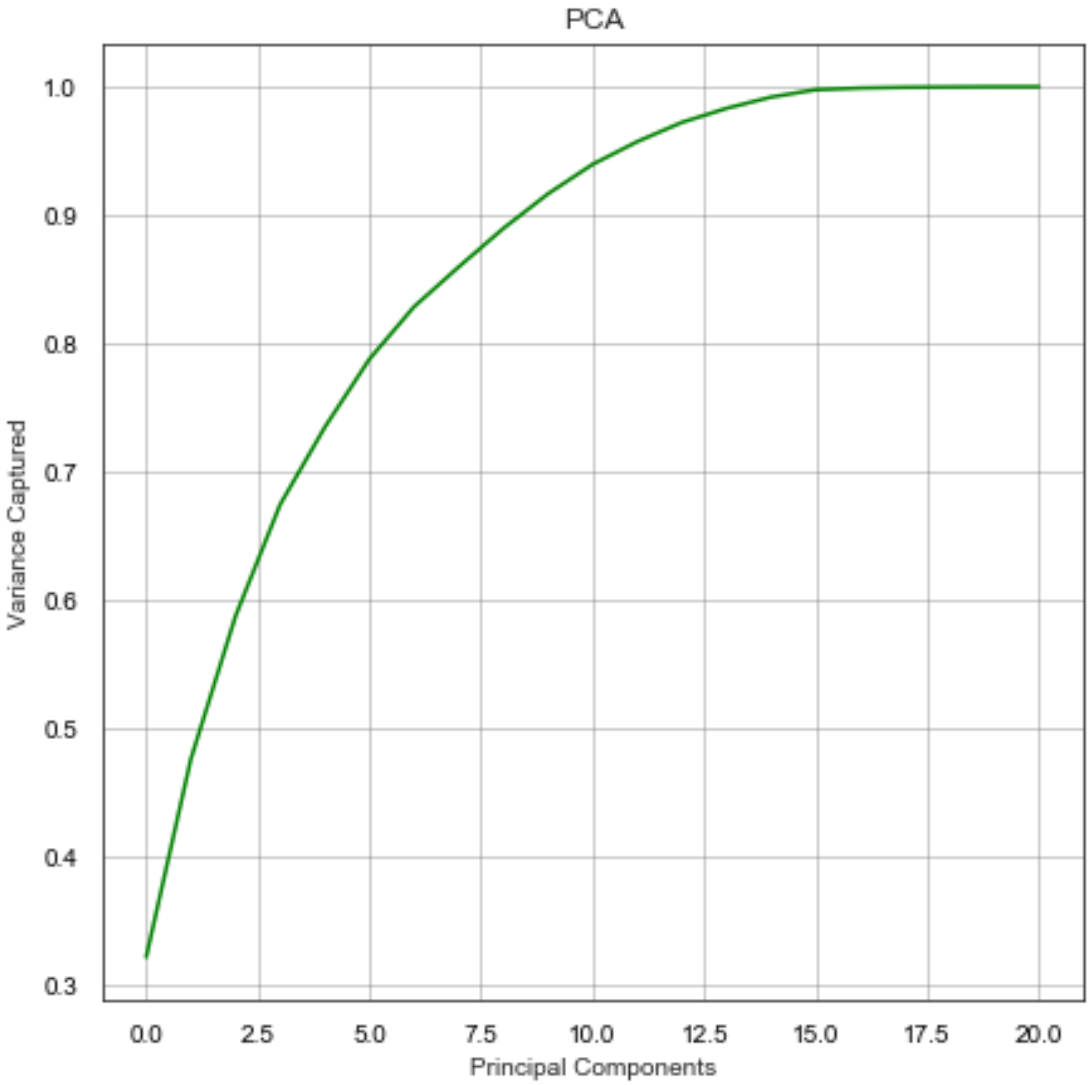
In [128]:
```
#Picking Number of dimensions to reduce to: scree plot

pr_var = np.zeros(len(reduced_list.columns)) #stddev^2
prop_var = np.zeros(len(reduced_list.columns)) #proportion of variance

for i in np.arange(len(reduced_list.columns)): #going through each principal compone
    stddev = np.std(reduced_list.iloc[:,i]) #standard deviation of each principal co
    pr_var_i = stddev**2
    pr_var[i] = pr_var_i #adding the the array

prop_var = pr_var/np.sum(pr_var)

plt.figure()
plt.plot(prop_var)
plt.xlabel("Feature")
plt.ylabel("Proportion of Variance Explained")
#plt.ylim((-1,1))
plt.show()
```



In [427]:
```
#pca for n = 283
pca = PCA(n_components = 283)
principal_components = pca.fit_transform(reduced_list)
exvar = pca.explained_variance_

cumulative_variance = np.zeros(len(exvar)) #computing cumulative variance
for i in np.arange(len(exvar)):
    cumulative_variance[i] = exvar[i]/np.sum(exvar)

plt.figure()
plt.plot(cumulative_variance)
plt.xlabel('Principal Components')
plt.ylabel('Cumulative Variance')
plt.title('n = 283')
plt.grid()
plt.xticks(np.arange(0,20,1))
plt.show()

cumsum = np.zeros(len(exvar)) #where does it catch 90% of the variance?
cumsum[0] = cumulative_variance[0]
for i in range(1,len(exvar)):
    cumsum[i] = cumsum[i-1]+cumulative_variance[i]

cumsum
```

```
plt.figure(figsize = (7,7))
sns.set_style('white')
plt.plot(cumsum,c='g')
plt.xlabel('Principal Components')
plt.ylabel('Variance Captured')
plt.title('PCA')
plt.tick_params(direction='out', length=6, width=2, colors='black',
                grid_color='gray', grid_alpha=0.5)
plt.savefig('/Users/mkocher/Desktop/ARTChat/figures_week2/pca_variance.png')
plt.grid()
plt.show()
```



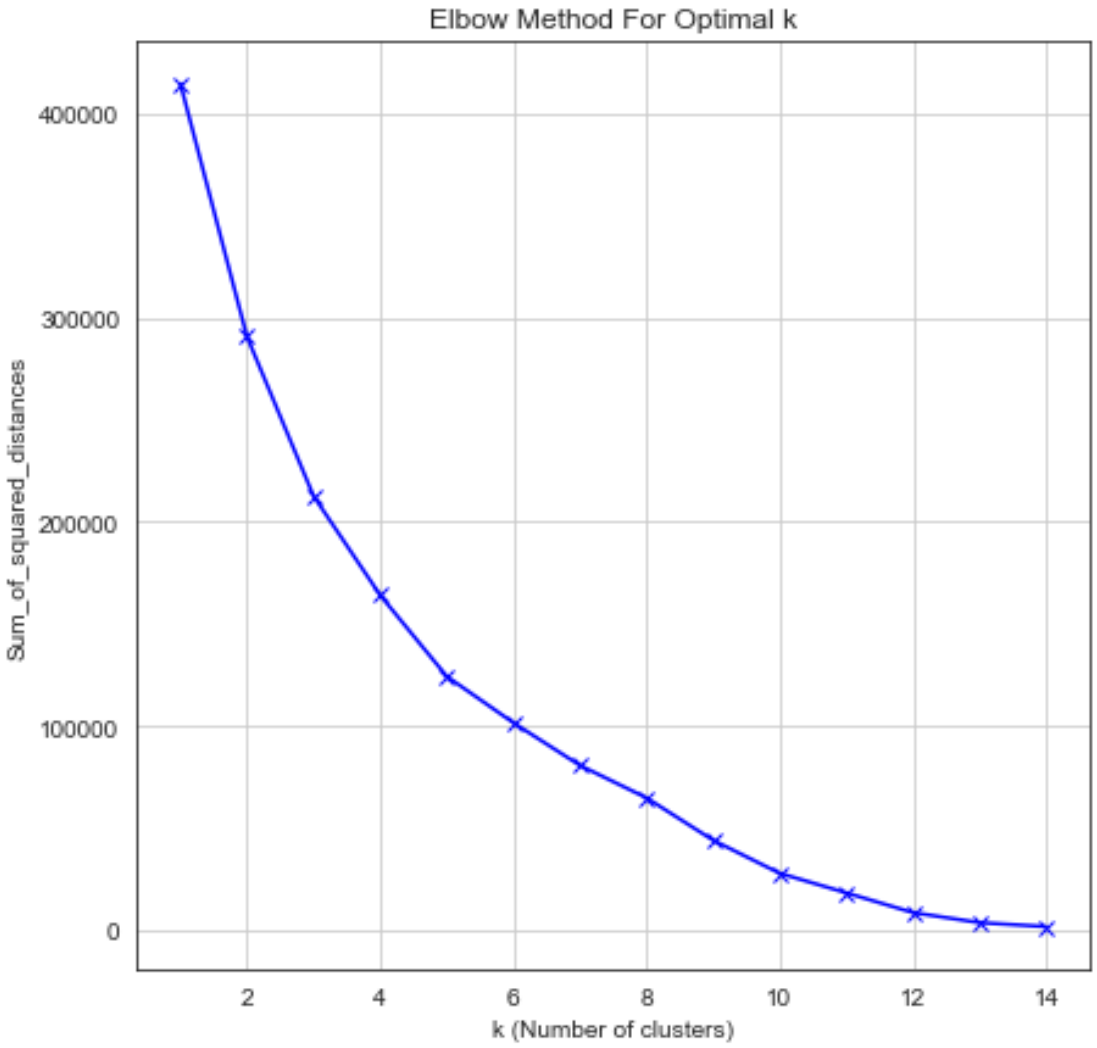


n = 10 captures 90% of the Variance. Dimensions reduced from 283 -> 10

1.0.9 Now to find the number of clusters for K-Means clustering

```
In [33]: #pca for n = 10
         pca = PCA(n_components = 10)
         principal_components9 = pca.fit_transform(reduced_list)
         principal_df9 = pd.DataFrame(data = principal_components9, columns=['Principal_Compone

         Sum_of_squared_distances = []
         K = range(1,15)       #why is this range 1 to 15?
         for k in K:
             km = KMeans(n_clusters=k)
             km = km.fit(principal_df9.values)
```

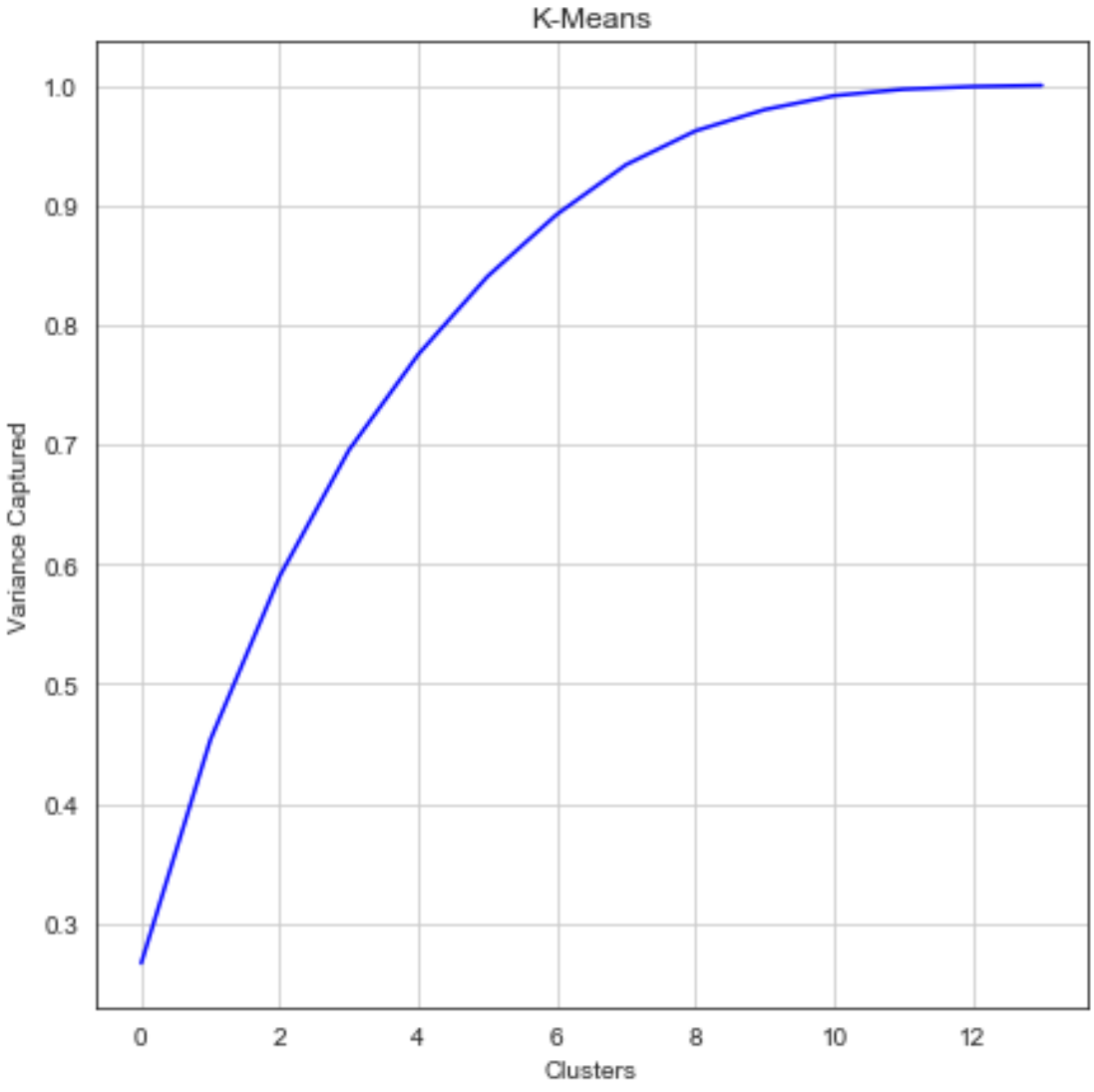
```
    Sum_of_squared_distances.append(km.inertia_)

plt.figure(figsize = (7,7))
plt.plot(K, Sum_of_squared_distances, 'bx-')
plt.xlabel('k (Number of clusters)')
plt.ylabel('Sum_of_squared_distances')
plt.title('Elbow Method For Optimal k')
plt.grid()
plt.show()
```



From the above plot it is difficult to determine what the appropriate number of clusters should be. Attempting the cumulative sum.

```
In [34]: cumsum = np.zeros(len(K)) #where does it catch 90% of the variance?
         cumsum[0] = Sum_of_squared_distances[0]/np.sum(Sum_of_squared_distances)
         for i in range(1,len(K)):
```

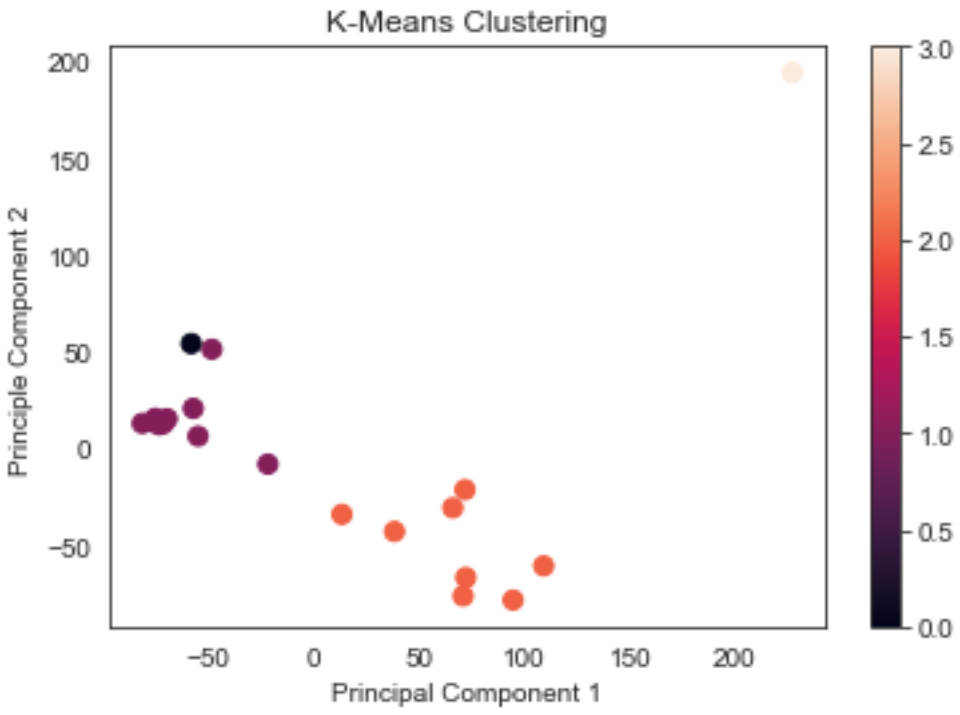
```
    cumsum[i] = (cumsum[i-1]+Sum_of_squared_distances[i])/np.sum(Sum_of_squared_distan
#Not sure if this metric works
variance_captured = np.cumsum(Sum_of_squared_distances)/np.sum(Sum_of_squared_distance


plt.figure(figsize = (7,7))
plt.grid()
plt.plot(variance_captured,c='b')
plt.xlabel('Clusters')
plt.ylabel('Variance Captured')
plt.title('K-Means')
plt.savefig('/Users/mkocher/Desktop/ARTChat/figures_week2/kmeans_variance.png')
plt.show()
```



n = 4 captures >90% of the variance

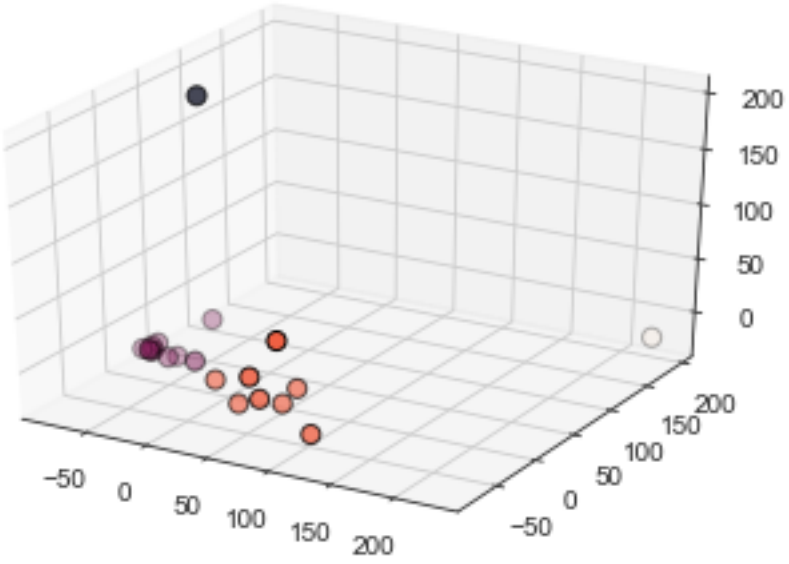
1.0.10 K-Means Clustering

In [35]:
```
model9 = KMeans(n_clusters=4,n_init=100)
y=model9.fit(principal_df9.values)
clust_labels5 = model9.predict(principal_df9.values)
center5 = model9.cluster_centers_

kmeans5 = pd.DataFrame(clust_labels5)
principal_df9.insert((principal_df9.shape[1]),'kmeans_n_5',kmeans5)

fig = plt.figure()
ax = fig.add_subplot(111)
ax.set_facecolor('xkcd:white')
scatter = ax.scatter(principal_df9['Principal_Component_1'],principal_df9['Principal_
                     c=kmeans5[0],s=50)
ax.set_title('K-Means Clustering')
ax.set_xlabel('Principal Component 1')
ax.set_ylabel('Principle Component 2')
plt.colorbar(scatter)
plt.show()
```



In [36]:
```
#3Dimensional Scatterplot
from mpl_toolkits.mplot3d import Axes3D
```

```
fig = plt.figure(facecolor='white')
#ax.set_facecolor('xkcd:white')
sns.set_style('white')
#fig.patch.set_alpha(0)
#ax.patch.set_alpha(0)
#ax.patch.set_facecolor('white')
#fig.set_facecolor('xkcd:white')
ax = fig.add_subplot(111, projection='3d')
ax.scatter(principal_df9['Principal_Component_1'],principal_df9['Principal_Component_
plt.savefig('/Users/mkocher/Desktop/ARTChat/figures_week2/clustering4.png')
plt.show()
```




```
In [37]: principal_df9.to_pickle('/Users/mkocher/Desktop/ARTChat/pickled_data/principal_df9.pk
```

1.0.11 Ranking how far each cluster is from all other clusters using Eucledian Distance

```
In [38]: #computing eucledian distance between centers and ranking the distance between cluste
         center5 #contains the coordinates of the centroids of the 4 clusters in 10-dimensiona
         distance_metric = sklearn.metrics.pairwise.euclidean_distances(center5)
         print(distance_metric)

         #for each row, where is the maximum value of distance?
         ranks_dist = np.zeros((len(distance_metric),len(distance_metric)))

         i=0
         while(i<len(distance_metric)):
             temp = distance_metric[i,:].argsort()
```

```
            ranks = np.empty_like(temp)
            ranks[temp] = np.arange(len(distance_metric[0,:]))
            ranks_dist[i,:] = ranks
            i+=1

        ranks_dist = ranks_dist
        print(ranks_dist)
        with open('/Users/mkocher/Desktop/ARTChat/pickled_data/ranks_dist.pkl','wb') as f: pi
```

```
[[  0.         230.1778403  260.86322633 393.63661631]
 [230.1778403    0.         150.10000233 343.31237034]
 [260.86322633 150.10000233   0.         296.49284934]
 [393.63661631 343.31237034 296.49284934   0.        ]]
[[0. 1. 2. 3.]
 [2. 0. 1. 3.]
 [2. 1. 0. 3.]
 [3. 2. 1. 0.]]
```

Interpreting the above table: For cluster no. 1, Cluster no. 4 is the farthest, then 3 then 2 ...

In [39]:
```
#Drugs and what clusters they belong to
cluster_results = pd.DataFrame(columns=['Drug','Cluster_no'])
cluster_results['Drug'] = reduced_list.index
cluster_results['Cluster_no'] = clust_labels5
cluster_results

cluster_results.to_pickle('/Users/mkocher/Desktop/ARTChat/pickled_data/cluster_results
cluster_results

#Creating a new dataframe with drugs,cluster_no, and side-effect frequencies
clusters_side_effects = pd.merge(left=reduced_list,right=cluster_results, right_on='D
clusters_side_effects.head()
```

Out[39]:

	Abdominal pain	Gastrointestinal pain	Anaemia	Decreased appetite	\
0	0.0	0.0	0.0	50.0	
1	50.0	50.0	0.0	2.0	
2	11.0	19.0	10.0	7.0	
3	1.0	1.0	10.0	0.0	
4	5.1	5.1	4.0	4.2	

	Anxiety	Asthenia	Back pain	Bronchitis	Chest pain	Infection	\
0	5.18	50.00	0.0	0.0	0.0	9.88	
1	50.00	50.00	0.0	0.0	0.0	0.00	
2	0.00	3.12	0.0	5.8	0.0	21.00	
3	0.00	4.00	0.0	0.0	0.0	0.00	
4	0.90	6.40	0.0	0.0	0.0	0.00	

...	Nephritis	Ocular icterus	Hepatitis toxic	Rash vesicular	\

```
0     ...            0.0             0.0             0.0             0.0
1     ...            0.0             0.0             0.0             0.0
2     ...            0.0             0.0             0.0             0.0
3     ...            0.0             0.0             0.0             0.0
4     ...            0.0             0.0             0.0             0.0

   Anogenital warts  Apocrine and eccrine gland disorders  \
0               0.0                                   0.0
1               0.0                                   0.0
2               0.0                                   0.0
3               0.0                                   0.0
4               0.0                                   0.0

   Urinary tract signs and symptoms  Vascular hypertensive disorders  \
0                               0.0                               0.0
1                               0.0                               0.0
2                               0.0                               0.0
3                               0.0                               0.0
4                               0.0                               0.0

         Drug  Cluster_no
0    abacavir           2
1   efavirenz           2
2  lamivudine           1
3  nevirapine           1
4   ritonavir           1

[5 rows x 286 columns]
```

1.0.12 Validating the cluster_results

In [302]:
```
#a = clusters_side_effects.groupby('Cluster_no') #group by the groups (doesn't displ
#a.get_group(1) #I can get the different groups
```

Out[302]:
```
    Abdominal pain  Gastrointestinal pain  Anaemia  Decreased appetite  \
0              0.0                    0.0      0.0                50.0
1             50.0                   50.0      0.0                 2.0
7             50.0                   50.0     10.0                 0.0
9             50.0                   50.0      0.0                 0.0
10            50.0                   50.0      0.0                10.0
11            50.0                   50.0     10.0                10.0
16            50.0                   50.0      0.0                 0.0
19            50.0                   50.0      0.0                 0.0

    Anxiety  Asthenia  Back pain  Bronchitis  Chest pain  Infection  \
0      5.18      50.0        0.0         0.0         0.0       9.88
1     50.00      50.0        0.0         0.0         0.0       0.00
7      0.00       8.0        0.0         0.0         0.0      44.00
```

```
9      0.00      50.0        0.0         0.0         0.0       0.00
10    10.00      50.0        0.0         0.0        10.0       0.00
11     0.00      50.0        0.0         0.0         0.0      10.00
16     0.00      50.0        0.0         0.0         0.0       0.00
19     0.00      50.0        0.0         0.0         0.0       0.00

       ...      Nephritis  Ocular icterus  Hepatitis toxic  Rash vesicular  \
0      ...            0.0             0.0              0.0             0.0
1      ...            0.0             0.0              0.0             0.0
7      ...            0.0             0.0              0.0             0.0
9      ...            0.0             0.0              0.0             0.0
10     ...            0.0            50.0              0.0             0.0
11     ...            0.0             0.0             10.0             0.0
16     ...            0.0             0.0              0.0             0.0
19     ...            0.0            50.0              0.0             0.0

    Anogenital warts  Apocrine and eccrine gland disorders  \
0                0.0                                   0.0
1                0.0                                   0.0
7                0.0                                   0.0
9                0.0                                   0.0
10               0.0                                   0.0
11               0.0                                   0.0
16               0.0                                   0.0
19               0.0                                   0.0

    Urinary tract signs and symptoms  Vascular hypertensive disorders  \
0                                0.0                               0.0
1                                0.0                               0.0
7                                0.0                               0.0
9                                0.0                               0.0
10                               0.0                               0.0
11                               0.0                               0.0
16                               0.0                               0.0
19                               0.0                               0.0

            Drug  Cluster_no
0        abacavir           1
1       efavirenz           1
7   emtricitabine           1
9   fosamprenavir           1
10     atazanavir           1
11     tipranavir           1
16   elvitegravir           1
19     cobicistat           1

[8 rows x 286 columns]
```

In [40]:
```
#Find the top 5 side-effects for 1 element in each cluster
#values_count, GROUPBY,getgroup
cluster_val = pd.DataFrame(columns=['lamivudine','val_0','abacavir','val_1','enfuvirti
cluster_val['abacavir']=clusters_side_effects.iloc[0,0:len(clusters_side_effects.colu
cluster_val['val_1'] = clusters_side_effects.iloc[0,0:len(clusters_side_effects.columm
cluster_val['lamivudine']=clusters_side_effects.iloc[2,0:len(clusters_side_effects.col
cluster_val['val_0'] = clusters_side_effects.iloc[2,0:len(clusters_side_effects.columm
cluster_val['saquinavir']=clusters_side_effects.iloc[6,0:len(clusters_side_effects.col
cluster_val['val_3'] = clusters_side_effects.iloc[6,0:len(clusters_side_effects.columm
cluster_val['val_2'] = clusters_side_effects.iloc[17,0:len(clusters_side_effects.colu
cluster_val['enfuvirtide']=clusters_side_effects.iloc[17,0:len(clusters_side_effects.
cluster_val
```

Out[40]:

	lamivudine	val_0	abacavir	val_1	\
0	Arthralgia	50	Rash	50	
1	Abdominal pain upper	50	Lethargy	50	
2	Myopathy	50	Hyperlactacidaemia	50	
3	Hyperlactacidaemia	50	Diarrhoea	50	
4	Alopecia	50	Dermatitis	50	
5	Musculoskeletal discomfort	50	Nausea	50	
6	Myalgia	50	Vomiting	50	
7	Pruritus	50	Body temperature increased	50	
8	Muscle spasms	50	Asthenia	50	
9	Infection	21	Fatigue	50	
10	Gastrointestinal pain	19	Decreased appetite	50	
11	Respiratory tract infection	17	Headache	50	
12	Chills	12	Pruritus	17	
13	Hepatomegaly	11	Myalgia	13	
14	Abdominal pain	11	Musculoskeletal discomfort	13	
15	Thrombocytopenia	10	Chills	12	
16	Anaemia	10	Infection	9.88	
17	Neutropenia	10	Insomnia	9.33	
18	Cough	9.72	Drug hypersensitivity	9.11	
19	Musculoskeletal pain	9.72	Pain	7.41	
20	Discomfort	9.6	Abdominal discomfort	7.41	
21	Dizziness	9.3	Cough	7.23	
22	Lymphadenopathy	9	Sleep disorder	7.23	
23	Wheezing	9	Musculoskeletal pain	7.23	
24	Breath sounds abnormal	9	Depression	6.74	
25	Neuropathy peripheral	8.5	Anxiety	5.18	
26	Pain	8.33	Dizziness	4.95	
27	Sleep disorder	8.1	Abnormal dreams	4.92	
28	Oropharyngeal discomfort	8	Ill-defined disorder	4.9	
29	Oropharyngeal pain	8	Discomfort	4.9	
..	...	...	...	...	
254	Renal failure acute	0	Respiration abnormal	0	
255	Hypercholesterolaemia	0	Respiratory disorder	0	
256	Angioedema	0	Disorientation	0	

257	Aphthous stomatitis	0	Hepatobiliary disease	0
258	Suicide attempt	0	Immune system disorder	0
259	Immune system disorder	0	Hyperbilirubinaemia	0
260	Rhabdomyolysis	0	Suicide attempt	0
261	Hepatobiliary disease	0	Aphthous stomatitis	0
262	Disorientation	0	Oropharyngeal discomfort	0
263	Connective tissue disorder	0	Oropharyngeal pain	0
264	Blood pressure increased	0	Angioedema	0
265	Nightmare	0	Dysthymic disorder	0
266	Bronchospasm	0	Nightmare	0
267	Aggression	0	Bronchospasm	0
268	Hypocalcaemia	0	Aggression	0
269	Herpes zoster	0	Renal failure acute	0
270	Hypernatraemia	0	Hypocalcaemia	0
271	Drug hypersensitivity	0	Hypernatraemia	0
272	Induration	0	Induration	0
273	Nodule	0	Nodule	0
274	Thinking abnormal	0	Lymphadenopathy	0
275	Paraesthesia oral	0	Thinking abnormal	0
276	Hypophosphataemia	0	Paraesthesia oral	0
277	Amnesia	0	Liver function test abnormal	0
278	Rash maculo-papular	0	Hypophosphataemia	0
279	Dermatitis bullous	0	Myopathy	0
280	Hyperbilirubinaemia	0	Amnesia	0
281	Dermatitis exfoliative	0	Rash maculo-papular	0
282	Blood creatinine increased	0	Dermatitis bullous	0
283	Hyperglycaemia	0	Abdominal pain	0

	enfuvirtide	val_2	saquinavir	\
0	Pain	96	Abdominal pain	
1	Discomfort	96	Nausea	
2	Erythema	91	Paraesthesia	
3	Induration	90	Pruritus	
4	Cyst	80	White blood cell count decreased	
5	Nodule	80	Haemoglobin decreased	
6	Pruritus	65	Platelet count decreased	
7	Diarrhoea	33.5	Lip dry	
8	Nausea	23.7	Increased appetite	
9	Asthenia	17.4	Vomiting	
10	Fatigue	17.4	Dry skin	
11	Neuropathy peripheral	15.4	Dry mouth	
12	Sinusitis	9.5	Eructation	
13	Decreased appetite	8.6	Diabetes mellitus	
14	Ecchymosis	8	Aspartate aminotransferase increased	
15	Weight decreased	7.9	Alanine aminotransferase increased	
16	Anxiety	7.5	Blood bilirubin increased	
17	Musculoskeletal discomfort	7	Abdominal pain upper	
18	Myalgia	7	Amylase increased	

19	Skin papilloma	6.6	Alopecia
20	Influenza	6.5	Blood triglycerides increased
21	Lymphadenopathy	5.9	Fatigue
22	Dry skin	5	Feeling abnormal
23	Gastrointestinal pain	4.7	Malaise
24	Abdominal pain	4.7	Discomfort
25	Cough	4.7	Ill-defined disorder
26	Influenza like illness	4.5	Eczema
27	Herpes simplex	4.1	Flatulence
28	Conjunctivitis	4.1	Blood creatinine increased
29	Pneumonia	3.9	Libido decreased
..	...	...	...
254	Oropharyngeal discomfort	0	Hyperlactacidaemia
255	Aphthous stomatitis	0	Rhabdomyolysis
256	Suicide attempt	0	Hepatobiliary disease
257	Immune system disorder	0	Disorientation
258	Rhabdomyolysis	0	Respiratory disorder
259	Hepatobiliary disease	0	Respiration abnormal
260	Disorientation	0	Connective tissue disorder
261	Respiratory disorder	0	Blood pressure increased
262	Respiration abnormal	0	Nightmare
263	Connective tissue disorder	0	Bronchospasm
264	Blood pressure increased	0	Aggression
265	Bronchospasm	0	Renal failure acute
266	Aggression	0	Hypocalcaemia
267	Renal failure acute	0	Hypernatraemia
268	Hypocalcaemia	0	Drug hypersensitivity
269	Hypernatraemia	0	Herpes simplex
270	Hyperlactacidaemia	0	Induration
271	Drug hypersensitivity	0	Nodule
272	Thinking abnormal	0	Lymphadenopathy
273	Paraesthesia oral	0	Thinking abnormal
274	Liver function test abnormal	0	Paraesthesia oral
275	Hypophosphataemia	0	Liver function test abnormal
276	Myopathy	0	Hypophosphataemia
277	Amnesia	0	Myopathy
278	Rash maculo-papular	0	Amnesia
279	Dermatitis bullous	0	Rash maculo-papular
280	Hyperbilirubinaemia	0	Hyperbilirubinaemia
281	Dermatitis exfoliative	0	Dermatitis exfoliative
282	Blood creatinine increased	0	Herpes zoster
283	Hyperglycaemia	0	Hyperglycaemia

	val_3
0	50
1	50
2	50
3	50

```
4       50
5       50
6       50
7       50
8       50
9       50
10      50
11      50
12      50
13      50
14      50
15      50
16      50
17      50
18      50
19      50
20      50
21      50
22      50
23      50
24      50
25      50
26      50
27      50
28      50
29      50
..     ...
254      0
255      0
256      0
257      0
258      0
259      0
260      0
261      0
262      0
263      0
264      0
265      0
266      0
267      0
268      0
269      0
270      0
271      0
272      0
273      0
274      0
```

```
275     0
276     0
277     0
278     0
279     0
280     0
281     0
282     0
283     0

[284 rows x 8 columns]
```

In [41]:
```
#comparing similar clusters:
a = clusters_side_effects.groupby('Cluster_no') #group by the groups (doesn't display

cluster_val2 = pd.DataFrame(columns=['abacavir','val_0','efavirenz','val_1','emtricita
cluster_val2['abacavir']=clusters_side_effects.iloc[0,0:len(clusters_side_effects.colu
cluster_val2['val_0'] = clusters_side_effects.iloc[0,0:len(clusters_side_effects.colum
cluster_val2['efavirenz']=clusters_side_effects.iloc[1,0:len(clusters_side_effects.col
cluster_val2['val_1'] = clusters_side_effects.iloc[1,0:len(clusters_side_effects.colum
cluster_val2['emtricitabine']=clusters_side_effects.iloc[7,0:len(clusters_side_effects
cluster_val2['val_2'] = clusters_side_effects.iloc[7,0:len(clusters_side_effects.colum
cluster_val2['fosamprenavir']=clusters_side_effects.iloc[9,0:len(clusters_side_effects
cluster_val2['val_3'] = clusters_side_effects.iloc[9,0:len(clusters_side_effects.colum
```

```
a.get_group(1) #I can get the different groups
cluster_val2.head()
```

Out[41]:

	abacavir	val_0	efavirenz	val_1	emtricitabine	val_2	fosamprenavir	val_3
0	Rash	50	Abdominal pain	50	Hyperglycaemia	50	Abdominal pain	50
1	Lethargy	50	Hypertriglyceridaemia	50	Blood triglycerides increased	50	Dizziness	50
2	Hyperlactacidaemia	50	Nausea	50	Rash maculo-papular	50	Vomiting	50
3	Diarrhoea	50	Rash	50	Dermatitis bullous	50	Flatulence	50
4	Dermatitis	50	Dermatitis	50	Hyperbilirubinaemia	50	Fatigue	50

1.0.13 Co-administered Drug Database:

UCSF Database of Antiretroviral Drug Interactions

```
In [42]: #Getting list of URLs:

         url_list = [
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=21&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=15&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=10&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=329&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=341&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=25&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=337&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=16&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=17&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=235&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=347&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=9&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=259&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=225&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=261&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=23&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=11&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=1&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=24&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=14&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=18&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=3&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=2&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=12&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=19&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=5&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=205&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=8&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=4&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=13&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=335&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=7&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=6&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=22&post=4',
             'http://hivinsite.ucsf.edu/insite?page=ar-00-02&param=20&post=4'
         ]
```

The following function takes a URL and outputs the drug interaction table and the Name of the HIV/ART drug

```
In [43]: def get_drugdrug_interaction(url):

             url1=url #inputted URL
             user_agent = 'Mozilla/5.0 (Macintosh; Intel Mac OS X 10_14_1) AppleWebKit/537.36
             raw_html = requests.get(url1,
```

```
                                auth=('user', 'pass'),
                                headers={'User-Agent': user_agent})

        soup = BeautifulSoup(raw_html.text)
        soup.prettify()

        my_table = soup.find('table',{'class':'datatable'}) #get the table of class 'data

        rows = soup.find_all('tr')  #prints only table rows
        drug_name=soup.find('p',{'class':'kbrsec1'}) #gets you name of the drug
        drug_name=drug_name.getText()

        #deleting the undesirable td's:
        for div in soup.find_all("td", {'class':'cellleft'}):
            div.decompose()

        for div in soup.find_all("td", {'class':'cellrightblue'}):
            div.decompose()

        for div in soup.find_all("a"):
            div.decompose()

        coadmin_drugname=[]
        drug_dose=[]
        parsed_data=[]
        for tr in rows:
            td = tr.find_all('td')
            row = [i.text for i in td]
            parsed_data.append(row)

        #clean the dataset
        parsed_data=parsed_data[3:] #removing first three rows, not useful

        for i in parsed_data: #going through each element in parsed_data
            if i==[]:         #if the element is emppty
                parsed_data.remove(i) #go ahead and remove it

        dd=pd.DataFrame(parsed_data)
        dd=dd.dropna(axis=0)

        return(dd,drug_name)
```

Compiling complete list of Drug-Drug Interactions to implement Regular Expressions on interaction notes

```
In [44]: dd_list = [] #compiled list of drug-drug interaction table
         drug_name_list = [] #list of drug names (needs to be extracted using Re)
         length_eachdrug = [] #number of rows for each drug (will be used to add another colum
```

```
sum=0 #total number of rows in the interaction database

for i in np.arange(len(url_list)):
    dd,drug_name=get_drugdrug_interaction(url_list[i])
    dd_list.append(dd)
    drug_name_list.append(drug_name)
    length_eachdrug.append(len(dd))
    sum+=len(dd)

dd_compiled=pd.concat(dd_list)

drug_name_list[14] = 'All Interactions with Elvitegravir' #some forcing
```

Extract drug names from titles using Regular Expressions

```
In [45]: drug_name_list
         drug_brand_dd = [] #contains a list of the drug and its components/other names

         for element in drug_name_list:
              extract = re.findall('(?<=\().*?(?=\))',element) #getting anything inside braces
              if(len(extract) != 0):
                 drug_brand_dd.append(extract[0])
              else:
                 drug_brand_dd.append(element[22:])

         brand_names_dd_temp = [] #Brand names scaled for the drug-drug interaction list
         for i in np.arange(0,len(length_eachdrug)):
             temp_var = [drug_brand_dd[i]]*length_eachdrug[i]
             brand_names_dd_temp.append(temp_var)

         brand_names_dd = [item for sublist in brand_names_dd_temp for item in sublist] #colla
         dd_compiled['Brand_Names'] = brand_names_dd #adding the brand name to the column
         dd_compiled.columns = ['Interacting_Drug','Dosage_Intr','Dosage_ART','Effect_Intr_leve
         dd_compiled.to_pickle('/Users/mkocher/Desktop/ARTChat/pickled_data/dd_compiled.pkl')

In [46]: #Saving the interacting drugs into a list for Dash
         interacting_drug_dash = dd_compiled['Interacting_Drug'].unique()
         interacting_drug_dash.tolist()

         with open('/Users/mkocher/Desktop/ARTChat/data/interacting_drug.txt', 'w') as f:
             for item in interacting_drug_dash:
                 f.write("%s;" % item)
```

Codifying the Management of Drug-Drug Interactions

```
In [47]: safe_keywords = ['NO DOSE ADJUSTMENT NECESSARY']
         caution_keywords = ['DOSE ADJUSTMENT NOT ESTABLISHED','MONITOR','MONITORING','CAUTION
```

```
danger_keywords = ['AVOID','DO NOT COADMINISTER','AVOID COADMINISTRATION','AVOID COMBI

interaction_metric = []
for i in np.arange(0,len(dd_compiled['Management'])):
    if(((dd_compiled.iloc[i,7].upper()).find(caution_keywords[0]) != -1) | ((dd_compil
        interaction_metric.append(2)
    elif(((dd_compiled.iloc[i,7].upper()).find(safe_keywords[0]) != -1)):
        interaction_metric.append(1)
    elif(((dd_compiled.iloc[i,7].upper()).find(danger_keywords[0]) != -1) | ((dd_compi
        interaction_metric.append(3)
    else:
        interaction_metric.append(4)

dd_compiled['Management_Code'] = interaction_metric
dd_compiled_art= pd.merge(left=drugs_art,right=dd_compiled, left_on='Brand_Names', rig
dd_compiled_art.to_pickle('/Users/mkocher/Desktop/ARTChat/pickled_data/dd_compiled_art

dd_compiled_art.head()
```

Out[47]:

	Brand_Names	Generic_Name/Other_Names	Drug_Class	\
0	Ziagen	[abacavir]	NRTI	
1	Ziagen	[abacavir]	NRTI	
2	Ziagen	[abacavir]	NRTI	
3	Ziagen	[abacavir]	NRTI	
4	Ziagen	[abacavir]	NRTI	

	Interacting_Drug	Dosage_Intr	\
0	Amprenavir(APV)(Agenerase)	900 mg BID x 3 weeks	
1	Ethanol, (Alcohol, Ethanol, Wine, Liquor, Beer...	0.7 g/kg body weight	
2	Lamivudine, (3TC)(Epivir)	150 mg x 1 dose	
3	Methadone(Dolophine)(Dolophine)	40 mg QD; 90 mg QD	
4	Mycophenolate(CellCept)(CellCept)	500 mg BID x 8 weeks	

	Dosage_ART	Effect_Intr_level	\
0	300 mg BID x 3 weeks	Amprenavir Cmax: increased 47%; AUC: increased...	
1	600 mg QD	No significant change	
2	600 mg x 1 dose	Lamivudine Cmax: decreased 35%; AUC: decreased...	
3	600 mg BID	Methadone clearance: increased 22%	
4	300 mg BID	Not studied	

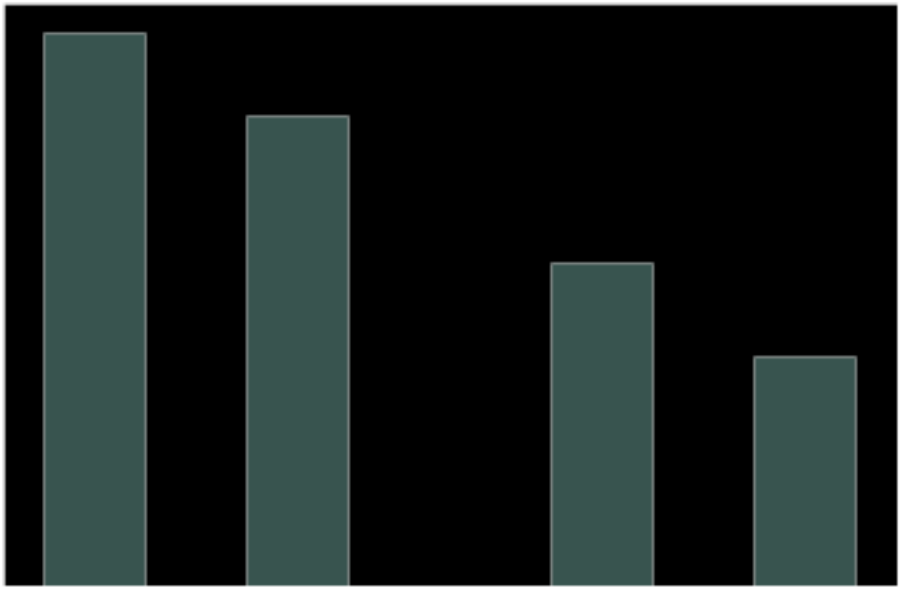
	Effect_ART_level	\
0	Not studied	
1	Abacavir AUC: increased 41%; half-life: increa...	
2	No significant change	
3	No significant change	
4	No significant change	

	Clinical_Effects	\

```
0                                                  -
1                                                  -
2                                                 -
3  Decreased methadone effects (eg, withdrawal)
4                                                  -

                                          Interactions  \
0                                                    -
1  Decreased abacavir metabolism by alcohol dehyd...
2                        Delayed lamivudine absorption
3                                                    -
4                                                    -

                                           Management Brand_Name  \
0                  Dose adjustment not established      Ziagen
1                      No dose adjustment necessary     Ziagen
2                     No dose adjustment necessary      Ziagen
3  Monitor for signs and symptoms of methadone wi...     Ziagen
4                      No dose adjustment necessary     Ziagen

   Management_Code
0                2
1                1
2                1
3                2
4                1
```

In [48]:
```
#Historgram of drug-drug interaction Management code:
plt.figure()
plt.style.use('dark_background')
sns.distplot(dd_compiled_art['Management_Code'],kde=False)
plt.show()
```

```
/Users/mkocher/anaconda3/lib/python3.7/site-packages/scipy/stats/stats.py:1713: FutureWarning:
  return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval
```



1.0.14 Extracting side-effect data for a user-inputted HIV/ART drug

1.0.15 ARTChat Version 1.0 Output Channel :

Provides 1 component recommendation

Here are 5 functions that go into the recommendation framework

```
In [54]: def drugs_to_avoid(drug_name, side_effect_user):
             '''
             Identify the drugs to avoid based on the side-effect frequency
             '''
             print('------------------------DRUGS TO AVOID--------------------------')
             #1. Finding the location of the drug taken in the HIV/ART database
             drug_taken = drugs_art.loc[drugs_art['Brand_Names'].str.lower() ==
                                        drug_user.lower()]

             #2. Checking if it is combination drug
             if drugs_art['Drug_Class'][drug_taken.index[0]] == 'Comb':
                 print('Your therapy is a cocktail of the following drugs:')
             else:
                 print('The generic name of your drug is:')

             #3. Extracting the ingredients of the combination drugs
             ingr_list = drugs_art['Generic_Name/Other_Names'][drug_taken.index[0]]
```

```
    print(ingr_list)  #print statement

    #4. Which drug(s) contributes most to the side-effect in question
    freq_side_effect_user = np.zeros(len(ingr_list))
    for i in np.arange(0, len(ingr_list) - 1):

        #5. First check if the drug is represented in the side-effect database:
        if ((ingr_list[i] in reduced_list.index) == True):
            freq_side_effect_user[i] = reduced_list.loc[ingr_list[i],
                                                        side_effect_user]
        else:
            freq_side_effect_user[
                i] = np.nan  #if the drug doesn't exit in the side-effect database
            #assign NaN to the frequency
            print('{0} does not exist in the SIDER database'.format(
                ingr_list[i]))

    #6. Which drugs contribute most of these side-effects? We will avoid them in the
    max_freq = np.nanmax(freq_side_effect_user)

    ingr_list = np.asarray(ingr_list)  #converting ingr_list to numpy array
    drugs_avoid = ingr_list[np.where(freq_side_effect_user == max_freq)]

    print(
        'The drug(s) that contribute(s) most to your {0} side-effect is(are): {1}'
        .format(side_effect_user, drugs_avoid))
    return(drugs_avoid)


def cluster_identifier(drug_name, rank):
    '''
    Identifies the cluster based on rank requested and returns drugs in the cluster
    '''
    #Step 1: Finding clusters that the undesirable drugs are seated in
    print('------------------------CLUSTER IDENTIFIER-------------------------')
    cluster_nos=[]
    cluster_desired_all=[]
    for i in np.arange(0,len(drug_name)):

        index = cluster_results.loc[cluster_results['Drug'].str.lower() == drug_name[

        cluster_no = index['Cluster_no'].values  #gives you cluster number of the dru
        print(cluster_no)
        cluster_no = cluster_no[0]  #collapses numpy array to a number for ease in in
        cluster_nos.append(cluster_no) #cluster numbers

        #Step 2: Find the cluster at the nth (rank) largest distance
        loc_array = heapq.nlargest(3,range(len(ranks_dist[cluster_no])), key=ranks_dis
```

```
        #above: list of farthest to closest cluster
        cluster_desired = loc_array[rank]
        cluster_desired_all.append(cluster_desired)

    #Step 3: Make sure cluster_desired_all has no values from cluster_nos
    cluster_desired_shaved=[]
    for i in np.arange(0,len(cluster_desired_all)):
        if cluster_desired_all[i] not in cluster_nos:
            cluster_desired_shaved.append(cluster_desired_all[i])

    #Step 4: Make cluster_desired_shaved into a Series
    cluster_desired_shaved = pd.DataFrame({'desired_cluster':cluster_desired_shaved})

    #Step 5: Find the drugs within these desired clusters
    index_dr = pd.merge(left=cluster_results,right=cluster_desired_shaved,left_on='Clu

    return(index_dr['Drug']) #returns a pandas Series


def frequency_check(possible_drugs_1,side_effect):
    '''
    This function reduces a list of drug to ones where frequency of undesirable sidee
    '''
    #possible_drugs_1 = possible_drugs_1.tolist() #convert the drug series to a list

    drug_frequency_option = reduced_list.loc[possible_drugs_1,side_effect] #
    possible_drugs_2 = drug_frequency_option[drug_frequency_option.values < 50.00]
    return(possible_drugs_2.index)

def interaction_checker(drugs_recommended,coadmin_drug_user):

    string_1 = drugs_recommended['Drug'].tolist() #list of drugs that match a frequen
    #string_1 = drugs_recommended
    #Cleaning up columns in Compiled ART and their drug-drug interaction database
    dd_compiled_art['Generic_Name/Other_Names'] = [str(i).replace('[', '').replace(']
    dd_compiled_art['Generic_Name/Other_Names'] = [str(i).replace("\'", '') for i in c

    #Identifying ARTs that interact
    interactions_only = dd_compiled_art.loc[(dd_compiled_art['Generic_Name/Other_Names

    to_drop = interactions_only['Generic_Name/Other_Names']
    to_drop_name = to_drop.values.tolist()
    for i in np.arange(0,len(to_drop_name)):
        drugs_recommended = drugs_recommended[drugs_recommended.Drug != to_drop_name[i

    return(drugs_recommended)

def class_check(possible_drugs_2):
```

```
        '''
        returns a confidence value, if desired combination of 2 NRTIs and 1 PI/Insti is a
        '''
        #Step 1: Create a dataframe with drugs & their labels
        drugs_copy = copy.deepcopy(drugs_art)
        drugs_copy['Generic_Name/Other_Names'] = [str(i).replace('[', '').replace(']', ''
        drugs_copy['Generic_Name/Other_Names'] = [str(i).replace("\'", '') for i in drugs_
        drugs_labeled = drugs_copy.loc[(drugs_copy['Generic_Name/Other_Names'].isin(possi

        return(drugs_labeled)

    def combination_recommender(drugs_recommended_final):
        a = drugs_art.groupby('Drug_Class')
        comb_df = a.get_group('Comb').reset_index()
        comb_rec = []
        for i in np.arange(0,len(comb_df)):
            check = len(comb_df.loc[i]['Generic_Name/Other_Names']) #number of components
            truth = drugs_recommended_final['Generic_Name/Other_Names'].isin(comb_df.loc[
            check_i = np.sum(truth.values) #number of trues
            if check == check_i:
                comb_rec.append(comb_df.loc[i]['Brand_Names'])
        return(comb_rec)
```

1.0.16 Function to check if the a drug has an interaction with another drug:

In [55]:
```
drug_user = 'Genvoya'
coadmin_drug_user = 'Amiodarone'
side_effect_user = 'Asthenia,Gastrointestinal pain'

#If the user inputs one drug and multiple side-effects
#drug_user = str(input('What HIV/ART drug or drugs are you taking?')) #Loop this inca
#side_effect_user = str(input('What side-effect are you experiencing?'))
#coadmin_drug_user = str(input('What drug are you co-administering?'))
side_effect_user = side_effect_user.split(',') #useful if you have multiple inputs an
coadmin_drug_user = coadmin_drug_user.split(',')
print(side_effect_user)
#Step 1: Culprit Identification:
drugs_avoid_all=[]

for i in np.arange(0,len(side_effect_user)):
    drugs_avoid = drugs_to_avoid(drug_name = drug_user, side_effect_user = side_effect
    drugs_avoid = drugs_avoid.tolist()
    drugs_avoid_all.append(drugs_avoid) #appends all drugs to avoid

drugs_avoid_all = [item for sublist in drugs_avoid_all for item in sublist]
print(drugs_avoid_all)
drugs_avoid_all = list(dict.fromkeys(drugs_avoid_all))
```

```
print(drugs_avoid_all)

print('List of drugs to avoid based on contribution to side-effects are {0}'.format(dr

rank_1 = 0
count_nrti = 0
count_ii = 0
count_pi = 0

drugs_recommended_final = pd.DataFrame(columns=['Brand_Names','Generic_Name/Other_Name

loop_end = 0
while((loop_end != 1) & (rank_1 < 3)):

    #Step 2: Cluster Identification:
    drugs_1 = cluster_identifier(drug_name = drugs_avoid_all, rank = rank_1) #returns
    print('Drugs in clusters at rank {0} are {1}'.format(rank_1,drugs_1))


    #Step 3: Frequency Check
    drugs_2 = copy.deepcopy(drugs_1)
    for i in np.arange(len(side_effect_user)): #Going through each side-effect
        drugs_1 = copy.deepcopy(drugs_2)
        drugs_2 = frequency_check(possible_drugs_1 = drugs_1, side_effect = side_effec
                  #for each side-effect returning only the drugs that have side-effec
        drugs_2 = drugs_2.tolist()

    drugs_2 = pd.DataFrame({'Drug':drugs_2})#input for interaction checker is a dataf

    #Step 4: Ensuring the drugs don't interact with anything else
    drugs_25 = interaction_checker(drugs_recommended = drugs_2,coadmin_drug_user = coa

    #Step 5: What are the different classes of the drugs?
    drugs_3 = class_check(possible_drugs_2 = drugs_25) #input is a dataframe of drugs

    drugs_3 = drugs_3.drop_duplicates('Generic_Name/Other_Names') #drop duplicate val

    #Step 6: Confidence value
    count_nrti = count_nrti + len(drugs_3[drugs_3['Drug_Class'] == 'NRTI']) #can doub
    count_ii   = count_ii   + len(drugs_3[drugs_3['Drug_Class'] == 'INSTI'])
    count_pi   = count_pi   + len(drugs_3[drugs_3['Drug_Class'] == 'PI'])

    if (count_nrti >= 2):
        if ((count_pi >= 1) | (count_ii >= 1)):
            loop_end = 1 #exit out of the loop

    rank_1 +=1 #move to the next cluster
    drugs_recommended_final = drugs_recommended_final.append(drugs_3)
```

```
        combinations_final = combination_recommender(drugs_recommended_final)

        if (len(combinations_final) == 0):
            output_combinations = 'No existing brands offer an appropriate combination based
        else:
            output_combinations = str(combinations_final)


        print('We went to the {0} farthest cluster to find combinations'.format(rank_1-1))
        print('All drugs recommended are:')
        drugs_recommended_final = drugs_recommended_final.drop_duplicates('Generic_Name/Other
        drugs_recommended_final
```

```
['Asthenia', 'Gastrointestinal pain']
-----------------------DRUGS TO AVOID-------------------------
Your therapy is a cocktail of the following drugs:
['elvitegravir', 'cobicistat', 'emtricitabine', 'tenofovir']
The drug(s) that contribute(s) most to your Asthenia side-effect is(are): ['elvitegravir' 'cobi
-----------------------DRUGS TO AVOID-------------------------
Your therapy is a cocktail of the following drugs:
['elvitegravir', 'cobicistat', 'emtricitabine', 'tenofovir']
The drug(s) that contribute(s) most to your Gastrointestinal pain side-effect is(are): ['elvite
['elvitegravir', 'cobicistat', 'elvitegravir', 'cobicistat', 'emtricitabine']
['elvitegravir', 'cobicistat', 'emtricitabine']
List of drugs to avoid based on contribution to side-effects are ['elvitegravir', 'cobicistat'
-----------------------CLUSTER IDENTIFIER-------------------------
[2]
[2]
[2]
Drugs in clusters at rank 0 are 0    saquinavir
1    saquinavir
2    saquinavir
Name: Drug, dtype: object
-----------------------CLUSTER IDENTIFIER-------------------------
[2]
[2]
[2]
Drugs in clusters at rank 1 are 0    enfuvirtide
1    enfuvirtide
2    enfuvirtide
Name: Drug, dtype: object
-----------------------CLUSTER IDENTIFIER-------------------------
[2]
[2]
[2]
Drugs in clusters at rank 2 are 0       lamivudine
1       lamivudine
```

```
2       lamivudine
3       nevirapine
4       nevirapine
5       nevirapine
6        ritonavir
7        ritonavir
8        ritonavir
9       zidovudine
10      zidovudine
11      zidovudine
12       tenofovir
13       tenofovir
14       tenofovir
15      etravirine
16      etravirine
17      etravirine
18       darunavir
19       darunavir
20       darunavir
21       maraviroc
22       maraviroc
23       maraviroc
24     rilpivirine
25     rilpivirine
26     rilpivirine
27     raltegravir
28     raltegravir
29     raltegravir
30    dolutegravir
31    dolutegravir
32    dolutegravir
Name: Drug, dtype: object
We went to the 2 farthest cluster to find combinations
All drugs recommended are:
```

Out[55]:

	Brand_Names	Generic_Name/Other_Names	Drug_Class
17	Fuzeon	enfuvirtide	FI
2	Epivir	lamivudine	NRTI
3	Viread	tenofovir	NRTI
4	Retrovir	zidovudine	NRTI
7	Intelence	etravirine	NNRTI
8	Viramune	nevirapine	NNRTI
10	Edurant	rilpivirine	NNRTI
12	Prezista	darunavir	PI
18	Selzentry	maraviroc	CCR5
19	Tivicay	dolutegravir	INSTI
20	Isentress	raltegravir	INSTI

```
In [381]: print(output_combinations)

['Dovato', 'Juluca', 'Cimduo', 'Combivir']


In [53]: drugs_copy = copy.deepcopy(drugs_art)
         drugs_copy['Generic_Name/Other_Names'] = [str(i).replace('[', '').replace(']', '') fo
         drugs_copy['Generic_Name/Other_Names'] = [str(i).replace("\'", '') for i in drugs_copy
         drugs_copy = drugs_copy.loc[(drugs_copy['Generic_Name/Other_Names'].isin(drugs_25['Dru
```

The code to deploy this prescription recommender as an app is laid out separately. Please email manan.kocher@gmail.com incase of any questions.