Data Methods for Health Research

National Healthcare Service (NHS) review

Despite improvements in the NHS, the public healthcare system has been facing unrelenting pressure over the past years. Thus, a better understanding of its costs is a pressing need, so that potential areas for improvement can be identified and available resources can be allocated more efficiently. Herein, we have carried out a review which aims to document and assess GP prescribing costs for the NHS England in April 2018. The data used for this review comes from two different .csv files. The first file captures the number of patients registered at a GP practice (https://digital.nhs.uk/data-and-information/publications/statistical/practice-level-prescribing-data/april-2018)) and the second file the practice level prescribing-data/april-2018) (https://digital.nhs.uk/data-and-information/publications/statistical/practice-level-prescribing-data/april-2018) (https://digital.nhs.uk/data-and-information/publications/statistical/practice-level-prescribing-data/april-2018)), both from April 2018.

In [1]:

```
import numpy as np # We import numpy and abbreviate as np
import pandas as pd # We import pandas and abbreviate as pd
import matplotlib.pyplot as plt # We import matplotlib and abbreviate as plt
from scipy import stats # We import stats from scipy to work with statistical packages
# We ensure our plots open in the notebook
%matplotlib inline
```

First, an exploratory data analysis of the file containing the number of patients registered at a GP practice in April 2018 has been performed.

```
In [2]:
```

```
df1=pd.read_csv('https://files.digital.nhs.uk/71/B59D99/gp-reg-pat-prac-all.csv')
```

In [3]:

```
# Number of rows and columns
df1.shape
```

Out[3]:

(7241, 10)

In [4]:

```
# Exploration of the first rows of the DataFrame
df1.head()
```

Out[4]:

_	PUBLICATION	EXTRACT_DATE	TYPE	CCG_CODE	ONS_CCG_CODE	CODE	POSTC
_	0 GP_PRAC_PAT_LIST	01APR2018	GP	00C	E38000042	A83005	DL1
	1 GP_PRAC_PAT_LIST	01APR2018	GP	00C	E38000042	A83006	DL3
	2 GP_PRAC_PAT_LIST	01APR2018	GP	00C	E38000042	A83010	DL3
	3 GP_PRAC_PAT_LIST	01APR2018	GP	00C	E38000042	A83013	DL1
	4 GP_PRAC_PAT_LIST	01APR2018	GP	00C	E38000042	A83031	DL3

In [5]:

No missing values present in any of the columns
df1.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 7241 entries, 0 to 7240
Data columns (total 10 columns):

7241 non-null object PUBLICATION 7241 non-null object EXTRACT_DATE 7241 non-null object TYPE CCG_CODE 7241 non-null object ONS_CCG_CODE 7241 non-null object 7241 non-null object CODE POSTCODE 7241 non-null object 7241 non-null object SEX 7241 non-null object AGE NUMBER OF PATIENTS 7241 non-null int64

dtypes: int64(1), object(9)
memory usage: 565.8+ KB

In [6]:

Summary statistics
df1.describe()

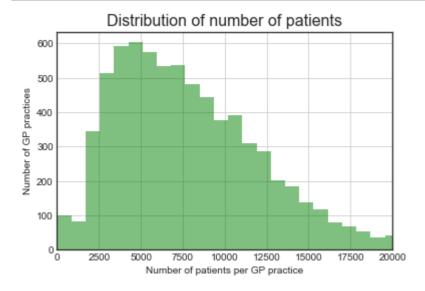
Out[6]:

NUMBER_OF_PATIENTS

count	7241.000000
mean	8153.514017
std	5184.888435
min	1.000000
25%	4501.000000
50%	7235.000000
75%	10711.000000
max	72227.000000

In [7]:

```
# Plot of histogram
plt.style.use('seaborn-white')
bins=int(np.sqrt(len(df1['NUMBER_OF_PATIENTS'])))
plt.hist(df1['NUMBER_OF_PATIENTS'], bins=bins, alpha=0.5, histtype='stepfilled', color='gre
plt.xlabel('Number of patients per GP practice')
plt.xlim(-10,20000)
plt.ylabel('Number of GP practices')
plt.title('Distribution of number of patients', fontsize=16)
plt.grid()
plt.show()
# Analysing skewness and kurtosis can also provide us useful information about our data wit
from scipy.stats import kurtosis
from scipy.stats import skew
k=round(kurtosis(df1['NUMBER_OF_PATIENTS']),2)
print('Kurtosis is {}. The distribution has a positive kurtosis.'.format(k))
s=round(skew(df1['NUMBER_OF_PATIENTS']),2)
print('Skewness is {}. The distribution is positively skewed.'.format(s))
```



Kurtosis is 13.59. The distribution has a positive kurtosis. Skewness is 2.27. The distribution is positively skewed.

Now, an exploratory analysis of the file containing the practice prescription level has been carried out.

In [8]:

```
df2=pd.read_csv('Prescribing.csv') # https://files.digital.nhs.uk/38/03EC1C/T201804PDPI%20E
```

In [9]:

```
df2.shape
```

Out[9]:

(9748354, 11)

In [10]:

df2.head()

Out[10]:

	SHA	PCT	PRACTICE	BNF CODE	BNF NAME	ITEMS	NIC	ACT COST	QUANTITY
0	Q44	RTV	Y04937	0401010Z0AAAAA	Zopiclone_Tab 7.5mg	6	1.56	2.12	63
1	Q44	RTV	Y04937	0401020K0AAAHAH	Diazepam_Tab 2mg	4	0.87	1.15	73
2	Q44	RTV	Y04937	0401020K0AAAIAI	Diazepam_Tab 5mg	2	0.46	0.56	35
3	Q44	RTV	Y04937	0402010ABAAABAB	Quetiapine_Tab 25mg	1	2.60	2.52	14
4	Q44	RTV	Y04937	0402010ADAAAAAA	Aripiprazole_Tab 10mg	1	1.53	1.53	14

In [11]:

df2.info(verbose=True, null_counts=True) # for large datasets, it is needed to display full

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 9748354 entries, 0 to 9748353

Data columns (total 11 columns):

SHA	9748354 non-null object
PCT	9748354 non-null object
PRACTICE	9748354 non-null object
BNF CODE	9748354 non-null object
BNF NAME	9748354 non-null object
ITEMS	9748354 non-null int64
NIC	9748354 non-null float64
ACT COST	9748354 non-null float64
QUANTITY	9748354 non-null int64
PERIOD	9748354 non-null int64
	9748354 non-null object

dtypes: float64(2), int64(3), object(6)

memory usage: 818.1+ MB

In order to make the information present in the prescribing dataset more understandable to the reader, column indexes with acronyms have been renamed with the full description and columns which are not relevant for the analysis have been dropped, too.

In [12]:

Out[12]:

	PRACTICE	BNF_CODE	BNF_NAME	ITEMS	NET_INGREDIENT_COST	ACTUAL_C
0	Y04937	0401010Z0AAAAA	Zopiclone_Tab 7.5mg	6	1.56	
1	Y04937	0401020K0AAAHAH	Diazepam_Tab 2mg	4	0.87	
2	Y04937	0401020K0AAAIAI	Diazepam_Tab 5mg	2	0.46	
3	Y04937	0402010ABAAABAB	Quetiapine_Tab 25mg	1	2.60	
4	Y04937	0402010ADAAAAA	Aripiprazole_Tab 10mg	1	1.53	

In [13]:

```
df2.describe(include='all')
```

Out[13]:

	PRACTICE	BNF_CODE	BNF_NAME	ITEMS	NET_INGREDIENT_COST	AC
count	9748354	9748354	9748354	9.748354e+06	9.748354e+06	ξ
unique	9578	22358	19227	NaN	NaN	
top	M85063	0603020T0AAACAC	GlucoRX FinePoint Needles Pen Inj Screw	NaN	NaN	
freq	4003	7964	16287	NaN	NaN	
mean	NaN	NaN	NaN	9.115409e+00	7.078242e+01	6
std	NaN	NaN	NaN	2.999382e+01	1.918400e+02	1
min	NaN	NaN	NaN	0.000000e+00	0.000000e+00	(
25%	NaN	NaN	NaN	1.000000e+00	7.920000e+00	7
50%	NaN	NaN	NaN	2.000000e+00	2.250000e+01	2
75%	NaN	NaN	NaN	6.000000e+00	6.286000e+01	Ę
max	NaN	NaN	NaN	5.147000e+03	3.391873e+04	3

Once a preliminar exploratory analysis has been done, we have delved into two specific locations in the UK: Cambridge and London.

For each of these cities, the total number of practices, patients registered, prescriptions, actual cost of these prescriptions and the top 10 and bottom 10 drugs prescribed will be reported. Since the same operations had to be performed twice, functions have been defined, so that they can be called when appropriate and the code is kept as concise as possible.

First, the practices in London and Cambridge have to be collated from the dataset.

The Organisation Data Service at NHS Digital is responsible for the publication of the definitive list of organisation codes and names across the NHS. Thus, it assigns the clinical commissioning groups (CCGs) authorisations. In London, the CCG codes of the healthcare services range from '07L' to '09A'. Consequently, all the practices labelled with these codes are located in London.

The CCG code for Cambridge would be 06H. However, this CCG code covers the NHS in Cambridgeshire and Peterborough and this would not be specific enough. Thus, we have used the postcode as an identifier instead. The postcodes for the city of Cambridge range from CB1 to CB5 according to https://data.gov.uk/dataset/9bd39552-5b5c-4a87-9fdc-fb2b0142b3c8/cambridgeshire-postcodes).

In [14]:

```
# We define a function to identify the practices in each city
def practice(city):
    # Regular expressions to identify city-specific GP practices
    if city=='London':
        city_practice=df1[df1.CCG_CODE.str.match('07[L-Z]|08[A-Y]|09A')]
    if city=='Cambridge':
        city_practice=df1[df1.POSTCODE.str.match('CB[1-5]')]

list_city_practice=city_practice.CODE.tolist()
return list_city_practice, city_practice
```

After having identified the practices located in the city of interest, the rest of the parameters can be determined.

In [15]:

```
def no_patients(city):
    no_patients_tot=np.sum(df1['NUMBER_OF_PATIENTS'])
    no_patients_city=np.sum(practice(city)[1].NUMBER_OF_PATIENTS) # Sum number of patients
    ratio_patients=np.round(np.divide(no_patients_city,no_patients_tot)*100,2) # Calculatic
    return no_patients_city, ratio_patients
```

In [16]:

```
def no_prescriptions(city):
    no_prescriptions_tot=np.sum(df2['ITEMS'])
    no_prescriptions_city=np.sum(df2[df2['PRACTICE'].isin(practice(city)[0])].ITEMS) # Sum
    ratio_prescriptions_city=np.round(np.divide(no_prescriptions_city,no_prescriptions_tot)
    return no_prescriptions_city, ratio_prescriptions_city
```

In [17]:

```
def total_cost(city):
    total_cost_global=np.sum(df2['ACTUAL_COST'])
    total_cost_city=np.round(np.sum(df2[df2['PRACTICE'].isin(practice(city)[0])].ACTUAL_COS
    ratio_cost_city=np.round(np.divide(total_cost_city,total_cost_global)*100,2)
    return total_cost_city, ratio_cost_city
```

In [18]:

```
def freq_city(city):
    #We first define a function which cleans the DataFrame from irrelevant columns and rese
    df2_city_freq=df2[df2['PRACTICE'].isin(practice(city)[0])][['BNF_NAME','BNF_CODE','ITEM
    freq1_city=df2_city_freq.reset_index(0, drop=True)
    return freq1_city
```

In [19]:

```
def top10_drugs(city):
    # freq_city function is called
    freq1_city=freq_city(city)

# Frequencies grouped by the first 9 characters of the BNF CODE (describe the chemical
    freq2_city=freq1_city.groupby(lambda e: freq1_city.iloc[e, 1][:9]).agg({'BNF_NAME': lam
    # Since we grouped by chemical substances, strength or formulation of the drug might di
    # Irrelevant information often comes after the '_' following the drug name
    freq2_city['BNF_NAME']=freq2_city.apply(lambda z: z['BNF_NAME'].split()[0].split('_')[@]
    return freq2_city
```

In order to determine the bottom 10 less frequent prescribed drugs, we had to consider the fact that several drugs could be prescribed with low frequencies. Therefore, we have devised a method by which we report all of the drugs prescribed with frequencies ranging from 1 to 10. Of note, some of the names of the drugs prescribed with lower frequency might not be informative enough (especially if we take the first word of the string of the drug). However, having the BNF CODE available, the actual drug could be easily tracked in the British National Formulary (BNF).

In [20]:

```
def bottom10 drugs(city):
   # Top10 drugs are reversed, so that we start from bottom 10
   freq3_city=top10_drugs(city).sort_values(by='ITEMS',ascending=True).reset_index(0, drop
    # keys for dictionaries are in a list
    keys=list(np.arange(1,11))
    # Index of the last drug being prescribed 10 times is located
    index=freq3_city[freq3_city['ITEMS']==10].index[-1]
    # Loop-filled dictionaries are created
   freq_dict1={} # This dictionary will contain BNF NAME
   freq_dict2={} # This dictionary will contain BNF_CODE
    j=0 # We set counter j at 0, so that we start with the first value from the list 'keys'
    # We start a loop ranging from 0 to 'index'
   for i in range(0,index+1):
        if keys[j] not in freq_dict1: #Only unique drugs will be added
            freq_dict1[keys[j]]=list()
            freq_dict2[keys[j]]=list()
        # Prescription frequency has to match the corresponding key in 'keys'
        if freq3_city.iloc[i,2]==keys[j]:
            freq_dict1[keys[j]].append(freq3_city.iloc[i,0]) #Adding the BNF_NAME
            freq_dict2[keys[j]].append(freq3_city.iloc[i,1].rstrip()) #Adding the BNF_CODE
            j=j+1 # When the key has been filled with all the drugs with that frequency, mo
   # Conversion of dictionaries into DataFrames
   freq_dict1=pd.DataFrame.from_dict(freq_dict1, orient='index').transpose().fillna('')
   freq_dict2=pd.DataFrame.from_dict(freq_dict2, orient='index').transpose().fillna('')
    # Concatenation of DataFrames
    bttm10_city=pd.concat([freq_dict1,freq_dict2], axis=1)
    # Defining column names for the concatenated DataFrame
    bttm10_city=bttm10_city[list(set(sum(zip(freq_dict1.columns, freq_dict2.columns),())))]
    iterables=[[str(i) for i in range(1,11)],['BNF_NAME','BNF_CODE']]
    bttm10 city.columns=pd.MultiIndex.from product(iterables).rename('prescription frequence
    return bttm10_city
```

For further descriptive statistical analysis, it might also be relevant to display the number of registered patients, prescriptions and total costs detailed by practice.

In [21]:

```
def no_patients_city_bypractice(city):
    no_patients_city_bypractice=pd.DataFrame(practice(city)[1][['CODE','NUMBER_OF_PATIENTS'
    return no_patients_city_bypractice
```

```
In [22]:
```

Once all the functions have been defined, we have proceeded with the analysis of the London GP practices.

Identification of all GP practices located in London
list_ldn_practice=practice('London')[0]
print('There are {} registered GP practices in London in April 2018.\nThe codes of the GP p

There are 1323 registered GP practices in London in April 2018. The codes of the GP practices in London are the following: ['F82001', 'F82003', 'F82005', 'F82012', 'F82015', 'F82017', 'F82018', 'F820 25', 'F82027', 'F82034', 'F82038', 'F82040', 'F82042', 'F82051', 'F82604', 'F82612', 'F82621', 'F82625', 'F82634', 'F82642', 'F82647', 'F82650', 'F8266 0', 'F82661', 'F82668', 'F82676', 'F82677', 'F82678', 'F82679', 'F82680', 'F 86040', 'Y01280', 'Y01719', 'Y01795', 'Y02575', 'Y02583', 'Y04786', 'E8300 3', 'E83005', 'E83006', 'E83007', 'E83008', 'E83009', 'E83010', 'E83011', 'E 83012', 'E83013', 'E83016', 'E83017', 'E83018', 'E83020', 'E83021', 'E8302 4', 'E83025', 'E83026', 'E83027', 'E83028', 'E83030', 'E83031', 'E83032', 'E 83034', 'E83035', 'E83036', 'E83037', 'E83038', 'E83039', 'E83041', 'E8304 4', 'E83045', 'E83046', 'E83049', 'E83050', 'E83053', 'E83600', 'E83613', 'E 83621', 'E83622', 'E83624', 'E83629', 'E83631', 'E83632', 'E83633', 'E8363 7', 'E83638', 'E83639', 'E83644', 'E83649', 'E83650', 'E83653', 'E83657', 'E 83668', 'Y00105', 'Y00316', 'Y01697', 'Y02986', 'Y03663', 'Y03664', 'G8300 2', 'G83004', 'G83005', 'G83006', 'G83009', 'G83010', 'G83018', 'G83024', 'G 83025', 'G83028', 'G83029', 'G83033', 'G83037', 'G83046', 'G83047', 'G8304 9', 'G83052', 'G83053', 'G83057', 'G83061', 'G83062', 'G83064', 'G83066', 'G 83630', 'G83642', 'G83672', 'E83654', 'E84002', 'E84003', 'E84006', 'E8400 7', 'E84011', 'E84012', 'E84013', 'E84015', 'E84017', 'E84020', 'E84021', 'E 84023', 'E84025', 'E84026', 'E84028', 'E84030', 'E84031', 'E84032', 'E8403 3', 'E84036', 'E84042', 'E84048', 'E84049', 'E84051', 'E84056', 'E84063', 'E 84066', 'E84067', 'E84074', 'E84076', 'E84077', 'E84078', 'E84080', 'E8408 3', 'E84084', 'E84086', 'E84620', 'E84624', 'E84626', 'E84635', 'E84637', 'E 84638', 'E84645', 'E84656', 'E84665', 'E84667', 'E84669', 'E84674', 'E8467 8', 'E84684', 'E84685', 'E84690', 'E84696', 'E84699', 'E84701', 'E84702', 'E 84704', 'E84705', 'E84709', 'Y00206', 'Y01090', 'Y02692', 'G84001', 'G8400 2', 'G84003', 'G84004', 'G84005', 'G84006', 'G84007', 'G84008', 'G84009', 'G 84010', 'G84011', 'G84013', 'G84015', 'G84016', 'G84017', 'G84018', 'G8401 9', 'G84020', 'G84021', 'G84022', 'G84023', 'G84024', 'G84025', 'G84027', 'G 84028', 'G84029', 'G84030', 'G84032', 'G84033', 'G84035', 'G84039', 'G8404 0', 'G84041', 'G84604', 'G84607', 'G84609', 'G84621', 'G84624', 'G84625', 'G 84627', 'G84628', 'G84629', 'G84630', 'Y00542', 'Y02811', 'F83003', 'F8300 5', 'F83006', 'F83011', 'F83017', 'F83018', 'F83019', 'F83020', 'F83022', 'F 83023', 'F83025', 'F83042', 'F83043', 'F83044', 'F83048', 'F83050', 'F8305 2', 'F83055', 'F83057', 'F83058', 'F83059', 'F83061', 'F83615', 'F83623', 'F 83632', 'F83633', 'F83635', 'F83658', 'F83665', 'F83672', 'F83677', 'F8368 2', 'F83683', 'Y02674', 'F84003', 'F84008', 'F84013', 'F84015', 'F84018', 'F 84021', 'F84033', 'F84035', 'F84036', 'F84038', 'F84041', 'F84043', 'F8406 0', 'F84063', 'F84069', 'F84072', 'F84080', 'F84096', 'F84105', 'F84115', 'F 84117', 'F84119', 'F84601', 'F84619', 'F84620', 'F84621', 'F84624', 'F8463 2', 'F84635', 'F84636', 'F84640', 'F84659', 'F84668', 'F84685', 'F84686', 'F 84692', 'F84694', 'F84711', 'F84716', 'F84719', 'F84720', 'Y00403', 'Y0304 9', 'H83001', 'H83004', 'H83005', 'H83006', 'H83007', 'H83008', 'H83009', 'H 83010', 'H83011', 'H83012', 'H83013', 'H83014', 'H83015', 'H83016', 'H8301 7', 'H83018', 'H83019', 'H83020', 'H83021', 'H83022', 'H83023', 'H83024', 'H 83027', 'H83028', 'H83029', 'H83030', 'H83031', 'H83033', 'H83034', 'H8303 7', 'H83039', 'H83040', 'H83042', 'H83043', 'H83044', 'H83046', 'H83048', 'H 83049', 'H83050', 'H83051', 'H83052', 'H83053', 'H83608', 'H83609', 'H8361 1', 'H83620', 'H83622', 'H83624', 'H83625', 'H83626', 'H83627', 'H83631', 'Y 00182', 'Y02962', 'Y05317', 'Y05318', 'E84059', 'E85006', 'E85012', 'E8501 3', 'E85014', 'E85019', 'E85021', 'E85023', 'E85026', 'E85028', 'E85034', 'E 85041', 'E85046', 'E85049', 'E85050', 'E85051', 'E85053', 'E85054', 'E8505

```
7', 'E85061', 'E85064', 'E85066', 'E85069', 'E85075', 'E85083', 'E85088', 'E
85090', 'E85091', 'E85096', 'E85098', 'E85099', 'E85103', 'E85105', 'E8510
7', 'E85108', 'E85109', 'E85111', 'E85112', 'E85116', 'E85119', 'E85120', 'E
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3', 'E85628', 'E85630', 'E85633', 'E85635', 'E85640', 'E85643', 'E85656', 'E
85657', 'E85663', 'E85677', 'E85680', 'E85682', 'E85687', 'E85694', 'E8571
2', 'E85714', 'E85715', 'E85721', 'E85723', 'E85725', 'E85726', 'E85728', 'E
85733', 'E85740', 'E85743', 'E85745', 'Y01221', 'Y02342', 'Y04225', 'F8500
2', 'F85003', 'F85004', 'F85010', 'F85015', 'F85016', 'F85020', 'F85023', 'F
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6', 'F85039', 'F85043', 'F85044', 'F85048', 'F85053', 'F85055', 'F85058', 'F
85072', 'F85076', 'F85625', 'F85634', 'F85642', 'F85650', 'F85652', 'F8565
4', 'F85656', 'F85663', 'F85666', 'F85676', 'F85678', 'F85681', 'F85682', 'F
85684', 'F85686', 'F85687', 'F85700', 'F85701', 'F85703', 'F85707', 'Y0005
7', 'Y00612', 'Y03402', 'E85001', 'E85004', 'E85007', 'E85015', 'E85018', 'E
85024', 'E85030', 'E85035', 'E85040', 'E85045', 'E85052', 'E85056', 'E8505
8', 'E85059', 'E85060', 'E85062', 'E85071', 'E85113', 'E85114', 'E85115', 'E
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2', 'E85693', 'E85696', 'E85697', 'E85699', 'E85700', 'E85707', 'E85708', 'E
85713', 'E85716', 'E85718', 'E85732', 'E85734', 'E85735', 'E85736', 'E8573
9', 'E85744', 'E85746', 'E85750', 'Y02671', 'Y02672', 'G83001', 'G83003', 'G
83012', 'G83013', 'G83015', 'G83016', 'G83019', 'G83021', 'G83022', 'G8302
6', 'G83027', 'G83030', 'G83031', 'G83034', 'G83039', 'G83044', 'G83058', 'G
83060', 'G83065', 'G83067', 'G83628', 'G83631', 'G83633', 'G83635', 'G8364
1', 'G83647', 'G83651', 'G83654', 'G83663', 'G83673', 'G83680', 'Y02222', 'Y
02974', 'Y03296', 'Y03755', 'E85003', 'E85005', 'E85008', 'E85016', 'E8502
0', 'E85025', 'E85029', 'E85032', 'E85033', 'E85038', 'E85042', 'E85048', 'E
85055', 'E85074', 'E85077', 'E85118', 'E85124', 'E85125', 'E85128', 'E8562
4', 'E85636', 'E85649', 'E85659', 'E85672', 'E85685', 'E85719', 'E85748', 'Y
02589', 'Y02906', 'F85007', 'F85008', 'F85013', 'F85014', 'F85017', 'F8501
9', 'F85028', 'F85030', 'F85031', 'F85034', 'F85045', 'F85046', 'F85052', 'F
85060', 'F85061', 'F85063', 'F85064', 'F85065', 'F85066', 'F85067', 'F8506
9', 'F85071', 'F85615', 'F85623', 'F85628', 'F85640', 'F85645', 'F85669', 'F
85675', 'F85688', 'F85697', 'F85705', 'F85711', 'Y01655', 'Y02117', 'Y0303
5', 'Y03135', 'Y05330', 'E84004', 'E84005', 'E84008', 'E84009', 'E84014', 'E
84018', 'E84022', 'E84024', 'E84039', 'E84040', 'E84044', 'E84053', 'E8405
7', 'E84058', 'E84061', 'E84062', 'E84068', 'E84069', 'E84070', 'E84075', 'E
84601', 'E84617', 'E84646', 'E84647', 'E84653', 'E84657', 'E84658', 'E8466
3', 'E84676', 'E84680', 'E84681', 'E84693', 'E84713', 'Y03528', 'Y05080', 'F
82002', 'F82006', 'F82007', 'F82008', 'F82009', 'F82010', 'F82011', 'F8201
3', 'F82014', 'F82016', 'F82019', 'F82021', 'F82022', 'F82023', 'F82028', 'F
82030', 'F82031', 'F82033', 'F82039', 'F82045', 'F82053', 'F82055', 'F8260
7', 'F82609', 'F82610', 'F82614', 'F82619', 'F82624', 'F82627', 'F82630', 'F
82638', 'F82639', 'F82648', 'F82649', 'F82653', 'F82663', 'F82666', 'F8267
0', 'F82671', 'F82674', 'F82675', 'F82686', 'Y00312', 'Y02973', 'E86001', 'E
86003', 'E86004', 'E86005', 'E86006', 'E86007', 'E86009', 'E86010', 'E8601
1', 'E86012', 'E86014', 'E86015', 'E86016', 'E86017', 'E86018', 'E86019', 'E
86020', 'E86022', 'E86024', 'E86026', 'E86027', 'E86028', 'E86029', 'E8603
0', 'E86033', 'E86034', 'E86036', 'E86038', 'E86041', 'E86042', 'E86605', 'E
86609', 'E86610', 'E86612', 'E86615', 'E86618', 'E86619', 'E86620', 'E8662
5', 'E86626', 'E86629', 'E86632', 'E86637', 'E86640', 'Y00352', 'Y02812', 'F
83002', 'F83004', 'F83007', 'F83008', 'F83010', 'F83012', 'F83015', 'F8302
1', 'F83027', 'F83032', 'F83033', 'F83034', 'F83039', 'F83045', 'F83051', 'F
83053', 'F83056', 'F83060', 'F83063', 'F83064', 'F83624', 'F83652', 'F8366
0', 'F83664', 'F83666', 'F83671', 'F83673', 'F83674', 'F83678', 'F83680', 'F
83681', 'F83686', 'Y01066', 'H84010', 'H84015', 'H84016', 'H84020', 'H8402
5', 'H84027', 'H84030', 'H84033', 'H84034', 'H84042', 'H84049', 'H84050', 'H
84051', 'H84053', 'H84054', 'H84061', 'H84062', 'H84618', 'H84619', 'H8462
9', 'H84635', 'H84637', 'H85055', 'Y03054', 'G85002', 'G85010', 'G85011', 'G
85014', 'G85016', 'G85021', 'G85022', 'G85025', 'G85028', 'G85039', 'G8504
1', 'G85044', 'G85045', 'G85047', 'G85053', 'G85054', 'G85073', 'G85083', 'G
```

85086', 'G85096', 'G85100', 'G85102', 'G85109', 'G85113', 'G85118', 'G8512 3', 'G85127', 'G85129', 'G85130', 'G85133', 'G85135', 'G85136', 'G85137', 'G 85647', 'G85662', 'G85673', 'G85674', 'G85690', 'G85695', 'G85706', 'G8570 8', 'G85724', 'Y00020', 'Y01962', 'Y03063', 'G85003', 'G85004', 'G85005', 'G 85008', 'G85015', 'G85020', 'G85023', 'G85024', 'G85026', 'G85027', 'G8503 2', 'G85035', 'G85036', 'G85038', 'G85046', 'G85048', 'G85055', 'G85057', 'G 85061', 'G85076', 'G85081', 'G85085', 'G85089', 'G85104', 'G85105', 'G8511 4', 'G85120', 'G85121', 'G85124', 'G85633', 'G85696', 'G85698', 'G85711', 'G 85716', 'G85717', 'G85722', 'G85727', 'G85736', 'Y02957', 'F84004', 'F8400 6', 'F84009', 'F84010', 'F84014', 'F84017', 'F84022', 'F84047', 'F84050', 'F 84052', 'F84053', 'F84070', 'F84074', 'F84077', 'F84086', 'F84088', 'F8408 9', 'F84092', 'F84093', 'F84097', 'F84111', 'F84121', 'F84124', 'F84631', 'F 84641', 'F84642', 'F84657', 'F84658', 'F84660', 'F84661', 'F84666', 'F8466 9', 'F84670', 'F84672', 'F84673', 'F84677', 'F84679', 'F84681', 'F84706', 'F 84708', 'F84717', 'F84724', 'F84729', 'F84730', 'F84734', 'F84735', 'F8473 9', 'F84740', 'F84741', 'F84742', 'F84749', 'Y02928', 'Y04273', 'F86007', 'F 86008', 'F86009', 'F86010', 'F86012', 'F86013', 'F86020', 'F86022', 'F8602 3', 'F86025', 'F86028', 'F86032', 'F86034', 'F86042', 'F86057', 'F86060', 'F 86064', 'F86066', 'F86081', 'F86082', 'F86083', 'F86085', 'F86087', 'F8661 2', 'F86624', 'F86637', 'F86641', 'F86642', 'F86652', 'F86655', 'F86657', 'F 86658', 'F86691', 'F86692', 'F86698', 'F86702', 'F86703', 'F86704', 'F8670 7', 'F86731', 'Y00090', 'Y00155', 'Y00918', 'Y02987', 'H84002', 'H84005', 'H 84006', 'H84007', 'H84012', 'H84014', 'H84017', 'H84018', 'H84023', 'H8403 1', 'H84032', 'H84039', 'H84040', 'H84041', 'H84043', 'H84044', 'H84048', 'H 84055', 'H84057', 'H84059', 'H84060', 'H84608', 'H84623', 'H84625', 'H8463 0', 'H84632', 'H84639', 'Y01206', 'G85001', 'G85006', 'G85009', 'G85013', 'G 85019', 'G85029', 'G85030', 'G85031', 'G85034', 'G85040', 'G85042', 'G8505 0', 'G85051', 'G85052', 'G85082', 'G85084', 'G85087', 'G85091', 'G85097', 'G 85106', 'G85112', 'G85119', 'G85125', 'G85132', 'G85134', 'G85138', 'G8562 3', 'G85632', 'G85642', 'G85644', 'G85651', 'G85681', 'G85685', 'G85705', 'G 85712', 'G85715', 'G85721', 'G85723', 'G85726', 'Y00454', 'Y00812', 'H8502 0', 'H85024', 'H85026', 'H85027', 'H85028', 'H85029', 'H85033', 'H85035', 'H 85037', 'H85038', 'H85051', 'H85070', 'H85072', 'H85076', 'H85078', 'H8509 0', 'H85092', 'H85101', 'H85110', 'H85112', 'H85634', 'H85649', 'H85656', 'Y 02968', 'H85018', 'H85019', 'H85021', 'H85022', 'H85023', 'H85025', 'H8503 0', 'H85031', 'H85032', 'H85053', 'H85054', 'H85063', 'H85095', 'H85103', 'H 85105', 'H85113', 'H85115', 'H85116', 'H85618', 'H85653', 'H85662', 'H8566 5', 'H85683', 'H85686', 'H85693', 'F84012', 'F84016', 'F84025', 'F84030', 'F 84031', 'F84034', 'F84039', 'F84044', 'F84046', 'F84051', 'F84054', 'F8405 5', 'F84062', 'F84079', 'F84081', 'F84083', 'F84087', 'F84114', 'F84118', 'F 84122', 'F84123', 'F84647', 'F84656', 'F84676', 'F84682', 'F84696', 'F8469 8', 'F84702', 'F84710', 'F84714', 'F84718', 'F84731', 'F84733', 'F84747', 'Y 00212', 'Y03023', 'F86001', 'F86004', 'F86005', 'F86006', 'F86011', 'F8601 8', 'F86026', 'F86030', 'F86036', 'F86038', 'F86044', 'F86045', 'F86049', 'F 86058', 'F86062', 'F86073', 'F86074', 'F86078', 'F86086', 'F86088', 'F8660 7', 'F86616', 'F86621', 'F86625', 'F86626', 'F86627', 'F86638', 'F86644', 'F 86650', 'F86664', 'F86666', 'F86679', 'F86689', 'F86696', 'F86700', 'F8670 1', 'F86705', 'F86708', 'F86712', 'Y00092', 'Y01291', 'Y01839', 'Y02585', 'H 85001', 'H85002', 'H85003', 'H85005', 'H85006', 'H85007', 'H85008', 'H8500 9', 'H85011', 'H85012', 'H85041', 'H85045', 'H85047', 'H85048', 'H85049', 'H 85052', 'H85056', 'H85057', 'H85061', 'H85065', 'H85066', 'H85067', 'H8506 9', 'H85075', 'H85077', 'H85082', 'H85087', 'H85088', 'H85100', 'H85111', 'H 85114', 'H85637', 'H85643', 'H85659', 'H85664', 'H85680', 'H85682', 'H8569 1', 'H85695', 'Y00367', 'Y01132', 'Y02423', 'Y02946', 'E87003', 'E87004', 'E 87007', 'E87009', 'E87013', 'E87016', 'E87021', 'E87024', 'E87026', 'E8702 9', 'E87038', 'E87043', 'E87047', 'E87048', 'E87050', 'E87057', 'E87061', 'E 87063', 'E87065', 'E87067', 'E87637', 'E87665', 'E87682', 'E87701', 'E8770 2', 'E87706', 'E87711', 'E87715', 'E87720', 'E87722', 'E87733', 'E87735', 'E 87738', 'E87742', 'E87746', 'E87750', 'E87751', 'E87755', 'E87762', 'Y0020 0', 'Y00507', 'Y01011', 'Y02842', 'Y03441', 'E87002', 'E87005', 'E87006', 'E 87008', 'E87010', 'E87011', 'E87017', 'E87034', 'E87037', 'E87045', 'E8704

```
6', 'E87052', 'E87066', 'E87069', 'E87070', 'E87609', 'E87648', 'E87663', 'E
87677', 'E87681', 'E87691', 'E87694', 'E87714', 'E87737', 'E87739', 'E8774
0', 'E87741', 'E87745', 'E87753', 'E87754', 'E87756', 'E87768', 'E87772', 'Y
00230', 'Y00902', 'Y02260'].
```

In [24]:

```
# Total number of registered patients
no_patients_ldn=no_patients('London')
print('The number of patients registered in London GP practices in April 2018 is {}, which

# Total number of prescriptions
no_prescriptions_ldn=no_prescriptions('London')
print('The number of prescriptions issued by London GP practices in April 2018 is {}, which

# Total actual cost of the prescriptions
total_cost_ldn=total_cost('London')
print('The total actual cost of the prescriptions issued by London GP practices in April 20
print('The data is captured in the following table:')
d_ldn={'number of practices':len(list_ldn_practice),'number of patients':no_patients_ldn[0]
i_ldn=['London']
df_ldn=pd.DataFrame(data=d_ldn, index=i_ldn).T
df_ldn
```

The number of patients registered in London GP practices in April 2018 is 98 51208, which is 16.69% of the total.

The number of prescriptions issued by London GP practices in April 2018 is 1 0416926, which is 11.72% of the total.

The total actual cost of the prescriptions issued by London GP practices in April 2018 is $76586738.71 \pm$, which is 11.91% of the total.

The data is captured in the following table:

Out[24]:

-	London
number of practices	1323.00
number of patients	9851208.00
number of prescriptions	10416926.00
total actual cost	76586738.71

In [25]:

```
# Top 10 most frequent drugs prescribed in London GP practices
freq2_ldn=top10_drugs('London')
top10_ldn=pd.DataFrame(freq2_ldn.head(10).reset_index(0, drop=True))
top10_ldn['%']=(top10_ldn['ITEMS']/top10_ldn['ITEMS'].sum())*100
top10_ldn
```

Out[25]:

	BNF_NAME	BNF_CODE	ITEMS	%
0	Atorvastatin	0212000B0AAAAA	449846	15.486059
1	Amlodipine	0206020A0AAAAAA	354663	12.209361
2	Metformin	0601022B0AAABAB	295603	10.176206
3	Colecal	0906040G0AAANAN	294817	10.149147
4	Levothyrox	0602010V0AABWBW	285559	9.830438
5	Ramipril	0205051R0AAAAAA	274274	9.441950
6	Omeprazole	0103050P0AAAAAA	269995	9.294644
7	Aspirin	0209000A0AAABAB	235565	8.109383
8	Lansoprazole	0103050L0AAAAAA	223527	7.694972
9	Simvastatin	0212000Y0AAAAAA	220996	7.607841

In [26]:

bottom10_ldn=bottom10_drugs('London')
bottom10_ldn

Out[26]:

prescription frequency (items)

1

2

BNF_N	NAME	BNF_CODE	BNF_NAME	BNF_CODE
0	SASH	23304153002	Coloplast	23601006100
1	Frador	120301000BCBCAM	Spring	21060100210
2	Coloplast	23941010107	Jade	23602406008
3	Hyaluronidase	1003010P0AAAAAA	Coloplast	23601006400
4	Benzbromarone	1001040A0AAAAAA	Paromomycin	0504050T0AAADAC
5	Triamcinol	1001022Y0AAADAD	Respond	23753377500
6	Ward	23305303004	Levocarnitine	0908010Z0AAABAE
7	Pelican	23963459702	Noristerat	0703022N0BBAAAA
8	Timolol/Bendroflumeth	020400030AAAEAE	Pro-Plus	0404000D0BBAAAA
9	Repatha	0212000AHBBABAB	Salts	23964109637
10	Jade	23962409609	Dibromprop	1103010E0AAAAA
11	M.Sauer	23102951012	Peak	23945909490
12	Erythromycin	1103010I0AAAAAA	Rochester	22803958000
13	Tixylix	0309020H0BHACAE	Nefazodone	0403040T0AAAAA
14	Cefotaxime	0501021D0AAABAB	Salts	23754107507
15	Clomethi	0401010D0AAACAC	Reflectant	1308010U0AAAJAJ
16	Trientine	0908010S0AAACAC	Humulin	0601011R0BEAAAE
17	Sod	0908010P0AAAGAG	Flurbiprofen	1104020G0AAACAC
18	U-drain	22806208000	Dansac	23600706060
19	Cefuroxime	0501021J0AAABAB	Proguanil	0504010M0AAAAAA
20	Mercaptamine	0908010E0AAABAB	Unomedical	22055050501
21	Dolenio	1001050B0BCABAB	Lofexidine	0410030D0AAAAA
22	Buttercup	030902000BEDSA0	Phenindione	0208020N0AAAAA
23	Tocofersolan	0906050U0AAAAAA	Bullen	23250602501
24	B.Braun	23350453702	Elas	21060200110
25	Meropenem	0501022A0AAAAAA	Tretinoin	1306010V0AAANAN
26	Ward	22505305002	M.Sauer	22052950501
27	Sod	0101010U0AAAAAA	Nandrolone	0604030L0AAABAE
28	HealthAid	090602300BBBJA0	Camellia	1307000W0AAAAA
29	Betacarotene	0906012B0AAADAD	Gentamicin	1310012I0AAAEAE

	BNF_NAME	BNF_CODE	BNF_NAME	BNF_CODE
102	Marlen	23603056309		
103	Jade	23752407509		
104	Coloplast	23751007516		
105	Caffeine	0404000E0AAAMAM		
106	Buserelin	0607020B0AAABAB		
107	GF	22801978004		
108	Genvoya	050301000BBAEA0		
109	Forsteo	0606010U0BBABAC		
110	Ketamine	1501010F0AAAAAA		
111	Alirocumab	0212000AIAAABAB		
112	Macrogol	0106040X0AAAAAA		
113	Loxley	23452704509		
114	Chorion	0605010D0AAACAC		
115	Suspen	21070100990		
116	Truvada	0503010AABBAAAA		
117	Anadin	0407010AABCAAAB		
118	C&G	22900879003		
119	Abacavir	0503010E0AAAAAA		
120	DBT	23601256218		
121	Fenofibrate/Simvastatin	0212000AJAAABAB		
122	Respond	23253372500		
123	Salts	23604106123		
124	Salts	23604106285		
125	Ins	0601012U0AAAAAA		
126	Cortisone	0603020F0AAAHAH		
127	Elas	21060200220		
128	Efavirenz/Emtricitabine/Tenofovir	0503010ANAAAAAA		
129	Veracur	1307000C0BBAAAB		
130	Ward	23605306035		
131	Nevirapine	0503010B0AAAAA		

In [27]:

```
# Number of registered patients in London by practice
no_patients_ldn_bypractice = no_patients_city_bypractice('London')

# Number of prescriptions and actual cost by practice in London
no_presc_cost_ldn=no_presc_cost_city('London')

df2_ldn=pd.merge(no_presc_cost_ldn,no_patients_ldn_bypractice,how='outer',left_on='PRACTICE_right_on='CODE')
list_column=['CODE','NUMBER_OF_PATIENTS','ITEMS','ACTUAL_COST']
df2_ldn=df2_ldn[list_column]
df2_ldn.head()
```

Out[27]:

	CODE	NUMBER_OF_PATIENTS	ITEMS	ACTUAL_COST
0	E83003	8911	11740.0	89607.38
1	E83005	6224	6724.0	47240.62
2	E83006	6885	6327.0	54746.99
3	E83007	5706	6181.0	53459.56
4	E83008	7900	8909.0	71808.73

In [28]:

```
df2_ldn.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 1323 entries, 0 to 1322
Data columns (total 4 columns):
```

CODE 1323 non-null object
NUMBER_OF_PATIENTS 1323 non-null int64
ITEMS 1299 non-null float64
ACTUAL_COST 1299 non-null float64
dtypes: float64(2), int64(1), object(1)

memory usage: 51.7+ KB

While in df1 1323 GP practices have been identified to be located in London, in df2 only 1299 GP practices from London are displayed. This might be either due to the fact that some GP practices from London might not have prescribed anything during April 2018 or because of missing data or data that has not been collected for these practices during that month. The characteristics of these GP practices will be studied, in order to see if there is any overlooked underlying pattern that might explain this situation.

In [29]:

```
ldn_practices_missing=df2_ldn[df2_ldn['ITEMS'].isnull()][['CODE','NUMBER_OF_PATIENTS']]
ldn_practices_missing.shape
```

Out[29]:

(24, 2)

In [30]:

ldn_practices_missing

Out[30]:

	CODE	NUMBER_OF_PATIENTS
1299	E83644	1362
1300	Y01697	6
1301	E84056	111
1302	E84084	496
1303	F84659	61
1304	E85728	252
1305	E85732	419
1306	F85711	4
1307	E84657	383
1308	H84049	231
1309	H84637	170
1310	Y03054	184
1311	G85113	801
1312	F84089	24
1313	G85009	246
1314	G85097	1007
1315	Y00812	1
1316	Y02968	1286
1317	F86049	398
1318	H85056	541
1319	H85643	264
1320	Y00367	32
1321	E87017	764
1322	Y00230	8

In [31]:

ldn_practices_missing.describe()

Out[31]:

NUMBER_OF_PATIENTS

count	24.000000
mean	377.125000
std	400.096218
min	1.000000
25%	53.750000
50%	249.000000
75%	507.250000
max	1362.000000

In [32]:

```
meanpointprops = dict(marker='+', markeredgecolor='black', markerfacecolor='firebrick') # se
medianprops = dict(linewidth=1.5,color='orange') # settings median representation
plt.boxplot(ldn_practices_missing['NUMBER_OF_PATIENTS'], showmeans=True, meanprops=meanpoir
plt.title('Boxplot', fontsize=15)
plt.ylabel('number of patients', fontsize=11)
plt.xticks([1],['London missing practices'], fontsize=12)
plt.annotate('+ mean', xy=(1.25,1300), fontsize=11)
plt.show()
```



In [33]:

```
# We drop from df2_ldn practices which have missing values for ITEMS and ACTUAL_COST, they
df2_ldn=df2_ldn.dropna()
df2_ldn.shape
```

Out[33]:

(1299, 4)

In [34]:

```
no_patients_ldn_bypractice.describe()
```

Out[34]:

NUMBER OF PATIENTS

count	1323.000000
mean	7446.113379
std	4649.138337
min	1.000000
25%	4330.000000
50%	6659.000000
75%	9779.500000
max	72227.000000

A quick analysis of descriptive statistics parameters of these practices reveals that these GP practices tend to have a lower number of patients than the rest of London GP practices which appear on the prescribing dataset. While it could be plausible that a low number of patients is correlated with no prescriptions in April 2018, there are many other factors that are not known. Notwithstanding, these practices have been removed from further analysis, since missing values might add ambiguity to the results.

Herein, we have analysed the GP practices located in Cambridge.

In [35]:

```
# Identification of all GP practices located in Cambridge
list_cb_practice=practice('Cambridge')
print('There are {} registered GP practices in the city of Cambridge in April 2018.\nThe co
```

There are 37 registered GP practices in the city of Cambridge in April 2018. The codes of the GP practices in the city of Cambridge are the following: ['D81001', 'D81002', 'D81003', 'D81005', 'D81009', 'D81012', 'D81013', 'D81016', 'D81017', 'D81025', 'D81028', 'D81033', 'D81035', 'D81037', 'D81041', 'D81042', 'D81043', 'D81044', 'D81051', 'D81055', 'D81055', 'D81056', 'D81058', 'D81066', 'D81070', 'D81078', 'D81084', 'D81085', 'D81086', 'D81602', 'D81607', 'D81612', 'D81637', 'Y00056', 'F81009', 'F81015', 'F81034'].

In [36]:

```
# Number of registered patients per GP practice in the city of Cambridge
no_patients_cb=no_patients('Cambridge')
print('The number of patients registered in Cambridge GP practices in April 2018 is {}, whi
#Number of prescriptions issued per GP practice in the city of Cambridge
no_prescriptions_cb=no_prescriptions('Cambridge')
print('The number of prescriptions issued by Cambridge GP practices in April 2018 is {}, wh
#Actual cost of prescriptions in Cambridge GP practices
total_cost_cb=total_cost('Cambridge')
print('The total actual cost of the prescriptions issued by Cambridge GP practices in April
print('The data is captured in the following table:')
d_cb={'number of practices':len(list_cb_practice[1]),'number of patients':no_patients_cb[0]
i_cb=['Cambridge']
df_cb=pd.DataFrame(data=d_cb, index=i_cb).T
df_cb
```

The number of patients registered in Cambridge GP practices in April 2018 is 366333, which is 0.62% of the total.

The number of prescriptions issued by Cambridge GP practices in April 2018 is 417095, which is 0.47% of the total.

The total actual cost of the prescriptions issued by Cambridge GP practices in April 2018 is 2931133.94 £, which is 0.46% of the total.

The data is captured in the following table:

Out[36]:

	Cambridge
number of practices	37.00
number of patients	366333.00
number of prescriptions	417095.00
total actual cost	2931133.94

In [37]:

Out[37]:

	CODE	NUMBER_OF_PATIENTS	ITEMS	ACTUAL_COST
0	D81001	12057	6679	65873.09
1	D81002	16939	13885	90156.76
2	D81003	9927	11572	71266.77
3	D81005	14941	6918	63413.35
4	D81009	9071	11378	84364.61

In [38]:

```
df2_cb.isnull().any()
```

Out[38]:

CODE False
NUMBER_OF_PATIENTS False
ITEMS False
ACTUAL_COST False

dtype: bool

Unlike London GP Practices, both df1 and df2 contain the same number of GP Practices in Cambridge in April 2018.

In [39]:

```
# Top 10 most frequent drugs prescribed in Cambridge GP practices
freq2_cb=top10_drugs('Cambridge')
top10_cb=pd.DataFrame(freq2_cb.head(10).reset_index(0, drop=True))
top10_cb['%']=(top10_cb['ITEMS']/top10_cb['ITEMS'].sum())*100
top10_cb
```

Out[39]:

	BNF_NAME	BNF_CODE	ITEMS	%
0	Omeprazole	0103050P0AAAAA	15291	14.064311
1	Atorvastatin	0212000B0AAAAA	15097	13.885874
2	Levothyrox	0602010V0AABWBW	14400	13.244789
3	Amlodipine	0206020A0AAAAAA	10476	9.635584
4	Colecal	0906040G0AAANAN	9979	9.178455
5	Aspirin	0209000A0AAABAB	9446	8.688214
6	Simvastatin	0212000Y0AAAAA	9401	8.646824
7	Bisoprolol	0204000H0AAAAAA	8902	8.187855
8	Lisinopril	0205051L0AAAAAA	8675	7.979066
9	Salbutamol	0301011R0AAAPAP	7055	6.489027

In [40]:

```
# Bottom 10 less frequent drugs prescribed in Cambridge GP practices
bottom10_cb=bottom10_drugs('Cambridge')
bottom10_cb
```

Out[40]:

prescription frequency (items)

1 2 3

	BNF_NAME	BNF_CODE	BNF_NAME	BNF_CODE	BNF_N
0	ConvaTec	23964809625	Dansac	23600706278	
1	Lamb	0906025P0BJAABF	Loprofin	0904010AQBBACAA	Meth
2	Levocarnitine	0908010Z0AAABAB	Pot	090602800AAANAN	
3	Ibuprofen	1001010APAAAAAA	Optimum	22056150501	C
4	Sativex	1002020Y0BBABAB	Mevalia	0904010T0BIAEAD	Fonda
5	Transvasin	1003020T0BBAAAA	Colifoam	0105020B0BBAAAA	С
6	Deep	1003020Y0BDABAC	Glutafin	0904010AABEACAL	Had
7	Ferric	0901011Y0AAAAAA	Jade	22502405011	
8	GF	22801978004	Dansac	23960709625	
9	Degarelix	0803042R0AAAAAA	Loperamide	0104020P0AAAAAA	Far
10	Nonoxinol	0703030G0AAAIAI	Fluoresc	1108020K0AAAAAA	Darl
11	Neomycin	0501040N0AAADAD	Dansac	22600706000	
12	Chloramphen	0501070F0AAAAAA	Macrogol	0106040X0AAAAAA	Mox
13	Vancomycin	0501070U0AAAAAA	Klean-Prep	0106050B0BBAAA0	Isc
14	Tinidazole	0501110G0AAABAB	Mag	0106050M0AAAAAA	
15	Saxagliptin/Metformin	0601023AHAAABAB	Flexicare	22601756000	C
16	Dapagliflozin/Metformin	0601023ALAAAAAA	Mag	0905013A0AAAHAH	F
17	Eudemine	0601040E0BBAAAA	Salts	23964109727	Podoph
18	Nature-Throid	0602010Z0BDAAAB	Mesterolone	0604020F0AAAAAA	Mom
19	Dexameth	0603020H0AAALAL	Hollister	22300103021	Eryth
20	Selenium	090504700AABCBC	Optimum	22506155005	C
21	Osvaren	0905022U0BBAAAA	Salts	23604106515	
22	Magnesium	0905013P0AAAAAA	ConvaTec	23944810024	
23	Mevalia	0904010V0BGAAAD	Kaolin	0104020N0AAABAB	
24	Sucralfate	0103030S0AAAAAA	Invicorp	0704050ADBBAAAA	Мусо
25	Germoloids	0107010N0BFAAA0	Torasemide	0202020U0AAAAAA	Tiı
26	Xipamide	0202010Y0AAAAAA	Amiloride	0202040D0AAAAAA	(
27	Lasilactone	0202040T0BBAAAA	Unomedical	22805058002	Ubidec
28	Furosemide/Pot	0202080K0AAABAB	Hollister	23700107000	Flur
29	Dronedarone	0203020X0AAAAAA	Waxsol	1201030F0BEAAAB	С

2

3

	BNF_NAME	BNF_CODE	BNF_NAME	BNF_CODE	BNF_N
158	Amobarb	0401030E0AAAAA			
159	Felodipine/Ramipril	0205051S0AAABAB			
160	Quinapril	0205051P0AAAAAA			
161	Fosinopril	0205051J0AAABAB			
162	L.IN.C	22502655017			
163	Aspirin/Codeine	0407010W0AAADAD			
164	Cutimed	20030800150			
165	MicardisPlus	0205052R0BBAAAA			
166	ActiLymph	21270000798			
167	ConvaTec	22604806001			
168	Teleflex	22704887000			
169	Beambridge	22800758000			
170	ConvaTec	22404804001			
171	Haddenham	21270002480			
172	Sigvaris	21270002192			
173	Sigvaris	21270001036			
174	Tegaderm	20032400003			
175	Kapitex	20050100102			
176	Insight	20050500005			
177	Aquacel	20031600110			
178	Class	21070520140			
179	Imperm	20100000240			
180	Eesiness	20170000100			
181	DermaSilk	20200000119			
182	Estriol	21010100101			
183	Unspecified	21020000105			
184	GentleCath	21020001507			
185	Elas	21060200110			
186	Comfifast	20090001037			
187	Amielle	21250000102			

188 rows × 20 columns

While London is the most populated city in Western Europe and amongst the most populated worldwide, Cambridge is a middle-sized city with a population of ~125,000 inhabitants. The idiosyncrasy of the lifestyles of the peoples living in these two cities might impact in a different fashion the way the healthcare system is run. This is why in the next lines of code, a statistical descriptive analysis has been performed, so that a conclusion about the potentially contrasting tendencies of these two urban areas could be drawn.

In [41]:

```
df_abs=df_ldn.merge(df_cb, right_index=True, left_index=True)
df_abs['Ratio London / Cambridge']=np.round(np.divide(df_abs['London'],df_abs['Cambridge'])
df_abs.index.name=r'$\Sigma$'
df_abs
```

Out[41]:

	London	Cambridge	Ratio London / Cambridge
Σ			
number of practices	1323.00	37.00	35.8
number of patients	9851208.00	366333.00	26.9
number of prescriptions	10416926.00	417095.00	25.0
total actual cost	76586738.71	2931133.94	26.1

As expected, the absolute number of practices, patients, prescriptions and the costs of the whole London GP practices are higher than the same parameters for the city of Cambridge. However, a closer look at these variables depending on the city might shed some light on the statistical analysis for this report.

In [42]:

```
def ratio(a, b):
    ratio=np.round(np.divide(a,b),2)
    return ratio
```

In [43]:

```
iterables=[['number of patients','items','actual cost'],
        ['mean', 'median',r'$\Sigma$']]
index=pd.MultiIndex.from_product(iterables)
df_rel=pd.DataFrame(index=index, columns=['London', 'Cambridge', 'Ratio London/Cambridge'])
df_rel['London']=[int(df2_ldn['NUMBER_OF_PATIENTS'].mean()),int(df2_ldn['NUMBER_OF_PATIENTS']
                  int(df2_ldn['ITEMS'].mean()),int(df2_ldn['ITEMS'].quantile(.5)),df_abs.ld
                  int(df2_ldn['ACTUAL_COST'].mean()),int(df2_ldn['ACTUAL_COST'].quantile(.5
df_rel['Cambridge']=[np.round(df2_cb['NUMBER_OF_PATIENTS'].mean(),0),int(df2_cb['NUMBER_OF_
                     np.round(df2_cb['ITEMS'].mean(),0),int(df2_cb['NUMBER_OF_PATIENTS'].qu
                     np.round(df2 cb['ACTUAL COST'].mean(),2),int(df2 cb['ACTUAL COST'].qua
df_rel['Ratio London/Cambridge']=[ratio(df_rel.loc[('number of patients', 'mean'), 'London'],
                                  ratio(df_rel.loc[('number of patients', 'median'), 'London'
                                  df_abs.loc['number of practices','Ratio London / Cambridg
                                  ratio(df_rel.loc[('items','mean'),'London'],df_rel.loc[('
                                  ratio(df_rel.loc[('items', 'median'), 'London'], df_rel.loc[
                                  df_abs.loc['number of prescriptions','Ratio London / Camb
                                  ratio(df_rel.loc[('actual cost', 'mean'), 'London'], df_rel.
                                  ratio(df_rel.loc[('actual cost','median'),'London'],df_re
                                  df_abs.loc['total actual cost', 'Ratio London / Cambridge'
df_rel
```

Out[43]:

		London	Cambridge	Ratio London/Cambridge
number of patients	mean	7576.00	9901.00	0.77
	median	6815.00	9063.00	0.75
	Σ	9851208.00	366333.00	35.80
items	mean	8019.00	11273.00	0.71
	median	6712.00	9063.00	0.74
	Σ	10416926.00	417095.00	25.00
actual cost	mean	58958.00	79219.84	0.74
	median	50571.00	71695.00	0.71
	Σ	76586738.71	2931133.94	26.10

By analysing the measures of central tendency displayed in this table, it is possible to claim that overall, a Cambridge GP practice has a higher number of patients than a practice in London. It is thus logical that number of prescriptions is also higher and hence the total cost as well. With the aim to further understand this statement, we have explored the distribution of these parameters in both cities by plotting histograms and checked the normality of data (graphically and analytically with skewness and kurtosis symmetry measures) and boxplots comparing them and identifying outliers.

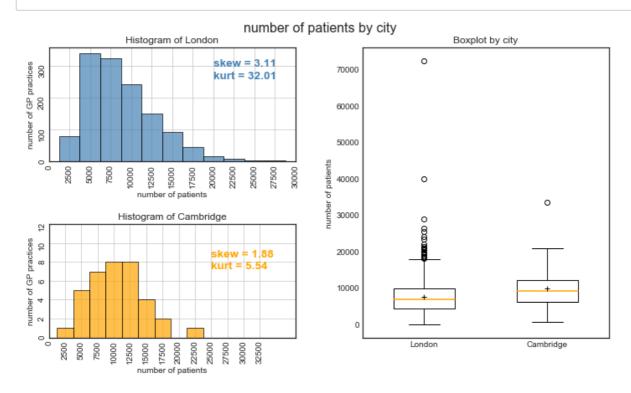
```
In [44]:
```

```
def plot_hist(var1):
    multiply1=1
    if var1=='patients':
        column='NUMBER OF PATIENTS'
        var1='number of patients'
        title='number of patients by city'
    if var1=='prescriptions':
        column='ITEMS'
        var1='number of prescriptions'
        title='number of prescriptions by city'
    if var1=='cost':
        column='ACTUAL COST'
        var1='cost/f'
        title='practice cost by city'
        multiply1=10 #correction factor to scale representations for 'ACTUAL_COST'
    plt.figure(figsize=(10,6))
    ax1=plt.subplot(221)
    ax2=plt.subplot(223)
    ax3=plt.subplot(122)
    bins1=np.arange(0,round(max(df2_ldn[column])/500*multiply1)*500*multiply1, 2500*multipl
    bins2=np.arange(0,round(max(df2_cb[column])/500*multiply1)*500*multiply1, 2500*multiply
    ax1.hist(df2_ldn[column],bins=bins1,color='steelblue', edgecolor='black', alpha=0.7, al
    ax1.set_xticks(bins1)
    ax1.tick_params(labelrotation=90)
    ax1.set_xlim(0,30000*multiply1)
    ax1.set_xlabel(var1)
    ax1.set_ylabel('number of GP practices')
    ax1.set_title('Histogram of London')
    ax1.grid(True)
    ax1.text(20000*multiply1,300,'skew = '+str(np.round(skew(df2_ldn[column]),2)),fontsize=
         color='steelblue', fontweight='bold')
    ax1.text(20000*multiply1,260,'kurt = '+str(np.round(kurtosis(df2_ldn[column]),2)),fonts
         color='steelblue', fontweight='bold')
    ax1.get_xaxis().get_major_formatter().set_scientific(False)
    ax2.hist(df2_cb[column],bins=bins2,color='orange', edgecolor='black', alpha=0.7, align=
    ax2.set_xticks(bins2)
    ax2.tick_params(labelrotation=90)
    ax2.set_xlim(0,38000*multiply1)
    ax2.set ylim(0,12)
    ax2.set_xlabel(var1)
    ax2.set_ylabel('number of GP practices')
    ax2.set title('Histogram of Cambridge')
    ax2.grid(True)
    ax2.text(25000*multiply1,8.5,'skew = '+str(np.round(skew(df2_cb[column]),2)),fontsize=1
         color='orange', fontweight='bold')
    ax2.text(25000*multiply1,7.25,'kurt = '+str(np.round(kurtosis(df2_cb[column]),2)),fonts
         color='orange', fontweight='bold')
    ax2.get_xaxis().get_major_formatter().set_scientific(False)
    boxplot=[df2 ldn[column],df2 cb[column]]
    ax3.boxplot(boxplot,showmeans=True, meanprops=meanpointprops, medianprops=medianprops,
    ax3.set_ylabel(var1)
    ax3.set_title('Boxplot by city')
    plt.xticks([1,2],['London','Cambridge'])
```

```
plt.suptitle(title, fontsize=16, y=1)
plt.subplots_adjust(wspace=5, hspace=3)
plt.tight_layout()
plt.show()
```

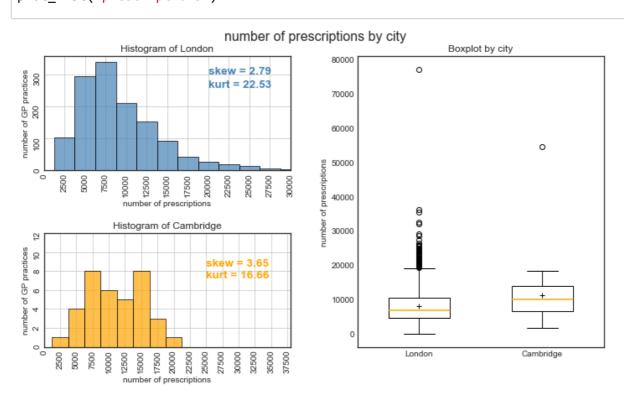
In [45]:

```
plot_hist('patients')
```



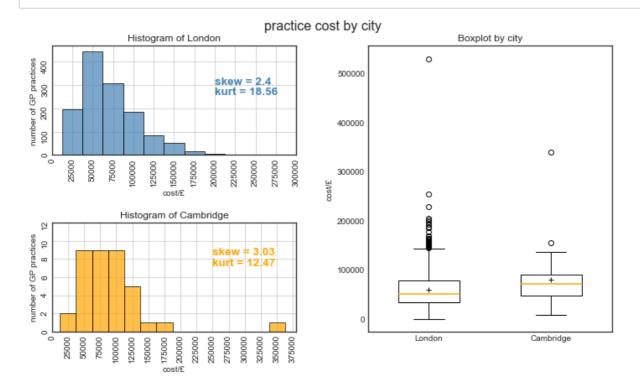
In [46]:

plot_hist('prescriptions')



In [47]:

plot_hist('cost')



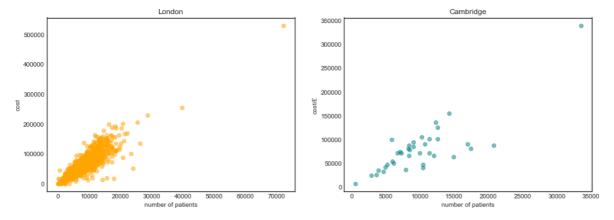
Previously, it was surmised that a higher number of patients could imply higher costs for a practice. In the next graphs, we have represented scatterplots to help understanding the tendencies both in London and Cambridge. Admittedly, regression lines could have been fitted, but the purpose of these charts was only illustrative so that the treader could see general trends and correlations. Regression fitting would potentially require further data manipulation and assumptions checking which are beyond the scope of this report.

In [48]:

```
fig,(ax1,ax2)=plt.subplots(nrows=1,ncols=2, figsize=(12,5))
ax1.scatter(df2_ldn['NUMBER_OF_PATIENTS'],df2_ldn['ACTUAL_COST'], c='orange', alpha=0.5)
ax1.set_xlabel('number of patients')
ax1.set_ylabel('cost')
ax1.set_title('London')

ax2.scatter(df2_cb['NUMBER_OF_PATIENTS'],df2_cb['ACTUAL_COST'], alpha=0.5,c='teal')
ax2.set_xlabel('number of patients')
ax2.set_ylabel('cost/f')
ax2.set_title('Cambridge')

plt.subplots_adjust(left=0.01, right=1)
plt.show()
```



Despite the fact that linear trends can be appreciated, it has been preferred to remove outliers or points with high leverage or influence in both graphs so that relationships can be more clearly appreciated.

In [49]:

```
df2_ldn_clean=df2_ldn[df2_ldn['NUMBER_OF_PATIENTS']<20000]
df2_ldn_clean_pat=df2_ldn_clean['NUMBER_OF_PATIENTS']
df2_ldn_clean_cost=df2_ldn_clean['ACTUAL_COST']</pre>
```

In [50]:

```
df2_cb_clean=df2_cb.sort_values(by='NUMBER_OF_PATIENTS')[:-1]
df2_cb_clean_pat=df2_cb_clean['NUMBER_OF_PATIENTS']
df2_cb_clean_cost=df2_cb_clean['ACTUAL_COST']
```

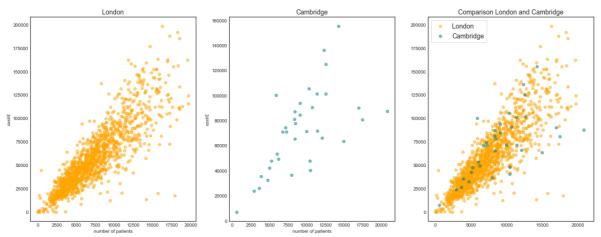
In [135]:

```
fig,(ax1,ax2,ax3)=plt.subplots(nrows=1,ncols=3, figsize=(12,8))
ax1.scatter(df2_ldn_clean_pat,df2_ldn_clean_cost,c='orange', alpha=0.5)
ax1.set_xlabel('number of patients')
ax1.set_ylabel('cost/f')
ax1.set_title('London', fontsize=14)

ax2.scatter(df2_cb_clean_pat,df2_cb_clean_cost, alpha=0.5,c='teal')
ax2.set_xlabel('number of patients')
ax2.set_ylabel('cost/f')
ax2.set_title('Cambridge', fontsize=14)

ax3.scatter(df2_ldn_clean_pat,df2_ldn_clean_cost,c='orange', alpha=0.5)
ax3.scatter(df2_cb_clean_pat,df2_cb_clean_cost, alpha=0.5,c='teal')
ax3.legend(['London', 'Cambridge'], frameon=True, loc='upper left', prop={'size':14})
ax3.set_title('Comparison London and Cambridge', fontsize=14)

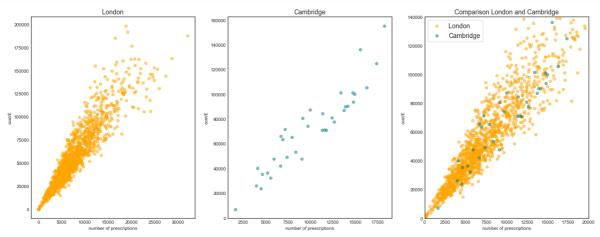
plt.subplots_adjust(left=0.01, right=1.4)
plt.show()
```



Here, it is possible to identify a linear correlation between number of patients and total cost for both cities. The variance increases as the number of patients per practice does. It is worth mentioning however that there is great variance for the datapoints from practices in Cambridge and thus hasty conclusions should be guarded.

In [136]:

```
fig,(ax1,ax2, ax3)=plt.subplots(nrows=1,ncols=3, figsize=(12,8))
ax1.scatter(df2_ldn_clean['ITEMS'],df2_ldn_clean_cost,c='orange', alpha=0.5)
ax1.set xlabel('number of prescriptions')
ax1.set_ylabel('cost/f')
ax1.set_title('London', fontsize=14)
ax2.scatter(df2_cb_clean['ITEMS'],df2_cb_clean_cost, alpha=0.5,c='teal')
ax2.set_xlabel('number of prescriptions')
ax2.set ylabel('cost/f')
ax2.set_title('Cambridge', fontsize=14)
ax3.scatter(df2_ldn_clean['ITEMS'],df2_ldn_clean_cost,c='orange', alpha=0.5)
ax3.scatter(df2_cb_clean['ITEMS'],df2_cb_clean_cost, alpha=0.5,c='teal')
ax3.set_xlabel('number of prescriptions')
ax3.set_ylabel('cost/f')
ax3.set_xlim(0,20000)
ax3.set_ylim(0,140000)
ax3.legend(['London','Cambridge'], frameon=True, loc='upper left', prop={'size':14})
ax3.set_title('Comparison London and Cambridge', fontsize=14)
plt.subplots_adjust(left=0.01, right=1.4)
plt.show()
```

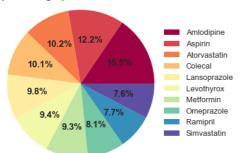


As one would expect, there is a high linear correlation between the number of prescriptions per GP practice and the total cost in both cities. In London practices, there is a greater variance as the number of prescriptions increases.

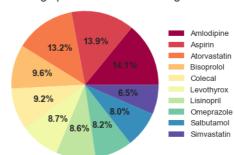
In [53]:

```
fig, (ax1, ax2)=plt.subplots(1,2, figsize=(10,5))
cmap = plt.get_cmap('Spectral')
colors = [cmap(i) for i in np.linspace(0, 1, 10)] #Set the colors from Spectral colormap
sizes1=top10_ldn['%'].tolist()
labels1=top10_ldn['BNF_NAME'].sort_values().tolist()
patches1, texts1, autotexts1=ax1.pie(sizes1, colors=colors, autopct='%1.1f%%')
ax1.axis('equal')
ax1.legend(labels1,loc='center left',bbox to anchor=(0.8, 0, 0, 1), prop={'size': 13})
ax1.set_title('Top 10 drugs prescribed in London', size=20)
plt.setp(autotexts1, size=15, weight="bold")
sizes2=top10_cb['%'].tolist()
labels2=top10_cb['BNF_NAME'].sort_values().tolist()
patches2, texts2, autotexts2=ax2.pie(sizes2, colors=colors, autopct='%1.1f%%', textprops=di
ax2.axis('equal')
ax2.legend(labels2,loc='center left',bbox_to_anchor=(0.8, 0, 0, 1), prop={'size': 13}) # Le
ax2.set_title('Top 10 drugs prescribed in Cambridge', size=20)
plt.subplots_adjust(left=0.1, right=1.4)
plt.setp(autotexts2, size=15, weight="bold")
plt.show()
```

Top 10 drugs prescribed in London



Top 10 drugs prescribed in Cambridge



Interestingly, there are drugs in common in the top 10 drugs prescribed in each city (Amlodipine, Aspirin, Atorvastatin, Colecal, Levothyrox, Omeprazol and Simvastatin). However, the proportion they represent is slightly different.

The NHS uses the British National Formulary (BNF) to classify the prescriptions issued by their GP practices. The BNF code structure specifies the BNF chapter in the characters 1 and 2 and the subsection in the characters 3 and 4 (please refer to https://digital.nhs.uk/data-and-information/areas-of-interest/prescribing/practice-level-prescribing-in-england-a-summary/practice-level-prescribing-glossary-of-terms) for more details).

In the following lines of code, we have analysed and compared prescriptions for each therapeutic area in London and Cambridge as defined by the BNF.

In [54]:

```
look_up_chapter=pd.DataFrame(columns=['BNF Chapter','Therapeutic Area'])
look_up_chapter['BNF Chapter']=['01','02','03','04','05','06','07','08','09','10','11','12'
look_up_chapter['Therapeutic Area']=['Gastro-Intestinal System','Cardiovascular System','Re
look_up_chapter
```

Out[54]:

	BNF Chapter	Therapeutic Area
0	01	Gastro-Intestinal System
1	02	Cardiovascular System
2	03	Respiratory System
3	04	Central Nervous System
4	05	Infections
5	06	Endocrine System
6	07	Obstetrics, Gynae+Urinary Tract Disorders
7	08	Malignant Disease & Immunosuppression
8	09	Nutrition and Blood
9	10	Musculoskeletal & Joint Diseases
10	11	Eye
11	12	Ear, Nose and Oropharynx
12	13	Skin
13	14	Immunological Products & Vaccines
14	15	Anaesthesia
15	18	Preparations used in Diagnosis
16	19	Other Drugs and Preparations
17	20	Dressings
18	21	Appliances
19	22	Incontinence Appliances
20	23	Stoma Appliances

In [55]:

```
def freq_chapter_city(city):
    freq1_city=freq_city(city) #We call a function already defined
    #Grouping by therapeutic area (first characters of BNF_CODES)
    freq_chapter_city=freq1_city.groupby(lambda c: freq1_city.iloc[c,1][:2]).sum().reset_ir
    freq_chapter_city=pd.DataFrame(freq_chapter_city).rename(columns={'index':'BNF Chapter'
    #Left join with look_up_chapter table
    freq_chapter_city=pd.merge(freq_chapter_city,look_up_chapter, how='left', left_on='BNF
    #Calculation of percentage
    freq_chapter_city['Percentage']= np.round((freq_chapter_city['Number of prescriptions']
    #Sorting by descending order
    freq_chapter_city=freq_chapter_city.sort_values(by='Percentage', ascending=False).reset
    return freq_chapter_city
```

In [56]:

```
#Drug prescriptions by therapeutic area in London
freq_chapter_ldn=freq_chapter_city('London')
freq_chapter_ldn
```

Out[56]:

	BNF Chapter	Number of prescriptions	Therapeutic Area	Percentage
0	02	3104617	Cardiovascular System	29.80
1	04	1651463	Central Nervous System	15.85
2	06	1209221	Endocrine System	11.61
3	01	892921	Gastro-Intestinal System	8.57
4	09	735620	Nutrition and Blood	7.06
5	03	645567	Respiratory System	6.20
6	13	401393	Skin	3.85
7	05	348466	Infections	3.35
8	21	309387	Appliances	2.97
9	07	291407	Obstetrics, Gynae+Urinary Tract Disorders	2.80
10	10	276505	Musculoskeletal & Joint Diseases	2.65
11	11	204628	Eye	1.96
12	12	124301	Ear, Nose and Oropharynx	1.19
13	20	53817	Dressings	0.52
14	14	50725	Immunological Products & Vaccines	0.49
15	23	42357	Stoma Appliances	0.41
16	08	39182	Malignant Disease & Immunosuppression	0.38
17	15	12669	Anaesthesia	0.12
18	19	11075	Other Drugs and Preparations	0.11
19	22	11604	Incontinence Appliances	0.11
20	18	1	Preparations used in Diagnosis	0.00

In [57]:

```
# Drug prescriptions by therapeutic area in Cambridge
freq_chapter_cb=freq_chapter_city('Cambridge')
freq_chapter_cb
```

Out[57]:

	BNF Chapter	Number of prescriptions	Therapeutic Area	Percentage
0	02	120136	Cardiovascular System	28.80
1	04	77571	Central Nervous System	18.60
2	06	43041	Endocrine System	10.32
3	01	37674	Gastro-Intestinal System	9.03
4	03	27244	Respiratory System	6.53
5	09	23928	Nutrition and Blood	5.74
6	05	15904	Infections	3.81
7	07	13897	Obstetrics, Gynae+Urinary Tract Disorders	3.33
8	13	13793	Skin	3.31
9	10	12368	Musculoskeletal & Joint Diseases	2.97
10	21	9829	Appliances	2.36
11	11	7740	Eye	1.86
12	12	4726	Ear, Nose and Oropharynx	1.13
13	08	2494	Malignant Disease & Immunosuppression	0.60
14	23	1739	Stoma Appliances	0.42
15	20	1586	Dressings	0.38
16	14	1112	Immunological Products & Vaccines	0.27
17	15	944	Anaesthesia	0.23
18	22	801	Incontinence Appliances	0.19
19	19	568	Other Drugs and Preparations	0.14

In [58]:

Out[58]:

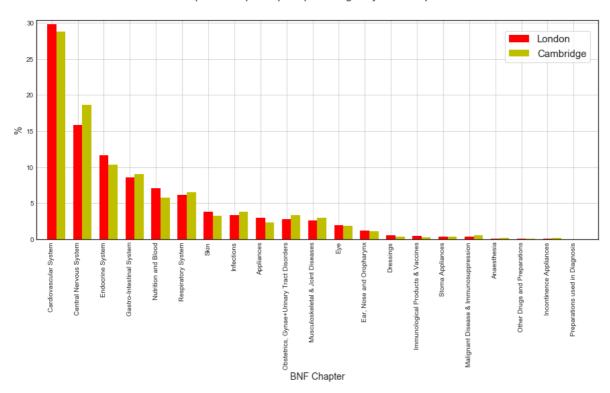
	Therapeutic Area	Percentage London	Percentage Cambridge
0	Cardiovascular System	29.80	28.80
1	Central Nervous System	15.85	18.60
2	Endocrine System	11.61	10.32
3	Gastro-Intestinal System	8.57	9.03
4	Nutrition and Blood	7.06	5.74
5	Respiratory System	6.20	6.53
6	Skin	3.85	3.31
7	Infections	3.35	3.81
8	Appliances	2.97	2.36
9	Obstetrics, Gynae+Urinary Tract Disorders	2.80	3.33
10	Musculoskeletal & Joint Diseases	2.65	2.97
11	Eye	1.96	1.86
12	Ear, Nose and Oropharynx	1.19	1.13
13	Dressings	0.52	0.38
14	Immunological Products & Vaccines	0.49	0.27
15	Stoma Appliances	0.41	0.42
16	Malignant Disease & Immunosuppression	0.38	0.60
17	Anaesthesia	0.12	0.23
18	Other Drugs and Preparations	0.11	0.14
19	Incontinence Appliances	0.11	0.19
20	Preparations used in Diagnosis	0.00	0.00

In [59]:

```
#Bar chart comparing prescription by therapeutic area by city
fig, ax=plt.subplots(figsize=(15,6))
ind=np.arange(len(freq_chapter_compare))
width=0.35

p1=ax.bar(ind, freq_chapter_compare['Percentage London'], width, color='r')
p2=ax.bar(ind+width, freq_chapter_compare['Percentage Cambridge'], width, color='y')
ax.set(xticks=ind,xticklabels=freq_chapter_compare['Therapeutic Area'])
ax.tick_params(axis='x', rotation=90)
ax.legend(['London','Cambridge'], frameon=True,loc='upper left',bbox_to_anchor=(0.825, 0, 0)
ax.grid(True)
ax.set_ylabel('%', size=14)
ax.set_ylabel('BNF Chapter', size=14)
fig.suptitle('Comparison of prescription percentages by BNF Chapter', size=16)
plt.margins(0.02)
plt.show()
```

Comparison of prescription percentages by BNF Chapter



Trends in London and Cambridge with regard to prescription depending on therapeutic area do not vary substantially. Cardiovascular system, central nervous system and endocrine system are the most prevalent drugs to be prescribed in both cities.

Since our interest is to describe the number of prescriptions and total actual cost across all NHS practices for drugs related to cardiovascular disease (CVD) and antidepressants (AD), we will be looking for the corresponding BNF codes in the coming lines of code.

In [60]:

```
# CVD BNF codes should start with '02', while BNF codes for AD with '0403'
# Total number of prescriptions for CVD
cvd_code=df2.BNF_CODE.str.match('^02')==True
no prescriptions cvd=np.sum(df2[cvd code].ITEMS)
print('The total number of prescriptions for cardiovascular disease in the NHS is {} prescr
# Actual cost of prescriptions for CVD
total_cost_prescriptions=np.round(np.sum(df2.ACTUAL_COST),2)
actual_cost_cvd=np.round(np.sum(df2[cvd_code].ACTUAL_COST),2)
print('The total cost of prescriptions for cardiovascular disease in the NHS is {} £.'.form
# Total number of prescriptions for AD
ad_code=df2.BNF_CODE.str.match('^0403')==True
no_prescriptions_ad=np.sum(df2[ad_code].ITEMS)
print('The total number of antidepressants prescribed in the NHS is {}.'.format(no_prescrip
# Actual cost of prescriptions for AD
actual_cost_ad =np.round(np.sum(df2[ad_code].ACTUAL_COST),2)
print('The total cost of prescriptions for antidepressants in the NHS is {} f.'.format(actu
```

The total number of prescriptions for cardiovascular disease in the NHS is 2 6449832 prescriptions.

The total cost of prescriptions for cardiovascular disease in the NHS is 901 93834.02 f.

The total number of antidepressants prescribed in the NHS is 5715873.

The total cost of prescriptions for antidepressants in the NHS is 16853470.8 6 \pm .

Once the impact of diseases from the cardiovascular and depression therapeutic areas has been assessed, we have described the total spending and relative costs per patient across the NHS system. This is particularly relevant to be able to track the expenses of GP practices, identify those which spend more and make informed decisions about how to tackle financial issues in the healthcare system.

In [61]:

Out[61]:

	CODE	NUMBER_OF_PATIENTS	PRACTICE	ACTUAL_COST	RELATIVE_SPENDING
0	A83005	11826	A83005	156599.88	13.241999
1	A83006	8044	A83006	89694.95	11.150541
2	A83010	14070	A83010	210441.47	14.956750
3	A83013	11298	A83013	137665.38	12.184934
4	A83031	10109	A83031	128457.68	12.707259

In [62]:

df3.describe()

Out[62]:

	NUMBER_OF_PATIENTS	ACTUAL_COST	RELATIVE_SPENDING
count	7191.000000	7191.000000	7191.000000
mean	8207.557224	87842.769907	11.606497
std	5161.846053	59133.286587	38.868946

0.001724 min 3.000000 3.250000 25% 4557.000000 8.875578 45118.630000 50% 7278.000000 76206.840000 10.914659 75% 10742.500000 117871.110000 12.690038 72227.000000 842838.180000 2830.020000 max

In [63]:

df3.info()

<class 'pandas.core.frame.DataFrame'>
Int64Index: 7191 entries, 0 to 7190
Data columns (total 5 columns):

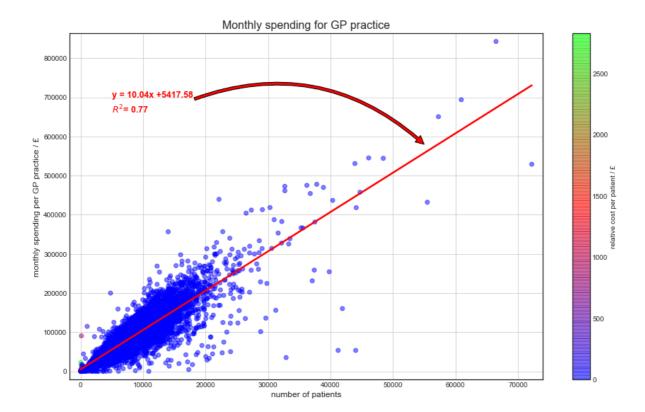
CODE 7191 non-null object
NUMBER_OF_PATIENTS 7191 non-null int64
PRACTICE 7191 non-null object
ACTUAL_COST 7191 non-null float64
RELATIVE_SPENDING 7191 non-null float64
dtypes: float64(2), int64(1), object(2)

memory usage: 337.1+ KB

In [64]:

```
#Scatter plot
fig, ax=plt.subplots(figsize=(15,9))
plt.style.use('seaborn-white')
# Scatterplot with colourbar
scatter=ax.scatter(df3['NUMBER_OF_PATIENTS'],df3['ACTUAL_COST'], c=df3['RELATIVE_SPENDING']
                   cmap='brg', vmin=0, vmax=df3['RELATIVE_SPENDING'].max(), alpha=0.5)
# Axis
plt.xlabel('number of patients', size=12)
plt.ylabel('monthly spending per GP practice / f', size=12)
plt.yticks(np.arange(0,900000,100000))
plt.title('Monthly spending for GP practice', fontsize=16)
cbar=fig.colorbar(scatter) # colorbar set up
cbar.set_label('relative cost per patient / f')
#Trend line
slope, intercept, r_value, p_value, std_err = stats.linregress(df3['NUMBER_OF_PATIENTS'],df
print('The slope for this trendline is {} and the intercept is {}.'.format(np.round(slope,2
x=df3['NUMBER_OF_PATIENTS'].sort_values() # ordering of x values
yfit=[n*slope for n in x]+intercept
# Trendline plotting
ax.plot(x, yfit,c='r',linestyle='-', linewidth=2.5)
# Annotation in the graph
ax.annotate('y = ' +str(np.round(slope,2))+'x +'+str(np.round(intercept,2)), xy=(55000,5800)
            arrowprops=dict(facecolor='r', connectionstyle='arc3, rad=-0.3'), color='r', fd
ax.annotate(r'\$R^2 = '+str(np.round(r_value**2,2)), xy=(5000,660000),color='r', fontsize=12
ax.grid()
plt.margins(0.025)
plt.show()
```

The slope for this trendline is 10.04 and the intercept is 5417.58.



A close inspection into the graph shown above reveals that there is a linear trend for GP practices, so that the greater the number of patients, the higher the monthly spending. Notably, the relative cost per patient is fairly homogeneous across all practices (<500£/patient month).

In order to get a more detailed visualisation of the relative cost per patient, a histogram has been plotted, so that the distribution of this variable could be interpreted more easily.

In [65]:

```
def remove_outliers(df,column):
    from scipy.stats import iqr

    iqr=iqr(df[column]) #Interquartilic range
    Q1=df[column].quantile(0.25)
    Q3=df[column].quantile(0.75)

#
    outliers_1=Q1-1.5*iqr
    outliers_2=Q3+1.5*iqr

clean=df[column][(df[column]>outliers_1)&(df[column]<outliers_2)] #Reject datapoints column clean</pre>
```

In [66]:

```
#First, outliers are removed
spending=remove_outliers(df3,'RELATIVE_SPENDING') #Call remove_outliers function
spending.describe()
```

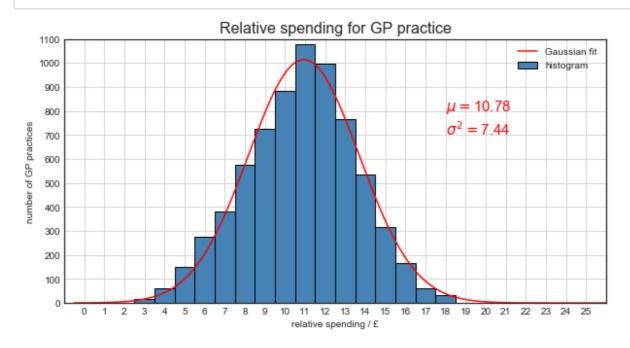
Out[66]:

count	7025.000000
mean	10.777284
std	2.727275
min	3.183002
25%	8.944339
50%	10.922939
75%	12.642940
max	18.357644

Name: RELATIVE_SPENDING, dtype: float64

In [67]:

```
# Histogram plot
plt.subplots(figsize=(10,5))
bins=int(np.sqrt(len(spending))) # Square root of n to determine number of bins
# bin_h is an array with the height of the bins and bin_b is an array with the 'borders' of
bin_h,bin_b,_=plt.hist(spending, bins=np.arange(bins)-0.5,
                       color='steelblue', edgecolor='black', label='histogram')
# Axis
plt.xlim(-1,26)
plt.ylim(-1,1100)
plt.ylabel ('number of GP practices')
plt.xlabel ('relative spending / f')
plt.xticks(np.arange(0,26,1))
plt.yticks(np.arange(0,1200,100))
plt.title('Relative spending for GP practice', fontsize=16)
from scipy.optimize import curve_fit
# Gaussian function to model the data
def gaussian(x, mean, amplitude, sd):
    return amplitude * np.exp( - ((x - mean) / sd) ** 2) #
bin_c=bin_b[:-1]+np.diff(bin_b)/2 # bin_c is an array with the bin centres, that is, the va
popt, _ = curve_fit(gaussian, bin_c, bin_h) # popt returns the best fit values for paramete
lnspc=np.linspace(bin_b[0],bin_b[-1], 10000) # array of x values for Gaussian function
plt.plot(lnspc,gaussian(lnspc,*popt), color='red', label='Gaussian fit') # plot it
plt.legend()
plt.text(18,800,r'$\mu = $'+str(np.round(spending.mean(),2)), fontsize=15, color='r') # med
plt.text(18,700,r'$\sigma^2 = $'+str(np.round(np.var(spending),2)), fontsize=15, color='r')
plt.grid(True)
plt.show()
```



One of the most salient features of this histogram is that the relative cost per patient follows a normal distribution N~(10.78,7.44).

World Health Organization (WHO) Mortality Database

In this section, an analysis of the data provided in the WHO Mortality Database has been performed. The Database contains relevant information about the cause of each death according to the 10th revision of the International Classification of Diseases (ICD-10) by country.

The analysis has been carried out for selected countries, where several data and descriptive statistical parameters have been reported, so that the reader gets a grasp of demographics and mortality characteristics of these countries.

In [68]:

```
# The relevant datasets are read
country_codes=pd.read_csv('country_codes.csv') # https://www.who.int/healthinfo/statistics/
pop=pd.read_csv('pop.csv') # https://www.who.int/healthinfo/Pop.zip?ua=1

# Low_memory entails that the whole file is read before deciding the type of each column
morticd10_1=pd.read_csv('Morticd10_part1.csv', low_memory=False) # https://www.who.int/heal
morticd10_2=pd.read_csv('Morticd10_part2.csv', low_memory=False) # https://www.who.int/heal
```

First, we have explored the datasets.

In [69]:

country_codes DataFrame is a look-up table which contains the four digit numeric code for country_codes.head()

Out[69]:

	country	name
0	1010	Algeria
1	1020	Angola
2	1025	Benin
3	1030	Botswana
4	1035	Burkina Faso

In [70]:

```
# country_codes DataFrame has 227 entries with no null values
country_codes.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 227 entries, 0 to 226
Data columns (total 2 columns):
country 227 non-null int64
name 227 non-null object
dtypes: int64(1), object(1)
memory usage: 3.6+ KB
```

In [71]:

pop DataFrame contains columns total (Pop1) and age-stratified populations (Pop to Pop26)
pop.head()

Out[71]:

	Country	Admin1	SubDiv	Year	Sex	Frmat	Pop1	Pop2	Pop3	Pop4	 Pop'
0	1060	NaN	NaN	1980	1	7	137100.0	3400.0	15800.0	NaN	
1	1060	NaN	NaN	1980	2	7	159000.0	4000.0	18400.0	NaN	
2	1125	NaN	NaN	1955	1	2	5051500.0	150300.0	543400.0	NaN	 1102
3	1125	NaN	NaN	1955	2	2	5049400.0	145200.0	551000.0	NaN	 1221
4	1125	NaN	NaN	1956	1	2	5353700.0	158700.0	576600.0	NaN	 1169

5 rows × 33 columns

In [72]:

```
pop.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 9349 entries, 0 to 9348
Data columns (total 33 columns):
Country
           9349 non-null int64
           82 non-null float64
Admin1
SubDiv
           138 non-null object
           9349 non-null int64
Year
           9349 non-null int64
Sex
           9349 non-null int64
Frmat
Pop1
           9349 non-null float64
           9213 non-null float64
Pop2
           9213 non-null float64
Pop3
           5152 non-null float64
Pop4
Pop5
           5152 non-null float64
           5152 non-null float64
Pop6
           9213 non-null float64
Pop7
Pop8
           9195 non-null float64
           9213 non-null float64
Pop9
Pop10
           9195 non-null float64
           9213 non-null float64
Pop11
           9195 non-null float64
Pop12
           9213 non-null float64
Pop13
           9195 non-null float64
Pop14
Pop15
           9213 non-null float64
Pop16
           9195 non-null float64
           9213 non-null float64
Pop17
Pop18
           9195 non-null float64
Pop19
           9213 non-null float64
           9151 non-null float64
Pop20
Pop21
           9057 non-null float64
           8197 non-null float64
Pop22
           8197 non-null float64
Pop23
           1148 non-null float64
Pop24
Pop25
           1148 non-null float64
           9195 non-null float64
Pop26
           9125 non-null float64
Lb
dtypes: float64(28), int64(4), object(1)
memory usage: 2.4+ MB
```

The DataFrame pop has been preprocessed before use. Columns not considered to be relevant for the analysis (i.e. Admin1, SubDiv, etc.) will be dropped. The DataFrame has also been merged with the pop DataFrame, so that all the information is contained in a single DataFrame. Indeed, there are some columns with high missingness rates. However, this might not impact our analysis, since we are only going to focus on selected countries.

In [73]:

Left join of both DataFrames and dropping of Admin1 and SubDiv columns
pop_country=pd.merge(pop, country_codes, how='left',left_on='Country',right_on='country').c
pop_country.head()

Out[73]:

	Country	Year	Sex	Frmat	Pop1	Pop2	Pop3 Pop4		Pop5	Pop6	 Pop19
0	1060	1980	1	7	137100.0	3400.0	15800.0	NaN	NaN	NaN	 5300.0
1	1060	1980	2	7	159000.0	4000.0	18400.0	NaN	NaN	NaN	 6200.0
2	1125	1955	1	2	5051500.0	150300.0	543400.0	NaN	NaN	NaN	 51100.0
3	1125	1955	2	2	5049400.0	145200.0	551000.0	NaN	NaN	NaN	 51100.0
4	1125	1956	1	2	5353700.0	158700.0	576600.0	NaN	NaN	NaN	 54100.0

5 rows × 32 columns

In [74]:

Since morticd10_1 and morticd10_2 DataFrames are part of the same file split in two parts
morticd10=pd.concat([morticd10_1,morticd10_2]).drop(columns=['Admin1','SubDiv'])
morticd10.info(verbose=True, null_counts=True)

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 3587860 entries, 0 to 2199753
Data columns (total 37 columns):
             3587860 non-null int64
Country
              3587860 non-null int64
Year
              3587860 non-null object
List
              3587860 non-null object
Cause
Sex
              3587860 non-null int64
              3587860 non-null int64
Frmat
IM Frmat
              3587860 non-null int64
Deaths1
              3587860 non-null int64
Deaths2
              3585618 non-null float64
Deaths3
              3585618 non-null float64
              3420612 non-null float64
Deaths4
              3420612 non-null float64
Deaths5
              3420612 non-null float64
Deaths6
Deaths7
              3585618 non-null float64
              3582633 non-null float64
Deaths8
              3585618 non-null float64
Deaths9
              3582633 non-null float64
Deaths10
Deaths11
              3585618 non-null float64
Deaths12
              3582633 non-null float64
              3585618 non-null float64
Deaths13
              3582633 non-null float64
Deaths14
              3585618 non-null float64
Deaths15
Deaths16
              3582633 non-null float64
              3585618 non-null float64
Deaths17
              3582633 non-null float64
Deaths18
              3585618 non-null float64
Deaths19
              3582309 non-null float64
Deaths20
              3585294 non-null float64
Deaths21
Deaths22
              3574442 non-null float64
Deaths23
              3574442 non-null float64
              3109293 non-null float64
Deaths24
              3109293 non-null float64
Deaths25
              3585618 non-null float64
Deaths26
              3585617 non-null float64
IM Deaths1
              2779471 non-null float64
IM Deaths2
              2868691 non-null float64
IM_Deaths3
IM Deaths4
              2868691 non-null float64
dtypes: float64(29), int64(6), object(2)
memory usage: 1.0+ GB
```

In [75]:

```
# Exploration of the DataFrame
morticd10.head()
```

Out[75]:

	Country	Year	List	Cause	Sex	Frmat	IM_Frmat	Deaths1	Deaths2	Deaths3	 Deaths2
0	1400	2001	101	1000	1	7	8	332	8.0	2.0	 95.
1	1400	2001	101	1000	2	7	8	222	11.0	1.0	 112.
2	1400	2001	101	1001	1	7	8	24	0.0	0.0	 5.
3	1400	2001	101	1001	2	7	8	14	0.0	0.0	 6.
4	1400	2001	101	1002	1	7	8	0	0.0	0.0	 0.

5 rows × 37 columns

In [76]:

```
# Merge with country_code DataFrame
morticd10_country=pd.merge(morticd10, country_codes, how='left',left_on='Country',right_on=
morticd10_country.head()
```

Out[76]:

	Country	Year	List	Cause	Sex	Frmat	IM_Frmat	Deaths1	Deaths2	Deaths3	 Deaths2
0	1400	2001	101	1000	1	7	8	332	8.0	2.0	 Nal
1	1400	2001	101	1000	2	7	8	222	11.0	1.0	 Nal
2	1400	2001	101	1001	1	7	8	24	0.0	0.0	 Nal
3	1400	2001	101	1001	2	7	8	14	0.0	0.0	 Nal
4	1400	2001	101	1002	1	7	8	0	0.0	0.0	 Nal

5 rows × 38 columns

Once the datasets to be used have been cleaned, we will proceed with the data analysis. In the first instance, missingness was checked. Since this was not an issue, the total population and deaths of Iceland, Italy and New Zealand in 2010 were reported without further data manipulation.

In [77]:

pop_country[(pop_country['name'].str.match('Australia'))&(pop_country['Year']==2010)].isna(

Out[77]:

Country 0 Year 0 Sex 0 0 Frmat Pop1 0 Pop2 0 0 Pop3 Pop4 0 0 Pop5 0 Pop6 0 Pop7 0 Pop8 Pop9 0 0 Pop10 Pop11 0 Pop12 0 0 Pop13 Pop14 0 0 Pop15 Pop16 0 Pop17 0 0 Pop18 Pop19 0 Pop20 0 0 Pop21 Pop22 0 0 Pop23 Pop24 0 0 Pop25 0 Pop26 Lb 0 name dtype: int64

In [78]:

pop_country[(pop_country['name'].str.match('Italy'))&(pop_country['Year']==2010)].isna().su

Out[78]:

Country 0 Year 0 Sex 0 0 Frmat Pop1 0 Pop2 0 0 Pop3 Pop4 0 0 Pop5 0 Pop6 0 Pop7 0 Pop8 Pop9 0 0 Pop10 Pop11 0 0 Pop12 0 Pop13 Pop14 0 0 Pop15 Pop16 0 Pop17 0 0 Pop18 Pop19 0 Pop20 0 0 Pop21 Pop22 0 0 Pop23 Pop24 0 0 Pop25 0 Pop26 Lb 0 name dtype: int64

```
In [79]:
```

```
pop_country[(pop_country['name'].str.match('Iceland'))&(pop_country['Year']==2010)].isna().
Out[79]:
Country
           0
           0
Year
Sex
           0
           0
Frmat
Pop1
           0
           0
Pop2
           0
Pop3
           0
Pop4
Pop5
           0
           0
Pop6
Pop7
           0
           0
Pop8
           0
Pop9
Pop10
           0
Pop11
           0
Pop12
           0
           0
Pop13
Pop14
           0
           0
Pop15
Pop16
           0
           0
Pop17
Pop18
           0
Pop19
           0
Pop20
           0
Pop21
           0
Pop22
           0
Pop23
           0
           0
Pop24
Pop25
           0
Pop26
           0
Lb
name
dtype: int64
In [80]:
# Function to calculate population and total number of deaths in 2010 (for all ages and all
def country pop():
    while True:
        x=input('Choose the country: Iceland, Italy or New Zealand:')
        if x=='Iceland' or x=='Italy' or x=='New Zealand':
            # Calculate the total population
            locations_pop=pop_country[(pop_country['name'].str.match(x))&(pop_country['Year
            total_pop=np.sum(pop_country.iloc[locations_pop].Pop1.sum())
            # Calculate total number of deaths
            locations_death=morticd10_country[(morticd10_country['name'].str.match(x))&(mor
            total death=morticd10 country.iloc[locations death,7].sum()
            print('According to WHO Mortality Database, the population of {} in 2010 was {}
            break
        else:
            print('Error! Please type only Iceland, Italy or New Zealand.')
```

In [81]:

country_pop()

Choose the country: Iceland, Italy or New Zealand:Iceland According to WHO Mortality Database, the population of Iceland in 2010 was 3 18041.0 inhabitants and the total number of deaths was 4038.

In [82]:

country_pop()

Choose the country: Iceland, Italy or New Zealand:Italy According to WHO Mortality Database, the population of Italy in 2010 was 604 83386.0 inhabitants and the total number of deaths was 1169230.

In [83]:

country_pop()

Choose the country: Iceland, Italy or New Zealand: New Zealand According to WHO Mortality Database, the population of New Zealand in 2010 w as 4367360.0 inhabitants and the total number of deaths was 57298.

Afterwards, we analysed the distribution of total deaths in Italy by age group across all the dataset. First, we created a new column for the 0-4 year old age group and then we plotted it in an horizontal bar chart, as customary for demographic analysis.

In [84]:

```
# Distribution of deaths by age group in Italy (for all causes and years)
# Creation of the age group 0-4 yrs
morticd10_country['0-4 yrs']=np.sum(morticd10_country.iloc[:,8:12], axis=1)
# Renaming, dropping and reordering of morticd10_country colums for clarification purposes
morticd10_country=morticd10_country.rename(index=str,columns={'name':'Name','Deaths7':'5-9
morticd10_country=morticd10_country[['Country','Name','Year','List','Sex','Cause','0-4 yrs'
morticd10_country.head()
```

Out[84]:

	Country	Name	Year	List	Sex	Cause	0-4 yrs	5-9 yrs	10- 14 yrs	15- 19 yrs	 85- 89 yrs	90- 94 yrs	>95 yrs	Age uns
0	1400	Seychelles	2001	101	1	1000	10.0	1.0	NaN	9.0	 NaN	NaN	NaN	
1	1400	Seychelles	2001	101	2	1000	12.0	1.0	NaN	1.0	 NaN	NaN	NaN	
2	1400	Seychelles	2001	101	1	1001	0.0	0.0	NaN	1.0	 NaN	NaN	NaN	
3	1400	Seychelles	2001	101	2	1001	0.0	0.0	NaN	0.0	 NaN	NaN	NaN	
4	1400	Seychelles	2001	101	1	1002	0.0	0.0	NaN	0.0	 NaN	NaN	NaN	

5 rows × 33 columns

In [85]:

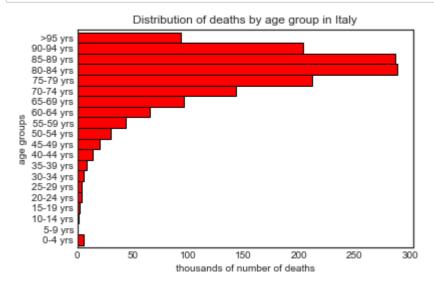
```
# Checking missingness
morticd10_country.loc[morticd10_country['Name']=='Italy','0-4 yrs':'>95 yrs'].isna().sum()
```

Out[85]:

```
0-4 yrs
              0
5-9 yrs
              0
10-14 yrs
              0
15-19 yrs
20-24 yrs
             0
25-29 yrs
30-34 yrs
              0
35-39 yrs
40-44 yrs
             0
45-49 yrs
              0
50-54 yrs
              0
55-59 yrs
             0
60-64 yrs
             0
65-69 yrs
             0
70-74 yrs
75-79 yrs
             0
80-84 yrs
              0
85-89 yrs
              0
90-94 yrs
>95 yrs
dtype: int64
```

In [86]:

```
# Analysis and representation of the distribution
# Selection of columns with age groups (age unspecified is not considered as cannot be cate
distr_deaths=pd.DataFrame(np.sum(morticd10_country.loc[morticd10_country['Name']=='Italy','
# In demographic pyramids, the distribution of age groups tends to be plotted horizontally
distr_deaths.plot(kind='barh', legend=False, color='red', width=1, edgecolor='black')
plt.xlabel('thousands of number of deaths')
plt.ylabel('age groups')
plt.title('Distribution of deaths by age group in Italy')
plt.show()
```



Having analysed the distribution of total deaths in Italy in 2010, we then put the focus on neoplasm, which is a prevalent disease in developed countries. In the first place, we have identified the top-5 causes of deaths for this disease with the ICD-10 codes. Importantly, ICD-10 have a minimum of three characters which indicate the cause of the disease. However, further granularity is allowed and the code can be extended with up to seven characters. Consequently, we have taken two different approaches to identify the top-5 causes: a 'specific' approach which considers all the characters and a 'generic' approach which only considers the first three characters.

In [87]:

```
# Generation of a table with the cause of death, number of deaths and proportion of overall
# First, a variable with the relevant columns is created (including unspecified age)
italy_neoplasm=morticd10_country[(morticd10_country['Name']=='Italy')&morticd10_country['Ca
# Second, all the deaths per age group are added and ordered in descending order
no_deaths_neoplasm_it_specific=np.sum(italy_neoplasm.groupby('Cause').sum(), axis=1).sort_v
# Third, the proportion of overall deaths is calculated
proportion_specific= np.divide(no_deaths_neoplasm_it_specific.head(5),no_deaths_neoplasm_it
# The data is captured in a DataFrame
data={'number of deaths':no_deaths_neoplasm_it_specific.head(5),'proportion of overall deat
no_deaths_neoplasm_it_specific_df=pd.DataFrame(data=data).rename({'C349':'Bronchus or lung.
no_deaths_neoplasm_it_specific_df.index.names=['Malignant Neoplasm']
no_deaths_neoplasm_it_specific_df
```

Out[87]:

number of deaths proportion of overall deaths

Malignant Neoplasm

Bronchus or lung. Unspecified	426449.0	0.189670
Breast. Unspecified	155895.0	0.069337
Colon. Unspecified	143188.0	0.063685
Stomach. Unspecified	125679.0	0.055898
Pancreas. Unspecified	120069.0	0.053402

When considering whole ICD-10 codes for neoplasms, the 'Unspecified' category is frequently selected. This reveals that it might be complicated to give a precise diagnosis on neoplasm and thus descriptions as kept as general as possible. Indeed, this tendency was found to be replicated for the top-10, as shown below.

In [88]:

```
no_deaths_neoplasm_it_df2=pd.DataFrame(no_deaths_neoplasm_it_specific.head(10))
no_deaths_neoplasm_it_df2.columns=['number of deaths']
no_deaths_neoplasm_it_df2.rename({'C349':'Bronchus or lung. Unspecified','C509':'Breast. Ur
'C189':'Colon. Unspecified','C169':'Stomach. Unspecified'
'C61':'Prostate', 'C679':'Bladder. Unspecified','C229':'Li
'C220':'Liver cell carcinoma','C809':'Primary site. Unspecified'
```

Out[88]:

number of deaths

Cause

Bronchus or lung. Unspecified	426449.0
Breast. Unspecified	155895.0
Colon. Unspecified	143188.0
Stomach. Unspecified	125679.0
Pancreas. Unspecified	120069.0
Prostate	95903.0
Bladder. Unspecified	71097.0
Liver. Unspecified	58340.0
Liver cell carcinoma	54392.0
Primary site. Unspecified	54149.0

In [89]:

```
# Now, we analyse the ICD-10 codes following the 'generic' approach
# Grouping by cause, sorting and identifying top 5 generic causes
no_deaths_neoplasm_it_generic=italy_neoplasm
no_deaths_neoplasm_it_generic['Cause']=no_deaths_neoplasm_it_generic['Cause'].str[:3] #In h
no_deaths_neoplasm_it_generic_tot=np.sum(no_deaths_neoplasm_it_generic.groupby('Cause').sum
no_deaths_neoplasm_it_generic5=no_deaths_neoplasm_it_generic_tot.head(5)
no_deaths_neoplasm_it_other=no_deaths_neoplasm_it_generic_tot.tail(len(no_deaths_neoplasm_i
proportion_generic5=np.divide(no_deaths_neoplasm_it_generic5, no_deaths_neoplasm_it_generic
data={'number of deaths': no_deaths_neoplasm_it_generic5, 'proportion of overall deaths':pr
no_deaths_neoplasm_it_generic5=pd.DataFrame(data=data).rename({'C34':'Bronchus and lungs','
no_deaths_neoplasm_it_generic5.index.names=['Malignant Neoplasm']
no_deaths_neoplasm_it_generic5
```

Out[89]:

number of deaths proportion of overall deaths

Malignant Neoplasm

Bronchus and lungs	430067.0	0.416058
Colon	182802.0	0.176847
Breast	156002.0	0.150920
Stomach	132676.0	0.128354
Pancreas	132124.0	0.127820

Interestingly, top-5 neoplasms following the more 'generic' approach leads to very similar results in terms of ranks, albeit the total number of deaths is logically higher in these categories. Since the results obtained with the more 'specific' approach were been found to be vague and did not differ substantially from the 'generic' ones, a pie chart was plotted following the data from the 'generic' diagnoses.

In [90]:

```
#Calculation of proportion top5 and other
proportion_generic_tot1=np.divide(no_deaths_neoplasm_it_other, no_deaths_neoplasm_it_generic_proportion_generic_tot2=1-proportion_generic_tot1

#We construct a DataFrame with the data just calculated
no_deaths_neoplasm_it_total=pd.DataFrame(columns=['number of deaths','proportion of deaths'
no_deaths_neoplasm_it_total.index.names=['Malignant Neoplasm']
no_deaths_neoplasm_it_total['number of deaths']=no_deaths_neoplasm_it_generic5['number of cono_deaths_neoplasm_it_total['proportion of deaths']=proportion_generic_tot2,proportion_generic_deaths_neoplasm_it_total
```

Out[90]:

number of deaths proportion of deaths

Malignant Neoplasm

Top 5	1033671.0	0.459741
Other	1214708.0	0.540259

In [91]:

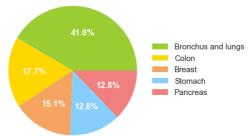
```
# Display pie chart to visualise the proportion of deaths
fig, (ax1, ax2)=plt.subplots(1,2, figsize=(10,5))
colors1=['yellowgreen','lightcoral']
sizes1=no_deaths_neoplasm_it_total['proportion of deaths'].tolist()
labels1='Top 5','Other'
patches1, texts1, autotexts1=ax1.pie(sizes1, labels=labels1,colors=colors1, autopct='%1.1f%
ax1.axis('equal')
ax1.legend(loc='center left',bbox_to_anchor=(0.8, 0, 0, 1), prop={'size': 15})
ax1.set_title('Overall proportion of deaths for neoplasm in Italy', size=20)
plt.setp(autotexts1, size=16, weight="bold")
colors2=['yellowgreen', 'gold','sandybrown','lightskyblue', 'lightcoral']
sizes2=proportion_generic5.tolist()
labels2='Bronchus and lungs', 'Colon', 'Breast', 'Stomach', 'Pancreas'
patches2,texts2,autotexts2=ax2.pie(sizes2, labels=labels2,colors=colors2, autopct='%1.1f%'
ax2.axis('equal') # Equally sized circumference
ax2.legend(loc='center left',bbox_to_anchor=(0.8, 0, 0, 1), prop={'size': 15}) # legend loc
ax2.set_title('Top 5 proportion of deaths for neoplasm in Italy', size=20)
plt.subplots adjust(left=0.1, right=1.5)
plt.setp(autotexts2, size=16, weight="bold")
plt.show()
```

Overall proportion of deaths for neoplasm in Italy

46.0%

Top 5
Other

Top 5 proportion of deaths for neoplasm in Italy



Top-5 neoplasms represent over 45% of the total neoplasm diagnoses in Italy. By far, the most common neoplasm amongst the top-5 is located in the bronchus and lungs. Notably, breast neoplasm has also a high prevalence, despite only affecting women.

The age group distribution for deaths due to neoplasm in Australia was analysed in the code below.

In [92]:

```
# Elimination of the 'Cause' column as it is not of interest anymore (we are only intereste
aus_neoplasm=morticd10_country[(morticd10_country['Name']=='Australia')&(morticd10_country[
no_deaths_neoplasm_aus=aus_neoplasm.sum()
no_deaths_neoplasm_aus_sorted=no_deaths_neoplasm_aus.sort_values(ascending=False)
no_deaths_neoplasm_aus_sorted5=no_deaths_neoplasm_aus_sorted.head(5) # Identification of to
no_deaths_neoplasm_aus_sorted=pd.DataFrame(no_deaths_neoplasm_aus_sorted) # Convert to Data
no_deaths_neoplasm_aus_sorted.columns=['Number of deaths'] # Renaming of column
print('As shown in the following table, there are indeed differences by age group for death
no_deaths_neoplasm_aus_sorted
```

As shown in the following table, there are indeed differences by age group f or deaths from Neoplasms in Australia in 2010.

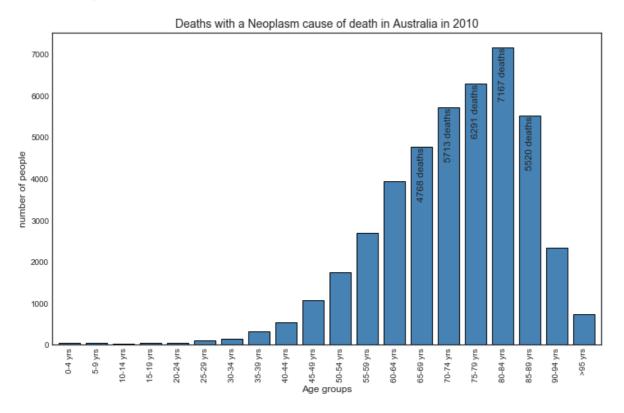
Out[92]:

	Number of deaths
80-84 yrs	7167.0
75-79 yrs	6291.0
70-74 yrs	5713.0
85-89 yrs	5520.0
65-69 yrs	4768.0
60-64 yrs	3938.0
55-59 yrs	2695.0
90-94 yrs	2336.0
50-54 yrs	1756.0
45-49 yrs	1065.0
>95 yrs	735.0
40-44 yrs	548.0
35-39 yrs	323.0
30-34 yrs	138.0
25-29 yrs	97.0
20-24 yrs	52.0
15-19 yrs	50.0
5-9 yrs	46.0
0-4 yrs	36.0
10-14 yrs	31.0

Certainly, the top-5 age groups in Australia dying because of neoplasm can be identified in the above table. This was also displayed in the next bar chart, so that it could be visualised.

In [93]:

The top 5 age groups dying by Neoplasms in Australia in 2010 can be easily i dentified graphically, too.



Having collated and analysed the data both for Australia and Italy with regard to neoplasm deaths, we calculated frequencies and compared the trends amongst both countries. Despite both Italy and Australia being Western developed countries, they do differ socioeconomically. Hence, it has been deemed to be interesting to analyse potential contrasting trends and evaluate the neoplasm burden in 2010 in these two countries.

In [94]:

```
# As done before, we create a new column grouping the age group comprised between 0 and 4 y pop_country['Pop 0-4 yrs']=np.sum(pop_country.iloc[:,5:10], axis=1) cols=pop_country.columns.tolist() cols=cols[0:10]+cols[-1:]+cols[10:32] pop_country=pop_country[cols] pop_country.columns
```

Out[94]:

Considering that sex and age could be potential confounders, most analysis have been carried out stratifying by the different categories of sex and age groups available.

In [95]:

```
# We define a function which allows us to identify total neoplasm deaths by sex
def neoplasm_sex(country):
    neoplasm_sex=morticd10_country[(morticd10_country['Name']==country)&(morticd10_country[
    neoplasm_sex=neoplasm_sex.groupby('Sex').sum()
    return neoplasm_sex
```

In [96]:

```
aus_neoplasm_sex=neoplasm_sex('Australia')
aus_neoplasm_sex
```

Out[96]:

```
20-
                               25-
                                     30-
            10-
                  15-
0-4
      5-9
                                           35-39 40-44
                                                          45-49
                                                                  50-54
                                                                         55-59
                                                                                  60-64
                                                                                           65-69
            14
                  19
                         24
                               29
                                     34
                                                                  yrs
                                                                         yrs
                                                                                  yrs
                                                                                          yrs
vrs
      yrs
                                           yrs
                                                   vrs
                                                          yrs
                  yrs
                                     yrs
                               yrs
            vrs
                        yrs
```

Sex

```
1 18.0 28.0 20.0 26.0 24.0 50.0 79.0 139.0 247.0 535.0 919.0 1507.0 2267.0 2926.0 2 18.0 18.0 11.0 24.0 28.0 47.0 59.0 184.0 301.0 530.0 837.0 1188.0 1671.0 1842.0
```

In [97]:

```
it_neoplasm_sex=neoplasm_sex('Italy')
it_neoplasm_sex
```

Out[97]:

```
10-
                 15-
0-4
     5-9
                       20-24 25-29 30-34 35-39 40-44
                                                          45-49
                                                                  50-54
                                                                          55-59
                                                                                  60-64
           14
                 19
yrs
     yrs
                             yrs
                                    yrs
                                           yrs
                                                  yrs
                                                          yrs
                                                                  yrs
                                                                          yrs
                                                                                  yrs
                 yrs
```

Sex

- **1** 40.0 44.0 43.0 72.0 100.0 131.0 218.0 421.0 829.0 1602.0 2904.0 4900.0 8656.0
- **2** 42.0 46.0 54.0 61.0 63.0 103.0 225.0 514.0 1096.0 1835.0 2781.0 3653.0 5393.0

In [98]:

```
# This function allows us to calculate the population by sex and age group for 2010 def pop_sex(country):
```

country_pop_country[(pop_country['name']==country)&(pop_country['Year']==20
return country_pop_country

In [99]:

```
aus_pop_sex=pop_sex('Australia')
aus_pop_sex
```

Out[99]:

	Pop 0-4 yrs	Pop7	Pop8	Pop9	Pop10	Pop11	Pop12	Pop13	Pop14	F
0	743953.0	700989.0	719857.0	770176.0	848684.0	841085.0	765441.0	801732.0	769275.0	7
1	706015.0	664365.0	683971.0	728073.0	793579.0	816353.0	763552.0	814291.0	780335.0	7

In [100]:

```
it_pop_sex=pop_sex('Italy')
it_pop_sex
```

Out[100]:

	Pop 0-4 yrs	Pop7	Pop8	Pop9	Pop10	Pop11	Pop12	Pop13	Pop
0	1462245.0	1458918.0	1447417.0	1519990.0	1596439.0	1757263.0	2082019.0	2411477.0	247
1	1383308.0	1379303.0	1364393.0	1431000.0	1530065.0	1730638.0	2050852.0	2388466.0	247

In [101]:

This function calculates the frequency of deaths caused by neoplasm for every 100,000 pec
def freq_neoplasm_death(country):
 country_freq=np.divide(neoplasm_sex(country),pop_sex(country))*100000
 return country_freq

In [102]:

```
aus_freq=freq_neoplasm_death('Australia')
aus_freq
```

Out[102]:

	0-4 yrs	5-9 yrs	10-14 yrs	15-19 yrs	20-24 yrs	25-29 yrs	30-34 yrs	35-39 yrs	40-44 y
Sex									
1	2.419508	3.994357	2.778330	3.375852	2.827908	5.944702	10.320848	17.337464	32.1081
2	2.549521	2.709354	1.608255	3.296373	3.528319	5.757313	7.727044	22.596345	38.5731

In [103]:

```
it_freq=freq_neoplasm_death('Italy')
it_freq
```

Out[103]:

	0-4 yrs	5-9 yrs	10-14 yrs	15-19 yrs	20-24 yrs	25-29 yrs	30-34 yrs	35-39 yrs	40-44 yrs
Sex									
1	2.73552	3.015934	2.970809	4.736873	6.263941	7.454775	10.470606	17.458180	33.46624
2	3.03620	3.335018	3.957804	4.262753	4.117472	5.951562	10.971050	21.520089	44.33594

In [104]:

```
aus_it_freq=pd.DataFrame(columns=['median male','median female'],index=['Australia','Italy'
aus_it_freq.index.names=['Death rate (x100,000)']
aus_it_freq.iloc[0,0]=np.round(aus_freq.iloc[0,:].quantile(.50),2)
aus_it_freq.iloc[0,1]=np.round(aus_freq.iloc[1,:].quantile(.50),2)
aus_it_freq.iloc[1,0]=np.round(it_freq.iloc[0,:].quantile(.50),2)
aus_it_freq.iloc[1,1]=np.round(it_freq.iloc[1,:].quantile(.50),2)
aus_it_freq
```

Out[104]:

median male median female

Death rate (x100,000)

Australia	97.63	89.67
Italy	106.46	105.28

Since the death rate distribution is not normal, the median death rate has been reported instead of a mean. The death rate tends to be higher in Italy than in Australia and amongst man over women. To further illustrate this, we have estimated the ratio of neoplasm death rates (per 100,000 people) in Italy vs. Australia for all age groups.

In [105]:

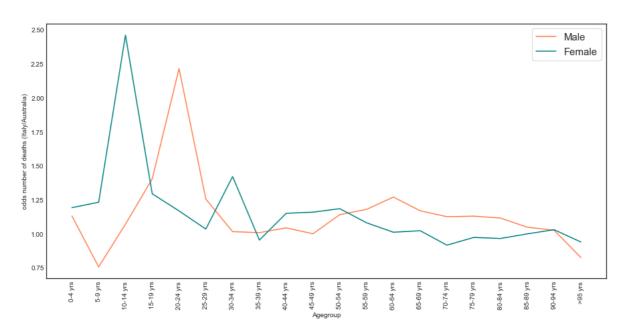
```
odds_m=np.divide(it_freq.iloc[0,:],aus_freq.iloc[0,:])
odds_f=np.divide(it_freq.iloc[1,:],aus_freq.iloc[1,:])
```

In [106]:

```
fig, ax=plt.subplots(figsize=(15,7))
ind=np.arange(len(odds_m))

ax.plot(ind,odds_m, color='coral')
ax.plot(ind,odds_f, color='teal')
ax.set(xticks=ind,xticklabels=odds_m.index)
ax.tick_params(axis='x', rotation=90)
ax.legend(['Male','Female'], frameon=True, prop={'size':15})
ax.set_ylabel('odds number of deaths (Italy/Australia)')
ax.set_xlabel('Agegroup')
fig.suptitle('Odds of death by neoplasm by age group', size=15)
plt.show()
```

Odds of death by neoplasm by age group



The frequency of death in Italy is higher in low age groups for both sexes. However, this is not very significant demographically as the number of deaths amongst young people for neoplasm is not very high when compared to older age groups. Indeed, the frequency of deaths for people over 40 years old is quite similar in both countries and sexes. The next graphs make these claims clearer, as frequencies are displayed in bars and the absolute number of deaths can be traced with the overlaid linear plot.

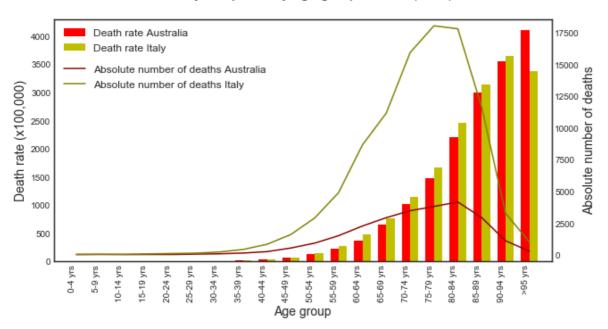
In [107]:

```
def plot death ageg(country1,country2, sex):
    fig, ax1=plt.subplots(figsize=(10,5))
    ind=np.arange(len(freq_neoplasm_death(country1).columns))
   width=0.35
    ax2=ax1.twinx()
   if sex=='male':
        a=0
    if sex=='female':
        a=1
    p1=ax1.bar(ind, freq_neoplasm_death(country1).iloc[a,:], width, color='r')
    11=ax2.plot(ind+(width/2),neoplasm_sex(country1).iloc[a,:], color='darkred')
    p2=ax1.bar(ind+width, freq_neoplasm_death(country2).iloc[a,:], width, color='y')
    12=ax2.plot(ind+(width/2),neoplasm_sex(country2).iloc[a,:], color='olive')
    ax1.set(xticks=ind,xticklabels=freq_neoplasm_death(country1).columns)
    ax1.tick_params(axis='x', rotation=90)
    ax1.legend(['Death rate ' + str(country1), 'Death rate ' + str(country2)], frameon=False
           prop={'size': 12})
    ax2.legend(['Absolute number of deaths ' + str(country1), 'Absolute number of deaths ' +
           bbox_to_anchor=(0, 0, 0, 0.85),loc='upper left',prop={'size': 12})
    ax1.set_ylabel('Death rate (x100,000)', size=14)
    ax2.set ylabel('Absolute number of deaths', size=14)
    ax1.set_xlabel('Age group', size=14)
    fig.suptitle('Deaths by Neoplasm by age group in 2010 (' + str(sex)+ ')', size=16)
    plt.margins(0.03)
    plt.show()
```

In [108]:

```
plot_death_ageg('Australia','Italy','male')
```

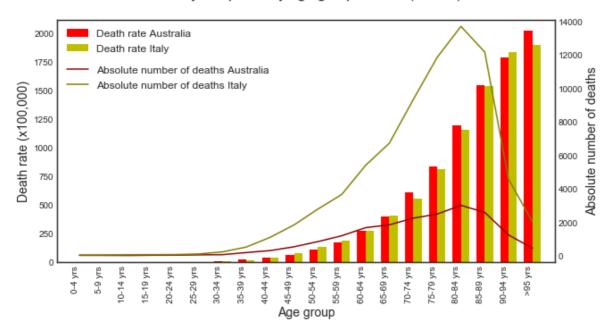
Deaths by Neoplasm by age group in 2010 (male)



In [109]:

```
plot_death_ageg('Australia','Italy','female')
```

Deaths by Neoplasm by age group in 2010 (female)



The absolute number of deaths in Italy is higher than in Australia, but this is due to the fact that Italy's population is ~2.5-fold higher than Australia's. It is thus more informative to compare frequencies of neoplasm death by 100,000 people. An examination of these previous graphs further strengthens the conclusion that, generally, frequency of neoplasm death increases with age at similar rates regardless country. Notably, frequencies are almost halved amongst females compared to males.

It is also relevant to assess the impact that different types of neoplasms might have in both countries. Thus, the top-5 most burdensome neoplasms for both countries are identified and plotted together in a bar chart.

In [110]:

```
# This function allows us to group by 'generic' causes of cancer by sex and country
def neoplasm_sex_type(country):
    neoplasm_type=morticd10_country[(morticd10_country['Name']==country)&(morticd10_country
    neoplasm_type['Cause']=neoplasm_type['Cause'].str[:3]
    neoplasm_sex_type=np.sum(neoplasm_type.groupby(['Cause','Sex']).sum(), axis=1) # Now we
    neoplasm_sex_type=pd.DataFrame(neoplasm_sex_type, columns=['Number of deaths'])
    return neoplasm_sex_type
```

In [111]:

```
aus_neoplasm_sex_type=neoplasm_sex_type('Australia')
aus_neoplasm_sex_type.head()
```

Out[111]:

Number of deaths

Cause	Sex	
C00	1	4.0
	2	7.0
C01	1	20.0
	2	7.0
C02	1	124.0

In [112]:

```
# This is a function used for selecting the appropriate columns and rows in the multiindexe
def country_sorted_sex(country,sex):
    idx=pd.IndexSlice # it helps us with slicing multiindexed DataFrames more easily

if sex=='male':
    a=1
    if sex=='female':
    a=2

country_sorted_s=neoplasm_sex_type(country).loc[idx[:,a],:].reset_index(level=1, drop=1 country_sorted_s.columns=['Number of deaths '+str(country)]

return country_sorted_s
```

In [113]:

```
# Frequency calculation by type
def freq_neoplasm_type(country,sex):
    if sex=='male':
        a=0
    if sex=='female':
        a=1

#Calling pop_sex, summing over the corresponding sex across all age groups
frequency=np.divide(country_sorted_sex(country,sex),pop_sex(country).sum(axis=1)[a])*10

freq_neoplasm_type=pd.DataFrame(frequency)
    freq_neoplasm_type.columns=['Frequency in '+str(country)]

return freq_neoplasm_type
```

In [114]:

freq_neoplasm_type('Australia','female').sort_values(by=['Frequency in Australia'], ascendi

Out[114]:

Frequency in Australia

Cause	
C34	28.274747
C50	25.381184
C80	11.538526
C25	10.725828
C18	9.162947

In [115]:

freq_neoplasm_type('Italy','female').sort_values(by=['Frequency in Italy'], ascending=False

Out[115]:

Frequency in Italy

Cause	
C50	38.913629
C34	26.544138
C18	21.925252
C25	17.438060
C16	13.670360

In [116]:

#Comparison of frequency of death by type of Neoplasm by males
aus_it_freq_m=pd.merge(freq_neoplasm_type('Australia','male'), freq_neoplasm_type('Italy','
aus_it_freq_m.head()

Out[116]:

Frequency in Australia Frequency in Italy

Cause		
C34	44.431456	86.649748
C61	29.152512	25.577212
C80	13.432137	15.011749
C25	11.107864	17.318365
C18	10.107886	26.306335

In [117]:

```
#Comparison of frequency of death by type of Neoplasm by females
aus_it_freq_f=pd.merge(freq_neoplasm_type('Australia','female'), freq_neoplasm_type('Italy'
aus_it_freq_f.head()
```

Out[117]:

Frequency in Australia Frequency in Italy

Cause		
C34	28.274747	26.544138
C50	25.381184	38.913629
C80	11.538526	11.659635
C25	10.725828	17.438060
C18	9.162947	21.925252

In [118]:

```
def country1_country2_sorted_sex(country1,country2,sex):
    #We construct a merged DataFrame with the absolute number of deaths by type of neoplasm
    c_sorted_s=pd.merge(country_sorted_sex(country1,sex), country_sorted_sex(country2,sex),
    c_sorted_s.columns=['Deaths in '+str(country1), 'Deaths in '+str(country2)]
    #We standardise the absolute deaths and sort by the sum of the standardised absolute de
    a=np.divide(c_sorted_s.iloc[:,0],c_sorted_s.iloc[:,0].max())
    b=np.divide(c_sorted_s.iloc[:,1],c_sorted_s.iloc[:,1].max())
    c_sorted_s['Sum']=a+b
    c_sorted_s.sort_values(['Sum'], inplace=True, ascending=False)
    c_sorted_s=c_sorted_s.drop(columns=['Sum'])
    #Determine number of columns to display for top5 of each country
    no_cols=len(pd.merge(country_sorted_sex(country1,sex).head(5),country_sorted_sex(country_sorted_sex)
    c_freq_s=pd.merge(freq_neoplasm_type(country1,sex), freq_neoplasm_type(country2,sex), freq_neoplasm_type(country2,sex)
    #Merge absolute deaths with frequencies
    c sorted s=pd.merge(c sorted s,c freq s, how='left',left on='Cause',right on='Cause')
    c_sorted_s.index.names=['Malignant Neoplasm']
    return c_sorted_s.head(no_cols)
```

In [119]:

Out[119]:

	Deaths in Australia	Deaths in Italy	Frequency in Australia	Frequency in Italy
Malignant Neoplasm				
Bronchus and lung	4932.0	25432.0	44.431456	86.649748
Prostate	3236.0	7507.0	29.152512	25.577212
Colon	1122.0	7721.0	10.107886	26.306335
Without specification of site	1491.0	4406.0	13.432137	15.011749
Pancreas	1233.0	5083.0	11.107864	17.318365
Liver and intrahepatic bile ducts	888.0	6057.0	7.999824	20.636895
Stomach	719.0	5819.0	6.477335	19.826002

In [120]:

Out[120]:

	Deaths in Australia	Deaths in Italy	Frequency in Australia	Frequency in Italy
Malignant Neoplasm				
Breast	2842.0	12115.0	25.381184	38.913629
Bronchus and lung	3166.0	8264.0	28.274747	26.544138
Colon	1026.0	6826.0	9.162947	21.925252
Pancreas	1201.0	5429.0	10.725828	17.438060
Without specification of site	1292.0	3630.0	11.538526	11.659635
Ovary	912.0	3193.0	8.144842	10.255982

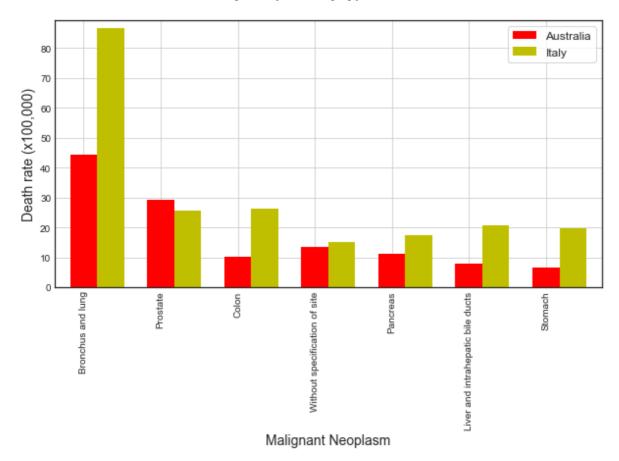
In [121]:

```
def plot neoplasm bytype(country1,country2,sex):
    fig, ax=plt.subplots(figsize=(10,5))
    ccss=country1_country2_sorted_sex(country1,country2,sex) # We call a previously defined
    ind=np.arange(len(ccss))
    width=0.35
    if sex=='male':
        labels=['Bronchus and lung','Prostate','Colon','Without specification of site','Par
                'Liver and intrahepatic bile ducts', 'Stomach']
    if sex=='female':
        labels=['Bronchus and lung','Colon','Without specification of site','Pancreas','Ova
    p1=ax.bar(ind, ccss.iloc[:,2], width, color='r')
    p2=ax.bar(ind+width, ccss.iloc[:,3], width, color='y')
    ax.set(xticks=ind,xticklabels=labels)
    ax.tick_params(axis='x', rotation=90)
    ax.legend([str(country1),str(country2)], frameon=True, loc='upper right', prop={'size':
    ax.grid()
    ax.set_ylabel('Death rate (x100,000)', size=14)
    ax.set_xlabel('Malignant Neoplasm', size=14)
    fig.suptitle('Deaths by Neoplasm by type in 2010 '+str(sex), size=16)
    plt.margins(0.03)
    plt.show()
```

In [122]:

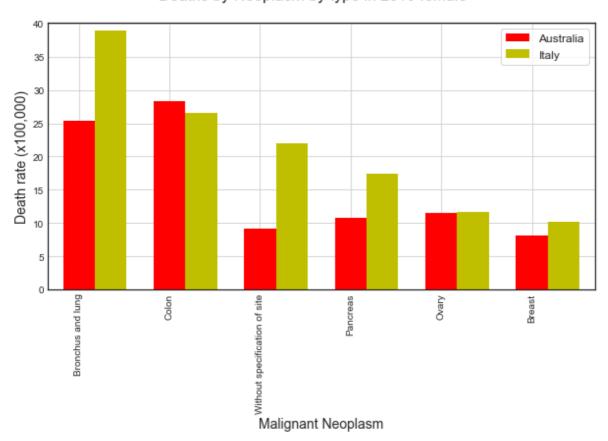
```
plot_neoplasm_bytype('Australia','Italy','male')
```

Deaths by Neoplasm by type in 2010 male



plot_neoplasm_bytype('Australia','Italy','female')

Deaths by Neoplasm by type in 2010 female



'Bronchus and lung' neoplasm are prevalent in both countries, albeit the death rate is higher in Italy than in Australia. However, these plots unveil something which had not been previously seen as clearly: sex-related neoplasms (i.e. prostate, ovary and breast) are common causes of death, as they figure in the top-5 of at least one of the analysed countries.

END OF THE REPORT

Word count: 2,500 words

This report has been posted in Github (https://github.com/BVWC3/DMHR-Assignment))