Predictive Health Care

Project Description

PwC is working closely with a network of doctors from Germany. The doctors are interested in finding the possible adverse effects of drugs used to treat neurological pain.

Besides treatment with usual drugs such as gapapentin or lyrica, doctors have found tramal to be a good remedy against neurological pain. If all of these have a similar effect, it would be interesting for the doctors to compare the adverse effects of tramal to gabapentin or lyrica. Depending on the patient, they could then prescribe the medication with fewer adverse effects.

The US has a central database, hosted by the FDA. The FDA Adverse Event Reporting System (FAERS) is a database that contains information on adverse event and medication error reports submitted to FDA. The database is designed to support the FDA's post-marketing safety surveillance programme for drug and therapeutic biologic products.

Data Description

Code for a patient outcome (See table below)

CODE MEANING_TEXT

DE Death

LT Life-Threatening

HO Hospitalization - Initial or Prolonged

DS Disability

CA Congenital Anomaly

RI Required Intervention to Prevent Permanent Impairment/Damage

OT Other Serious (Important Medical Event)

NOTE: The outcome from the latest version of a case is provided. If there is more than one outcome, the codes will be line listed.

Import Libraries

In [1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import random

import statsmodels.api as sm
import statsmodels.formula.api as smf
from statsmodels.formula.api import ols

import datetime
from datetime import datetime, timedelta

import scipy.stats

import pandas_profiling
from pandas_profiling import ProfileReport


%matplotlib inline
#sets the default autosave frequency in seconds
%autosave 60
sns.set_style('dark')
sns.set(font_scale=1.2)

plt.rc('axes', titlesize=9)
plt.rc('axes', labelsize=14)
plt.rc('xtick', labelsize=12)
plt.rc('ytick', labelsize=12)

import warnings
warnings.filterwarnings('ignore')

# Webscraping
#import requests
#from bs4 import BeautifulSoup

# Use Folium library to plot values on a map.
#import folium

# Use Feature-Engine library
#import feature_engine
#import feature_engine.missing_data_imputers as mdi
#from feature_engine.outlier_removers import Winsorizer
#from feature_engine import categorical_encoders as ce
#from feature_engine.discretisation import EqualWidthDiscretiser, EqualFrequencyDiscretiser, DecisionTreeDis
#from feature_engine.encoding import OrdinalEncoder

pd.set_option('display.max_columns',None)
#pd.set_option('display.max_rows',None)
pd.set_option('display.width', 1000)
pd.set_option('display.float_format','{:.2f}'.format)

random.seed(0)
np.random.seed(0)
np.set_printoptions(suppress=True)
```

```
Autosaving every 60 seconds
```

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In [2]:
```
df_19Q1_drug = pd.read_table("DRUG19Q1.txt",sep='$')
```

In [3]:
```
df_19Q1_drug
```

Out[3]:

	primaryid	caseid	drug_seq	role_cod	drugname	prod_ai	val_vbm	route	dose_vbm	cum_dose_chr
0	1000661812	10006618	1	PS	LIPITOR	ATORVASTATIN CALCIUM	1	NaN	UNK	nan
1	1000661812	10006618	2	SS	BENTYL	DICYCLOMINE HYDROCHLORIDE	1	NaN	UNK	nan
2	1000661812	10006618	3	SS	DICYCLOMINE	DICYCLOMINE HYDROCHLORIDE	1	NaN	UNK	nan
3	1000808590	10008085	1	PS	SANDOSTATIN LAR DEPOT	OCTREOTIDE ACETATE	1	Intramuscular	20 MG, BIW	nan
4	1000808590	10008085	2	SS	SANDOSTATIN LAR DEPOT	OCTREOTIDE ACETATE	1	Intramuscular	30 MG, QMO	nan
...	...	...	...	...	...	...	...	...	...	...
1648982	99978793	9997879	3	C	DOLIPRANE	ACETAMINOPHEN	1	NaN	UNK	nan
1648983	99978793	9997879	4	C	INDOCOLLYRE	INDOMETHACIN	1	NaN	UNK	nan
1648984	99978793	9997879	5	C	LEDERFOLIN	LEUCOVORIN CALCIUM	1	NaN	UNK	nan
1648985	99998153	9999815	1	PS	SUTENT	SUNITINIB MALATE	1	Oral	37.5 MG, CYCLIC (DAILY, 4 WEEKS ON, 2 WEEKS OFF)	nan
1648986	99998153	9999815	2	C	L-THYROXIN [LEVOTHYROXINE SODIUM]	NaN	2	NaN	UNK	nan

1648987 rows × 20 columns

In [4]:
```
df_19Q1_drug.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1648987 entries, 0 to 1648986
Data columns (total 20 columns):
 #   Column         Non-Null Count    Dtype
---  ------         --------------    -----
 0   primaryid      1648987 non-null  int64
 1   caseid         1648987 non-null  int64
 2   drug_seq       1648987 non-null  int64
 3   role_cod       1648987 non-null  object
 4   drugname       1648977 non-null  object
 5   prod_ai        1617259 non-null  object
 6   val_vbm        1648987 non-null  int64
 7   route          1185339 non-null  object
 8   dose_vbm       985266 non-null   object
 9   cum_dose_chr   47009 non-null    float64
 10  cum_dose_unit  47023 non-null    object
 11  dechal         856330 non-null   object
 12  rechal         258523 non-null   object
 13  lot_num        289346 non-null   object
 14  exp_dt         3496 non-null     object
 15  nda_num        531373 non-null   float64
 16  dose_amt       656764 non-null   float64
 17  dose_unit      656759 non-null   object
 18  dose_form      706391 non-null   object
 19  dose_freq      417653 non-null   object
dtypes: float64(3), int64(4), object(13)
memory usage: 251.6+ MB
```

In [5]:
```
df_19Q1_drug.describe()
```

Out[5]:

	primaryid	caseid	drug_seq	val_vbm	cum_dose_chr	nda_num	dose_amt
count	1648987.00	1648987.00	1648987.00	1648987.00	47009.00	531373.00	656764.00
mean	190114742.75	15453701.21	6.92	1.02	42283.39	95447814.91	1031.45
std	198681637.69	1119314.35	11.64	0.14	1859674.13	13611129397.52	170499.67
min	37624583.00	3762458.00	1.00	1.00	0.00	0.00	0.00
25%	156449482.00	15530068.00	1.00	1.00	75.00	21829.00	5.00
50%	158806961.00	15867207.00	4.00	1.00	600.00	90071.00	30.00
75%	160128414.00	15997378.50	8.00	1.00	4980.00	202439.00	150.00
max	1593052612.00	16156981.00	397.00	2.00	390000000.00	3400955762713.00	78000000.00

In [6]:
```
df_19Q1_drug.columns
```

Out[6]:
```
Index(['primaryid', 'caseid', 'drug_seq', 'role_cod', 'drugname', 'prod_ai', 'val_vbm', 'route', 'dose_vbm',
'cum_dose_chr', 'cum_dose_unit', 'dechal', 'rechal', 'lot_num', 'exp_dt', 'nda_num', 'dose_amt', 'dose_uni
t', 'dose_form', 'dose_freq'], dtype='object')
```

In [7]:
```
df_19Q1_drug.drop(['caseid', 'drug_seq', 'prod_ai', 'val_vbm', 'route', 'dose_vbm', 'cum_dose_chr', 'cum_dos
```

In [8]:
```
df_19Q1_drug
```

Out[8]:

	primaryid	role_cod	drugname
0	1000661812	PS	LIPITOR
1	1000661812	SS	BENTYL
2	1000661812	SS	DICYCLOMINE
3	1000808590	PS	SANDOSTATIN LAR DEPOT
4	1000808590	SS	SANDOSTATIN LAR DEPOT
...	...	...	...
1648982	99978793	C	DOLIPRANE
1648983	99978793	C	INDOCOLLYRE
1648984	99978793	C	LEDERFOLIN
1648985	99998153	PS	SUTENT
1648986	99998153	C	L-THYROXIN [LEVOTHYROXINE SODIUM]

1648987 rows × 3 columns

Load the outcome file

In [9]:
```
df_19Q1_OUT = pd.read_table("OUTC19Q1.txt", sep='$')
```

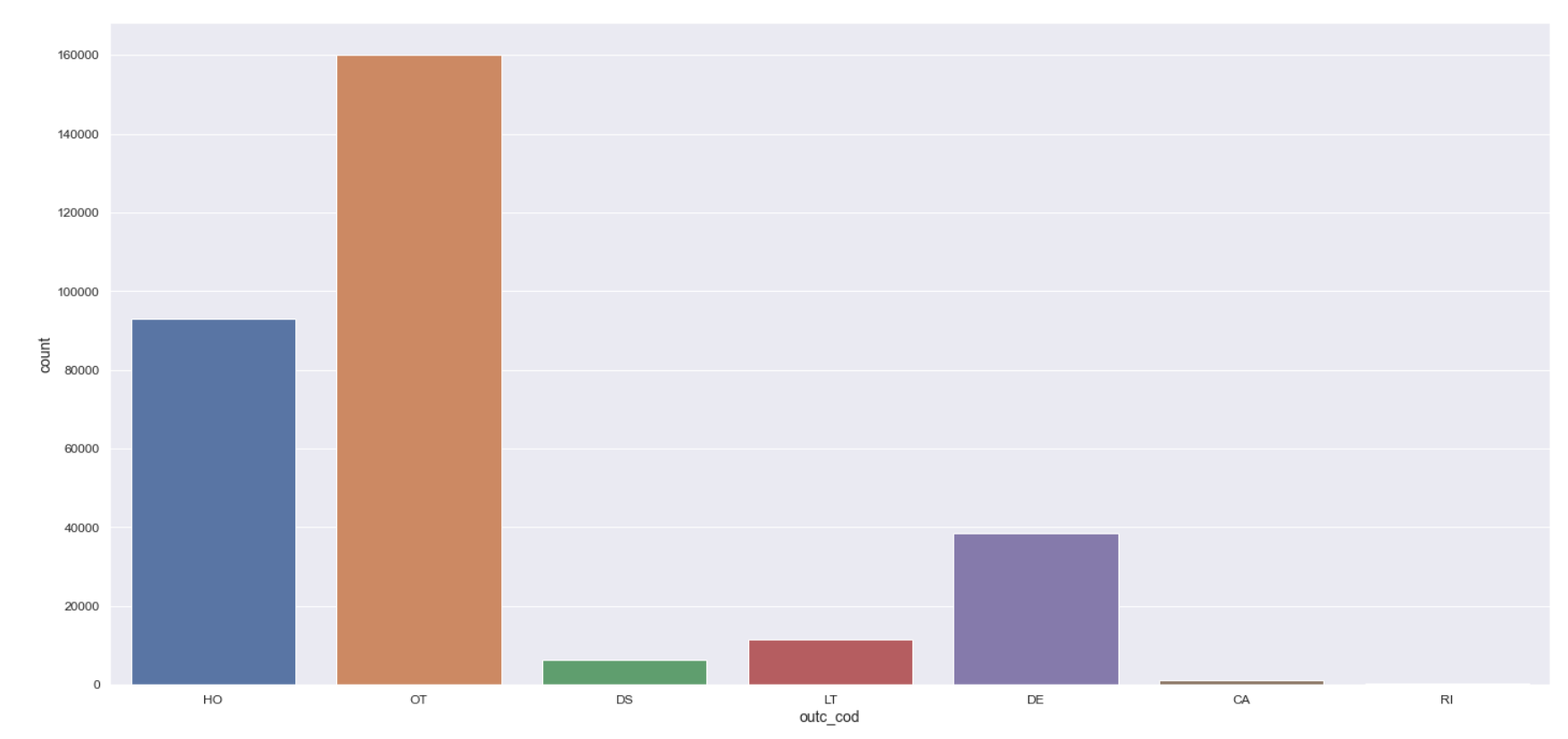
In [10]:
```
df_19Q1_OUT
```

Out[10]:

	primaryid	caseid	outc_cod
0	1000808590	10008085	HO
1	1000808590	10008085	OT
2	100107484	10010748	OT
3	100107484	10010748	HO
4	100171328	10017132	OT
...	...	...	...
310657	99885794	9988579	DS
310658	99885794	9988579	OT
310659	99924278	9992427	HO
310660	99978793	9997879	HO
310661	99998153	9999815	HO

310662 rows × 3 columns

In [11]:
```
plt.figure(figsize=(20,10))
sns.countplot(x=df_19Q1_OUT.outc_cod)
plt.suptitle('Patient Outcome 2019 Q1', x=0.5, y=1.02, ha='center', fontsize=20)
plt.tight_layout()
plt.show()
```



In [12]:
```
dfQ1 = pd.merge(left=df_19Q1_drug, right=df_19Q1_OUT, how='inner', on='primaryid')
```

In [13]:
```
dfQ1
```

Out[13]:

	primaryid	role_cod	drugname	caseid	outc_cod
0	1000808590	PS	SANDOSTATIN LAR DEPOT	10008085	HO
1	1000808590	PS	SANDOSTATIN LAR DEPOT	10008085	OT
2	1000808590	SS	SANDOSTATIN LAR DEPOT	10008085	HO
3	1000808590	SS	SANDOSTATIN LAR DEPOT	10008085	OT
4	1000808590	SS	SANDOSTATIN LAR DEPOT	10008085	HO
...	...	...	...	...	...
1684340	99978793	C	DOLIPRANE	9997879	HO
1684341	99978793	C	INDOCOLLYRE	9997879	HO
1684342	99978793	C	LEDERFOLIN	9997879	HO
1684343	99998153	PS	SUTENT	9999815	HO
1684344	99998153	C	L-THYROXIN [LEVOTHYROXINE SODIUM]	9999815	HO

1684345 rows × 5 columns

In [14]:
```
dfQ1['drugname'].value_counts()
```

Out[14]:
```
HUMIRA                                                                19293
NEXIUM                                                                17213
PREDNISONE.                                                           16567
XOLAIR                                                                15772
METHOTREXATE.                                                         14815
                                                                      ...
ALIVIATOS                                                                 1
THERAGRAN [ASCORBIC ACID;BIOTIN;CALCIUM PANTOTHENATE;CYANOCOBALAMIN;ER    1
CIMICIFUGA                                                                1
morphine sul                                                              1
Multi vitamin infusion (Ascorbic acid, Pyridoxine hydrochloride, Tocop    1
Name: drugname, Length: 50808, dtype: int64
```

In [15]:
```
(dfQ1['drugname'] == "LYRICA").value_counts()
```

Out[15]:
```
False    1677652
True        6693
Name: drugname, dtype: int64
```

In [16]:
```
(dfQ1['drugname'] == "TRAMAL").value_counts()
```

Out[16]:
```
False    1684095
True         250
Name: drugname, dtype: int64
```

In [17]:
```
(dfQ1['drugname'] == "GABAPENTIN.").value_counts()
```

Out[17]:
```
False    1675573
True        8772
Name: drugname, dtype: int64
```

Select the three medications

In [18]:
```
df2Q1 = dfQ1[(dfQ1['drugname'] == "LYRICA") | (dfQ1['drugname'] == "TRAMAL") | (dfQ1['drugname'] == "GABAPEN
```

In [19]:
```
df2Q1
```

Out[19]:

	primaryid	role_cod	drugname	caseid	outc_cod
194	100442633	SS	GABAPENTIN.	10044263	OT
195	100442633	SS	GABAPENTIN.	10044263	DS
896	100716802	SS	LYRICA	10071680	OT
938	100904069	PS	LYRICA	10090406	HO
939	100904069	PS	LYRICA	10090406	OT
...	...	...	...	...	...
1683997	992278323	C	GABAPENTIN.	9922783	OT
1684012	99252085	SS	LYRICA	9925208	HO
1684120	99314732	SS	LYRICA	9931473	HO
1684322	99885794	C	TRAMAL	9988579	DS
1684323	99885794	C	TRAMAL	9988579	OT

15715 rows × 5 columns

In [20]:
```
df2Q1.groupby(by=['outc_cod','drugname'])['primaryid'].count()
```

Out[20]:
```
outc_cod  drugname
CA        GABAPENTIN.      15
          LYRICA            2
DE        GABAPENTIN.    1358
          LYRICA          352
          TRAMAL           37
DS        GABAPENTIN.     213
          LYRICA          162
          TRAMAL            4
HO        GABAPENTIN.    2814
          LYRICA         2200
          TRAMAL           86
LT        GABAPENTIN.     223
          LYRICA          201
          TRAMAL           22
OT        GABAPENTIN.    4147
          LYRICA         3776
          TRAMAL          101
RI        GABAPENTIN.       2
Name: primaryid, dtype: int64
```

In [21]:
```
df2Q1.to_csv("dfQ1.csv", index=False)
```

In [22]:
```
tabledf2Q1 = pd.pivot_table(data=df2Q1, index=['outc_cod'], columns=['drugname'], aggfunc='count')['caseid']
```

In [23]:
```
tabledf2Q1
```

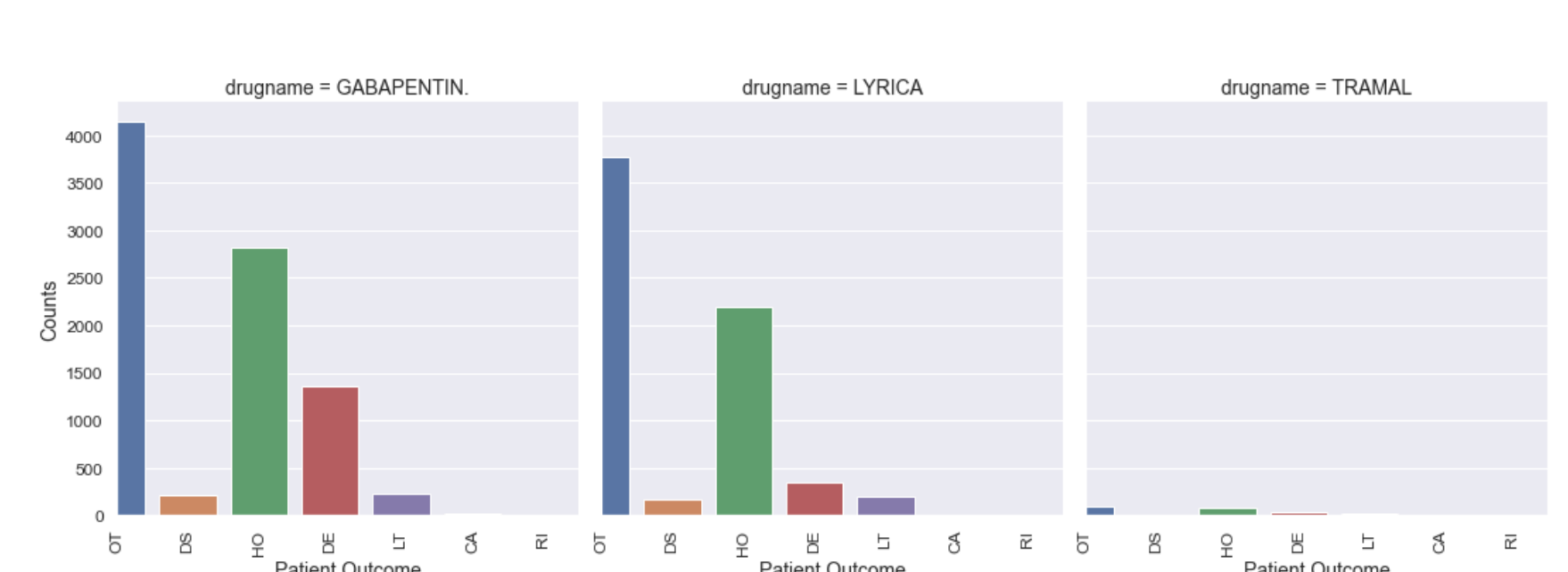
Out[23]:

drugname	GABAPENTIN.	LYRICA	TRAMAL
outc_cod			
CA	15.00	2.00	nan
DE	1358.00	352.00	37.00
DS	213.00	162.00	4.00
HO	2814.00	2200.00	86.00
LT	223.00	201.00	22.00
OT	4147.00	3776.00	101.00
RI	2.00	nan	nan

Data Visualization

In [24]:
```
plt.figure(figsize=(20,20))


g = sns.catplot(x='outc_cod', col = 'drugname',
            kind='count', data=df2Q1,
            height = 5, aspect = 1)

g.set_xlabels("Patient Outcome")
g.set_ylabels("Counts")

g.set(xlim=(0,None))
g.set_xticklabels(rotation=90)

plt.suptitle("Comparison of 3 Drugs 2019 Q1", x=0.5, y=1.2, ha='center', fontsize=20)

plt.show()
```

```
<Figure size 1440x1440 with 0 Axes>
```



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In [25]:
```
df_19Q2_drug = pd.read_table("DRUG19Q2.txt",sep='$')
```

In [26]:
```
df_19Q2_drug
```

Out[26]:

	primaryid	caseid	drug_seq	role_cod	drugname	prod_ai	val_vbm	route	dose_vbm	cum_dose_ch
0	1000661813	10006618	1	PS	LIPITOR	ATORVASTATIN CALCIUM	1	NaN	UNK	na
1	1000661813	10006618	2	SS	BENTYL	DICYCLOMINE HYDROCHLORIDE	1	NaN	UNK	na
2	1000661813	10006618	3	SS	DICYCLOMINE	DICYCLOMINE HYDROCHLORIDE	1	NaN	UNK	na
3	1000808410	10008084	1	PS	INFLIXIMAB, RECOMBINANT	INFLIXIMAB	1	Intravenous (not otherwise specified)	NaN	na
4	1000808410	10008084	2	C	METHOTREXATE.	METHOTREXATE	1	Unknown	NaN	na
...	...	...	...	...	...	...	...	...	...	.
1863005	999981612	9999816	15	C	CALCIUM +VIT D	CALCIUM\VITAMIN D	1	Oral	1 DF, 3X/DAY	na
1863006	999981612	9999816	16	C	RESTASIS	CYCLOSPORINE	1	NaN	1 GTT, 2X/DAY (1 GTT IN EACH AFFECTED EYE EVER...	na
1863007	999981612	9999816	17	C	TRAZODONE	TRAZODONE HYDROCHLORIDE	1	Oral	100 MG, 3X/DAY	na
1863008	999981612	9999816	18	C	TIZANIDINE.	TIZANIDINE	1	Oral	8 MG, DAILY	na
1863009	999981612	9999816	19	C	BOTOX	ONABOTULINUMTOXINA	1	NaN	UNK, EVERY 3 MONTHS	na

1863010 rows × 20 columns

In [27]:
```
df_19Q2_drug.info(null_counts=True)
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1863010 entries, 0 to 1863009
Data columns (total 20 columns):
 #   Column         Non-Null Count    Dtype
---  ------         --------------    -----
 0   primaryid      1863010 non-null  int64
 1   caseid         1863010 non-null  int64
 2   drug_seq       1863010 non-null  int64
 3   role_cod       1863010 non-null  object
 4   drugname       1862993 non-null  object
 5   prod_ai        1827186 non-null  object
 6   val_vbm        1863010 non-null  int64
 7   route          1321842 non-null  object
 8   dose_vbm       1068362 non-null  object
 9   cum_dose_chr   47352 non-null    float64
 10  cum_dose_unit  47247 non-null    object
 11  dechal         956418 non-null   object
 12  rechal         285765 non-null   object
 13  lot_num        319696 non-null   object
 14  exp_dt         5092 non-null     object
 15  nda_num        578843 non-null   float64
 16  dose_amt       783999 non-null   float64
 17  dose_unit      783979 non-null   object
 18  dose_form      824588 non-null   object
 19  dose_freq      482814 non-null   object
dtypes: float64(3), int64(4), object(13)
memory usage: 284.3+ MB
```

In [28]:
```
df_19Q2_drug.describe()
```

Out[28]:

	primaryid	caseid	drug_seq	val_vbm	cum_dose_chr	nda_num	dose_amt
count	1863010.00	1863010.00	1863010.00	1863010.00	47352.00	578843.00	783999.00
mean	197427186.64	15771903.29	7.21	1.02	46024.45	97522295.22	851.59
std	210867983.25	1135669.67	10.49	0.14	1699622.09	14333987978.39	157949.90
min	39490342.00	3949034.00	1.00	1.00	0.00	0.00	0.00
25%	159405832.00	15806260.00	2.00	1.00	78.00	21344.00	3.00
50%	162233237.50	16204212.50	4.00	1.00	600.00	78787.00	20.00
75%	163698028.50	16349342.00	9.00	1.00	5850.00	202192.00	108.00
max	1636576010.00	16517055.00	326.00	2.00	199000000.00	2280000731000.00	72000000.00

In [29]:
```
df_19Q2_drug.columns
```

Out[29]:
```
Index(['primaryid', 'caseid', 'drug_seq', 'role_cod', 'drugname', 'prod_ai', 'val_vbm', 'route', 'dose_vbm',
'cum_dose_chr', 'cum_dose_unit', 'dechal', 'rechal', 'lot_num', 'exp_dt', 'nda_num', 'dose_amt', 'dose_uni
t', 'dose_form', 'dose_freq'], dtype='object')
```

In [30]:
```
df_19Q2_drug.drop(['caseid', 'drug_seq', 'prod_ai', 'val_vbm', 'route', 'dose_vbm', 'cum_dose_chr', 'cum_dos
```

In [31]:
```
df_19Q2_drug
```

Out[31]:

	primaryid	role_cod	drugname
0	1000661813	PS	LIPITOR
1	1000661813	SS	BENTYL
2	1000661813	SS	DICYCLOMINE
3	1000808410	PS	INFLIXIMAB, RECOMBINANT
4	1000808410	C	METHOTREXATE.
...	...	...	...
1863005	999981612	C	CALCIUM +VIT D
1863006	999981612	C	RESTASIS
1863007	999981612	C	TRAZODONE
1863008	999981612	C	TIZANIDINE.
1863009	999981612	C	BOTOX

1863010 rows × 3 columns

Load the outcome file

In [32]:
```
df_19Q2_OUT = pd.read_table("OUTC19Q2.txt", sep='$')
```

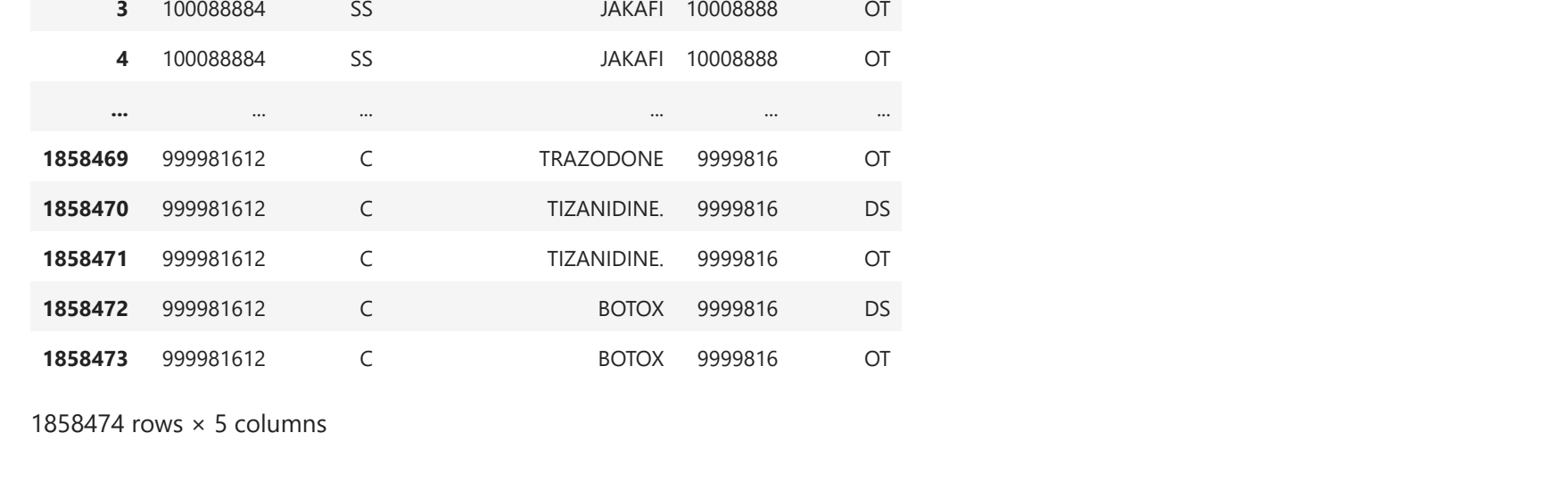
In [33]:
```
df_19Q2_OUT
```

Out[33]:

	primaryid	caseid	outc_cod
0	1000808410	10008084	OT
1	100088884	10008888	OT
2	100097843	10009784	OT
3	1001163924	10011639	OT
4	1001443222	10014432	HO
...	...	...	...
324733	99924843	9992484	OT
324734	99943572	9994357	OT
324735	99943572	9994357	LT
324736	999981612	9999816	DS
324737	999981612	9999816	OT

324738 rows × 3 columns

In [34]:
```
plt.figure(figsize=(20,10))
sns.countplot(x=df_19Q2_OUT.outc_cod)
plt.suptitle('Patient Outcome 2019 Q2', x=0.5, y=1.02, ha='center', fontsize=20)
plt.tight_layout()
plt.show()
```



In [35]:
```
dfQ2 = pd.merge(left=df_19Q2_drug, right=df_19Q2_OUT, how='inner', on='primaryid')
```

In [36]:
```
dfQ2
```

Out[36]:

	primaryid	role_cod	drugname	caseid	outc_cod
0	1000808410	PS	INFLIXIMAB, RECOMBINANT	10008084	OT
1	1000808410	C	METHOTREXATE.	10008084	OT
2	100088884	PS	JAKAFI	10008888	OT
3	100088884	SS	JAKAFI	10008888	OT
4	100088884	SS	JAKAFI	10008888	OT
...	...	...	...	...	...
1858469	999981612	C	TRAZODONE	9999816	OT
1858470	999981612	C	TIZANIDINE.	9999816	DS
1858471	999981612	C	TIZANIDINE.	9999816	OT
1858472	999981612	C	BOTOX	9999816	DS
1858473	999981612	C	BOTOX	9999816	OT

1858474 rows × 5 columns

In [37]:
```
dfQ2['drugname'].value_counts()
```

Out[37]:
```
NEXIUM                                                       31346
PRILOSEC                                                     23346
PREVACID                                                     23202
PREDNISONE.                                                  19329
HUMIRA                                                       18779
                                                               ...
VISINE ORIGINAL REDNESS RELIEF                                   1
fluocin acet                                                     1
SALINE [BORIC ACID;EDETATE DISODIUM;SODIUM BORATE;SORBIC ACID]   1
Doxycyc mono                                                     1
levocetrizine                                                    1
Name: drugname, Length: 54011, dtype: int64
```

In [38]:
```
(dfQ2['drugname'] == "LYRICA").value_counts()
```

Out[38]:
```
False    1849217
True        9257
Name: drugname, dtype: int64
```

In [39]:
```
(dfQ2['drugname'] == "TRAMAL").value_counts()
```

Out[39]:
```
False    1858239
True         235
Name: drugname, dtype: int64
```

In [40]:
```
(dfQ2['drugname'] == "GABAPENTIN.").value_counts()
```

Out[40]:
```
False    1849234
True        9240
Name: drugname, dtype: int64
```

Select the three medications

In [41]:
```
df2Q2 = dfQ2[(dfQ2['drugname'] == "LYRICA") | (dfQ2['drugname'] == "TRAMAL") | (dfQ2['drugname'] == "GABAPEN
```

In [42]:
```
df2Q2
```

Out[42]:

	primaryid	role_cod	drugname	caseid	outc_cod
126	1001443222	SS	LYRICA	10014432	HO
127	1001443222	SS	LYRICA	10014432	OT
355	100242679	PS	LYRICA	10024267	DS
356	100242679	PS	LYRICA	10024267	HO
357	100242679	PS	LYRICA	10024267	OT
...	...	...	...	...	...
1858439	999981612	SS	LYRICA	9999816	OT
1858440	999981612	SS	LYRICA	9999816	DS
1858441	999981612	SS	LYRICA	9999816	OT
1858442	999981612	SS	LYRICA	9999816	DS
1858443	999981612	SS	LYRICA	9999816	OT

18732 rows × 5 columns

In [43]:
```
df2Q2.groupby(by=['outc_cod','drugname'])['primaryid'].count()
```

Out[43]:
```
outc_cod  drugname
CA        GABAPENTIN.      18
          LYRICA            4
          TRAMAL            1
DE        GABAPENTIN.     662
          LYRICA          356
          TRAMAL           36
DS        GABAPENTIN.     236
          LYRICA          268
          TRAMAL            1
HO        GABAPENTIN.    2908
          LYRICA         3093
          TRAMAL           80
LT        GABAPENTIN.     271
          LYRICA          222
          TRAMAL           25
OT        GABAPENTIN.    5137
          LYRICA         5314
          TRAMAL           92
RI        GABAPENTIN.       8
Name: primaryid, dtype: int64
```

In [44]:
```
df2Q2.to_csv("dfQ2.csv", index=False)
```

In [45]:
```
tabledf2Q2 = pd.pivot_table(data=df2Q2, index=['outc_cod'], columns=['drugname'], aggfunc='count')['caseid']
```

In [46]:
```
tabledf2Q2
```

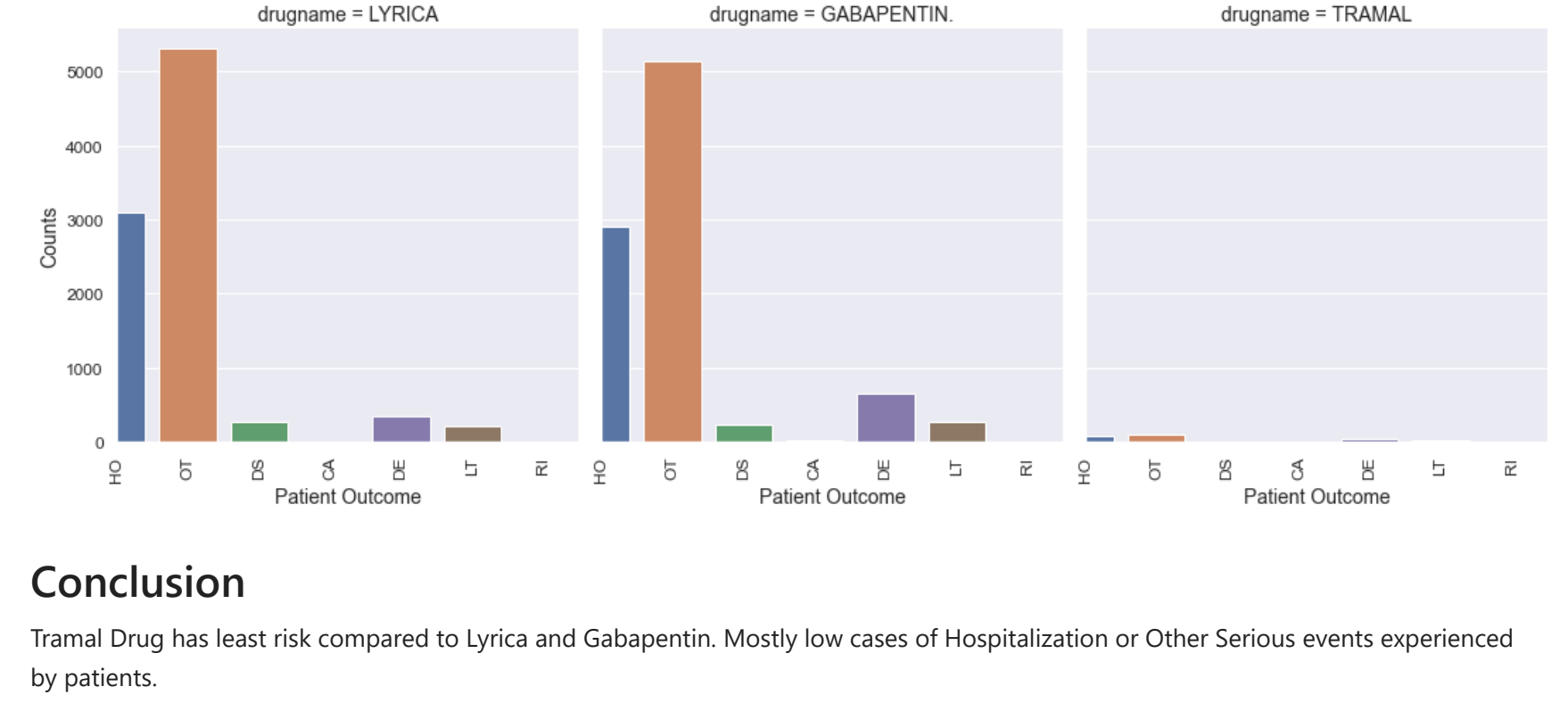
Out[46]:

drugname	GABAPENTIN.	LYRICA	TRAMAL
outc_cod			
CA	18.00	4.00	1.00
DE	662.00	356.00	36.00
DS	236.00	268.00	1.00
HO	2908.00	3093.00	80.00
LT	271.00	222.00	25.00
OT	5137.00	5314.00	92.00
RI	8.00	nan	nan

Data Visualization

In [47]:
```
plt.figure(figsize=(20,20))


g = sns.catplot(x='outc_cod', col = 'drugname',
            kind='count', data=df2Q2,
            height = 5, aspect = 1)

g.set_xlabels("Patient Outcome")
g.set_ylabels("Counts")

g.set(xlim=(0,None))
g.set_xticklabels(rotation=90)

plt.suptitle("Comparison of 3 Drugs in 2019 Q2", x=0.5, y=1.2, ha='center', fontsize=20)

plt.show()
```

```
<Figure size 1440x1440 with 0 Axes>
```



Conclusion

Tramal Drug has least risk compared to Lyrica and Gabapentin. Mostly low cases of Hospitalization or Other Serious events experienced by patients.

Python code done by Dennis Lam