Logistic Regression-1 & 2

Data: h1n1_vaccine_prediction.csv

Libraries

```
# Jesus is my Saviour!
import os
os.chdir('C:\\Users\\Dr Vinod\\Desktop\\WD_python')
import pandas as pd
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import statsmodels.api as sm
from statsmodels.formula.api import ols
from scipy.stats import chi2_contingency
from sklearn.preprocessing import LabelEncoder

df = pd.read_csv('h1n1_vaccine_prediction.csv') #26707; 34 , 1st is unique id
df.info()
```

```python
df = pd.read_csv('h1n1_vaccine_prediction.csv') #26707; 34 , 1st is unique id
df.info()
```

```
In [3]: df.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 26707 entries, 0 to 26706
Data columns (total 34 columns):
 #   Column                       Non-Null Count  Dtype
---  ------                       --------------  -----
 0   unique_id                    26707 non-null  int64
 1   h1n1_worry                   26615 non-null  float64
 2   h1n1_awareness               26591 non-null  float64
 3   antiviral_medication         26636 non-null  float64
 4   contact_avoidance            26499 non-null  float64
 5   bought_face_mask             26688 non-null  float64
 6   wash_hands_frequently        26665 non-null  float64
 7   avoid_large_gatherings       26620 non-null  float64
 8   reduced_outside_home_cont    26625 non-null  float64
 9   avoid_touch_face             26579 non-null  float64
 10  dr_recc_h1n1_vacc            24547 non-null  float64
 11  dr_recc_seasonal_vacc        24547 non-null  float64
 12  chronic_medic_condition      25736 non-null  float64
 13  cont_child_undr_6_mnths      25887 non-null  float64
 14  is_health_worker             25903 non-null  float64
 15  has_health_insur             14433 non-null  float64
 16  is_h1n1_vacc_effective       26316 non-null  float64
 17  is_h1n1_risky                26319 non-null  float64
 18  sick_from_h1n1_vacc          26312 non-null  float64
 19  is_seas_vacc_effective       26245 non-null  float64
 20  is_seas_risky                26193 non-null  float64
 21  sick_from_seas_vacc          26170 non-null  float64
 22  age_bracket                  26707 non-null  object
 23  qualification                25300 non-null  object
 24  race                         26707 non-null  object
 25  sex                          26707 non-null  object
 26  income_level                 22284 non-null  object
 27  marital_status               25299 non-null  object
 28  housing_status               24665 non-null  object
 29  employment                   25244 non-null  object
 30  census_msa                   26707 non-null  object
 31  no_of_adults                 26458 non-null  float64
 32  no_of_children               26458 non-null  float64
 33  h1n1_vaccine                 26707 non-null  int64
dtypes: float64(23), int64(2), object(9)
memory usage: 6.9+ MB
```

Drop

```
# lets drop 1st unique_id
df33 = df.drop(['unique_id'], axis = 1)
df33.info() # now 33 columns
# droping all will give 11794 rows only 50% values
dfnomissing = df33.dropna()
dfnomissing.info() # # 11,794 rows; 33 columns
# its not a good idea to carry with 11,794 rows
## note that index identification remains same as in
# the original file
'''
so, we will remove the column- "has_health_insur" (14433 rows only)
and create a new file name 'df32'. This is shown below.
'''
df32 = df33.drop(['has_health_insur'], axis = 1)
```

```
32  df32.info() # observe many missing values in many columns, now 32 columns
```

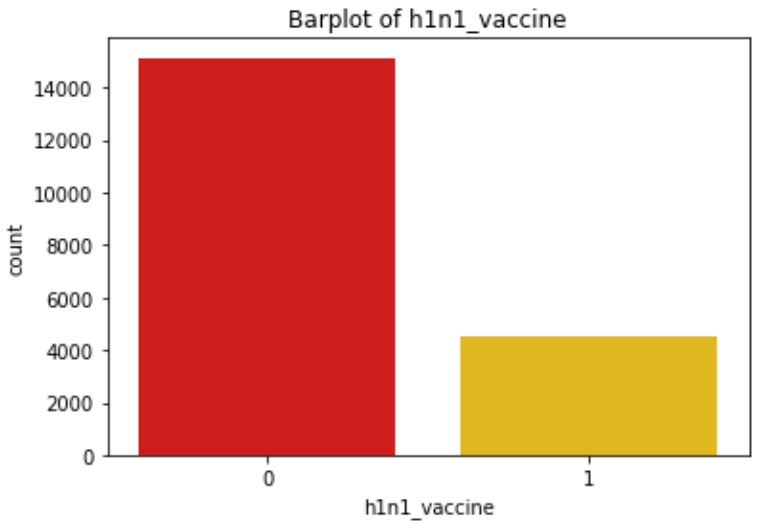
```
In [5]: df32.info() # observe many missing values in many columns, now 32 columns
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 26707 entries, 0 to 26706
Data columns (total 32 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   h1n1_worry                26615 non-null  float64
 1   h1n1_awareness            26591 non-null  float64
 2   antiviral_medication      26636 non-null  float64
 3   contact_avoidance         26499 non-null  float64
 4   bought_face_mask          26688 non-null  float64
 5   wash_hands_frequently     26665 non-null  float64
 6   avoid_large_gatherings    26620 non-null  float64
 7   reduced_outside_home_cont 26625 non-null  float64
 8   avoid_touch_face          26579 non-null  float64
 9   dr_recc_h1n1_vacc         24547 non-null  float64
 10  dr_recc_seasonal_vacc     24547 non-null  float64
 11  chronic_medic_condition   25736 non-null  float64
 12  cont_child_undr_6_mnths   25887 non-null  float64
 13  is_health_worker          25903 non-null  float64
 14  is_h1n1_vacc_effective    26316 non-null  float64
 15  is_h1n1_risky             26319 non-null  float64
 15  is_h1n1_risky             26319 non-null  float64
 16  sick_from_h1n1_vacc       26312 non-null  float64
 17  is_seas_vacc_effective    26245 non-null  float64
 18  is_seas_risky             26193 non-null  float64
 19  sick_from_seas_vacc       26170 non-null  float64
 20  age_bracket               26707 non-null  object
 21  qualification             25300 non-null  object
 22  race                      26707 non-null  object
 23  sex                       26707 non-null  object
 24  income_level              22284 non-null  object
 25  marital_status            25299 non-null  object
 26  housing_status            24665 non-null  object
 27  employment                25244 non-null  object
 28  census_msa                26707 non-null  object
 29  no_of_adults              26458 non-null  float64
 30  no_of_children            26458 non-null  float64
 31  h1n1_vaccine              26707 non-null  int64
dtypes: float64(22), int64(1), object(9)
memory usage: 6.5+ MB
```

```
# lets remove all missing values from df32
df_vac = df32.dropna() # 19642 , 32
df_vac.info()
## now , 19642 is a good no to go with!
```

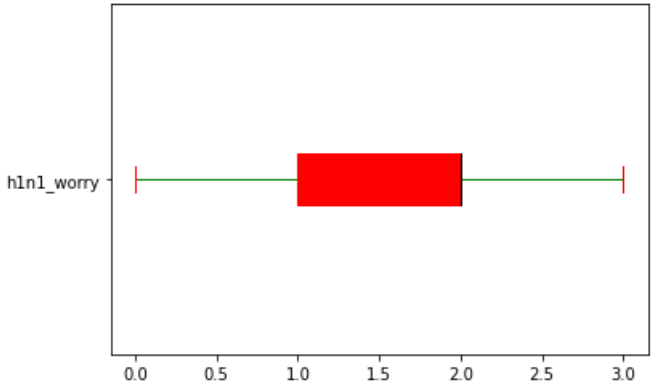
```
In [6]: df_vac = df32.dropna() # 19642 , 32

In [7]: df_vac.info()
<class 'pandas.core.frame.DataFrame'>
Int64Index: 19642 entries, 0 to 26706
Data columns (total 32 columns):
 #   Column                     Non-Null Count  Dtype
---  ------                     --------------  -----
 0   h1n1_worry                 19642 non-null  float64
 1   h1n1_awareness             19642 non-null  float64
 2   antiviral_medication       19642 non-null  float64
 3   contact_avoidance          19642 non-null  float64
 4   bought_face_mask           19642 non-null  float64
 5   wash_hands_frequently      19642 non-null  float64
 6   avoid_large_gatherings     19642 non-null  float64
 7   reduced_outside_home_cont  19642 non-null  float64
 8   avoid_touch_face           19642 non-null  float64
 9   dr_recc_h1n1_vacc          19642 non-null  float64
 10  dr_recc_seasonal_vacc      19642 non-null  float64
 11  chronic_medic_condition    19642 non-null  float64
 12  cont_child_undr_6_mnths    19642 non-null  float64
 13  is_health_worker           19642 non-null  float64
 14  is_h1n1_vacc_effective     19642 non-null  float64
 15  is_h1n1_risky              19642 non-null  float64
 16  sick_from_h1n1_vacc        19642 non-null  float64
 17  is_seas_vacc_effective     19642 non-null  float64
 18  is_seas_risky              19642 non-null  float64
 19  sick_from_seas_vacc        19642 non-null  float64
 20  age_bracket                19642 non-null  object
 21  qualification              19642 non-null  object
 22  race                       19642 non-null  object
 23  sex                        19642 non-null  object
 24  income_level               19642 non-null  object
 25  marital_status             19642 non-null  object
 26  housing_status             19642 non-null  object
 27  employment                 19642 non-null  object
 28  census_msa                 19642 non-null  object
 29  no_of_adults               19642 non-null  float64
 30  no_of_children             19642 non-null  float64
 31  h1n1_vaccine               19642 non-null  int64
dtypes: float64(22), int64(1), object(9)
memory usage: 4.9+ MB
```

```
###_________________1 ALWAYS START WITH TARGET VARIABLE
# 1 h1n1_vaccine - Target Variable
```

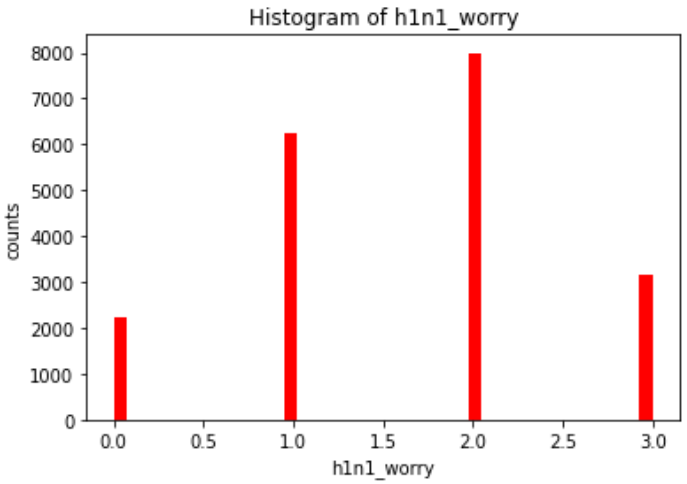
```
###_________________1 ALWAYS START WITH TARGET VARIABLE
# 1 h1n1_vaccine - Target Variable
df_vac.h1n1_vaccine.isnull().sum() #No Missing values
df_vac.h1n1_vaccine.value_counts()
'''
0    15128
1     4514
Name: h1n1_vaccine, dtype: int64
'''
# Bar Plot
sns.countplot(x = 'h1n1_vaccine', data = df_vac , palette = 'hot')
plt.title('Barplot of h1n1_vaccine')
```



```
#_________________ 2 h1n1_worry [0,1,2,3] ordered
#_____histogram
#_run in block
plt.hist(df_vac.h1n1_worry, bins = 'auto', facecolor = 'red')
plt.xlabel('h1n1_worry')
plt.ylabel('counts')
plt.title('Histogram of h1n1_worry')
```




```
#____boxplot
props2 = dict(boxes = 'red', whiskers = 'green', medians = 'black', caps = 'red')
df_vac['h1n1_worry'].plot.box(color=props2, patch_artist = True, vert = False) #No outliers
```



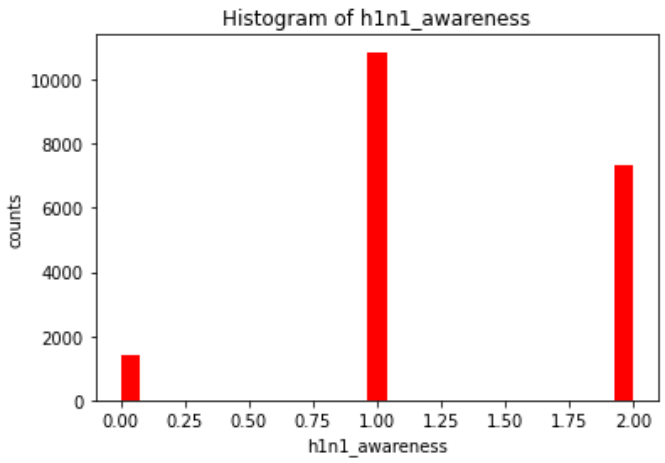

```
In [13]: df_vac.h1n1_worry.isnull().sum() #0 Missing values
Out[13]: 0

In [14]: df_vac.h1n1_worry.value_counts()
Out[14]:
2.0    7989
1.0    6229
3.0    3175
0.0    2249
Name: h1n1_worry, dtype: int64
```

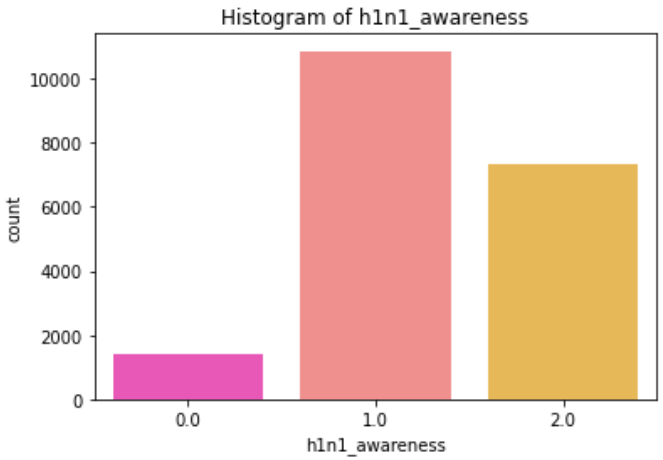
Is h1n1_worry a good predictor?

```
#Hypothesis Testing
import statsmodels.api as sm
from statsmodels.formula.api import ols
mod = ols('h1n1_worry ~ h1n1_vaccine', data = df_vac).fit()
aov_table = sm.stats.anova_lm(mod)
print(aov_table)
# 1.564e-79 ie p_value is <0.05; Ho Reject; Good Predictor
```

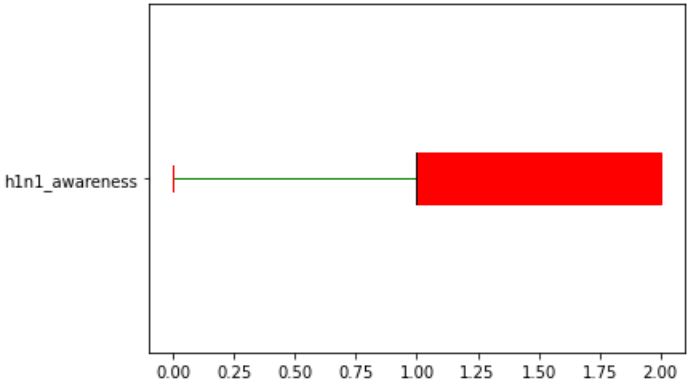
```
In [15]: import statsmodels.api as sm
    ...: from statsmodels.formula.api import ols
    ...: mod = ols('h1n1_worry ~ h1n1_vaccine', data = df_vac).fit()
    ...: aov_table = sm.stats.anova_lm(mod)
    ...: print(aov_table)
                  df        sum_sq     mean_sq           F        PR(>F)
h1n1_vaccine     1.0    278.817902  278.817902  359.846071  1.564062e-79
Residual     19640.0  15217.572282    0.774825         NaN           NaN
```

```
#_____________________________# 3 h1n1_awareness [0,1,2] ordered
```





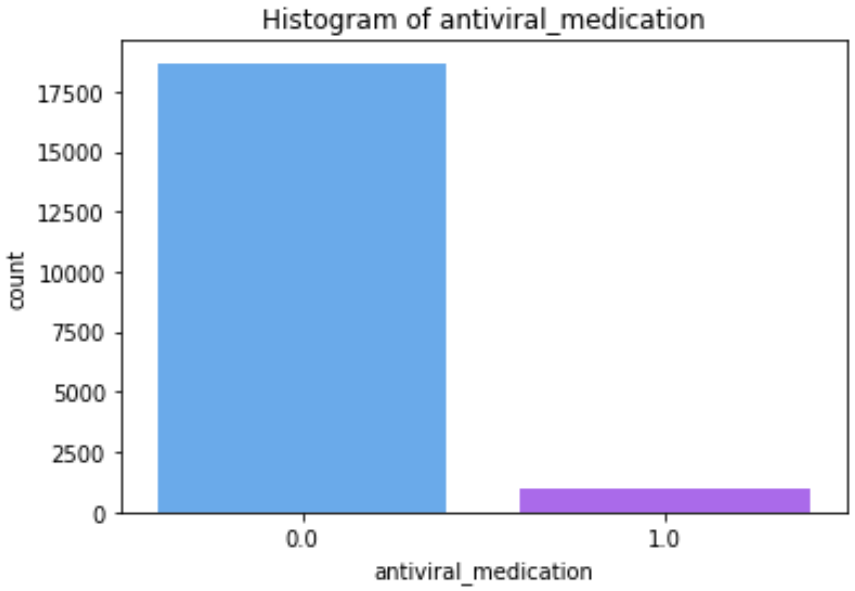

```
In [23]: df_vac.h1n1_awareness.value_counts()
Out[23]:
1.0    10861
2.0     7362
0.0     1419
Name: h1n1_awareness, dtype: int64
```




```
#Hypothesis Testing
import statsmodels.api as sm
from statsmodels.formula.api import ols
mod = ols('h1n1_awareness ~ h1n1_vaccine', data = df_vac).fit()
aov_table = sm.stats.anova_lm(mod)
print(aov_table)
#3.442e-70 ie  p_value is <0.05; Ho Reject; Good Predictor
```

```
#_______________ 4 antiviral_medication [0 and 1]
```

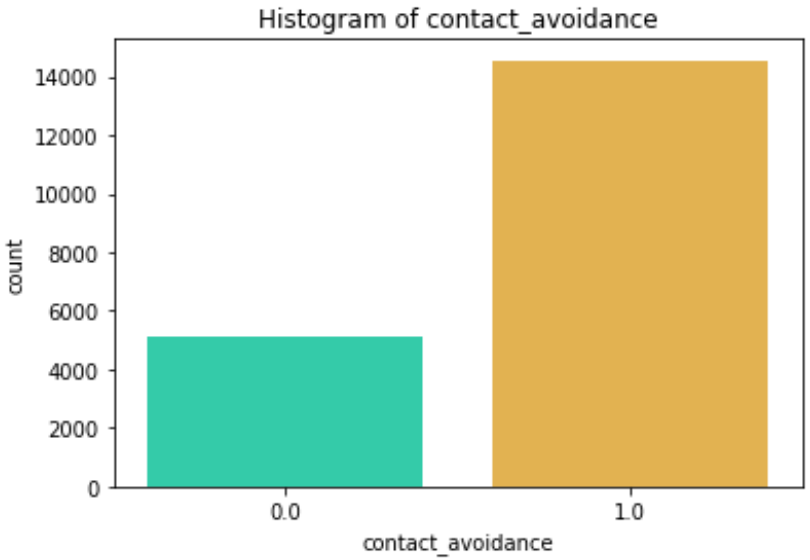
```
In [27]: df_vac.antiviral_medication.value_counts()
Out[27]:
0.0    18671
1.0      971
Name: antiviral_medication, dtype: int64
```



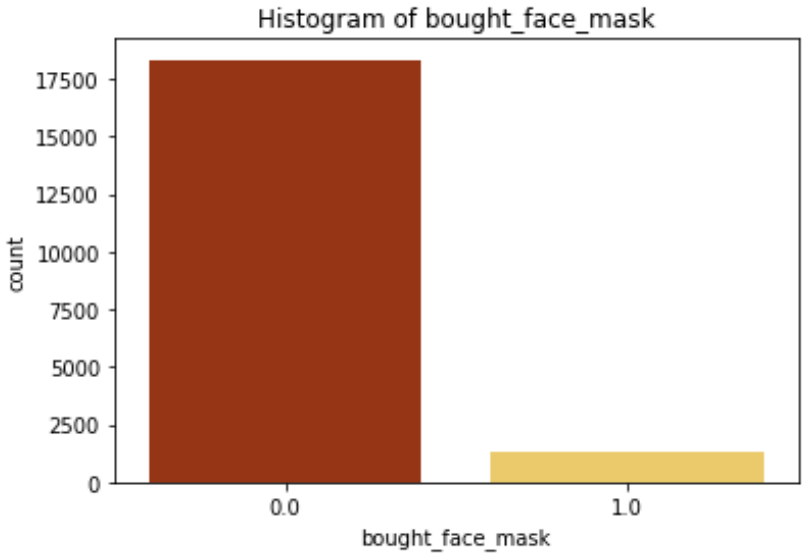

```
#Hypothesis Testing
from scipy.stats import chi2_contingency
ct_antiviral = pd.crosstab(df_vac.h1n1_vaccine, df_vac.antiviral_medication)
chi2_contingency(ct_antiviral, correction = False)
# p_val = 3.9e-7, Ho reject, hence association exists, good predictor
```

```
#_______________ 5 contact_avoidance [0 and 1]

df_vac.contact_avoidance.isnull().sum() #0 Missing values
df_vac.contact_avoidance.value_counts()
'''
1.0    14544
0.0     5098'''
```

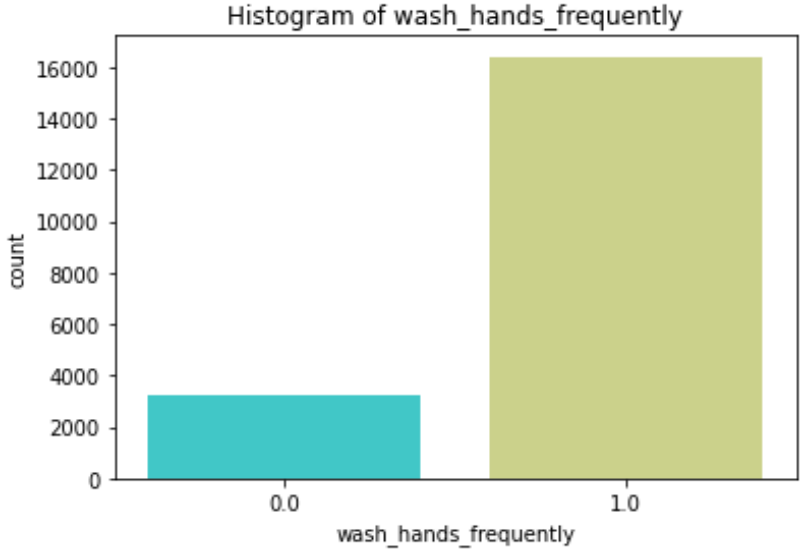
```
#Hypothesis Testing
from scipy.stats import chi2_contingency
ct_avoid = pd.crosstab(df_vac.h1n1_vaccine, df_vac.contact_avoidance)
chi2_contingency(ct_avoid, correction = False)
# p_val = 6.6 e-10, Ho reject, hence association exists, good predictor
```



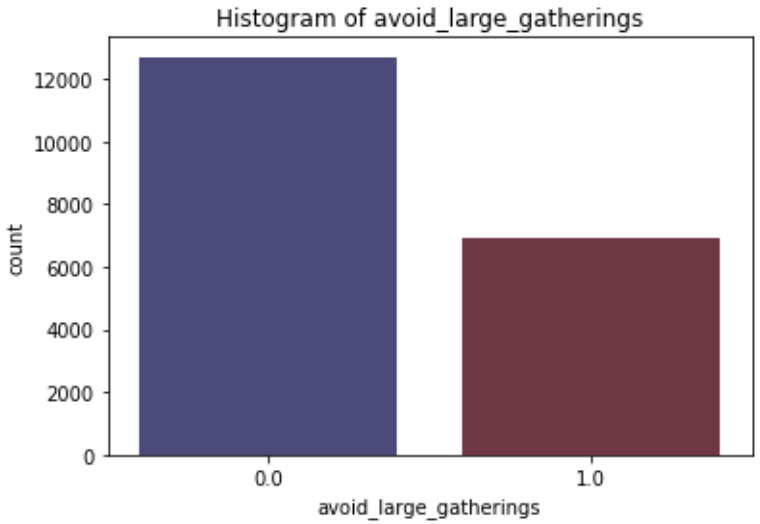
```
#_________________ 6 bought_face_mask [0 and 1]

df_vac.bought_face_mask.isnull().sum() #0 Missing values
df_vac.bought_face_mask.value_counts()
'''
0.0    18312
1.0     1330'''
# Bar Plot
sns.countplot(x = 'bought_face_mask', data = df_vac , palette = 'afmhot')
plt.title('Histogram of bought_face_mask')
#Hypothesis Testing
ct_mask = pd.crosstab(df_vac.h1n1_vaccine, df_vac.bought_face_mask)
chi2_contingency(ct_mask, correction = False)
# p_val = 4.9 e-26, Ho reject, hence association exists, good predictor
```



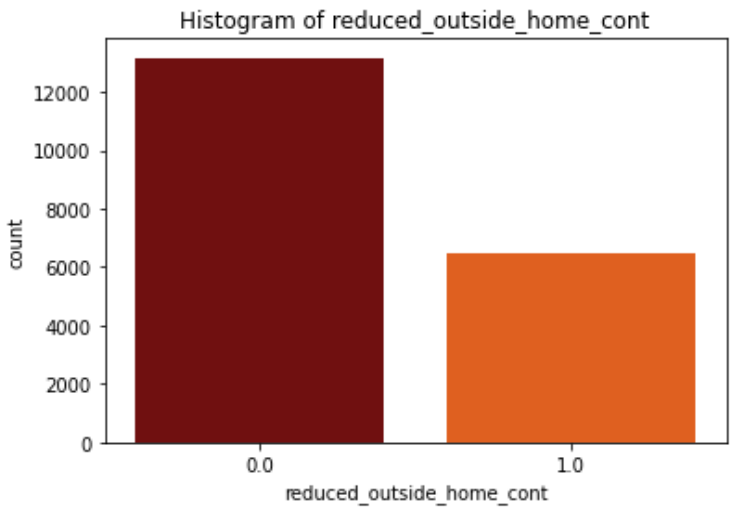
```
#_______________ 7 wash_hands_frequently [0 and 1]

df_vac.wash_hands_frequently.isnull().sum() #0 Missing values
df_vac.wash_hands_frequently.value_counts()
'''
1.0    16399
0.0     3243'''
# Bar Plot
sns.countplot(x = 'wash_hands_frequently', data = df_vac , palette = 'rainbow')
plt.title('Histogram of wash_hands_frequently')

#Hypothesis Testing
ct_wash = pd.crosstab(df_vac.h1n1_vaccine, df_vac.wash_hands_frequently)
chi2_contingency(ct_wash, correction = False)
# p_val = 4.3 e-26, Ho reject, hence association exists, good predictor
```



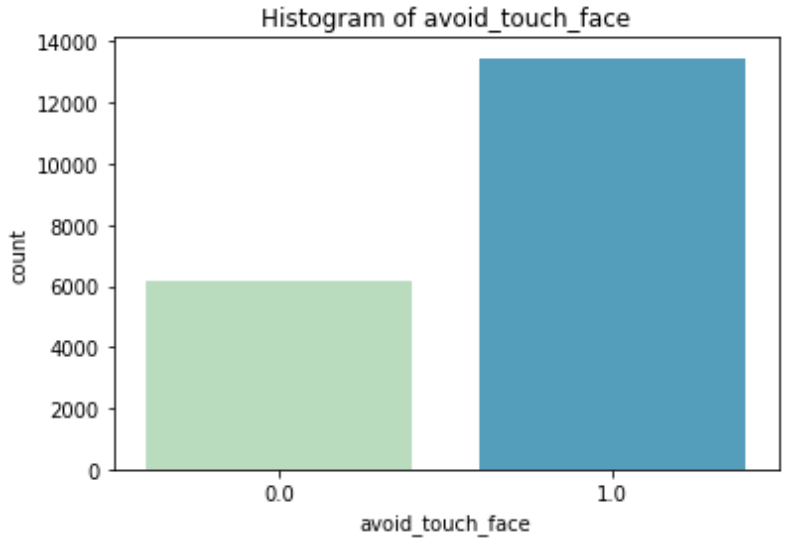
```
#_________________ 8 avoid_large_gatherings [0 and 1]

df_vac.avoid_large_gatherings.isnull().sum() #0 Missing values
df_vac.avoid_large_gatherings.value_counts()
'''
0.0    12703
1.0     6939'''
# Bar Plot
sns.countplot(x = 'avoid_large_gatherings', data = df_vac , palette = 'icefire')
plt.title('Histogram of avoid_large_gatherings')
#Hypothesis Testing
ct_gath = pd.crosstab(df_vac.h1n1_vaccine, df_vac.avoid_large_gatherings)
chi2_contingency(ct_gath, correction = False)
# p_val = 0.004, Ho reject, hence association exists, good predictor
```



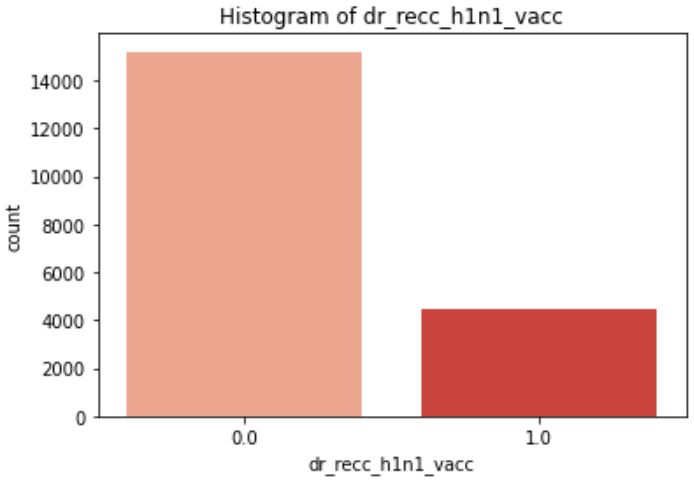
```
#_____________ 9 reduced_outside_home_cont [0 and 1]
df_vac.reduced_outside_home_cont.isnull().sum() #0 Missing values
df_vac.reduced_outside_home_cont.value_counts()
'''
0.0    13159
1.0     6483'''
# Bar Plot
sns.countplot(x = 'reduced_outside_home_cont', data = df_vac , palette = 'gist_heat')
plt.title('Histogram of reduced_outside_home_cont')
#Hypothesis Testing
ct_outside = pd.crosstab(df_vac.h1n1_vaccine, df_vac.reduced_outside_home_cont)
chi2_contingency(ct_outside, correction = False)
# p_val = 0.015, Ho reject, hence association exists, good predictor
```



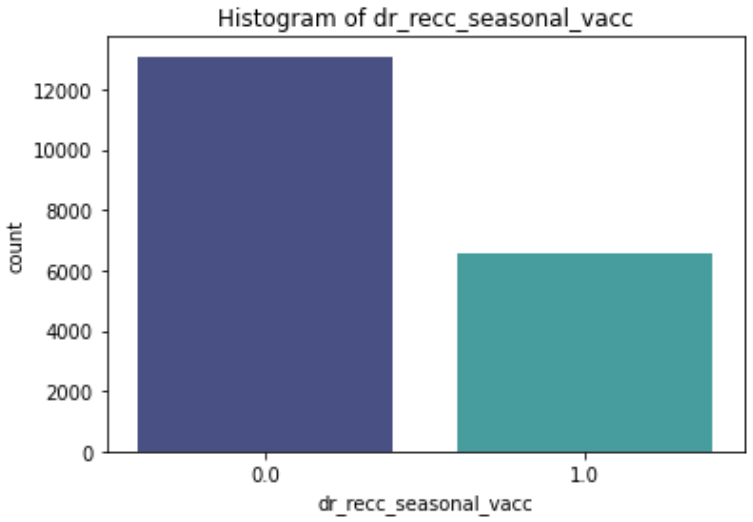
```
#_________________10 avoid_touch_face [0 and 1]
df_vac.avoid_touch_face.isnull().sum() #0 Missing values
df_vac.avoid_touch_face.value_counts()
'''
1.0    13455
0.0     6187'''
# Bar Plot
sns.countplot(x = 'avoid_touch_face', data = df_vac , palette = 'GnBu')
plt.title('Histogram of avoid_touch_face')
#Hypothesis Testing
ct_face = pd.crosstab(df_vac.h1n1_vaccine, df_vac.avoid_touch_face)
chi2_contingency(ct_face, correction = False)
# p_val = 1.5e-23, Ho reject, hence association exists, good predictor
```



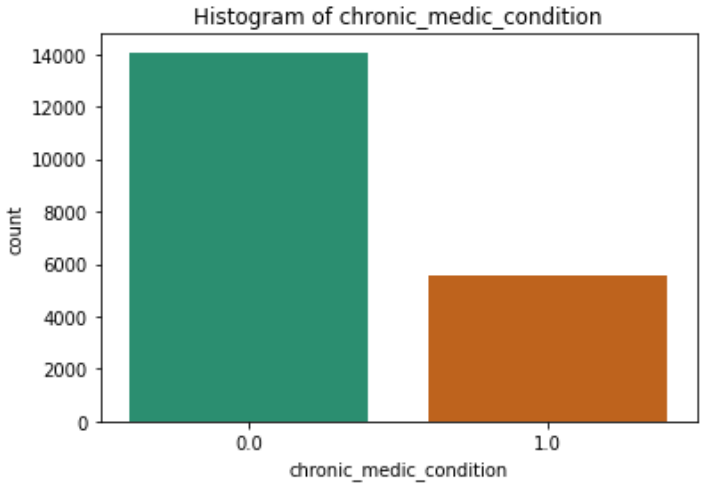
```
#_____________________ 11 dr_recc_h1n1_vacc [0 and 1]
df_vac.dr_recc_h1n1_vacc.isnull().sum() #0 Missing values
df_vac.dr_recc_h1n1_vacc.value_counts()
'''
0.0    15203
1.0     4439'''
# Bar Plot
sns.countplot(x = 'dr_recc_h1n1_vacc', data = df_vac , palette = 'Reds')
plt.title('Histogram of dr_recc_h1n1_vacc')
#Hypothesis Testing
ct_drrec = pd.crosstab(df_vac.h1n1_vaccine, df_vac.dr_recc_h1n1_vacc)
chi2_contingency(ct_drrec, correction = False)
# p_val = 0, Ho reject, hence association exists, good predictor
```



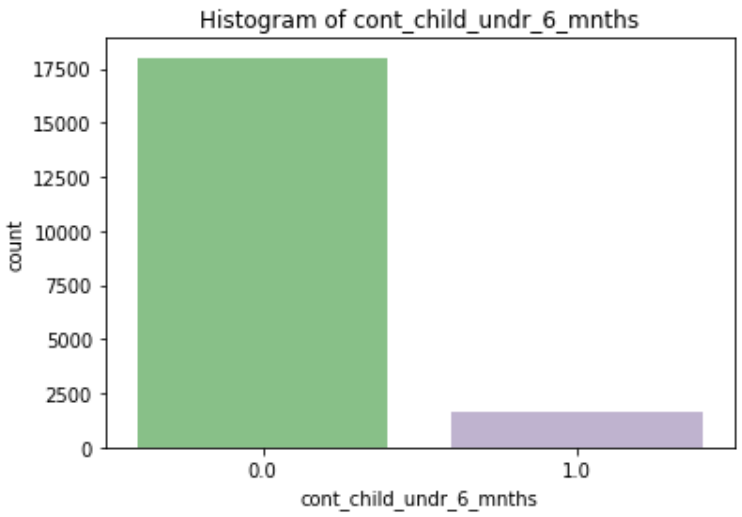
```
#_______________ 12 dr_recc_seasonal_vacc [0 and 1]
df_vac.dr_recc_seasonal_vacc.isnull().sum() #0 Missing values
df_vac.dr_recc_seasonal_vacc.value_counts()
'''
0.0    13091
1.0     6551'''
# Bar Plot
sns.countplot(x = 'dr_recc_seasonal_vacc', data = df_vac , palette = 'mako')
plt.title('Histogram of dr_recc_seasonal_vacc')
#Hypothesis Testing
ct_drseason = pd.crosstab(df_vac.h1n1_vaccine, df_vac.dr_recc_seasonal_vacc)
chi2_contingency(ct_drseason, correction = False)
# p_val = 2.2e-192, Ho reject, hence association exists, good predictor
```



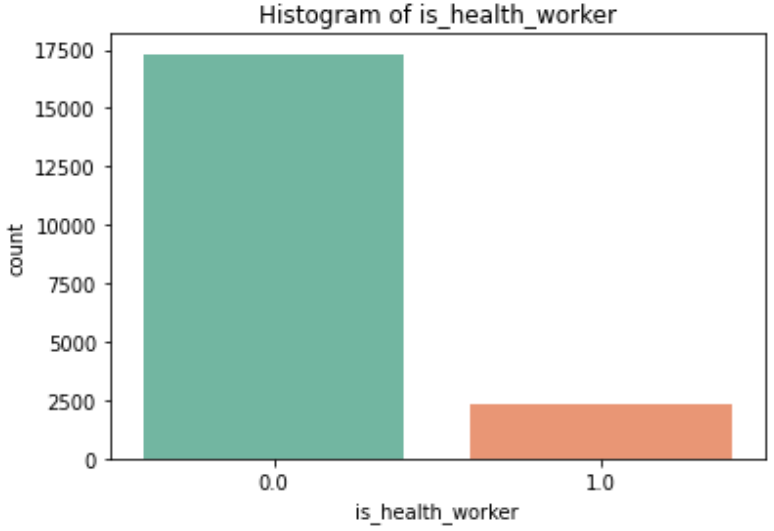
```
#_____________________ 13 chronic_medic_condition [0 and 1]
df_vac.chronic_medic_condition.isnull().sum() #0 Missing values
df_vac.chronic_medic_condition.value_counts()
'''
0.0    14066
1.0     5576'''
# Bar Plot
sns.countplot(x = 'chronic_medic_condition', data = df_vac , palette = 'Dark2')
plt.title('Histogram of chronic_medic_condition')
#Hypothesis Testing
ct_chronic = pd.crosstab(df_vac.h1n1_vaccine, df_vac.chronic_medic_condition)
chi2_contingency(ct_chronic, correction = False)
# p_val = 1.3e-49, Ho reject, hence association exists, good predictor
```



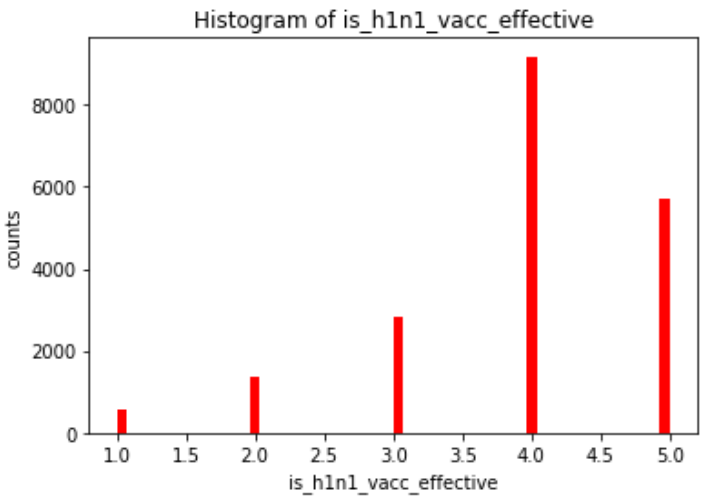
```
#_________________ 14 cont_child_undr_6_mnths [0 and 1]
df_vac.cont_child_undr_6_mnths.isnull().sum() #0 Missing values
df_vac.cont_child_undr_6_mnths.value_counts()
'''
0.0    17995
1.0     1647'''
# Bar Plot
sns.countplot(x = 'cont_child_undr_6_mnths', data = df_vac , palette = 'Accent')
plt.title('Histogram of cont_child_undr_6_mnths')
#Hypothesis Testing
ct_child = pd.crosstab(df_vac.h1n1_vaccine, df_vac.cont_child_undr_6_mnths)
chi2_contingency(ct_child, correction = False)
# p_val = 9.2e-26, Ho reject, hence association exists, good predictor
```

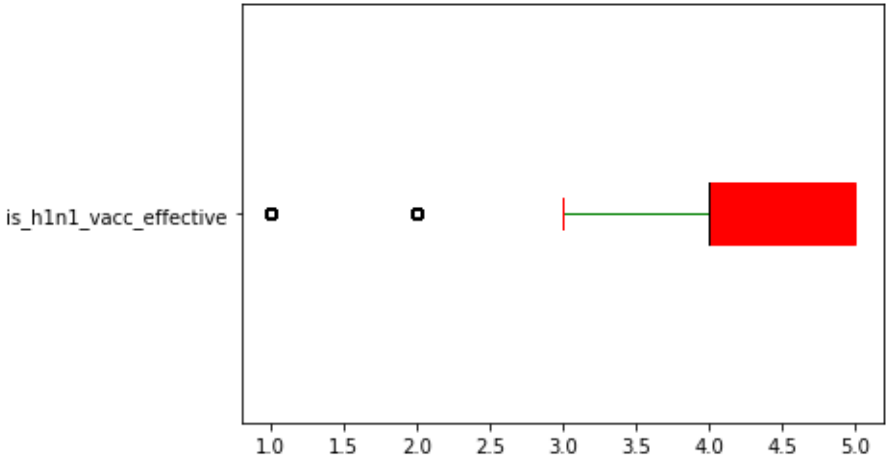


```
#_________________ 15 is_health_worker [0 and 1]
df_vac.is_health_worker.isnull().sum() #0 Missing values
df_vac.is_health_worker.value_counts()
'''
0.0    17310
1.0     2332'''
# Bar Plot
sns.countplot(x = 'is_health_worker', data = df_vac , palette = 'Set2')
plt.title('Histogram of is_health_worker')
#Hypothesis Testing
ct_hw = pd.crosstab(df_vac.h1n1_vaccine, df_vac.is_health_worker)
chi2_contingency(ct_hw, correction = False)
# p_val = 4e-152, Ho reject, hence association exists, good predictor
```

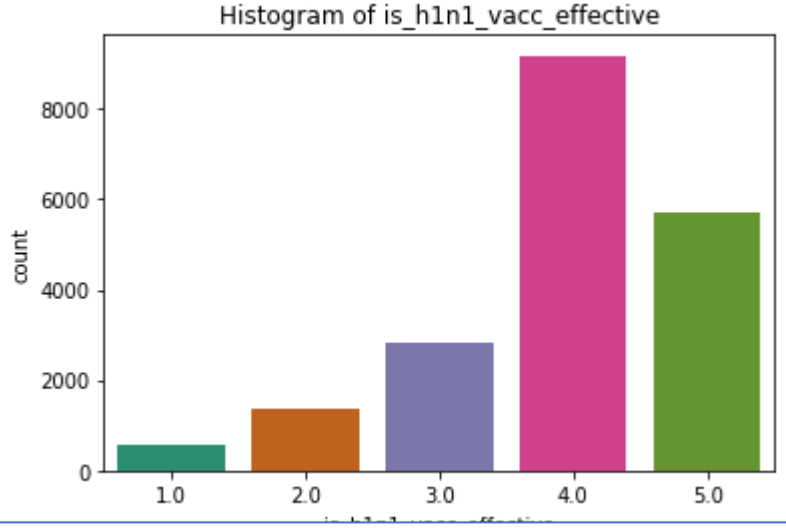


```
#_____________________ 16 is_h1n1_vacc_effective [1,2,3,4,5] ordered
```





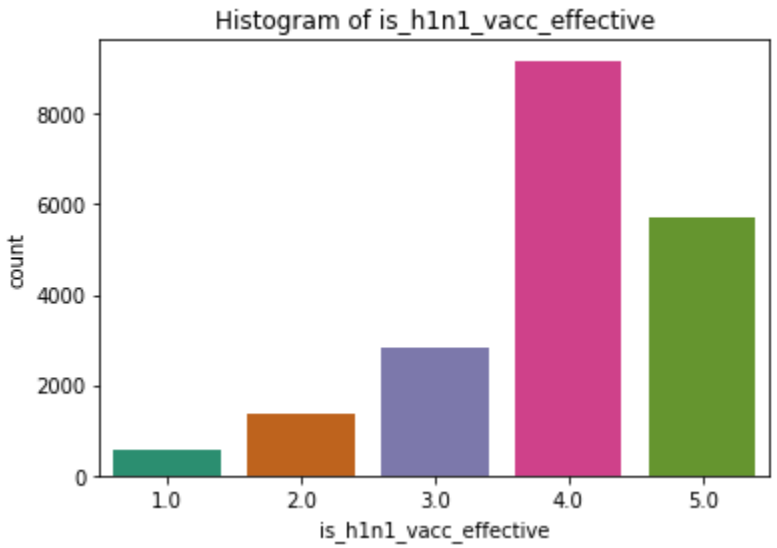

```
#_____________________ 16 is_h1n1_vacc_effective [1,2,3,4,5] ordered
#_____histogram
#_run in block
plt.hist(df_vac.is_h1n1_vacc_effective, bins = 'auto', facecolor = 'red')
plt.xlabel('is_h1n1_vacc_effective')
plt.ylabel('counts')
plt.title('Histogram of is_h1n1_vacc_effective')
#____boxplot
props2 = dict(boxes = 'red', whiskers = 'green', medians = 'black', caps = 'red')
df_vac['is_h1n1_vacc_effective'].plot.box(color=props2, patch_artist = True, vert = False)
# few outliers on lower side; IGNORE!
df_vac.is_h1n1_vacc_effective.isnull().sum() #0 Missing values
df_vac.is_h1n1_vacc_effective.value_counts()
'''
4.0    9172
5.0    5715
3.0    2838
2.0    1347
1.0     570'''
```

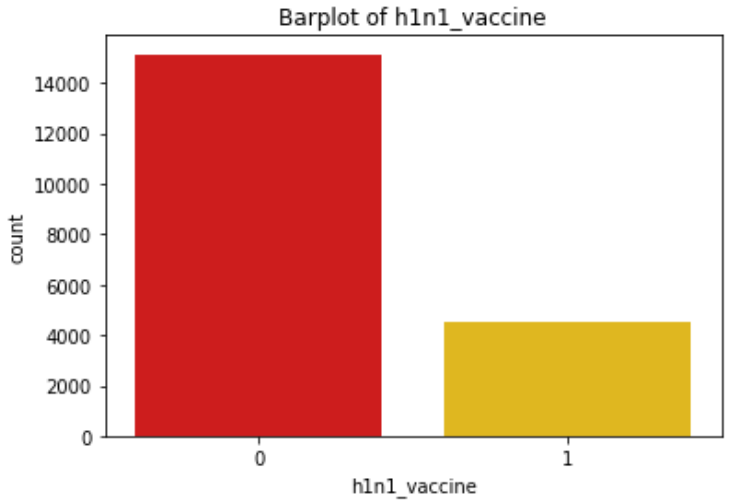



```
# Bar Plot
sns.countplot(x = 'is_h1n1_vacc_effective', data = df_vac , palette = 'Dark2')
plt.title('Histogram of is_h1n1_vacc_effective')
```

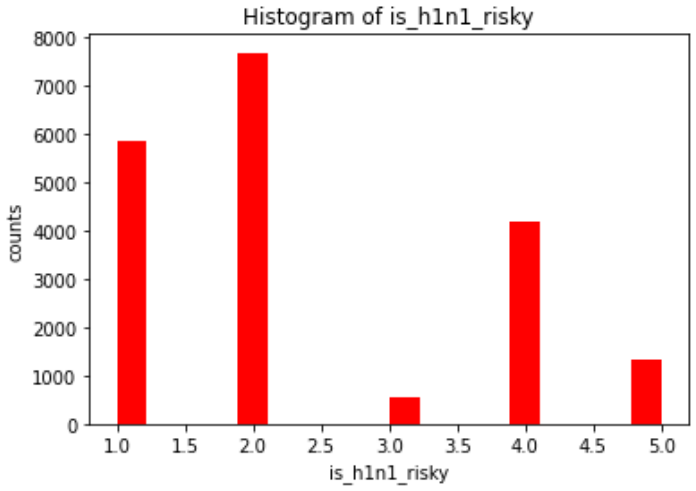
Is this a good predictor?

```
#Hypothesis Testing
import statsmodels.api as sm
from statsmodels.formula.api import ols
mod = ols('is_h1n1_vacc_effective~ h1n1_vaccine', data = df_vac).fit()
aov_table = sm.stats.anova_lm(mod)
print(aov_table)
#0.0  ie p_value which is <0.05; Ho Reject; Good Predictor
```

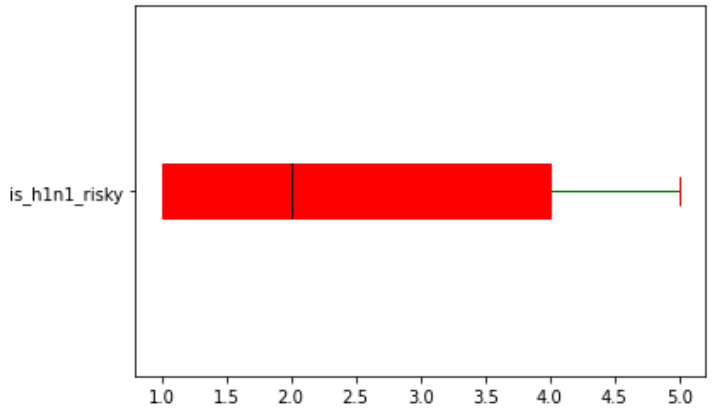


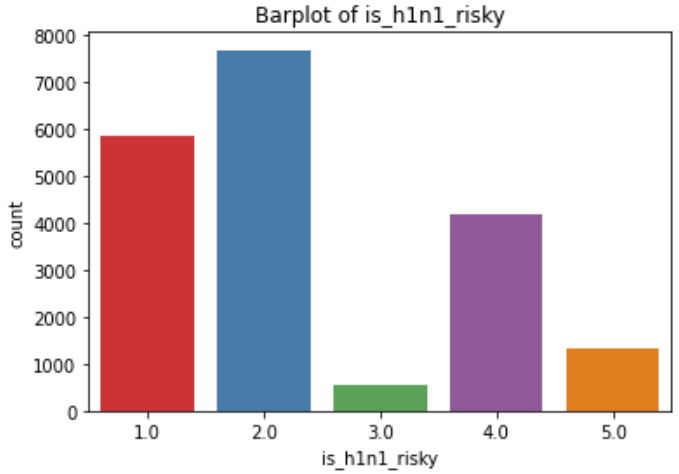


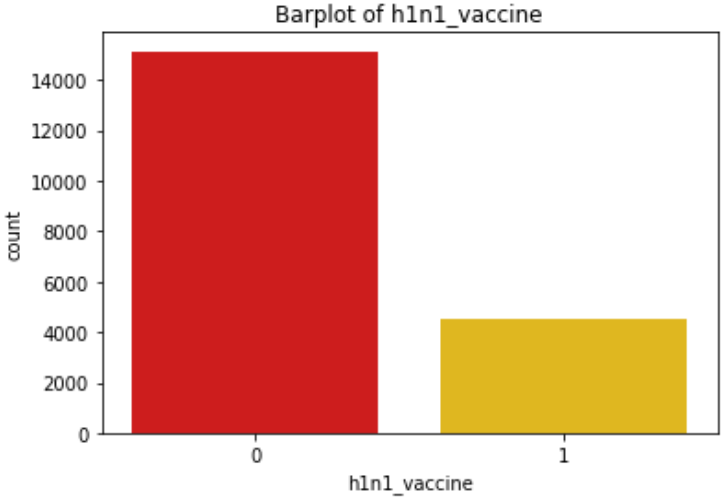
```
#_____________________ 17 is_h1n1_risky [1,2,3,4,5] ordered
```



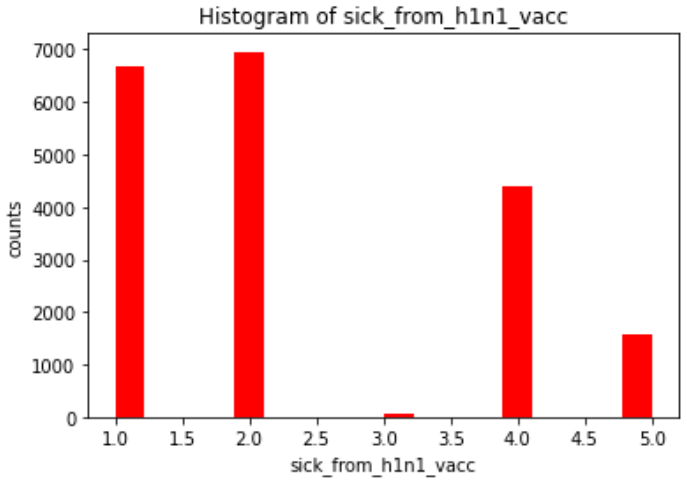

```
#Hypothesis Testing
import statsmodels.api as sm
from statsmodels.formula.api import ols
mod = ols('is_h1n1_risky ~ h1n1_vaccine', data = df_vac).fit()
aov_table = sm.stats.anova_lm(mod)
print(aov_table)
#0.0  ie p_value is <0.05; Ho Reject; Good Predictor
```

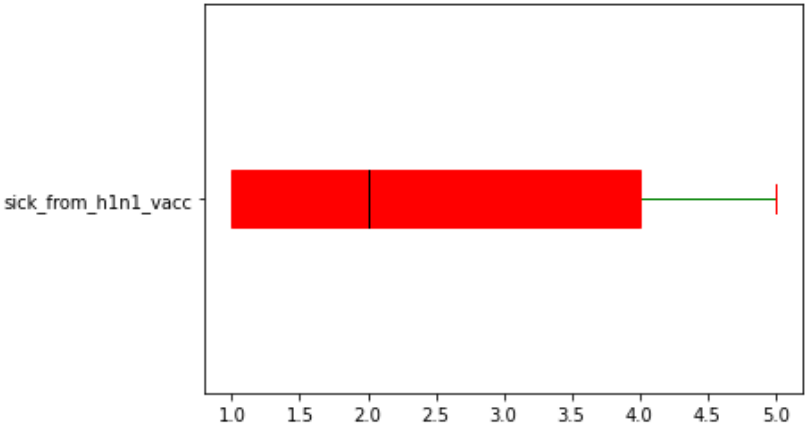




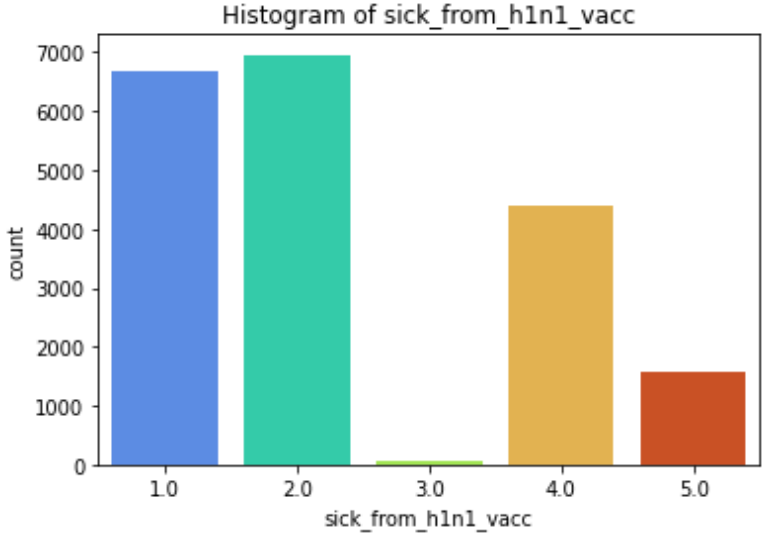


#_____ 18 sick_from_h1n1_vacc [1,2,3,4,5] ordered



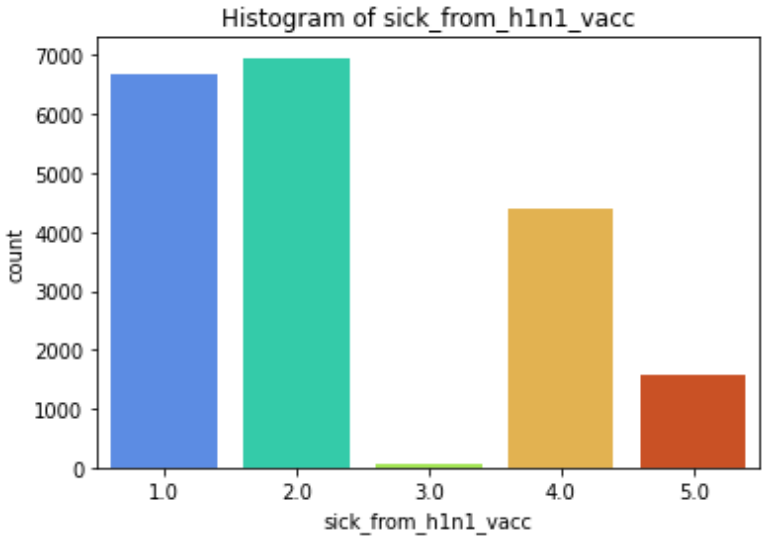


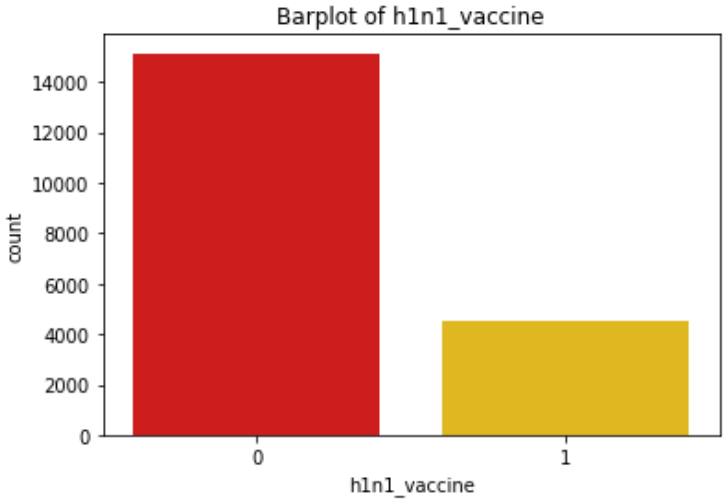

```
#_____ 18 sick_from_h1n1_vacc [1,2,3,4,5] ordered
#_____histogram
#_run in block
plt.hist(df_vac.sick_from_h1n1_vacc, bins = 'auto', facecolor = 'red')
plt.xlabel('sick_from_h1n1_vacc')
plt.ylabel('counts')
plt.title('Histogram of sick_from_h1n1_vacc')
#____boxplot
props2 = dict(boxes = 'red', whiskers = 'green', medians = 'black', caps = 'red')
df_vac['sick_from_h1n1_vacc'].plot.box(color=props2, patch_artist = True, vert = False)

df_vac.sick_from_h1n1_vacc.isnull().sum() #0 Missing values
df_vac.sick_from_h1n1_vacc.value_counts()
'''
2.0    6956
1.0    6684
4.0    4390
5.0    1560
3.0      52'''
```



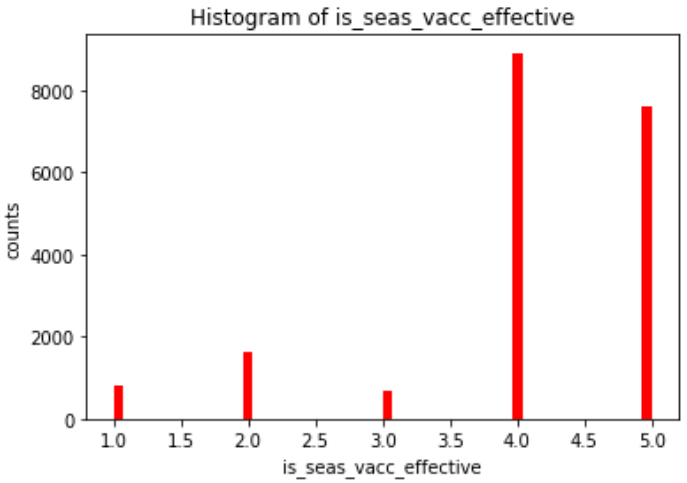
Is this a good predictor?

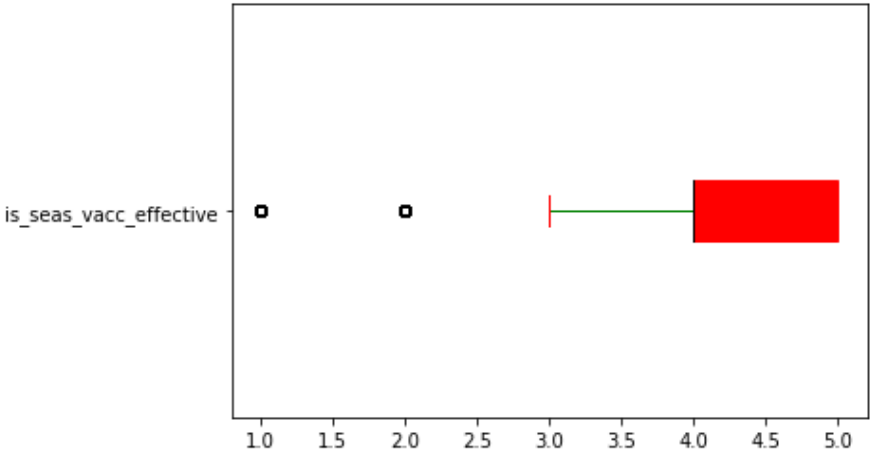
```
#Hypothesis Testing
import statsmodels.api as sm
from statsmodels.formula.api import ols
mod = ols('sick_from_h1n1_vacc ~ h1n1_vaccine', data = df_vac).fit()
aov_table = sm.stats.anova_lm(mod)
print(aov_table)
#3.62e-31  ie p_value is <0.05; Ho Reject; Good Predictor
```





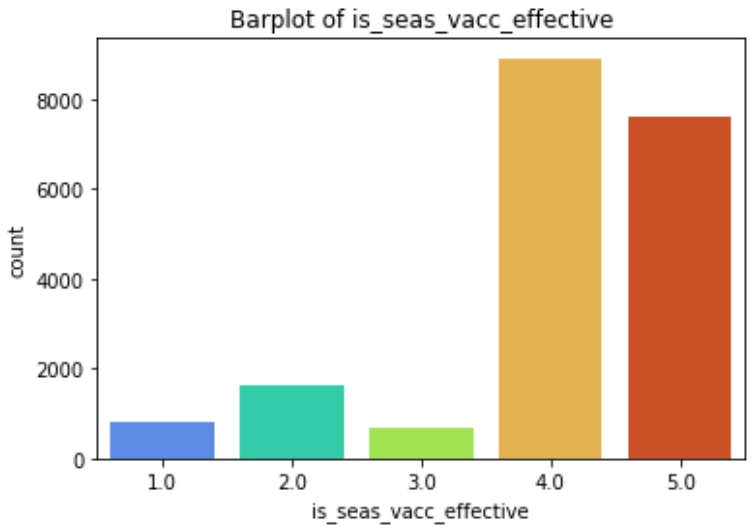
```
#_____________ 19 is_seas_vacc_effective [1,2,3,4,5] ordered
#_____histogram
#_run in block
plt.hist(df_vac.is_seas_vacc_effective, bins = 'auto', facecolor = 'red')
plt.xlabel('is_seas_vacc_effective')
plt.ylabel('counts')
plt.title('Histogram of is_seas_vacc_effective')
#____boxplot
props2 = dict(boxes = 'red', whiskers = 'green', medians = 'black', caps = 'red')
df_vac['is_seas_vacc_effective'].plot.box(color=props2, patch_artist = True, vert = False)
# few are on lower side; Ignore outliers

df_vac.is_seas_vacc_effective.isnull().sum() #0 Missing values
df_vac.is_seas_vacc_effective.value_counts()
'''
4.0    8906
5.0    7603
2.0    1638
1.0     822
3.0     673'''
```

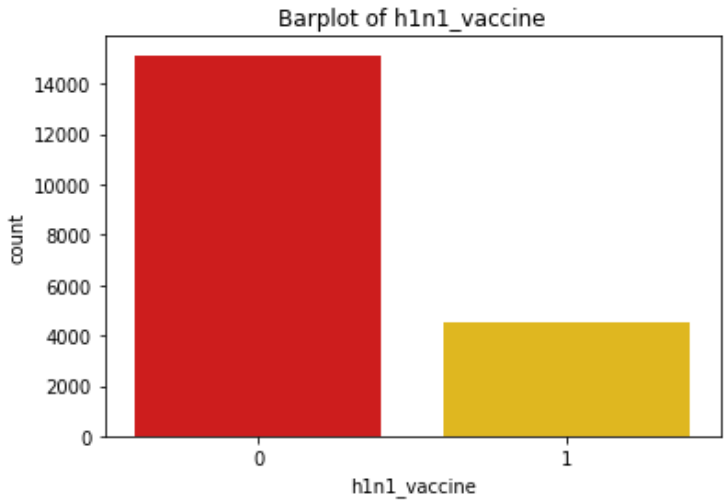




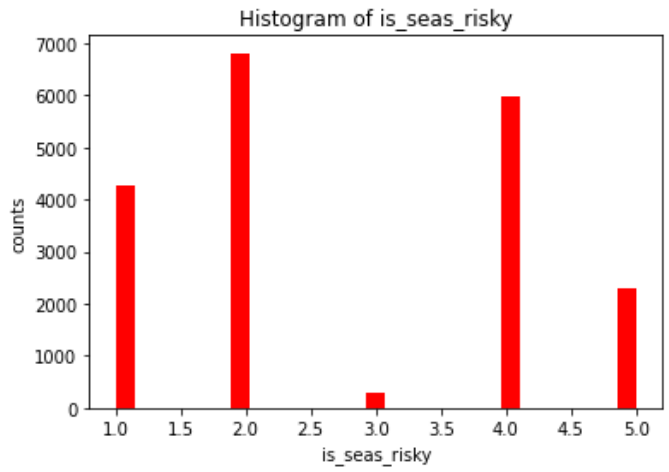
Is this a good predictor?

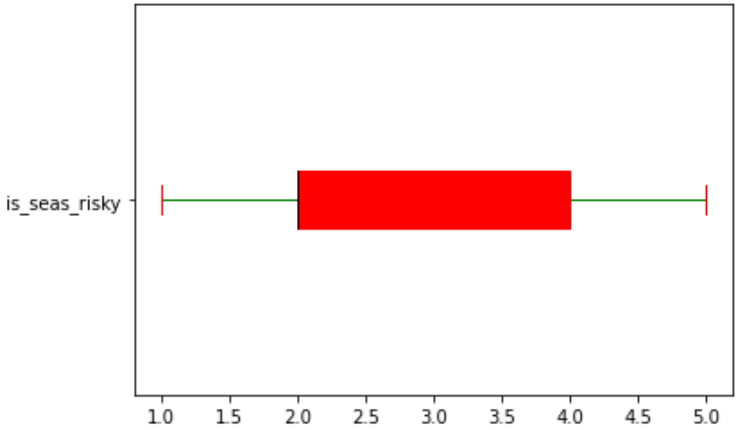
```
#Hypothesis Testing
import statsmodels.api as sm
from statsmodels.formula.api import ols
mod = ols('is_seas_vacc_effective ~ h1n1_vaccine', data = df_vac).fit()
aov_table = sm.stats.anova_lm(mod)
print(aov_table)
#9.2e-152 ie p_value is <0.05; Ho Reject; Good Predictor
```



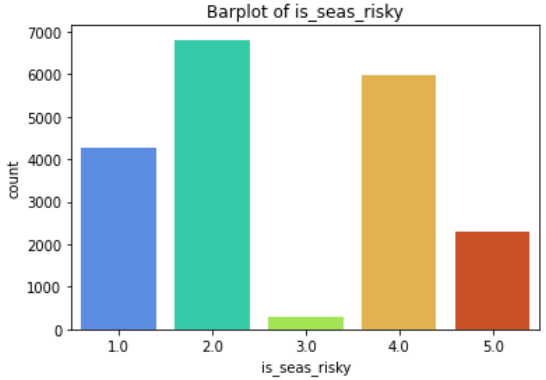


#_____ 20 is_seas_risky [1,2,3,4,5] ordered



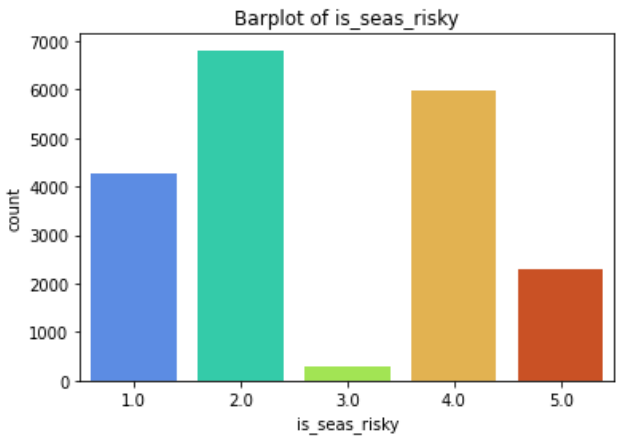


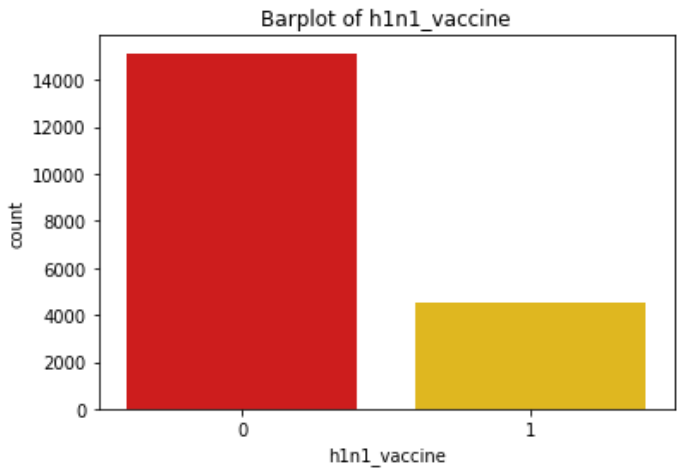

```
#_____histogram
#_run in block
plt.hist(df_vac.is_seas_risky, bins = 'auto', facecolor = 'red')
plt.xlabel('is_seas_risky')
plt.ylabel('counts')
plt.title('Histogram of is_seas_risky')
#____boxplot
props2 = dict(boxes = 'red', whiskers = 'green', medians = 'black', caps = 'red')
df_vac['is_seas_risky'].plot.box(color=props2, patch_artist = True, vert = False)
# no outliers
df_vac.is_seas_risky.isnull().sum() #0 Missing values
df_vac.is_seas_risky.value_counts()
'''
2.0    6811
4.0    5984
1.0    4258
5.0    2286
3.0     303'''
# Bar Plot
sns.countplot(x = 'is_seas_risky', data = df_vac , palette = 'turbo')
plt.title('Barplot of is_seas_risky')
```

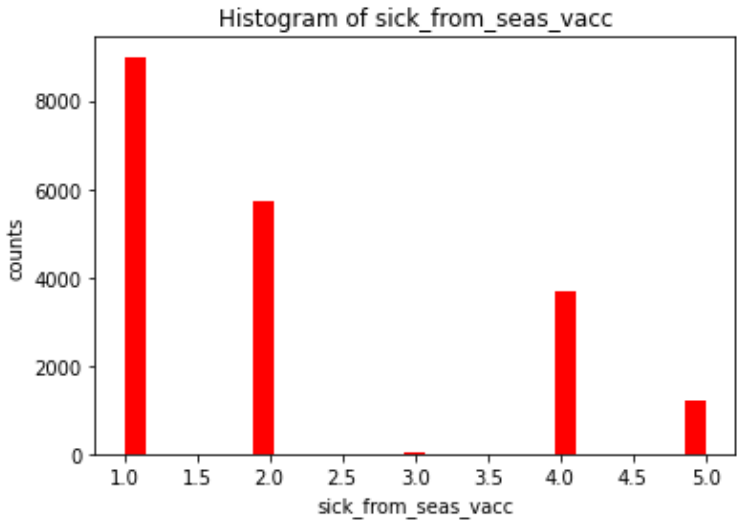


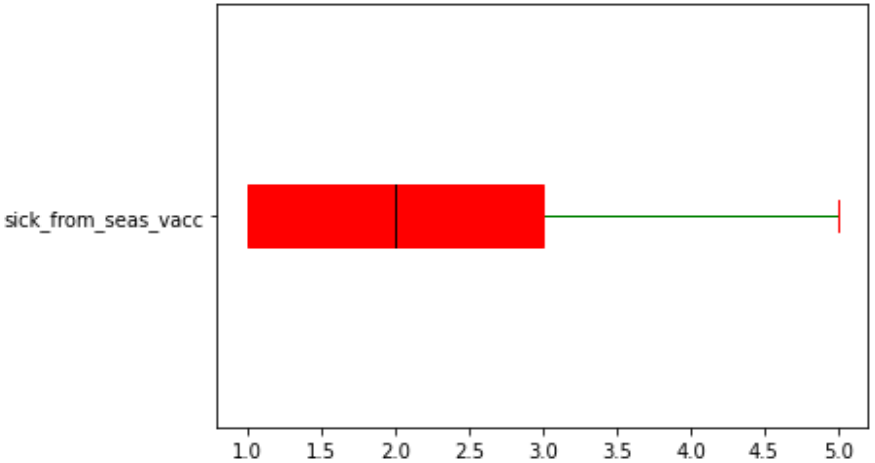
Is this a good predictor?

```
#Hypothesis Testing
import statsmodels.api as sm
from statsmodels.formula.api import ols
mod = ols('is_seas_risky ~ h1n1_vaccine', data = df_vac).fit()
aov_table = sm.stats.anova_lm(mod)
print(aov_table)
#0.0 ie p_value which is <0.05; Ho Reject; Good Predictor
```

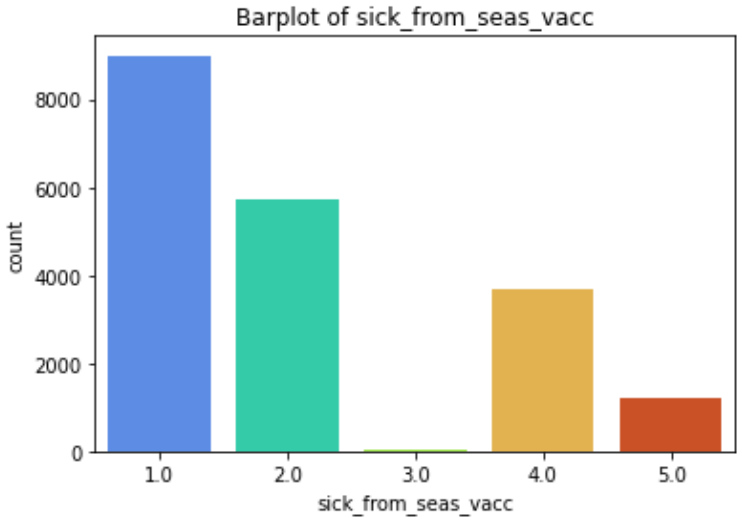






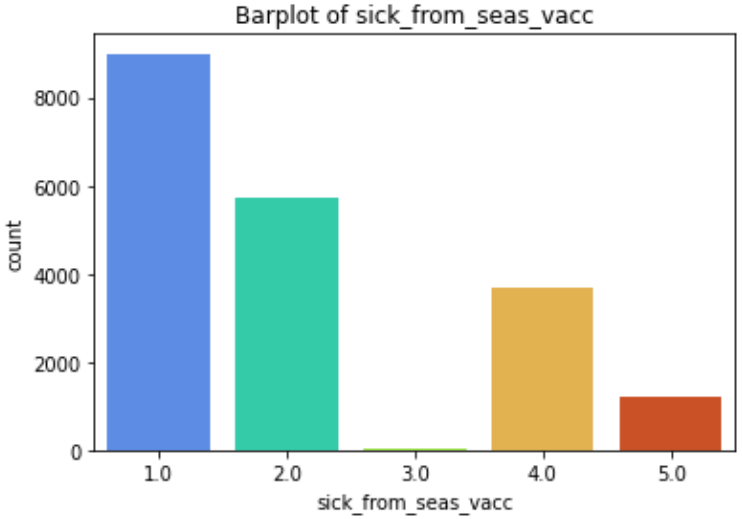


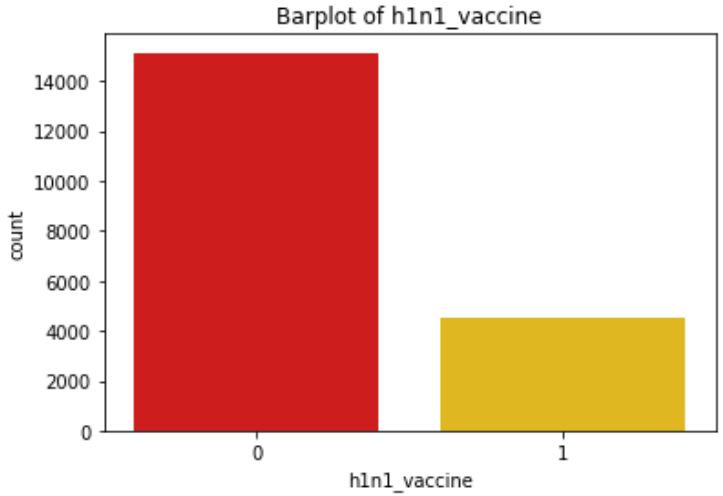

```
#_________________ 21 sick_from_seas_vacc [1,2,3,4,5] ordered
#_____histogram
#_run in block
plt.hist(df_vac.sick_from_seas_vacc, bins = 'auto', facecolor = 'red')
plt.xlabel('sick_from_seas_vacc')
plt.ylabel('counts')
plt.title('Histogram of sick_from_seas_vacc')
#____boxplot
props2 = dict(boxes = 'red', whiskers = 'green', medians = 'black', caps = 'red')
df_vac['sick_from_seas_vacc'].plot.box(color=props2, patch_artist = True, vert = Fals

df_vac.sick_from_seas_vacc.isnull().sum() #0 Missing values
df_vac.sick_from_seas_vacc.value_counts()
'''
1.0    8996
2.0    5713
4.0    3683
5.0    1221
3.0      29'''
# Bar Plot
sns.countplot(x = 'sick_from_seas_vacc', data = df_vac , palette = 'turbo')
plt.title('Barplot of sick_from_seas_vacc')
```



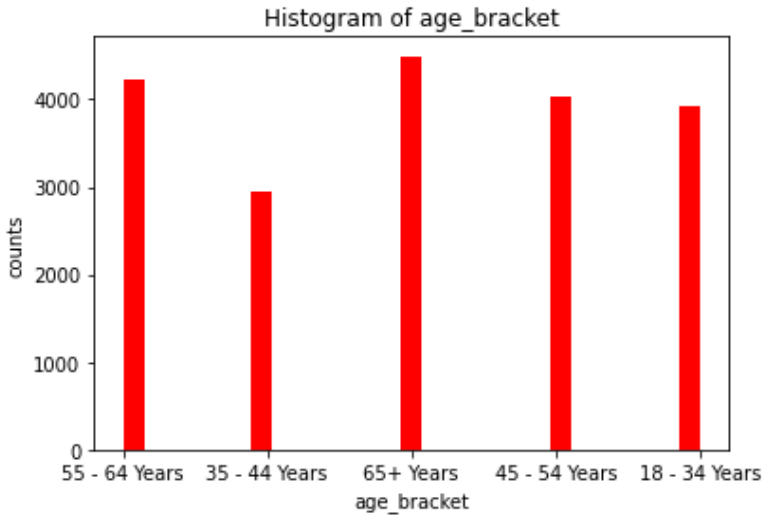
Is this a good predictor?

```
#Hypothesis Testing
import statsmodels.api as sm
from statsmodels.formula.api import ols
mod = ols('sick_from_seas_vacc ~ h1n1_vaccine', data = df_vac).fit()
aov_table = sm.stats.anova_lm(mod)
print(aov_table)
#0.36 ie p_value is >0.05; Ho accepted; Bad Predictor
```



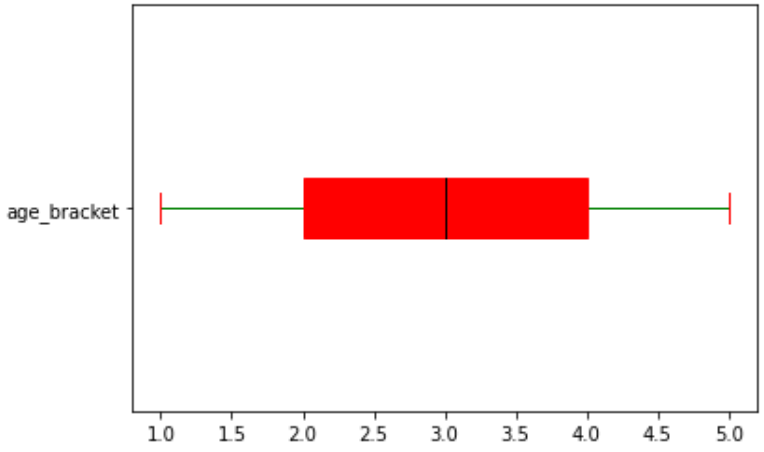


```
#_____________ 22 age_bracket [actually ordered]
```




```
#____boxplot
props2 = dict(boxes = 'red', whiskers = 'green', medians = 'black', caps = 'red')
df_vac['age_bracket'].plot.box(color=props2, patch_artist = True, vert = False)
## oops, its object, lets change to 1,2,3 like; first see value counts
df_vac.age_bracket.isnull().sum() #0 Missing values
df_vac.age_bracket.value_counts()
'''
65+ Years        4491
55 - 64 Years    4234
45 - 54 Years    4038
18 - 34 Years    3925
35 - 44 Years    2954
'''
```

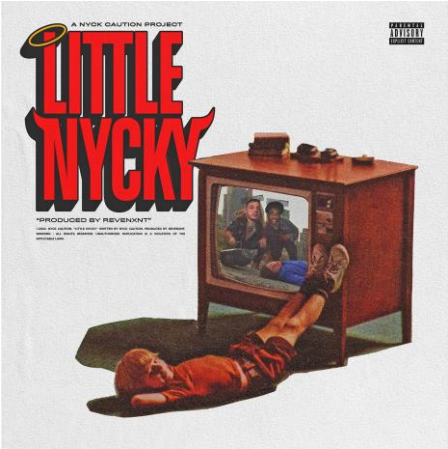
```
# let categories be in order

df_vac['age_bracket'] =df_vac.get('age_bracket').replace('65+ Years', 5)
df_vac['age_bracket'] =df_vac.get('age_bracket').replace('55 - 64 Years', 4)
df_vac['age_bracket'] =df_vac.get('age_bracket').replace('45 - 54 Years', 3)
df_vac['age_bracket'] =df_vac.get('age_bracket').replace('18 - 34 Years', 1)
df_vac['age_bracket'] =df_vac.get('age_bracket').replace('35 - 44 Years', 2)
# ignore warnings !

df_vac.age_bracket.isnull().sum() #0 Missing values
df_vac.age_bracket.value_counts()
'''
5    4491
4    4234
3    4038
1    3925
2    2954
Name: age_bracket, dtype: int64
'''
# now boxplot will come
props2 = dict(boxes = 'red', whiskers = 'green', medians = 'black', caps = 'red')
df_vac['age_bracket'].plot.box(color=props2, patch_artist = True, vert = False) #No outliers
```

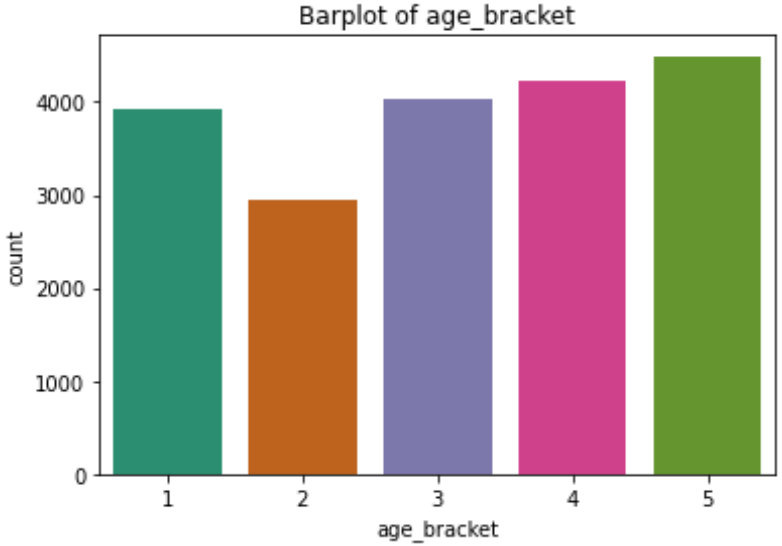


Caution!

```
#_________________________we could have followed a more easier way!
# label encoding the data ; its good for nominal data , not good for ordered data
# like in our present case!
# DO NOT TRY AS IT HAS ALREAY BEING DONE !!!!
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()
```

```
# Bar Plot
sns.countplot(x = 'age_bracket', data = df_vac , palette = 'Dark2')
plt.title('Barplot of age_bracket')
```

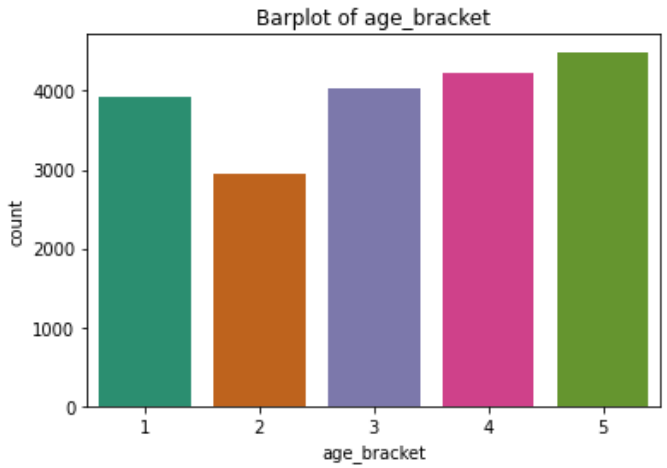


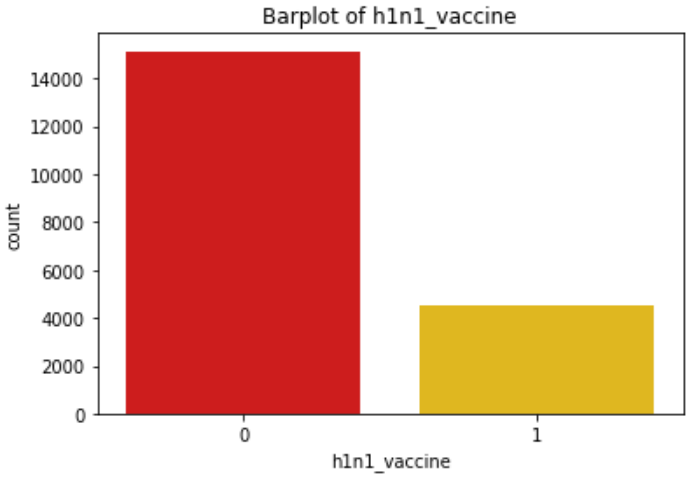


Dr Vinod on h1n1 Log Reg 8971073111
vinodanalytics@gmail.com

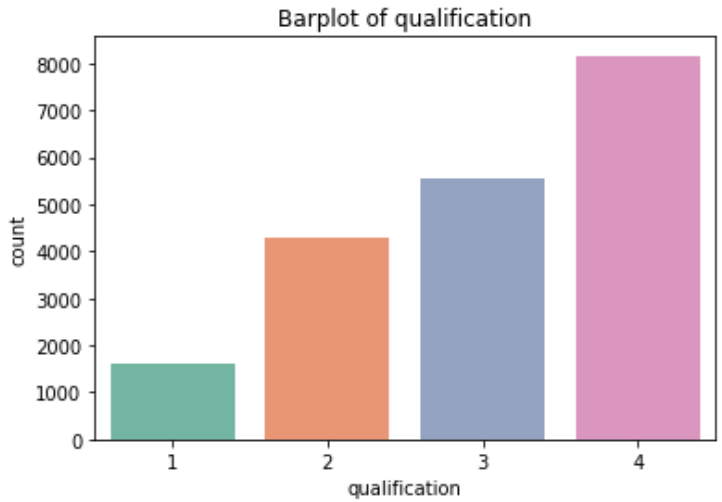
Is this a good predictor?

```
#Hypothesis Testing
import statsmodels.api as sm
from statsmodels.formula.api import ols
mod = ols('age_bracket ~ h1n1_vaccine', data = df_vac).fit()
aov_table = sm.stats.anova_lm(mod)
print(aov_table)
#1.5e-10 ie p_value is <0.05; Ho rejected; Good Predictor
```



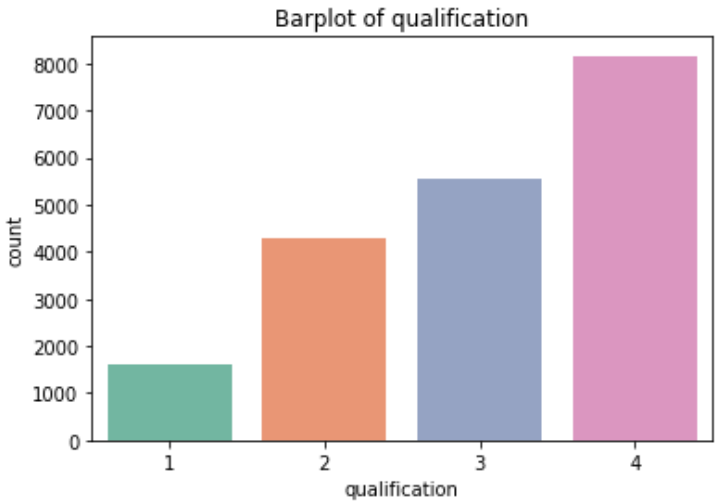


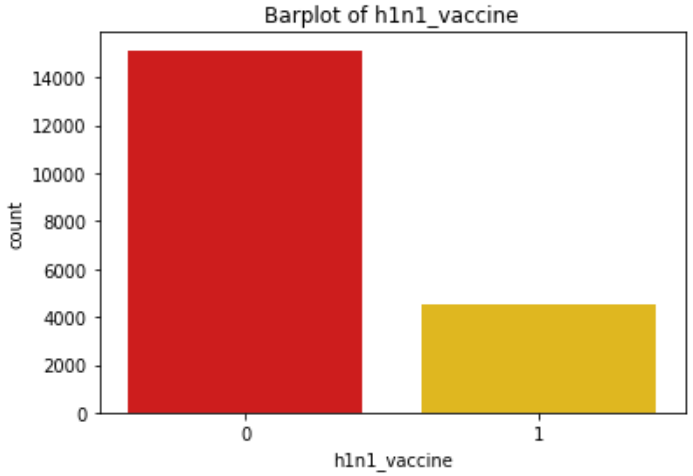
```
#_________________ 23 qualification - object, Actually ordered! 3 levels
df_vac.qualification.isnull().sum()
df_vac.qualification.value_counts()
'''
College Graduate    8165
Some College        5570
12 Years            4287
< 12 Years          1620'''

# let's put them in order
df_vac['qualification'] =df_vac.get('qualification').replace('College Graduate', 4)
df_vac['qualification'] =df_vac.get('qualification').replace('Some College', 3)
df_vac['qualification'] =df_vac.get('qualification').replace('12 Years', 2)
df_vac['qualification'] =df_vac.get('qualification').replace('< 12 Years', 1)

df_vac.qualification.value_counts()
'''
4    8165
3    5570
2    4287
1    1620
'''
# Bar Plot
sns.countplot(x = 'qualification', data = df_vac , palette = 'Set2')
plt.title('Barplot of qualification')
```



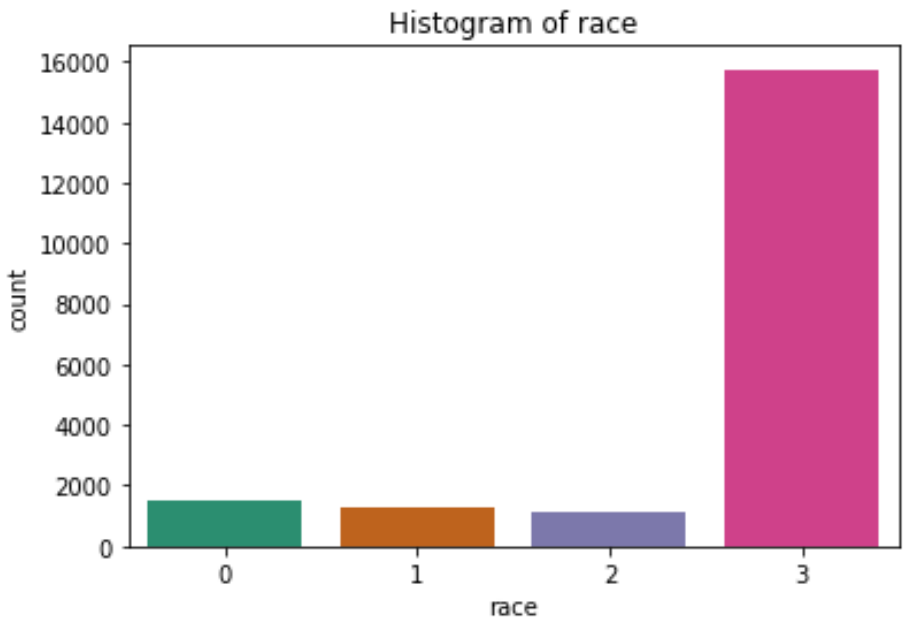
Is this a good predictor?

```
#Hypothesis Testing
import statsmodels.api as sm
from statsmodels.formula.api import ols
mod = ols('qualification ~ h1n1_vaccine', data = df_vac).fit()
aov_table = sm.stats.anova_lm(mod)
print(aov_table)
#1.57e-22 ie p_value is <0.05; Ho rejected; Good Predictor
```



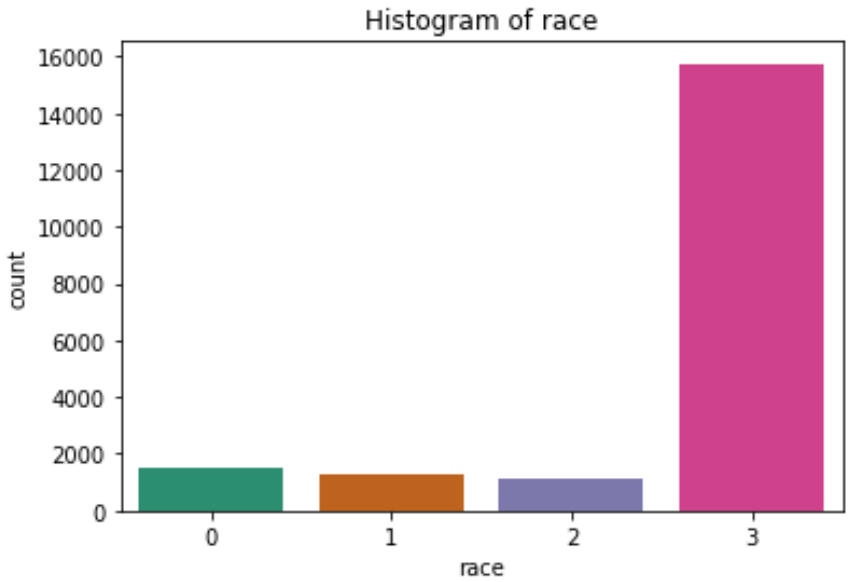


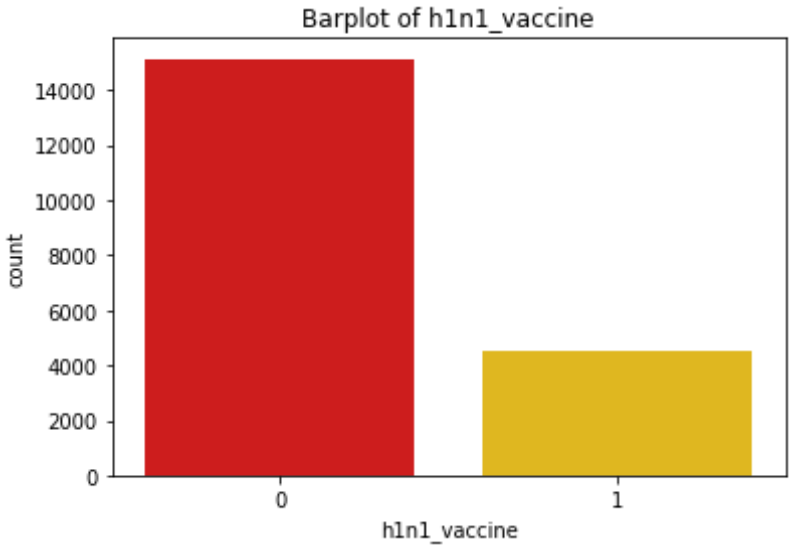
```
#_________________ 24 race - object [NO ORDER, NOMINAL]; 4 levels
df_vac.race.isnull().sum() #No Missing values
df_vac.race.value_counts()
'''
White                 15745
Black                  1474
Hispanic               1295
Other or Multiple      1128'''

# label encoding 'race' ; does alphabetically!
# HERE WE CAN USE LabelEncoder!
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()

df_vac['race']= le.fit_transform(df_vac['race'])
df_vac.race.value_counts()
'''
3    15745
0     1474
1     1295
2     1128'''

# Bar Plot
sns.countplot(x = 'race', data = df_vac , palette = 'Dark2')
plt.title('Histogram of race')
```



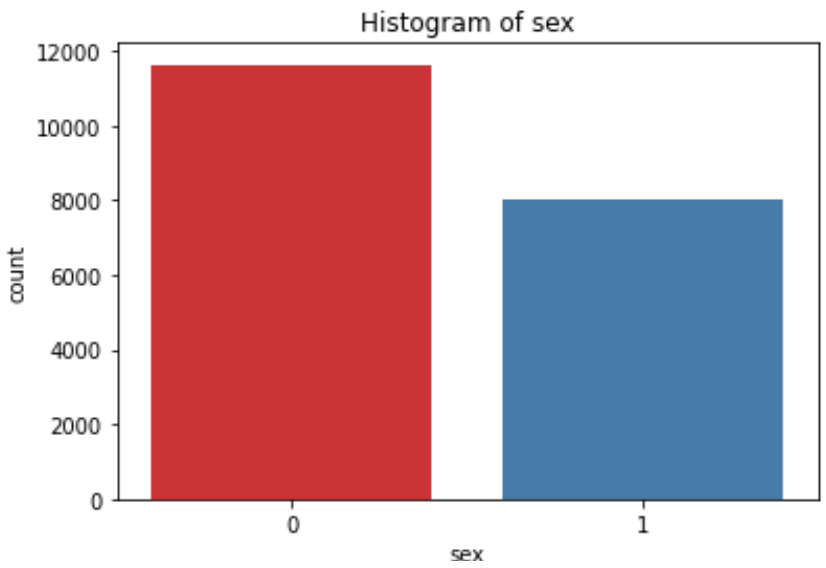
Is this a good predictor?

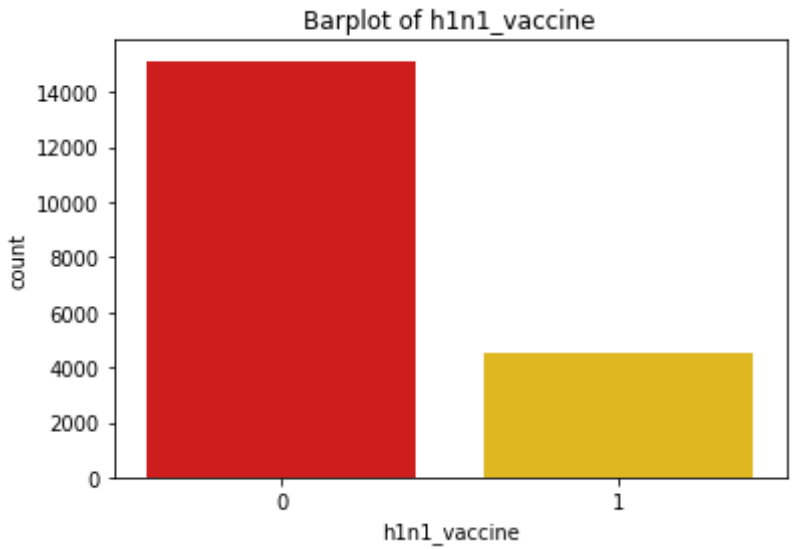
```
#Hypothesis Testing
from scipy.stats import chi2_contingency
ct_race = pd.crosstab(df_vac.h1n1_vaccine, df_vac.race)
chi2_contingency(ct_race, correction = False)
# p_val = 2.4e-10, Ho reject, hence association exists, good predictor
```



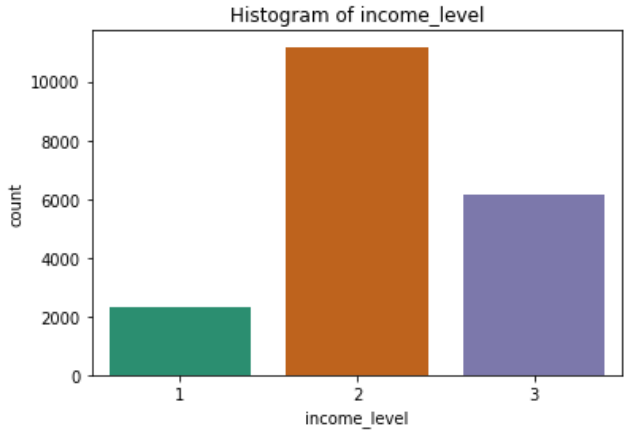


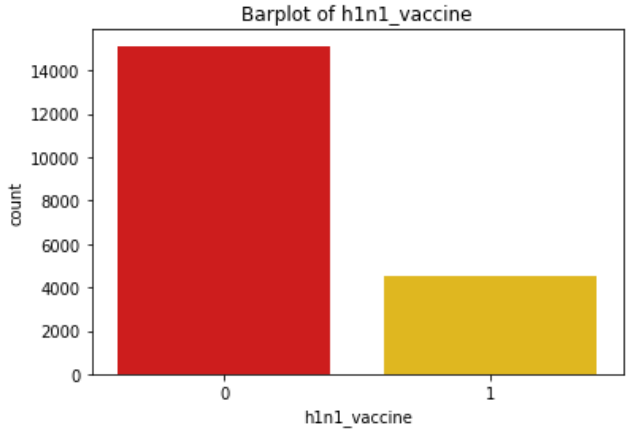
```python
#_____________________ 25 sex - object [female, male]
df_vac.sex.isnull().sum() #No Missing values
df_vac.sex.value_counts()
'''
Female    11638
Male       8004'''

# label encoding the data
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()

df_vac['sex']= le.fit_transform(df_vac['sex'])
df_vac.sex.value_counts()
'''
0    11638
1     8004'''
# Bar Plot
sns.countplot(x = 'sex', data = df_vac , palette = 'Set1')
plt.title('Histogram of sex')

#Hypothesis Testing
from scipy.stats import chi2_contingency
ct_sex = pd.crosstab(df_vac.h1n1_vaccine, df_vac.sex)
chi2_contingency(ct_sex, correction = False)
# p_val = 00, Ho reject, hence association exists, good predictor
```



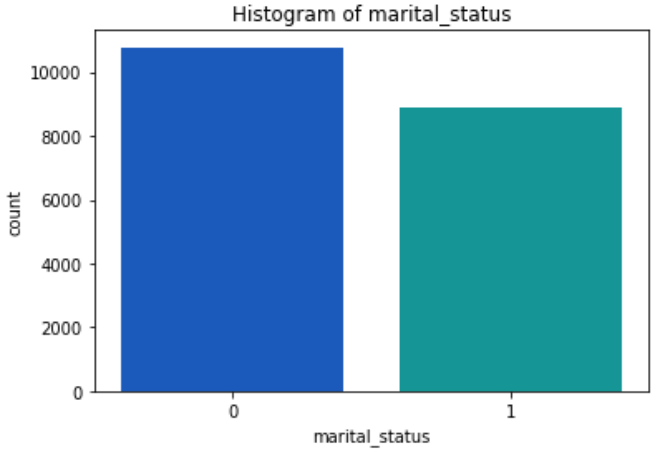


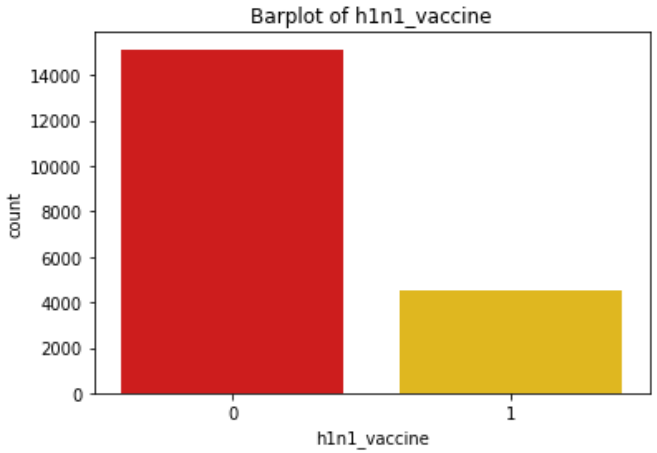
```
#_____________ 26 income_level - object, its ordered
df_vac.income_level.isnull().sum() # no missing values
df_vac.income_level.value_counts()
'''
<= $75,000, Above Poverty    11185
> $75,000                     6159
Below Poverty                  2298'''

#Converting to numeric/ integer
df_vac['income_level']=df_vac.get('income_level').replace('Below Poverty', 1)
df_vac['income_level']=df_vac.get('income_level').replace('<= $75,000, Above Poverty', 2)
df_vac['income_level']=df_vac.get('income_level').replace('> $75,000', 3)

df_vac.income_level.value_counts()
'''
2    11185
3     6159
1     2298
'''
df_vac.info()

# Bar Plot
sns.countplot(x = 'income_level', data = df_vac , palette = 'Dark2')
plt.title('Histogram of income_level')
#Hypothesis Testing
import statsmodels.api as sm
from statsmodels.formula.api import ols
mod = ols('income_level ~ h1n1_vaccine', data = df_vac).fit()
aov_table = sm.stats.anova_lm(mod)
print(aov_table)
# 2.62e-15 ie p_value is <0.05; Ho rejected; Good Predictor
```



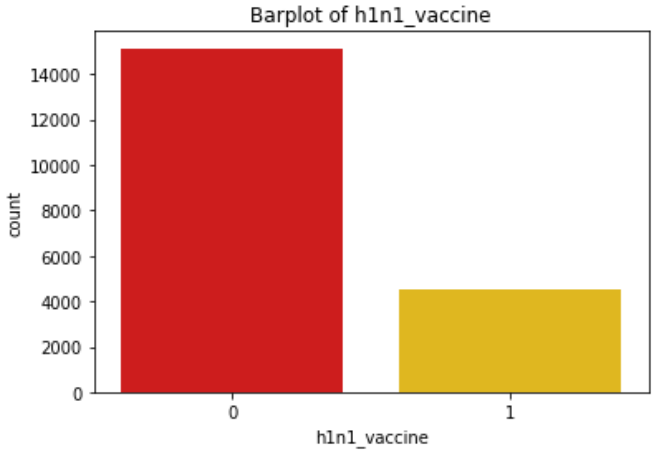


```
#_________________27 marital_status - object [0,1]
df_vac.marital_status.isnull().sum() #471 Missing values
df_vac.marital_status.value_counts()
'''
Married        10768
Not Married     8874'''

# label encoding the data
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()

df_vac['marital_status']= le.fit_transform(df_vac['marital_status'])
df_vac.marital_status.value_counts()
'''
0    10768
1     8874'''
df_vac.info()

# Bar Plot
sns.countplot(x = 'marital_status', data = df_vac , palette = 'winter')
plt.title('Histogram of marital_status')

#Hypothesis Testing
from scipy.stats import chi2_contingency
ct_mari = pd.crosstab(df_vac.h1n1_vaccine, df_vac.marital_status)
chi2_contingency(ct_mari, correction = False)
# p_val = 2.14e-13, Ho reject, hence association exists, good predictor
```

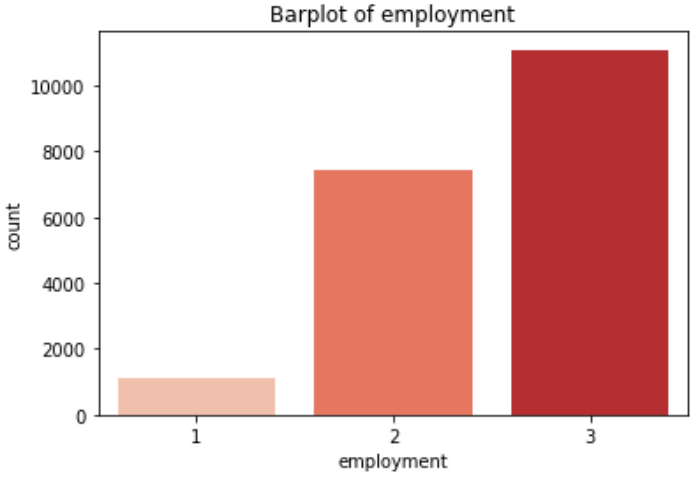




```
#__________28 housing_status - object [own, rent]
df_vac.housing_status.isnull().sum()
df_vac.housing_status.value_counts()
'''
Own      14980
Rent      4662'''
# label encoding the data
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()
df_vac['housing_status']= le.fit_transform(df_vac['housing_status'])
df_vac.housing_status.value_counts()
'''
0    14980
1     4662'''
# Bar Plot
sns.countplot(x = 'housing_status', data = df_vac , palette = 'Set2')
plt.title('Histogram of housing_status')
#Hypothesis Testing
from scipy.stats import chi2_contingency
ct_house = pd.crosstab(df_vac.h1n1_vaccine, df_vac.housing_status)
chi2_contingency(ct_house, correction = False)
# p_val = 7.1e-07, Ho reject, hence association exists, good predictor
```

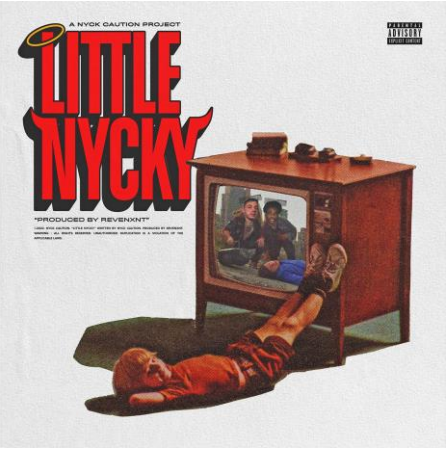


```
# _______________ 29 employment - object [3 levels] actually ordered
df_vac.employment.isnull().sum()
df_vac.employment.value_counts()
'''
Employed              11093
Not in Labor Force     7417
Unemployed             1132'''

#Converting to numeric/ integer
df_vac['employment']=df_vac.get('employment').replace('Employed', 3)
df_vac['employment']=df_vac.get('employment').replace('Not in Labor Force', 2)
df_vac['employment']=df_vac.get('employment').replace('Unemployed', 1)

df_vac.employment.value_counts()
'''
3    11093
2     7417
1     1132
'''
```



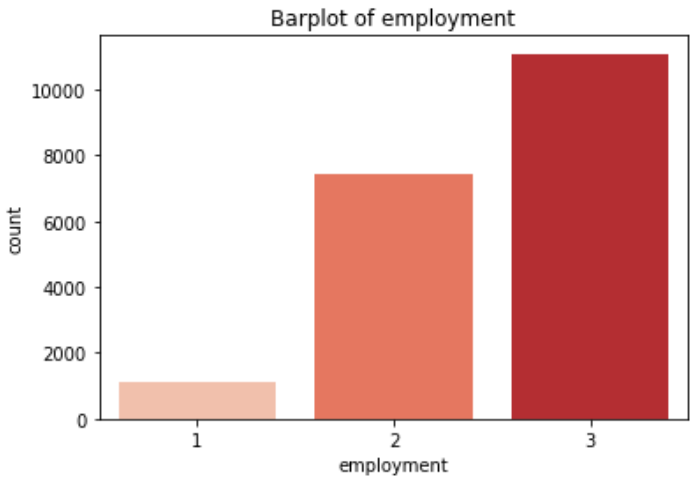
```
#_____________________LabelEncoder giving opposite notation!
# label encoding the data ; DO NOT TRY THIS
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()

df_vac['employment']= le.fit_transform(df_vac['employment'])
df_vac.employment.value_counts()
'''
0    11093
1     7417
2     1132'''
```

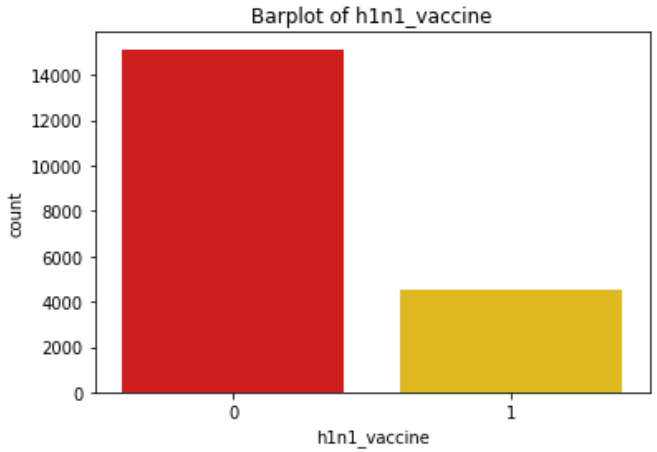
```
Employed                11093
Not in Labor Force       7417
Unemployed               1132'''
```



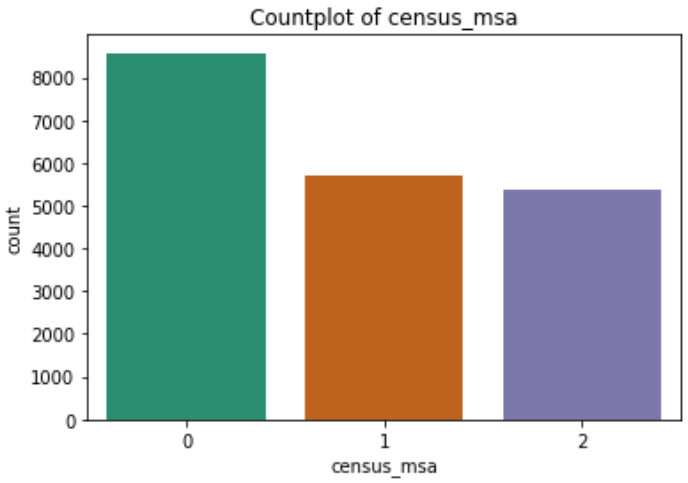
Is this a good predictor?

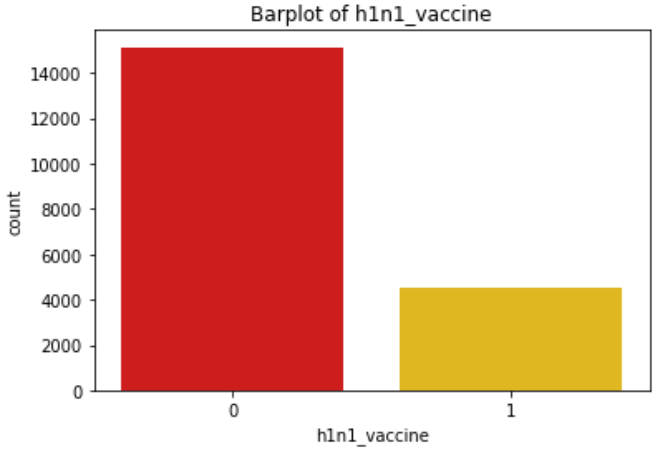
```
#Hypothesis Testing
import statsmodels.api as sm
from statsmodels.formula.api import ols
mod = ols('employment ~ h1n1_vaccine', data = df_vac).fit()
aov_table = sm.stats.anova_lm(mod)
print(aov_table)
#0.015 ie p_value is <0.05; Ho rejected; Good Predictor
```



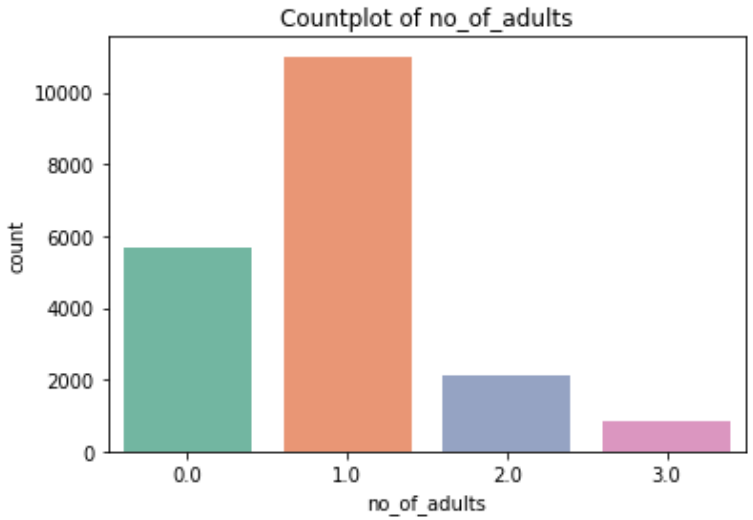


```
#___________30 census_msa - object, 3 levels, NOMINAL
df_vac.census_msa.isnull().sum() #No Missing values
df_vac.census_msa.value_counts()
'''
MSA, Not Principle  City    8571
MSA, Principle City         5717
Non-MSA                     5354'''

# label encoding the data
from sklearn.preprocessing import LabelEncoder
le = LabelEncoder()

df_vac['census_msa']= le.fit_transform(df_vac['census_msa'])
df_vac.census_msa.value_counts()
'''
0    8571
1    5717
2    5354'''

# Bar Plot
sns.countplot(x = 'census_msa', data = df_vac , palette = 'Dark2')
plt.title('Countplot of census_msa')
#Hypothesis Testing
from scipy.stats import chi2_contingency
ct_msa = pd.crosstab(df_vac.h1n1_vaccine, df_vac.census_msa)
ct_msa
chi2_contingency(ct_msa, correction = False)
# p_val = 0.76, > 0.05 Ho accept, hence association does not exists, bad predictor
```

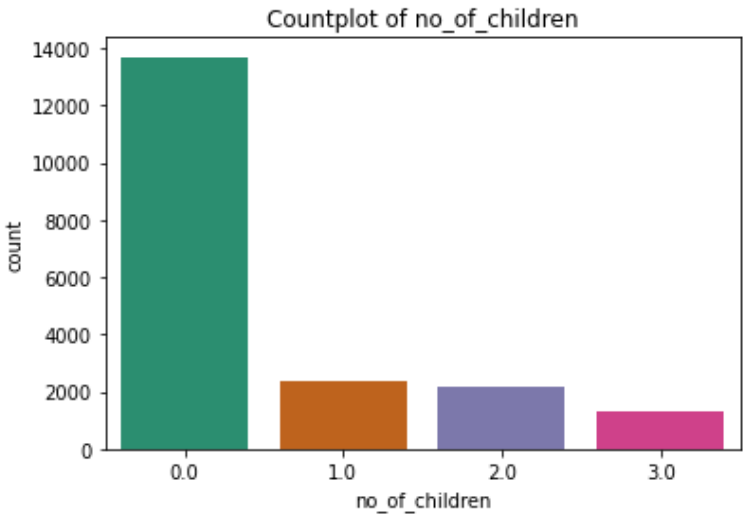




```
#_____________31 no_of_adults, ordered
df_vac.no_of_adults.isnull().sum() #No Missing values
df_vac.no_of_adults.value_counts()
'''
1.0    11006
0.0     5683
2.0     2124
3.0      829'''

# Bar Plot
sns.countplot(x = 'no_of_adults', data = df_vac , palette = 'Set2')
plt.title('Countplot of no_of_adults')

#Hypothesis Testing
import statsmodels.api as sm
from statsmodels.formula.api import ols
mod = ols('no_of_adults ~ h1n1_vaccine', data = df_vac).fit()
aov_table = sm.stats.anova_lm(mod)
print(aov_table)
#0.55 ie p_value is >0.05; Ho accepted; Bad Predictor
```



```python
#_______________ 32 no_of_children , ordered
df_vac.no_of_children.isnull().sum() #No Missing values
df_vac.no_of_children.value_counts()
'''
0.0    13697
1.0     2402
2.0     2207
3.0     1336'''
# Bar Plot
sns.countplot(x = 'no_of_children', data = df_vac , palette = 'Dark2')
plt.title('Countplot of no_of_children')
#Hypothesis Testing
import statsmodels.api as sm
from statsmodels.formula.api import ols
mod = ols('no_of_children ~ h1n1_vaccine', data = df_vac).fit()
aov_table = sm.stats.anova_lm(mod)
print(aov_table)
#0.63 ie p_value is >0.05; Ho accepted; Bad Predictor
```



We are almost near to our final data!

```
#+++++++++++++++++++++++
df_vac.info()
'''
lets delete
index 19, sick_from_seas_vacc
index 28, census_msa
index 29, no_of_adults
index 30, no_of_children

AND SAVE NEW DATA AS hn and export to wd and
THEN START A NEW SCRIPT
'''
hn = df_vac.drop(['sick_from_seas_vacc','census_msa','no_of_adults','no_of_children'], axis = 1)
hn.info() # 19642, 28 columns

hn.to_csv('hn.csv')
```

```
#_______lets create dummy variables for 'race'

df2 = pd.get_dummies(hn.race, drop_first = True, prefix = 'race')

hnd = pd.concat([hn, df2], axis = 1)

# we must remove the original col 'race'

hnc = hnd.drop(['race'], axis = 1)
hnc.info() #19642, 30 columns

hnc.to_csv('hnc.csv')
```

hnc - Excel

I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE
reduced_c	avoid_tou	dr_recc_h	dr_recc_se	chronic_m	cont_child	is_health_	is_h1n1_va	is_h1n1_ri	sick_from_	is_seas_va	is_seas_ris	age_brack	qualificatio	sex	income_le	marital_st	housing_st	employme	h1n1_vacc	race_1	race_2	race_3
1	1	0	0	0	0	0	3	1	2	2	1	4	1	0	1	1	0	2	0	0	0	1
1	1	0	0	0	0	0	5	4	4	4	2	2	2	1	1	1	1	3	0	0	0	1
0	0	0	1	1	0	0	3	3	5	5	4	5	2	0	1	1	1	2	0	0	0	1
0	1	0	0	0	0	0	3	3	2	3	1	3	3	0	2	0	0	3	0	0	0	1
0	1	0	1	0	0	0	5	2	1	5	4	5	2	1	2	0	0	3	0	0	0	1
0	0	0	0	0	0	0	4	1	1	4	2	4	1	1	2	1	0	3	0	0	0	1
0	1	1	0	1	0	0	5	2	1	4	2	3	3	0	2	0	0	3	1	0	0	1
1	1	0	0	0	0	0	4	1	1	4	2	3	4	1	3	0	0	3	0	0	0	1
0	1	0	0	1	0	0	4	2	2	4	2	4	2	1	2	1	0	2	0	0	0	1
0	0	0	0	1	1	0	4	1	2	5	4	3	2	1	2	0	1	3	1	0	0	1
0	0	0	0	0	0	0	3	2	2	4	2	4	4	1	3	0	0	3	1	0	0	1
0	1	0	1	0	0	0	3	2	1	5	4	5	4	1	2	0	0	2	0	0	0	1
0	1	0	0	1	1	0	3	1	4	4	2	2	3	1	3	0	0	3	0	0	0	1
1	1	0	0	0	0	0	5	4	2	4	4	4	2	1	2	0	0	2	0	0	0	1
0	0	0	1	0	0	0	4	2	2	2	1	2	4	0	3	0	0	3	0	0	0	1
0	1	1	1	0	0	0	2	2	4	4	2	2	3	0	2	1	0	3	0	0	0	1
0	1	1	1	0	0	0	5	2	2	5	4	5	4	1	3	0	0	3	0	0	0	1
1	1	0	0	0	0	0	4	2	1	5	2	4	3	0	2	0	0	2	0	0	0	0
1	1	1	1	0	0	0	4	2	2	4	2	4	4	0	2	1	1	2	0	0	0	0
0	1	1	0	0	0	0	3	3	1	3	3	4	3	0	3	1	0	3	0	0	0	1
0	1	1	1	0	0	0	4	2	2	4	1	3	4	0	3	0	0	3	0	0	0	1
1	1	0	0	0	0	0	5	5	4	4	4	1	1	0	1	1	1	2	0	0	0	0
0	1	0	0	0	0	0	3	2	2	2	4	3	3	0	2	0	1	3	0	0	0	1
1	1	0	0	0	0	0	4	2	2	2	2	5	3	0	2	0	0	2	0	0	0	1
0	0	0	0	0	0	0	1	1	1	2	1	4	2	1	2	0	0	2	0	0	0	1
1	1	1	1	0	0	0	2	1	2	4	2	2	4	0	2	1	0	3	0	0	0	1
0	1	0	0	0	0	0	4	2	2	4	2	2	3	1	2	0	0	1	0	0	0	0
0	0	1	1	0	0	0	5	4	4	5	2	5	2	0	2	1	0	2	1	0	0	1

hnc

Ready Accessibility: Unavailable

Part 1 is Done! Congratulations!!

Lets build model

Libraries

```
# Jesus is my Saviour!
import os
os.chdir('C:\\Users\\Dr Vinod\\Desktop\\WD_python')
import pandas as pd
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import statsmodels.api as sm
from statsmodels.formula.api import ols
from scipy.stats import chi2_contingency
from sklearn.preprocessing import LabelEncoder
from statsmodels.stats.outliers_influence import variance_inflation_factor
from sklearn.linear_model import LogisticRegression
from sklearn import metrics
from sklearn.metrics import classification_report, confusion_matrix
from sklearn.metrics import classification_report
from sklearn.metrics import roc_curve, auc, roc_auc_score
from sklearn.utils import resample
```

```
In [2]: df = pd.read_csv('hnc.csv') #19642; 31 , 1st is unique id

In [3]: df.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 19642 entries, 0 to 19641
Data columns (total 31 columns):
 #   Column                     Non-Null Count  Dtype
---  ------                     --------------  -----
 0   Unnamed: 0                 19642 non-null  int64
 1   h1n1_worry                 19642 non-null  float64
 2   h1n1_awareness             19642 non-null  float64
 3   antiviral_medication       19642 non-null  float64
 4   contact_avoidance          19642 non-null  float64
 5   bought_face_mask           19642 non-null  float64
 6   wash_hands_frequently      19642 non-null  float64
 7   avoid_large_gatherings     19642 non-null  float64
 8   reduced_outside_home_cont  19642 non-null  float64
 9   avoid_touch_face           19642 non-null  float64
 10  dr_recc_h1n1_vacc          19642 non-null  float64
 11  dr_recc_seasonal_vacc      19642 non-null  float64
 12  chronic_medic_condition    19642 non-null  float64
 13  cont_child_undr_6_mnths    19642 non-null  float64
 14  is_health_worker           19642 non-null  float64
 15  is_h1n1_vacc_effective     19642 non-null  float64
 16  is_h1n1_risky              19642 non-null  float64
 17  sick_from_h1n1_vacc        19642 non-null  float64
 18  is_seas_vacc_effective     19642 non-null  float64
 19  is_seas_risky              19642 non-null  float64
 20  age_bracket                19642 non-null  int64
 21  qualification              19642 non-null  int64
 22  sex                        19642 non-null  int64
 23  income_level               19642 non-null  int64
 24  marital_status             19642 non-null  int64
 25  housing_status             19642 non-null  int64
 26  employment                 19642 non-null  int64
 27  h1n1_vaccine               19642 non-null  int64
 28  race_1                     19642 non-null  int64
 29  race_2                     19642 non-null  int64
 30  race_3                     19642 non-null  int64
dtypes: float64(19), int64(12)
memory usage: 4.6 MB
```

```python
#_______________VIF
from statsmodels.stats.outliers_influence import variance_inflation_factor

# first put your predictors in x
x = df.iloc[:, [1,2,15,16,17,18,19,20,21,23,26]] # x is a data frame
# VIF dataframe
vif_data = pd.DataFrame()
vif_data["feature"] = x.columns

# calculating VIF for each feature
vif_data["VIF"] = [variance_inflation_factor(x.values, i)
                          for i in range(len(x.columns))]

print(vif_data) # two columns, feature & VIF will appear
'''
 feature        VIF
0              h1n1_worry   5.759713
1          h1n1_awareness   6.628330
2   is_h1n1_vacc_effective  21.390106
3           is_h1n1_risky   7.203521
4      sick_from_h1n1_vacc   4.689096
5   is_seas_vacc_effective  20.908152
6           is_seas_risky   8.017402
7             age_bracket   5.406338
8           qualification  13.411080
9            income_level  16.792285
10             employment  15.695942
'''
```

Drop vif>10 and ‘Unnamed: 0’

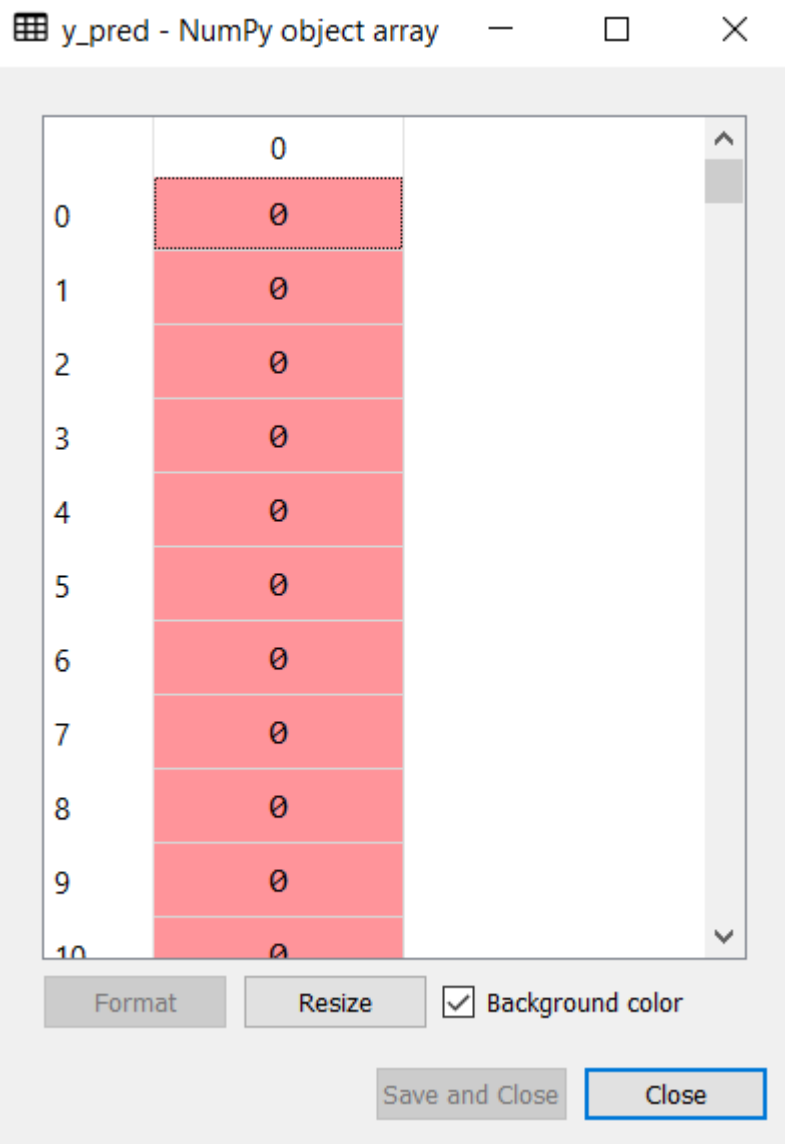
```
# drop VIF> 10
df = df.drop(['is_h1n1_vacc_effective', 'is_seas_vacc_effective',
              'qualification', 'employment'], axis = 1)
df.info() # 19642, 27 [with 1st as Unnamed: 0, lets remove this]
df = df.drop(['Unnamed: 0'], axis = 1)
df.info() # 19642, 26

# X and y
X = df.loc[:, df.columns != 'h1n1_vaccine']
y = df.loc[:, df.columns == 'h1n1_vaccine']
```

Model

```
from sklearn.linear_model import LogisticRegression
model1 = LogisticRegression(solver='liblinear', random_state=0)
model1.fit(X, y)
model1.intercept_
model1.coef_
```

```
In [26]: model1.intercept_
Out[26]: array([-4.77922475])

In [27]: model1.coef_
Out[27]:
array([[-0.04498622,  0.23585606,  0.08002789, -0.02169607,  0.11127946,
         0.06433461, -0.18866288, -0.09143327,  0.0279202 ,  2.01272438,
        -0.55614951,  0.13015874,  0.23410973,  0.86014732,  0.45516232,
        -0.06153378,  0.21774852,  0.15974545,  0.20150469,  0.09885106,
        -0.12242907, -0.01306603,  0.13690518,  0.37603554,  0.35276398]])
```

```python
#Predictions
y_pred = model1.predict(X)

#Confusion matrix
from sklearn import metrics
cm = metrics.confusion_matrix(y, y_pred)
print(cm)
'''
[[14200   928]
 [ 2608  1906]]
'''
```



```python
#Predictions
y_pred = model1.predict(X)

#Confusion matrix
from sklearn import metrics
cm = metrics.confusion_matrix(y, y_pred)
print(cm)
'''
[[14200   928]
 [ 2608  1906]]
'''
```

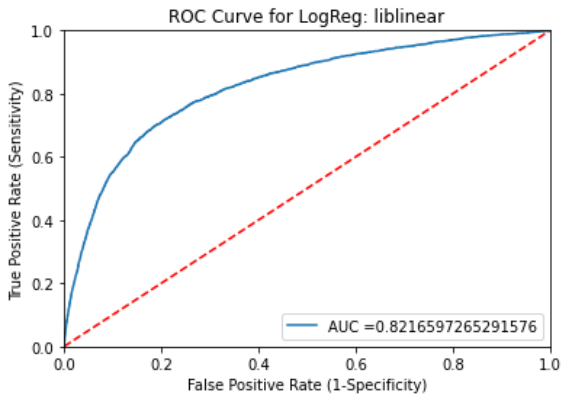
```python
#Accuracy Score - correct predictions / total number of data points
model1.score(X,y) #.0.82
(14200+1906)/(14200+928+2608+1906) # 0.82
```

```
In [32]: model1.score(X,y) #.0.82
Out[32]: 0.8199775990225028

In [33]: (14200+1906)/(14200+928+2608+1906) # 0.82
Out[33]: 0.8199775990225028
```

```python
#Classification report
from sklearn.metrics import classification_report
print(classification_report(y, y_pred))
```

```
In [34]: from sklearn.metrics import classification_report

In [35]: print(classification_report(y, y_pred))
              precision    recall  f1-score   support

           0       0.84      0.94      0.89     15128
           1       0.67      0.42      0.52      4514

    accuracy                           0.82     19642
   macro avg       0.76      0.68      0.70     19642
weighted avg       0.81      0.82      0.80     19642
```

```python
#ROC Curve - Receiver Operating Characteristic curve
#tpr = True Positive Rate
#fpr = False Positive Rate
from sklearn.metrics import roc_curve, auc, roc_auc_score
y_pred_prob = model1.predict_proba(X)
fpr, tpr, thresholds =roc_curve(df["h1n1_vaccine"], y_pred_prob[:,1])
roc_auc = auc(fpr, tpr) #Area under Curve 0.82
print(roc_auc)

#ROC Curve
plt.title('ROC Curve for LogReg: liblinear')
plt.xlabel('False Positive Rate (1-Specificity)')
plt.ylabel('True Positive Rate (Sensitivity)')
plt.plot([0, 1], [0, 1],'r--')
plt.xlim([0, 1])
plt.ylim([0, 1])
plt.plot(fpr, tpr, label = 'AUC =' +str(roc_auc))
plt.legend(loc=4) #Location of label
plt.show()
```



y_pred_prob - NumPy object ...

	0	1
0	0.966744	0.0332555
1	0.834273	0.165727
2	0.892517	0.107483
3	0.905644	0.0943557
4	0.869147	0.130853
5	0.935931	0.0640693
6	0.573655	0.426345
7	0.913557	0.0864425
8	0.89974	0.10026
9	0.880152	0.119848
10	0.831641	0.168359

Format Resize Background color

Save and Close Close

SMOTE

```
#_____________________SMOTE

novac = df[df.h1n1_vaccine == 0] #15128,26
vac = df[df.h1n1_vaccine == 1] #4514, 26
#_____________________________________ oversample minority_with replacement
from sklearn.utils import resample
vac_oversample = resample(vac,
                          replace=True, # sample with replacement
                          n_samples=len(novac), # match number in majority class
                          random_state=27) # reproducible results

# combine majority and oversampled minority

dfsmote = pd.concat([novac, vac_oversample])
dfsmote.h1n1_vaccine.value_counts()
'''
1    15128
0    15128
'''
```

```
#_________________lets re do log reg
# X and y
X2 = dfsmote.loc[:, dfsmote.columns != 'h1n1_vaccine']
y2 = dfsmote.loc[:, dfsmote.columns == 'h1n1_vaccine']
y2.value_counts() # both 15,128

# solver = liblinear
'''
liblinear [library for linear classification]: good for small data
newton-cg [newton conjugate]: can be used in this case
lbfgs[limited memory BFGS]: for multiclass problems
BFGS:Broyden-Fletcher-Goldfarb-Shanno algorithm
sag [Stochastic Average Gradient Descent]: good for large data sets
saga: a little variant of sag
'''
from sklearn.linear_model import LogisticRegression
model2 = LogisticRegression(solver='liblinear', random_state=0)
model2.fit(X2, y2)
model2.intercept_
model2.coef_
```

Coefficients

```
In [54]: model2.intercept_
Out[54]: array([-3.55103733])

In [55]: model2.coef_
Out[55]:
array([[-0.01118147,  0.2210547 ,  0.1371775 , -0.00679728,  0.14257456,
         0.09421023, -0.2000553 , -0.11595893, -0.01936164,  2.10424968,
        -0.63670885,  0.14104786,  0.19295641,  0.93630368,  0.43867647,
        -0.05666603,  0.22833308,  0.1551444 ,  0.23000128,  0.10607717,
        -0.11945158,  0.07376133,  0.04801412,  0.26810969,  0.24540742]])
```

With and Without SMOTE

```
#Confusion matrix
from sklearn import metrics
cm2 = metrics.confusion_matrix(y2, y_pred2)
print(cm2)
'''
WITH SMOTE=
[[11848  3280]
 [ 4154 10974]]

WITHOUT SMOTE =
[[14200   928]
 [ 2608  1906]]
'''
```

```
#Accuracy Score - correct predictions / total number of data points
model2.score(X2,y2) #WITH SMOTE = 0.75; without = #.0.82
(11848+10974)/(11848+3200+4154+10974) # 0.75

#Classification report
from sklearn.metrics import classification_report
print(classification_report(y2, y_pred2))
```

```
In [61]: from sklearn.metrics import classification_report

In [62]: print(classification_report(y2, y_pred2))
              precision    recall  f1-score   support

           0       0.74      0.78      0.76     15128
           1       0.77      0.73      0.75     15128

    accuracy                           0.75     30256
   macro avg       0.76      0.75      0.75     30256
weighted avg       0.76      0.75      0.75     30256
```

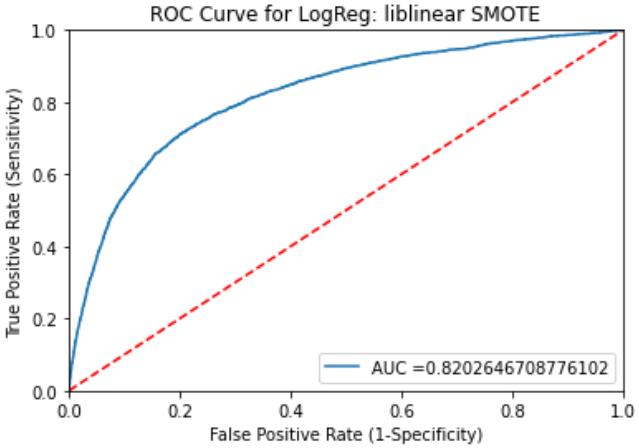
AUC

```
#ROC Curve - Receiver Operating Characteristic curve
#tpr = True Positive Rate
#fpr = False Positive Rate
from sklearn.metrics import roc_curve, auc, roc_auc_score
y_pred_prob2 = model2.predict_proba(X2)
fpr2, tpr2, thresholds2 =roc_curve(dfsmote["h1n1_vaccine"], y_pred_prob2[:,1])
roc_auc2 = auc(fpr2, tpr2) #Area under Curve 0.82
print(roc_auc2) # 0.82, same as without smote
```

```
In [63]: from sklearn.metrics import roc_curve, auc, roc_auc_score
    ...: y_pred_prob2 = model2.predict_proba(X2)
    ...: fpr2, tpr2, thresholds2 =roc_curve(dfsmote["h1n1_vaccine"], y_pred_prob2[:,1])
    ...: roc_auc2 = auc(fpr2, tpr2) #Area under Curve 0.82
    ...: print(roc_auc2) # 0.82, same as without smote
0.8202646708776102
```

ROC

```
#ROC Curve
plt.title('ROC Curve for LogReg: liblinear SMOTE')
plt.xlabel('False Positive Rate (1-Specificity)')
plt.ylabel('True Positive Rate (Sensitivity)')
plt.plot([0, 1], [0, 1],'r--')
plt.xlim([0, 1])
plt.ylim([0, 1])
plt.plot(fpr2, tpr2, label = 'AUC =' +str(roc_auc2))
plt.legend(loc=4) #Location of label
plt.show()
```



GLM Method

```python
# Jesus is my Saviour!
import os
os.chdir('C:\\Users\\Dr Vinod\\Desktop\\WD_python')
import pandas as pd
import pandas as pd
pd.set_option('display.max_column',None)
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import statsmodels.api as sm
from statsmodels.formula.api import ols
from scipy.stats import chi2_contingency
from sklearn.preprocessing import LabelEncoder
from statsmodels.stats.outliers_influence import variance_inflation_factor
from sklearn.linear_model import LogisticRegression
from sklearn import metrics
from sklearn.metrics import classification_report, confusion_matrix
from sklearn.metrics import classification_report
from sklearn.metrics import roc_curve, auc, roc_auc_score
from sklearn.utils import resample

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

df = pd.read_csv('hnsmote.csv') #30256; 27 , 1st is 'Unnamed: 0'
df.info()
```

GLM Method

```
#Logistic Regression model - GLM method
import statsmodels.api as sm
import statsmodels.formula.api as smf
model3 = smf.glm(formula='''h1n1_vaccine~h1n1_worry+h1n1_awareness+antiviral_medication
                +contact_avoidance+bought_face_mask+wash_hands_frequently+avoid_large_gatherings+
                reduced_outside_home_cont+avoid_touch_face+dr_recc_h1n1_vacc+dr_recc_seasonal_vacc+
                chronic_medic_condition+cont_child_undr_6_mnths+is_health_worker
                +is_h1n1_risky+sick_from_h1n1_vacc+is_seas_risky+
                age_bracket+sex+income_level+
                marital_status+housing_status
                +race_1+race_2+race_3''', data=df, family=sm.families.Binomial())
result = model3.fit()
print(result.summary())
```

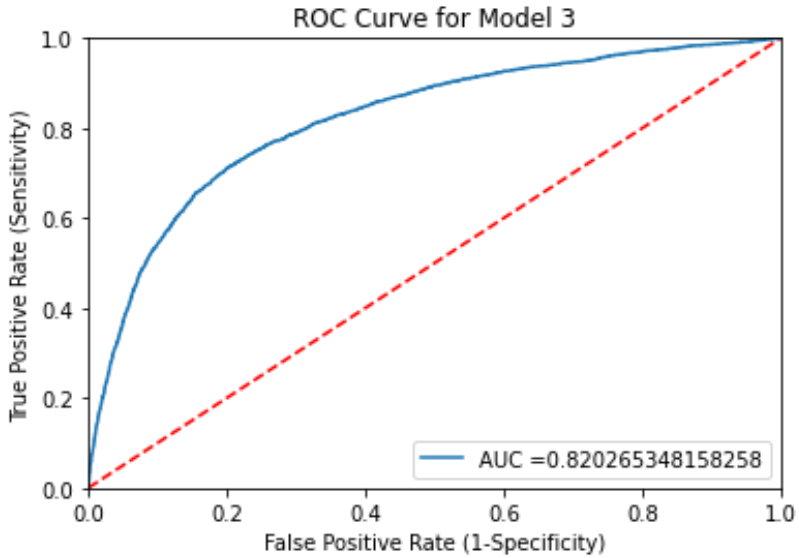
```
                 Generalized Linear Model Regression Results
==============================================================================
Dep. Variable:           h1n1_vaccine   No. Observations:                30256
Model:                            GLM   Df Residuals:                    30230
Model Family:                Binomial   Df Model:                           25
Link Function:                  logit   Scale:                          1.0000
Method:                          IRLS   Log-Likelihood:                -15780.
Date:                Wed, 14 Dec 2022   Deviance:                       31560.
Time:                        06:46:37   Pearson chi2:                 3.14e+04
No. Iterations:                     5
Covariance Type:            nonrobust
==============================================================================================
                                 coef    std err          z      P>|z|      [0.025      0.975]
----------------------------------------------------------------------------------------------
Intercept                     -3.5978      0.110    -32.588      0.000      -3.814      -3.381
h1n1_worry                    -0.0105      0.019     -0.564      0.573      -0.047       0.026
h1n1_awareness                 0.2226      0.025      8.963      0.000       0.174       0.271
antiviral_medication           0.1396      0.065      2.159      0.031       0.013       0.266
contact_avoidance             -0.0059      0.035     -0.166      0.868      -0.075       0.063
bought_face_mask               0.1425      0.056      2.559      0.011       0.033       0.252
wash_hands_frequently          0.0976      0.044      2.242      0.025       0.012       0.183
avoid_large_gatherings        -0.2005      0.037     -5.425      0.000      -0.273      -0.128
reduced_outside_home_cont     -0.1155      0.038     -3.073      0.002      -0.189      -0.042
avoid_touch_face              -0.0185      0.034     -0.543      0.587      -0.085       0.048
```

	coef	std err	z	P>|z|	[0.025	0.975]
dr_recc_h1n1_vacc	2.1099	0.043	49.157	0.000	2.026	2.194
dr_recc_seasonal_vacc	-0.6408	0.041	-15.692	0.000	-0.721	-0.561
chronic_medic_condition	0.1415	0.032	4.439	0.000	0.079	0.204
cont_child_undr_6_mnths	0.1947	0.050	3.929	0.000	0.098	0.292
is_health_worker	0.9385	0.041	22.659	0.000	0.857	1.020
is_h1n1_risky	0.4393	0.013	33.287	0.000	0.413	0.465
sick_from_h1n1_vacc	-0.0560	0.011	-4.968	0.000	-0.078	-0.034
is_seas_risky	0.2288	0.012	18.685	0.000	0.205	0.253
age_bracket	0.1569	0.011	14.494	0.000	0.136	0.178
sex	0.2326	0.029	7.907	0.000	0.175	0.290
income_level	0.1116	0.026	4.310	0.000	0.061	0.162
marital_status	-0.1159	0.030	-3.809	0.000	-0.176	-0.056
housing_status	0.0783	0.037	2.102	0.036	0.005	0.151
race_1	0.0614	0.078	0.785	0.433	-0.092	0.215
race_2	0.2819	0.081	3.502	0.000	0.124	0.440
race_3	0.2583	0.059	4.367	0.000	0.142	0.374

```
# following 4 had high p_value
'''
h1n1_worry, contact_avoidance,
avoid_touch_face, race_1
IN OUR NEXT MODEL, WE WILL REMOVE THESE 4
'''
predictions3 = result.predict()
predictions_nominal3 = [0 if x < 0.5 else 1 for x in predictions3]
predictions_nominal3
#Confusion matrix
from sklearn.metrics import confusion_matrix, classification_report
print(confusion_matrix(df["h1n1_vaccine"], predictions_nominal3))

'''
glm with 4 high p values; Model 3
[[11852  3276]
 [ 4150 10978]]

Solver-liblinear, hnsmote
WITH SMOTE=
[[11848  3280]
 [ 4154 10974]]

WITHOUT SMOTE =
[[14200   928]
 [ 2608  1906]]
'''
```

Almost same

```python
#ROC & AUC
from sklearn.metrics import roc_curve, auc, roc_auc_score
fpr3, tpr3, thresholds3 =roc_curve(df["h1n1_vaccine"], predictions3)
roc_auc3 = auc(fpr3, tpr3) #Area under Curve 0.82
print(roc_auc3)

#ROC Curve
plt.title('ROC Curve for Model 3')
plt.xlabel('False Positive Rate (1-Specificity)')
plt.ylabel('True Positive Rate (Sensitivity)')
plt.plot([0, 1], [0, 1],'r--')
plt.xlim([0, 1])
plt.ylim([0, 1])
plt.plot(fpr3, tpr3, label = 'AUC =' +str(roc_auc3))
plt.legend(loc=4)
plt.show()
```



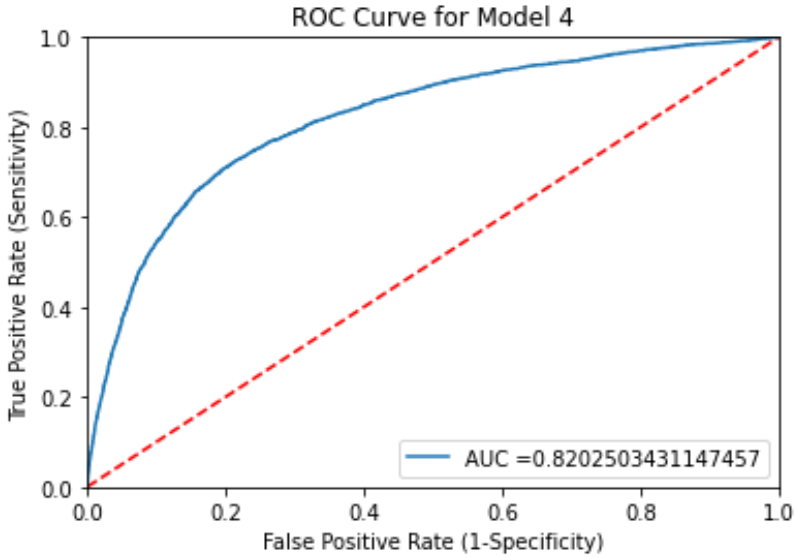
```
#Classification Report
print(classification_report(df["h1n1_vaccine"], predictions_nominal3, digits = 3))

'''
              precision    recall  f1-score   support

           0      0.741     0.783     0.761     15128
           1      0.770     0.726     0.747     15128

    accuracy                          0.755     30256
   macro avg      0.755     0.755     0.754     30256
weighted avg      0.755     0.755     0.754     30256


'''
```

```
######################################## Model 4
# following 4 had high p_value, removed
'''
h1n1_worry, contact_avoidance,
avoid_touch_face, race_1
'''
import statsmodels.api as sm
import statsmodels.formula.api as smf
model4 = smf.glm(formula='''h1n1_vaccine~h1n1_awareness+antiviral_medication
                +bought_face_mask+wash_hands_frequently+avoid_large_gatherings+
                reduced_outside_home_cont+dr_recc_h1n1_vacc+dr_recc_seasonal_vacc+
                chronic_medic_condition+cont_child_undr_6_mnths+is_health_worker
                +is_h1n1_risky+sick_from_h1n1_vacc+is_seas_risky+
                age_bracket+sex+income_level+
                marital_status+housing_status
                +race_2+race_3''', data=df, family=sm.families.Binomial())
result4 = model4.fit()
print(result4.summary())
```

	coef	std err	z	P>|z|	[0.025	0.975]
Intercept	-3.5773	0.101	-35.424	0.000	-3.775	-3.379
h1n1_awareness	0.2215	0.025	8.953	0.000	0.173	0.270
antiviral_medication	0.1397	0.065	2.162	0.031	0.013	0.266
bought_face_mask	0.1414	0.056	2.547	0.011	0.033	0.250
wash_hands_frequently	0.0849	0.041	2.089	0.037	0.005	0.165
avoid_large_gatherings	-0.2041	0.037	-5.563	0.000	-0.276	-0.132
reduced_outside_home_cont	-0.1205	0.037	-3.244	0.001	-0.193	-0.048
dr_recc_h1n1_vacc	2.1096	0.043	49.161	0.000	2.026	2.194
dr_recc_seasonal_vacc	-0.6419	0.041	-15.721	0.000	-0.722	-0.562
chronic_medic_condition	0.1411	0.032	4.430	0.000	0.079	0.204
cont_child_undr_6_mnths	0.1941	0.050	3.919	0.000	0.097	0.291
is_health_worker	0.9375	0.041	22.714	0.000	0.857	1.018
is_h1n1_risky	0.4379	0.013	33.640	0.000	0.412	0.463
sick_from_h1n1_vacc	-0.0575	0.011	-5.214	0.000	-0.079	-0.036
is_seas_risky	0.2284	0.012	18.772	0.000	0.205	0.252
age_bracket	0.1558	0.011	14.490	0.000	0.135	0.177
sex	0.2362	0.029	8.093	0.000	0.179	0.293
income_level	0.1112	0.026	4.308	0.000	0.061	0.162
marital_status	-0.1171	0.030	-3.876	0.000	-0.176	-0.058
housing_status	0.0797	0.037	2.140	0.032	0.007	0.153
race_2	0.2518	0.070	3.575	0.000	0.114	0.390
race_3	0.2305	0.044	5.189	0.000	0.143	0.318

```
predictions4 = result4.predict()
predictions_nominal4 = [0 if x < 0.5 else 1 for x in predictions4]
predictions_nominal4
#Confusion matrix
from sklearn.metrics import confusion_matrix, classification_report
print(confusion_matrix(df["h1n1_vaccine"], predictions_nominal4))

'''
Model 4
[[11864  3264]
 [ 4141 10987]]
SLIGHT IMPROVEMENT !
glm with 4 high p values; Model 3
[[11852  3276]
 [ 4150 10978]]

Solver-liblinear, hnsmote
WITH SMOTE=
[[11848  3280]
 [ 4154 10974]]

WITHOUT SMOTE =
[[14200   928]
 [ 2608  1906]]

'''
```

```python
#ROC & AUC
from sklearn.metrics import roc_curve, auc, roc_auc_score
fpr4, tpr4, thresholds4 =roc_curve(df["h1n1_vaccine"], predictions4)
roc_auc4 = auc(fpr4, tpr4) #Area under Curve 0.82
print(roc_auc4)

#ROC Curve
plt.title('ROC Curve for Model 4')
plt.xlabel('False Positive Rate (1-Specificity)')
plt.ylabel('True Positive Rate (Sensitivity)')
plt.plot([0, 1], [0, 1],'r--')
plt.xlim([0, 1])
plt.ylim([0, 1])
plt.plot(fpr4, tpr4, label = 'AUC =' +str(roc_auc4))
plt.legend(loc=4)
plt.show()
```



```
#Classification Report
print(classification_report(df["h1n1_vaccine"], predictions_nominal4, digits = 3))

'''
              precision    recall  f1-score   support

           0      0.741     0.784     0.762     15128
           1      0.771     0.726     0.748     15128

    accuracy                          0.755     30256
   macro avg      0.756     0.755     0.755     30256
weighted avg      0.756     0.755     0.755     30256


'''
```

Multi Class Logistic Regression

```python
# Jesus is my saviour!

import os
os.chdir('C:\\Users\\Dr Vinod\\Desktop\\WD_python')
import pandas as pd
pd.set_option('display.max_column',None)
#import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
#import statsmodels.api as sm
#import statsmodels.formula.api as smf
#from scipy.stats import chi2_contingency
#from sklearn.preprocessing import LabelEncoder
#from statsmodels.stats.outliers_influence import variance_inflation_factor
from sklearn.linear_model import LogisticRegression
from sklearn import metrics
from sklearn.metrics import classification_report, confusion_matrix
#from sklearn.metrics import roc_curve, auc, roc_auc_score
#from sklearn.utils import resample

# we need below also
from sklearn.preprocessing import MinMaxScaler
```

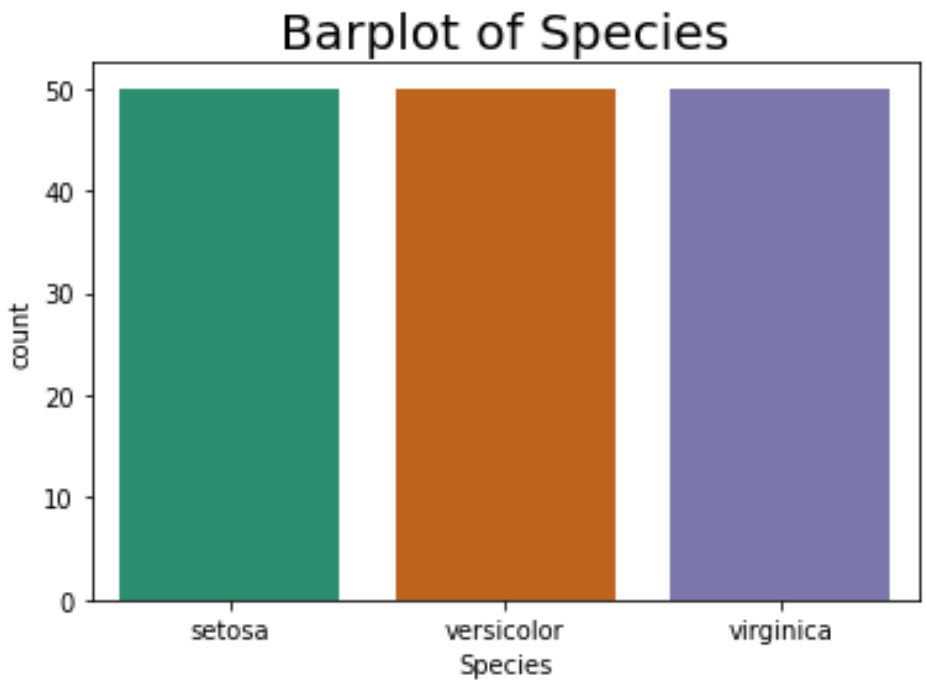
```python
df = pd.read_csv('iris.csv') #150; 5
df.info()
'''
 #   Column        Non-Null Count  Dtype
---  ------        --------------  -----
 0   Sepal.Length  150 non-null    float64
 1   Sepal.Width   150 non-null    float64
 2   Petal.Length  150 non-null    float64
 3   Petal.Width   150 non-null    float64
 4   Species       150 non-null    object
'''
df.Species.value_counts()
'''
virginica     50
setosa        50
versicolor    50

'''
```

df - DataFrame

Index	epal.Lengt	epal.Widt	etal.Lengt	etal.Widtl	Species
0	5.10	3.50	1.40	0.20	setosa
1	4.90	3.00	1.40	0.20	setosa
2	4.70	3.20	1.30	0.20	setosa
3	4.60	3.10	1.50	0.20	setosa
4	5.00	3.60	1.40	0.20	setosa
5	5.40	3.90	1.70	0.40	setosa
6	4.60	3.40	1.40	0.30	setosa
7	5.00	3.40	1.50	0.20	setosa
8	4.40	2.90	1.40	0.20	setosa
9	4.90	3.10	1.50	0.10	setosa
10	5.40	3.70	1.50	0.20	setosa
11	4.80	3.40	1.60	0.20	setosa

Format | Resize | Background color | Column min/max | Save and Close | Close

```python
# Bar Plot of Species
sns.countplot(x = 'Species', data = df, palette='Dark2')
plt.title('Barplot of Species', fontsize = 20)
```



```
# as Species levels are in text, we need to
# put nos, see a new way! other than LabelEncoder!

df['target'] = df.Species.astype('category').cat.codes
df.target.value_counts()
'''
2    50; virginica
1    50; versicolar
0    50; setosa
'''
```

```
'''
virginica     50
setosa        50
versicolor    50

'''
```

Scaling

```
# predictors and target var, X and y
X = df.drop(['Species', 'target'], axis = 1)
y = df.target

from sklearn.preprocessing import MinMaxScaler
scaler = MinMaxScaler()
X = scaler.fit_transform(X)
```

X - NumPy object array

	0	1	2	3
0	0.222222	0.625	0.0677966	0.0416667
1	0.166667	0.416667	0.0677966	0.0416667
2	0.111111	0.5	0.0508475	0.0416667
3	0.0833333	0.458333	0.0847458	0.0416667
4	0.194444	0.666667	0.0677966	0.0416667
5	0.305556	0.791667	0.118644	0.125
6	0.0833333	0.583333	0.0677966	0.0833333
7	0.194444	0.583333	0.0847458	0.0416667
8	0.0277778	0.375	0.0677966	0.0416667
9	0.166667	0.458333	0.0847458	0
10	0.305556	0.708333	0.0847458	0.0416667

Format Resize Background color

Save and Close Close

One Over Rest model

```
from sklearn.preprocessing import MinMaxScaler
scaler = MinMaxScaler()
X = scaler.fit_transform(X)

df_ovr = LogisticRegression(multi_class= 'ovr')
df_ovr.fit(X,y)

print("oaa_ovr=", df_ovr.score(X,y)) # 0.89
'''
oaa_ovr= 0.8933333333333333
'''
```

```
# predictions
pred_ovr = df_ovr.predict(X)

print("ovr\n")
print(metrics.confusion_matrix(y, pred_ovr, labels = [0,1,2]))
print(metrics.classification_report(y, pred_ovr, labels = [0,1,2]))
'''
ovr

[[50  0  0]
 [ 0 37 13]
 [ 0  3 47]]
              precision    recall  f1-score   support

           0       1.00      1.00      1.00        50
           1       0.93      0.74      0.82        50
           2       0.78      0.94      0.85        50

    accuracy                           0.89       150
   macro avg       0.90      0.89      0.89       150
weighted avg       0.90      0.89      0.89       150

'''
```

Multinomial Model

```
#_____________another way! not ovr but , multinomial way!
df_mul = LogisticRegression(multi_class= 'multinomial')
df_mul.fit(X,y)

print("oaa=", df_mul.score(X,y)) # ovr =0.89, mul = 0.94
'''
oaa; ovr= 0.8933333333333333
oaa; mul = oaa= 0.94, BETTER!
'''
# predictions
pred_mul = df_mul.predict(X)

print("mul\n")
print(metrics.confusion_matrix(y, pred_mul, labels = [0,1,2]))
print(metrics.classification_report(y, pred_mul, labels = [0,1,2]))

'''
mul

[[50  0  0]
 [ 0 45  5]
 [ 0  4 46]]
              precision    recall  f1-score   support

           0       1.00      1.00      1.00        50
           1       0.92      0.90      0.91        50
           2       0.90      0.92      0.91        50

    accuracy                           0.94       150
   macro avg       0.94      0.94      0.94       150
weighted avg       0.94      0.94      0.94       150

'''
```

Multinomial is better than One Over Rest

Awesome so far!