In [1]:
```
import os
from os import listdir
from os.path import isfile, join
import struct
import random
import operator
import gzip
import pandas as pd
import numpy as np
import seaborn as sns
%matplotlib inline
import matplotlib.pyplot as plt
```

Type *Markdown* and LaTeX: α^2

In [2]:
```
mypath= r'C:\Users\dwijj\Downloads\chsi_dataset'
os.chdir(mypath)
onlyfiles = [f for f in listdir(mypath) if isfile(join(mypath, f))]
onlyfiles
```

Out[2]:
```
['CHSI DataSet.xls',
 'CSV File Index.txt',
 'DATAELEMENTDESCRIPTION.csv',
 'DEFINEDDATAVALUE.csv',
 'DEMOGRAPHICS.csv',
 'HEALTHYPEOPLE2010.csv',
 'LEADINGCAUSESOFDEATH.csv',
 'MEASURESOFBIRTHANDDEATH.csv',
 'MEASURESOFBIRTHANDDEATH.ipynb',
 'PREVENTIVESERVICESUSE.csv',
 'RELATIVEHEALTHIMPORTANCE.csv',
 'RISKFACTORSANDACCESSTOCARE.csv',
 'SUMMARYMEASURESOFHEALTH.csv',
 'VUNERABLEPOPSANDENVHEALTH.csv']
```

In [34]:
```
df_mbd = pd.read_csv('MEASURESOFBIRTHANDDEATH.csv')
df_mbd = df_mbd[['State_FIPS_Code','County_FIPS_Code','CHSI_County_Name','CHSI_St
ListofNans = [-9999,-2222,-2222.2,-2,-1111,-1,-9998.9,-1111.10000]
df_mbd=df_mbd.replace([i for i in ListofNans], np.NAN)
df_mbd.head()
```

Out[34]:

	State_FIPS_Code	County_FIPS_Code	CHSI_County_Name	CHSI_State_Abbr	CHSI_State_Name
0	1	1	Autauga	AL	Alabama
1	1	3	Baldwin	AL	Alabama
2	1	5	Barbour	AL	Alabama
3	1	7	Bibb	AL	Alabama
4	1	9	Blount	AL	Alabama

5 rows × 29 columns

Granularity: Every record in the dataframe is record of one county in the US

In [35]:
```
BirthStats = df_mbd['Total_Births'].describe()
DeathStats = df_mbd['Total_Deaths'].describe()
print("Births Across Counties Stats\n", BirthStats,"\n\n")
print("Deaths Across Counties Stats\n", DeathStats)
```

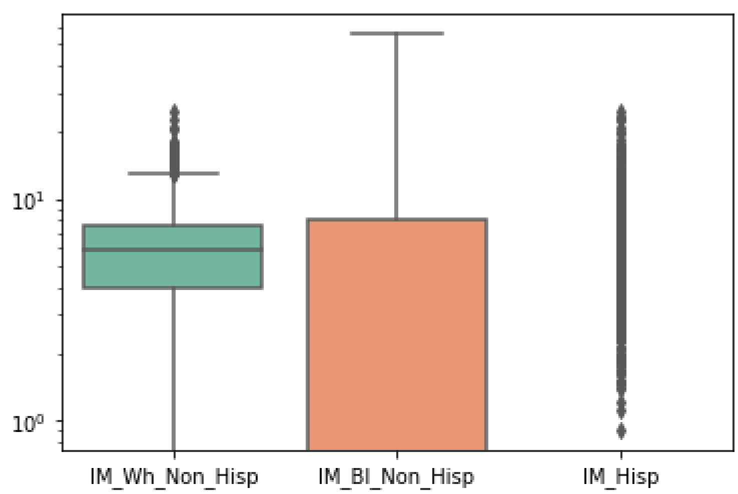
```
Births Across Counties Stats
 count      3140.000000
mean       4838.878344
std       13754.598791
min           2.000000
25%        1319.750000
50%        2283.000000
75%        3936.000000
max      457033.000000
Name: Total_Births, dtype: float64


Deaths Across Counties Stats
 count      3140.000000
mean       3107.701592
std        6432.756342
min           5.000000
25%        1164.000000
50%        1887.000000
75%        2858.250000
max      181018.000000
Name: Total_Deaths, dtype: float64
```

In [36]:
```
Races_df = df_mbd[['IM_Wh_Non_Hisp','IM_Bl_Non_Hisp','IM_Hisp']]
Races_df.rename(columns = {'IM_Wh_Non_Hisp':'White', 'IM_Bl_Non_Hisp':'Black','IM
print("Races \n\n", Races_df.describe())
```

```
Races

              White       Black    Hispanic
count  2712.000000  858.000000  618.000000
mean      6.580531   14.835548    6.377832
std       2.604574    5.790628    3.485414
min       0.000000    1.500000    0.000000
25%       5.000000   11.100000    4.100000
50%       6.300000   14.400000    5.900000
75%       7.900000   17.300000    7.775000
max      24.600000   55.600000   24.600000
```

Infant Mortality is the strongest over hispanic, then comes white, and then comes black genes

In [5]:
```
ax = sns.boxplot(data=df_mbd[['IM_Wh_Non_Hisp','IM_Bl_Non_Hisp','IM_Hisp']], pale
ax.set_yscale('log')
```



Mother with babies whose age is either under 18 or over 4o shows that both have more chances of mortality rate of their children

In [37]:
```
AgeBorn = df_mbd[['Under_18','Over_40']]
print("Age Groups \n",AgeBorn.describe())
```

```
Age Groups
          Under_18      Over_40
count  3062.000000  3011.000000
mean      4.750131     1.742976
std       2.291837     0.914043
min       0.300000     0.200000
25%       3.000000     1.100000
50%       4.400000     1.500000
75%       6.000000     2.100000
max      14.500000     9.100000
```

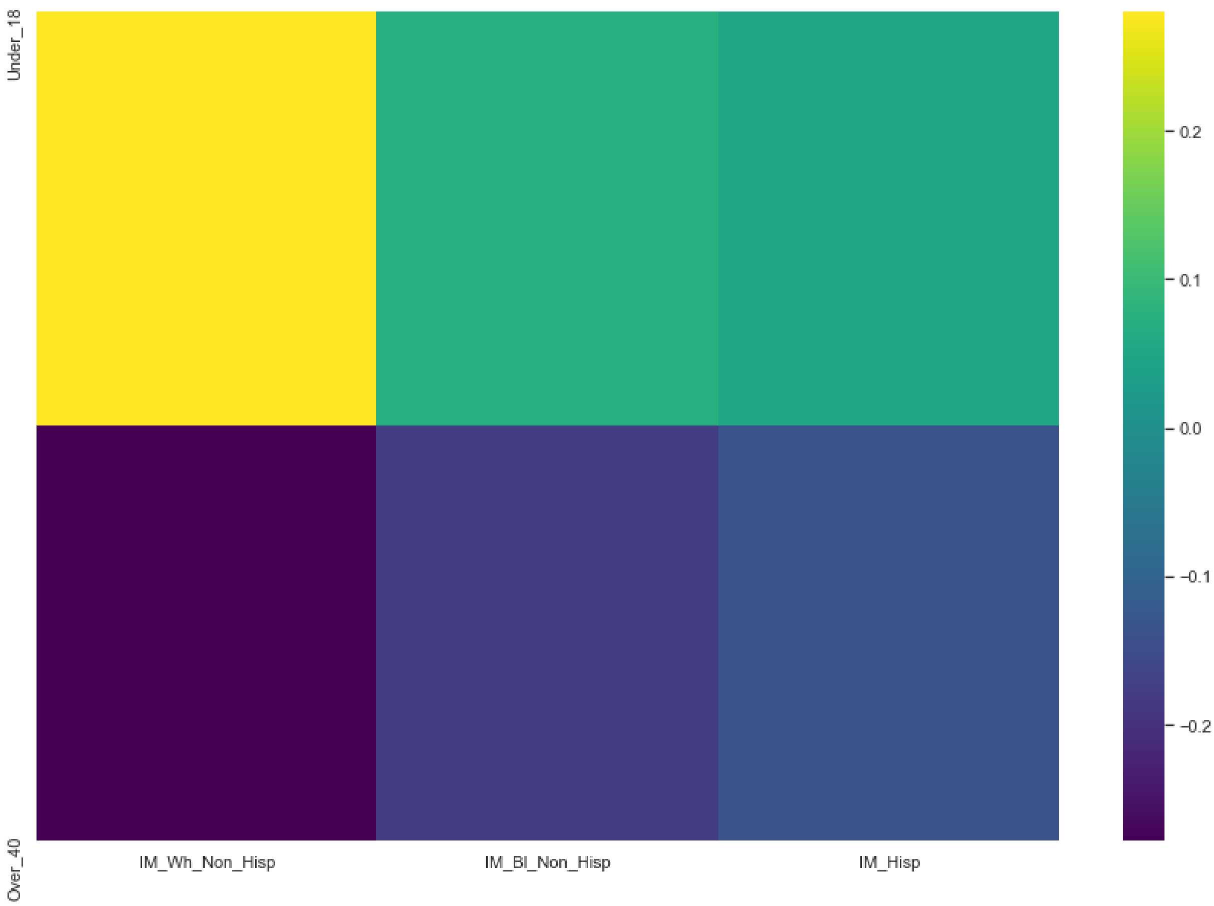
In [40]:
```
Race_Age = df_mbd[['IM_Wh_Non_Hisp','IM_Bl_Non_Hisp','IM_Hisp','Under_18','Over_4
Race_AgeCorr = pd.DataFrame(Race_Age.corr())
Race_AgeCorr = Race_AgeCorr[Race_AgeCorr.index.isin(['IM_Wh_Non_Hisp','IM_Bl_Non_
Race_AgeCorr = Race_AgeCorr[['Under_18','Over_40']]
print(Race_AgeCorr)
```

```
                Under_18   Over_40
IM_Wh_Non_Hisp  0.280604 -0.278369
IM_Bl_Non_Hisp  0.073517 -0.178707
IM_Hisp         0.051379 -0.136454
```

The table represents the correlation values among the features. We see races except white to be negatively correlated with the age groups of Under 18 and Over 40

This means that counties in which both age groups resides have less blacks and hispanics mothers getting pregnant whose age is under 18. hence they are negatively correlated to the age groups. In conclusion: white race has more chances of getting pregnant than hispanics and blacks.

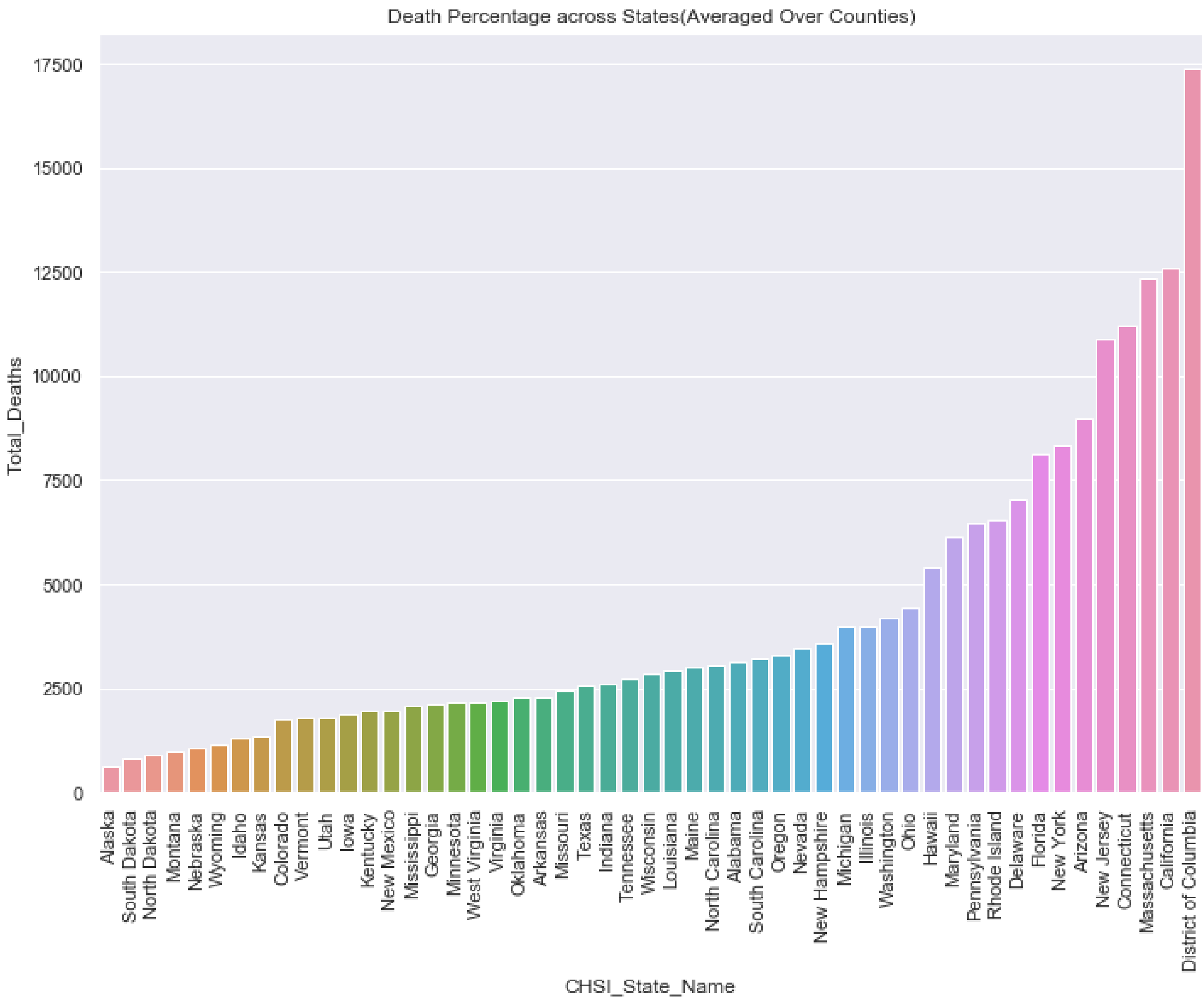
In [39]:
```
ax = sns.heatmap(Race_AgeCorr.transpose(),cmap='viridis')
```



Death Percentage in Numbers are shown below in the Graph over the Country which shows which state has more deaths

In [9]:
```
DeathDF = df_mbd[['Total_Deaths']].groupby(df_mbd['CHSI_State_Name']).mean().sort
sns.set(rc={'figure.figsize':(11.7,8.27)})
chart = sns.barplot(x=DeathDF.index, y='Total_Deaths', data=DeathDF)
plt.xticks(rotation=90)
plt.title('Death Percentage across States(Averaged Over Counties)')
```

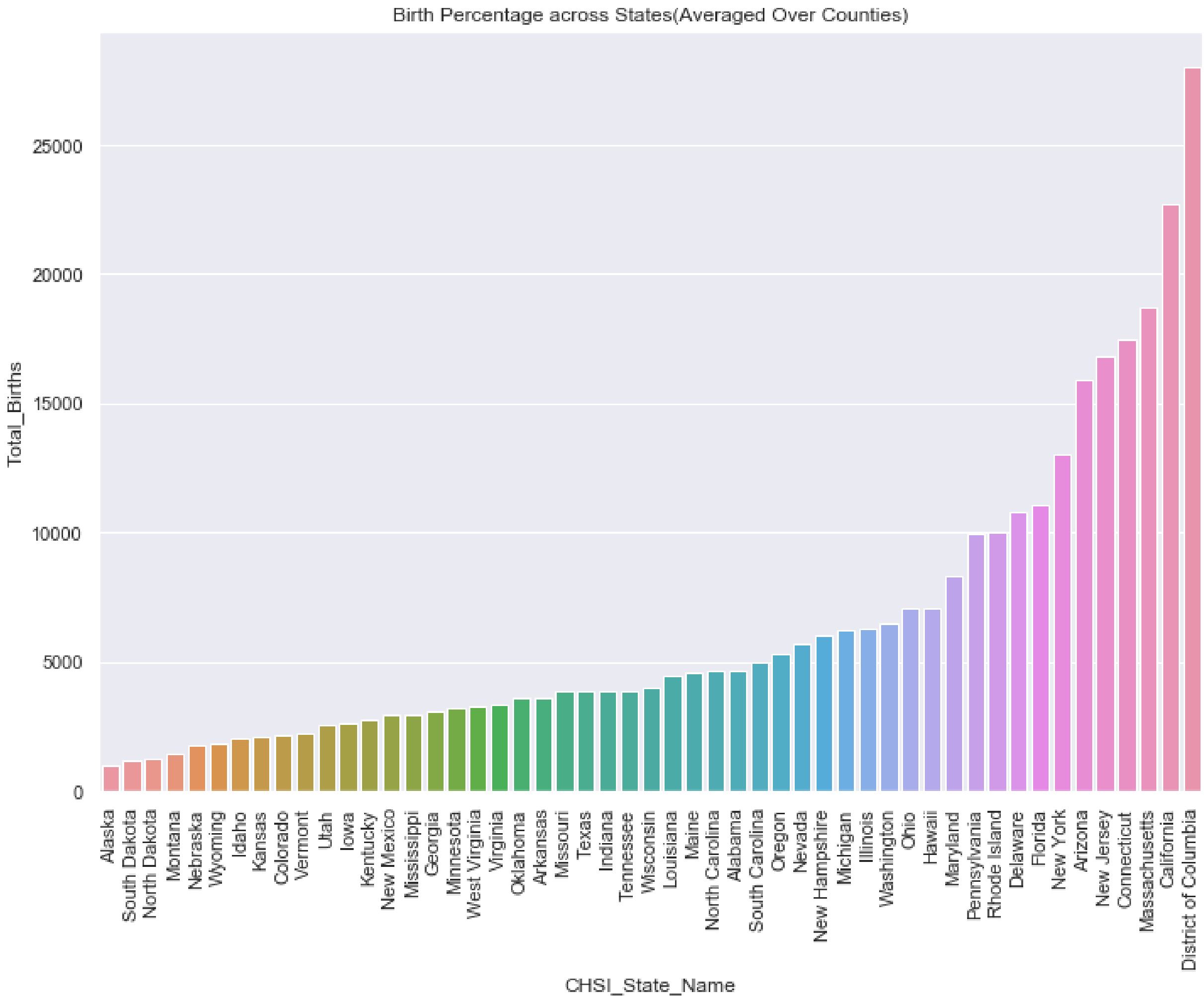
Out[9]:
```
Text(0.5, 1.0, 'Death Percentage across States(Averaged Over Counties)')
```



Birth Percentage in Numbers are shown below in the Graph over the Country which shows which state has more births

In [10]:
```
BirthDF = df_mbd[['Total_Births']].groupby(df_mbd['CHSI_State_Name']).mean().sort
sns.set(rc={'figure.figsize':(11.7,8.27)})
chart = sns.barplot(x=DeathDF.index, y='Total_Births', data=BirthDF)
plt.xticks(rotation=90)
plt.title('Birth Percentage across States(Averaged Over Counties)')
```

Out[10]:
```
Text(0.5, 1.0, 'Birth Percentage across States(Averaged Over Counties)')
```



Different Causes of Death which is related to our data

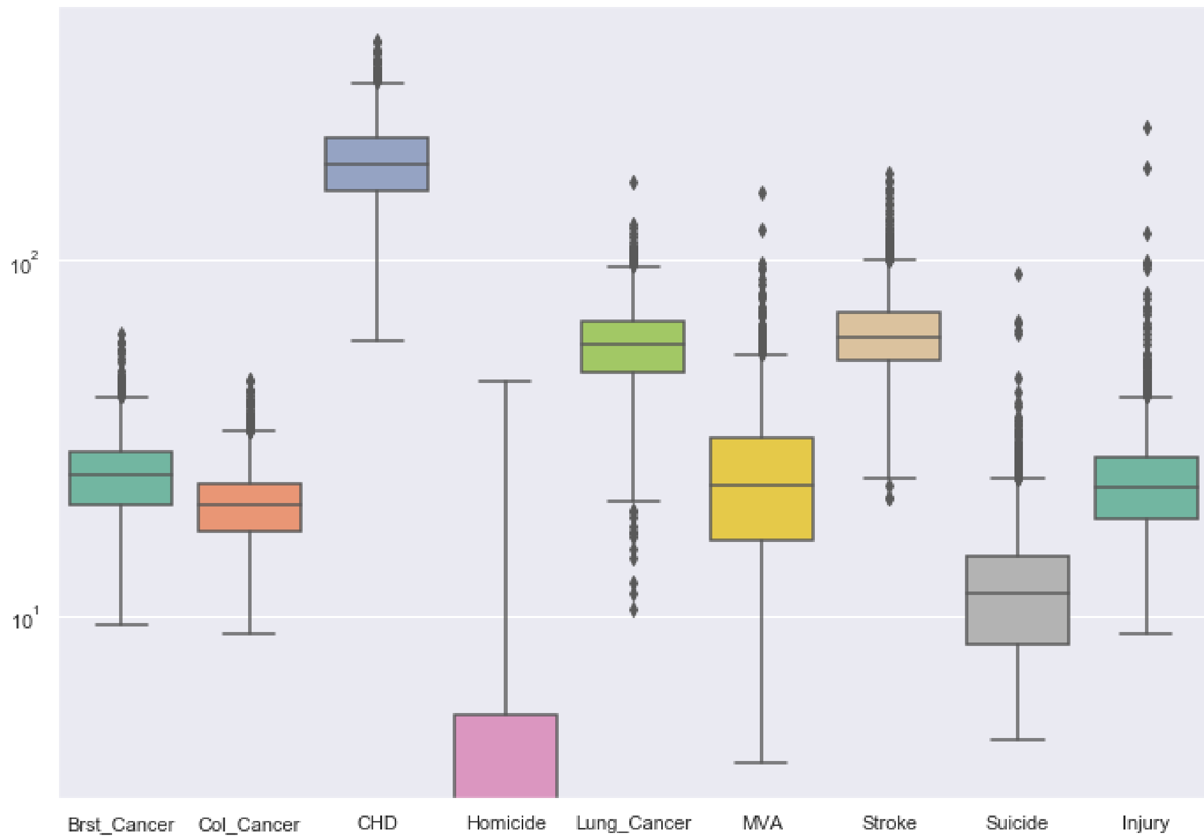
In [41]:
```
DReason_df = df_mbd[['Brst_Cancer','Col_Cancer','CHD','Homicide','Lung_Cancer','M
print("Death Types \n", DReason_df.describe())
```

```
Death Types
        Brst_Cancer   Col_Cancer          CHD     Homicide  Lung_Cancer  \
count  2750.000000  2916.000000  3122.000000  1208.000000   3063.00000
mean     26.325236    21.354870   191.066496     7.623675     58.63983
std       5.845011     4.673957    48.273544     4.842897     14.45984
min       9.500000     9.000000    59.800000     0.700000     10.50000
25%      22.600000    18.100000   156.900000     4.400000     49.30000
50%      25.800000    20.900000   187.400000     6.500000     58.40000
75%      29.500000    24.000000   221.575000     9.600000     67.85000
max      62.300000    46.300000   412.900000    46.000000    166.40000

               MVA       Stroke      Suicide       Injury
count  2960.000000  3074.000000  2618.000000  2957.000000
mean     25.879527    63.388484    13.544843    24.692459
std      11.866271    15.901792     5.328337     9.407172
min       3.900000    21.600000     4.500000     9.000000
25%      17.700000    52.800000    10.300000    19.500000
50%      24.200000    61.400000    12.700000    23.400000
75%      32.100000    71.600000    15.700000    28.200000
max     154.600000   175.800000    91.300000   236.200000
```

In [42]:
```
Death_Reason = df_mbd[['IM_Wh_Non_Hisp','IM_Bl_Non_Hisp','IM_Hisp','Brst_Cancer',
Death_ReasonCorr = pd.DataFrame(Death_Reason.corr())
Death_ReasonCorr = Death_ReasonCorr[Death_ReasonCorr.index.isin(['IM_Wh_Non_Hisp'
Death_ReasonCorr = Death_ReasonCorr[['Brst_Cancer','Col_Cancer','CHD','Homicide',
print(Death_ReasonCorr)
```

```
                Brst_Cancer  Col_Cancer       CHD  Homicide  Lung_Cancer  \
IM_Wh_Non_Hisp     0.036162    0.087951  0.193010  0.195028     0.208724
IM_Bl_Non_Hisp    -0.039616    0.014718  0.108016  0.052221     0.148257
IM_Hisp            0.122107    0.064680  0.072033  0.083570     0.071114

                     MVA    Stroke   Suicide    Injury
IM_Wh_Non_Hisp  0.246505  0.117336  0.155021  0.202378
IM_Bl_Non_Hisp  0.093742  0.053821  0.158443  0.093347
IM_Hisp         0.068416  0.071006  0.049346  0.090555
```

In [13]:
```
ax = sns.boxplot(data=df_mbd[['Brst_Cancer','Col_Cancer','CHD','Homicide','Lung_C
ax.set_yscale('log')
```



Leading Causes of Death in order is: CHD(Cardiovascular Heart Disease), Lung Cancer, Stroke, MVA(motor vehicle accidents), Breast Cancer, Injury, Colon Cancer, Suicide, and then at last Homicide this is correlated to the data over the states and deaths and negatively related to births

In [43]:
```
ax = sns.heatmap(Death_ReasonCorr.transpose(), cmap='viridis')
```