Visualizing high dimensional TEDS data

In [2]:
```
import matplotlib.pyplot as plt
import pandas as pd

import seaborn as sns

import numpy as np
import scipy.stats as ss

from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler
```

In [7]:
```
df=pd.read_csv('__TEDSCountyLevel2008-2017_2.csv')
```

In [3]:
```
%matplotlib inline
```

In [8]:
```
df.head(10)
```

Out[8]:

	Alcohol	Amphetamine	Barbiturates	Benzine	Age	State	Cocaine	County Name	Gender	Hal	...	Pr
0	0	0	0	0	18-24	Indiana	0	Pulaski	Male	0	...	0
1	1	0	0	0	55+	Indiana	0	Pulaski	Male	0	...	0
2	1	0	0	0	18-24	Indiana	0	Pulaski	Male	0	...	0
3	0	0	0	0	55+	Indiana	0	Pulaski	Male	0	...	0
4	0	0	0	0	55+	Indiana	0	Pulaski	Male	0	...	0
5	1	0	0	0	25-34	Indiana	0	Pulaski	Male	0	...	0
6	1	0	0	0	35-44	Indiana	0	Pulaski	Male	0	...	0
7	1	0	0	0	25-34	Indiana	0	Pulaski	Male	0	...	0
8	1	0	0	0	0-18	Indiana	0	Pulaski	Male	0	...	0
9	1	0	0	0	25-34	Indiana	0	Pulaski	Male	0	...	0

10 rows × 50 columns

In [9]:
```
#Limit the number of features
features = ['Year','County Name','Gender','Race','Age','Alcohol','Heroin','Marijuana','O
pioid','Cocaine','Other Drugs','Pain Killers', 'Methamphetamine', 'Synthetic Drugs']
df_subset = df[features]
df_subset.head()
```

Out[9]:

	Year	County Name	Gender	Race	Age	Alcohol	Heroin	Marijuana	Opioid	Cocaine	Other Drugs	Pain Killers	M
0	2009	Pulaski	Male	White	18-24	0	0	1	0	0	0	0	0
1	2009	Pulaski	Male	White	55+	1	0	0	0	0	0	0	0
2	2009	Pulaski	Male	White	18-24	1	0	1	0	0	0	0	0
3	2009	Pulaski	Male	White	55+	0	0	1	0	0	0	0	0
4	2009	Pulaski	Male	White	55+	0	0	1	0	0	0	0	0

In [10]:
```
import altair as alt
alt.renderers.enable('notebook')
```

Out[10]:
```
RendererRegistry.enable('notebook')
```

In [11]:
```
#Create a dataset for the 9 substances to use in correlations
features = ['Alcohol','Heroin','Marijuana','Opioid','Cocaine','Other Drugs','Pain Killer
s', 'Methamphetamine', 'Synthetic Drugs']
df_only_features = df_subset[features]
df_only_features.head()
```

Out[11]:

	Alcohol	Heroin	Marijuana	Opioid	Cocaine	Other Drugs	Pain Killers	Methamphetamine	Synthetic Drugs
0	0	0	1	0	0	0	0	0	0
1	1	0	0	0	0	0	0	0	0
2	1	0	1	0	0	0	0	0	0
3	0	0	1	0	0	0	0	0	0
4	0	0	1	0	0	0	0	0	0

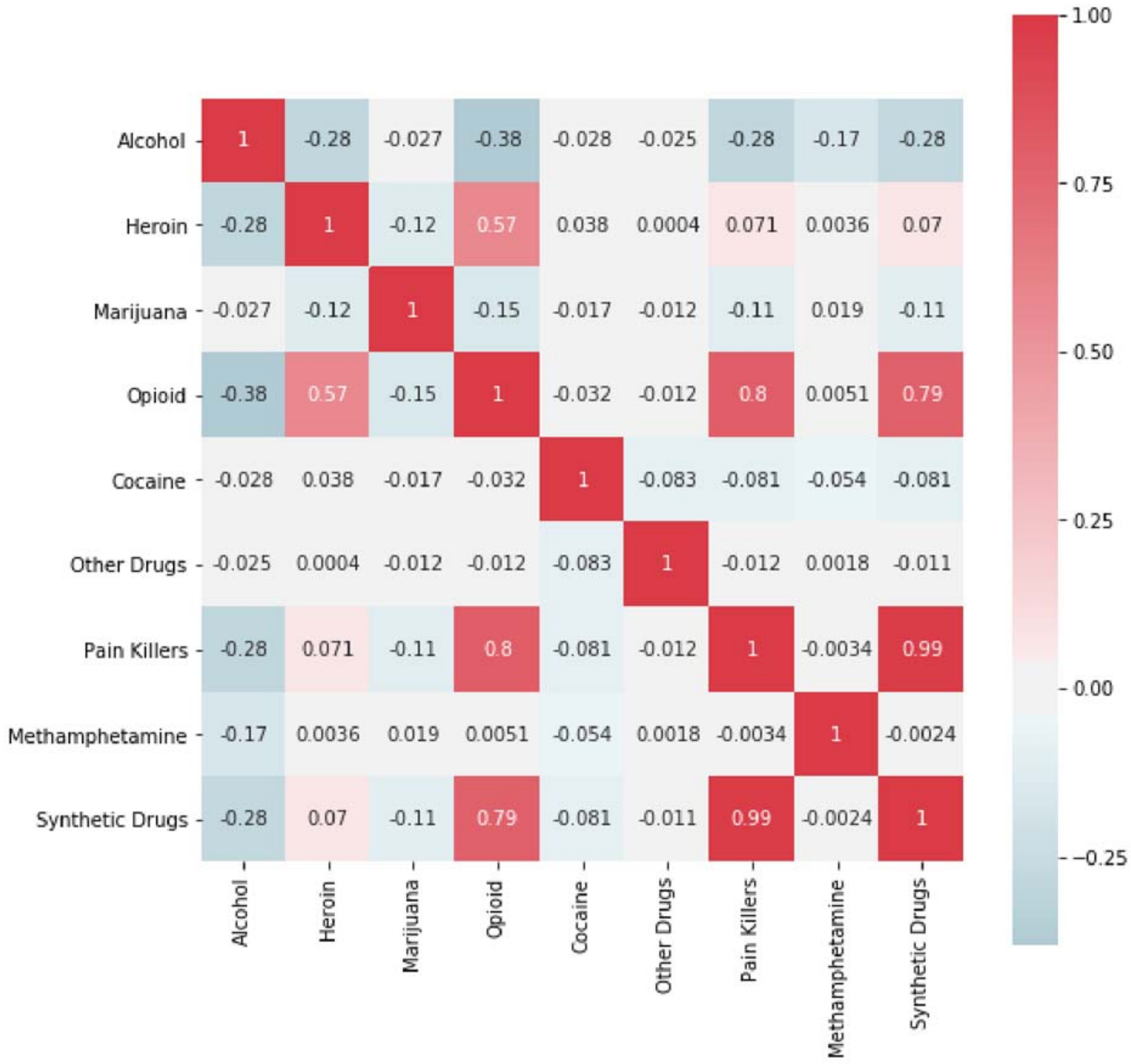
In [12]:
```
n_samples, n_features = df_only_features.shape
print(n_samples)
print(n_features)
```

```
335866
9
```

```
In [11]: #Check correlation between substances
         import seaborn as sns

         f, ax = plt.subplots(figsize=(9, 9))
         corr = df_only_features.corr()
         sns.heatmap(corr, mask=np.zeros_like(corr, dtype=np.bool), cmap=sns.diverging_palette(22
         0, 10, as_cmap=True), center=0,
                     square=True, ax=ax,annot=True)
```

```
Out[11]: <matplotlib.axes._subplots.AxesSubplot at 0x1bd9f9260b8>
```



	Alcohol	Heroin	Marijuana	Opioid	Cocaine	Other Drugs	Pain Killers	Methamphetamine	Synthetic Drugs
Alcohol	1	-0.28	-0.027	-0.38	-0.028	-0.025	-0.28	-0.17	-0.28
Heroin	-0.28	1	-0.12	0.57	0.038	0.0004	0.071	0.0036	0.07
Marijuana	-0.027	-0.12	1	-0.15	-0.017	-0.012	-0.11	0.019	-0.11
Opioid	-0.38	0.57	-0.15	1	-0.032	-0.012	0.8	0.0051	0.79
Cocaine	-0.028	0.038	-0.017	-0.032	1	-0.083	-0.081	-0.054	-0.081
Other Drugs	-0.025	0.0004	-0.012	-0.012	-0.083	1	-0.012	0.0018	-0.011
Pain Killers	-0.28	0.071	-0.11	0.8	-0.081	-0.012	1	-0.0034	0.99
Methamphetamine	-0.17	0.0036	0.019	0.0051	-0.054	0.0018	-0.0034	1	-0.0024
Synthetic Drugs	-0.28	0.07	-0.11	0.79	-0.081	-0.011	0.99	-0.0024	1

There is strong correlation between Pain Killers and Synthetic Drugs, supported by the Opioids. Heroin appears in 57% of the cases with Opioids. Alcohol is slightly negatively correlates with all four of them.

Remarkably, there appears to be no appreciable correlation between opioid use and such commonly accepted and complementary socio-economic markers as alcohol, marijuana, or methamphetamine use. In fact, these three factors are likely to be biased towards older population (alcohol), younger population (marijuana) and underprivileged rural population (methamphetamine).

Thus, it appears that opioid abuse have roots that are different from the common socio-economic maladies reflected in these three markers.

```
In [13]: df_subset['County Name'].nunique()

Out[13]: 93
```

```
In [13]: df_subset['Year'].nunique()

Out[13]: 10
```

```
In [14]: # Total number of records
         len(df_subset)

Out[14]: 335866
```

```
In [15]: #How many records per year
         df_subset['Year'].value_counts()

Out[15]: 2017    37459
         2015    34739
         2011    34677
         2014    34470
         2012    33984
         2013    33616
         2016    33170
         2009    32049
         2010    31827
         2008    29875
         Name: Year, dtype: int64
```

In [15]:
```
#How many records per county
df_subset['County Name'].value_counts()
```

```
Out[15]: Marion          41678
         Lake            25329
         Allen           16940
         Vanderburgh     14085
         Monroe          13842
         Saint Joseph    13359
         Delaware        10453
         Madison          9594
         Elkhart          8309
         Hamilton         8033
         Vigo             7895
         Howard           6235
         Bartholomew      6037
         Porter           5455
         LaPorte          5086
         Morgan           5057
         Lawrence         4557
         Tippecanoe       4514
         Wayne            4391
         Grant            4241
         Dearborn         3981
         Clark            3857
         Hendricks        3488
         Knox             3350
         Noble            3024
         Montgomery       3006
         Warrick          2969
         Kosciusko        2946
         Jefferson        2888
         Johnson          2834
                         ...
         Perry            1407
         Rush             1281
         Shelby           1246
         Vermillion       1241
         Wells            1195
         Jay              1193
         Orange           1174
         Franklin         1115
         Huntington       1107
         Parke            1084
         Whitley          1031
         Carroll           967
         Brown             922
         Pulaski           906
         Jasper            902
         Sullivan          812
         Blackford         759
         Washington        681
         Fountain          662
         Martin            638
         Tipton            563
         Switzerland       562
         Crawford          511
         Harrison          461
         Pike              433
         Benton            373
         Newton            315
         Ohio              293
         Union             284
```

```
Warren            229
Name: County Name, Length: 93, dtype: int64
```

In [16]:
```
# General method to variably group the data
def group_dataset(df, col1, col2):
    df_grouped=df.groupby([col1,col2])
    return df_grouped
```

In [17]:
```
#Group by Year and County
df_grouped=group_dataset(df_subset, 'Year','County Name')

#Excluded pain killers and synthetic drugs as highly correclated with opioids
feature=['Alcohol','Heroin','Marijuana','Opioid','Cocaine','Other Drugs','Methamphetamin
e']
df_grouped=df_grouped[feature].mean()

df_grouped.head()
```

Out[17]:

		Alcohol	Heroin	Marijuana	Opioid	Cocaine	Other Drugs	Methamphetamine
Year	**County Name**							
2008	**Adams**	0.905263	0.021053	0.684211	0.105263	0.231579	0.0	0.010526
	Allen	0.863495	0.012480	0.641186	0.048362	0.325273	0.0	0.017161
	Bartholomew	0.651106	0.004914	0.542998	0.226044	0.255528	0.0	0.299754
	Benton	0.840000	0.000000	0.520000	0.040000	0.160000	0.0	0.040000
	Blackford	0.833333	0.000000	0.620370	0.157407	0.175926	0.0	0.009259

In [18]:
```
#Group by County
df_grouped_c=group_dataset(df_subset,'County Name', 'Year')

#exclude pain killers and synthetic drugs as highly correclated with opioids
feature=['Alcohol','Heroin','Marijuana','Opioid','Cocaine','Other Drugs','Methamphetamin
e']
df_grouped_c=df_grouped_c[feature].mean()

df_grouped_c.head()
```

Out[18]:

		Alcohol	Heroin	Marijuana	Opioid	Cocaine	Other Drugs	Methamphetamine
County Name	**Year**							
Adams	**2008**	0.905263	0.021053	0.684211	0.105263	0.231579	0.000000	0.010526
	2009	0.877863	0.007634	0.549618	0.099237	0.175573	0.000000	0.030534
	2010	0.613497	0.141104	0.496933	0.300613	0.184049	0.147239	0.042945
	2011	0.655405	0.141892	0.540541	0.331081	0.155405	0.108108	0.060811
	2012	0.756098	0.073171	0.528455	0.203252	0.178862	0.138211	0.040650

```
In [19]: # Group by Year to genralize the output
         df_grouped_year1=df_subset.groupby('Year')
         df_grouped_year1=df_grouped_year1[feature].mean()

         df_grouped_year1.head()
```

Out[19]:

	Alcohol	Heroin	Marijuana	Opioid	Cocaine	Other Drugs	Methamphetamine
Year							
2008	0.661891	0.038226	0.506644	0.155213	0.223397	0.000000	0.087464
2009	0.682798	0.049237	0.514837	0.177821	0.194359	0.000000	0.091235
2010	0.632168	0.055833	0.490998	0.186006	0.157602	0.119553	0.096962
2011	0.606050	0.068662	0.483837	0.220607	0.146899	0.138593	0.103556
2012	0.590837	0.094191	0.471398	0.275012	0.156809	0.154926	0.112612

```
In [20]: # General method to pivot by two predictors
         def create_pivot_df(df, col_name, index_name, val_name):
             pivot_df = df.pivot_table(columns=col_name, index= index_name, values= val_name, agg
         func='mean')
             return pivot_df
```

```
In [21]: #create a pivot table for alcohol
         create_pivot_df(df_grouped,col_name='Year',index_name='County Name', val_name='Alcohol')
         .head()
```

Out[21]:

Year	2008	2009	2010	2011	2012	2013	2014	2015	2
County Name									
Adams	0.905263	0.877863	0.613497	0.655405	0.756098	0.812030	0.805195	0.697143	0.559
Allen	0.863495	0.834094	0.812057	0.794048	0.672963	0.736813	0.729648	0.674190	0.665
Bartholomew	0.651106	0.605505	0.442708	0.400815	0.458841	0.522551	0.501475	0.410745	0.345
Benton	0.840000	0.850000	0.684211	0.794118	0.852941	0.659091	0.708333	0.750000	0.780
Blackford	0.833333	0.787234	0.216216	0.523810	0.519231	0.386364	0.440678	0.454545	0.378

```
In [22]: def draw_heatmap(df, nrows, ncols):
             f, ax = plt.subplots(figsize=(nrows, ncols))
             sns.heatmap(df,  cmap=sns.cubehelix_palette(8, start=.5, rot=-.75),ax=ax,xticklabels
         =2, square=True, vmin=0, vmax=.9)
```

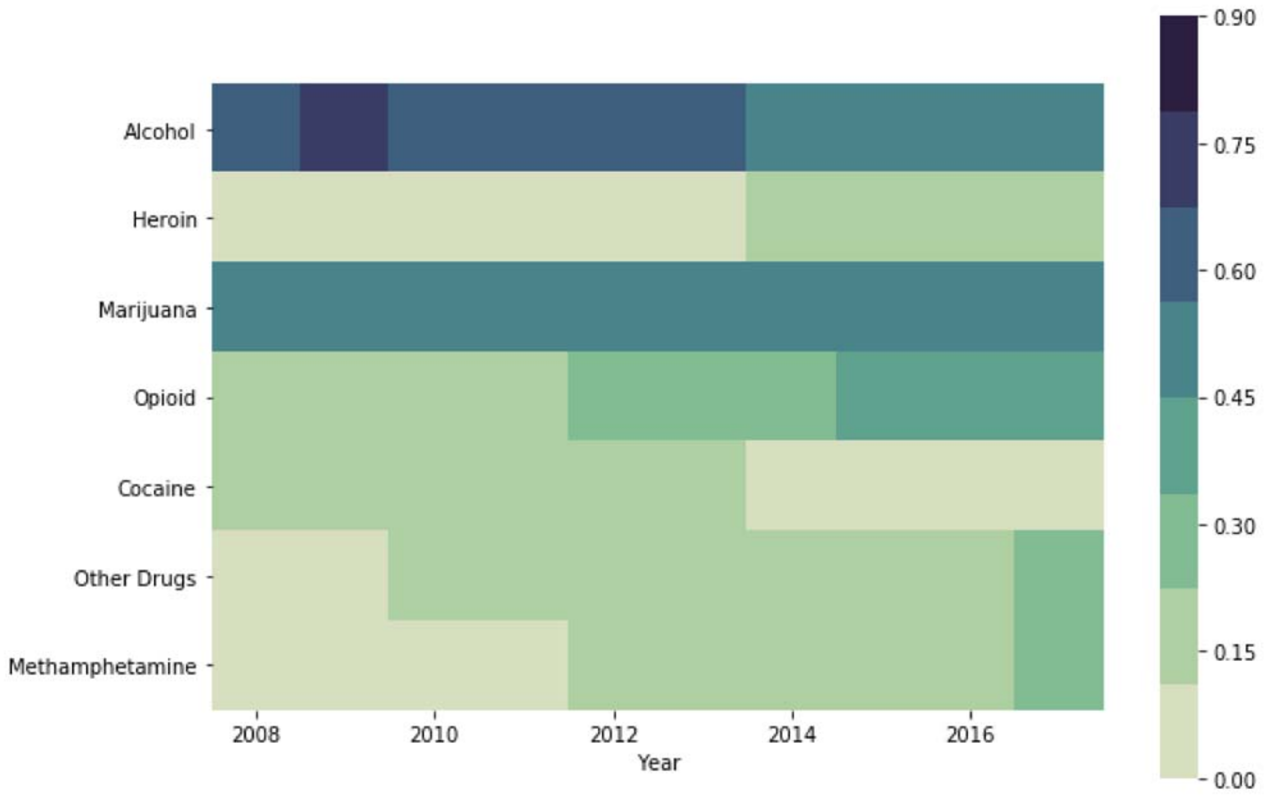
```
In [23]: def draw_heatmap_corr(df, nrows, ncols):
             f, ax = plt.subplots(figsize=(nrows, ncols))
             df=df.corr()
             sns.heatmap(df,  cmap=sns.diverging_palette(220, 10, as_cmap=True), center=0,ax=ax,
         square=True,annot=True,cbar_kws={"shrink": .5})
```

```
In [24]: #Transpose the matrix
         df_grouped_year_T= df_grouped_year1.T
         df_grouped_year_T
```

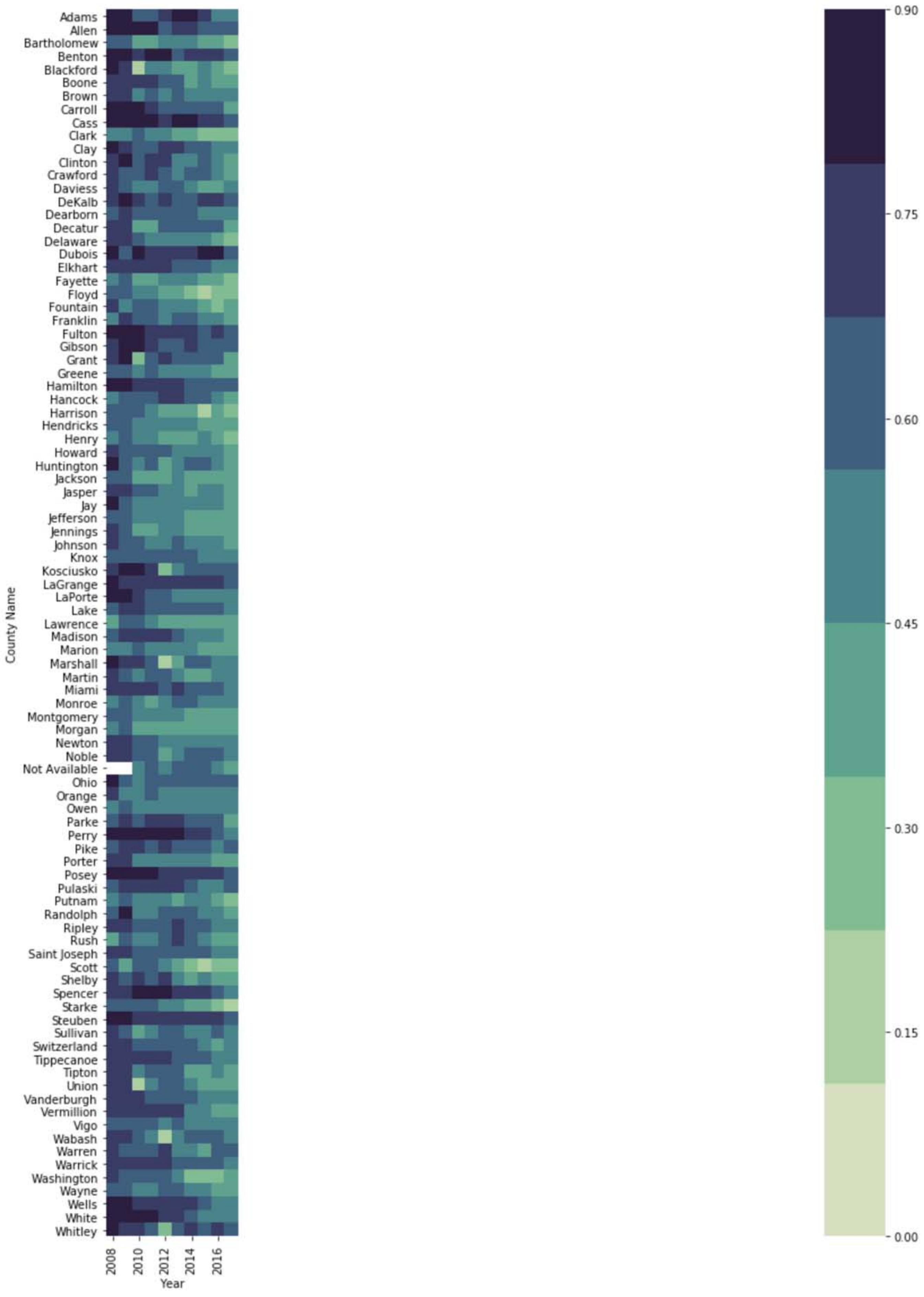
Out[24]:

Year	2008	2009	2010	2011	2012	2013	2014	2015
Alcohol	0.661891	0.682798	0.632168	0.606050	0.590837	0.585792	0.559066	0.528743
Heroin	0.038226	0.049237	0.055833	0.068662	0.094191	0.105396	0.121787	0.156625
Marijuana	0.506644	0.514837	0.490998	0.483837	0.471398	0.476172	0.478648	0.483462
Opioid	0.155213	0.177821	0.186006	0.220607	0.275012	0.303248	0.314244	0.339273
Cocaine	0.223397	0.194359	0.157602	0.146899	0.156809	0.131277	0.112446	0.106825
Other Drugs	0.000000	0.000000	0.119553	0.138593	0.154926	0.165516	0.177894	0.202654
Methamphetamine	0.087464	0.091235	0.096962	0.103556	0.112612	0.121995	0.141514	0.159936

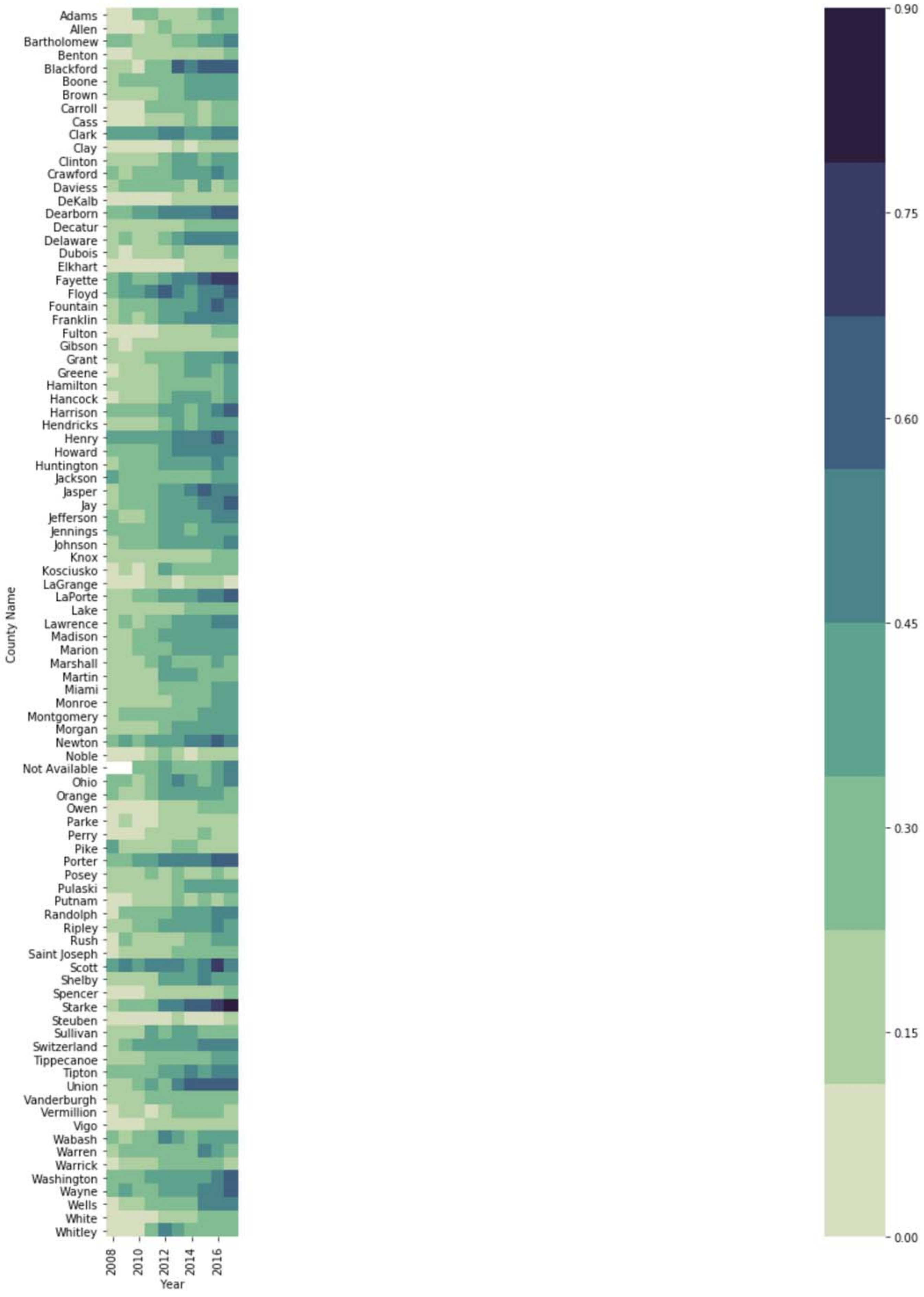
```
In [27]: # Show a trend relative to other substances
         draw_heatmap(df_grouped_year_T, 10, 7)
```



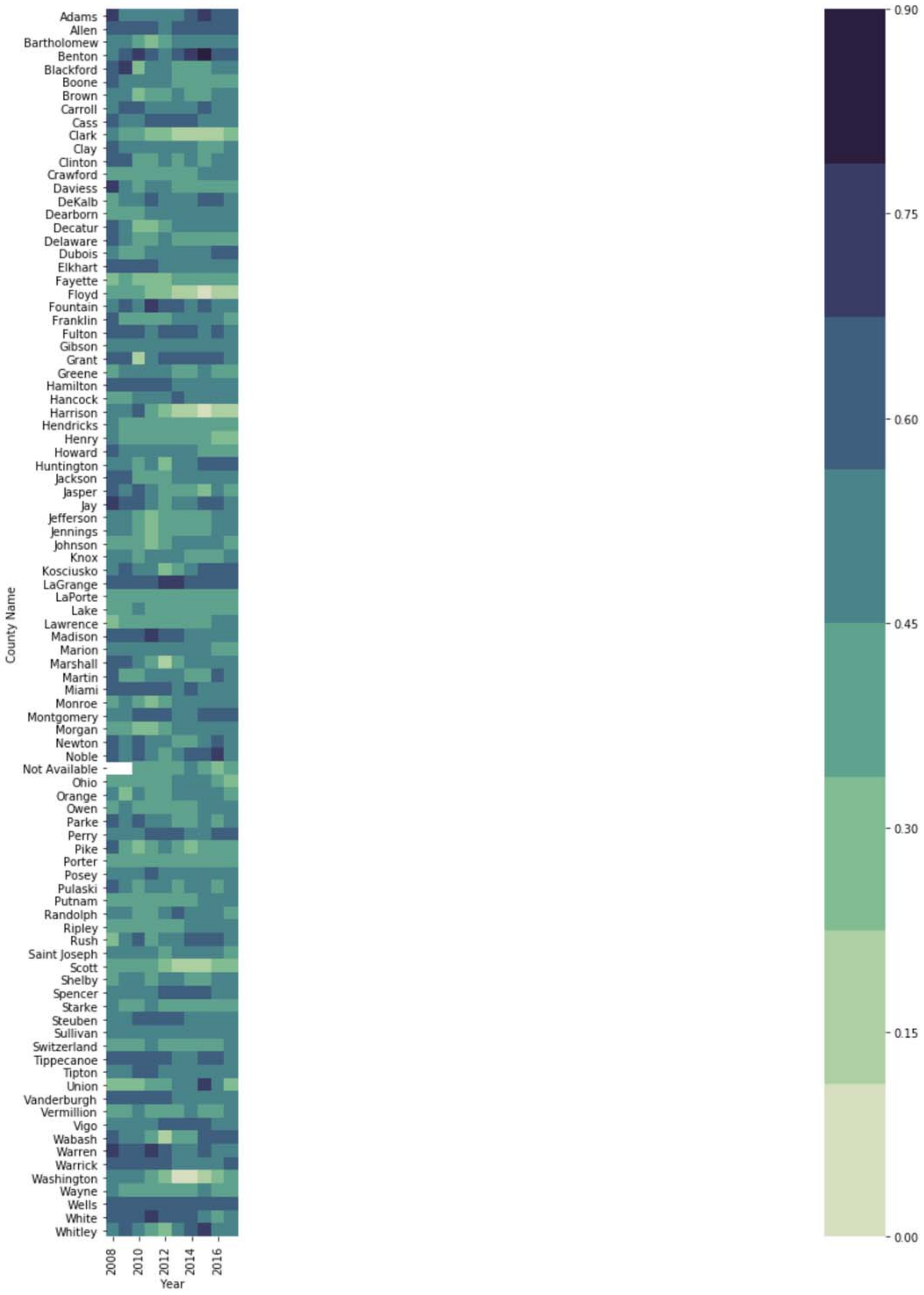
```
In [28]: # Draw a heatmap by County for Alcohol
         draw_heatmap(
         create_pivot_df(df_grouped,'Year','County Name', 'Alcohol'), 186, 20)
```



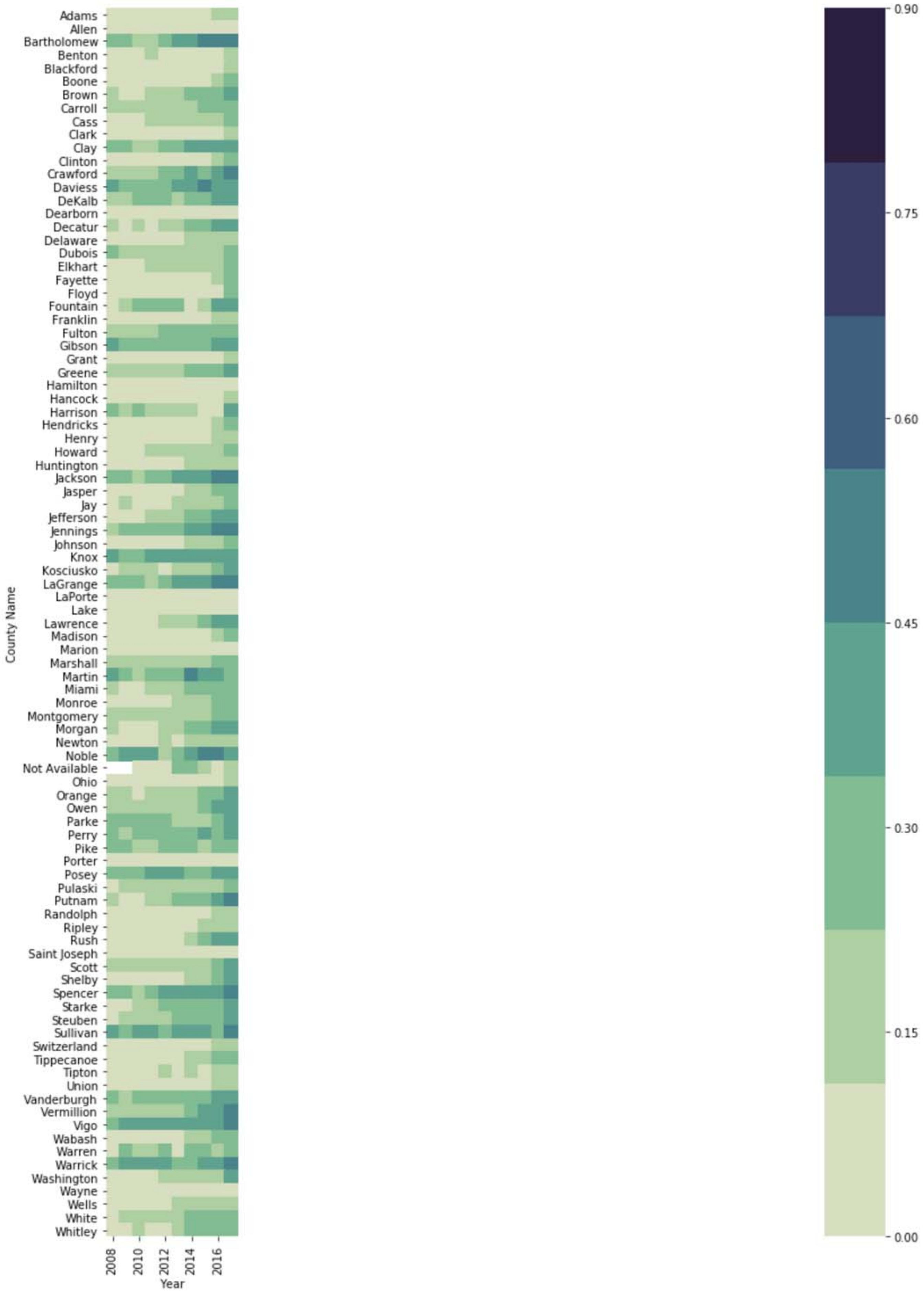
```
In [29]: #Opioid
         draw_heatmap(create_pivot_df(df_grouped,'Year','County Name', 'Opioid'), 186, 20)
```



In [30]:
```
#Marijuana
draw_heatmap(create_pivot_df(df_grouped,'Year','County Name', 'Marijuana'), 186, 20)
```



In [31]:
```
# Methamphetamine
draw_heatmap(create_pivot_df(df_grouped,'Year','County Name', 'Methamphetamine'), 186, 2
0)
```



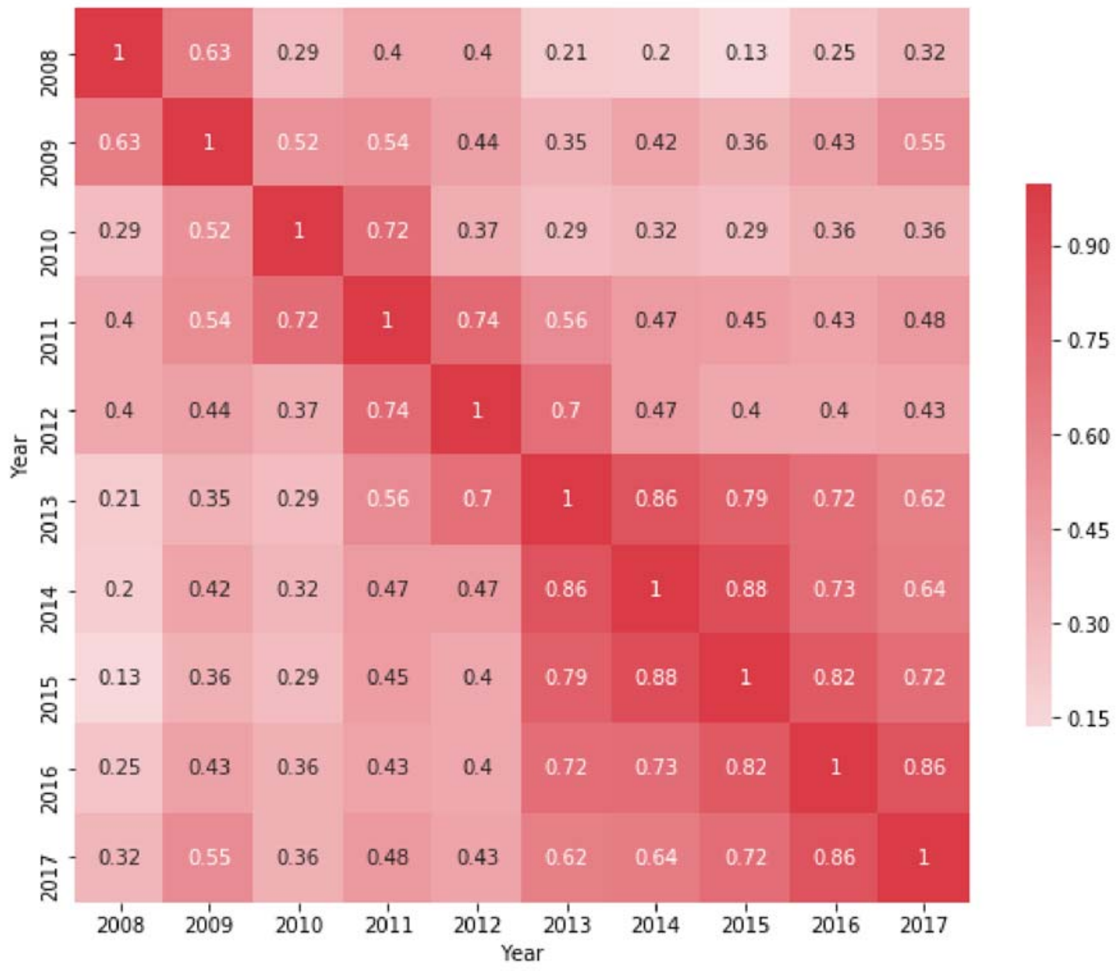
From the four heatmaps above, one could infer the following observations:

- while Alcohol remains the most commonly abused substance, its dominance is vaning as the prevalence of other substances, especially opiods and methamphethamine increases. At the same time, marijuana abuse remains fairly stable.

Suplimentary Analysis: Identify any years that differ from the majority

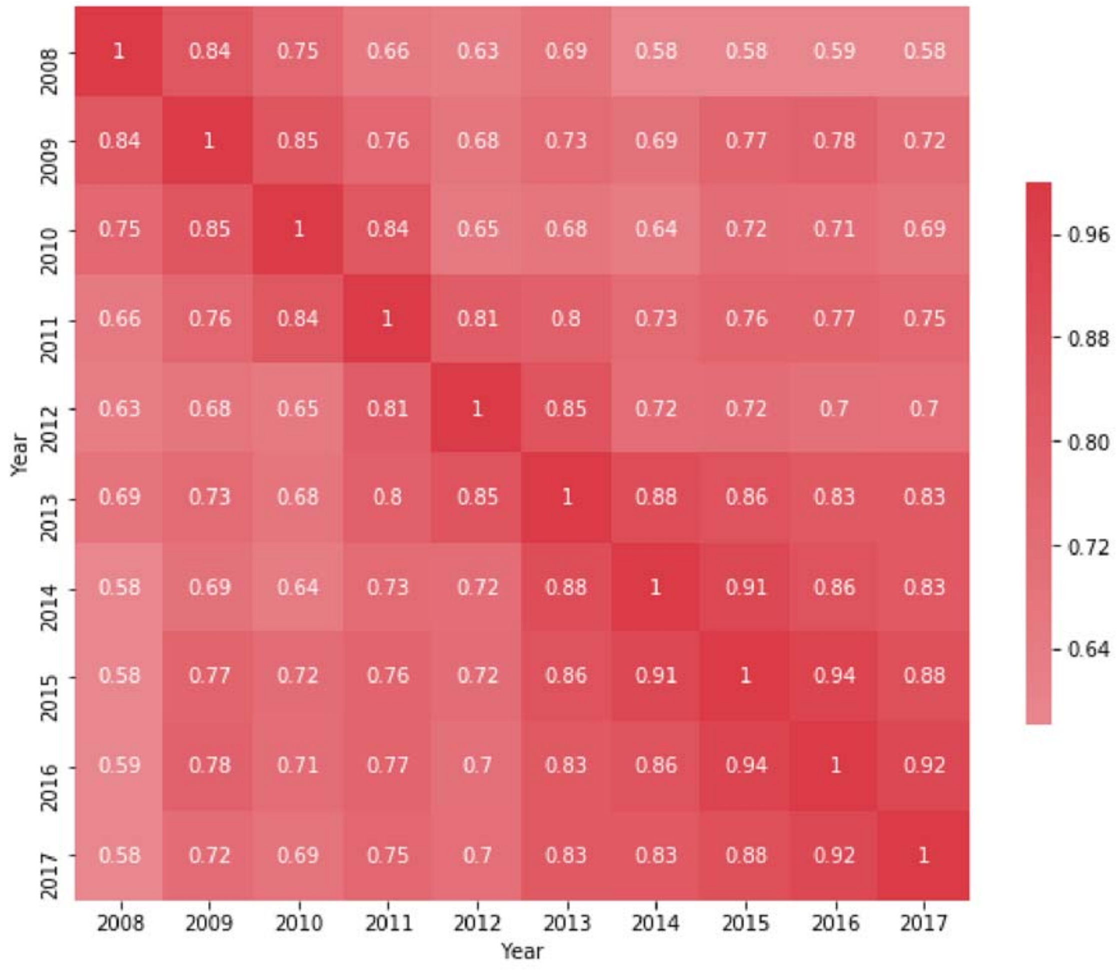
```
In [ ]: draw_heatmap_corr(create_pivot_df(df_grouped,'Year','County Name', 'Alcohol'), 10,10)
```

```
In [33]: #Marijuana
         draw_heatmap_corr(create_pivot_df(df_grouped,'Year','County Name', 'Marijuana'), 10,10)
```

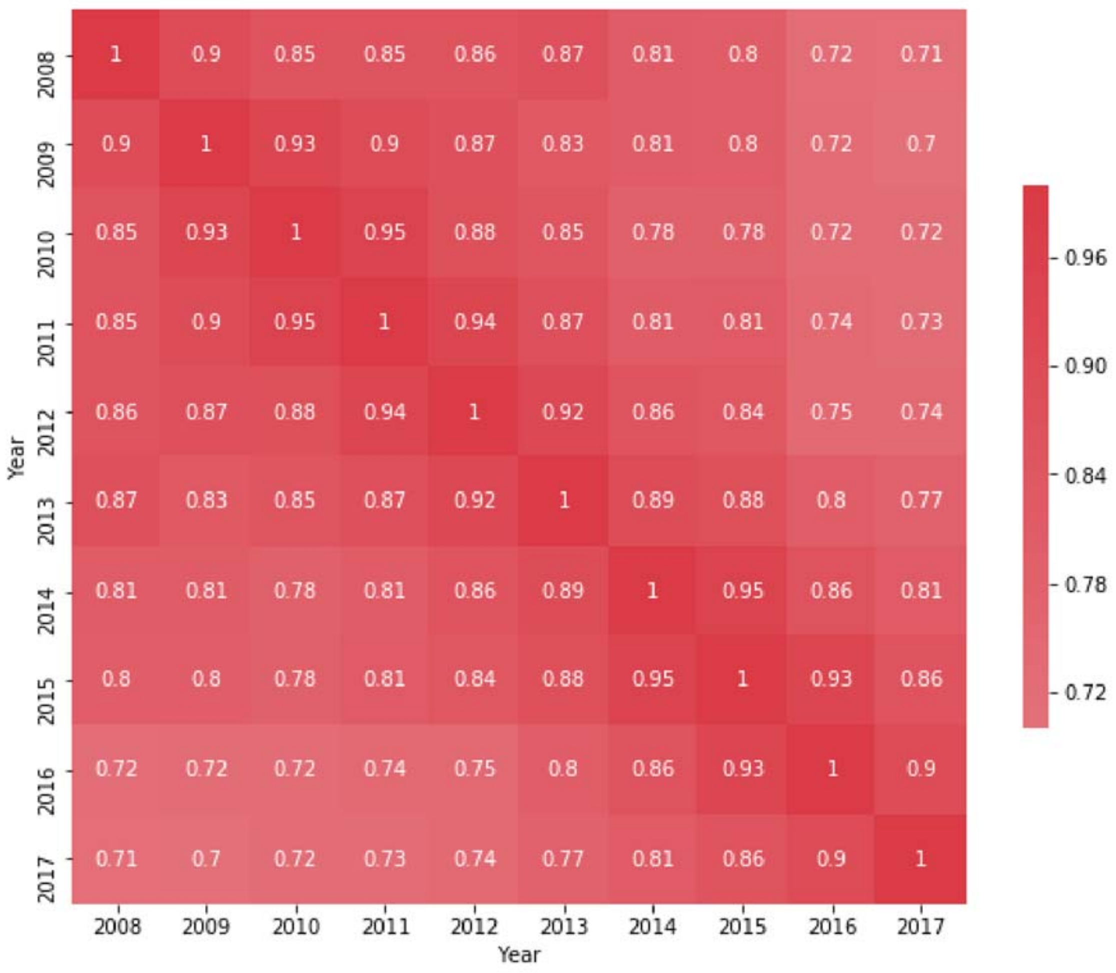


In [34]:

```
#Opioids
draw_heatmap_corr(create_pivot_df(df_grouped,'Year','County Name', 'Opioid'), 10,10)
```



```
In [35]: #Methamphetamine
         draw_heatmap_corr(create_pivot_df(df_grouped,'Year','County Name', 'Methamphetamine'), 1
         0,10)
```

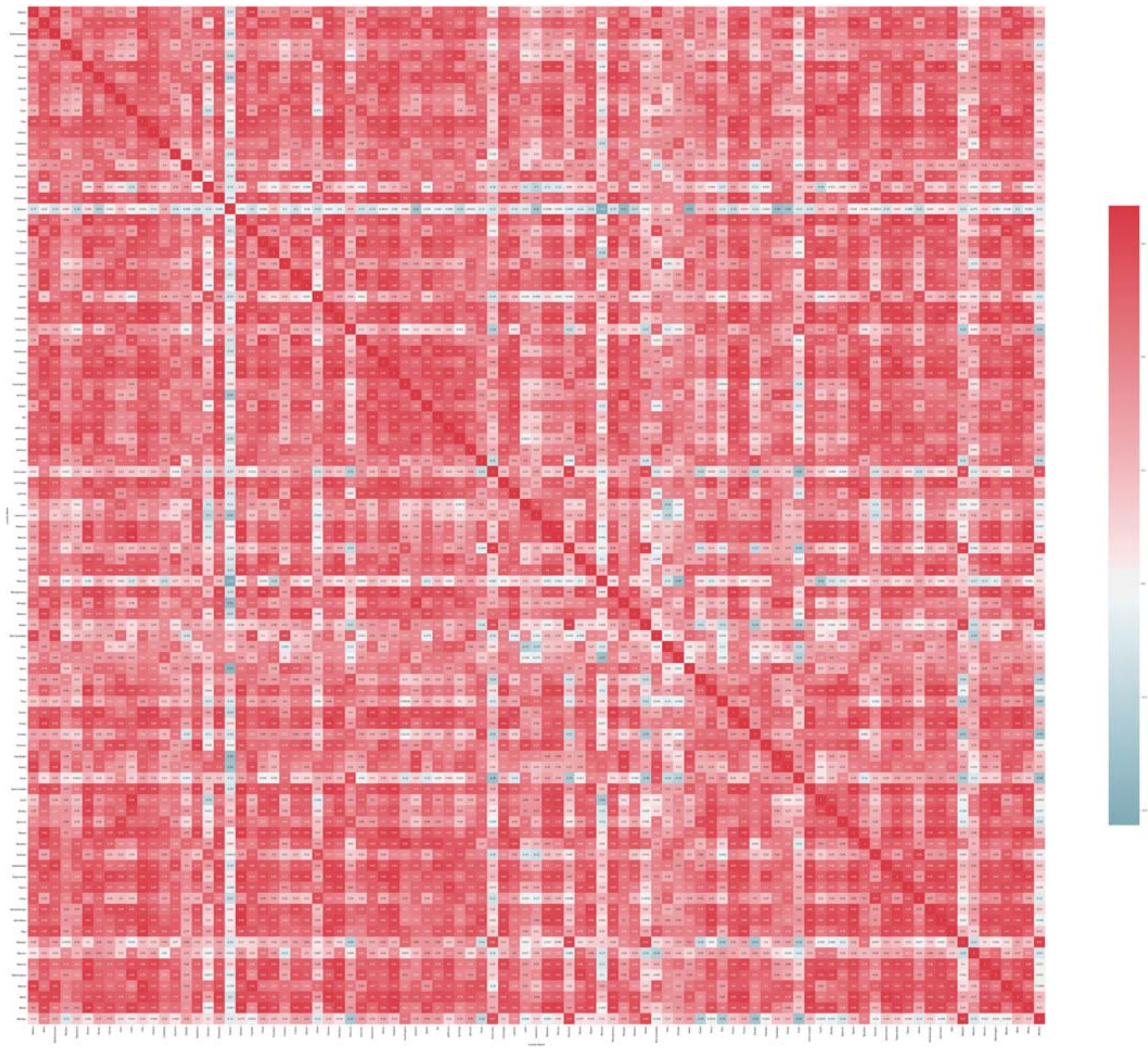


Year	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017
2008	1	0.9	0.85	0.85	0.86	0.87	0.81	0.8	0.72	0.71
2009	0.9	1	0.93	0.9	0.87	0.83	0.81	0.8	0.72	0.7
2010	0.85	0.93	1	0.95	0.88	0.85	0.78	0.78	0.72	0.72
2011	0.85	0.9	0.95	1	0.94	0.87	0.81	0.81	0.74	0.73
2012	0.86	0.87	0.88	0.94	1	0.92	0.86	0.84	0.75	0.74
2013	0.87	0.83	0.85	0.87	0.92	1	0.89	0.88	0.8	0.77
2014	0.81	0.81	0.78	0.81	0.86	0.89	1	0.95	0.86	0.81
2015	0.8	0.8	0.78	0.81	0.84	0.88	0.95	1	0.93	0.86
2016	0.72	0.72	0.72	0.74	0.75	0.8	0.86	0.93	1	0.9
2017	0.71	0.7	0.72	0.73	0.74	0.77	0.81	0.86	0.9	1

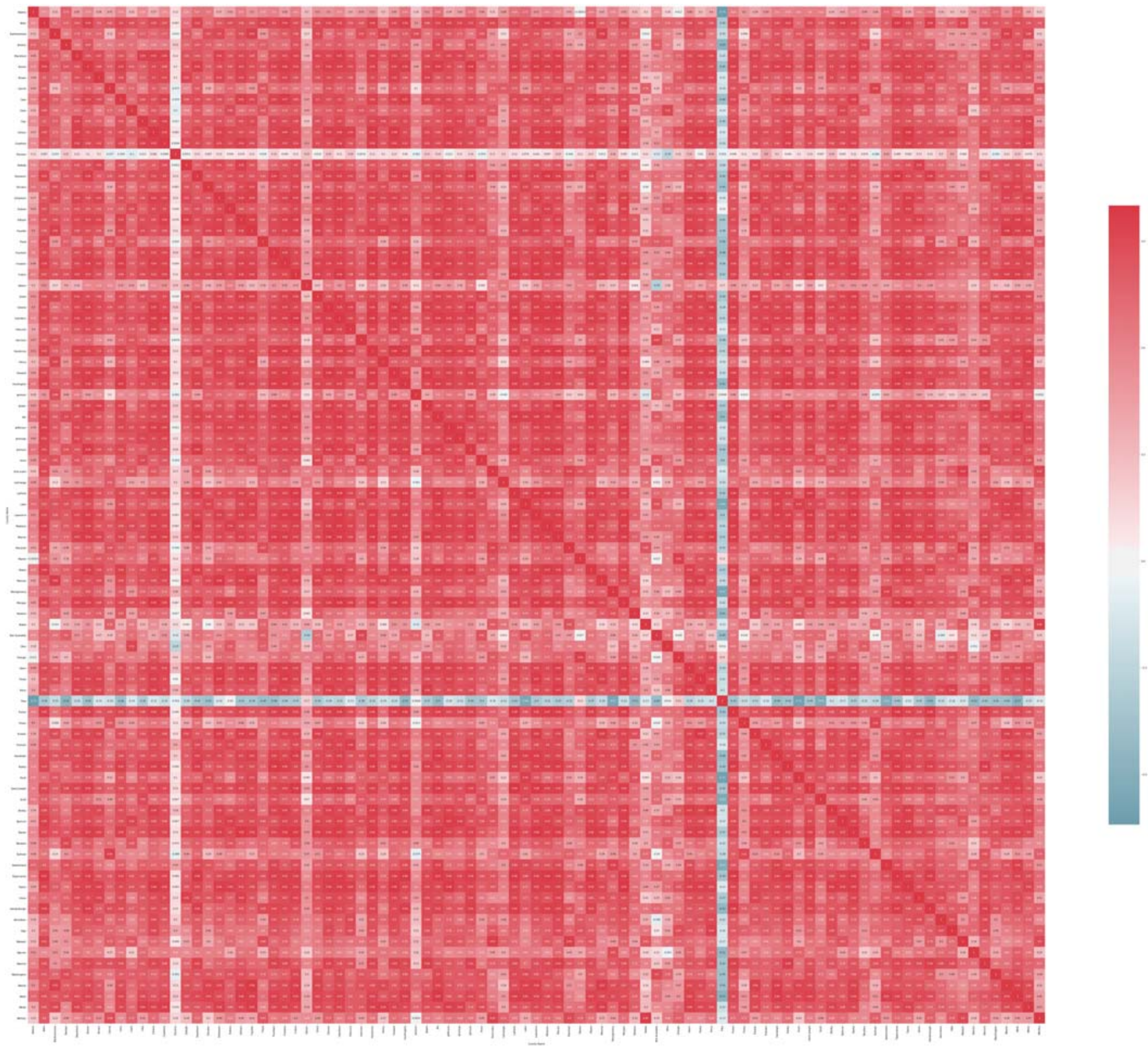
Beginning 2012 the usage patterns became very similar for the malority of the subjects that requested treatment in Indiana.

Suplimentary Analysis: Identify counties that differ from the majority

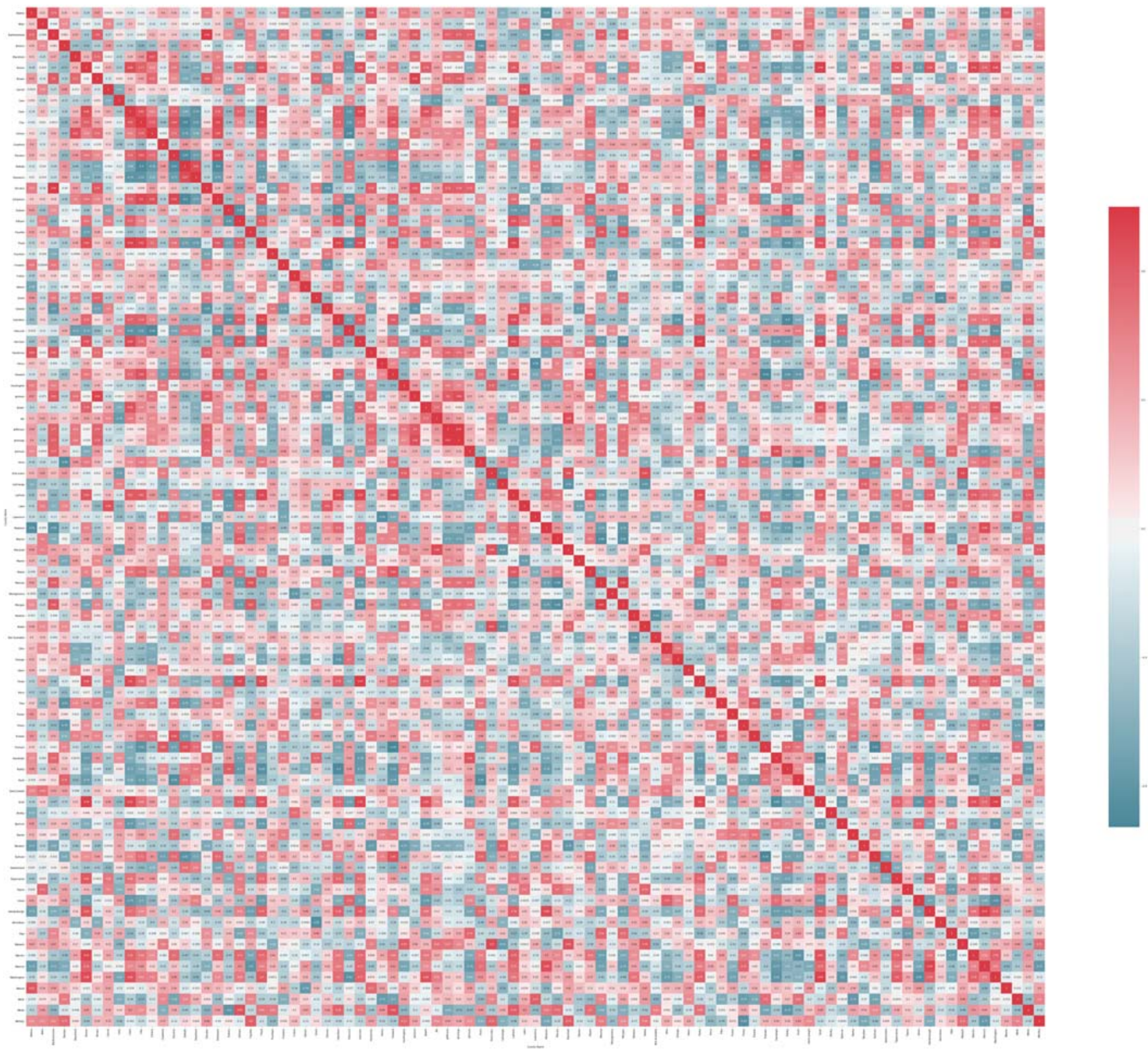
In [37]:
```
draw_heatmap_corr(create_pivot_df(df_grouped,'County Name','Year', 'Alcohol'), 93,93)
```



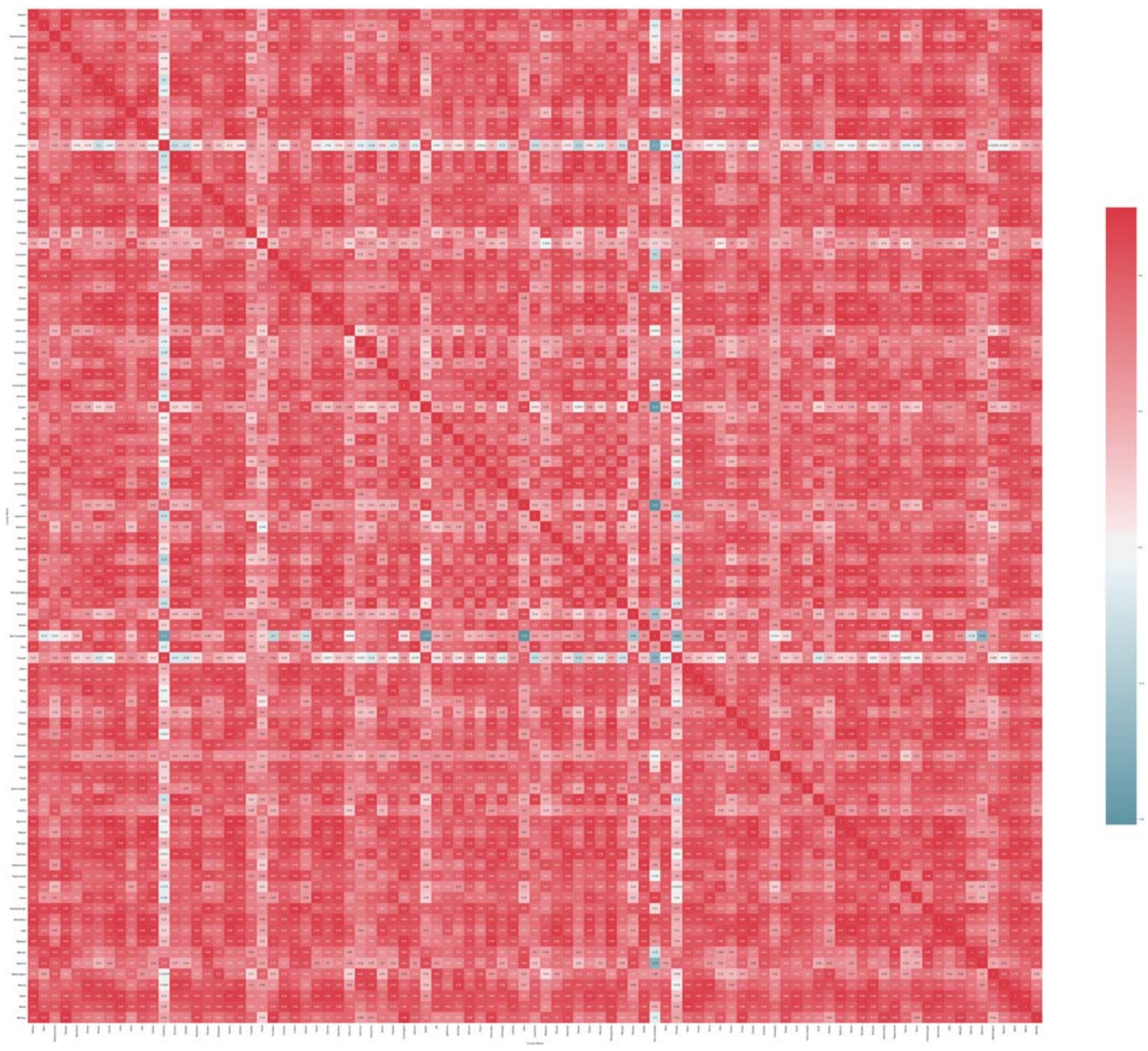
```
In [38]: draw_heatmap_corr(create_pivot_df(df_grouped,'County Name','Year', 'Opioid'), 93,93)
```



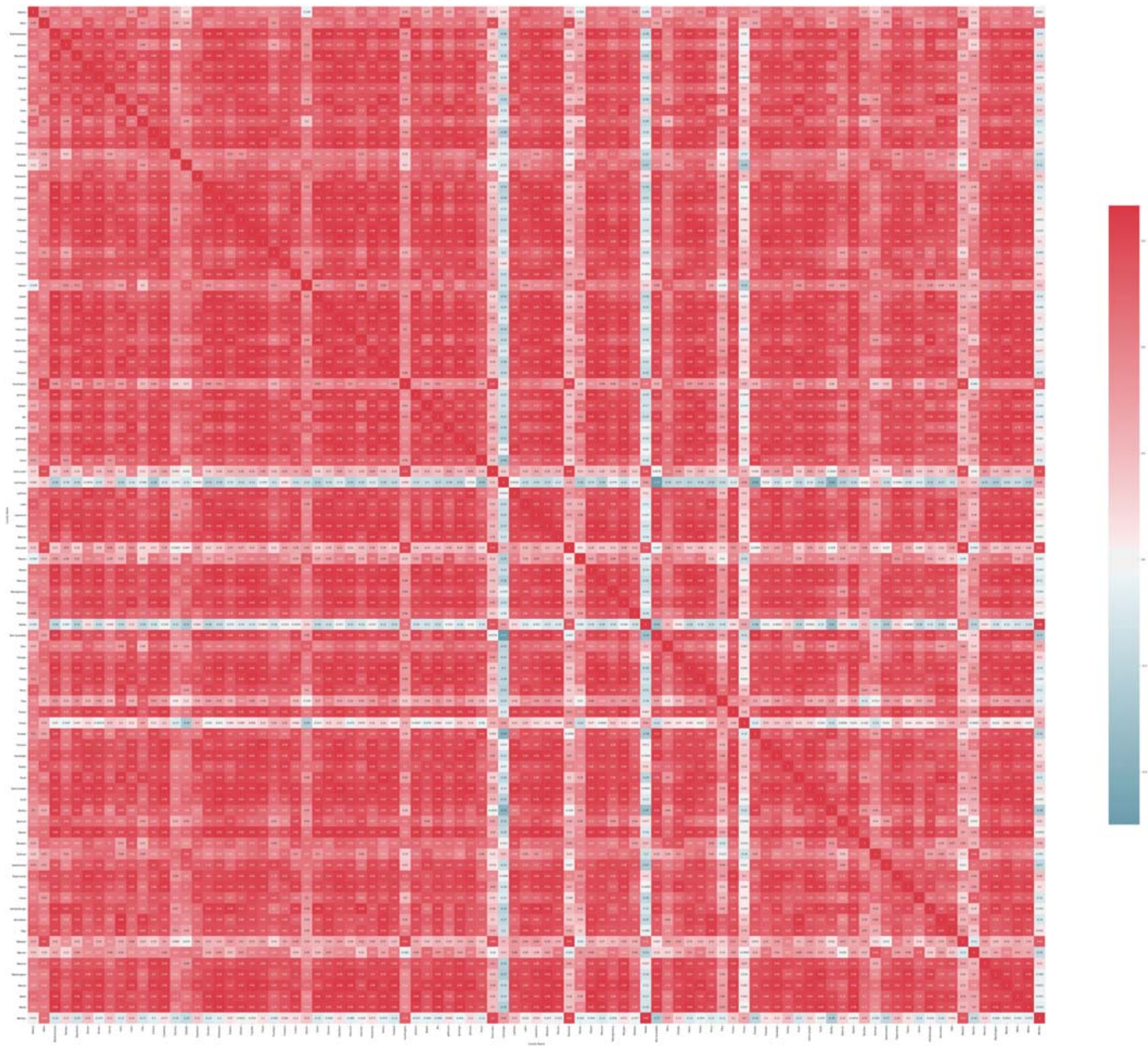
```
In [39]: draw_heatmap_corr(create_pivot_df(df_grouped,'County Name','Year', 'Marijuana'), 93,93)
```



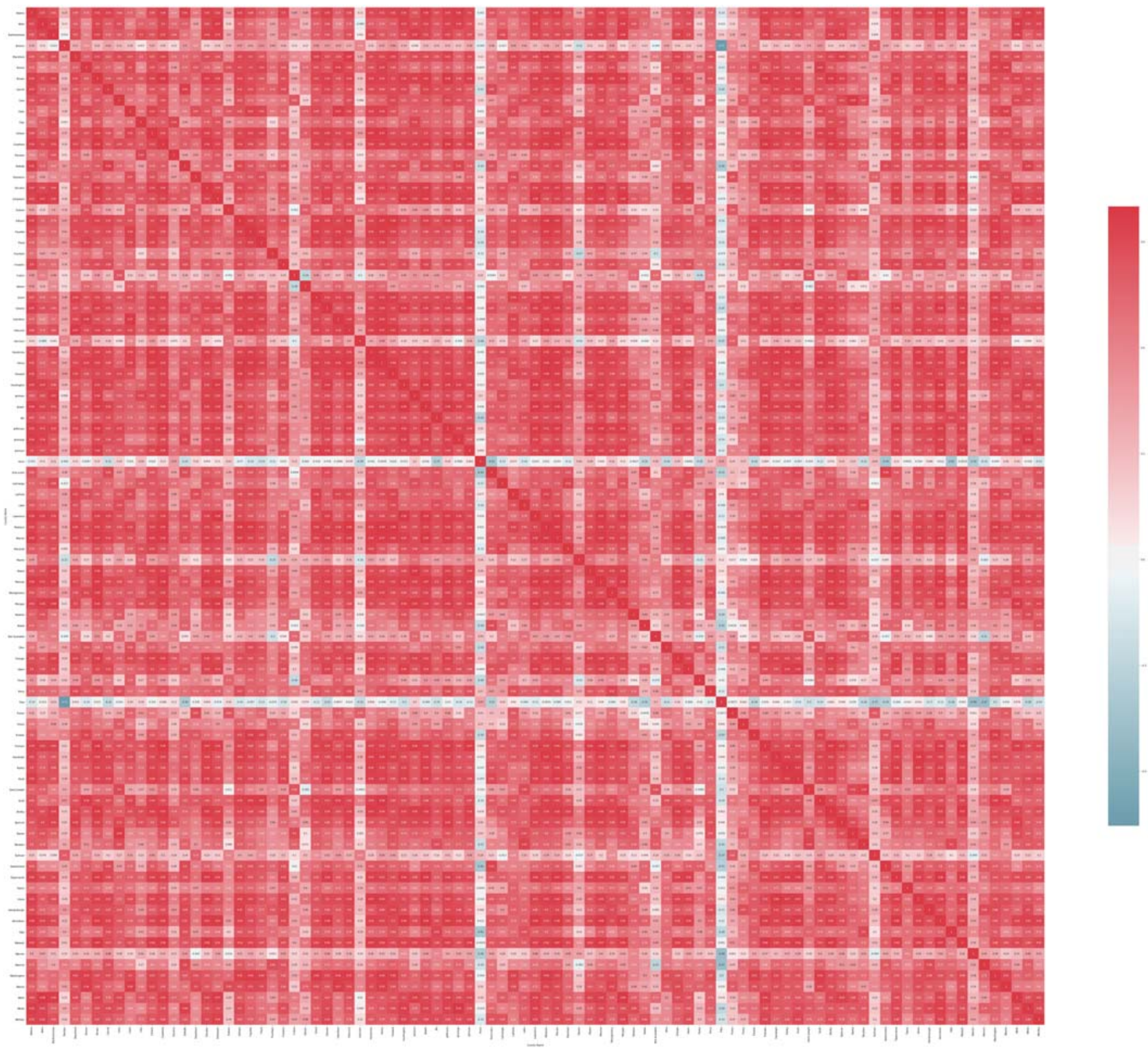
```
In [40]: draw_heatmap_corr(create_pivot_df(df_grouped,'County Name','Year', 'Other Drugs'), 93,93
         )
```



In [41]:
```
draw_heatmap_corr(create_pivot_df(df_grouped,'County Name','Year', 'Heroin'), 93,93)
```



```
In [42]: draw_heatmap_corr(create_pivot_df(df_grouped,'County Name','Year', 'Methamphetamine'), 9
         3,93)
```



Suplimentary analisys: PCA

The principal component analysis (PCA) (http://setosa.io/ev/principal-component-analysis/) is the most basic dimensionality reduction method. To run the PCA we want to isolate only the numerical columns.

```
In [43]: from sklearn.decomposition import PCA
         pca = PCA()
```

Now I ran `fit()` method to identify principal components.

```
In [44]: pca_df_fitted = pca.fit(df_only_features)
         print(pca.components_)
```

```
[[-3.85284978e-01  1.74017452e-01 -1.44132829e-01  5.72548369e-01
  -2.69179141e-02 -9.45944737e-04  4.88667622e-01  2.68324235e-02
   4.82126552e-01]
 [-4.18457857e-01 -5.05321504e-03  9.00800758e-01 -1.84296925e-02
  -5.53315489e-03  1.53651275e-03 -2.34787354e-02  1.09207683e-01
  -2.39850374e-02]
 [ 7.11756112e-01 -2.43212736e-01  3.74058306e-01  9.21887106e-02
  -1.39977393e-01 -4.67858705e-02  3.29558300e-01 -2.17148697e-01
   3.29070826e-01]
 [ 6.54654403e-02  2.33536949e-01  7.81258265e-02  1.44714164e-01
   6.66987977e-01 -5.86190546e-01 -6.12216977e-02 -3.43352728e-01
  -6.32252001e-02]
 [ 7.12073209e-02  4.07014556e-01  9.88869180e-02  2.09251566e-01
   5.82755415e-02  6.54588384e-01 -1.35008442e-01 -5.53985972e-01
  -1.36726374e-01]
 [-2.01654654e-01 -5.55680657e-01 -7.19214685e-02 -2.79439087e-01
   5.74989672e-01  3.75006655e-01  1.92924758e-01 -1.44138780e-01
   1.95080605e-01]
 [ 3.46163005e-01  2.35182719e-01  8.23741063e-02  1.93313001e-01
   4.47977083e-01  2.91666275e-01 -1.35950867e-02  7.03277331e-01
  -1.29745391e-02]
 [ 3.90868442e-04  5.68343537e-01  4.84514642e-03 -6.90996902e-01
   9.17264956e-03 -1.72477268e-03  2.33910579e-01  5.52881945e-03
   3.80333325e-01]
 [ 1.39976189e-03  5.68623039e-02  4.14804014e-04 -7.54235243e-02
   1.18822447e-03  5.79425375e-04  7.33450549e-01  1.74171781e-03
  -6.73142890e-01]]
```

'-Other Drugs', Marijuana,Opioid+Alcohol, Marijuana+Cocaine, Marijuana+Alcohol, -Marijuana-Heroin, Marijuana+Methamphetamine

```
In [45]: print(pca.explained_variance_)
```

```
[0.52332706 0.25520259 0.20435398 0.13614426 0.12185475 0.1103172
 0.10171866 0.00989851 0.00189358]
```

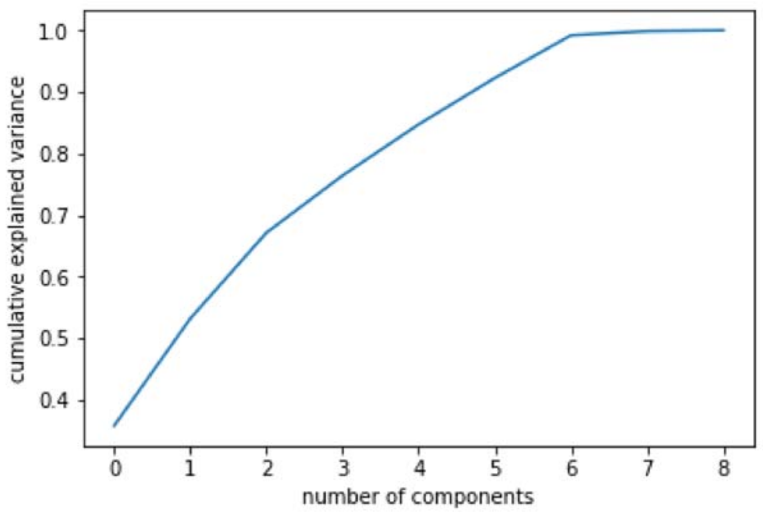
```
In [46]: pca_df_fitted.explained_variance_ratio_
```

```
Out[46]: array([0.35729042, 0.17423414, 0.13951833, 0.0929496 , 0.08319374,
                0.07531672, 0.06944625, 0.006758  , 0.0012928 ])
```

```
In [47]: pca.components_.shape
```

```
Out[47]: (9, 9)
```

In [48]:
```
plt.plot(np.cumsum(pca.explained_variance_ratio_))
plt.xlabel('number of components')
plt.ylabel('cumulative explained variance');
```



The first six components capture more than 95% of the variance in original dataset. This means that the PCA is not very effective on this dataset and six components will provide approximation for the rest of the dimensions.