In [1]:

```python
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
%matplotlib inline
```

Read and View Dataset

In [2]:

```python
df = pd.read_csv('placesCleanedUp.txt', sep="\s+", header=None,index_col=False)
df.columns = ["CommunityState","Climate","HousingCost","HlthCare", "Crime","Transp", "Ed
uc","Arts","Recreat","Econ","CaseNum","lat","lon","pop","statenum"]
df[['Community','State']] = df.CommunityState.apply(
    lambda x: pd.Series(str(x).split(",")))
df=df.drop(['CommunityState'],axis=1)
df
```

Out[2]:

	Climate	HousingCost	HlthCare	Crime	Transp	Educ	Arts	Recreat	Econ	CaseNum	lat	lon	pop	state
0	521	6200	237	923	4031	2757	996	1405	7633	1	-99.6890	32.5590	110932	
1	575	8138	1656	886	4883	2438	5564	2632	4350	2	-81.5180	41.0850	660328	
2	468	7339	618	970	2531	2560	237	859	5250	3	-84.1580	31.5750	112402	
3	476	7908	1431	610	6883	3399	4655	1617	5864	4	-73.7983	42.7327	835880	
4	659	8393	1853	1483	6558	3026	4496	2612	5727	5	-106.6500	35.0830	419700	
...	...	...	...	...	...	...	...	...	...	...	...	...	...	
324	562	8715	1805	680	3643	3299	1784	910	5040	325	-71.7950	42.2720	402918	
325	535	6440	317	1106	3731	2491	996	2140	4986	326	-120.5130	46.5950	172508	
326	540	8371	713	440	2267	2903	1022	842	4946	327	-76.7280	39.9600	381255	
327	570	7021	1097	938	3374	2920	2797	1327	3894	328	-80.7290	41.1700	531350	
328	608	7875	212	1179	2768	2387	122	918	4694	329	-121.6220	39.1280	101979	

329 rows × 16 columns

Step1: Normalize the data (StandardScaler uses Mean=0 and Stdev=1)

In [3]:

```python
from sklearn.preprocessing import MinMaxScaler
from sklearn.preprocessing import StandardScaler
```

In [4]:

```python
columns=['Climate', 'HousingCost','HlthCare','Crime','Transp','Educ','Arts','Recreat','Ec
on'] #,'CaseNum','lat','lon','pop','statenum'
dfScaler = df[columns]

#Initialize, fit(train) and transform data to normalize
```

```
scaler=StandardScaler()
scaler.fit(dfScaler)
scaled_data=scaler.transform(dfScaler)

#View in Frame
df_scaled = pd.DataFrame(scaled_data, columns=columns)
df_scaled = df_scaled.round(2)
df_scaled
```

Out[4]:

	Climate	HousingCost	HlthCare	Crime	Transp	Educ	Arts	Recreat	Econ
0	-0.15	-0.90	-0.95	-0.11	-0.12	-0.18	-0.46	-0.55	1.95
1	0.30	-0.09	0.47	-0.21	0.46	-1.18	0.52	0.97	-1.09
2	-0.59	-0.42	-0.57	0.03	-1.16	-0.80	-0.63	-1.22	-0.25
3	-0.52	-0.18	0.24	-0.98	1.84	1.82	0.32	-0.28	0.31
4	1.00	0.02	0.67	1.46	1.62	0.66	0.29	0.95	0.19
...	...	...	...	...	...	...	...	...	...
324	0.19	0.15	0.62	-0.79	-0.39	1.51	-0.29	-1.16	-0.45
325	-0.03	-0.80	-0.87	0.41	-0.33	-1.01	-0.46	0.36	-0.50
326	0.01	0.01	-0.47	-1.46	-1.34	0.28	-0.46	-1.24	-0.54
327	0.26	-0.56	-0.09	-0.06	-0.58	0.33	-0.08	-0.64	-1.51
328	0.57	-0.20	-0.97	0.61	-1.00	-1.34	-0.65	-1.15	-0.77

329 rows × 9 columns

How to select # of components?

Method 1: pass %

In [5]:

```
from sklearn.decomposition import PCA
```

In [6]:

```
pca = PCA(n_components = 0.95)
pca.fit(scaled_data)
reduced = pca.transform(scaled_data)
print('Original Dimensions: ',scaled_data.shape)   #14
print('Reduced Dimensions: ',reduced.shape)  #11
```

```
Original Dimensions:  (329, 9)
Reduced Dimensions:  (329, 7)
```

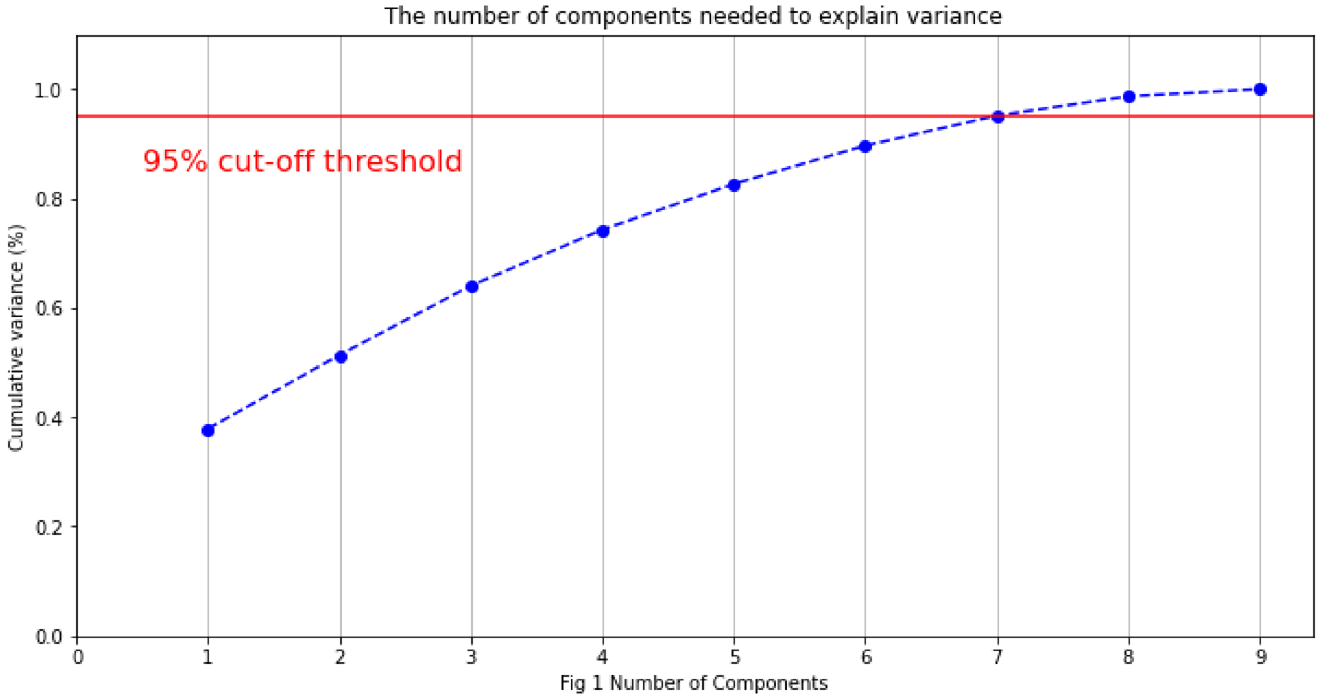
> `95%` **of variance is observed by** `7 dimensions`

Method 2: Select the number of components for PCA looking at plot

In [7]:

```
pca = PCA().fit(scaled_data)
plt.rcParams["figure.figsize"] = (12,6)

fig, ax = plt.subplots()
xi = np.arange(1, 10, step=1)
y = np.cumsum(pca.explained_variance_ratio_)
```

```
plt.ylim(0.0,1.1)
plt.plot(xi, y, marker='o', linestyle='--', color='b')

plt.xlabel('Fig 1 Number of Components')
plt.xticks(np.arange(0, 10, step=1)) #change from 0-based array index to 1-based human-r
eadable label
plt.ylabel('Cumulative variance (%)')
plt.title('The number of components needed to explain variance')

plt.axhline(y=0.95, color='r', linestyle='-')
plt.text(0.5, 0.85, '95% cut-off threshold', color = 'red', fontsize=16)

ax.grid(axis='x')
plt.show()
```



> `95%` **of variance is observed by** `7 components`

Step 2 Perform PCA

(use SVD or the eigenvalue decomposition of the covariance matrix)

In [8]:

```
pca=PCA(n_components=7)
```

In [9]:

```
pca.fit(scaled_data)
```

Out[9]:

```
PCA(copy=True, iterated_power='auto', n_components=7, random_state=None,
    svd_solver='auto', tol=0.0, whiten=False)
```

Step 3 Scree plot and Variance Explained

A Scree plot displays how much variation each principal component captures from the data. If the first two or three PCs have capture most of the information, then we can ignore the rest without losing anything important. A scree plot shows how much variation each PC captures from the data. The y axis is eigenvalues, which essentially stand for the amount of variation. A scree plot is used to select the principal components to keep. An

ideal curve should be steep, then bends at an "elbow" — this is the cutting-off point — and after that flattens out. In Figure 2 below, just PC 1, 2, and 3 seems enough to describe the data.

> A higher explained variance, captures more variability in dataset, which could potentially lead to better performance when training your model.

In [10]:

```
pca.explained_variance_
```

Out[10]:

```
array([3.41868293, 1.21767731, 1.14495927, 0.9237255 , 0.75558148,
       0.63248434, 0.49455091])
```

In [11]:

```
pca.explained_variance_ratio_
```

Out[11]:

```
array([0.37869909, 0.13488624, 0.12683102, 0.1023242 , 0.08369832,
       0.07006243, 0.05478308])
```

In [12]:

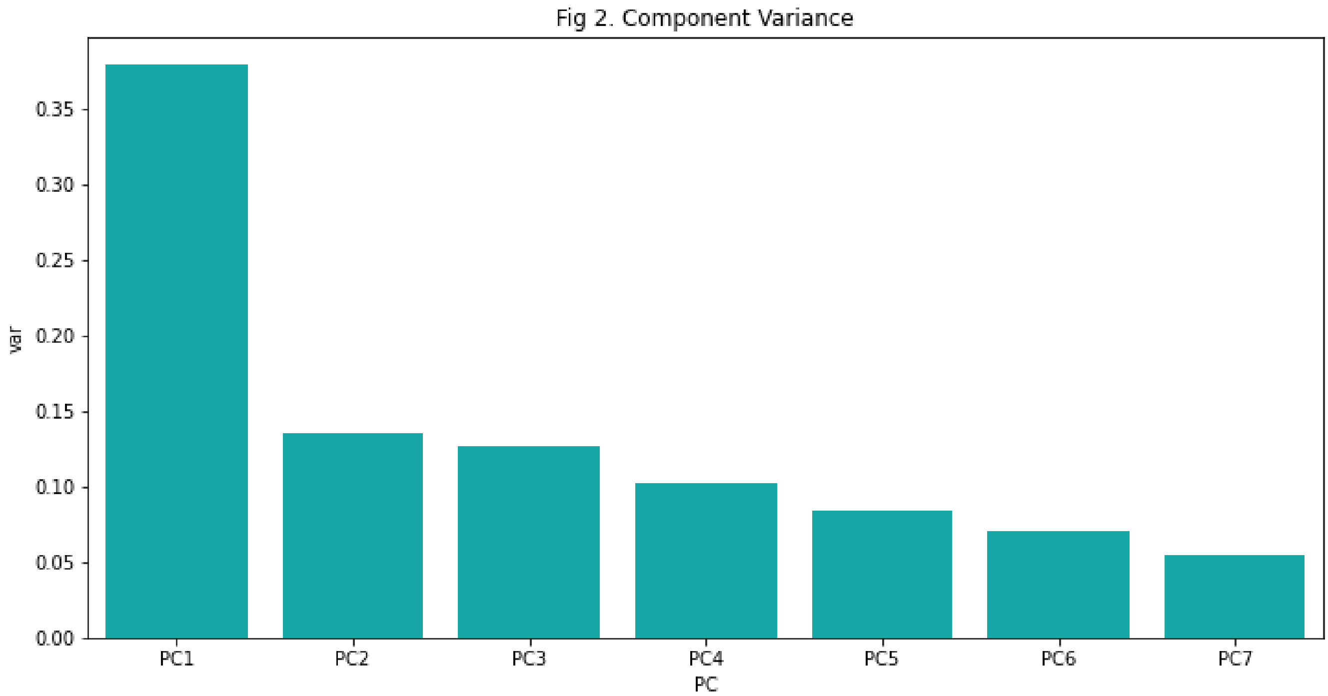
```
#cor_mat1 = np.corrcoef(scaled_data.T)
#eig_vals, eig_vecs = np.linalg.eig(cor_mat1)
#print('Eigenvectors \n%s' %eig_vecs)
#print('\nEigenvalues \n%s' %eig_vals)
```

In [13]:

```
import seaborn as sn
```

In [14]:

```
dfScree = pd.DataFrame({'var':pca.explained_variance_ratio_,'PC':['PC1','PC2','PC3','PC4
','PC5','PC6','PC7']})
sn.barplot(x='PC',y="var",data=dfScree, color="c").set_title('Fig 2. Component Variance'
);
```



In [15]:

```
x_pca=pca.transform(scaled_data)
```

In [16]:

```
scaled_data.shape
```

Out[16]:

```
(329, 9)
```

In [17]:

```
x_pca.shape
```

Out[17]:

```
(329, 7)
```

Compute the correlations between the original data and each principal component

In [18]:

```
import seaborn as sn
```

In [19]:

```
df_pc = pd.DataFrame(data = x_pca, columns = ['pc1','pc2','pc3','pc4','pc5','pc6','pc7']
)
df_pc=df_pc.drop(['pc4'],axis=1)
df_pc=df_pc.drop(['pc5'],axis=1)
df_pc=df_pc.drop(['pc6'],axis=1)
df_pc=df_pc.drop(['pc7'],axis=1)

df_col = pd.concat([df_pc,df_scaled], axis=1)
df_col
covMatrix = pd.DataFrame.cov(df_col)
sn.set(rc={'figure.figsize':(14,6)})
sn.heatmap(covMatrix, annot=True, fmt='g')
plt.figure(figsize=(28,18))
plt.show()
```


```
<Figure size 2016x1296 with 0 Axes>
```

Explain the Components observed

PCA 1 - The first principal component is strongly correlated with five of the original variables. It

PCA 1 - The first principal component is strongly correlated with five of the original variables. It increases with increasing `Arts`, `Health`, `Transportation`, `Housing` and `Recreation` scores. communities with high values tend to have a lot of arts available, in terms of theaters, orchestras, etc.

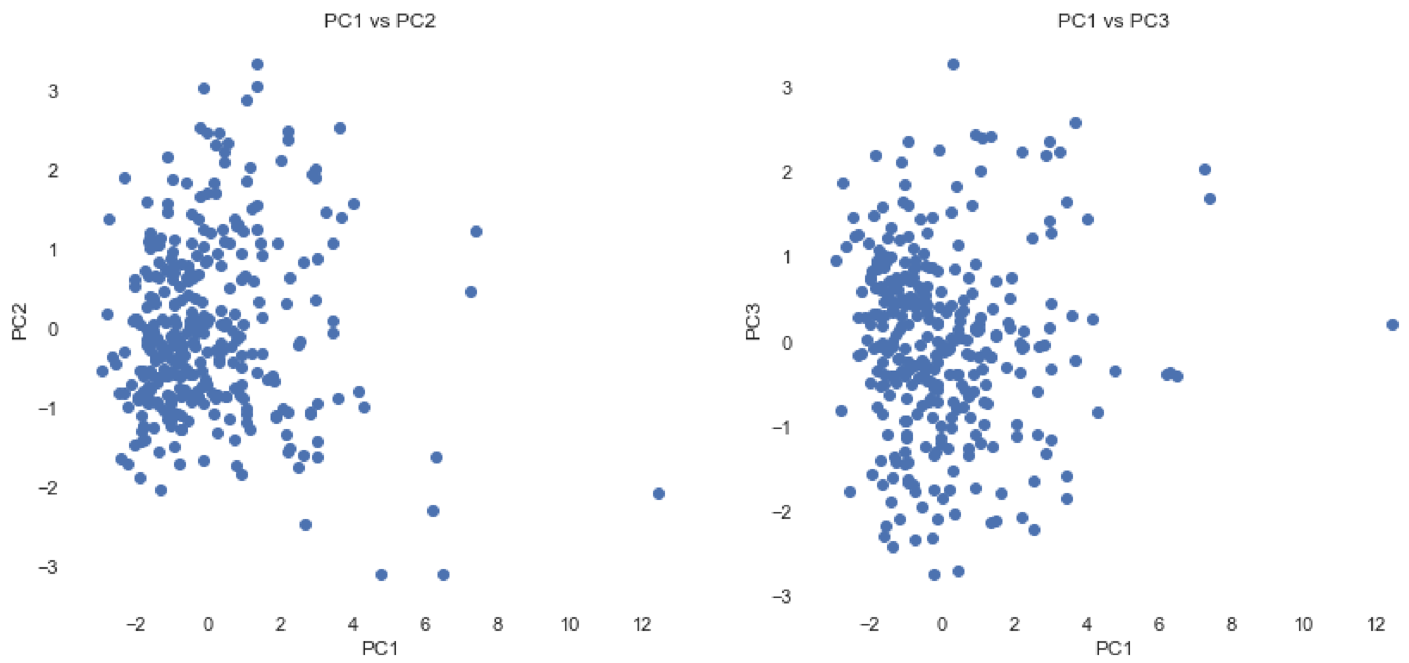
PCA 2 - The second principal component increases with decreasing `Education` and `Health`. This component can be viewed as a measure of how uneducated and unhealthy the location is in terms of education including available schools, universities and health care including doctors, hospitals, etc.

PCA 3 - The third principal component decreases with only one of the values, decreasing `Economy`. It can be viewed as measure of how poor the state is in terms of business environment, jobs market and growth.

Step 4 Scatter plot all communities along two of the PCs (PC1 vs PC2 or PC1 vs PC3)

In [20]:

```
fig = plt.figure()
ax1 = fig.add_subplot(121)
ax2 = fig.add_subplot(122)

ax1.scatter(x_pca[:,0],x_pca[:,1])
ax1.set_xlabel("PC1")
ax1.set_ylabel("PC2")
ax1.set_frame_on(False)
ax1.grid(True)
ax1.set_title('PC1 vs PC2')

ax2.scatter(x_pca[:,0],x_pca[:,2])
ax2.set_xlabel("PC1")
ax2.set_ylabel("PC3")
ax2.set_title('PC1 vs PC3')
ax2.grid(True)
ax2.set_frame_on(False)
```



PCA biplot = PCA score plot + loading plot

The left and bottom axes are of the PCA plot. It shows PCA scores of the samples (dots).

The top and right axes belong to the loading plot. It shows how strongly each characteristic (vector) influence the principal components.

In [21]:

```
import plotly.express as px
```

In [23]:

```
features = ['Climate', 'HousingCost','HlthCare','Crime','Transp','Educ','Arts','Recreat',
'Econ'] #,'CaseNum','lat','lon','pop','statenum'
loadings = pca.components_.T * np.sqrt(pca.explained_variance_)

fig = px.scatter(x_pca, x=0, y=1)
for i, feature in enumerate(features):
    fig.add_shape(
        type='line',
        x0=0, y0=0,
        x1=loadings[i, 0]*4.5,
        y1=loadings[i, 1]*4.5
    )
    fig.add_annotation(
        x=loadings[i, 0]*5.5,
        y=loadings[i, 1]*5.5,
        ax=0, ay=0,
        xanchor="center",
        yanchor="bottom",
        text=feature,
    )
fig.show()
```

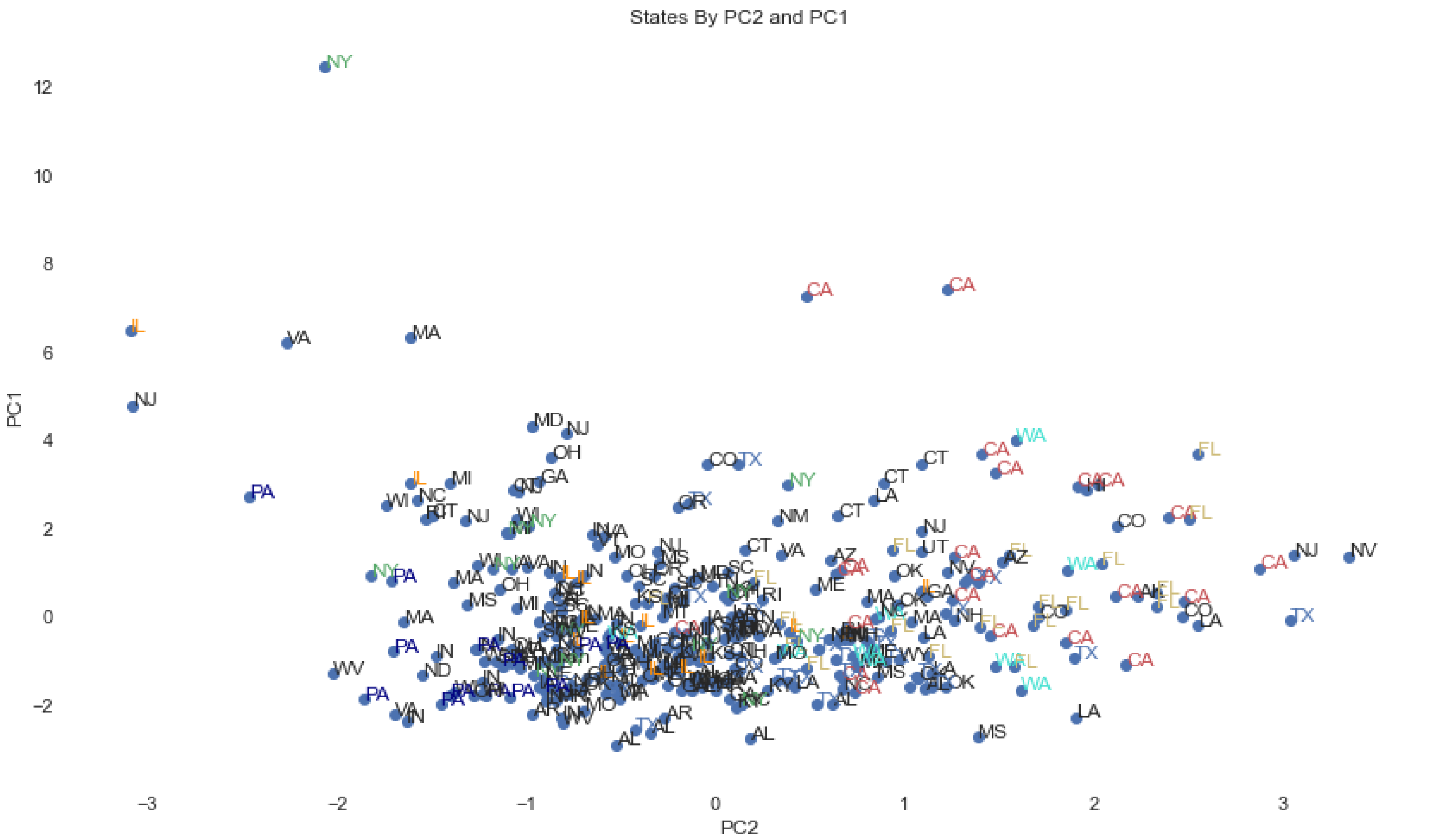
Plot STATES on principle components

In [24]:

```
def plotPCA(c1,c2):

    dict = {'NY':'g', 'FL':'y','TX':'b','CA':'r','PA':'navy','WA':'turquoise','IL':'darko
range'}
    fig, ax = plt.subplots(1, 1, figsize=(14, 8))
    ax.scatter(x_pca[:,c1-1],x_pca[:,c2-1])
    for i,(Community,u) in enumerate(zip(np.array(df),x_pca)):
        if df['State'][i] in dict:
            ax.annotate(df['State'][i],(u[c1-1],u[c2-1]),color=dict[df['State'][i]])
        else:
            ax.annotate(df['State'][i],(u[c1-1],u[c2-1]))

    ax.set_xlabel(f"PC{c1}")
    ax.set_ylabel(f"PC{c2}")
    ax.grid(True)
    ax.set_frame_on(False)
    title = 'States By ' + f"PC{c1}" + ' and ' + f"PC{c2}"
    ax.set_title(title)
    fig.savefig(title + '.png', dpi=75)

    return
```

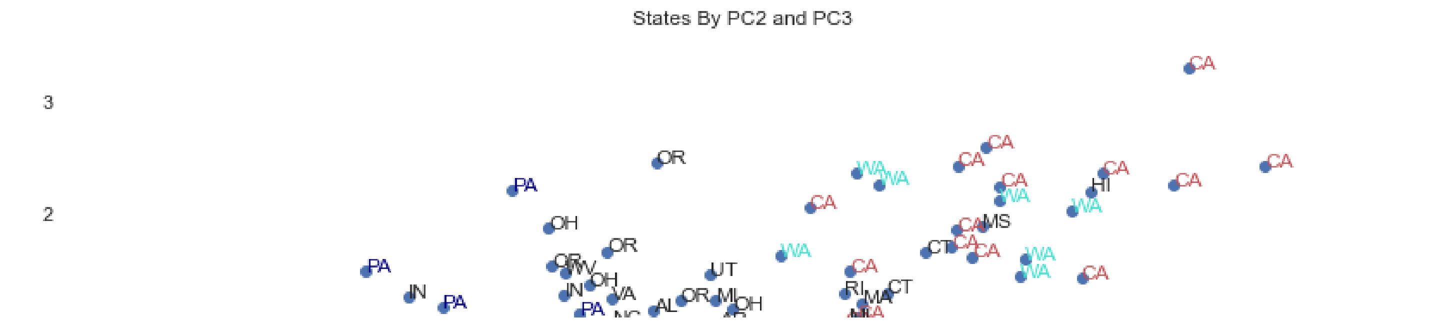
In [25]:

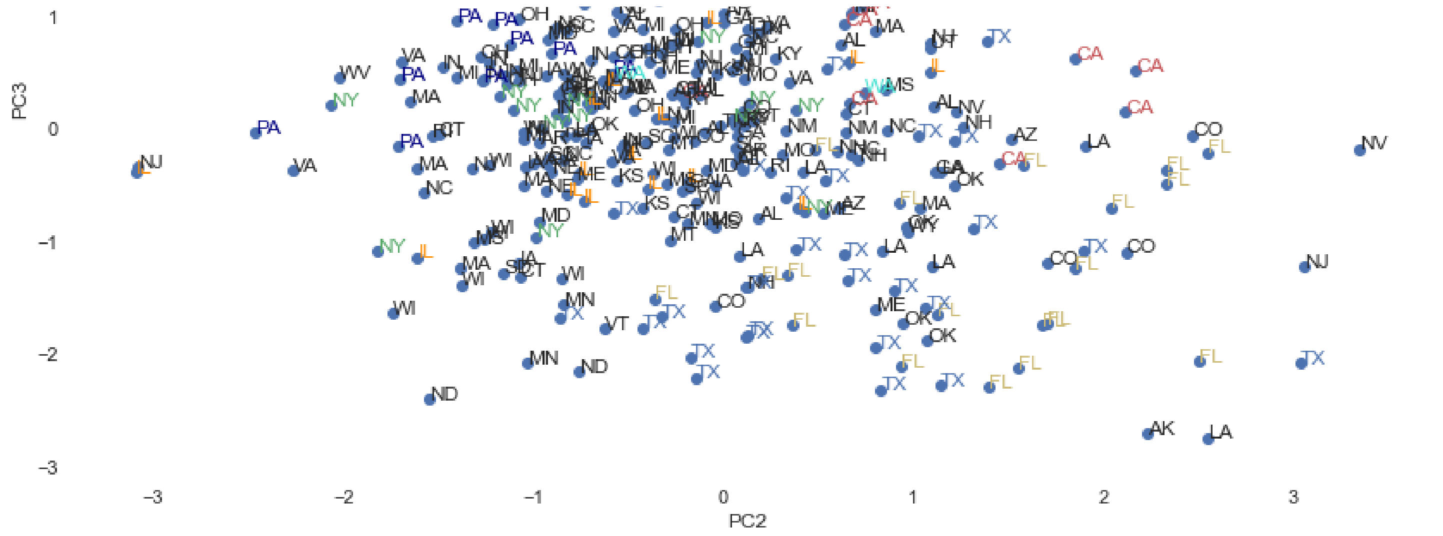
```
plotPCA(2, 1)
```



In [26]:

```
plotPCA(2, 3)
```



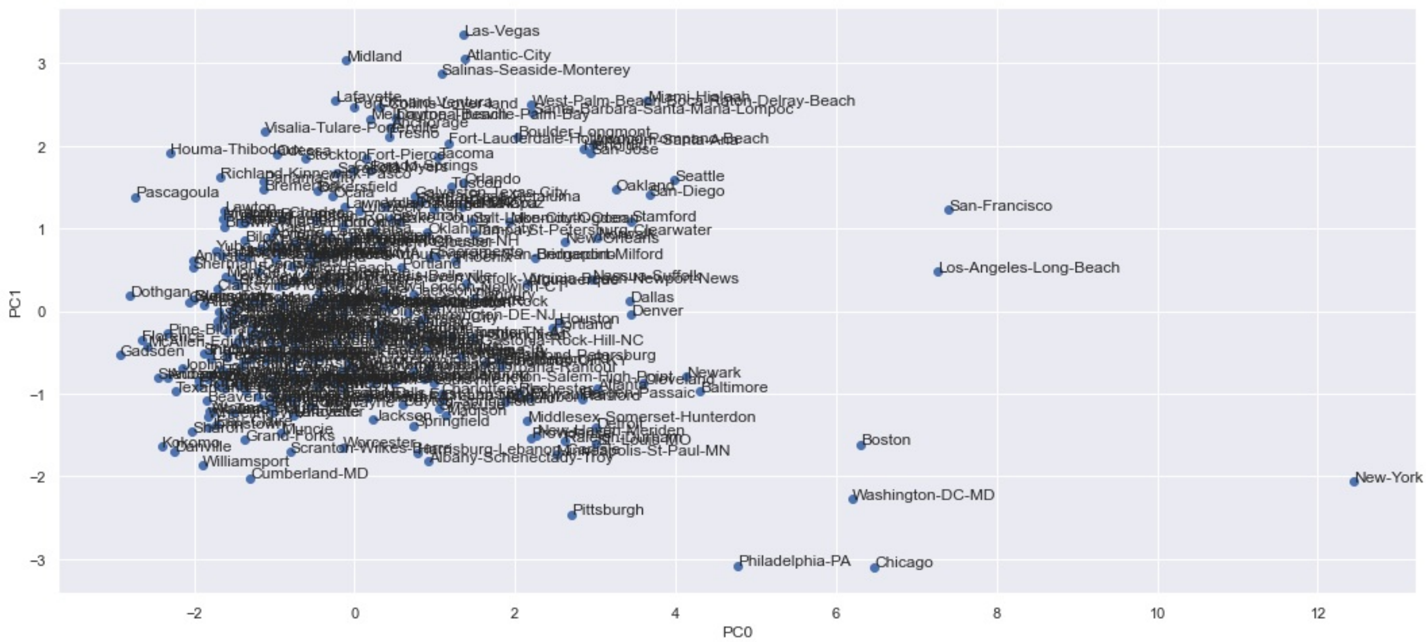


> **The angles between the vectors tell us how characteristics correlate with one another.**
>
> - **When two vectors are close, forming a small angle, the two variables they represent are positively correlated. Example: `TX` and `FL`. Similarly `CA` and `WA`**
> - **If they meet each other at `90°`, they are not likely to be correlated. Example: `TX` and `PA`, similarly `TX` and `CA`**
> - **When they diverge and form a large angle (close to `180°`), they are negative correlated. Example: `TX` and `OR`, similarly `PA` and `FL`.**

Plot Communities on principle components

In [27]:

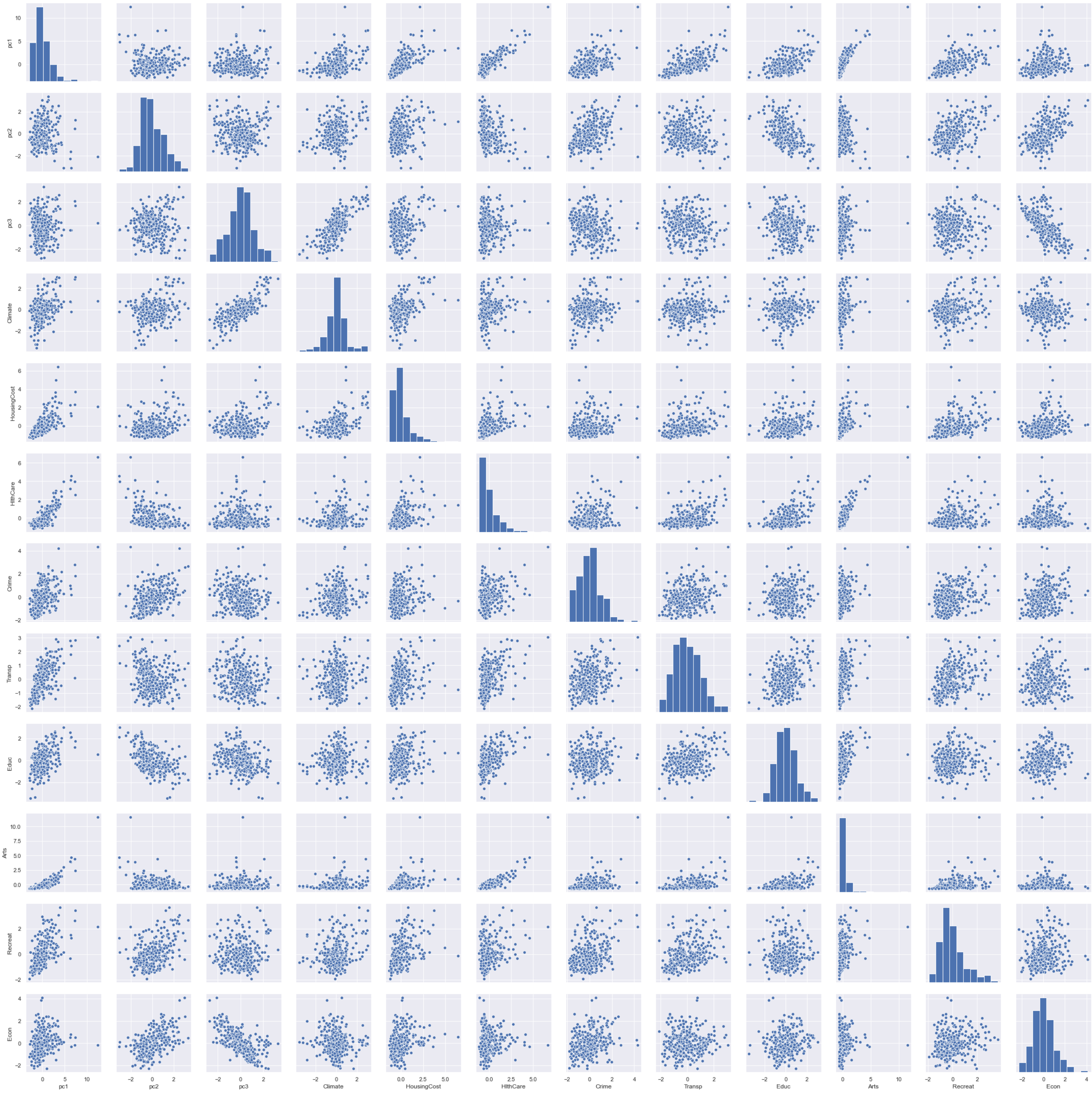
```
c1, c2 = 0, 1
fig, ax = plt.subplots(1, 1, figsize=(18, 8))
ax.scatter(x_pca[:,c1],x_pca[:,c2])
for i,(Community,u) in enumerate(zip(np.array(df),x_pca)):
    ax.annotate(df['Community'][i],(u[c1],u[c2]))
ax.grid(True)
ax.set_xlabel(f"PC{c1}")
ax.set_ylabel(f"PC{c2}")
ax.set_frame_on(True)
fig.savefig('Communities By PC1 PC2.png', dpi=75)
```



Step 5: Scatter plot all original dimensions in the space of PC0 and PC1.

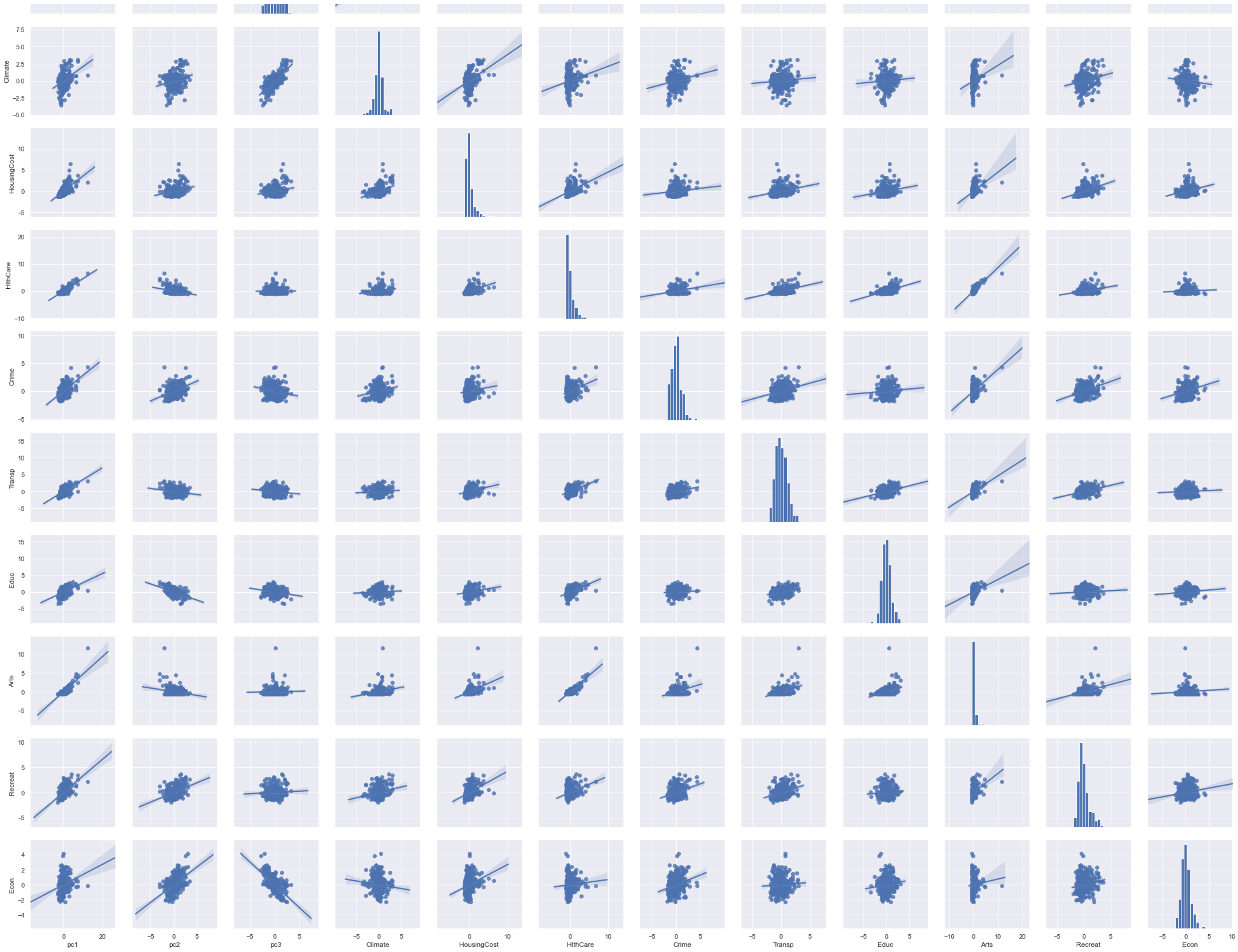
In [28]:

```
# without regression
sn.pairplot(df_col, kind="scatter")
plt.show()
```



In [39]:

```
# with regression
sn.pairplot(df_col, kind="reg")
plt.show()
```



Some interesting stuff

3D chart

In [21]:

```
from mpl_toolkits import mplot3d
```

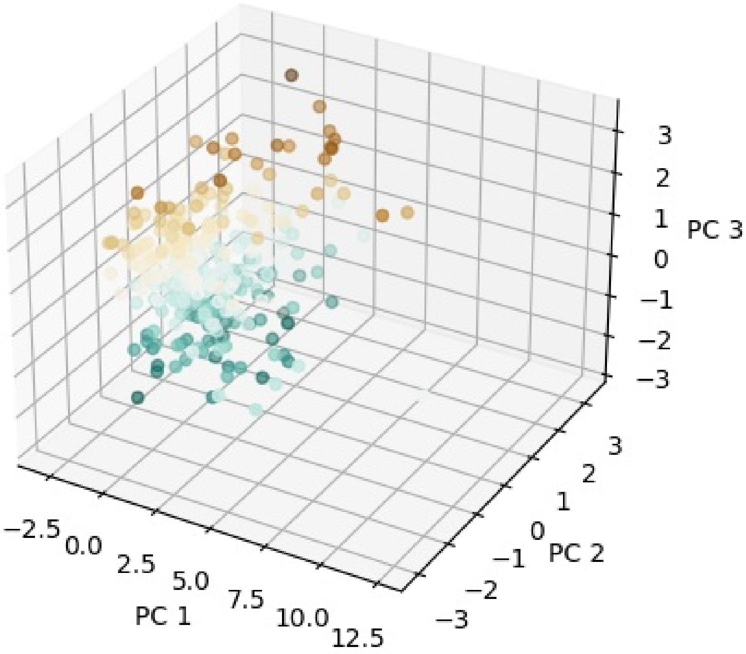
Add options for Interactions

In [22]:

```
%matplotlib notebook
import matplotlib.pyplot as plt
```

In [23]:

```
ax = plt.axes(projection='3d')
xline=x_pca[:,0]
yline=x_pca[:,1]
zline=x_pca[:,2]

ax.scatter3D(xline, yline, zline,c=zline,cmap='BrBG_r')
ax.set_xlabel('PC 1')
ax.set_ylabel('PC 2')
ax.set_zlabel('PC 3')
plt.show()
```



> **The scatter points transparency gives a sense of depth in the figure.**