Data Reduction

In [1]:
```
%matplotlib inline
import pandas as pd
import numpy as np
import scipy as sp
import scipy.stats as stats
import math
from IPython.display import display, HTML # This keeps the nice formatting whe
n printing more than 1 thing

import matplotlib.pyplot as plt # Required for plotting
np.random.seed(33)
```

Sampling in Pandas

In [2]:
```
df = pd.DataFrame(np.random.randn(50, 4), columns=list('ABCD'))
df.head(5)
```

Out[2]:

	A	B	C	D
0	-0.318854	-1.602981	-1.535218	-0.570401
1	-0.216728	0.254874	-0.149450	2.010783
2	-0.096784	0.422202	-0.225462	-0.637943
3	-0.016286	1.044217	-1.084880	-2.205925
4	-0.951219	0.832973	-1.000208	0.343463

In [3]:
```
#You can sample a fraction of the total dataframe
df.sample(frac=0.1,random_state=33)
```

Out[3]:

	A	B	C	D
5	1.546030	0.690081	-2.045853	0.334467
27	-0.769156	0.869197	0.371381	-0.628362
37	-0.352427	0.274527	-1.386049	-1.775175
15	1.054113	-0.615562	0.437443	-2.809395
40	0.578353	-0.103730	-0.161044	0.894541

In [4]:
```
#Or a raw number
df.sample(n=7,random_state=33)
```

Out[4]:

	A	B	C	D
5	1.546030	0.690081	-2.045853	0.334467
27	-0.769156	0.869197	0.371381	-0.628362
37	-0.352427	0.274527	-1.386049	-1.775175
15	1.054113	-0.615562	0.437443	-2.809395
40	0.578353	-0.103730	-0.161044	0.894541
45	0.000855	-0.146146	-0.261976	0.108848
4	-0.951219	0.832973	-1.000208	0.343463

In [5]:
```
#You can turn replacement on as well
df.sample(frac=0.3, replace=True)
```

Out[5]:

	A	B	C	D
46	1.017882	-1.144546	0.781887	-0.173980
3	-0.016286	1.044217	-1.084880	-2.205925
22	0.604432	0.941819	-0.620143	0.814865
48	-0.637681	1.507013	-1.017813	-1.446111
39	0.346235	-0.449622	-1.355818	1.192042
9	-0.777376	-0.414635	-1.145641	0.325040
1	-0.216728	0.254874	-0.149450	2.010783
46	1.017882	-1.144546	0.781887	-0.173980
47	-0.341525	-1.879558	-0.993942	1.021854
8	1.734299	-0.206790	-0.733189	0.774163
5	1.546030	0.690081	-2.045853	0.334467
40	0.578353	-0.103730	-0.161044	0.894541
36	-0.818514	-1.850421	0.397142	-0.946225
12	-0.682350	1.487670	-1.094711	-1.654707
48	-0.637681	1.507013	-1.017813	-1.446111

Stratified Sampling has it's own functions

In [6]:
```
from sklearn.cross_validation import StratifiedShuffleSplit
```

In [7]:
```
class_labels = []
for x in xrange(0,df.shape[0]):
    if x<20:
        class_labels.append(0)
    else:
        class_labels.append(1)

df['labels']= class_labels
display(df.head())
print('')
display(df.tail())
```

	A	B	C	D	labels
0	-0.318854	-1.602981	-1.535218	-0.570401	0
1	-0.216728	0.254874	-0.149450	2.010783	0
2	-0.096784	0.422202	-0.225462	-0.637943	0
3	-0.016286	1.044217	-1.084880	-2.205925	0
4	-0.951219	0.832973	-1.000208	0.343463	0

	A	B	C	D	labels
45	0.000855	-0.146146	-0.261976	0.108848	1
46	1.017882	-1.144546	0.781887	-0.173980	1
47	-0.341525	-1.879558	-0.993942	1.021854	1
48	-0.637681	1.507013	-1.017813	-1.446111	1
49	0.215798	-1.127582	0.439146	0.998467	1

In [8]:
```
sss = StratifiedShuffleSplit(df['labels'], 1, test_size=0.1, random_state=0)

for train_index, test_index in sss:
    population_remaining, population_sample = df.iloc[train_index], df.iloc[te
st_index]

population_sample
```

Out[8]:

	A	B	C	D	labels
15	1.054113	-0.615562	0.437443	-2.809395	0
12	-0.682350	1.487670	-1.094711	-1.654707	0
43	0.594309	-0.166302	1.272612	2.076016	1
27	-0.769156	0.869197	0.371381	-0.628362	1
26	-0.587376	1.751572	0.308274	-0.894283	1

In [9]:
```
#Cluster Data Reduction
import time
from sklearn.cluster import DBSCAN
from sklearn import metrics

df = pd.read_csv('cluster_reduce.csv', encoding='utf-8')
df.head()
```

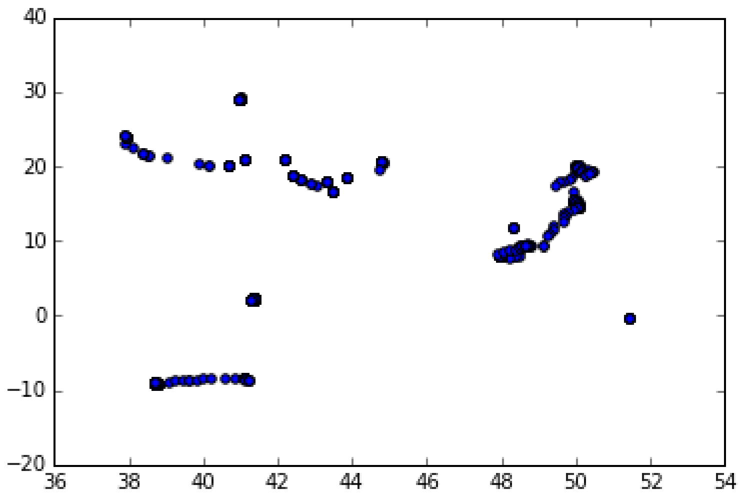
Out[9]:

	lat	lon	date	city	country
0	51.481292	-0.451011	05/14/2014 09:07	West Drayton	United Kingdom
1	51.474005	-0.450999	05/14/2014 09:22	Hounslow	United Kingdom
2	51.478199	-0.446081	05/14/2014 10:51	Hounslow	United Kingdom
3	51.478199	-0.446081	05/14/2014 11:24	Hounslow	United Kingdom
4	51.474146	-0.451562	05/14/2014 11:38	Hounslow	United Kingdom

In [10]:
```
plt.scatter(df['lat'],df['lon'])
print(df.shape)
```

```
(1759, 5)
```

```
/afs/crc.nd.edu/user/k/kfeldman/anaconda/lib/python2.7/site-packages/matplotl
ib/collections.py:590: FutureWarning: elementwise comparison failed; returnin
g scalar instead, but in the future will perform elementwise comparison
  if self._edgecolors == str('face'):
```



In [11]:
```
# represent points consistently as (lat, lon)
kms_per_radian = 6371.0088
coords = df.as_matrix(columns=['lat', 'lon'])
# define epsilon as 1.5 kilometers, converted to radians for use by haversine
epsilon = 1.5 / kms_per_radian

db = DBSCAN(eps=epsilon, min_samples=1, algorithm='ball_tree', metric='haversi
ne').fit(np.radians(coords))
cluster_labels = db.labels_

# get the number of clusters
num_clusters = len(set(cluster_labels))

# all done, print the outcome
message = 'Clustered {:,} points down to {:,} clusters, for {:.1f}% compressio
n'
print(message.format(len(df), num_clusters, 100*(1 - float(num_clusters) /
len(df))))
```

```
Clustered 1,759 points down to 138 clusters, for 92.2% compression
```

In [12]:
```
# turn the clusters in to a pandas series, where each element is a cluster of
 points
clusters = pd.Series([coords[cluster_labels==n] for n in range(num_clusters)])
```

In [13]:
```
def centeroidnp(arr):
    length = arr.shape[0]
    sum_x = np.sum(arr[:, 0])
    sum_y = np.sum(arr[:, 1])
    return sum_x/length, sum_y/length
```

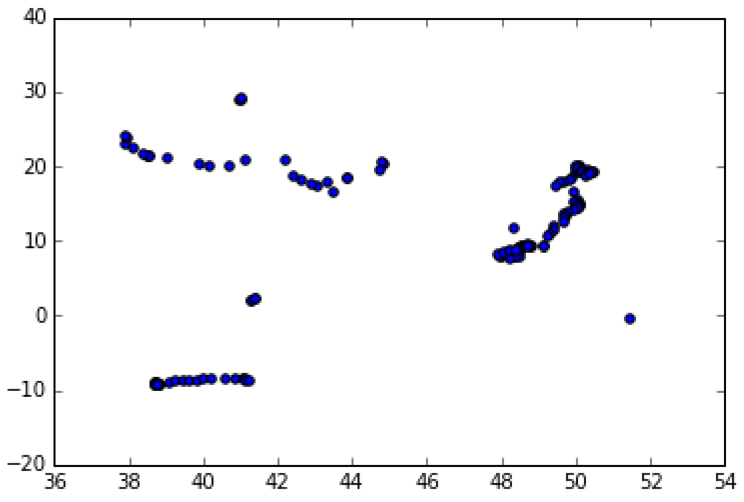
In [14]:
```
centermost_points = clusters.map(centeroidnp)
lats, lons = zip(*centermost_points)
# from these lats/lons create a new df of one representative point for each cl
uster
rep_points = pd.DataFrame({'lon':lons, 'lat':lats})
rep_points.tail()
```

Out[14]:

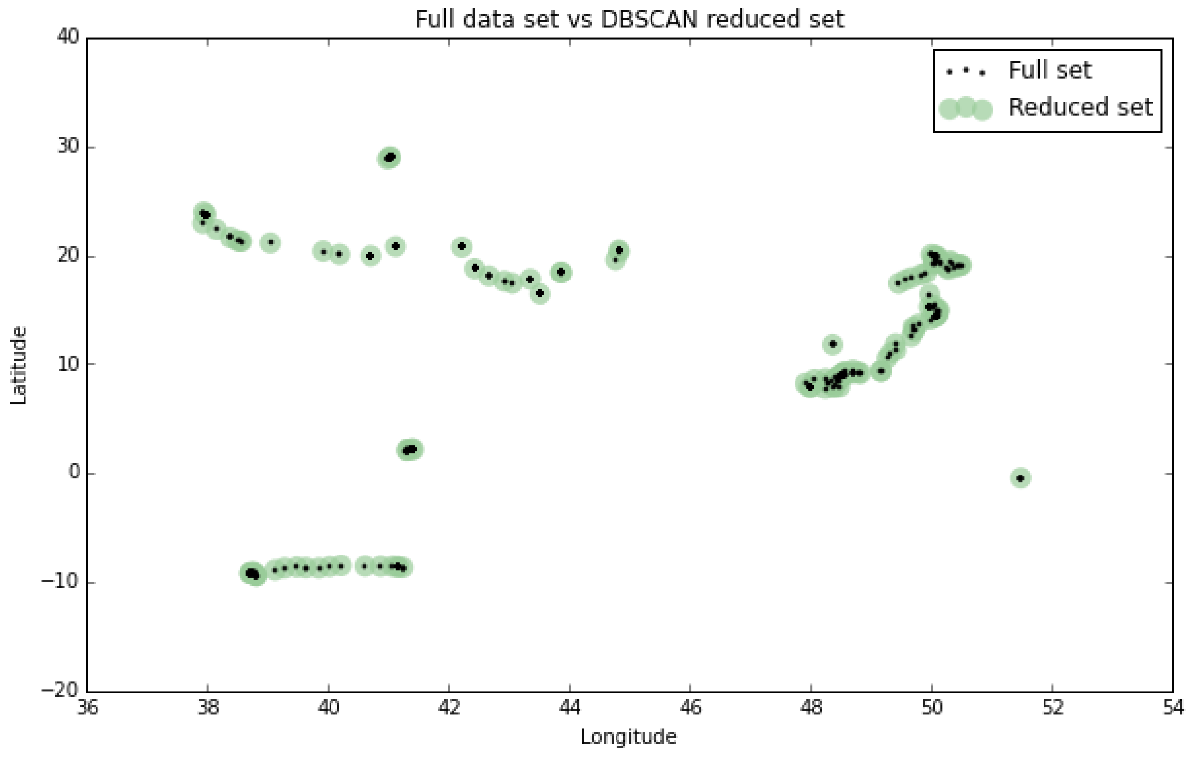
	lat	lon
133	37.933831	23.945850
134	40.979812	28.821654
135	41.032922	28.981427
136	41.016863	29.009547
137	48.356280	11.791802

In [15]:
```
plt.scatter(rep_points['lat'],rep_points['lon'])
print(rep_points.shape)
```

```
(138, 2)
```



In [16]:
```
# plot the final reduced set of coordinate points vs the original full set
fig, ax = plt.subplots(figsize=[10, 6])
rs_scatter = ax.scatter(rep_points['lat'],rep_points['lon'], c='#99cc99', edge
color='None', alpha=0.7, s=120)
df_scatter = ax.scatter(df['lat'], df['lon'], c='k', alpha=0.9, s=3)
ax.set_title('Full data set vs DBSCAN reduced set')
ax.set_xlabel('Longitude')
ax.set_ylabel('Latitude')
ax.legend([df_scatter, rs_scatter], ['Full set', 'Reduced set'], loc='upper ri
ght')
plt.show()
```



Feature Selection - Univariate

In [17]:
```
from sklearn.datasets import load_iris
fileURL = 'http://archive.ics.uci.edu/ml/machine-learning-databases/iris/iris.
data'
data = pd.read_csv(fileURL, names=['Sepal Length', 'Sepal Width', 'Petal Lengt
h', 'Petal Width', 'Name'], header=None)
iris_data = data.dropna()
iris_data.head()
```

Out[17]:

	Sepal Length	Sepal Width	Petal Length	Petal Width	Name
0	5.1	3.5	1.4	0.2	Iris-setosa
1	4.9	3.0	1.4	0.2	Iris-setosa
2	4.7	3.2	1.3	0.2	Iris-setosa
3	4.6	3.1	1.5	0.2	Iris-setosa
4	5.0	3.6	1.4	0.2	Iris-setosa

In [18]:
```
X = iris_data[['Sepal Length', 'Sepal Width', 'Petal Length', 'Petal
Width']].copy()
y = iris_data[['Name']].copy()
```

These objects take as input a scoring function that returns univariate scores and p-values (or only scores for SelectKBest and SelectPercentile):

For regression: *f_regression, mutual_info_regression*
For classification: *chi2, f_classif, mutual_info_classif*

The methods based on F-test estimate the degree of linear dependency between two random variables. On the other hand, mutual information methods can capture any kind of statistical dependency, but being nonparametric, they require more samples for accurate estimation.

In [19]:
```
from sklearn.feature_selection import SelectPercentile
from sklearn.feature_selection import SelectKBest
from sklearn.feature_selection import chi2
from sklearn.feature_selection import f_regression
Selector_f = SelectKBest(chi2,k=1)
Selector_f.fit(X,y)
scores = []
for n,s in zip(['Sepal Length', 'Sepal Width', 'Petal Length', 'Petal
Width'],Selector_f.scores_):
    scores.append((n,s))

scores = pd.DataFrame(scores)
scores.sort(1,ascending=False)
```

```
/afs/crc.nd.edu/user/k/kfeldman/anaconda/lib/python2.7/site-packages/sklearn/
utils/validation.py:449: DataConversionWarning: A column-vector y was passed
 when a 1d array was expected. Please change the shape of y to (n_samples, ),
for example using ravel().
  y = column_or_1d(y, warn=True)
```

Out[19]:

	0	1
2	Petal Length	116.169847
3	Petal Width	67.244828
0	Sepal Length	10.817821
1	Sepal Width	3.594499

In [20]:
```
from sklearn.datasets import make_friedman1
from sklearn.feature_selection import RFE
from sklearn.svm import SVR
X, y = make_friedman1(n_samples=50, n_features=10, random_state=0)
estimator = SVR(kernel="linear")
selector = RFE(estimator, 5, step=1)
selector = selector.fit(X, y)
selector.support_


selector.ranking_
```

Out[20]:
```
array([1, 1, 1, 1, 1, 6, 4, 3, 2, 5])
```

In [21]:
```
#Extra - Feature Importances
from sklearn.ensemble import RandomForestClassifier
rf = RandomForestClassifier(n_estimators=20, max_depth=4)
rfc = rf.fit(X,y)
print(rfc.feature_importances_)
scores = []
for n,s in zip(['Sepal Length', 'Sepal Width', 'Petal Length', 'Petal
Width'],rfc.feature_importances_):
    scores.append((n,s))

scores = pd.DataFrame(scores)
scores.sort(1,ascending=False)
```

```
[ 0.09318801  0.15037965  0.06433626  0.1112646   0.05650729  0.10239585
  0.0834941   0.07682496  0.15486122  0.10674807]
```

Out[21]:

	0	1
1	Sepal Width	0.150380
3	Petal Width	0.111265
0	Sepal Length	0.093188
2	Petal Length	0.064336

PCA

For a full tutorial of PCA in python see the link below
http://sebastianraschka.com/Articles/2014_pca_step_by_step.html
(http://sebastianraschka.com/Articles/2014_pca_step_by_step.html)

In [22]:
```
from sklearn.preprocessing import StandardScaler
fileURL = 'http://archive.ics.uci.edu/ml/machine-learning-databases/iris/iris.
data'
data = pd.read_csv(fileURL, names=['Sepal Length', 'Sepal Width', 'Petal Lengt
h', 'Petal Width', 'Name'], header=None)
iris_data = data.dropna()
iris_data.head()

X = iris_data[['Sepal Length', 'Sepal Width', 'Petal Length', 'Petal
Width']].copy()
y = iris_data[['Name']].copy()

X_std = StandardScaler().fit_transform(X)
display(X.head())
pd.DataFrame(X_std).head()
```

	Sepal Length	Sepal Width	Petal Length	Petal Width
0	5.1	3.5	1.4	0.2
1	4.9	3.0	1.4	0.2
2	4.7	3.2	1.3	0.2
3	4.6	3.1	1.5	0.2
4	5.0	3.6	1.4	0.2

Out[22]:

	0	1	2	3
0	-0.900681	1.032057	-1.341272	-1.312977
1	-1.143017	-0.124958	-1.341272	-1.312977
2	-1.385353	0.337848	-1.398138	-1.312977
3	-1.506521	0.106445	-1.284407	-1.312977
4	-1.021849	1.263460	-1.341272	-1.312977

In [23]:
```
mean_vec = np.mean(X_std, axis=0)
cov_mat = (X_std - mean_vec).T.dot((X_std - mean_vec)) / (X_std.shape[0]-1)
print('Covariance matrix \n%s' %cov_mat)
```

```
Covariance matrix
[[ 1.00671141 -0.11010327  0.87760486  0.82344326]
 [-0.11010327  1.00671141 -0.42333835 -0.358937  ]
 [ 0.87760486 -0.42333835  1.00671141  0.96921855]
 [ 0.82344326 -0.358937    0.96921855  1.00671141]]
```

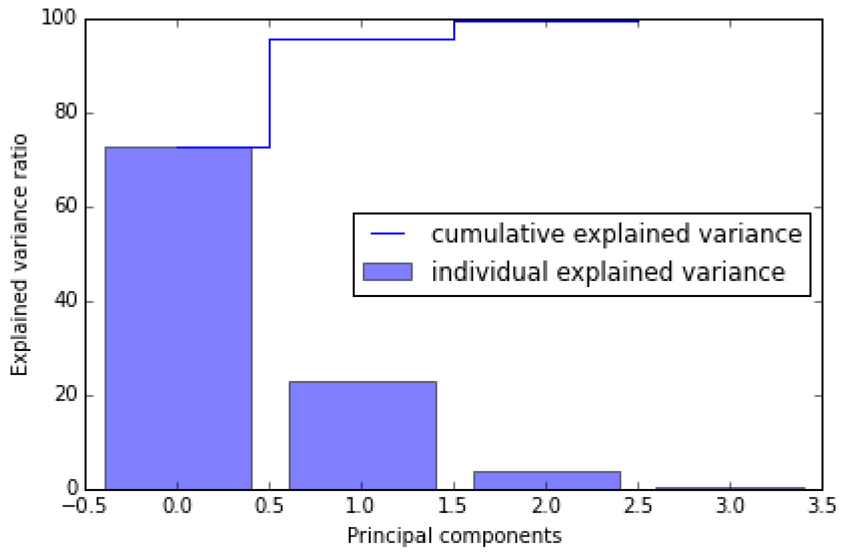
In [24]:
```
cov_mat = np.cov(X_std.T)

eig_vals, eig_vecs = np.linalg.eig(cov_mat)

print('Eigenvectors \n%s' %eig_vecs)
print('\nEigenvalues \n%s' %eig_vals)
```

```
Eigenvectors
[[ 0.52237162 -0.37231836 -0.72101681  0.26199559]
 [-0.26335492 -0.92555649  0.24203288 -0.12413481]
 [ 0.58125401 -0.02109478  0.14089226 -0.80115427]
 [ 0.56561105 -0.06541577  0.6338014   0.52354627]]

Eigenvalues
[ 2.93035378  0.92740362  0.14834223  0.02074601]
```

In [25]:
```
# Make a list of (eigenvalue, eigenvector) tuples
eig_pairs = [(np.abs(eig_vals[i]), eig_vecs[:,i]) for i in
range(len(eig_vals))]

# Sort the (eigenvalue, eigenvector) tuples from high to low
eig_pairs.sort(key=lambda x: x[0], reverse=True)

# Visually confirm that the list is correctly sorted by decreasing eigenvalues
print('Eigenvalues in descending order:')
for i in eig_pairs:
    print(i[0])
```

```
Eigenvalues in descending order:
2.93035377559
0.927403621517
0.148342226482
0.0207460139956
```

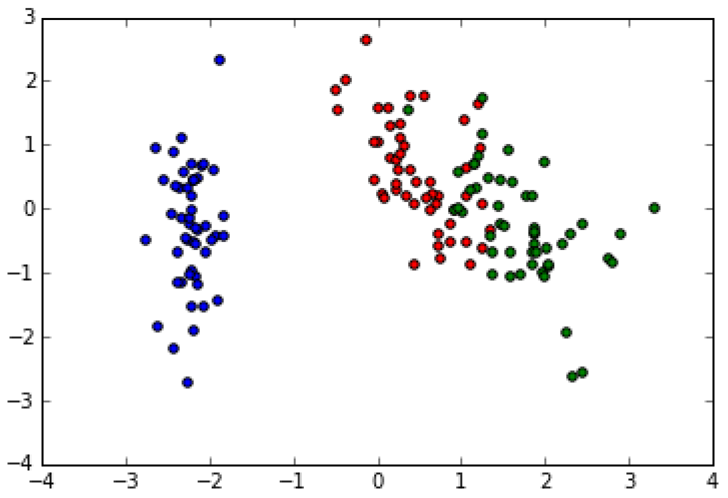
In [26]:
```
tot = sum(eig_vals)
var_exp = [(i / tot)*100 for i in sorted(eig_vals, reverse=True)]
cum_var_exp = np.cumsum(var_exp)
plt.figure(figsize=(6, 4))

plt.bar(range(4), var_exp, alpha=0.5, align='center',
        label='individual explained variance')
plt.step(range(4), cum_var_exp, where='mid',
         label='cumulative explained variance')
plt.ylabel('Explained variance ratio')
plt.xlabel('Principal components')
plt.legend(loc='best')
plt.tight_layout()
```



In [27]:
```
matrix_w = np.hstack((eig_pairs[0][1].reshape(4,1),
                      eig_pairs[1][1].reshape(4,1)))

print('Matrix W:')
print(matrix_w)
```

```
Matrix W:
[[ 0.52237162 -0.37231836]
 [-0.26335492 -0.92555649]
 [ 0.58125401 -0.02109478]
 [ 0.56561105 -0.06541577]]
```

In [28]:
```
Y = X_std.dot(matrix_w)
Y = pd.DataFrame(Y)
plt.figure(figsize=(6, 4))
#plt.scatter(Y[0],Y[1],c=y)
for lab, col in zip(('Iris-setosa', 'Iris-versicolor', 'Iris-virginica'),
                    ('blue', 'red', 'green')):
    plt.scatter(Y[Y.index.isin(y[y['Name']==lab].index)][0],
                Y[Y.index.isin(y[y['Name']==lab].index)][1],
                c=col)
```



In [29]:
```
existing_df = pd.read_csv('lecture5PCA.csv',index_col = 0, thousands  = ',')
existing_df.index.names = ['country']
existing_df.columns.names = ['year']
existing_df.head()
```

Out[29]:

year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	20
country													
Afghanistan	436	429	422	415	407	397	397	387	374	373	346	326	30
Albania	42	40	41	42	42	43	42	44	43	42	40	34	32
Algeria	45	44	44	43	43	42	43	44	45	46	48	49	50
American Samoa	42	14	4	18	17	22	0	25	12	8	8	6	5
Andorra	39	37	35	33	32	30	28	23	24	22	20	20	21

In [30]:
```
from sklearn.decomposition import RandomizedPCA

pca = RandomizedPCA(n_components=2)
pca.fit(existing_df)
```

Out[30]:
```
RandomizedPCA(copy=True, iterated_power=3, n_components=2, random_state=None,
       whiten=False)
```

In [31]:
```
existing_2d = pca.transform(existing_df)
existing_df_2d = pd.DataFrame(existing_2d)
existing_df_2d.index = existing_df.index
existing_df_2d.columns = ['PC1','PC2']
existing_df_2d.head()
```

Out[31]:

	PC1	PC2
country		
Afghanistan	732.215864	203.381495
Albania	-613.296510	4.715978
Algeria	-569.303713	-36.837051
American Samoa	-717.082766	5.464696
Andorra	-661.802241	11.037736

In [32]:
```
print(pca.explained_variance_ratio_)
```

```
[ 0.91808789  0.060556  ]
```

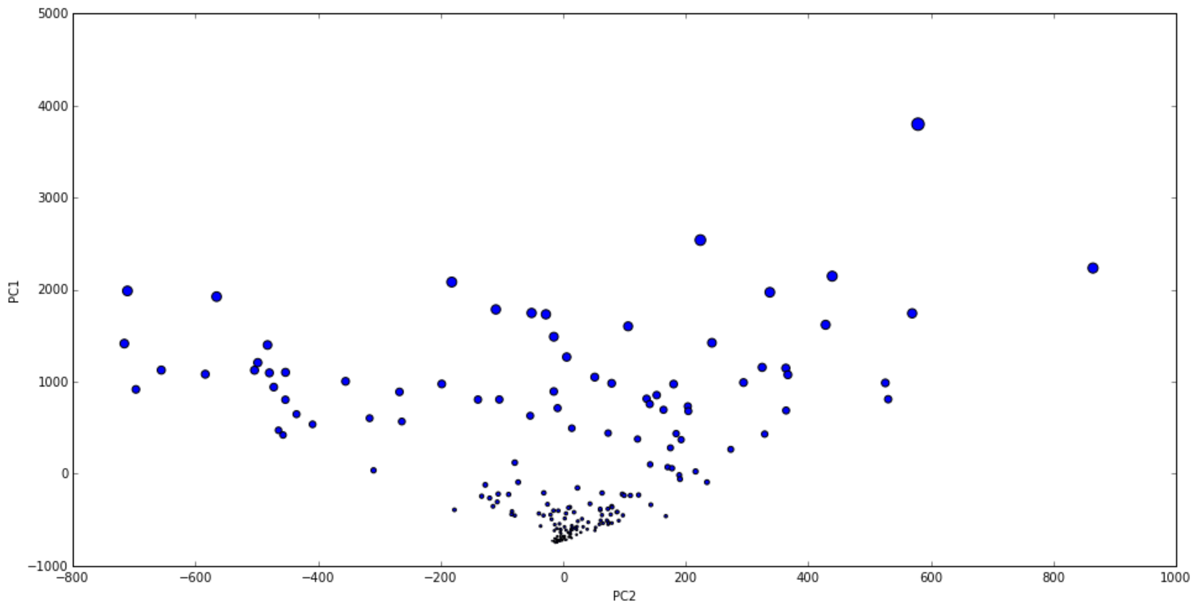
In [33]:
```
from sklearn.preprocessing import normalize
#We can scale the points by the countries mean value across the years, and can
 clearly see PCA seperate data based on the mean

existing_df_2d['country_mean'] = pd.Series(existing_df.mean(axis=1), index=exi
sting_df_2d.index)
country_mean_max = existing_df_2d['country_mean'].max()
country_mean_min = existing_df_2d['country_mean'].min()
country_mean_scaled = (existing_df_2d.country_mean-country_mean_min) / country
_mean_max
existing_df_2d['country_mean_scaled'] = pd.Series(
        country_mean_scaled,
        index=existing_df_2d.index)
existing_df_2d.head()
```

Out[33]:

	PC1	PC2	country_mean	country_mean_scaled
country				
Afghanistan	732.215864	203.381495	353.333333	0.329731
Albania	-613.296510	4.715978	36.944444	0.032420
Algeria	-569.303713	-36.837051	47.388889	0.042234
American Samoa	-717.082766	5.464696	12.277778	0.009240
Andorra	-661.802241	11.037736	25.277778	0.021457

```
In [34]: existing_df_2d.plot(
             kind='scatter',
             x='PC2',
             y='PC1',
             s=existing_df_2d['country_mean_scaled']*100,
             figsize=(16,8))
```

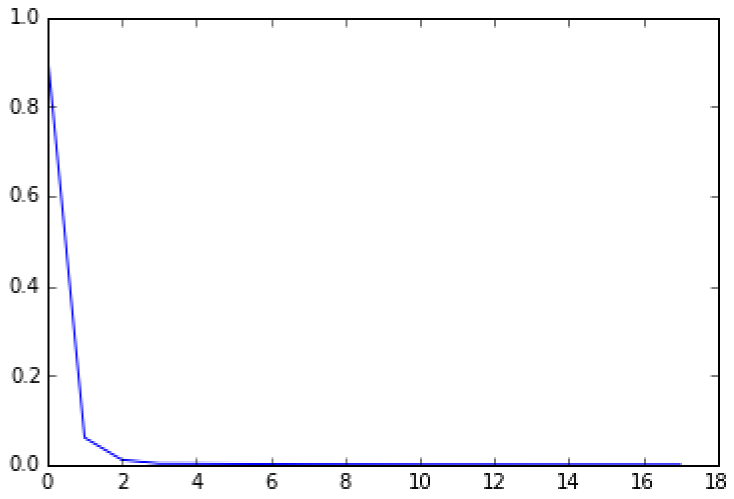
```
Out[34]: <matplotlib.axes._subplots.AxesSubplot at 0x7f9d7d4879d0>
```



```
In [35]: pca = RandomizedPCA()
         pca.fit(existing_df)
         print(pca.explained_variance_ratio_)
         plt.plot(pca.explained_variance_ratio_)
```

```
[  9.18087891e-01   6.05560009e-02   1.08051220e-02   2.39047545e-03
   2.19038229e-03   1.64732996e-03   1.19502740e-03   7.97856744e-04
   6.35817920e-04   4.61460559e-04   3.20989293e-04   2.66657191e-04
   2.42807240e-04   1.56998807e-04   1.08464204e-04   7.07768488e-05
   4.20518883e-05   2.38906112e-05]
```

```
Out[35]: [<matplotlib.lines.Line2D at 0x7f9ce2cf1990>]
```



1.0
0.8
0.6
0.4
0.2
0.0
0
2
4
6
8
10
12
14
16
18