Hands-on Exercise for Module 1: Exploratory Data Analysis

0.Importing important packages

In [1]:
```
# data loading and computing functionality
import pandas as pd
import numpy as np
import scipy as sp

# datasets in sklearn package
from sklearn import datasets
from sklearn.datasets import load_digits

# visualization packages
import seaborn as sns
import matplotlib.pyplot as plt
import matplotlib.cm as cm

#PCA, SVD, LDA
from sklearn.decomposition import PCA
from scipy.linalg import svd
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis
```

1. Loading data, determining samples, attributes, and types of attributes

Use Davis dataset avaialble at the url https://vincentarelbundock.github.io/Rdatasets/csv/carData/Davis.csv (https://vincentarelbundock.github.io/Rdatasets/csv/carData/Davis.csv)

Description of the data is provided at http://math.furman.edu/~dcs/courses/math47/R/library/car/html/Davis.html (http://math.furman.edu/~dcs/courses/math47/R/library/car/html/Davis.html)

Drop rows in the data set with missing values (NA), using dropna(inplace=True) function.

Question 1a: Based on the data description, ware the data points and what are the attributes i this data?

Answer: Each data point represents a man or women who is engaged in regular exercise The attributes are sex, measured weight, measured height, reported height, and reportec weight the the men and women.

Question 1b: Who are selected as subjects in the study?

Answer: Mean and women that are engaged in regular exercise

Question 1c: How many data points are in this dataset?

In [2]:
```
davis_df = pd.read_csv('https://vincentarelbundock.github.io/Rdatasets/csv/ca
```

In [3]:
```
davis_df.dropna(inplace=True);
```

In [4]:
```
davis_df.shape
```

Out[4]:
```
(181, 6)
```

Answer: There are 181 data points in this set.

Question 1d: How many attributes are in this dataset?

Answer: There are 6 attribute in this set.

Question 1e: What type of attributes are present in the dataset?

In [5]:
```
davis_df.dtypes
```

Out[5]:
```
Unnamed: 0      int64
sex            object
weight          int64
height          int64
repwt         float64
repht         float64
dtype: object
```

Answer: There are attributes of type int 64, object, and float 64.

2. Generating summary statistics

Use 'Davis' data. Do not include Unnamed attribute in this analysis.

In [6]:
```
davis_df.drop(columns=davis_df.columns[davis_df.columns.str.contains('unname
davis_df.head()
```

Out[6]:

	sex	weight	height	repwt	repht
0	M	77	182	77.0	180.0
1	F	58	161	51.0	159.0
2	F	53	161	54.0	158.0
3	M	68	177	70.0	175.0
4	F	59	157	59.0	155.0

Question 2a: What are range of values the numeric attributes take?
[Hint: Use exclude=object option in describe() function to ignore the attribute sex]

In [7]:
```
davis_df.describe(exclude=object)
```

Out[7]:

	weight	height	repwt	repht
count	181.000000	181.000000	181.000000	181.000000
mean	66.303867	170.154696	65.679558	168.657459
std	15.340992	12.312069	13.834220	9.394668
min	39.000000	57.000000	41.000000	148.000000
25%	56.000000	164.000000	55.000000	161.000000
50%	63.000000	169.000000	63.000000	168.000000
75%	75.000000	178.000000	74.000000	175.000000
max	166.000000	197.000000	124.000000	200.000000

Answer: Measured weight ranges from 38 to 166 kilograms. Measured height ranges from 57 t
197 centimeters. Reported height ranges from 41 to 124 kilograms. Reported height ranges fro
148 to 200 centimeters

Question 2b: What different values do categorical attributes take?
[Hint: Use include=object option in describe() function to ignore the attribute sex]

In [48]:
```
davis_df.describe(include=object)
```

Out[48]:

	sex
count	181
unique	2
top	F
freq	99

Answer: The different values for the categorical attribute is male and female.

Question 2c: What are the mean values for each of the numeric attributes?

In [9]:
```
from pandas.api.types import is_numeric_dtype

for col in davis_df.columns:
    if is_numeric_dtype(davis_df[col]):
        print('%s:' % (col))
        print('\t Mean = %.2f' % davis_df[col].mean())
```

```
weight:
         Mean = 66.30
height:
         Mean = 170.15
repwt:
         Mean = 65.68
repht:
         Mean = 168.66
```

Question 2d: What is the variance for each of the numeric attributes?

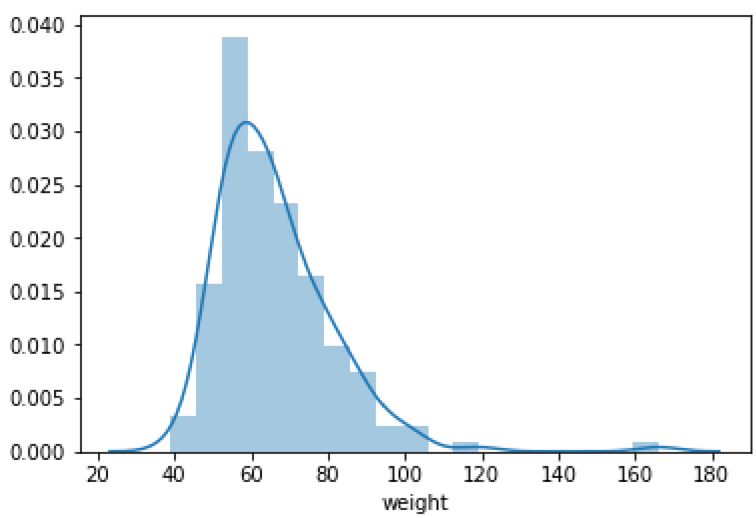
In [10]:
```
from pandas.api.types import is_numeric_dtype

for col in davis_df.columns:
    if is_numeric_dtype(davis_df[col]):
        print('%s:' % (col))
        print('\t Mean = %.2f' % davis_df[col].var())
```

```
weight:
         Mean = 235.35
height:
         Mean = 151.59
repwt:
         Mean = 191.39
repht:
         Mean = 88.26
```

Question 2e: Visually examine how the attribute 'weight' is distributed and comment if the distribution is more similar to a Gaussian distribution or to a uniform distribution?

In [11]:
```
sns.distplot(davis_df['weight']);
```

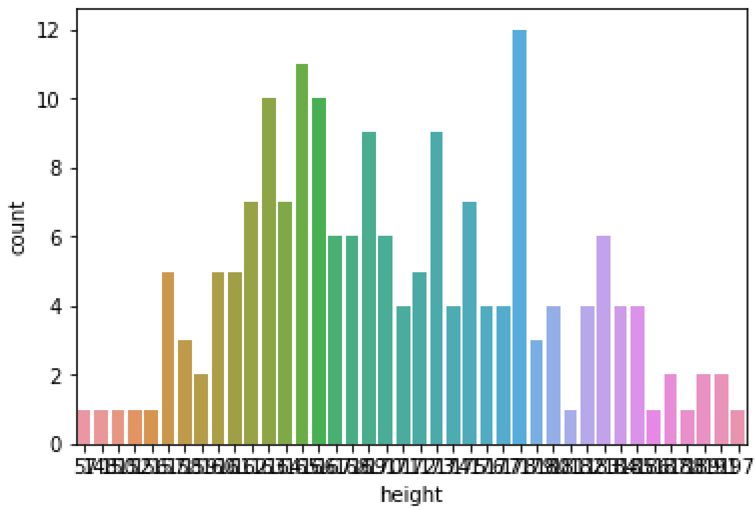
```
/usr/local/python/2.7-conda5.2/lib/python2.7/site-packages/scipy/stats/stats
y:1713: FutureWarning: Using a non-tuple sequence for multidimensional index
is deprecated; use `arr[tuple(seq)]` instead of `arr[seq]`. In the future th
will be interpreted as an array index, `arr[np.array(seq)]`, which will resu
either in an error or a different result.
  return np.add.reduce(sorted[indexer] * weights, axis=axis) / sumval
```



Answer: This distribution is not normally distributed. It is skewed to the right.

Question 2f: Visually examine how the attribute 'height' is distributed and comment if the distribution is more similar to a Gaussian distribution or to a uniform distribution?

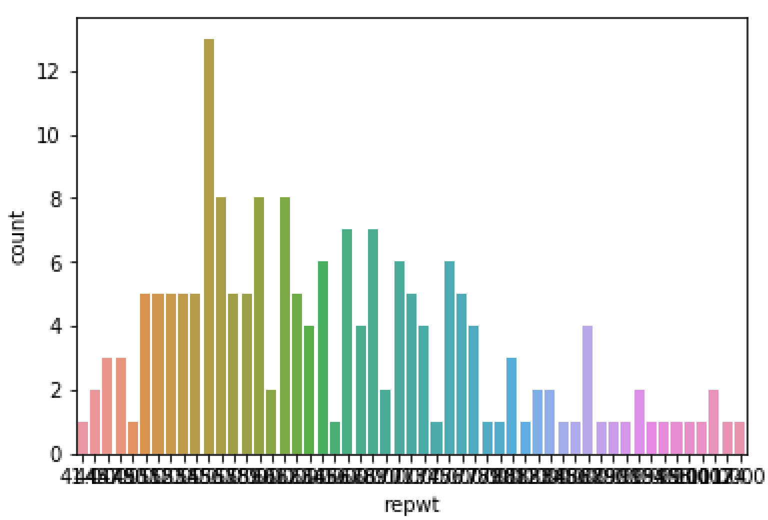
In [12]:
```python
sns.countplot(davis_df['height']);
```



Answer: This distribution looks more similar to a gaussian distribution than a uniform distributio

Question 2g: Visually examine how the attribute 'repwt' is distributed and comment if the distribution is more similar to a Gaussian distribution or to a uniform distribution?

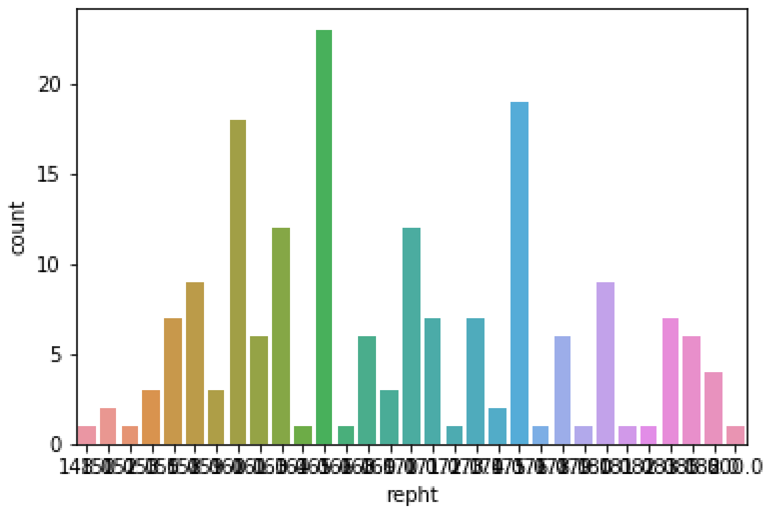
In [13]:
```python
sns.countplot(davis_df['repwt']);
```



Answer: This distribution, again, appears to look more Gaussian with a skew to the right.

Question 2h: Visually examine how the attribute 'repht' is distributed and comment if the distribution is more similar to a Gaussian distribution or to a uniform distribution?

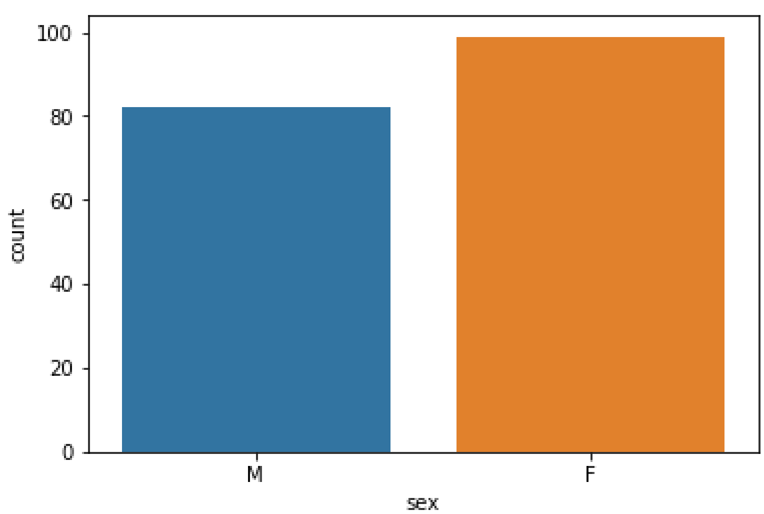
In [14]:
```
sns.countplot(davis_df['repht']);
```



Answer: This distribution looks like a sparse Gaussian distribution.

Question 2i: Visually examine how the attribute 'sex' is distributed and comment if the distribut is more similar to a Gaussian distribution or to a uniform distribution?

In [15]:
```
sns.countplot(davis_df['sex']);
```



Answer: This distriubtion looks more like a uniform distribution than a Gaussian distribution.

Question 2j: Is it possible for attribute 'sex' to follow a Gaussian distribution? Support your ans with a rationale.

Type *Markdown* and LaTeX: α^2

Answer: It would not be possible for sex to follow a gaussian distribution. This is do to there onl being two sexes measured. There can be no symmetry, except uniformity, that is characteristic Gaussian distribution.

Note: For this part, we will restrict to 'repwt' and 'repht' attributes in the davis dataset as we car only visualize 2D space.

In [16]:
```
davis_df_new = davis_df[['repwt','repht']]
```

In [17]:
```
davis_df_new.head()
```

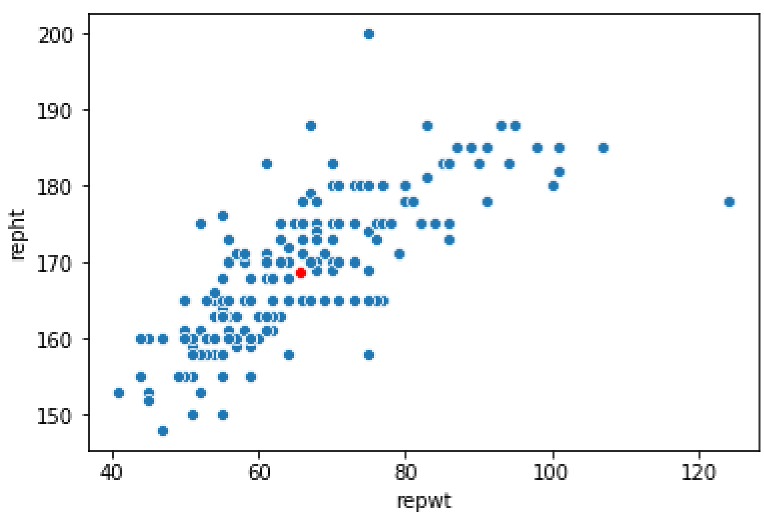
Out[17]:

	repwt	repht
0	77.0	180.0
1	51.0	159.0
2	54.0	158.0
3	70.0	175.0
4	59.0	155.0

Question 3a: Show the Geometric view of this data 'davis_df_new' on a 2D space along with tl mean.

In [18]:
```
fig, ax = plt.subplots()
sns.scatterplot(x='repwt',y='repht',data=davis_df_new,ax=ax)
mu = np.mean(davis_df_new.values,0)
sns.scatterplot(x=[mu[0], mu[0]],y=[mu[1], mu[1]],color='r',ax=ax)
```

Out[18]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x2b17a7c30210>
```



In [ ]:

Question 3b: From the geometric view, state your observations about the data and any relationships you observe between the attributes.

In [19]:
```
Based on my observation, there appears to be a positive correlation between
```

```
  File "<ipython-input-19-d945d96dc131>", line 1
    Based on my observation, there appears to be a positive correlation betw
repwt and repht.
           ^
SyntaxError: invalid syntax
```

We will further normalize the magnitude of each row in the data (davis_df_new) to 1 and use th new dataframe davis_df_new_row_norm.

In [20]:
```
from sklearn.preprocessing import normalize
davis_df_new_row_norm = normalize(davis_df_new, axis=1, norm='l2')
```

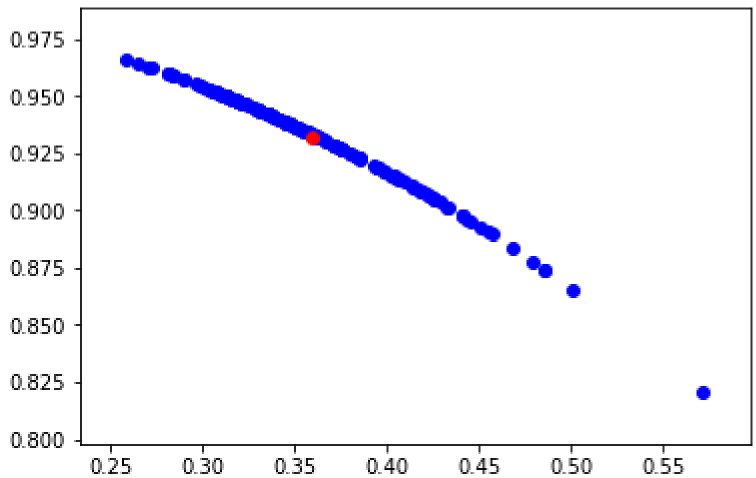
In [21]:
```
davis_df_new_row_norm[1:10,:]
```

Out[21]:
```
array([[0.30542755, 0.95221532],
       [0.32340548, 0.94626048],
       [0.37139068, 0.92847669],
       [0.35574458, 0.93458322],
       [0.41835989, 0.90828134],
       [0.42288547, 0.90618314],
       [0.37582461, 0.92669081],
       [0.37595091, 0.92663958],
       [0.35232976, 0.93587592]])
```

Question 3c: Show the Geometric view of this new row normalized data on a 2D space along the mean.

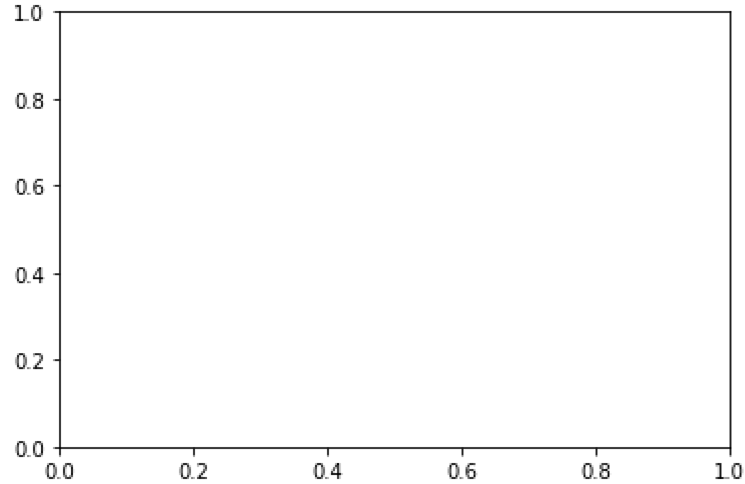
In [28]:
```
mu = np.mean(davis_df_new_row_norm,axis=0)
plt.figure()
plt.scatter(davis_df_new_row_norm[:, 0], davis_df_new_row_norm[:, 1], c='b')
plt.scatter(mu[0], mu[1], c='r')
```

Out[28]: <matplotlib.collections.PathCollection at 0x2b17a8145450>



In [26]:

```
AttributeErrorTraceback (most recent call last)
<ipython-input-26-dbee17f31b6f> in <module>()
      1 fig, ax = plt.subplots()
----> 2 sns.scatterplot(x='repwt',y='repht',data=davis_df_new_row_norm,ax=ax
      3 mu = np.mean(davis_df_new_row_norm.values,0)
      4 sns.scatterplot(x=[mu[0], mu[0]],y=[mu[1], mu[1]],color='r',ax=ax)

/usr/local/python/2.7-conda5.2/lib/python2.7/site-packages/seaborn/relationa
yc in scatterplot(x, y, hue, style, size, data, palette, hue_order, hue_norm
izes, size_order, size_norm, markers, style_order, x_bins, y_bins, units, es
ator, ci, n_boot, alpha, x_jitter, y_jitter, legend, ax, **kwargs)
   1333         x_bins=x_bins, y_bins=y_bins,
   1334         estimator=estimator, ci=ci, n_boot=n_boot,
-> 1335         alpha=alpha, x_jitter=x_jitter, y_jitter=y_jitter, legend=le
d,
   1336     )
   1337 

/usr/local/python/2.7-conda5.2/lib/python2.7/site-packages/seaborn/relationa
yc in __init__(self, x, y, hue, size, style, data, palette, hue_order, hue_n
m, sizes, size_order, size_norm, dashes, markers, style_order, x_bins, y_bin
 units, estimator, ci, n_boot, alpha, x_jitter, y_jitter, legend)
    850 
    851         plot_data = self.establish_variables(
--> 852             x, y, hue, size, style, units, data
    853         )
    854 

/usr/local/python/2.7-conda5.2/lib/python2.7/site-packages/seaborn/relationa
yc in establish_variables(self, x, y, hue, size, style, units, data)
    129             # Use variables as from the dataframe if specified
    130             if data is not None:
--> 131                 x = data.get(x, x)
    132                 y = data.get(y, y)
    133                 hue = data.get(hue, hue)

AttributeError: 'numpy.ndarray' object has no attribute 'get'
```



Answer:

Question 3d: Comment on the new geomateric view of the data in comparison to the view you observed in Question 3b. Provide a reason for the difference in the two geometric views.

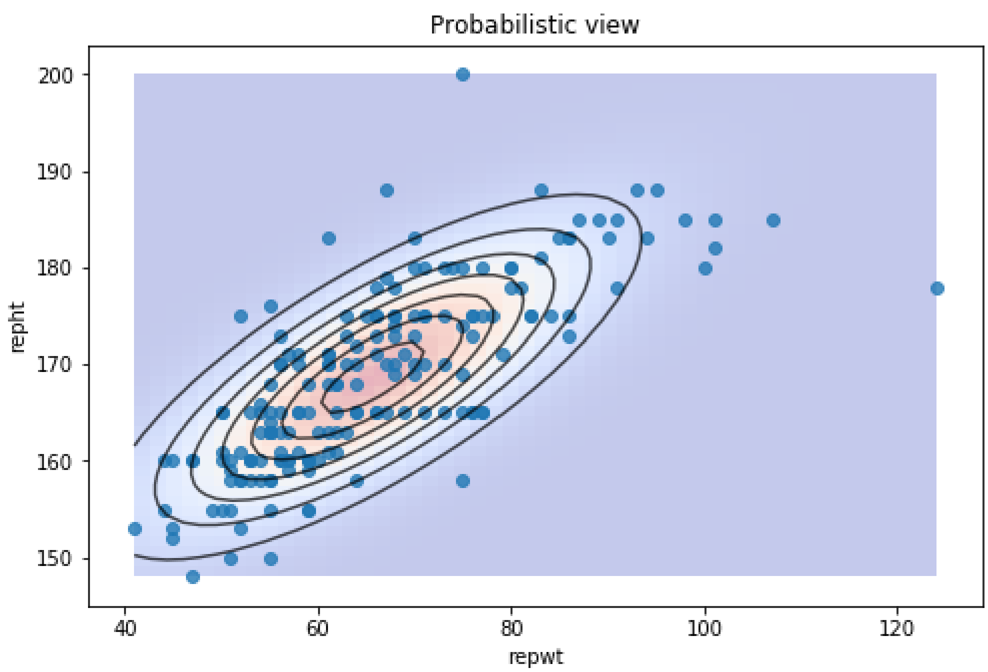
Answer: In the row normalized data, our scatterplot indicated a negative correlation, and it follo a smooth curve. The reason for this difference is that our data has been row normalized.

Question 3e: Show the Probabilistic view of the data davis_df_new.

In [29]:
```
from scipy.stats import multivariate_normal

mu = np.mean(davis_df_new.values,0)
Sigma = np.cov(davis_df_new.values.transpose())

min_length = np.min(davis_df_new.values[:,0]);
min_width = np.min(davis_df_new.values[:,1]);
max_length = np.max(davis_df_new.values[:,0]);
max_width = np.max(davis_df_new.values[:,1]);
x, y = np.mgrid[min_length:max_length:50j, min_width:max_width:50j]

positions = np.empty(x.shape + (2,))
positions[:, :, 0] = x;
positions[:, :, 1] = y

F = multivariate_normal(mu, Sigma)
Z = F.pdf(positions)
```

In [30]:
```
fig = plt.figure(figsize=(8,8))
ax = fig.gca()
ax.imshow(np.rot90(Z), cmap='coolwarm', extent=[min_length,max_length, min_w
cset = ax.contour(x, y, Z, colors='k', alpha=0.7)
plt.scatter(davis_df_new.values[:,0],davis_df_new.values[:,1],alpha=0.8)
ax.set_xlabel('repwt')
ax.set_ylabel('repht')
plt.title('Probabilistic view')
```

Out[30]:
```
Text(0.5,1,'Probabilistic view')
```



We will normalize the magnitude of each column in the data (davis_df_new) to 1 and use the n
dataframe davis_df_new_col_norm.

In [31]:
```
davis_df_new_col_norm = normalize(davis_df_new, axis=0, norm='l2')
```

In [32]:
```
davis_df_new_col_norm[1:10,:]
```

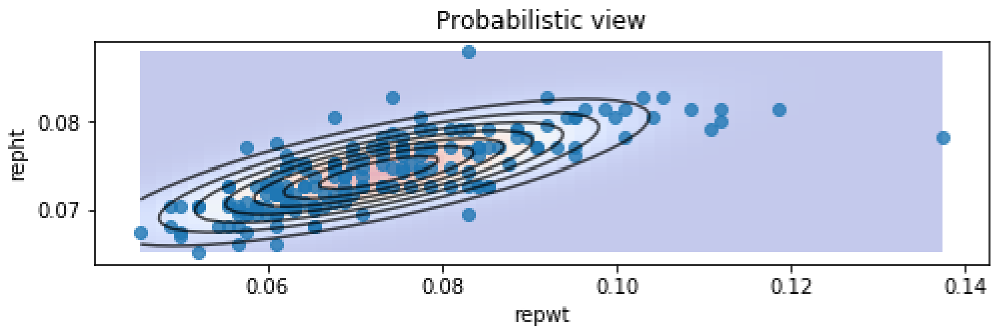
Out[32]:
```
array([[0.05648398, 0.06996539],
       [0.05980657, 0.06952536],
       [0.07752703, 0.07700594],
       [0.06534421, 0.06820526],
       [0.08417221, 0.0726056 ],
       [0.08527974, 0.0726056 ],
       [0.08084962, 0.07920611],
       [0.07863456, 0.07700594],
       [0.07088186, 0.07480577]])
```

Question 3f: Show the Probabilistic view of the data davis_df_new_col_norm.

In [33]:
```
from scipy.stats import multivariate_normal

mu = np.mean(davis_df_new_col_norm,0)
Sigma2 = np.cov(davis_df_new_col_norm.transpose())

min_length = np.min(davis_df_new_col_norm[:,0]);
min_width = np.min(davis_df_new_col_norm[:,1]);
max_length = np.max(davis_df_new_col_norm[:,0]);
max_width = np.max(davis_df_new_col_norm[:,1]);
x, y = np.mgrid[min_length:max_length:50j, min_width:max_width:50j]

positions = np.empty(x.shape + (2,))
positions[:, :, 0] = x;
positions[:, :, 1] = y

F = multivariate_normal(mu, Sigma2)
Z = F.pdf(positions)
```

In [34]:
```
fig = plt.figure(figsize=(8,8))
ax = fig.gca()
ax.imshow(np.rot90(Z), cmap='coolwarm', extent=[min_length,max_length, min_w
cset = ax.contour(x, y, Z, colors='k', alpha=0.7)
plt.scatter(davis_df_new_col_norm[:,0],davis_df_new_col_norm[:,1],alpha=0.8)
ax.set_xlabel('repwt')
ax.set_ylabel('repht')
plt.title('Probabilistic view')
```

Out[34]:
```
Text(0.5,1,'Probabilistic view')
```



Answer:

Question 3g: Compare the shape of the covariance structure in Question 3f with that of Questi
3e and comment if column normalization has affected the shape of the covariance structure.

```
<span style="color:green">Answer:</span>  Normalization has affected the sha
of the covariance structure slightly. The contour lines have been flattened
and expanded more towards the right.
```

4. Understanding the (in)dependencies among attributes using Covariance matrix

Use 'Davis' data. Do not include Unnamed attribute in this analysis.

Question 4a: Compute the covariance matrix.

In [ ]:
```
print('Covariance:')
davis_df.cov()
```

Question 4b: Which pairs of attributes co-vary in the opposite direction?

Answer: All of the values are positively correlated.

Question 4c: Compute the correlation matrix.

In [20]:
```python
print('Correlation:')
davis_df.corr()
```

```
Correlation:
```

Out[20]:

	weight	height	repwt	repht
weight	1.000000	0.154258	0.835376	0.631435
height	0.154258	1.000000	0.603737	0.739166
repwt	0.835376	0.603737	1.000000	0.761860
repht	0.631435	0.739166	0.761860	1.000000

Question 4d: Which pairs of attributes are highly correlated? Clearly specify the highly positive and highly negatively correlated attributes.

Answer: Highly positive correlated pairs: Measure Weight, Reported Weight Measured weight, Reported Height Measured Height, Reported Weight Measured Height, Reported Height Repor Weight, Reported Height

Question 4e: Which pairs of attributes are uncorrelated?

Answer: The only week correlation in this data set is between measured height, and measured weight.

Question 4f: What information did you gather from a correlation matrix that is not available in a covariance matrix?

```
<span style="color:green">Answer:</span> The extra information you get from
the correlation matrix is the relation between two variables that is not
affected by the scale of either. It is like measuring the angle between two
variables.
```

5. Dimensionality Reduction: Feature Selection

Data: Iris dataset from the practice notebook. (https://raw.githubusercontent.com/plotly/datasets/master/iris.csv (https://raw.githubusercontent.com/plotly/datasets/master/iris.csv))

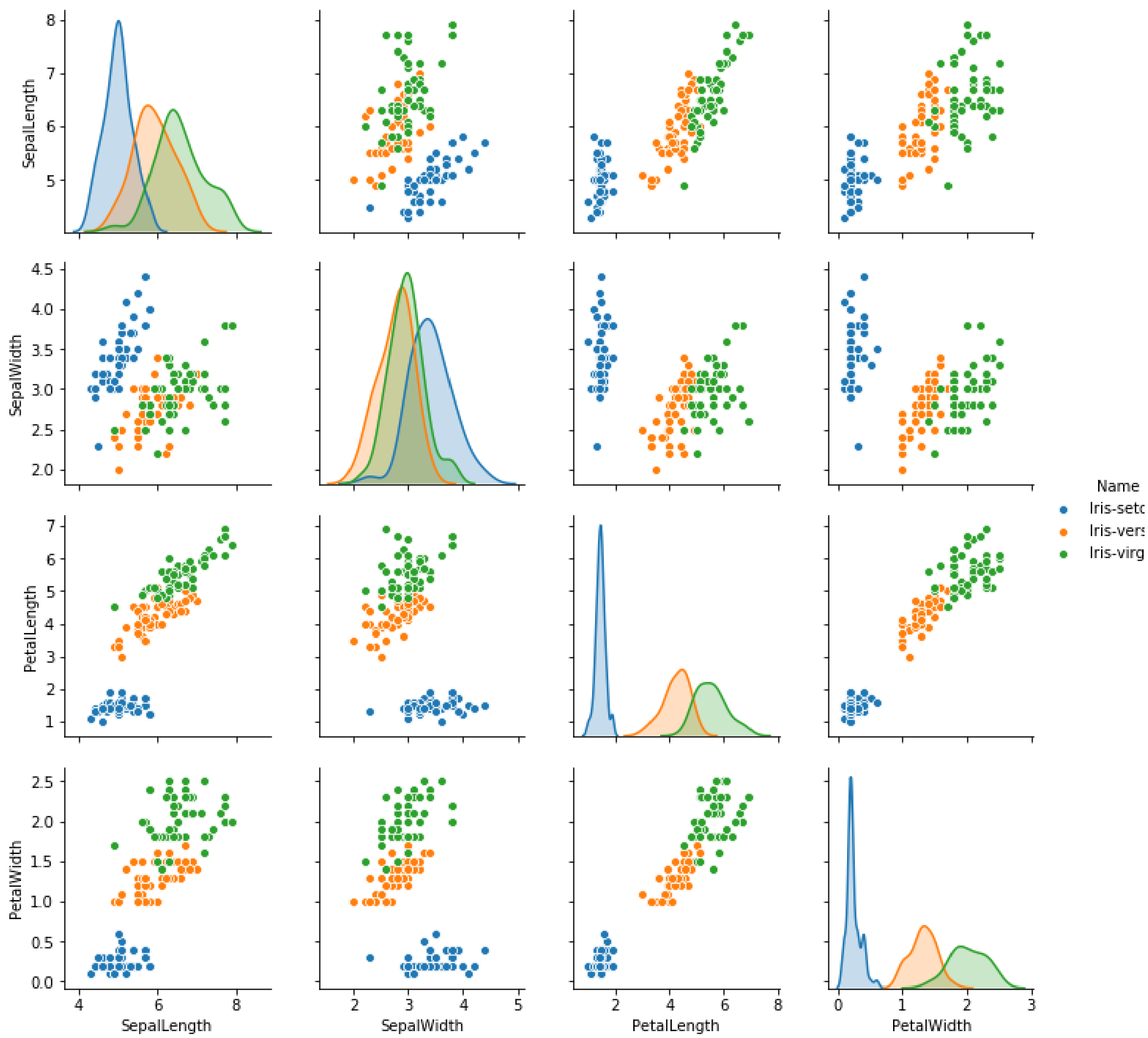
Assumption: Assume that your goal is to cluster the data to identify the species 'Name'. Clustering algorithm takes as input data points and attributes. It groups points that are similar t each other into a separate cluster. It puts points that are dissimilar in different cluster. Note that 'Name' attribute will be hidden from the clustering algorithm.

In [21]:
```
import seaborn as sns
iris_df = pd.read_csv('https://raw.githubusercontent.com/plotly/datasets/mas
```

Question 5a: If you are allowed to select only one attribute, which attribute would be highly use for the clustering task. Provide a reason. Use pairplot to answer this question.

In [22]:
```
sns.pairplot(iris_df, hue="Name")
```

Out[22]: <seaborn.axisgrid.PairGrid at 0x2b6a67e0de10>



Answer: If I had to choose one attribute for the clustering task, I would use PetalWidth. I would this attribute because it appears the area of overlap between the distributions of the flower type minimal. Due to the minimal overlap and high variance between classes, the clusters will be mo distinguished.

Question 5b: If you are allowed to select only two features, which feature would be highly usef for the clustering task. Provide a reason. Use pairplot to answer this question.

Answer: If I had to choose two attributes, I would choose PetalLength and PetalWidth. For the same reason as before, I would choose these two attributes. They have minimal overlap and hi variance between classes which will create more distinguishable clusters.

Question 5c: In real-world problems ground-truth (types of iris plants) will not be available to select the features, how do you perform **feature selection** in that case?

Answer: Without that types of plant information, I would perform feature selection using principa component analysis to capture the attributes that account for the most variance within the set o data.

6. Dimensionality Reduction: PCA on Iris Data

Question 6a: Perform PCA on Iris dataset and project the data onto the first two principal components. Use the attributes 'SepalLength','SepalWidth','PetalLength', and 'PetalWidth'.

Hint: Use iris_df[['SepalLength','SepalWidth','PetalLength','PetalWidth']] to use the specified attributes.

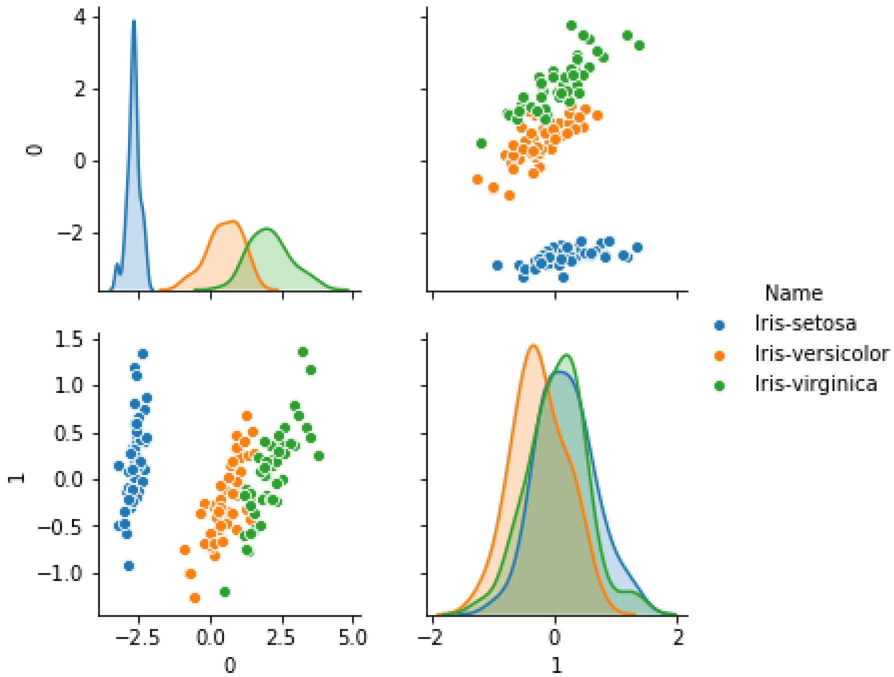
In [23]:
```
iris_df = pd.read_csv('https://raw.githubusercontent.com/plotly/datasets/mas
pca = PCA(2)
projected = pd.DataFrame(pca.fit_transform(iris_df[['SepalLength','SepalWidt
print(iris_df.shape)
print(projected.shape)
```

```
(150, 5)
(150, 2)
```

Question 6b: Generate a pairplot (along with colors for the different types of iris plants) betwee the two newly generated features using PCA in the above step.

In [24]:
```
projected['Name'] = iris_df['Name']
sns.pairplot(projected, hue='Name')
```

Out[24]: <seaborn.axisgrid.PairGrid at 0x2b6a68206410>



Question 6c: From the above pairplot, if only one newly generated attribute were to be used fc clustering the data which newly generated attribute is best suited. Provide a reason. Is the new generated attribute better than the feature selected in Question 5a?

Answer: The best attribute would be the attribute represented in the top right corner. This is because There is minimal overlap between the classes of flowers which makes the clusters mc distinguishable. This attribute seems like it would perform at about the same level as the attribu from 5a, because the distributions of the classes look alike and overlap similarly.

Question 6d: From the above pairplot, if two newly generated attributes were to be used for clustering the data, are the two newly generated attributes better than the features selected in Question 5b?

Answer: The two newly generated attributes together do not seem like they would be as effecte as the attributes selected in 5b. There is a lot of overlap between the class distributions of the second feature which does not make it very effective for classifying flower type.

Question 6e: In general, are principal components guaranteed to be more informative than the original features for the data mining task at hand?

Answer: Principal components are not guaranteed to be more informative for this task, becaus PCA does not optimize for this task.

Question 6f: In real-world problems ground-truth (types of iris plants) will not be available to determine if the principal compoents or original features are better suited for the data mining ta at hand. How should one proceed with the data mining task?

Answer: The best way to proceed would be to use linear discriminant analysis.

7. Dimensionality Reduction: PCA on synthetic datasets

Consider the following synthetic dataset we refer to as **Blobs**. This dataset has 500 data points centered around (-5, -5), (0,0) and (5,5). This dataset has 1500 data points and 2 attributes.

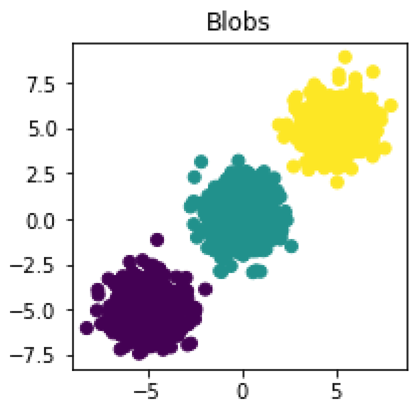
In [25]:
```
n_samples = 1500
random_state = 42
centers = [(-5, -5), (0, 0), (5, 5)]
Blobs_X, Blobs_y = datasets.make_blobs(n_samples=n_samples,centers=centers,r
Blobs_y = Blobs_y.astype(str)
```

In [26]:
```
Blobs_X.shape
```

Out[26]:
```
(1500, 2)
```

In [27]:
```
plt.figure(figsize=(3,3))
plt.scatter(Blobs_X[:, 0], Blobs_X[:, 1], c= Blobs_y)
plt.title('Blobs')
```

Out[27]: Text(0.5,1,'Blobs')



We generated a new dataset **Blobs1** by adding an extra attribute to this 2D Blobs dataset. The values for this new attribute are drawn from a normal distribution with mean 0 and variance 1.

In [28]:
```
Blobs1= pd.DataFrame(Blobs_X)
Blobs1['2'] = np.random.randn(1500)
Blobs1.head()
```

Out[28]:

	0	1	2
0	0.168461	1.317598	-0.165846
1	-3.534351	-5.225776	1.138630
2	-6.525525	-5.691908	-0.654892
3	-0.120948	0.419532	0.882061
4	-5.469474	-4.457440	0.397435

We generated a new dataset **Blobs2** by adding an extra attribute to the 2D Blobs dataset. The values for this new attribute are drawn from a normal distribution with mean 0 and variance 10(
Read more about how to do this at https://docs.scipy.org/doc/numpy-

1.15.1/reference/generated/numpy.random.randn.html (https://docs.scipy.org/doc/numpy-1.15.1/reference/generated/numpy.random.randn.html).

In [29]:
```
Blobs2= pd.DataFrame(Blobs_X)
Blobs2['2'] = np.random.randn(1500)*10
Blobs2.head()
```

Out[29]:

	0	1	2
0	0.168461	1.317598	-4.802351
1	-3.534351	-5.225776	-2.721057
2	-6.525525	-5.691908	-5.124457
3	-0.120948	0.419532	2.772398
4	-5.469474	-4.457440	-5.452522

We generated a new dataset **Blobs3** by adding two extra attributes to the 2D Blobs dataset. Th values for the two new attributes are drawn from a normal distribution with mean 0 and varianc 100.

In [30]:
```
Blobs3= pd.DataFrame(Blobs_X)
Blobs3['2'] = np.random.randn(1500)*10
Blobs3['3'] = np.random.randn(1500)*10
Blobs3.head()
```

Out[30]:

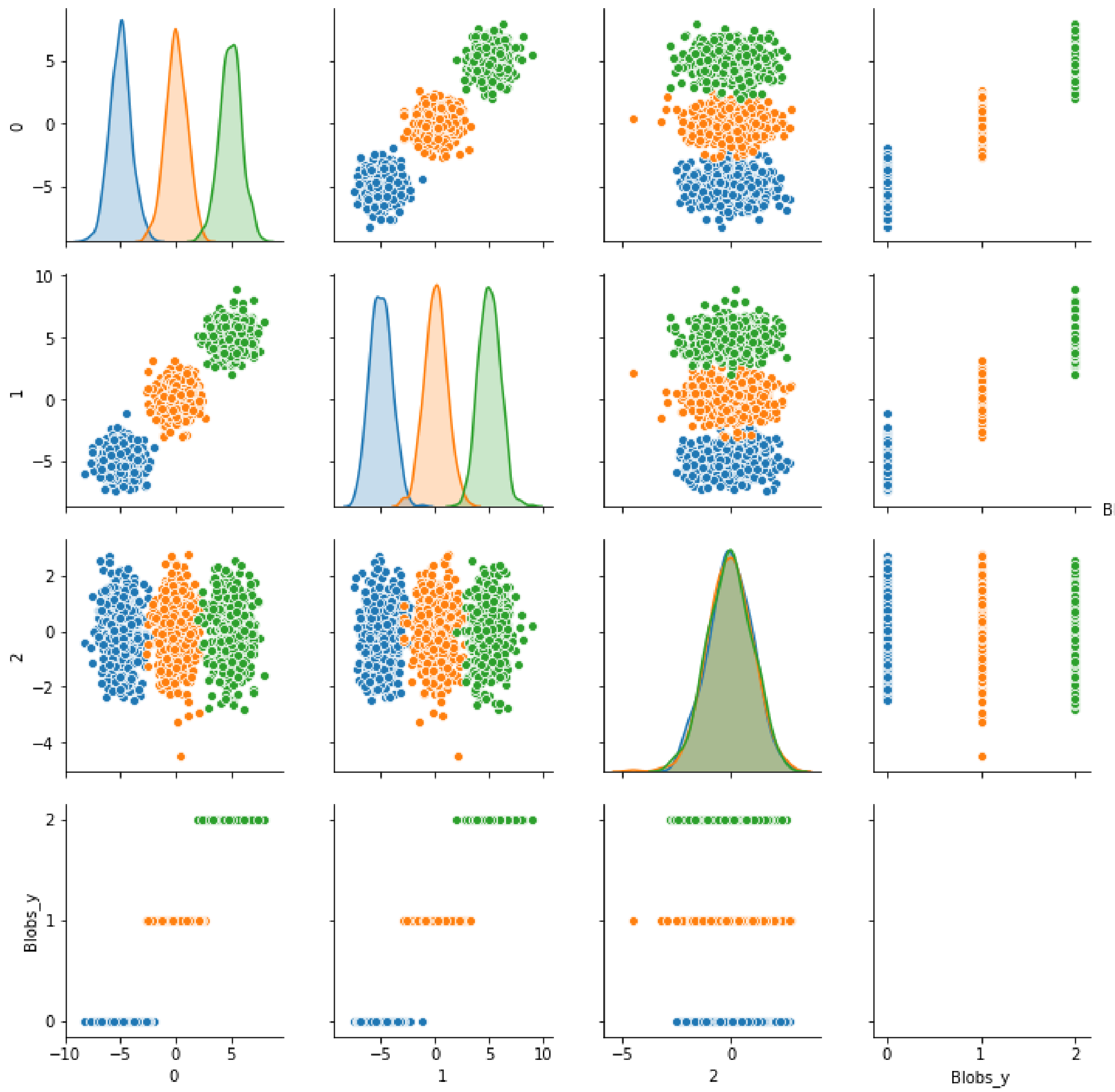
	0	1	2	3
0	0.168461	1.317598	-17.373495	-1.692865
1	-3.534351	-5.225776	-2.359591	5.461589
2	-6.525525	-5.691908	5.258740	-1.908480
3	-0.120948	0.419532	-6.959769	2.095838
4	-5.469474	-4.457440	-7.279706	-6.790430

Question 7a: Plot pairplot for **Blobs1** data. By visually examining this plot, comment on the variance of the third attribute in comparison to the first two attributes.

In [31]:
```
Blobs1['Blobs_y'] = Blobs_y
sns.pairplot(Blobs1, hue='Blobs_y')
```

```
/usr/local/python/2.7-conda5.2/lib/python2.7/site-packages/statsmodels/nonpa
etric/kde.py:488: RuntimeWarning: invalid value encountered in divide
  binned = fast_linbin(X, a, b, gridsize) / (delta * nobs)
/usr/local/python/2.7-conda5.2/lib/python2.7/site-packages/statsmodels/nonpa
etric/kde.py:488: RuntimeWarning: invalid value encountered in true_divide
  binned = fast_linbin(X, a, b, gridsize) / (delta * nobs)
/usr/local/python/2.7-conda5.2/lib/python2.7/site-packages/statsmodels/nonpa
etric/kdetools.py:34: RuntimeWarning: invalid value encountered in double_sc
rs
  FAC1 = 2*(np.pi*bw/RANGE)**2
```

Out[31]: <seaborn.axisgrid.PairGrid at 0x2b6a681caad0>



Answer: There appears to be less variance on the chart when the third attribute is present. The is also more overlap between classes.

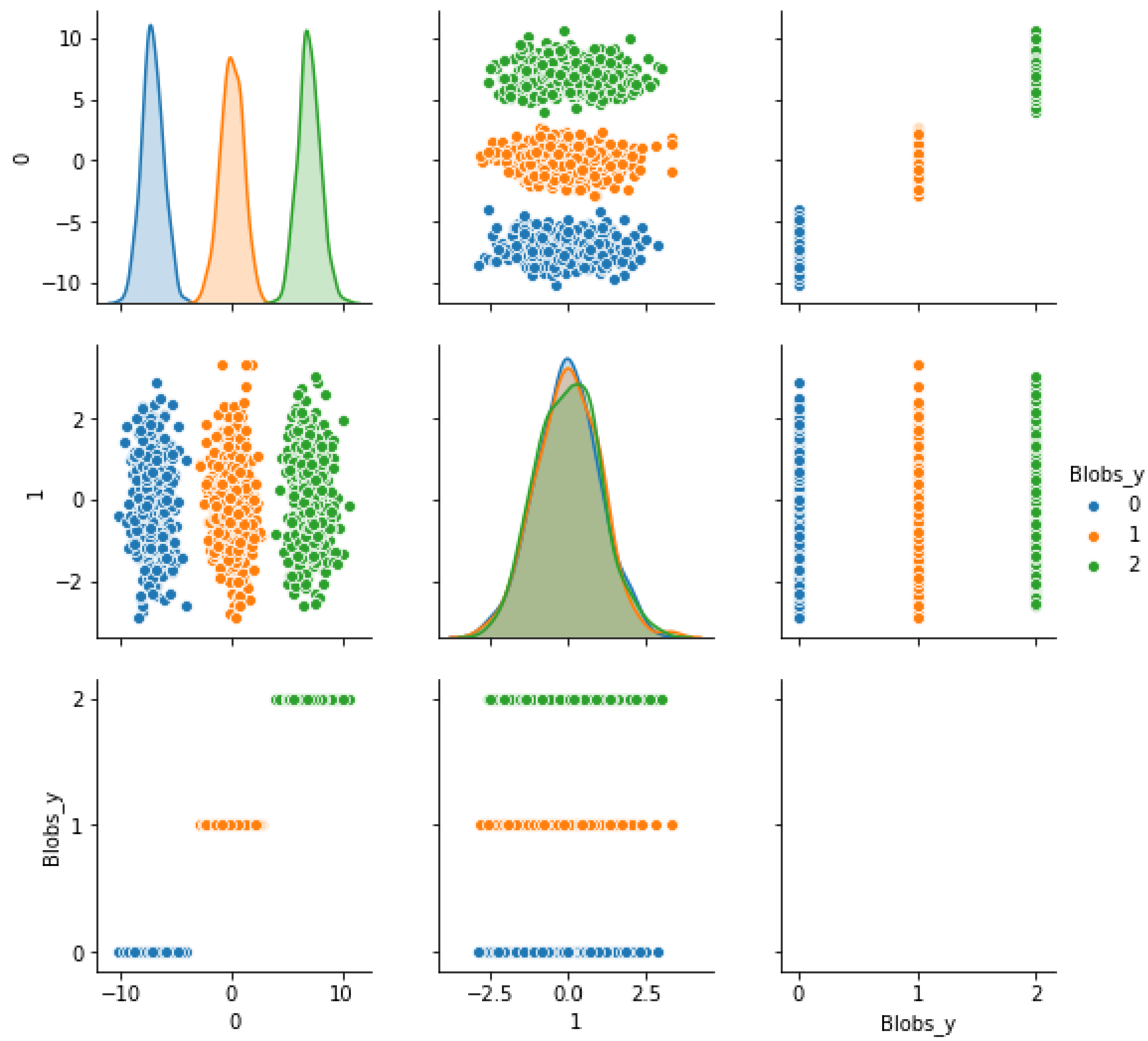
Question 7b: Perform PCA on **Blobs1** data. Project data onto the first two principal componen Generate a pairplot for the newly constructed attributes.

In [32]:
```
pca = PCA(2)
projected = pd.DataFrame(pca.fit_transform(Blobs1.iloc[:, 0:3]))
projected['Blobs_y'] = Blobs_y
print(projected.shape)
```

```
(1500, 3)
```

In [33]:
```
sns.pairplot(projected, hue='Blobs_y')
```

Out[33]: <seaborn.axisgrid.PairGrid at 0x2b6a6a8cc390>



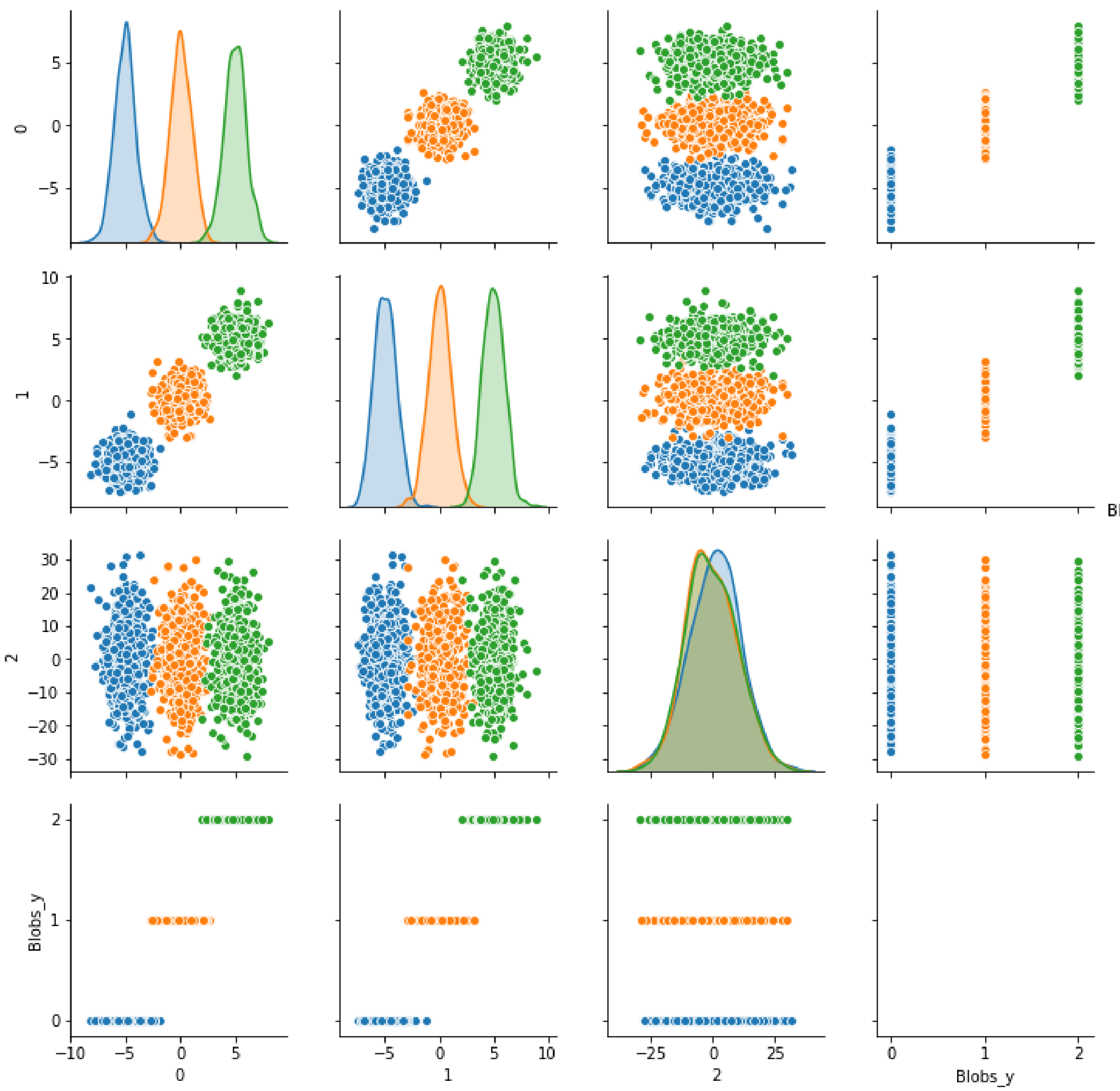
Question 7c: By comparing the distributions for the newly generated attributes in Question 7b the previous pairplot in Question 7a, determine which attribute is captured by the first principal component and which attribute is captured by the second principal component. Provide a reasc for your observations.

Answer: The first principal component appears to capture the essence of the first two attributes from the previous pairplot. There are three distinguished normal curves just like in the previous pairplot for the first two attributes. I looks like there is even less overlap between the classes wl makes me think it is a combination of the two. The second principal component looks like it captures the third attribute from the previous pairplot, because they both have three completely overlapping normal curves that look similar between the pairplots.

Question 7d: Plot pairplot for **Blobs2** data. By visually examining this plot, comment on the variance of the third attribute in comparison to the first two attributes.

In [34]:
```
Blobs2['Blobs_y'] = Blobs_y
sns.pairplot(Blobs2, hue='Blobs_y')
```

Out[34]: <seaborn.axisgrid.PairGrid at 0x2b6a6adb4090>



Answer: There appears to be greater variance on the chart when the third attribute is present. There is also more overlap between classes.

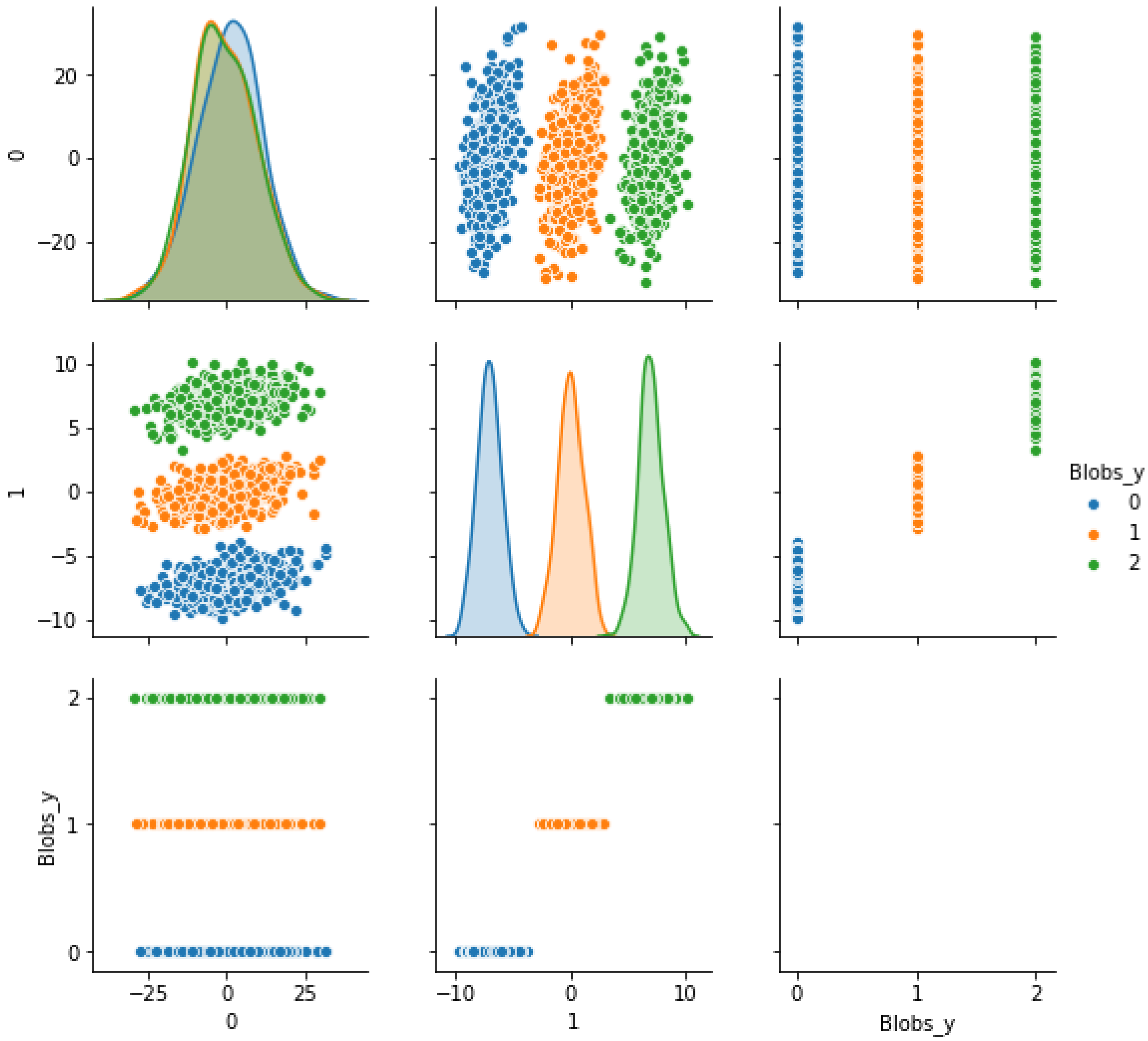
Question 7e: Perform PCA on **Blobs2** data. Project data onto the first two principal componen Generate a pairplot for the newly constructed attributes.

In [35]:
```
pca = PCA(2)
projected = pd.DataFrame(pca.fit_transform(Blobs2.iloc[:, 0:3]))
projected['Blobs_y'] = Blobs_y
print(projected.shape)
```

```
(1500, 3)
```

In [36]:
```
sns.pairplot(projected, hue='Blobs_y')
```

Out[36]: <seaborn.axisgrid.PairGrid at 0x2b6a6b4386d0>



Question 7f: By comparing the distributions for the newly generated attributes in Question 7e \
the previous pairplot in Question 7d, determine which attribute is captured by the first principal component and which attribute is captured by the second principal component. Why would hav caused this (in comparison to your observation in Question 7c)?

Answer: The first principal compenent is capturing the third attribute from the previous pairplot. second principal component is capturing the first and second attributes from the previous pairpl The first principal component captures the direction in which there is the most variance. The reason this differs from 7c is because in 7c the third attribute was responsible for less variance than the other two attributes. In contrast, the third attribute from Blobs2 is responsible for more variance.

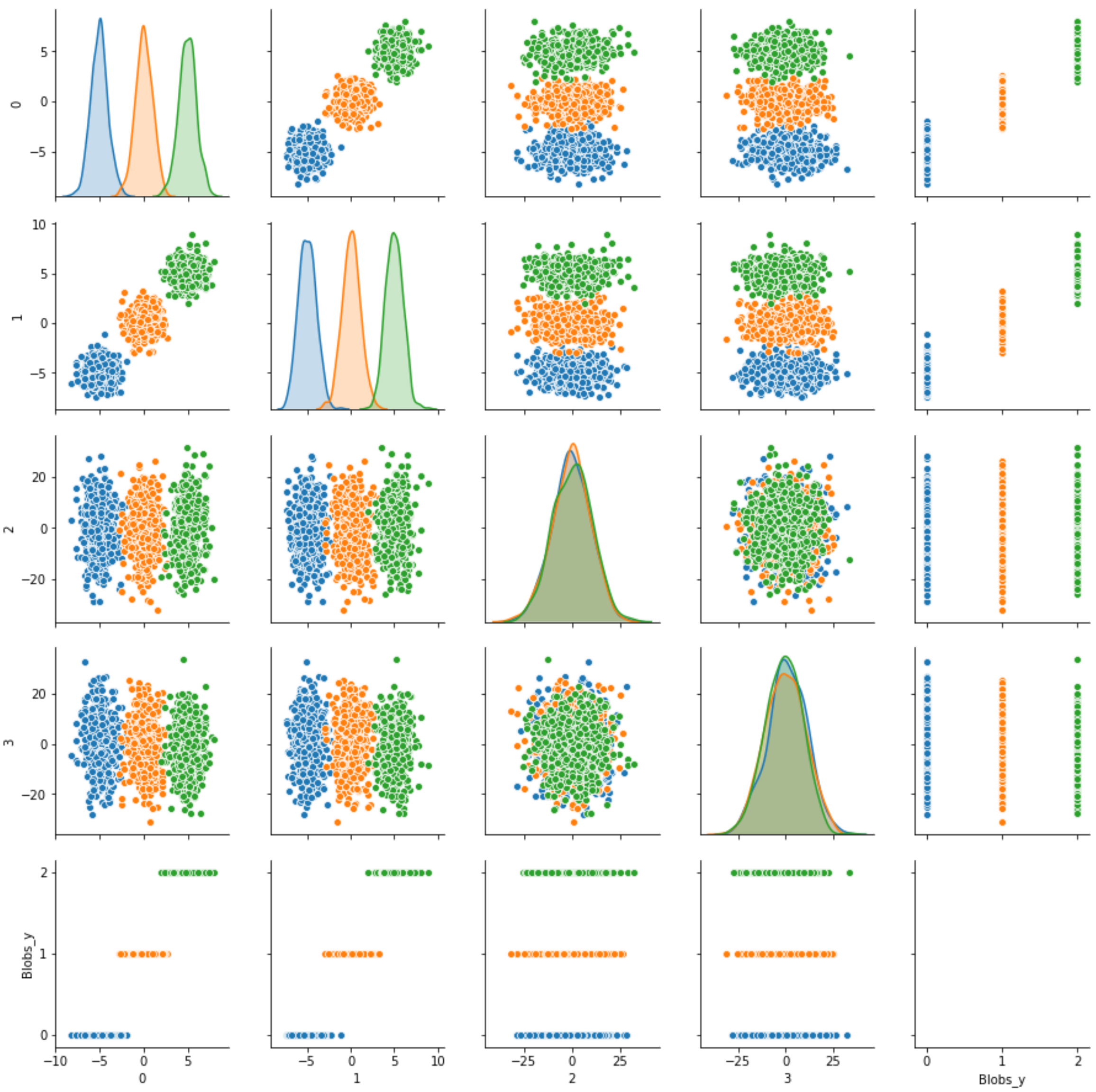
Question 7g: Are the three blobs separately visible after projection based on PCA in Question

Answer: Yes. The three blobs are separately visible.

Question 7h: Plot pairplot for **Blobs3** data. By visually examining this plot, comment on the strength of the correlation between the first two attributes. Also, comment on the strength of the correlation between the second two attributes.

In [37]:
```
Blobs3['Blobs_y'] = Blobs_y
sns.pairplot(Blobs3, hue='Blobs_y')
```

Out[37]: <seaborn.axisgrid.PairGrid at 0x2b6a70364910>



Answer: Between the first two attributes, there is a strong positive correlation as indicated by th
positive trend from left to right and bottom to top. Between the second two attributes, there is lit
correlation. There does not appear to be any clear positive or negative trend on either axis

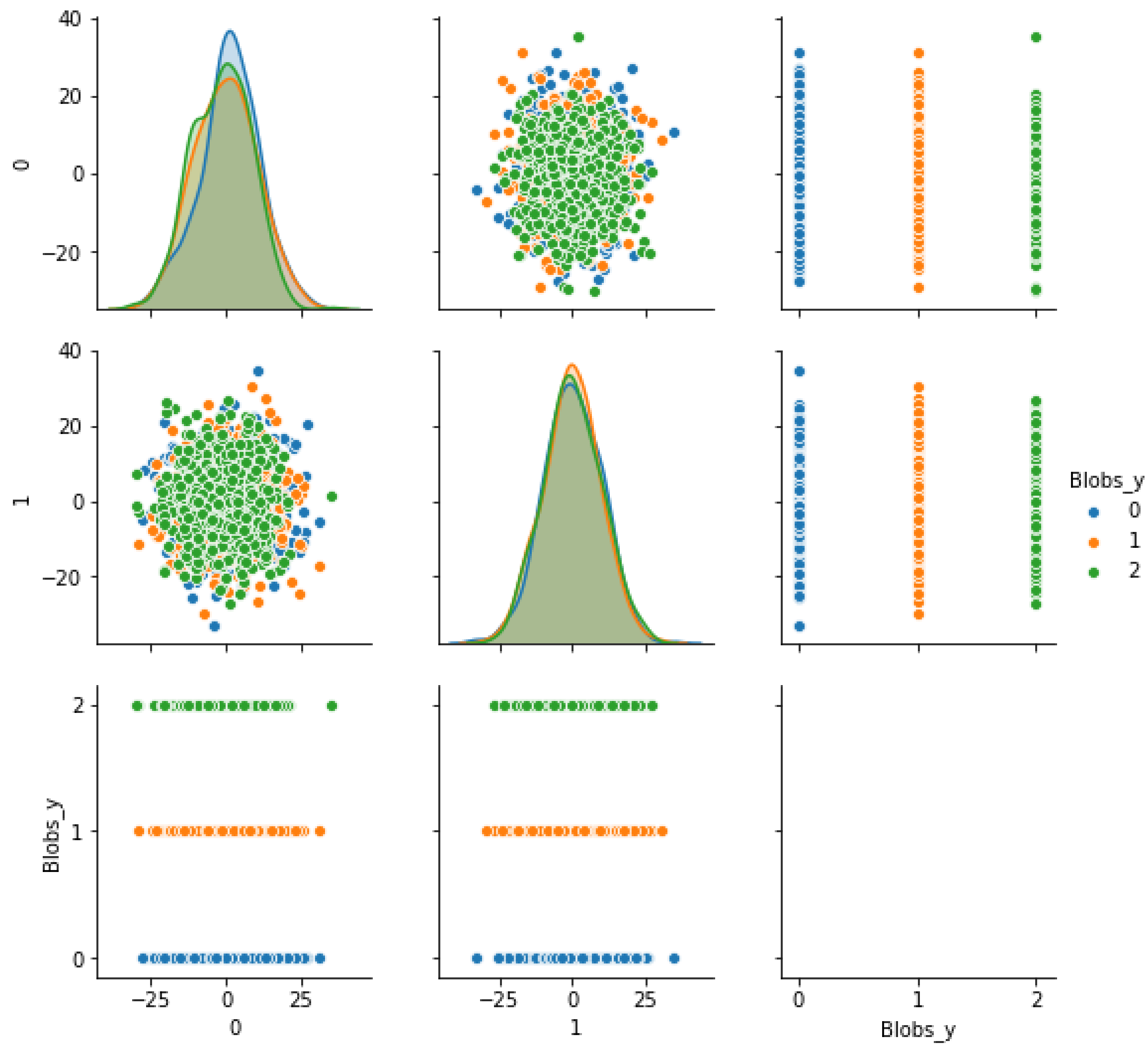
Question 7i: Perform PCA on **Blobs3** data. Project data onto the first two principal component
Generate a pairplot for the newly constructed attributes.

In [38]:
```
pca = PCA(2)
projected = pd.DataFrame(pca.fit_transform(Blobs3.iloc[:, 0:4]))
projected['Blobs_y'] = Blobs_y
print(projected.shape)
```

```
(1500, 3)
```

In [39]:
```
sns.pairplot(projected, hue='Blobs_y')
```

Out[39]:
```
<seaborn.axisgrid.PairGrid at 0x2b6a71851a10>
```



Question 7j: By comparing the distributions for the newly generated attributes in Question 7i w
the previous pairplot in Question 7h, determine which attribute is captured by the first principal
component and which attribute is captured by the second principal component. Why would hav

caused this (in comparison to your observation in Question 7f and 7c)?

Answer: The two principle components are captured by some combination of the third and fourt attributes. Both the third and fourth attributes contribute the greatest variance in Blobs 3 as indicated by their large spread on the charts. In contrast with this pairplot, in 7f and 7c, the first attributes were able to capture a significant portion of the variance. Here the third and fourth attributes dominate with their large varianc with a spread radius close to 40 on each.

Question 7k: Are the three blobs separately visible after projection based on PCA in Question What would have caused this, in comparison to your observation in Question 7g?

Answer: The three blobs are not separately visible after PCA. This is because the dimensions which captured the most variance were chosen, not the dimensions which best distinguished th classes. The distributions for the classes with the third and fourth attributes were almost completely overlapping which makes it impossible to separate these classes cleanly using only these attributes.

Question 7l: What limitation of PCA do your observations in Questions 7j, 7f, and 7c highlight?

Answer: PCA can capture the directions of most variance, however, the algorithm is not optimiz to distinguish between classes. The dimensions with most variance may not be the dimensions which distinguish class most clearly.

8. Singular Value Decomposition

(Optional) Question 8a: Using the code provided in the practice notebook for computing PCA, write your own SVD function (U,S,V = mysvd(A)) to factorize the matrix A into U,S, and V.

In [40]:
```python
def mysvd(A):
    lambda1, U = np.linalg.eig(np.matmul(A.T, A))
    lambda2, V = np.linalg.eig(np.matmul(A, A.T))
    eigval_U = np.linalg.eigvals(U)
    S = np.sqrt(eigval_U)

    return U, S, V.T
```

(Optional) Question 8b: Demonstrate that your code is correct by using your function on the following matrix A and showing that the product $USV^T = A$.

In [41]:
```
A = np.array([
    [1, 1, 1, 0, 0, 0],
    [3, 3, 3, 0, 0, 0],
    [4, 4, 4, 0, 0, 0],
    [5, 5, 5, 0, 0, 0],
    [0, 1, 0, 4, 4, 1],
    [0, 0, 0, 5, 5, 2],
    [0, 0, 0, 2, 2, 2]])
```

In [42]:
```
U, S, VT = svd(A)
S
```

Out[42]:
```
array([1.23907772e+01, 9.86730009e+00, 1.35561282e+00, 5.17051476e-01,
       2.41592441e-16, 6.70536613e-18])
```

Question 8c: Perform SVD on iris dataset and visualize the proportion of variance captured by each spectral value. List the dimensions that captures less than 10% of the total variance.

In [43]:
```
import pandas as pd
iris_df = pd.read_csv('https://raw.githubusercontent.com/plotly/datasets/mas
```

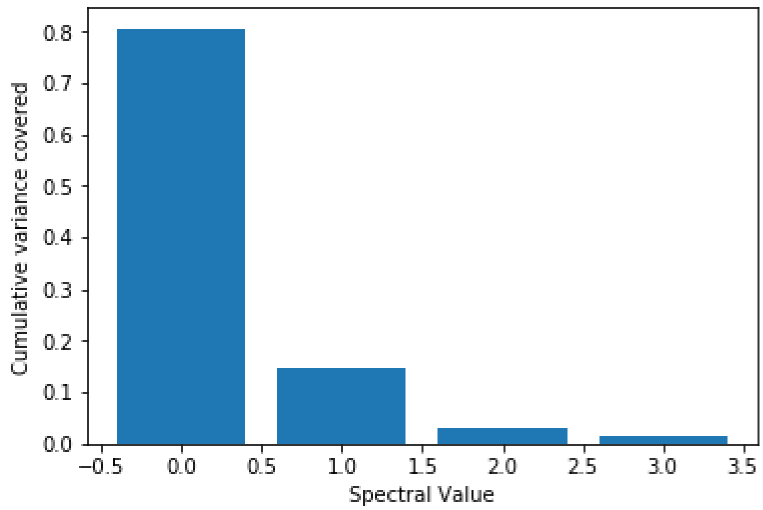
In [44]:
```
data = iris_df.values[:,0:4]
data = data.astype(float) #converts data format from object to numeric
```

In [62]:
```
U, S, V = svd(data, full_matrices = False)
U[0]
```

Out[62]:
```
array([-6.16171172e-02,  1.29969428e-01, -5.58364155e-05,  1.05847972e-03])
```

In [50]:
```
plt.bar(np.arange(4),S/np.sum(S))
plt.xlabel('Spectral Value')
plt.ylabel('Cumulative variance covered')
```

Out[50]:
```
Text(0,0.5,'Cumulative variance covered')
```

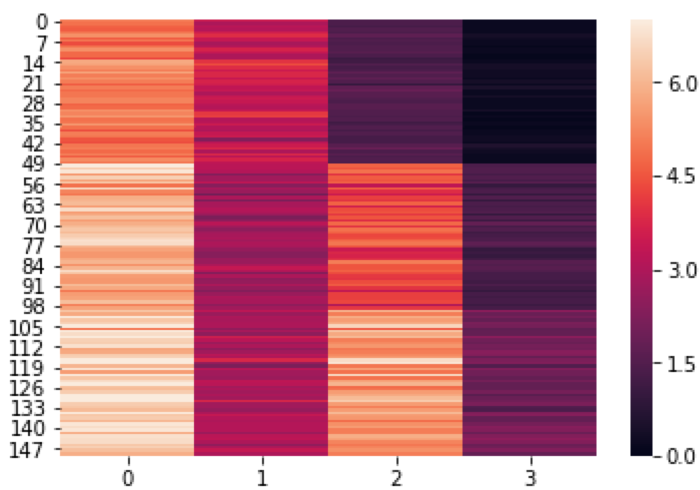


Answer: The Third and Fourth Spectral Values contain less than 10% of the total variance.

Question 8d: The heatmap of the full data is shown below. Plot all the four spectral decomposi matrices based on SVD.

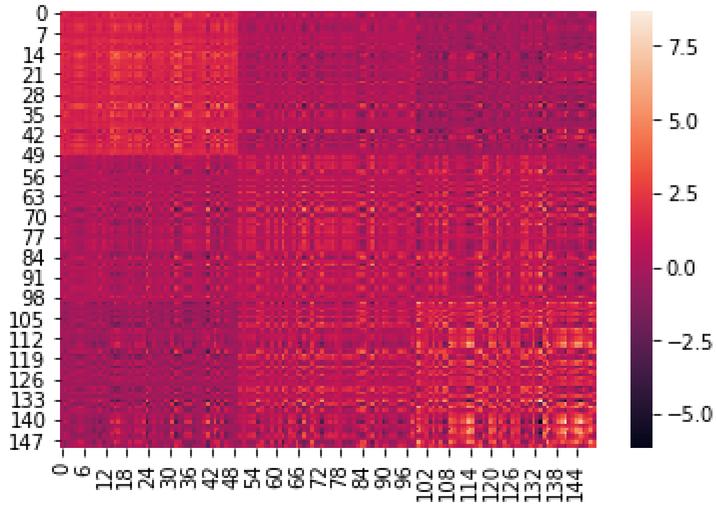
In [51]:
```
sns.heatmap(data,vmin=0, vmax=7)
```

Out[51]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x2b6a72666a10>
```



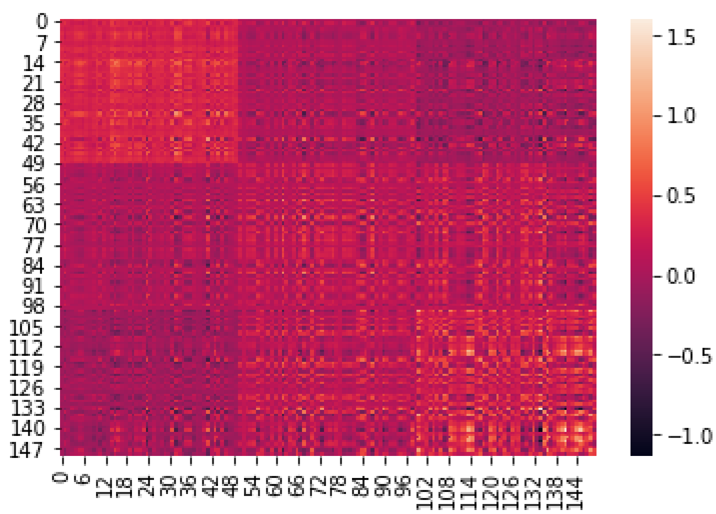
In [66]:
```
sns.heatmap(S[0]*np.matmul(U, U.T))
```

Out[66]: array([-6.16171172e-02, 1.29969428e-01, -5.58364155e-05, 1.05847972e-03])



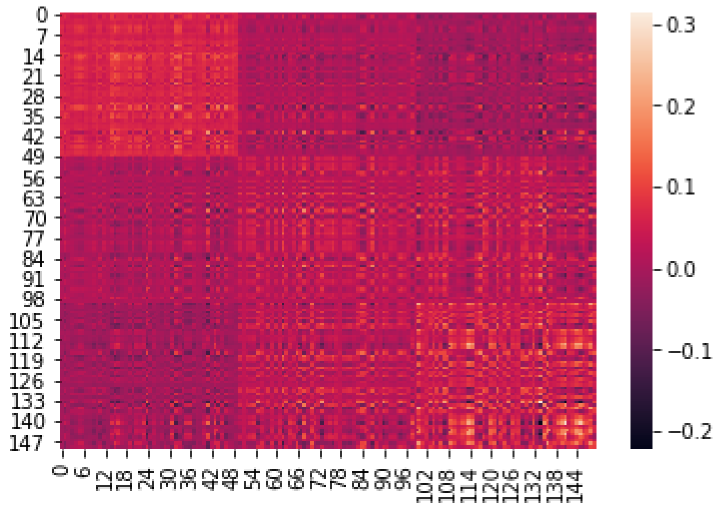
In [57]:
```
sns.heatmap(S[1]*np.matmul(U, U.T))
```

Out[57]: <matplotlib.axes._subplots.AxesSubplot at 0x2b6a73bfc2d0>



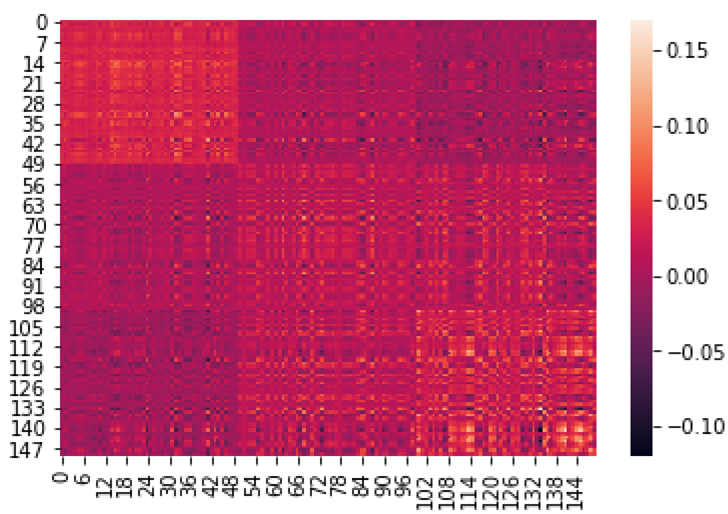
In [58]:
```
sns.heatmap(S[2]*np.matmul(U, U.T))
```

Out[58]: <matplotlib.axes._subplots.AxesSubplot at 0x2b6a73bfca10>



In [59]:
```
sns.heatmap(S[3]*np.matmul(U, U.T))
```

Out[59]: <matplotlib.axes._subplots.AxesSubplot at 0x2b6a73d2edd0>



Question 8e: Visually examine the magnitude of values present in each of the four spectral decomposition matrices and comment on which two of the four matrices have elements with relatively small magnitude in them. Provide a reason for this based on your obsevation in Ques 8c.

Answer:

9. Linear Discriminant Analysis

We will use digits data for studying the use of LDA.

In [35]:
```
digits = load_digits()
```

The data with 1797 samples and 64 attributes is in the object digits.data. These 64 attributes represent pixels in an 8x8 image.

In [36]:
```
digits.data.shape
```

Out[36]:
```
(1797, 64)
```

The 1797 images are digits from 0...9. This information is in the digits.target variable.

In [37]:
```
digits.target
```

Out[37]:
```
array([0, 1, 2, ..., 8, 9, 8])
```

For this part, we will only focus on digits 3 and 8. To this end, we generate indices of 183 samp
with 3s and indices of 174 samples with 8s.

In [38]:
```
Threes = np.where(digits.target==3)
Eights = np.where(digits.target==8)
[np.size(Threes), np.size(Eights)]
```

Out[38]:
```
[183, 174]
```

We will take samples from these indices and construct a matrix X such that the first 183 sample
represent 3s and the remaining ones represent 8s. The variable y captures this information.

In [39]:
```
indices = np.hstack((Threes[0], Eights[0]));
X = digits.data[indices,:]
y = np.hstack((3*np.ones(np.size(Threes)), 8*np.ones(np.size(Eights))))
```

In [40]:
```
X
```

Out[40]:
```
array([[ 0.,  0.,  7., ...,  9.,  0.,  0.],
       [ 0.,  2.,  9., ..., 11.,  0.,  0.],
       [ 0.,  1.,  8., ...,  2.,  0.,  0.],
       ...,
       [ 0.,  0.,  5., ...,  3.,  0.,  0.],
       [ 0.,  0.,  1., ...,  6.,  0.,  0.],
       [ 0.,  0., 10., ..., 12.,  1.,  0.]])
```

In [41]:
```
X.shape
```

Out[41]:
```
(357, 64)
```

In [42]:
```
y
```

Out[42]:
```
array([3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3.,
       3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3.,
       3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3.,
       3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3.,
       3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3.,
       3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3.,
       3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3.,
       3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3.,
       3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3.,
       3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3.,
       3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 3., 8., 8., 8., 8.,
       8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8.,
       8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8.,
       8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8.,
       8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8.,
       8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8.,
       8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8.,
       8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8.,
       8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8.,
       8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8.,
       8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8., 8.])
```

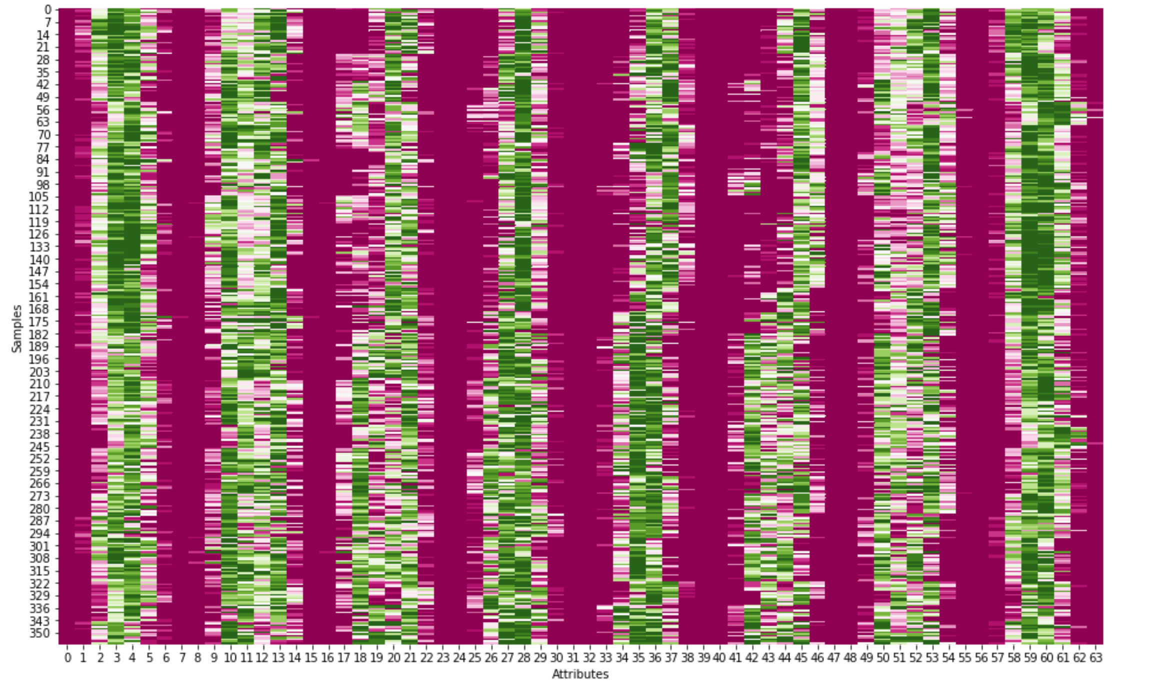
In [43]:
```
y.shape
```

Out[43]:
```
(357,)
```

Question 9a: Visually examine the following heatmap of the data X and comment which amon attributes 43 and 45 can separate the 3s from 8s better.

In [44]:
```
plt.figure(figsize=(20,10))
ax = sns.heatmap(X,cmap='PiYG')
ax.set(xlabel='Attributes', ylabel='Samples')
```

Out[44]: [Text(159,0.5,'Samples'), Text(0.5,69,'Attributes')]



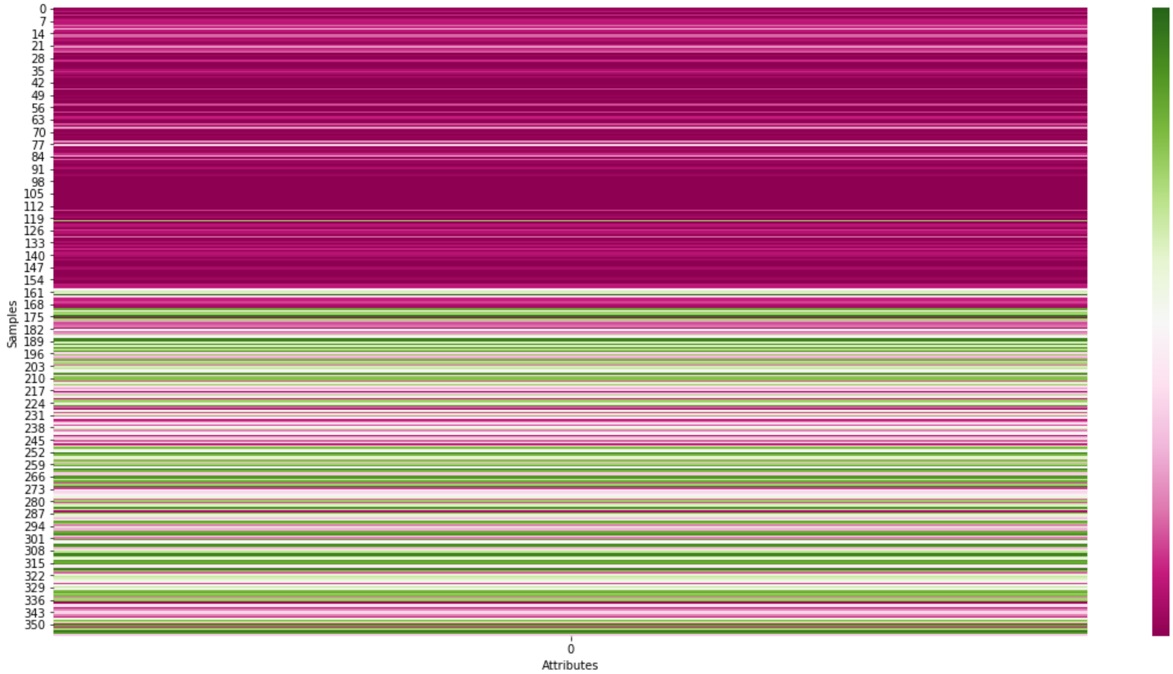
Answer: Attribute 43 seem the best amond these to separate the 3's from the 8's. this is because the attribute distinguishes the 3's and 8's most significantly due the the contrast betwee the top and bottom.

Question 9b: Perform LDA on this data. Plot the heatmap of the projected data and comment i the resultant projection is better than the best attribute between 43 and 45.

In [45]:
```
lda = LinearDiscriminantAnalysis(n_components=2)
X_r1 = lda.fit(X[:,43:45], y).transform(X[:,43:45])
```

In [46]:
```
plt.figure(figsize=(20,10))
ax = sns.heatmap(X_r1,cmap='PiYG')
ax.set(xlabel='Attributes', ylabel='Samples')
```

Out[46]: [Text(159,0.5,'Samples'), Text(0.5,69,'Attributes')]



```
<span style="color:green">Answer:</span> This heatmap for our LDA looks like
it separates that 3's and 8's about as well as attribute 43.
```

In [ ]: