Worksheet 7 and Worksheet 8

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1 Worksheet 7 – Clustering and Worksheet 8 – Matrix factorization

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1.2 3.5.2017

```
In [1]: import pandas as pd
        import numpy as np
        import math
        import sklearn
        from sklearn import metrics
        from sklearn import datasets
        import random
        import seaborn as sns
        from sklearn.cluster import KMeans
        from scipy.cluster.hierarchy import dendrogram, linkage
        from sklearn.decomposition import PCA
        import matplotlib.pyplot as plt
        import re

        %matplotlib inline
        from pylab import rcParams
        rcParams['figure.figsize'] = 10,10
```

```
C:\Users\Orysya\Anaconda\lib\site-packages\IPython\html.py:14: ShimWarning: The `IP
  "`IPython.html.widgets` has moved to `ipywidgets`.", ShimWarning)
```

2 Worksheet 7 – Clustering

2.1 Part 1

For this problem, we'll be using the animals with attributes data set. Go to

`http://attributes.kyb.tuebingen.mpg.de`

and, under "Downloads", choose the "base package" (the very first file in the list). Unzip it and look over the various text files.

```
In [2]: !cat ./AwA-base/Animals_with_Attributes/Features/README-features.txt
```

```
==========================================================================
   Pre-Extracted Image Features for the Animals_with_Attributes Dataset
==========================================================================

Names and IDs of all classes are in the file
- classes.txt

Predicate names andIDs are in the file
- predicates.txt

Training and test classnames for the attribute-based classifier are in
- trainclasses.txt, testclasses.txt

The class<->attribute matrix is given in three formats.
- predicate-matrix-numeric.txt (positive numeric entries, some missing
  entries encoded as -1)
- predicate-matrix-binary.txt (binarized with mean of feature, missing
  set to 0)
- predicate-matrix.png (PNG image file for visual inspection)

Note that the entries are in the order of the names/predicates files,
*not* alphabetically.

There are 6 feature representations:

- cq: (global) color histogram (1x1 + 2x2 + 4x4 spatial pyramid, 128 bins
      each, each histogram L1-normalized)
- lss[1]: local self similarity (2000 entry codebook, raw bag-of-visual-word
          counts)
- phog[2]: histogram of oriented gradients (1x1 + 2x2 + 4x4 spatial pyramid,
           12 bins each, each histogram L1-normalized or all zero)
- rgsift[3]: rgSIFT descriptors (2000 entry codebook, bag-of-visual-word counts,
             L1-normalized)
- sift[4]: SIFT descriptors (2000 entry codebook, raw bag-of-visual-word counts)
- surf[5]: SUFT descriptors (2000 entry codebook, raw bag-of-visual-word counts)

Each file consists of one sample per line in ASCII format.
All representations have non-negative entries.

-----------------------------------------------------------------
      Instructions for fixed-split Attribute-Based Classification
-----------------------------------------------------------------

- train using all examples of all 40 classes from "trainclasses.txt"
- test on all examples of 10 classes specified in the "testclasses.txt"
```

```
-----------------------------------------------------------------
      Instructions for CV-like Multi-Class Classification
-----------------------------------------------------------------

Follow a protocol similar to Caltech256:
- choose N_train \in {5,10,15,20,25,30,40,50} and set N_test=25
- train on N_train random training examples from each class
- test on N_test random examples out of the remaining images
  from each class
- calculate the mean of the confusion matrix (class averaged accuracy)
- report averaged results for 10-times this procedure

-----------------------------------------------------------------
      References
-----------------------------------------------------------------

[1] E. Shechtman, and M. Irani: "Matching Local Self-Similarities
    across Images and Videos", CVPR 2007.

[2] A. Bosch, A. Zisserman, and X. Munoz: "Representing shape with
    a spatial pyramid kernel", CIVR 2007.

[3] Koen E. A. van de Sande, Theo Gevers and Cees G. M. Snoek:
    "Evaluation of Color Descriptors for Object and Scene
    Recognition", CVPR 2008.

[4] D. G. Lowe, "Distinctive Image Features from Scale-Invariant
    Keypoints", IJCV 2004.

[5] H. Bay, T. Tuytelaars, and L. Van Gool: "SURF: Speeded Up
    Robust Features", ECCV 2006.
```

2.2 Part 2

This is a small data set that has information about 50 animals. The animals are listed in classes.txt. For each animal, the information consists of values for 85 features: does the animal have a tail, is it slow, does it have tusks, etc. The details of the features are in predicates.txt. The full data consists of a 50 x 85 matrix of real values, in predicate-matrix-continuous.txt. There is also a binarized version of this data, in predicate-matrix-binary.txt.

2.2.1 Examine the data files.

```
In [3]: !head -10 ./AwA-base/Animals_with_Attributes/classes.txt
```

```
     1        antelope
     2        grizzly+bear
     3        killer+whale
     4        beaver
     5        dalmatian
     6        persian+cat
     7        horse
     8        german+shepherd
     9        blue+whale
    10        siamese+cat
```

```
In [4]: !head -10 ./AwA-base/Animals_with_Attributes/predicates.txt
```

```
     1        black
     2        white
     3        blue
     4        brown
     5        gray
     6        orange
     7        red
     8        yellow
     9        patches
    10        spots
```

```
In [5]: !head -1 ./AwA-base/Animals_with_Attributes/predicate-matrix-continuous.txt
```

```
  -1.00  -1.00  -1.00  -1.00  12.34   0.00   0.00   0.00  16.11   9.19   0.00  38.0
```

```
In [6]: !head -1 ./AwA-base/Animals_with_Attributes/predicate-matrix-binary.txt
```

```
0 0 0 0 0 0 0 0 0 0 0 1 0 1 1 0 0 1 0 0 1 0 0 1 0 1 1 0 0 0 1 0 0 0 0 0 0 0 1 1 0 1
```

2.3 Part 3

Load the real-valued array, and also the animal names, into Python. Run k-means on the data (from sklearn.cluster) and ask for k = 10 clusters. For each cluster, list the animals in it. Does the clustering make sense?

2.3.1 Load the data into Python.

```
In [7]: samples_features = pd.read_fwf("./AwA-base/Animals_with_Attributes/predicat
        print 'The shape of the sample features is', samples_features.shape
```

```
The shape of the sample features is (50L, 85L)
```

```
In [8]: classes = pd.read_fwf('./AwA-base/Animals_with_Attributes/classes.txt', hea
        print classes
```

```
['antelope' 'grizzly+bear' 'killer+whale' 'beaver' 'dalmatian'
 'persian+cat' 'horse' 'german+shepherd' 'blue+whale' 'siamese+cat' 'skunk'
 'mole' 'tiger' 'hippopotamus' 'leopard' 'moose' 'spider+monkey'
 'humpback+whale' 'elephant' 'gorilla' 'ox' 'fox' 'sheep' 'seal'
 'chimpanzee' 'hamster' 'squirrel' 'rhinoceros' 'rabbit' 'bat' 'giraffe'
 'wolf' 'chihuahua' 'rat' 'weasel' 'otter' 'buffalo' 'zebra' 'giant+panda'
 'deer' 'bobcat' 'pig' 'lion' 'mouse' 'polar+bear' 'collie' 'walrus'
 'raccoon' 'cow' 'dolphin']
```

```
In [9]: feature_names=pd.read_fwf("./AwA-base/Animals_with_Attributes/predicates.tx
        classes_features = pd.DataFrame(data = samples_features, columns = feature_
        classes_features.index = classes
        classes_features.head()
```

```
Out[9]:               black  white  blue  brown   gray  orange  red  yellow  patche
        antelope      -1.00  -1.00  -1.0  -1.00  12.34     0.0  0.0     0.0    16.1
        grizzly+bear  39.25   1.39   0.0  74.14   3.75     0.0  0.0     0.0     1.2
        killer+whale  83.40  64.79   0.0   0.00   1.25     0.0  0.0     0.0    68.4
        beaver        19.38   0.00   0.0  87.81   7.50     0.0  0.0     0.0     0.0
        dalmatian     69.58  73.33   0.0   6.39   0.00     0.0  0.0     0.0    37.0

                       spots    ...     water  tree   cave  fierce  timid  smart  \
        antelope        9.19    ...      0.00  0.00   1.23   10.49  39.24  17.57
        grizzly+bear    0.00    ...      7.64  9.79  53.14   61.80  12.50  24.00
        killer+whale   32.69    ...     79.49  0.00   0.00   38.27   9.77  52.03
        beaver          7.50    ...     65.62  0.00   0.00    3.75  31.88  41.88
        dalmatian     100.00    ...      1.25  6.25   0.00    9.38  31.67  53.26

                      group  solitary  nestspot  domestic
        antelope      50.59      2.35      9.70      8.38
        grizzly+bear   3.12     58.64     20.14     11.39
        killer+whale  24.94     15.77     13.41     15.42
        beaver        23.44     31.88     33.44     13.12
        dalmatian     24.44     29.38     11.25     72.71

        [5 rows x 85 columns]
```

2.3.2 Ran KMeans clustering for 10 clusters.

```
In [10]: kmeans = KMeans(n_clusters=10, random_state=0).fit(samples_features)
         grouping = {i:[] for i in xrange(0,10)}

         for i,animal in enumerate(classes):
             grouping[kmeans.labels_[i]].append(animal)
         grouping
```

```
Out[10]: {0: ['antelope', 'horse', 'moose', 'giraffe', 'zebra', 'deer'],
          1: ['tiger', 'leopard', 'fox', 'wolf', 'weasel', 'bobcat', 'lion'],
          2: ['killer+whale', 'blue+whale', 'humpback+whale', 'walrus', 'dolphin'],
          3: ['skunk',
           'mole',
           'hamster',
           'squirrel',
           'rabbit',
           'rat',
           'mouse',
           'raccoon'],
          4: ['dalmatian',
           'persian+cat',
           'german+shepherd',
           'siamese+cat',
           'chihuahua',
           'collie'],
          5: ['hippopotamus',
           'elephant',
           'ox',
           'sheep',
           'rhinoceros',
           'buffalo',
           'giant+panda',
           'pig',
           'cow'],
          6: ['spider+monkey', 'gorilla', 'chimpanzee'],
          7: ['bat'],
          8: ['beaver', 'seal', 'otter'],
          9: ['grizzly+bear', 'polar+bear']}
```

2.4 Part 4

Now hierarchically cluster this data, using scipy.cluster.hierarchy.linkage. Choose Ward's method, and plot the resulting tree using the dendrogram method, setting the orientation parameter to 'right' and labeling each leaf with the corresponding animal name.

You will run into a problem: the plot is too cramped because the default figure size is so small. To make it larger, preface your code with the following:

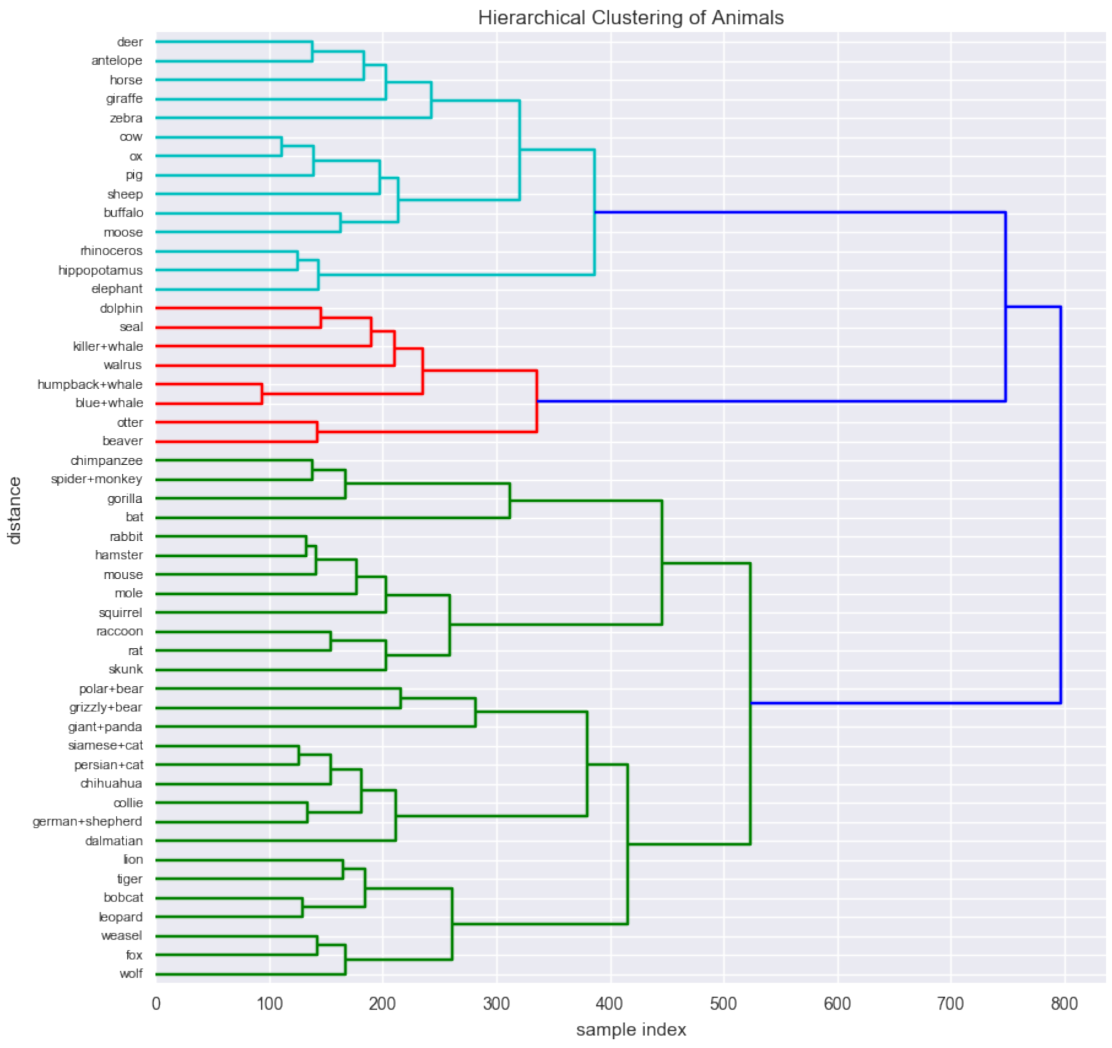
```
from pylab import rcParams
rcParams['figure.figsize'] = 5,10
```

(or try a different size if this doesn't seem quite right). Does the hierarchical clustering seem sensible to you?

For reference, used: https://joernhees.de/blog/2015/08/26/scipy-hierarchical-clustering-and-dendrogram-tutorial/

2.4.1 Ran hierarchical clustering on the data set to compare to the results from the KMeans clustering.

```
In [11]: Z = linkage(samples_features, 'ward')
In [12]: plt.title('Hierarchical Clustering of Animals')
         plt.xlabel('sample index')
         plt.ylabel('distance')
         dendrogram(Z, labels= classes, orientation='right')
         plt.show()
```



2.4.2 Yes, the hierarchical clustering seems sensible to me. It is easy to see which animals are most related to one another. From observation, it is interesting that the K-means clustering placed 'bat' into its own cluster, while hierarchical clustering shows that bat is most similar to gorilla, spider monkey, and chimpanzee.

3 Worksheet 8 – Matrix factorization

3.1 Part 4

Recall the animals with attributes data set from Worksheet 7, which has information about 50 animals, each represented as a vector in R_85.

We would like to visualize these animals in 2-d. Show how to do this with a PCA projection from R_85 to R_2. Show the position of each animal, and label them with their names. (Remember from Worksheet 7 how to enlarge the figure. This time you might want to ask for size 10,10.)

Does this embedding seem sensible to you?

3.1.1 Performed a PCA projection and examined the amount of variance explained when visualizing animals in 2-d

```
In [13]: print 'Before PCA, data shape', samples_features.shape
         pca_dg = PCA(2)
         samples_features2d = pca_dg.fit_transform(samples_features)
         print 'After PCA, data shape', samples_features2d.shape
         print "This PCA explains", np.sum(pca_dg.explained_variance_ratio_), "of t
```

```
Before PCA, data shape (50L, 85L)
After PCA, data shape (50L, 2L)
This PCA explains 0.389615467763 of the data set's variance
```

3.1.2 Repeated KMeans clustering and hierarchical clustering post PCA.

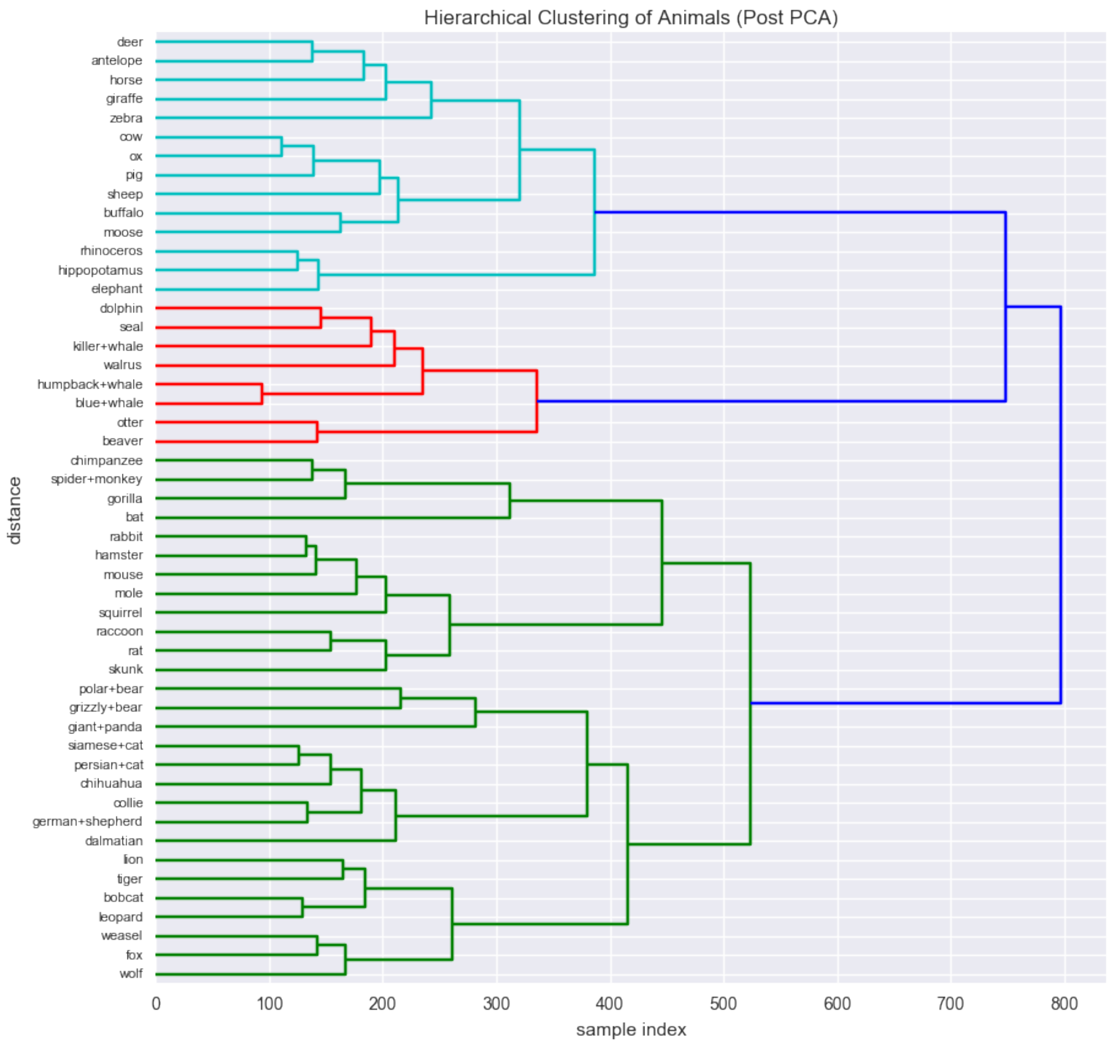
```
In [14]: kmeans = KMeans(n_clusters=10, random_state=0).fit(samples_features2d)
         grouping = {i:[] for i in xrange(0,10)}

         for i,animal in enumerate(classes):
             grouping[kmeans.labels_[i]].append(animal)
         print 'Post PCA: '
         grouping
```

```
Post PCA:
```

```
Out[14]: {0: ['tiger', 'leopard', 'fox', 'wolf', 'bobcat'],
          1: ['hamster', 'rabbit', 'giant+panda', 'mouse'],
          2: ['blue+whale', 'humpback+whale', 'walrus'],
          3: ['elephant', 'ox', 'buffalo', 'pig', 'cow'],
          4: ['grizzly+bear',
           'german+shepherd',
  'siamese+cat',
  'bat',
  'chihuahua',
  'rat',
  'weasel',
  'lion',
  'raccoon'],
 5: ['beaver', 'otter', 'polar+bear'],
 6: ['dalmatian',
  'persian+cat',
  'skunk',
  'mole',
  'spider+monkey',
  'gorilla',
  'chimpanzee',
  'squirrel',
  'collie'],
 7: ['hippopotamus', 'rhinoceros'],
 8: ['killer+whale', 'seal', 'dolphin'],
 9: ['antelope', 'horse', 'moose', 'sheep', 'giraffe', 'zebra', 'deer']}
```

```
In [15]: plt.title('Hierarchical Clustering of Animals (Post PCA)')
         plt.xlabel('sample index')
         plt.ylabel('distance')
         dendrogram(Z, labels= classes, orientation='right')
         plt.show()
```

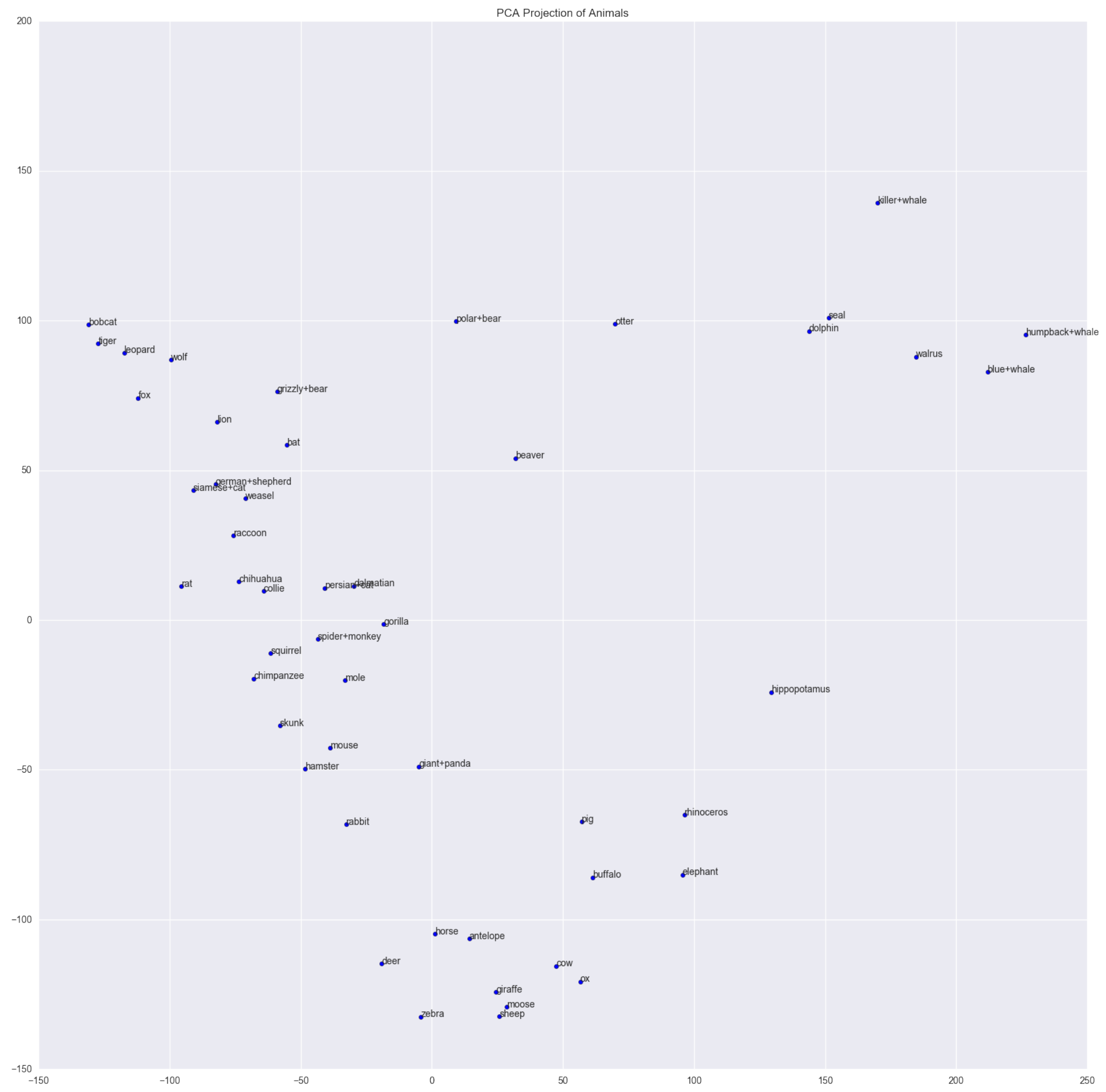


3.1.3 Visualized the position of the animals based on the PCA using a scatter plot.

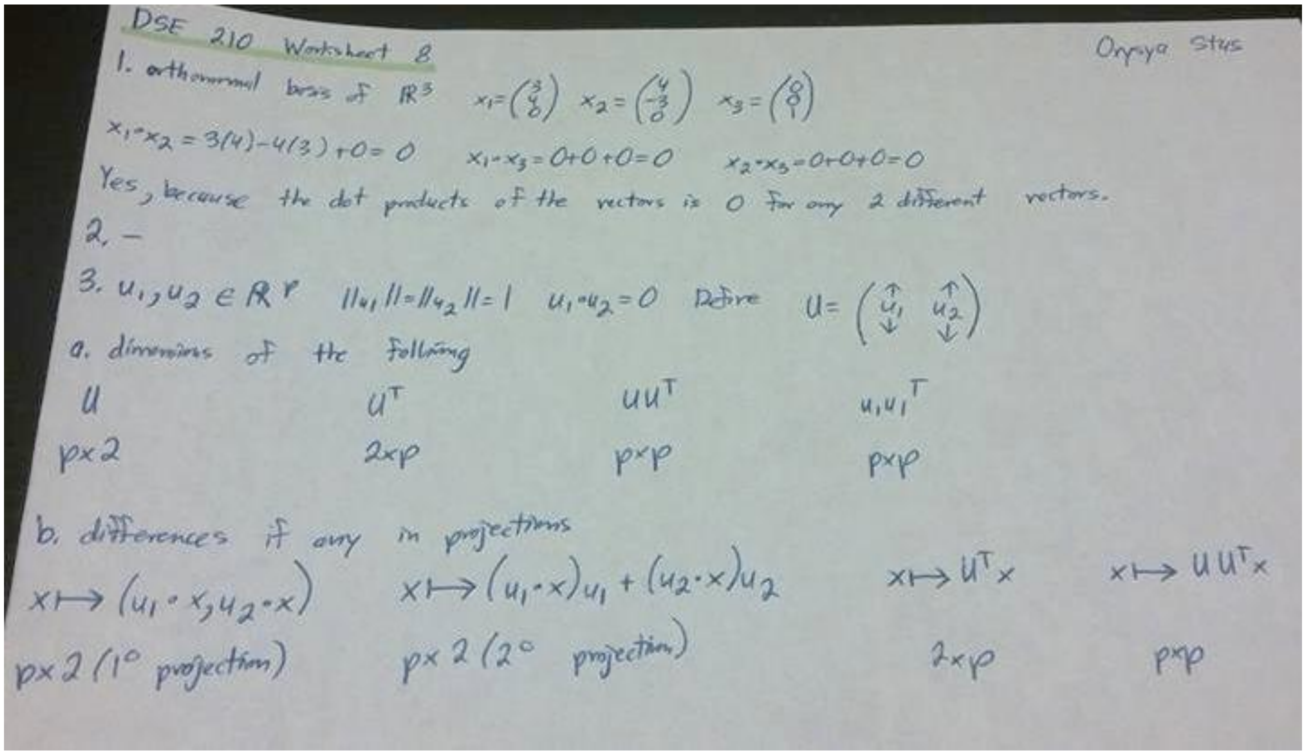
```
In [16]: fig = plt.figure(1, figsize=(20, 20))
         ax = fig.add_subplot(111)
         for i,point in enumerate(samples_features2d):
             ax.annotate(classes[i], xy=point, xytext=point)

         plt.scatter(samples_features2d[:,0], samples_features2d[:,1])
         plt.title('PCA Projection of Animals')

Out[16]: <matplotlib.text.Text at 0x10648c50>
```



3.1.4 Yes, the embedding seems sensible to me. It should be noted that the PCA projection from 85 to 2 dimensions, only explains 38.9% of the total variance.



DSE 210 Worksheet 8 Orysya Stus

1. orthonormal basis of $\mathbb{R}^3$ $x_1=\begin{pmatrix}3\\4\\0\end{pmatrix}$ $x_2=\begin{pmatrix}4\\-3\\0\end{pmatrix}$ $x_3=\begin{pmatrix}0\\0\\1\end{pmatrix}$

$x_1 \cdot x_2 = 3(4)-4(3)+0=0$ $x_1 \cdot x_3 = 0+0+0=0$ $x_2 \cdot x_3 = 0+0+0=0$

Yes, because the dot products of the vectors is 0 for any 2 different vectors.

2. –

3. $u_1, u_2 \in \mathbb{R}^p$ $\|u_1\|=\|u_2\|=1$ $u_1 \cdot u_2 = 0$ Define $U=\begin{pmatrix}\uparrow & \uparrow\\ u_1 & u_2\\ \downarrow & \downarrow\end{pmatrix}$

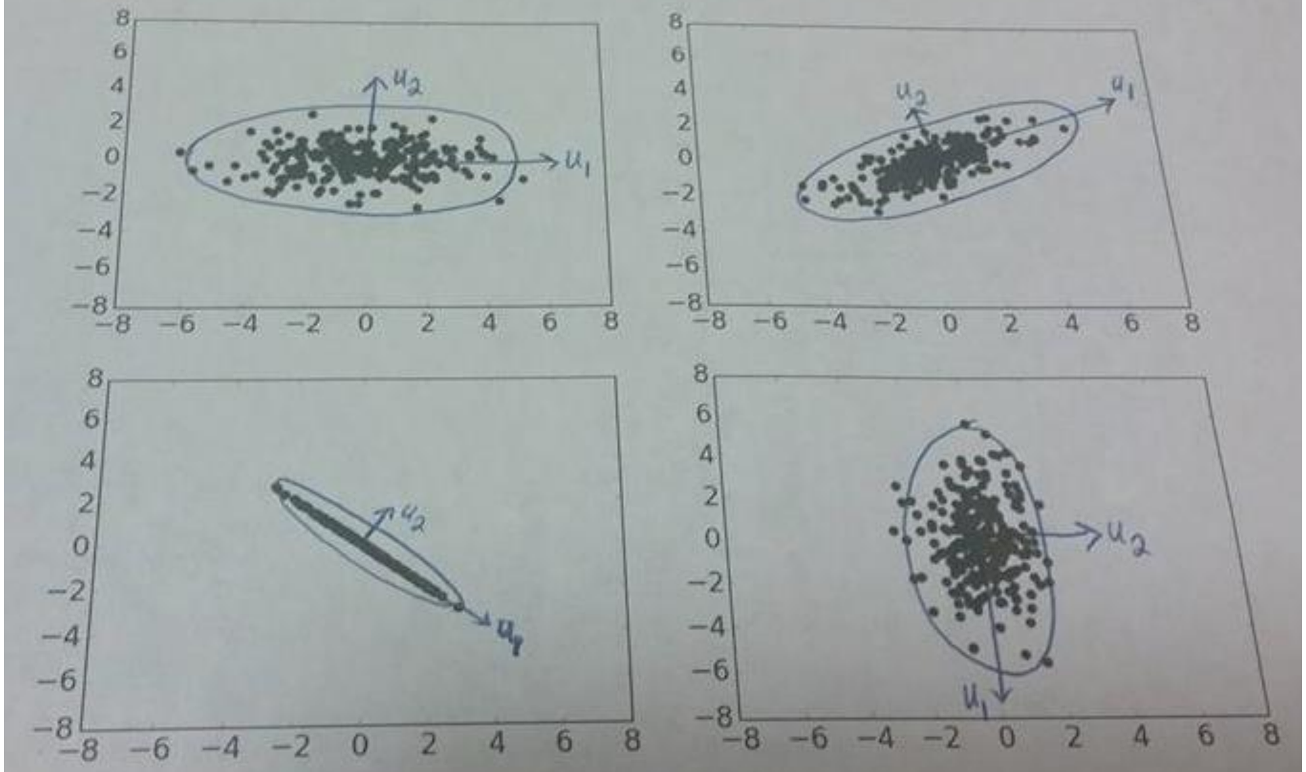
a. dimensions of the following

U	U^T	UU^T	$u_1u_1^T$
$p\times 2$	$2\times p$	$p\times p$	$p\times p$

b. differences if any in projections

$x \mapsto (u_1 \cdot x, u_2 \cdot x)$	$x \mapsto (u_1\cdot x)u_1 + (u_2 \cdot x)u_2$	$x \mapsto U^T x$	$x \mapsto UU^T x$
$p\times 2$ (1° projection)	$p\times 2$ (2° projection)	$2\times p$	$p\times p$

2. The following four figures show different 2-dimensional data sets. In each case, make a rough sketch of an ellipsoidal contour of the covariance matrix and indicate the directions of the first and second eigenvectors (mark which is which).



u_2
u_1
u_2
u_1
u_2
u_1
u_2
u_1