

Question 1 : (30 total points) Image data analysis with PCA

In this question we employ PCA to analyse image data

1.1 (3 points) Once you have applied the normalisation from Step 1 to Step 4 above, report the values of the first 4 elements for the first training sample in `Xtrn_nm`, i.e. `Xtrn_nm[0,:]` and the last training sample, i.e. `Xtrn_nm[-1,:]`.

```
First 4 elements of the first training sample in Xtrn_nm:  
[-3.13725490e-06 -2.26797386e-05 -1.17973856e-04 -4.07058824e-04]  
  
First 4 elements of the last training sample in Xtrn_nm:  
[-3.13725490e-06 -2.26797386e-05 -1.17973856e-04 -4.07058824e-04]
```

1.2 (4 points) Using **Xtrn** and Euclidean distance measure, for each class, find the two closest samples and two furthest samples of that class to the mean vector of the class.

A grid to show the mean vectors for each class along with the closest and furthest samples from these means



There is an interesting trend amongst the closest and furthest samples for each given class in the dataset. Notice that all the closest samples are a subtle gray, and in contrast all the furthest samples are very dark (almost black) or very light (almost white). We can deduce that this is due to the fact that the intensely dark/light colour pixels magnify the difference (and thus Euclidean distance) between corresponding pixel values in different samples.

This is a very important observation as it highlights the significance of colour intensity when calculating the similarity between different samples. This colour intensity could ultimately skew the performance of our classifier when predicting the type of clothing for uniquely dark/light samples. This is especially problematic if a given class (piece of clothing) is more likely to be dark/light as this will make it more likely to classify dark/light samples from other classes.

To prevent this issue, given that we are classifying the type of clothing and not the colour, we could either use a method specifically for classifying shapes (segmentation) or we could normalize the colour intensity of samples upon input (normalize the values of the pixels to be within a certain range).

1.3 (3 points) Apply Principal Component Analysis (PCA) to the data of `Xtrn_nm` using `sklearn.decomposition.PCA`, and report the variances of projected data for the first five principal components in a table. Note that you should use `Xtrn_nm` instead of `Xtrn`.

**Calculating the variances of the projected data in `Xtrn_nm`
for the first five principal components**

Principal Component #	Explained Variance
1	19.81
2	12.112
3	4.106
4	3.382
5	2.625

1.4 (3 points) Plot a graph of the cumulative explained variance ratio as a function of the number of principal components, K , where $1 \leq K \leq 784$. Discuss the result briefly.

A graph to show the relationship between the cumulative explained variance ratio and the number of principal components (K) for 'Xtrn_nm'

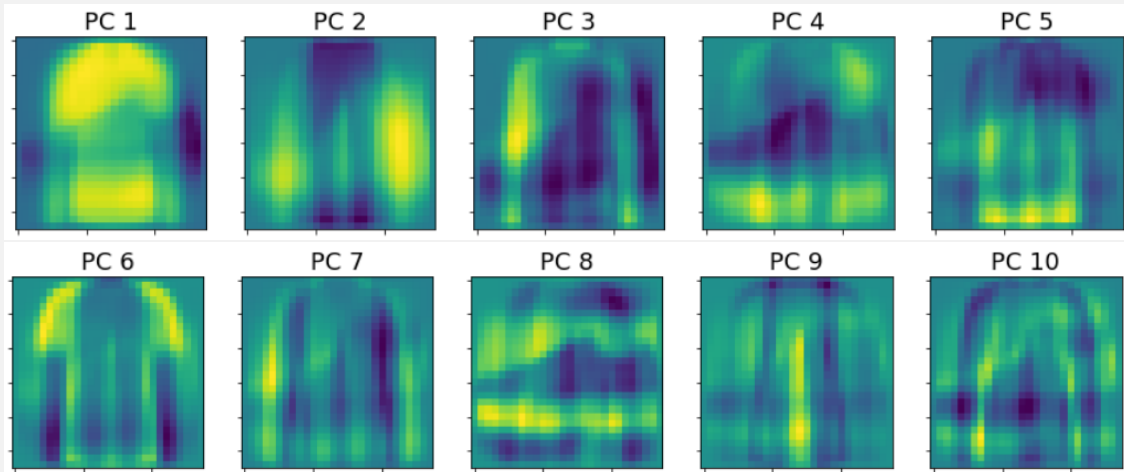


Given that the explained variance ratio for a given principal component represents the variance of that principal component divided by the total variance, we can see that the results of this graph showing the relationship between the cumulative explained ratio and the number of principal components (K) are as expected.

Although PCA chooses dimensions with maximum variance, as we increase the number of dimensions (K) we automatically increase the number of variances (which have been maximised by PCA) we must summate. We also know that the total variance is fixed throughout all different values of K so the value of all cumulative variance ratios are purely dependent on their respective explained variance ratios. Thereby, it is evident as illustrated by the plot that the number of principal components (K) is directly proportional to the cumulative explained ratio in a hyperbolic fashion.

1.5 (4 points) Display the images of the first 10 principal components in a 2-by-5 grid, putting the image of 1st principal component on the top left corner, followed by the one of 2nd component to the right. Discuss your findings briefly.

A grid to show the images of the first 10 principal components



Discuss your findings briefly...

We must note that these images are not distinct given they were calculated using the normalized dataset

***Should show UNnormalized photos too!

1.6 (5 points) Using `Xtrn_nm`, for each class and for each number of principal components $K = 5, 20, 50, 200$, apply dimensionality reduction with PCA to the first sample in the class, reconstruct the sample from the dimensionality-reduced sample, and report the Root Mean Square Error (RMSE) between the original sample in `Xtrn_nm` and reconstructed one.

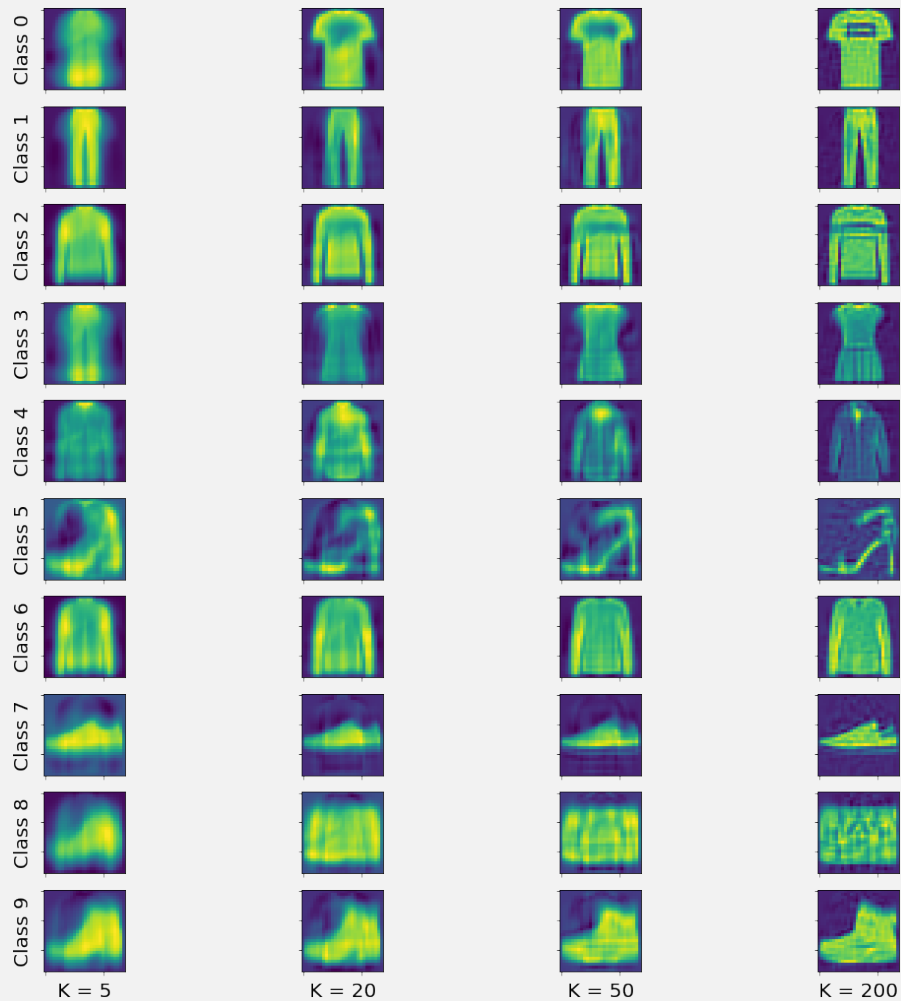
A table to show the RMSE between the original and the reconstructed version of the first sample for every class with varying numbers of PCA components (K)

*Each class sample is reconstructed by reducing the sample to K dimensions and then transforming it back to the original number of dimensions, this is all done via the sklearn PCA implementation.

RMSE	K = 5	K = 20	K = 50	K = 200
Class = 0	0.256	0.15	0.128	0.063
Class = 1	0.198	0.14	0.095	0.037
Class = 2	0.199	0.146	0.124	0.08
Class = 3	0.146	0.107	0.083	0.056
Class = 4	0.118	0.103	0.088	0.045
Class = 5	0.181	0.159	0.142	0.09
Class = 6	0.129	0.096	0.072	0.045
Class = 7	0.166	0.128	0.106	0.063
Class = 8	0.223	0.145	0.124	0.094
Class = 9	0.184	0.151	0.122	0.072

1.7 (4 points) Display the image for each of the reconstructed samples in a 10-by-4 grid, where each row corresponds to a class and each row column corresponds to a value of $K = 5, 20, 50, 200$.

A grid to show the images of the reconstructed class samples for varying amounts of dimension reductions (K)



As expected the reconstructed samples become more detailed as we increase the value of K. This is evident due to the increased number of dimensions to retain detail within the data. PCA reduces dataset dimensions by choosing dimensions which maximize variance in the data, this is evident to see as the reconstructed samples with small K highlight the more prominent features from their respective original samples.

1.8 (4 points) Plot all the test samples (`Xtrn_nm`) on the two-dimensional PCA plane you obtained in Question 1.3, where each sample is represented as a small point with a colour specific to the class of the sample. Use the 'coolwarm' colormap for plotting.



Give comments on the separation of the classes and explain findings briefly...

Question 2 : (25 total points) Logistic regression and SVM

In this question we will explore classification of image data with logistic regression and support vector machines (SVM) and visualisation of decision regions.

2.1 (3 points) Carry out a classification experiment with **multinomial logistic regression**, and report the classification accuracy and confusion matrix (in numbers rather than in graphical representation such as heatmap) for the test set.

FREQUENCY CONFUSION MATRIX:

Predicted Actual	0	1	2	3	4	5	6	7	8	9
0	819	5	27	31	0	2	147	0	7	0
1	3	953	4	15	3	0	3	0	1	0
2	15	4	731	14	115	0	128	0	6	0
3	50	27	11	866	38	1	46	0	11	1
4	7	5	133	33	760	0	108	0	3	0
5	4	0	0	0	2	911	0	32	7	15
6	89	3	82	37	72	0	539	0	15	1
7	1	1	2	0	0	56	0	936	5	42
8	12	2	9	4	10	10	28	1	945	0
9	0	0	1	0	0	20	1	31	0	941

PERCENTAGE CONFUSION MATRIX:

Predicted Actual	0	1	2	3	4	5	6	7	8	9
0	78.9	0.5	2.7	2.9	0.0	0.2	17.5	0.0	0.7	0.0
1	0.3	97.0	0.4	1.4	0.3	0.0	0.4	0.0	0.1	0.0
2	1.4	0.4	72.2	1.3	11.0	0.0	15.3	0.0	0.6	0.0
3	4.8	2.7	1.1	82.4	3.6	0.1	5.5	0.0	1.1	0.1
4	0.7	0.5	13.1	3.1	72.4	0.0	12.9	0.0	0.3	0.0
5	0.4	0.0	0.0	0.0	0.2	93.8	0.0	3.1	0.7	1.5
6	8.6	0.3	8.1	3.5	6.9	0.0	64.3	0.0	1.5	0.1
7	0.1	0.1	0.2	0.0	0.0	5.8	0.0	89.7	0.5	4.2
8	1.2	0.2	0.9	0.4	1.0	1.0	3.3	0.1	92.6	0.0
9	0.0	0.0	0.1	0.0	0.0	2.1	0.1	3.0	0.0	94.7

Classification accuracy = 84.01%

2.2 (3 points) Carry out a classification experiment with **SVM classifiers**, and report the mean accuracy and confusion matrix (in numbers) for the test set.

FREQUENCY CONFUSION MATRIX:

Predicted Actual	0	1	2	3	4	5	6	7	8	9
0	845	4	15	32	1	0	185	0	3	0
1	2	951	2	6	0	0	1	0	1	0
2	8	7	748	12	98	0	122	0	8	0
3	51	31	11	881	36	1	39	0	5	0
4	4	5	137	26	775	0	95	0	2	0
5	4	0	0	0	0	914	0	34	4	22
6	72	1	79	40	86	0	533	0	13	0
7	0	0	0	0	0	57	0	925	4	47
8	14	1	8	3	4	2	25	0	959	1
9	0	0	0	0	0	26	0	41	1	930

PERCENTAGE CONFUSION MATRIX:

Predicted Actual	0	1	2	3	4	5	6	7	8	9
0	77.9	0.4	1.5	3.0	0.1	0.0	22.5	0.0	0.3	0.0
1	0.2	98.8	0.2	0.6	0.0	0.0	0.1	0.0	0.1	0.0
2	0.7	0.7	74.6	1.1	9.4	0.0	14.8	0.0	0.8	0.0
3	4.7	3.2	1.1	83.5	3.4	0.1	4.7	0.0	0.5	0.0
4	0.4	0.5	13.7	2.5	74.2	0.0	11.5	0.0	0.2	0.0
5	0.4	0.0	0.0	0.0	0.0	93.5	0.0	3.3	0.4	2.2
6	6.6	0.1	7.9	3.8	8.2	0.0	64.7	0.0	1.3	0.0
7	0.0	0.0	0.0	0.0	0.0	5.8	0.0	89.5	0.4	4.7
8	1.3	0.1	0.8	0.3	0.4	0.2	3.0	0.0	94.3	0.1
9	0.0	0.0	0.0	0.0	0.0	2.7	0.0	4.0	0.1	93.2

Classification accuracy = 84.412%

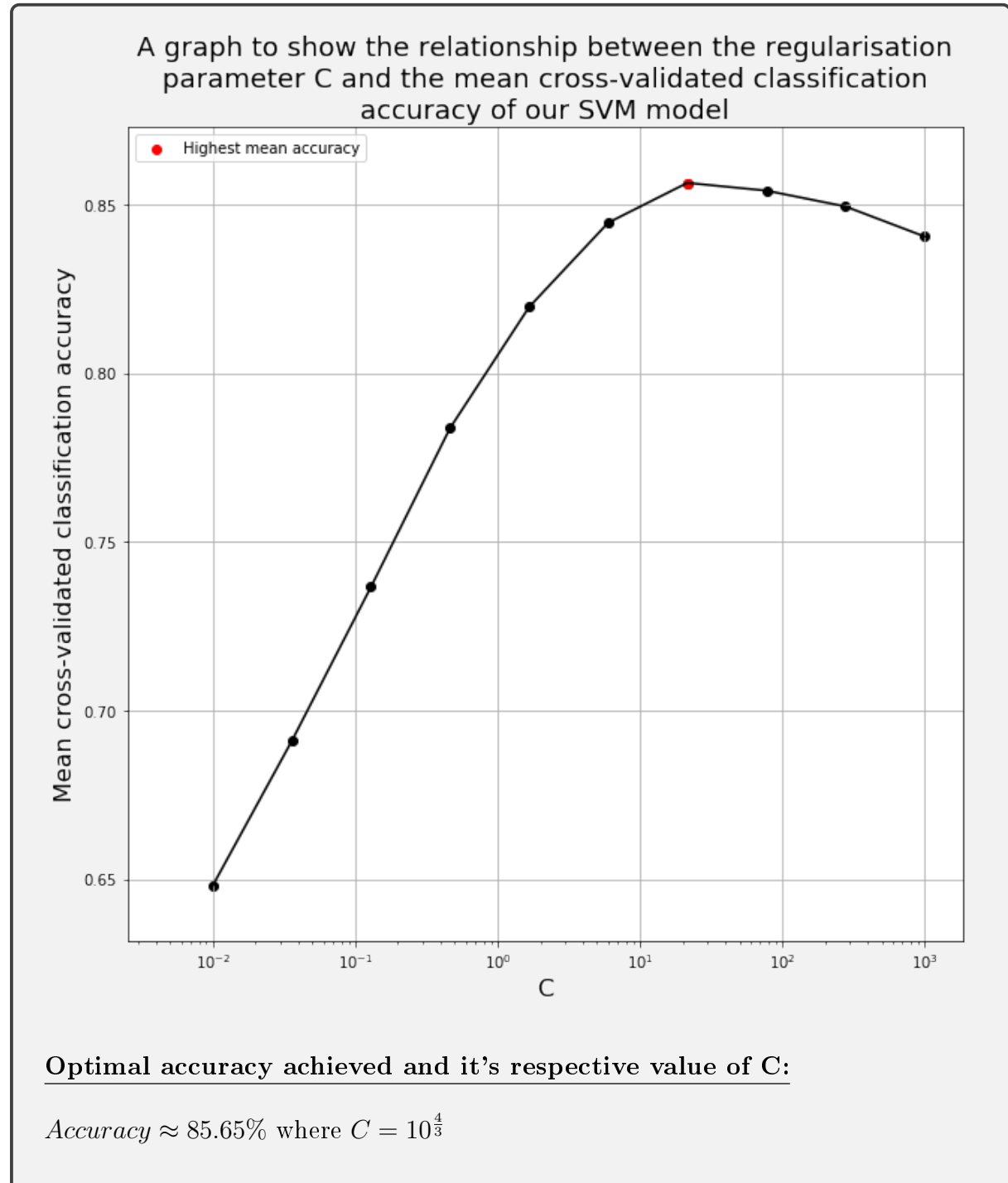
2.3 (6 points) We now want to visualise the decision regions for the logistic regression classifier we trained in Question 2.1.



2.4 (4 points) Using the same method as the one above, plot the decision regions for the SVM classifier you trained in Question 2.2. Comparing the result with that you obtained in Question 2.3, discuss your findings briefly.



2.5 (6 points) We used default parameters for the SVM in Question 2.2. We now want to tune the parameters by using cross-validation. To reduce the time for experiments, you pick up the first 1000 training samples from each class to create X_{small} , so that X_{small} contains 10,000 samples in total. Accordingly, you create labels, Y_{small} .



2.6 (3 points) Train the SVM classifier on the whole training set by using the optimal value of C you found in Question [2.5](#).

Classification accuracy of our trained SVM model using the optimal value of C found ($10^{\frac{4}{3}}$)

Training accuracy $\approx 90.842\%$

Testing accuracy $\approx 87.65\%$

Question 3 : (20 total points) Clustering and Gaussian Mixture Models

In this question we will explore K-means clustering, hierarchical clustering, and GMMs.

3.1 (3 points) Apply k-means clustering on `Xtrn` for $k = 22$, where we use `sklearn.cluster.KMeans` with the parameters `n_clusters=22` and `random_state=1`. Report the sum of squared distances of samples to their closest cluster centre, and the number of samples for each cluster.

```
Sum of squared distances (Euclidean) of samples to their closest cluster center:  
38185.81698349466
```

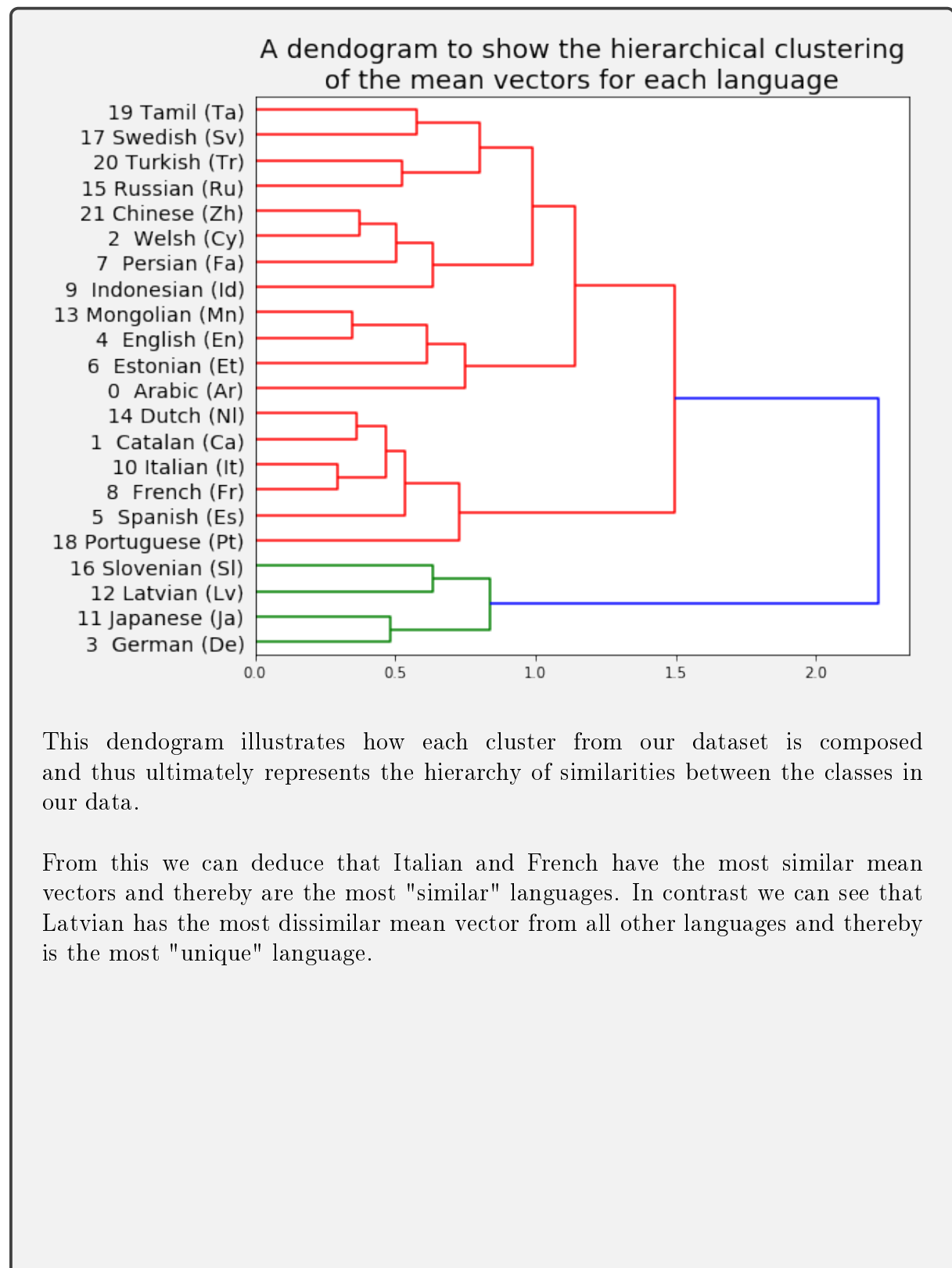
```
Number of samples for each cluster:
```

```
Cluster 1 = 1018  
Cluster 2 = 1125  
Cluster 3 = 1191  
Cluster 4 = 890  
Cluster 5 = 1162  
Cluster 6 = 1332  
Cluster 7 = 839  
Cluster 8 = 623  
Cluster 9 = 1400  
Cluster 10 = 838  
Cluster 11 = 659  
Cluster 12 = 1276  
Cluster 13 = 121  
Cluster 14 = 152  
Cluster 15 = 950  
Cluster 16 = 1971  
Cluster 17 = 1251  
Cluster 18 = 845  
Cluster 19 = 896  
Cluster 20 = 930  
Cluster 21 = 1065  
Cluster 22 = 1466
```

3.2 (3 points) Using the training set only, calculate the mean vector for each language, and plot the mean vectors of all the 22 languages on a 2D-PCA plane, where you apply PCA on the set of 22 mean vectors without applying standardisation. On the same figure, plot the cluster centres obtained in Question 3.1.



3.3 (3 points) We now apply hierarchical clustering on the training data set to see if there are any structures in the spoken languages.

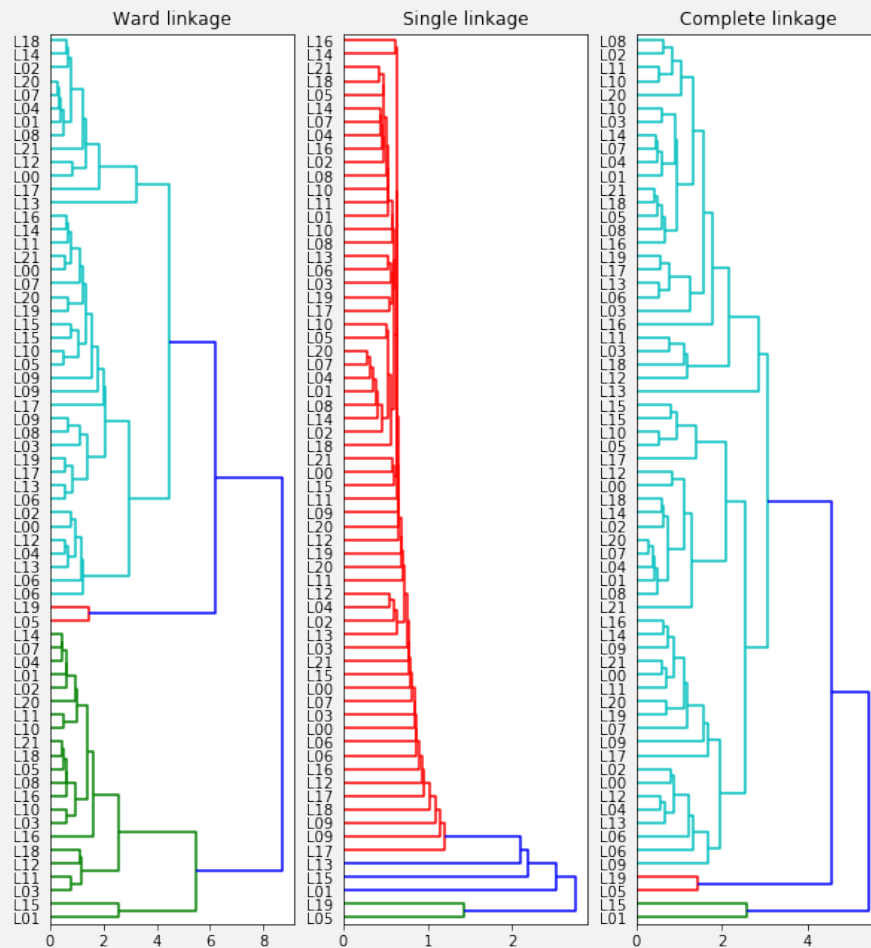


This dendrogram illustrates how each cluster from our dataset is composed and thus ultimately represents the hierarchy of similarities between the classes in our data.

From this we can deduce that Italian and French have the most similar mean vectors and thereby are the most "similar" languages. In contrast we can see that Latvian has the most dissimilar mean vector from all other languages and thereby is the most "unique" language.

3.4 (5 points) We here extend the hierarchical clustering done in Question 3.3 by using multiple samples from each language.

Hierarchical clustering dendrograms with varying linkage trained over the three cluster centers for each of the languages in the dataset



Discuss results briefly...

3.5 (6 points) We now consider Gaussian mixture model (GMM), whose probability distribution function (pdf) is given as a linear combination of Gaussian or normal distributions, i.e.,



Table to show the average per-sample log-likelihood scores for varying parameters of a GMM

Language 0 data	Σ type	K = 1	K = 3	K = 5	K = 10	K = 15
Training	Diagonal	14.28	15.399	16.014	16.895	17.653
Testing	Diagonal	13.843	15.041	15.882	16.375	19.942
Training	Full	16.394	18	19.129	21.018	22.889
Testing	Full	15.811	16.895	16.704	15.19	10.787

Discuss your findings...