

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 and last samples from the normalized training dataset `Xtrn_nm`

```
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 or very light (eg. the class 4 samples). 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 (type of clothing) is more likely to be dark/light as this will make it more likely to classify uniquely 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 (image segmentation) or we could normalize the colour intensity of samples upon input (normalize the values of the pixels to be within a certain range).

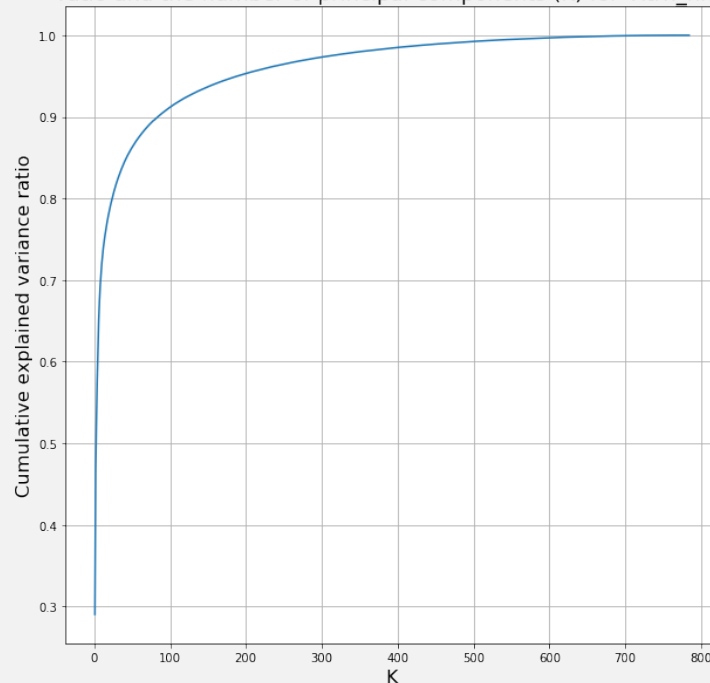
1.3 (3 points) Apply Principal Component Analysis (PCA) to the data of `Xtrn_nm` using `sklearn.decomposition.PCA`, and report the variances of projected data for the first five principal components in a table. Note that you should use `Xtrn_nm` instead of `Xtrn`.

**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'



$$\text{Cumulative explained variance ratio} = \frac{\sum_{k=1}^K \sigma_k^2}{\sigma_{\text{total}}^2}$$

***We must note that that the total variance as described in the equation above is the cumulative explained variance from the original 784 dimension dataset, and thereby is fixed for all ratio calculations where $1 \leq K \leq 784$.*

This cumulative explained variance ratio ultimately represents how much detail our new data retains from our original data. The reason the 'detail' of our data is measured by variance is because variance measures the average difference between all samples in the data, we want data with a high variance as this allows for more accurate classification.

Given this information it is evident to see that this graphing model ultimately represents the relationship between the 'detail' in the data and the number of dimensions. This is very useful when you have high dimensional data that you want to reduce whilst still keeping as much 'detail' in the data as possible.

We can see from the figure above that using just 100 dimensions (about 87.24% less data) already secures about 91.17% of the total cumulative variance from the original data.

Choosing the optimal number of dimensions for a given dataset depends entirely on the context of the data/classification model, as this directly denotes how important the trade-off between the size of the data and the quality of the data is. For example, when working with critical data we can not afford to lose any quality thus we would prefer to not reduce the dimensions. However, reducing dimensions can be very useful for many supervised methods, making problems that are not linearly separable into ones that are, reducing noise in the data, and being able to visually represent high-dimensional data.

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



These images represent the eigenvectors for each of their respective dimensions. Each of these eigenvectors has a direction and a corresponding eigenvalue. These are used for projecting data into new spaces.

What is useful is that we notice that many of the different clothing shapes are retained in these eigenvectors. In most of these images you can see the resemblances of most of the different clothing types from our dataset, however, what is truly interesting is the frequency and intensity of the different clothing shapes found amongst these. These factors are very important as these suggest what are the most significant features throughout all of our different classes for classification.

With regards to the frequency of the different clothing shapes, I am referring to the number of eigenvectors in which we can visibly see the resemblance of the different clothing types. For example, in contrast to other clothing shapes, we can see in almost all of the images the resemblance of a long sleeved shirt. This ultimately suggests that this long sleeved shirt shape was most common from our training data. This is evident as illustrated by the class images in Q1.2 where classes 2 (pullover), 4 (coat) and 6 (shirt) all appear to take very similar shapes, resembling that of a long sleeved shirt.

With regards to the intensity of the different clothing shapes, I am referring to the most prominent/visible shapes for each eigenvector. For example, PC 1 shows the resemblance of a long sleeved shirt, PC 2 shows the resemblance of trousers, PC 3 shows the resemblance of a boot, and PC 4 shows the resemblance of a sneaker. This ultimately represents how the separate dimensions in our dataset may be used predominantly for classifying certain classes. This makes perfect sense as this allows our model to apply different weightings to each dimension.

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.

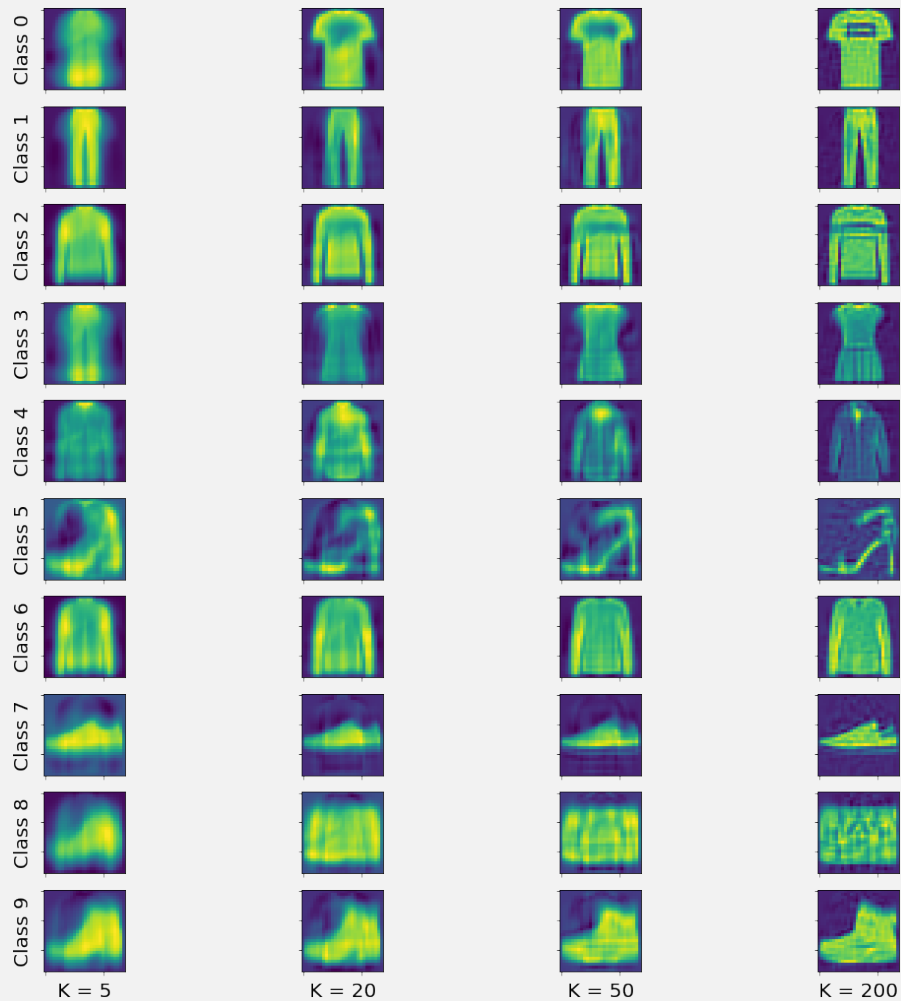
A table to show the RMSE between the original and the reconstructed version of the first sample for every class with varying numbers of PCA components (K)

*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.

Confusion matrices to show the classification accuracy of our trained multinomial logistic regression model on 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.

Confusion matrices to show the classification accuracy of our trained SVM model on 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.

Metrics for our trained k-means clustering model

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

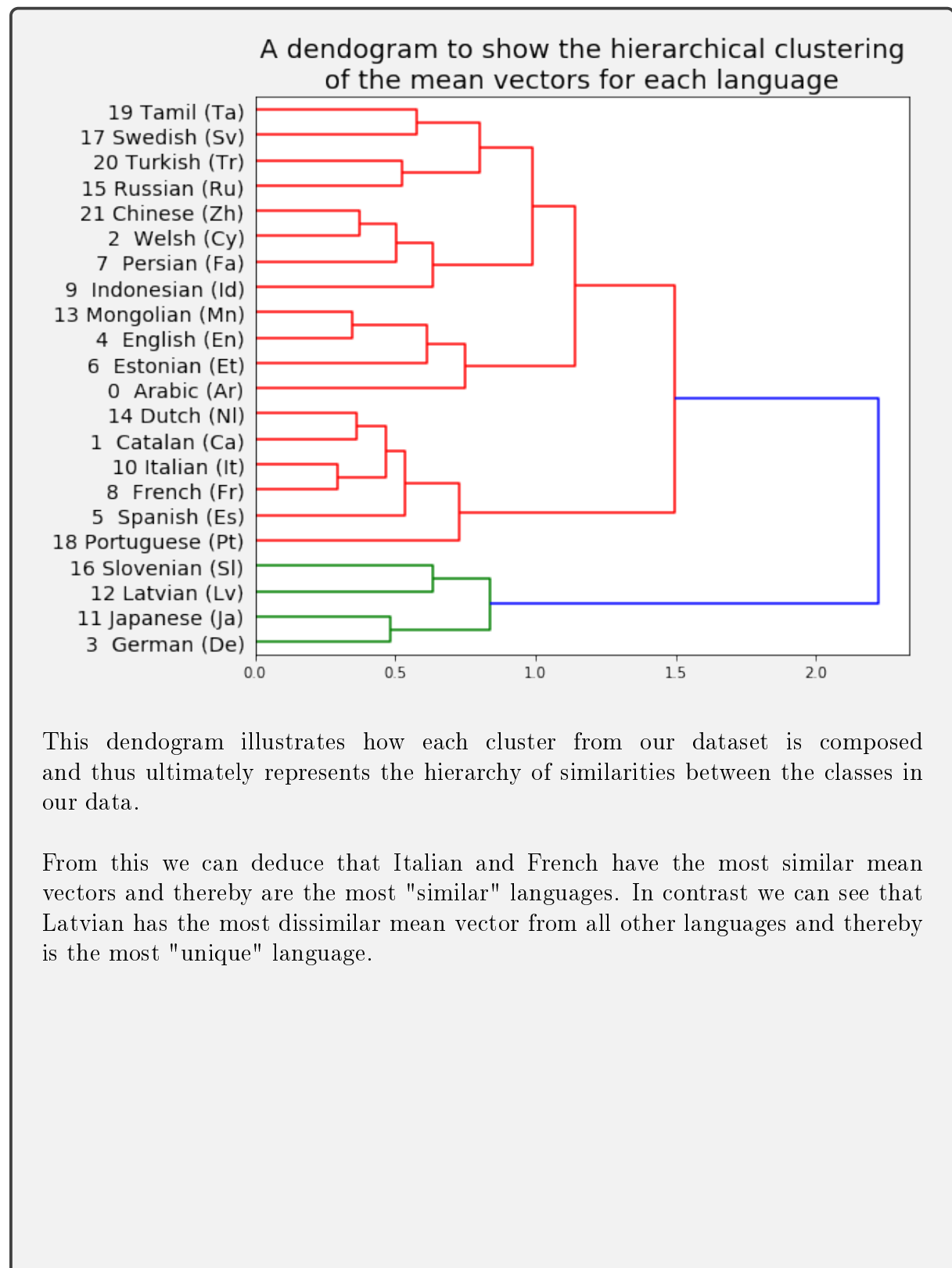
```
Number of samples for each cluster:
```

```
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.

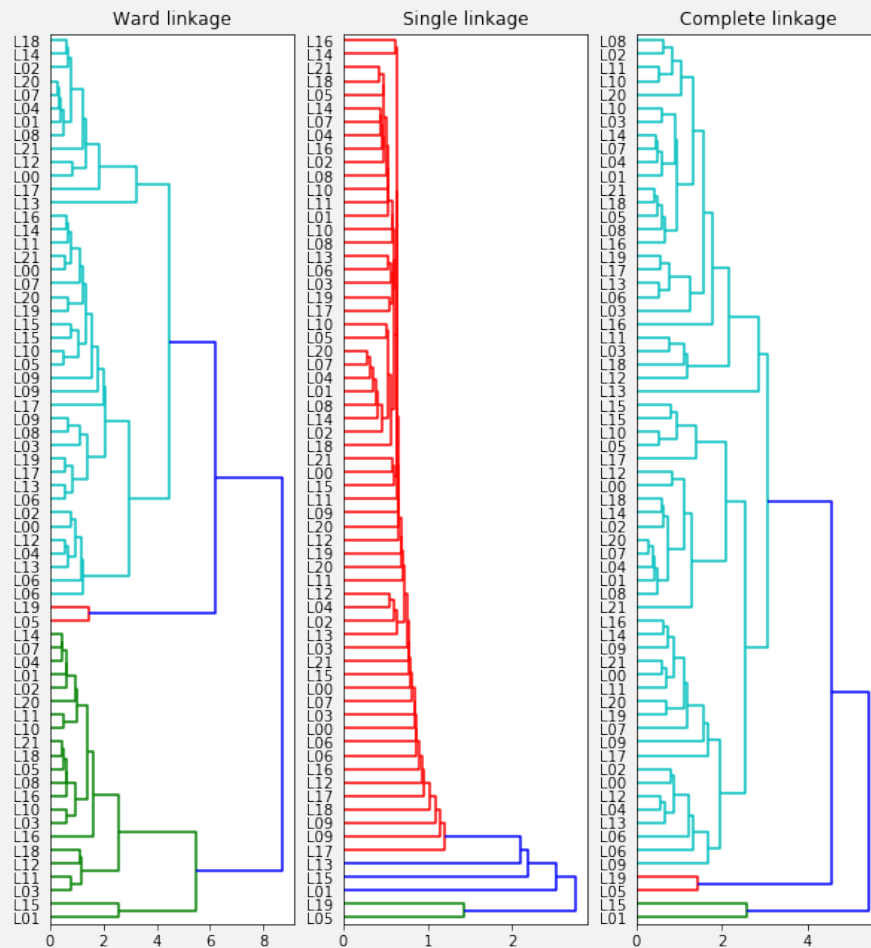


This dendrogram illustrates how each cluster from our dataset is composed and thus ultimately represents the hierarchy of similarities between the classes in our data.

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...