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DATASET USED

Human Gene DNA Sequences

The dataset constitutes of 311 DNA sequences in FASTA format

PREPROCESSING DONE ON DATA

The Proximity Matrix is preprocessed and stored in an 'out.txt' file. It is then loaded onto, when required.

FORMULAE USED

Single Linkage:

Shortest distance between two clusters is considered.

The minimum of which is taken as the metric

$$\min\,\{\,d(a,b):a\in A,\,b\in B\,\}.$$

DISTANCE METRIC

Global Sequence Alignment: Using Dynamic Programming

```
The similarity between two DNA sequences is assessed using
1. gap
2. substitution
3. match
for (int i = 1; i <= sequenceA.length(); i++)</pre>
   opt[i][0] = opt[i - 1][0] + gap;
for (int j = 1; j <= sequenceB.length(); j++)</pre>
   opt[0][j] = opt[0][j - 1] + gap;
for (int i = 1; i <= sequenceA.length(); i++) {</pre>
    for (int j = 1; j \le sequenceB.length(); <math>j++) {
       match : // same symbol
                   substitution); // different symbol
       int scoreLeft = opt[i][j - 1] + gap; // insertion
       int scoreUp = opt[i - 1][j] + gap; // deletion
       // we take the minimum
       opt[i][j] = Math.min(Math.min(scoreDiag, scoreLeft), scoreUp);
```

WHERE SINGLE LINKAGE WORKS

Single linkage works with irregular shaped clusters. But it is sensitive to outliers.

AVERAGE DISTANCE

Every pair of each cluster, is averaged out, and the distance is found.

This has been used in calculation of the Z Matrix.

Z-MATRIX

The Z-Matrix is (n-1)x4 matrix on SciPy

n-1 rows for every merge

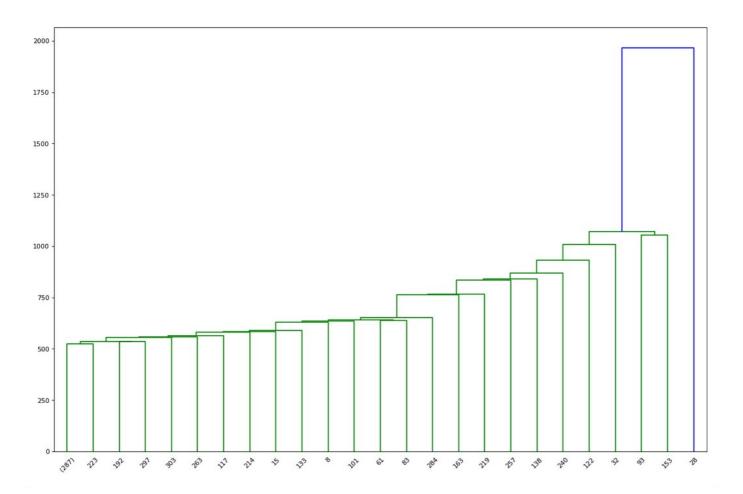
Column 1: ith cluster merging Column 2: jth cluster merging

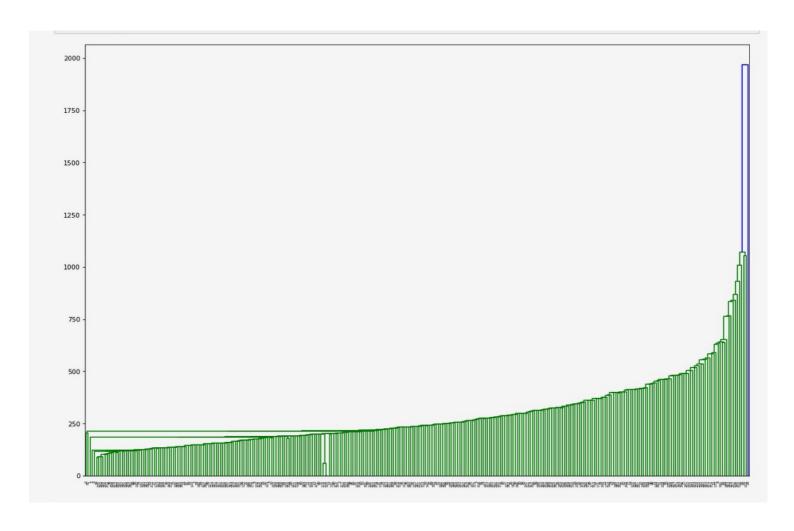
Column 3: distance between the clusters

Column 4: Number of original points in the cluster

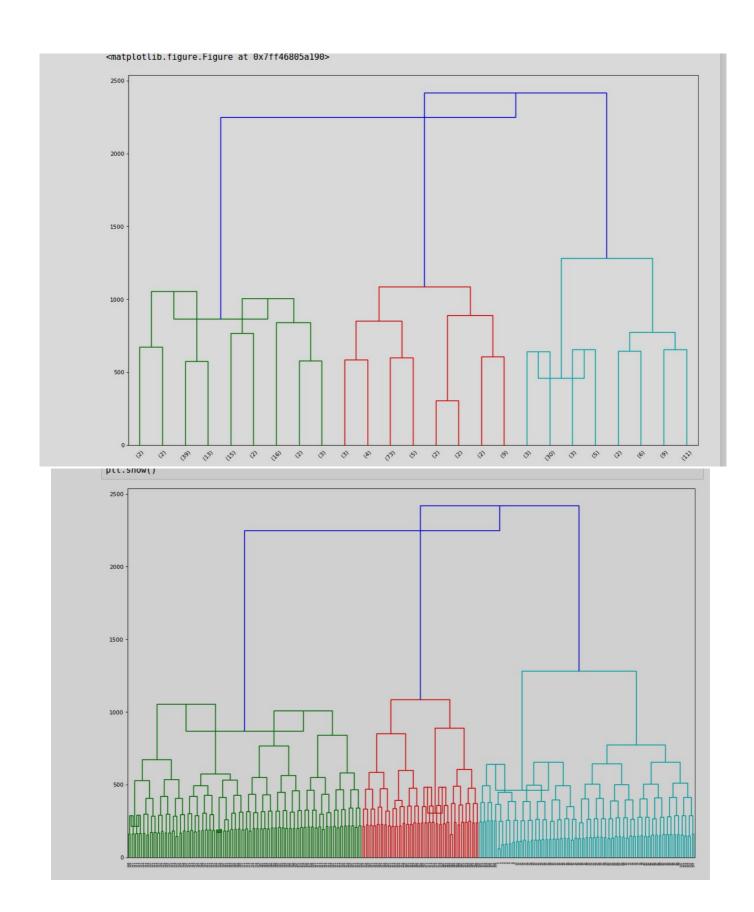
The Z matrix is an input in SciPy to plot Dendrograms.

AGGLOMERATIVE CLUSTERING





DIVISIVE CLUSTERING



The Agglomerative Clustering proves to be better for larger datasets. It scales better.

In Agglomerative Clustering shows a gradual connection between consecutive clusters.

The Divisive Clustering is required for more holistic view, that converges from a single cluster.