

CS690 Assignment 2 report

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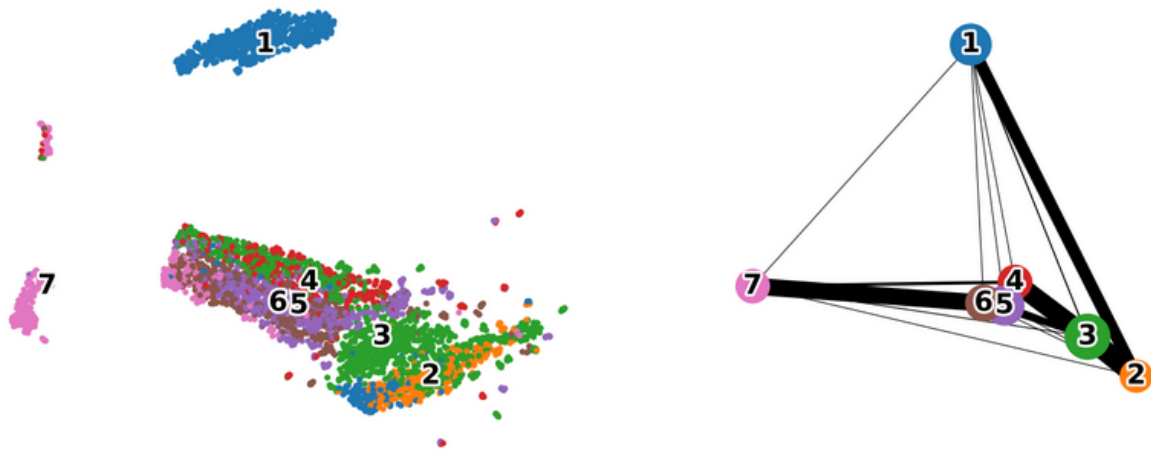
We used the ADEPT method for both clustering and imputation. The main core of the method uses an autoencoder to generate the spatial graph for k-means clustering. It then imputes the missing spatial transcriptomics data using its selection of the differentially expressed (DE) genes.

The authors' code was quite buggy, especially the part related to the loading of the datasets. The issues took quite some time to iron out, and we have raised an issue in the authors' github repo, which they will hopefully merge with the main project. With regards to the results, it was found that in most cases imputation made a significant (up to 30%) difference in the ARI score.

Spatial plots:

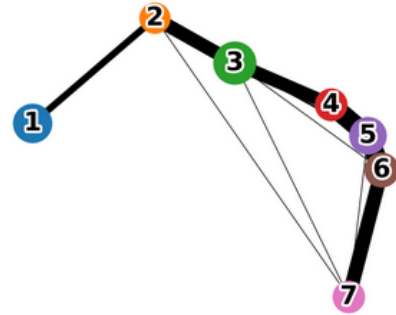
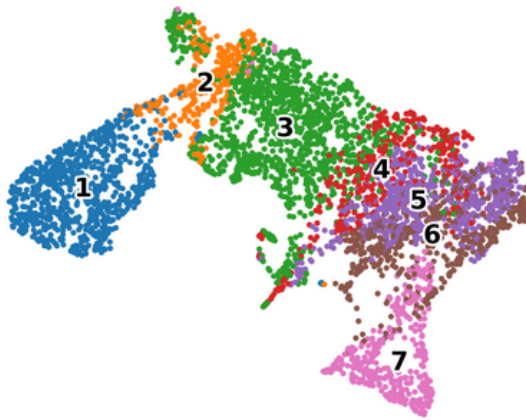
Imputation on

151507_ADePute



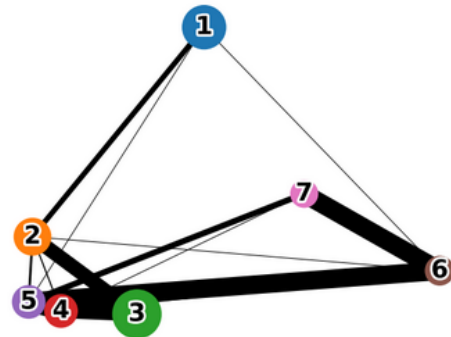
Imputation off

151507_ADePute



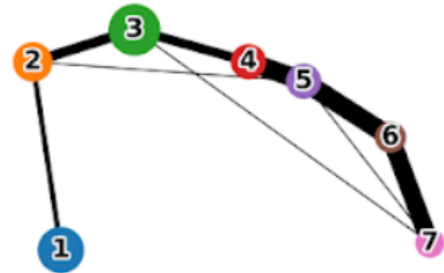
151509 Impute on

151509_ADePute



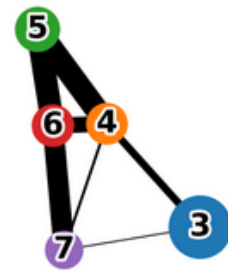
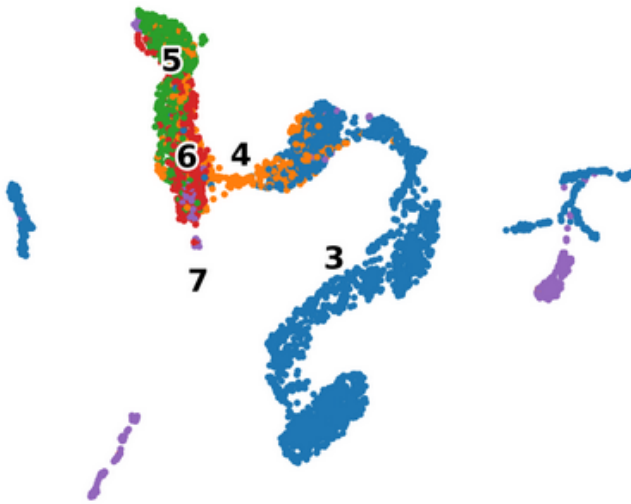
151509 Impute off

151509_ADePute



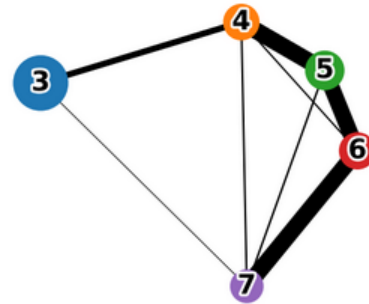
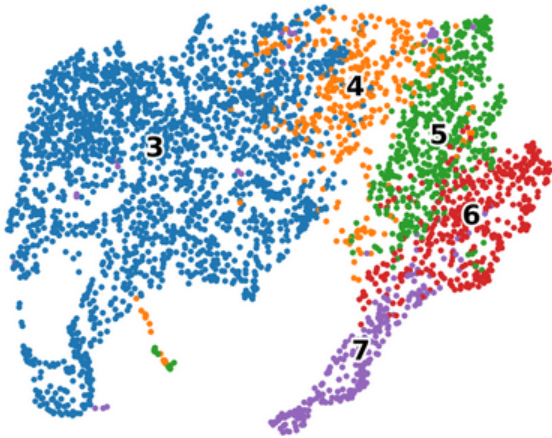
151669 Impute on

151669_ADePute



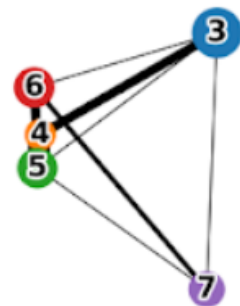
151669 Impute off

151669_ADePute



151671 Impute on

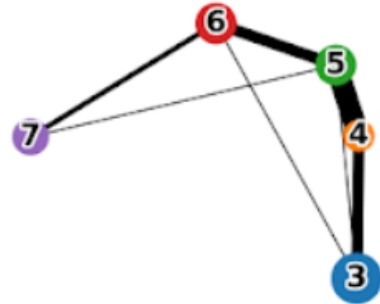
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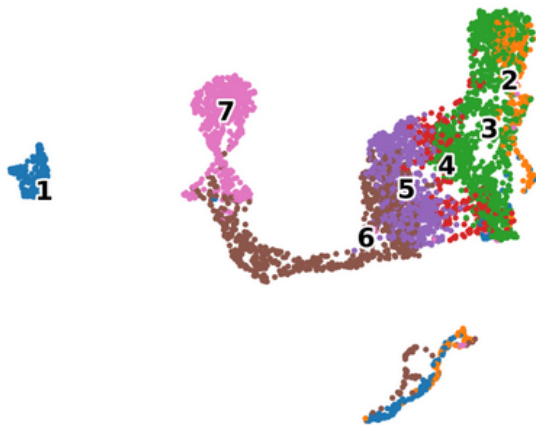
151671 Impute off



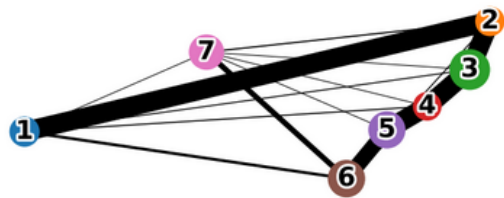
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151673 Impute on



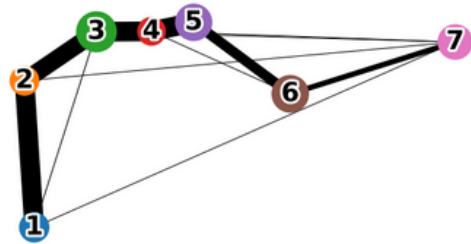
151673_ADePute



151673 Impute off



151673_ADePute



Contribution

Suyash Malik debugged and ran the ADEPT script, and generated the clustering predictions and spatial plots without imputation.

Mubashshir Uddin worked on the ConGI method.

Divyam Jain generated the clustering predictions for the ADEPT script without imputation.