April 8 2023

The similarity score module was implemented and the model was rerun on the new dataset. Entropy measure was used to compare the similarity matrices. Datamining was performed to find drug-gene associations and it was obtained from DGIdb. The drug names were matched against the drug bank database and the corresponding gene associations were obtained.

Results

Reported values for ten-fold cross-validation in the SNF-NN paper
Acc = 0.796
Rec= 0.816
F1 = 0.800
MCC = 0.593
AUC−ROC= 0.867
AUC−PR = 0.876

Our code after similarity selection
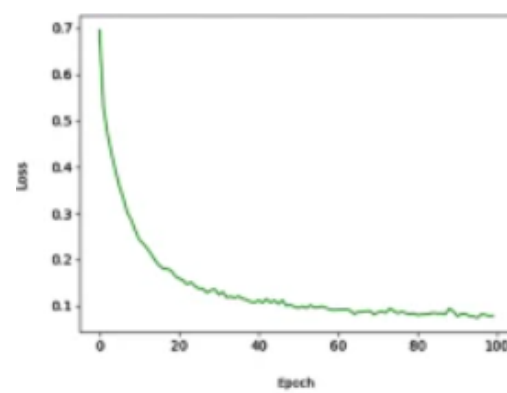Test accuracy: 0.83
F1-score: 0.75
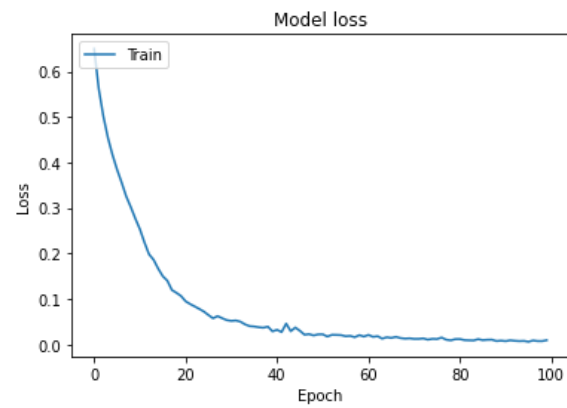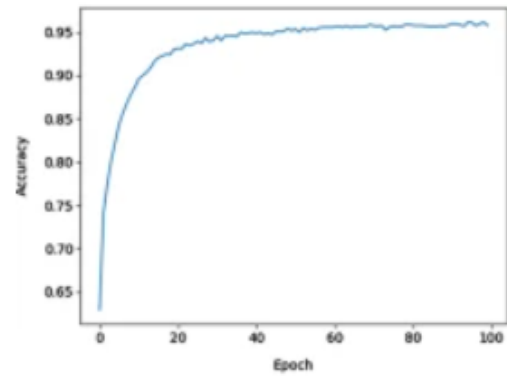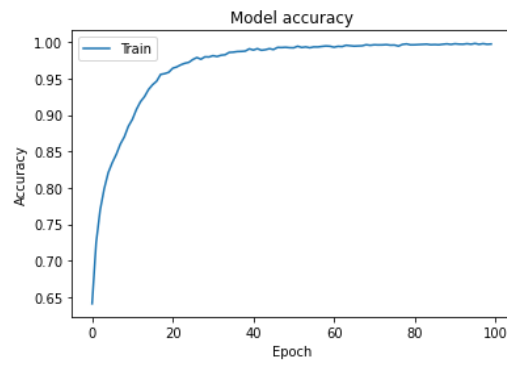Recall: 0.72
MCC: 0.62
AUC-ROC: 0.85
AUC-PR: 0.79

Below, on the left, are the graphs generated by us and on the right are those shown in the paper.

Takeaways

● Similarity network selection has improved the overall predictive ability of the model