HallmarkGraph: a cancer hallmark informed graph neural network for classifying hierarchical tumor subtypes

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This is the file library for HallmarkGraph

The current purpose of this file library is to provide reviewers with reproducible experimental results.

The repository contains the following:

```
code file:
```

06_BioGCN_load_model_and_test_pred.py

cleaned_data_and_target file :

Training and testing data: cleaned_data_out.csv

Training and testing label: cleaned_data_test_12_7.xlsx

adjacency_matrix file:

ten Hallmark related adjacency matrices

saved model file:

train: test = 0.6: 0.4: save_model(0.4)_18

analysis file:

Analysis file of experimental results: analysis

supplmentary materials file:

Supplementary documents for manuscript submission

If you wish to repeat our experiment, please refer to the following configuration:

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tensorflow=2.8.2=gpu_py39hc0c9373_0 keras=2.8.0=py39h06a4308_0 shap=0.45.1 scikit-learn=1.4.1.post1 matplotlib=3.9.2

We only use torch to clean up our GPU devices (our device storage space is insufficient), so this file is not limited by the torch version

how to get result:

- 1. The following files need to be downloaded from the repository: (1) code file, (2) clean data and target file, (3) adjacency matrix file, (4) saved model file
- 2、Modify the file path of the following tags in the *O6_BioGCN_load_model_and_test_pred.py* file:

data_path: training and testing data in cleaned_data_out.csv

graph_path: The adjacency matrix constructed based on the biological prior knowledge required for BioGCN in adjacency_matrix

target_path: training and testing label in cleaned_data_test_12_7.xlsx

best_model_path: Import the saved model in save_model(0.4)_18

Modify the file path of the cleaned_data_and_target file in the 06_BioGCN_load_model_and_test_pred.py file, and then run it. If you want to predict hard samples, please set **Whether_to_predict_hard_stamples = TRUE**, If you want to calculate the shap, please set **Whether_to_calculate_the_shap = TRUE**