CSAM-GAN is a model that can process multi-modal data of multiple cancer sets. Its input includes miRNA expression data, mRNA expression data and histopathological image data, and output is a prediction label corresponding to cancer patient samples. The approach can be divided into two sections. Firstly, we extract the features from each type of multi-modal data and learn the differences and connections between different modal data. Secondly, we used the classifier composed of deep neural network (DNN) to predict label for each patient.

Requirements

This is an implementation of CSAM-GAN in Python 3.8.

Keras (2.7.0)

Tensorflow (2.7.0)

xlrd (1.2.0)

scikit-learn (1.0.2)

Installation  
git clone https://github.com / CSAM-GAN.git  
cd CSAM-GAN  
Running Experiments  
Our proposed CSAM-GAN framework is in the ‘CSAM-GAN /GAN.py’ directorty.  
Before running the experiments, make sure the required environment is configured. After configuring the required environment, you can run CSAM-GAN by the following codes  
cd CSAM-GAN  
python GAN.py

the output file is stored in ./LGG/LGG.csv and the record model is in./model/LGG.h5  
Classification

python classification.py

Dataset

the input list of LGG multi-modal data set is in./inputs/. We can use the following command to finish process:   
python CSAM-GAN.py -m CSAM-GAN -t LGG -i ./inputs/LGG.list   
record the corresponding class label for each sample are in./LGG/label.csv