1. Install R packages

We need to install the following dependent packages:

Our method:

R version=4.0.3

Hmisc version=0.8

Rbsurv version=2.48.0

Survival version=3.2-7

Biobase version=2.50.0

randomForestSRC version=2.9.3

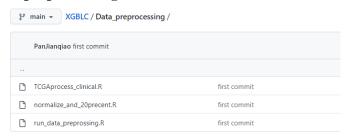survivalROC version=1.0.3

Matrix version=1.2-18

Baseline methods:

survivalsvm version=0.0.5

glmnet version=4.0-2

xgboost version=1.2.0.1

randomForestSRC version=2.9.3

2. Data preprocessing

The R codes are used for data preprocessing, and the raw datasets can be collected from biological labs or downloaded from public databases, such as TCGA.

3. If you plan to run the R script on one cancer data set

Please prepare these files as follows

Put xgblc.R file into the data folder, set the R directory to this caner datasets, and then run all of them.
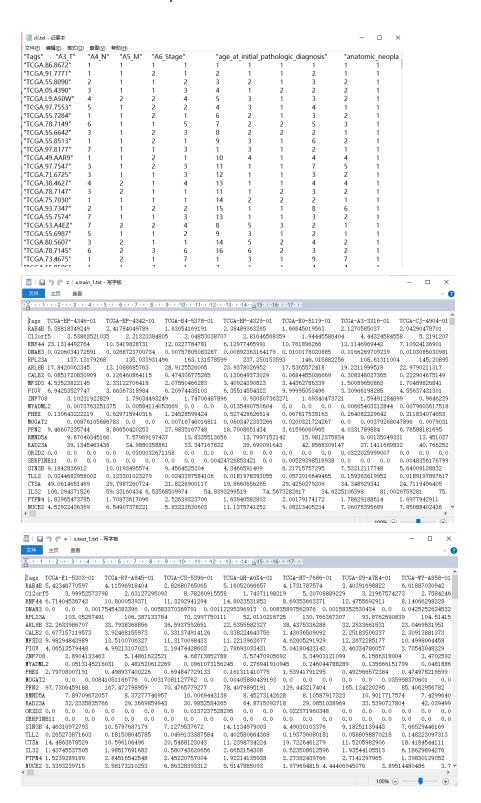
These files include RNA sequence data and corresponding clinical information

xgblc.R: xgblc model script

run.R: run script

cli.txt: clinical information

x.test and x.train: RNA sequence data for 5-fold cross validation

4. If you plan to run R script on several cancer data sets together

Place the file as follows

名称	日期	类型
BRCA	2021/7/11 10:30	文件夹
CESC	2021/7/11 10:30	文件夹
HNSC	2021/7/11 10:30	文件夹
KIRC	2021/7/11 10:30	文件夹
run.R	2021/7/10 2:31	R 文件
xgblc.R	2021/7/10 2:31	R 文件

 xgblc.R: xgblc model script
 run.R: run script

Modify the corresponding directories of run.R and xgblc.R, for example：
 Setwd("File path")

All programs can be downloaded from https://github.com/lab319/XGBLC