### Workflow

#### 1.Generating sequence feature

nohup ./sequence\_vector.sh {dataset} >{log\_file} 2>&1 &

parameters:

**dataset**: NPHN3265,NPHN4158,NPHN317,NPHN-Homo,NPHN-Mus

#### 2.Generating samples for train and Dividing data sets

nohup ./split\_cv\_edgelist.sh {dataset} {sampling\_type} >{log\_file} 2>&1 &

parameters:

**dataset**: NPHN3265,NPHN4158,NPHN317,NPHN-Homo,NPHN-Mus

**sampling\_type**:

0: random negative sampling

1: fire negative sampling

2: reliable negative sampling

3: 0 & 2

#### 3.Generating node feature vector and dataset for training

nohup ./five\_cv\_dataset.sh {dataset} {node\_feature\_type} {subgraph\_type} {sampling\_type} > {log\_file} 2>&1 &

parameters:

**dataset**: NPHN3265,NPHN4158,NPHN317,NPHN-Homo,NPHN-Mus

**node\_feature\_type**:

0: Nf,n2v,l

1: Np,n2v,l

2: Nn2v,l

**subgraph\_type**:

0: subgraph3

1: subgraph2

2: subgraph1

**sampling\_type**:

0: random negative sampling

1: fire negative sampling

2: reliable negative sampling

3: 0 & 2

#### 4.Running cross validation of RPI-HGNN and saving results

nohup ./five\_cv\_train.sh {dataset} {node\_feature\_type} {subgraph\_type} {sampling\_type} {cuda\_no} >{log\_file} 2>&1 &

parameters:

**dataset**: NPHN3265,NPHN4158,NPHN317,NPHN-Homo,NPHN-Mus

**node\_feature\_type**:

0: Nf,n2v,l

1: Np,n2v,l

2: Nn2v,l

**subgraph\_type**:

0: subgraph3

1: subgraph2

2: subgraph1

**sampling\_type**:

0: random negative sampling

1: fire negative sampling

2: reliable negative sampling

3: 0 & 2

**cuda\_no**: gpu number