

```
> library(PLIER)
```

## 1 HCC Dataset

Load data

```
> data(HCCdata)
> data(canonicalPathways)
> data(chemgenPathways)
> data(oncogenicPathways)
```

Construct a joint pathway matrix by merging canonicalPathways, chemgenPathways and oncogenicPathways and select genes appearing in both gene expression profile and the joint pathway matrix.

```
> HCCpath=combineGSmats(canonicalPathways, chemgenPathways, oncogenicPathways)
> cmHCC=commonRows(HCCdata, HCCpath)
```

Remove small pathways, not strictly necessary but saves computation time by making the pathway/geneset matrix smaller

```
> ii=which(colSums(HCCpath[cmHCC,])<20)
> HCCpath=HCCpath[, -ii]
```

Prescale the data

```
> HCCdataUse=rowNorm(HCCdata[cmHCC,cmSurvival])
```

Precompute the SVD for starting priorPCA and for comparison

```
> svdresHCC=svd(HCCdataUse)
```

Compute the number of latent variables by num.pc(HCCdataUse) and the result is 52. Then set max.iter = 250, L1 = 25, k = 52 and all other parameters are default.

```
> plierRes=PLIER(data=HCCdataUse, HCCpath[cmHCC,],svdres=svdresHCC, k=52, L1=25, max.iter=250)
```

```
[1] "L2 is set to 283.480769230769"
```

```
> plotMat(plierRes$U)
```

Check for a CTNNB1 mutation correlation. These are activating mutations so expect a positive correlation

```
> data(CTNNB1mut)
> plot(sort(corRes<-cor(t(plierRes$B), CTNNB1mut[cmSurvival], use = "p")), xlab="LV", ylab="CTNNB1mut")
```

The correlated LV is

```
> iBest=which(corRes==max(corRes))
```

Check the associated pathways

```
> which(plierRes$U[,iBest]>0)
```

```
      CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_UP
                                629
      BOYVAULT_LIVER_CANCER_SUBCLASS_G6_UP
                                2263
CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_DN
                                2924
```

Check survival

```
> survRaw=testSurvival(plierRes$B, survTime, survStatus)
```

Include the first 10 PCs from the SVD to correct for global subtype structure

```
> survCor=testSurvival(plierRes$B, survTime, survStatus, t(svdresHCC$v[, 1:10]))
```

Plot survival predictors

```
> iiSurv=which(survRaw$q.value<0.2)
> plotMat(plierRes$U[,iiSurv])
```

Plot structure corrected survival predictors

```
> iiSurv=which(survCor$q.value<0.2)
> plotMat(plierRes$U[,iiSurv])
```