README

Scripts and data included are:

.

├── CNV\_tf\_inference

│   ├── 2.Bulk.Panel.Sequencing.Tumor.fraction.from.CNV.R

│   ├── README.CNV.infer.TF.docx

│   ├── example\_data

│   │   └── 1901616S3CT-5.T.merge.cnr

│   └── result

│   ├── 1901616S3CT-5.T.merge.cnr.cnv\_fraction.json

│   ├── 1901616S3CT-5.T.merge.cnr.pdf

│   ├── 1901616S3CT-5.T.merge.cnr.txt

│   └── 1901616S3CT-5.T.merge.cnr\_mu\_df.info

├── scATAC

│   ├── ArchR\_CNV.R

│   ├── ArchR\_modified\_LSI.R

│   ├── ArchR\_modified\_getMatrixFromProject\_cnv.R

│   ├── ArchR\_modified\_ggFootprint.R

│   ├── ArchR\_slingshot.modified.R

│   ├── step.1.initiate.R

│   ├── step.1.initiate.for.subclass.R

│   ├── step.1.reinitiate.R

│   ├── step.2.2.T.cell.calculation.force.R

│   ├── step.2.T.cell.calculation.R

│   ├── step.2.create.arrow.files.blca.R

│   ├── step.2.epi.R

│   ├── step.3.make.lsi.and.umap.R

│   ├── step.3.make.lsi.and.umap.step2.R

│   ├── step.4.pmagic.R

│   ├── step.5.cnv.R

│   ├── step.6.cnv.plot.sample.R

│   ├── step.7.epithelial.re-lsi.R

│   └── step.8.epithelial.pure.R

├── scATAC\_CNV\_inference

│   ├── 1.scATAC\_CNV.R

│   └── README.CNV.infer.from.scATAC.docx

├── scATAC\_SNV\_inference

│   ├── README

│   ├── getvartrix.sh

│   └── liftover\_vcf.sh

├── scRNA

│   ├── CytoTrace.analysis.R

│   ├── NMF.on.scRNA.R

│   └── NMF.to.metagene.R

└── survival\_analysis

├── ICI\_survival\_analysis\_GSVA.R

├── TCGA.survival.R

└── survival.analysis.R

`CNV\_tf\_inference`: the codes and example data for computing tumor fraction from copy number variation profile.

`scATAC\_CNV\_inference`: the codes (plug-in for ArchR package) for computing copy number variation on single cell ATAC data.

`scATAC`: historical code records used for general purpose scATAC analysis using ArchR.

`scRNA`: the codes used for high-order scRNA analysis, namely CytoTrace and NMF-metagene analysis.

`scATAC\_SNV\_inference`: the codes for computing SNV carrier state of single cell ATAC data, using vartrix.

`survival\_analysis`: the codes for survival analysis.