

StromalCell_shiny

December 25, 2025

```
[ ]: library(shiny)
      library(Seurat)
      library(ShinyCell)
      library(stringr)
```

1 load data

```
[ ]: obj <- readRDS('obj.StromalCell.diet.rds')
      obj
      obj@meta.data %>% head(n = 2)
      conf <- createConfig(obj)
```

2 make shiny app

```
[ ]: makeShinyApp(obj,
                  conf,
                  gene.mapping = FALSE,
                  gex.slot = "data",
                  shiny.title = "SexTumorDB: Stromal cell landscape",
                  shiny.dir = "StromalShiny/",
                  shiny.footnotes = "Datasets covering the total tumor_
↪microenvironment can be accessed freely from Zenodo platform",
                  enableSubset = TRUE,
                  defPtSiz = .5
                  )
```

```
[ ]: rsconnect::setAccountInfo(name='sextumordb',
                               token='<SECRET>',
                               secret='<SECRET>')
```

```
[ ]: rsconnect::deployApp('StromalShiny/', account = 'sextumordb', appName = "
↪stromal")
```