

# 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")
```