

TumorCell_shiny

December 25, 2025

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

1 load load

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

```
[ ]: ## make shiny app
makeShinyApp(obj,
             conf,
             gene.mapping = FALSE,
             gex.slot = "data",
             shiny.title = "SexTumorDB: Tumor cell landscape",
             shiny.dir = "TumorShiny/",
             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('TumorShiny/', account = 'sextumordb', appName = "tumor")
```