

# 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")
```