

SexTumorDB_shiny

December 25, 2025

```
[ ]: ## load object
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.footnotes = "Datasets covering the total tumor_
↳microenvironment can be accessed freely from Zenodo platform",
  enableSubset = TRUE,
  defPtSiz = 1.3,
)

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

[ ]: rsconnect::deployApp('/project/sex_cancer/shinyApp/', account = 'sextumordb')
```