

RStudio

File Edit Code View Plots Session Build Debug Profile Tools Help

cor\_GSE122063 cor\_ad\_GSE122063 ggbox\_ad\_10 Astro.R NKX2-1A\_GSE122063 micro.R SUPPLEMENTARY CODER exp\_GSE122063

```
1 |
2 # snRNA analysis #####
3 library(Seurat)
4 library(tidyverse)
5 library(patchwork)
6 library(harmony)
7 if(!require(multtest))install.packages("multtest")
8 if(!require(Seurat))install.packages("Seurat")
9 if(!require(dplyr))install.packages("dplyr")
10 if(!require(mindr))install.packages("mindr")
11 if(!require(tidyverse))install.packages("tidyverse")
12
13 # Glial cell data extraction
14 astroRNA.sum <- subset(snRNA.sum_celltype_annotation,celltype.sum=="Astrocyte")
15 microRNA.sum <- subset(snRNA.sum_celltype_annotation,celltype.sum=="Microglia")
16 oligoRNA.sum <- subset(snRNA.sum_celltype_annotation,celltype.sum=="Oligodendrocyte")
17
18 #1. Glial sex-specific DEGs capturing #####
19 #1.1 screen DEGs #####
20 astro.deg <- FindMarkers(astroRNA.sum,ident.1 = "male",ident.2 = "female",group.by="sex")
21
```

Environment History Connections Tutorial

The learnr package is required to run tutorials for RStudio.  
Please [click here](#) to install the learnr package.

RStudio Tutorials powered by the learnr package.

Files Plots Packages Help Viewer

Zoom Export

Console Terminal Jobs

R 4.1.2 D:/summer/

You are welcome to redistribute it under certain conditions.  
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.  
Type 'contributors()' for more information and  
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.

[workspace loaded from D:/summer/.RData]

> |