**Files to download before running this script:**

Brain: [https://scope.aertslab.org/#/Davie\_et\_al\_Cell\_2018/\*/welcome](https://scope.aertslab.org/#/Davie_et_al_Cell_2018/*/welcome)

**Filename:** Aerts\_Fly\_AdultBrain\_Filtered\_57k.loom

VNC: <https://scope.aertslab.org/#/Davie_et_al_Cell_2018/Davie_et_al_Cell_2018%2FGoodwin_Fly_AdultVNC_elife54074.loom/gene>

**Filename:** Goodwin\_Fly\_AdultVNC\_elife54074.loom

Place the files in the 'input' directory: ITP scRNA analysis/**input**/

Folders provided

**input**

* Neuropeptides.rda
* Neuropeptide\_receptors.rda
* Monoamine\_receptors.rda
* Neurotransmitter\_receptors.rda
* brainITPcells.rda
* VNCITPcells.rda

\*Note: If you download the repo from github, this folder should already exist with the files above provided

The code checks to see if input/output folders exist, and will make them if they do not. However, without the input files provided (or needed from codex download), the rest of the script will not run

**A screenshot of a computer

AI-generated content may be incorrect.output**

**scripts**

Figure 13.R

Figure 13 supplement 3.R

After you run the Figure 13.R & Figure 13 supplement 3.R scripts, the folders should contain the following files:

A screenshot of a computer

AI-generated content may be incorrect.