This document contains README instructions for the various coding components needed to reproduce results for our manuscript: **Recurrent circuits encode de novo visual center-surround computations in the mouse superior colliculus**' by Cui et al.

1. Defining center and surround zones

Run the 'gridscan_EPSC' or 'gridscan_IPSC' for the excitatory postsynaptic current (EPSC) or inhibitory postsynaptic current (IPSC) GridScan recording file and put 'MAP_GRIDSCAN.mat' and 'stim_point2.mat' under the same folder. During the code running, it will ask for the name of recording file (.abf) under the same folder. The code will return two PNG image files for the current traces with stimulation points and the Center-Surround zones, and also the Plain Text documents of 'ON', 'OFF' and 'ON_OFF' for the software, PolyScan2, to read and generate stimulation patterns.

2. Trans-synaptic mapping

Rabies tracing analysis was done in R, codes are divided into two parts:

1. wholebrain.R
2. Rabies plotting.R

Part 1: wholebrain

This part uses R package "wholebrain", which was developed by Dr. Daniel Fürth, to mount the allen brain atlas mouse templates onto the actual pictures, and extract the coordinates of marked neurons for the following analysis. Coordinates of neurons of each brain section were then manually combined for each individual animal.

Codes were adapted from Daniel Fürth's instruction, please see:
https://github.com/tractatus/wholebrain for detailed explanation.

In summary:

```
### apply flat field correction to remove the grid-like pattern while stitching tiles
flat.field.correction(folder)
### stitch the corrected picture tiles
stitch(FFC_folder)
### set thresholds to locate neurons in the picture
seg<-segment(FFC_filename, filter = seg$filter) #, filter = seg$filter #use seg$filter$threshold.range to set the intensity range, form like <- c(min, max)
### register neurons onto the template
quartz()
regi<-registration(FFC_filename, coordinate = -3.85, filter=seg$filter)
### correct manually
regi<-add.corrpoints(regi, 1)
regi<-change.corrpoints(regi, c(36, 38))
regi<-remove.corrpoints(regi, 38)
### rerun registration after manual correction
regi<-registration(FFC_filename, coordinate = -3.85, filter=seg$filter, correspondance = regi)
### save all the data
dataset<-inspect.registration(regi, seg, forward.warps = TRUE)
save(seg, regi, dataset, file = '641_11_2.Rdata')
write.csv(dataset, file = "641_11_2_regi.csv")
### make a web map output of your result
pixel.resolution<-0.64
protein <- "EGFP"
makewebmap(FFC_filename, seg$filter, registration = regi, dataset = dataset, scale = pixel.resolution, fluorophore = protein)
```

Part 2: Rabies plotting

The plotting was mainly based on R package “ggplot2” (is included in "ggpubr" and "tidyverse"), please see https://ggplot2.tidyverse.org/ for the grammer, statistical comparison was done with R and ggpubr (see https://rpkgs.datanovia.com/ggpubr/).
Please see the notes and parameters in the actual codes for explanation.

3. cFos analysis

Variable names contain information about the brain hemisphere relative to the stimulation (ispi or contra), the area of the SCs relative to the fiber(medial, lateral, on) on being under the fiber, and the subject iD. The *fos_mean_num_ploter* function is used to plot the mean and standard error of the mean of Cfos-positive cells in any area and the code from lines 285-314 is used to make the GABA /total Cfos-positive cells comparison.

4. Compute synaptic conductances

Run 'compute_synaptic_conductance.m in Matlab. Place abf.files generated by 'pClamp10' in the same folder or 'addpath' to the location of the file. Enter filename when prompted. Ensure that time stamps correspond to the actual stimulation events. The routine implements a version of the method used by Wehr and Zador (Nature, 2003) for extracting synaptic conductances from current recordings performed in voltage clamp. Adjust time stamp values or axis size within the script as needed. It will generate a series of plots that can be used to directly visualize the conductances together with the current traces.

5. Neural network model

This is a simulation of a reduced model of superficial layer of the superior colliculus, referred to as SCs in the text.
The network consists of 6400 excitatory and 6400 inhibitory neurons. These neurons are placed on a uniform grid of size 80x80. Neurons are connected in a distance dependent manner and the network is folded to avoid boundary effects. For more information please see the methods section.
What you need to run this code
Network simulator: NEST 2.20
For more info visit: https://nest-simulator.readthedocs.io/en/v2.20.1/
Additional packages: PYTHON, numpy
Customized library for network connectivity: Several customised routines are provided in the folder lib to construct different types of spatial connectivity.
When you run the code in python
run sc_surround_suppression.py
This will create several simulations in which we have varied the strength of following connections E-E, E-I, I-I and I-E motifs.
If you do not want to run the full parameter scan you can change the corresponding parameter list in the code and then only your preferred simulation will be run.
The output is saved in a text file with .gdf ending. The file name is composed of the parameters that can be varied in this model. The gdf files store the simulated neural activity in two columns -- first column is neuron id and second column is the time when the neuron spiked. These files can be read in any scientific computing software and rendered as raster.