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

These two files simulated a data driven model of the Superior Colliculus.
We model this network as a Locally Connected Random Network (LCRN) with Excitatory and Inhibitory spiking neurons.

There are 12800 neuron. 6400 Exc. and 6400 Inh.
Neurons are arranged on a uniform grid.
Neurons are connected in a distance dependent manner.
Connection probability decreases in a Gaussian fashion.
The square grid is folded to form a torus to ensure that all neurons have same number of inputs and there are no boundary effects.

Neurons are driven by Poisson input.
Input corresponding to the stimulus is also provided as additional Poisson input to selected neurons

File names carry the weight information used.
Membrane potential and synaptic conductances are recorded in one file and spike in a separate
Both types of file have same initial prefix.

The code runs with NEST 3.4
sc_surround_supression_main.py -- This simulates the effect of local connections. Here we can show that Exc to Exc is the most important descriptor, of course this effect is mediated by Exc to Inh and Inh to Exc connections.

sc_surround_supression_weak_ee_compensate.py -- Here we can change Exc to Exc recurrent and corresponding synaptic weight to see the effect of connectivity and synaptic stength