

Granular layEr Simulator (GES) demo - *guidelines*

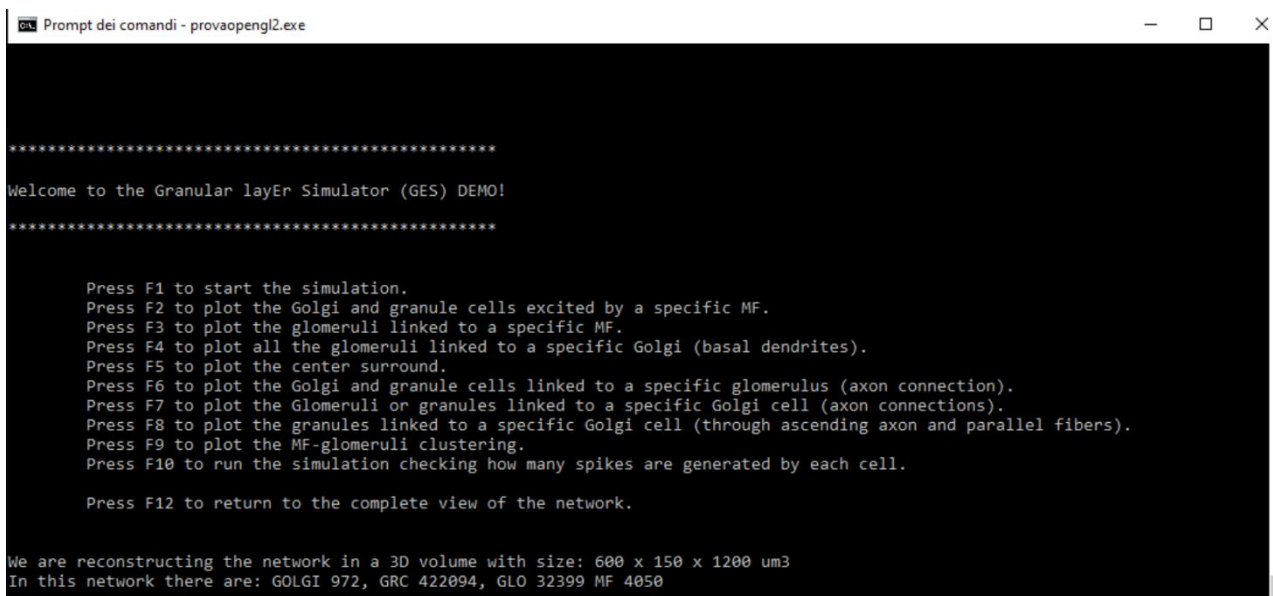
This demo refers to the simulator described in the “Granular layEr Simulator: design and multi-GPU simulation of the cerebellar granular layer” manuscript, submitted to *Neuroinformatics*.

Welcome in the Granular layEr Simulator (GES) demo!

This document presents some info to use the GES demo. In this demo, authors have simulated a network reconstructed in a 3D volume, whose size is 600 (*length*) \times 150 (*height*) \times 1200 (*depth*) μm^3 .

In this volume there are 422094 granule cells, 972 Golgi cells, 32399 glomeruli and 4050 mossy fibers: these elements are linked considering axonal/dendritic field geometries, oriented in the 3D space, and following convergence/divergence rates provided in literature.

When the user run the *ges_demo.exe*, two windows are opened: the former contains all the tasks that the user can select; the latter a top view of the network. In this last view, the glomeruli are shown in green, the Golgi soma in blue and the granule cells soma in red.



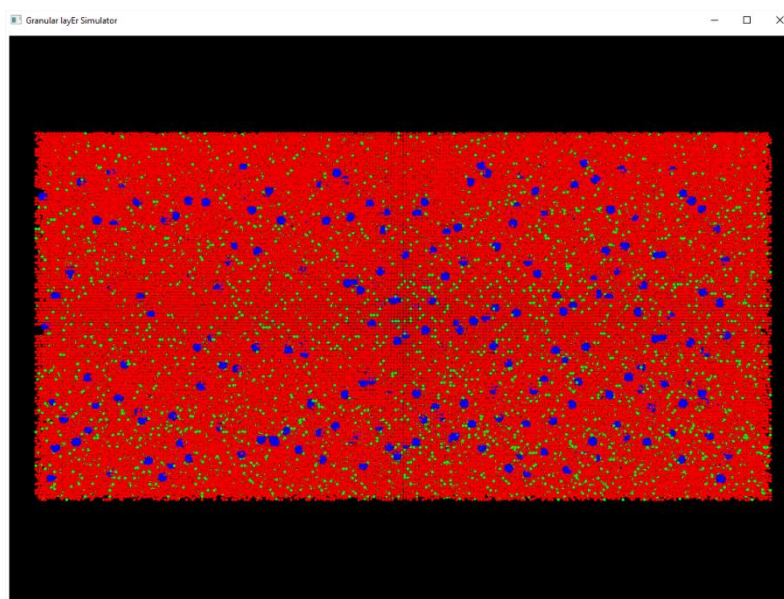
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Prompt dei comandi - provaopengl2.exe

*****
Welcome to the Granular layEr Simulator (GES) DEMO!
*****

Press F1 to start the simulation.
Press F2 to plot the Golgi and granule cells excited by a specific MF.
Press F3 to plot the glomeruli linked to a specific MF.
Press F4 to plot all the glomeruli linked to a specific Golgi (basal dendrites).
Press F5 to plot the center surround.
Press F6 to plot the Golgi and granule cells linked to a specific glomerulus (axon connection).
Press F7 to plot the Glomeruli or granules linked to a specific Golgi cell (axon connections).
Press F8 to plot the granules linked to a specific Golgi cell (through ascending axon and parallel fibers).
Press F9 to plot the MF-glomeruli clustering.
Press F10 to run the simulation checking how many spikes are generated by each cell.

Press F12 to return to the complete view of the network.

We are reconstructing the network in a 3D volume with size: 600 x 150 x 1200 um3
In this network there are: GOLGI 972, GRC 422094, GLO 32399 MF 4050
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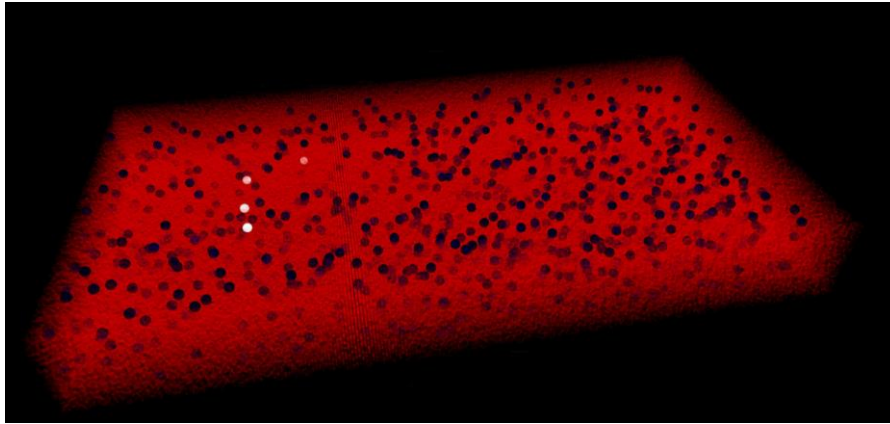


The user can rotate the network inside the 3D volume using the click and drag within the window. Moreover, the user can navigate within the network using the mouse scroll or the keyboards arrows. Every rotation or movement could take few seconds to be performed on the base of the system running the GUI.

The user can choose one of the following tasks.

F1 – start the simulation

GES is going to display only the Golgi soma (in blue) and the granule soma (in red) for clarity. When a cell generates a spike, its soma changes the color. In particular, the Golgi soma becomes white, while the granule soma becomes light blue.



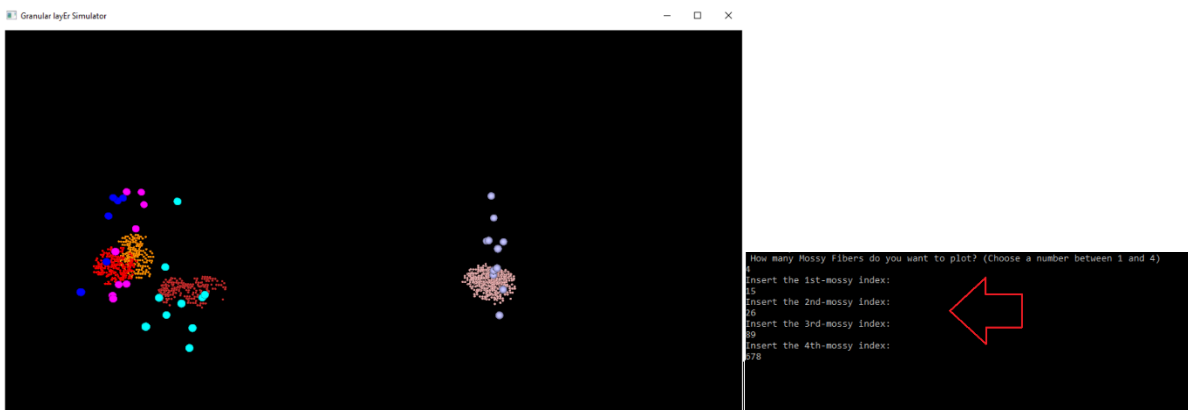
This simulation represents the reproduction of 3 s of network activity considering a time step of 0.025 ms, but it is important to notice that each time step in the graphical interface is displayed for 25 ms. This means that each cell changes its color for 25 ms. The network is stimulated with a protocol that combines two signals:

- Background: frequency = 1 Hz, duration = 3 s. This signal is applied on all the 4050 mossy fibers.
- Bursts: frequency = 150 Hz, duration = 50 ms. This signal is applied on the 1% of the mossy fibers.

Please, press F12 to return to the main window (complete network view).

F2 – plot the granule and Golgi cells linked to a specific mossy fiber

The user has to choose how many mossy fibers wants to consider (from 1 to 4). Then, he has to indicate the IDs of the mossy fibers he wants to consider. The GUI will display the Golgi and granule cells that are linked to that mossy fibers, from which they receive the input signals. In this case, the glomeruli are not shown. In the following image, the granule and Golgi cells linked to the mossy fibers with IDs 15, 26, 89 and 678 are shown.



Please, press F12 to return to the main window (complete network view).

F3 – plot the glomeruli linked to a specific MF

The user inserts the mossy fiber ID to plot all the glomeruli reached by this mossy fibers.

Please, press F12 to return to the main window (complete network view).

F4 – plot all the glomeruli linked to a specific Golgi (basal dendrites)

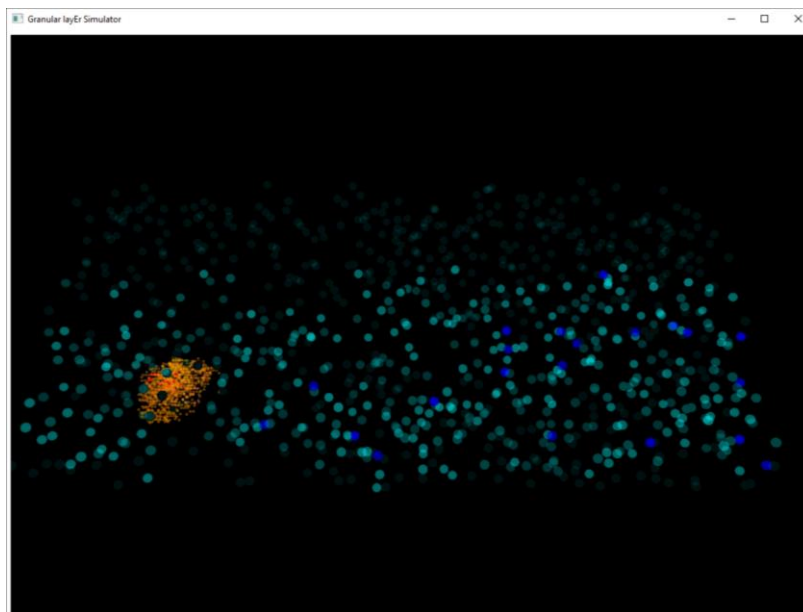
The user inserts the Golgi ID to show the glomeruli linked through the Golgi basal dendrites.



Please, press F12 to return to the main window (complete network view).

F5 – plot the center-surround organization

A particular technique is adopted to show the spiking neurons: at the beginning, all the neurons are not visible in the volume. As soon as a cell generates a spike, it will be shown with a color whose tone becomes darker as the spikes number increases.



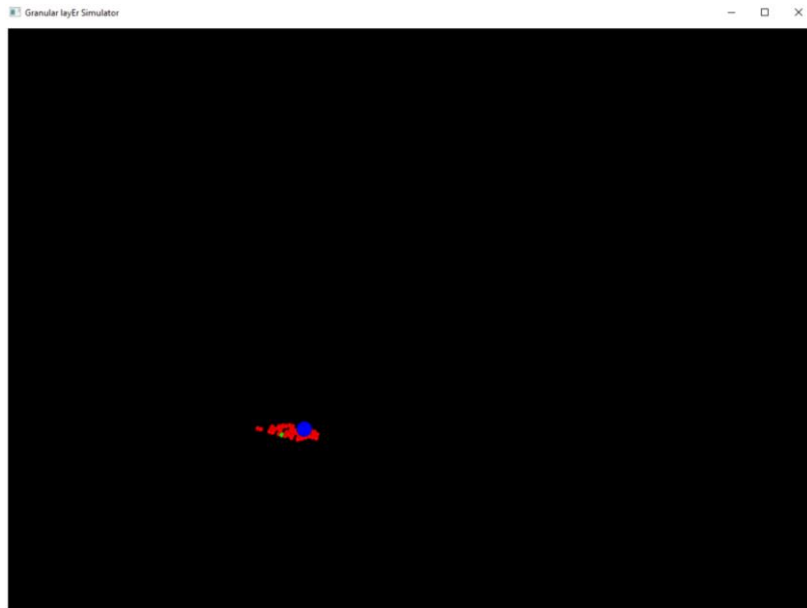
Please, press F12 to return to the main window (complete network view).

F6 - plot the Golgi and granule cells linked to a specific glomerulus (axon connection)

The user inserts the glomerulus ID. Then he can choose to display:

- 1) the glomerulus and the linked Golgi cells (axon connections);
- 2) the glomerulus and the linked granule cells;
- 3) the glomerulus and the linked granule and Golgi cells (axon connections).

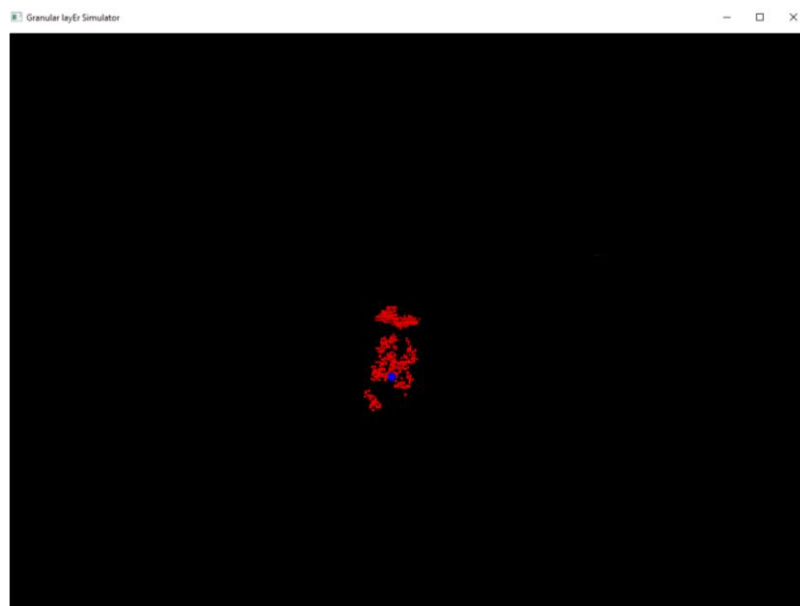
In the following image, the glomerulus ID1 is shown together with the Golgi cell (which spreads its axon into the glomerulus) and the granule cells linked to this glomerulus.



Please, press F12 to return to the main window (complete network view).

F7 - plot the Glomeruli or granules linked to a specific Golgi cell (axon connections)

The user has to insert the Golgi ID to display the glomeruli or the granule cells reached by the Golgi axon.

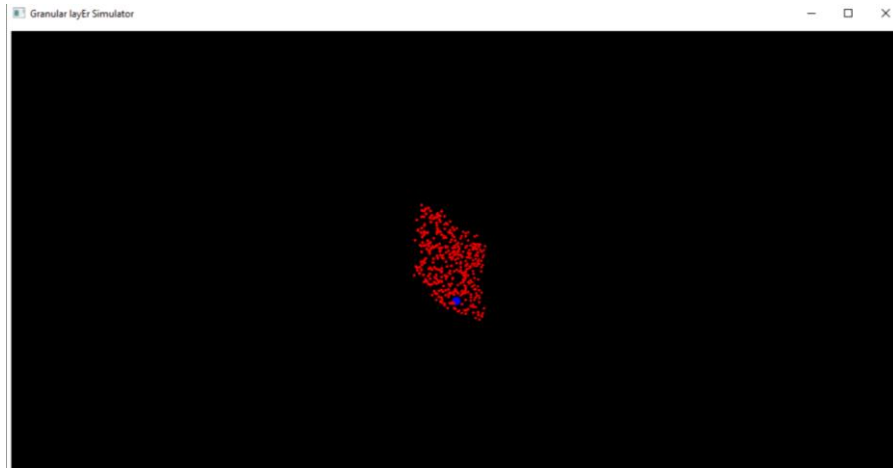


Please, press F12 to return to the main window (complete network view).

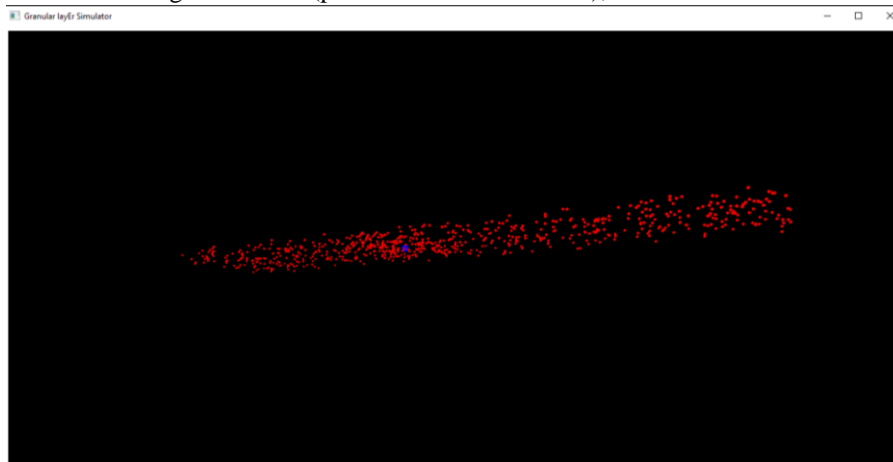
F8 - plot the granules linked to a specific Golgi cell (through ascending axon and parallel fibers)

The user has to insert a Golgi cell ID. Then, he can display:

- 1) the Golgi cell and the linked granules (ascending axon connection);



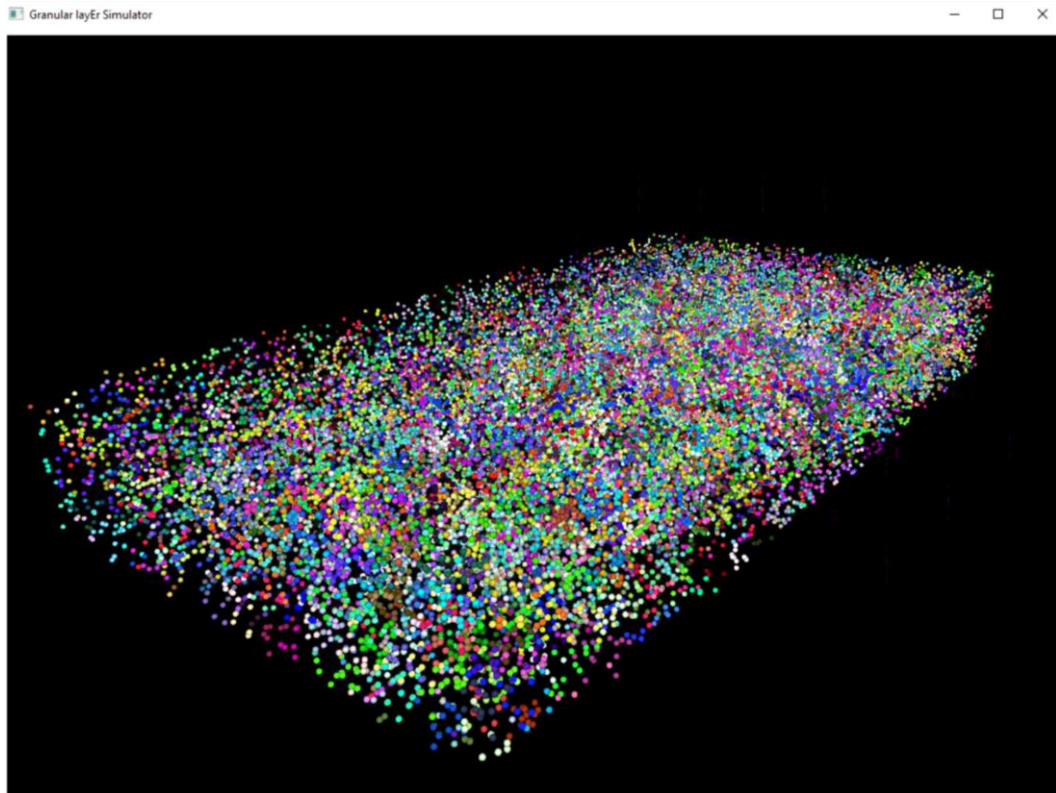
2) the Golgi cell and the linked granule cells (parallel fibers connection);



Please, press F12 to return to the main window (complete network view).

F9 - plot the MF-glomeruli clustering

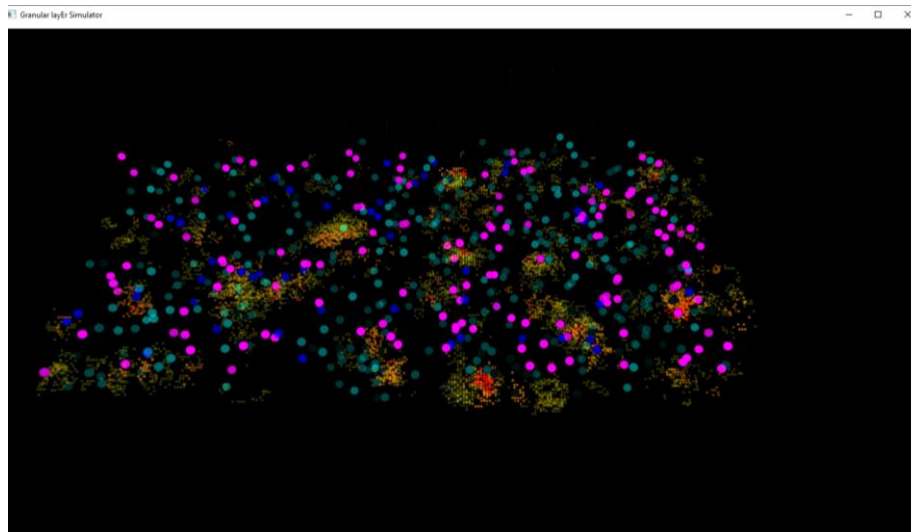
This task allows to display all the glomeruli grouped in clusters. Each cluster is characterized by a color. All the glomeruli within a cluster are reached by the same mossy fiber.



Please, press F12 to return to the main window (complete network view).

F10 - run the simulation checking how many spikes are generated by each cell

In this configuration, the user can run the same simulation described in F1 but, at the beginning, all the neurons are not visible in the volume. As soon as a cell generates a spike, it will be shown with a color whose tone becomes darker as the spikes number increases.



Please, press F12 to return to the main window (complete network view).