**CS – 590.21 Analysis and Modeling of Brain Networks**[**Department of Computer Science**](http://www.csd.uoc.gr/)**University of Crete**

**Description of the biological data– ReadMe file**

**General description**

Biological datasets were collected using two-photon calcium imaging in the neocortex of an animal. Simultaneously multiple layer 2/3 neurons were imaged using calcium indicator OGB-1. Several minutes of spontaneous activity were recorded, with different number of frames and duration for each of the datasets.

Each dataset contains a matrix (m x n), with the spike trains of n neurons for a specific animal. Each spike train is a vector of length m (number of recorded frames). Also there are information about the type and the coordinates of each neuron.

E.g., for the dataset saad16\_003 there are binary data for 126 neurons, for each neuron there are recorded 11972 frames.

**Structs**

**psm\_avalanche** is the matrix that contains binary data, containing calcium event onsets (0 -> no event or 1 -> event) for each neuron.

e.g.:

* psm\_avalanche(:, 1) returns a vector with the spike train (binary data) for the neuron with id 1.
* psm\_avalanche(3, 1) returns a number 0 -> no event or 1 -> event), for the neuron with id 1 for the third frame.

**com\_x** & **com\_y**: these are x and y coordinates of neurons in the physical field of view (FOV), in pixels.

**intereneurons**: indexes of neurons that are inhibitory interneurons.

**astrocytes:** denotes astrocyte indexes. Astrocytes are excluded from analysis, because they are not neurons (but can generate calcium spikes that are low amplitude, occur rarely and they are noisy).

**redcellz**: redcellz has indexes for all neurons that are not pyramidal (inteneurons and astrocytes).