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

**Directional STTC analysis– ReadMe file**

The STTC analysis introduces the script STTC\_Estimation that takes as input the biological data of an animal and a specific time window (lag) in order to estimate the directional STTC values among all possible pairs of neurons for the given dataset.

For the estimation of the directional STTC for a specific pair of neurons the function STTC\_AB is used. Also, this script estimates the significant edges and the percentage of them considering all possible edges. By changing the value of parameter dt you can estimate the directional STTC values for another time window.

The produced file STTCcirc (matrix) has the following format, each column represents:

1: The id of the first neuron of the pair

2: The id of the second neuron of the pair

3: The produced directional STTC value of a specific pair of neurons considering the first and second columns

4: Number of firing events of first neuron that occur within a defined interval Δt prior to firing events of the second neuron

5: Number of firing events of second neuron that occur within a defined interval Δt following firing events of the first neuron

6: Mean value of the directional STTC values considering the null distribution pool

7: Std value of the directional STTC values considering the null distribution pool

8: Binary value (0,1): 0 -> when the directional STTC value of the two neurons is not higher than the (mean value of null distribution pool + 3\*std), else 1.

While in the matrix STTC\_sign are stored only the significant edges, considering the strict criterion.

After that statistics and CDF plots are produced considering different types of pairs (e.g., interneuron-pyramidal, pyramidal-pyramidal).

This analysis can be produced by run the command STTC\_estimation on the command window of Matlab.

