

Reservoir Computing Model For Multi-Electrode Electrophysiological Data Analysis

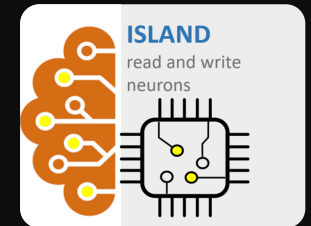
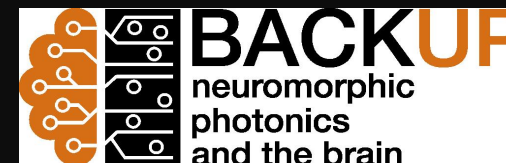
Ilya Ayslender, University of Trento



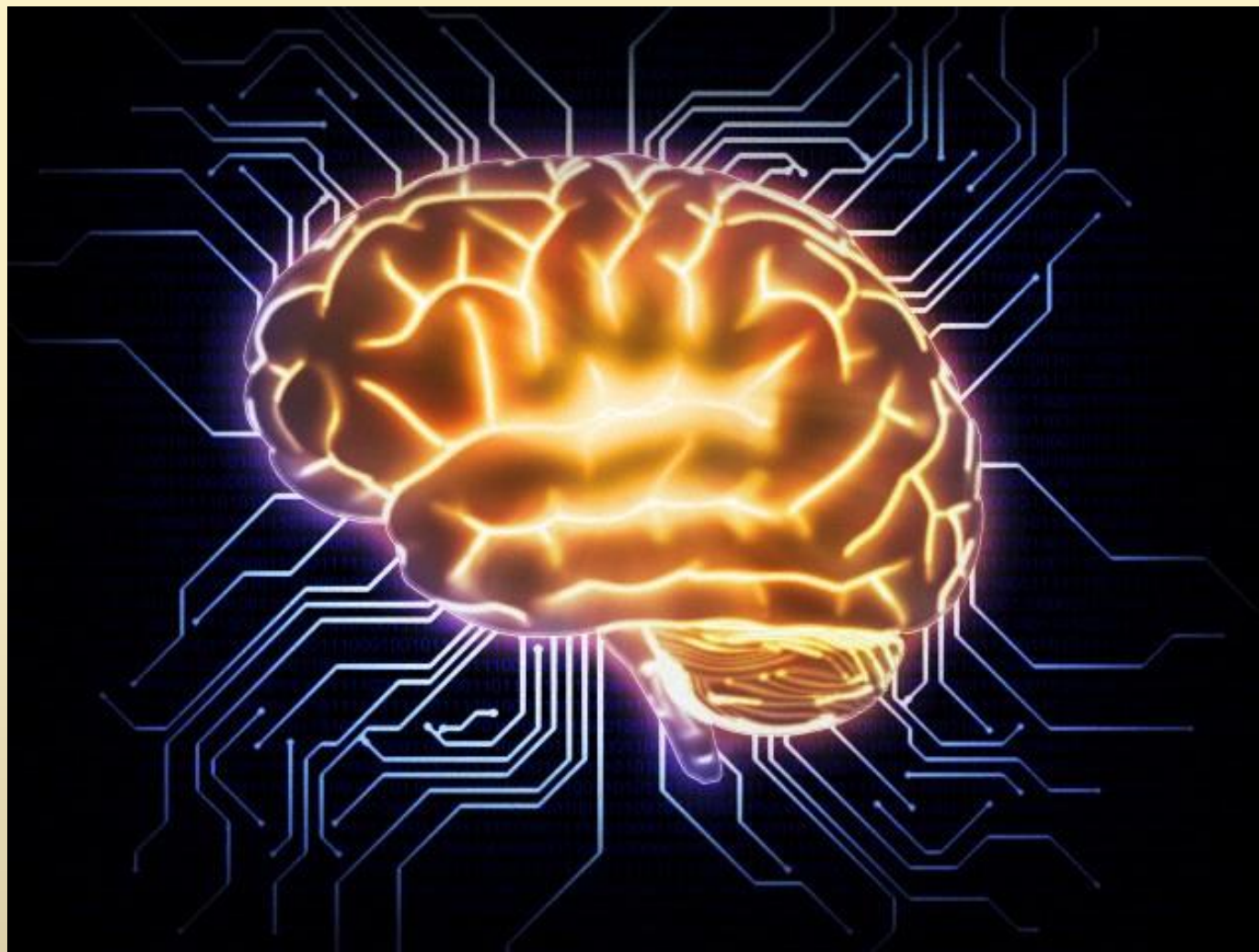
NanoLab
Department of Physics



UNIVERSITY
OF TRENTO - Italy

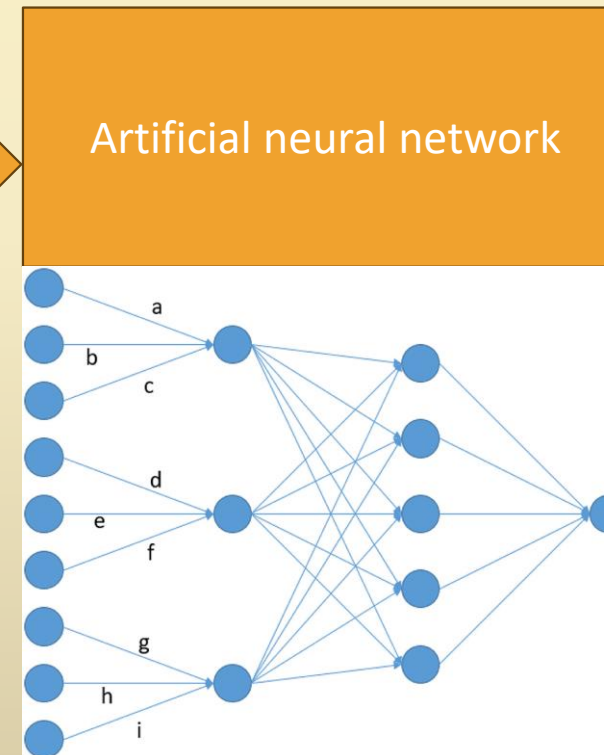
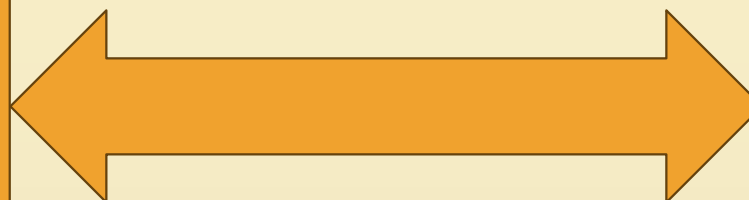
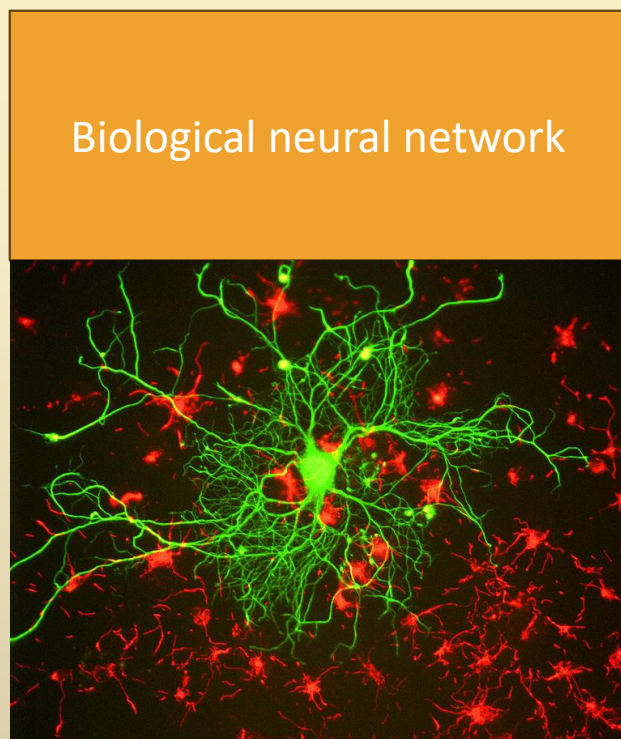






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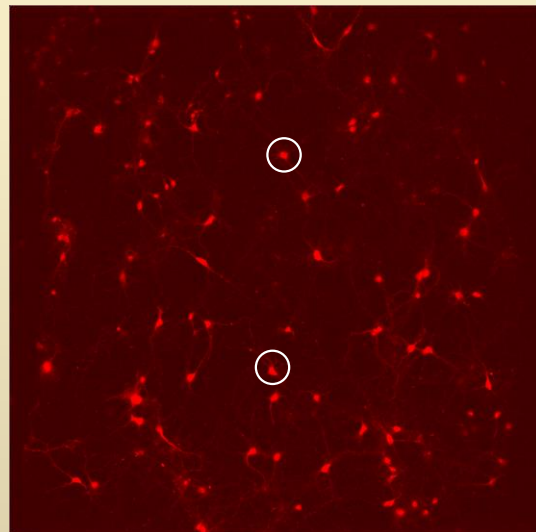
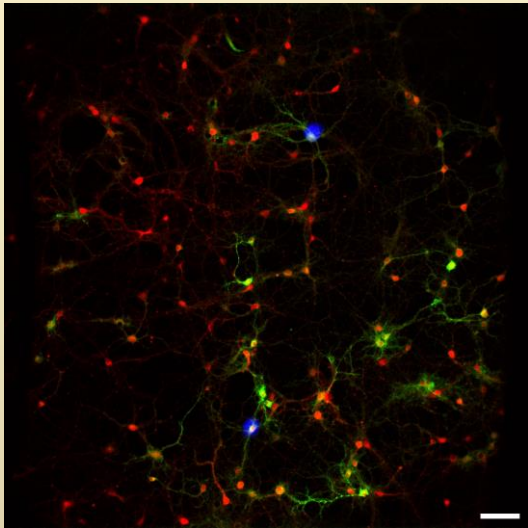
Biological Vs. Artificial NN



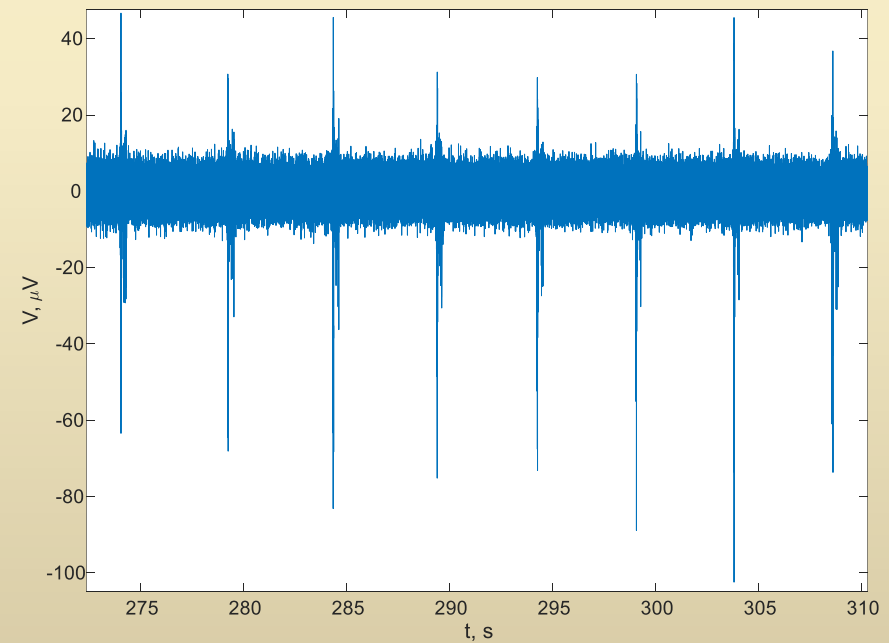
- Are they interchangeable?
- Can `they interact?

Studies of biological NN at NanoLab (UNITN)

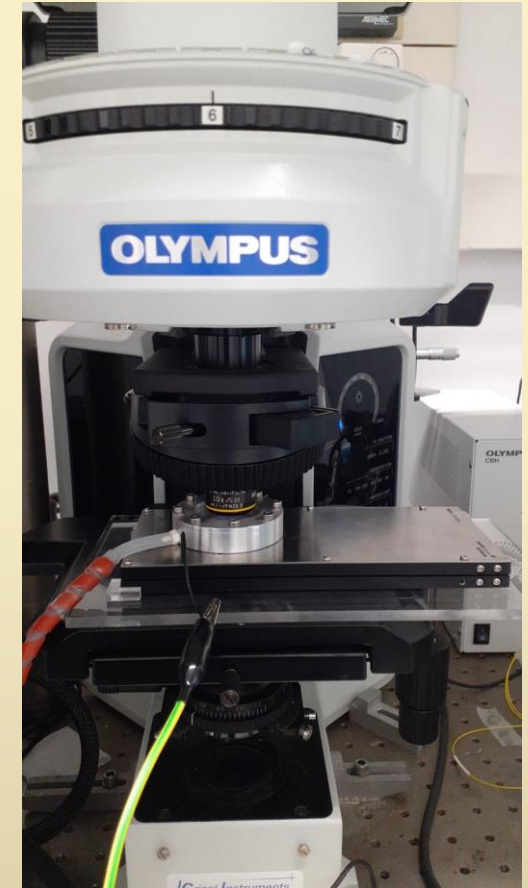
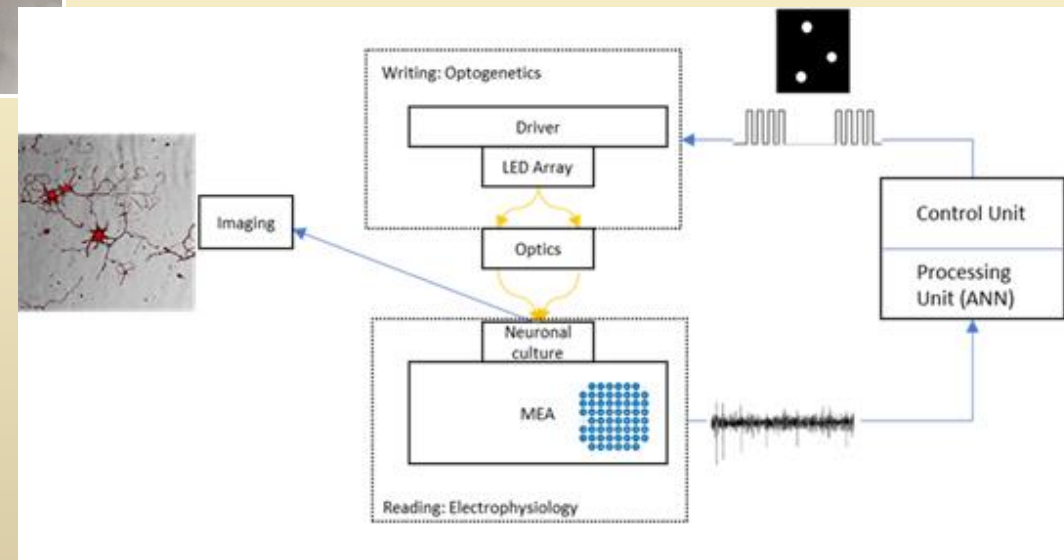
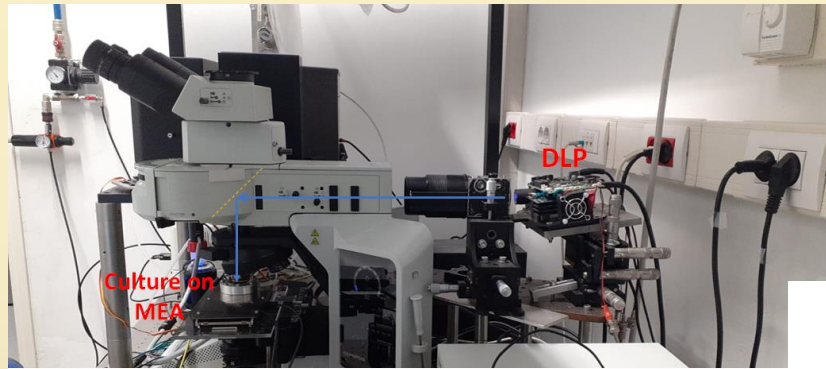
Optical imaging



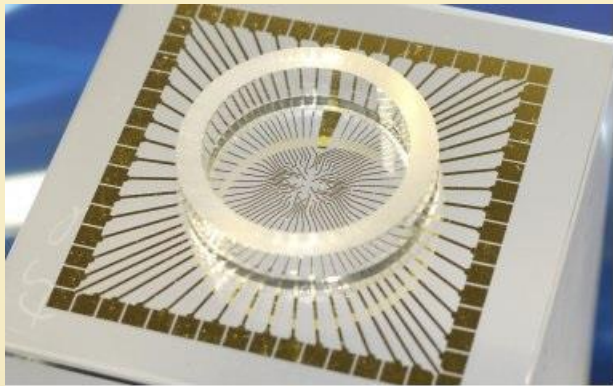
Electrophysiology



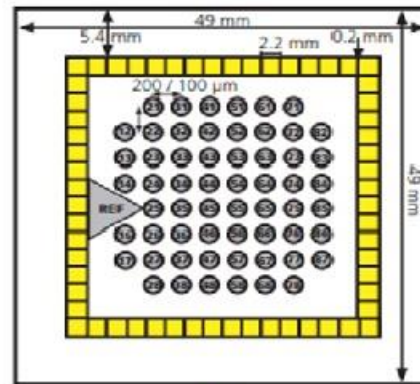
Optogenetic stimulation + Electrophysiological recording



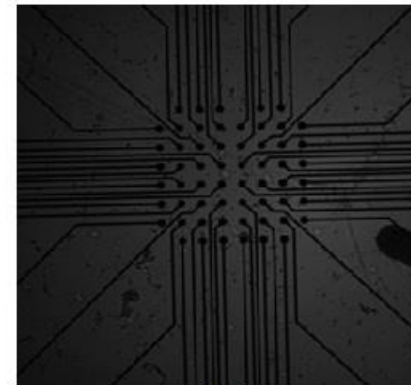
Microelectrode Array (MEA)



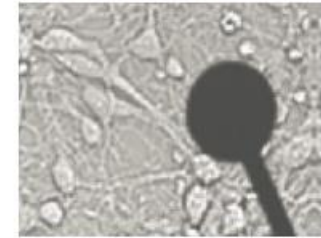
(a)



(b)



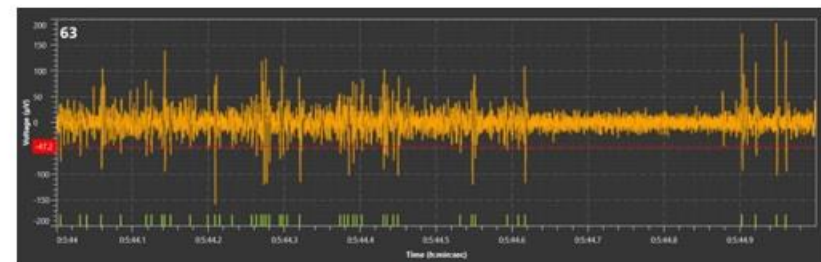
(c)



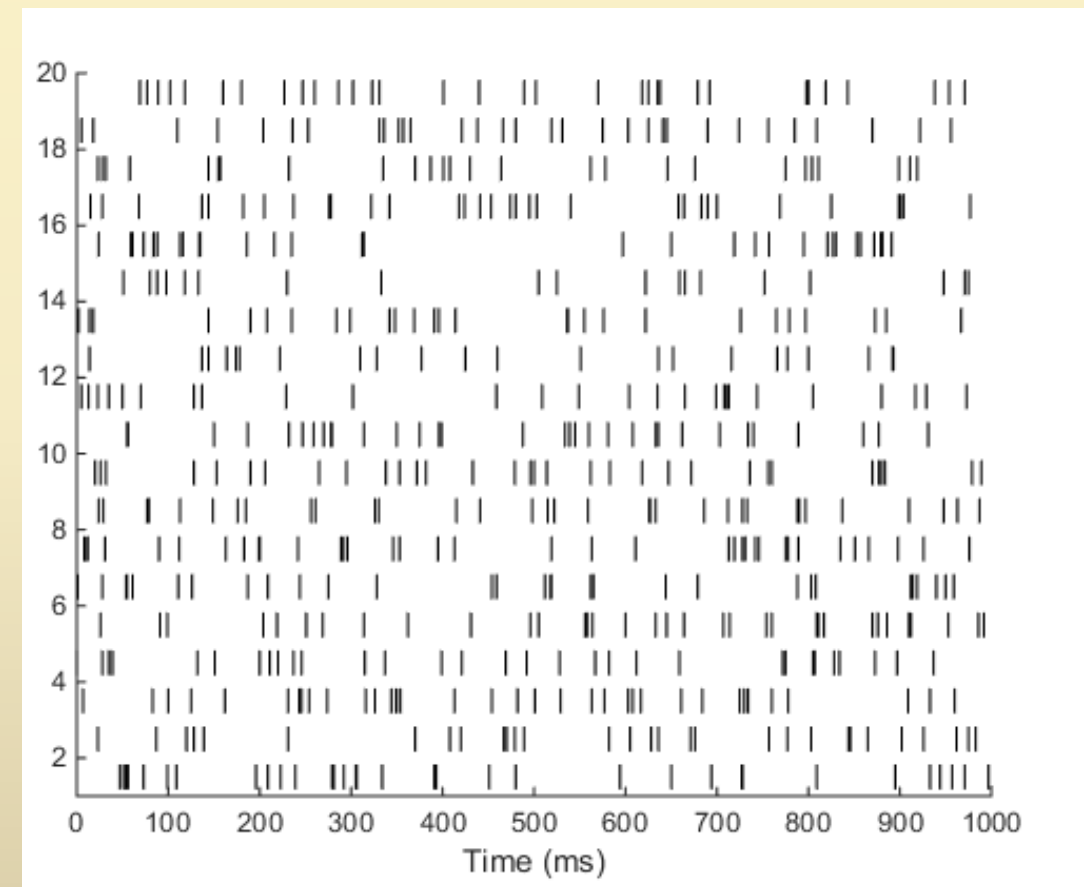
(d)



(e)



(f)



What can we learn?

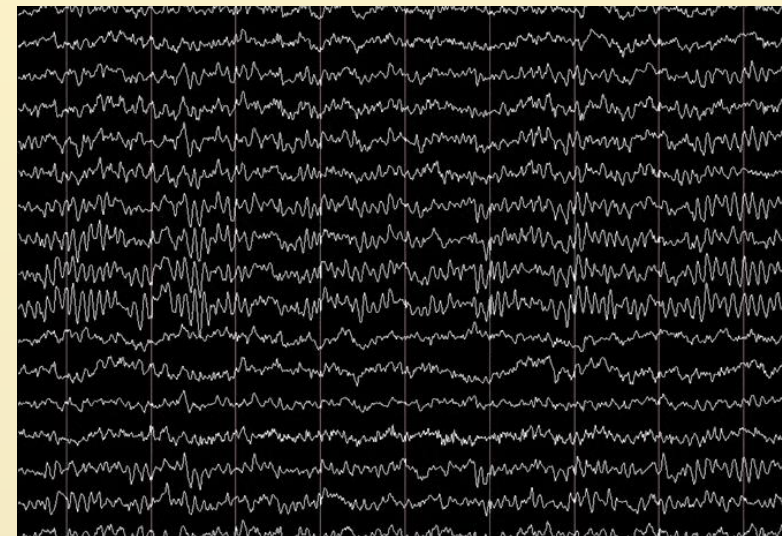
- Neuronal interactions macroscopically- Network of neuronal populations!
- Function of the network.
- Structural dynamics.



RC Model

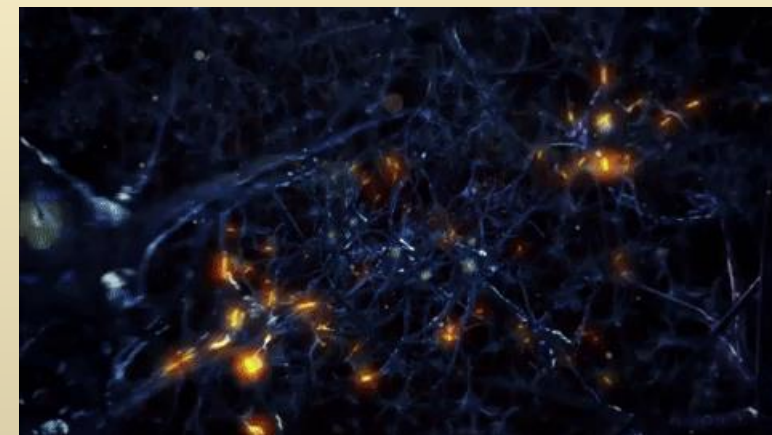


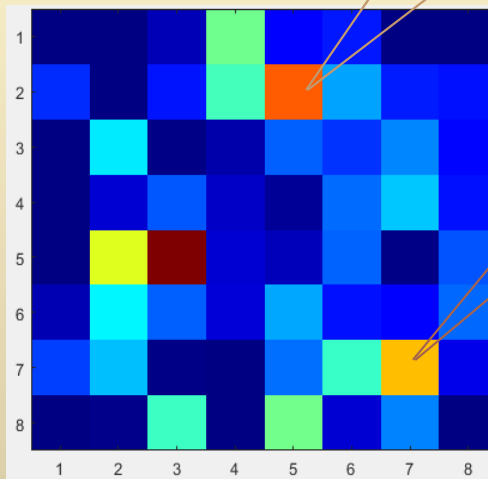
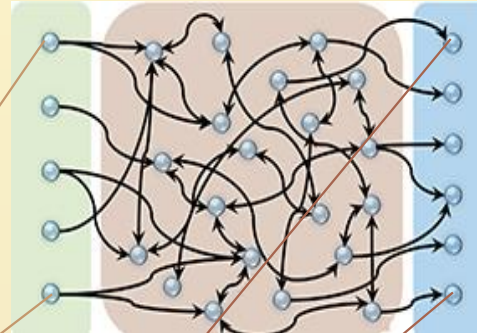
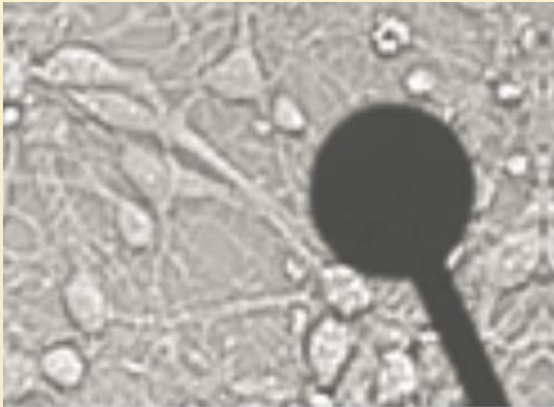
Neuronal
signals
measurement



Network
structure

Network
simulation

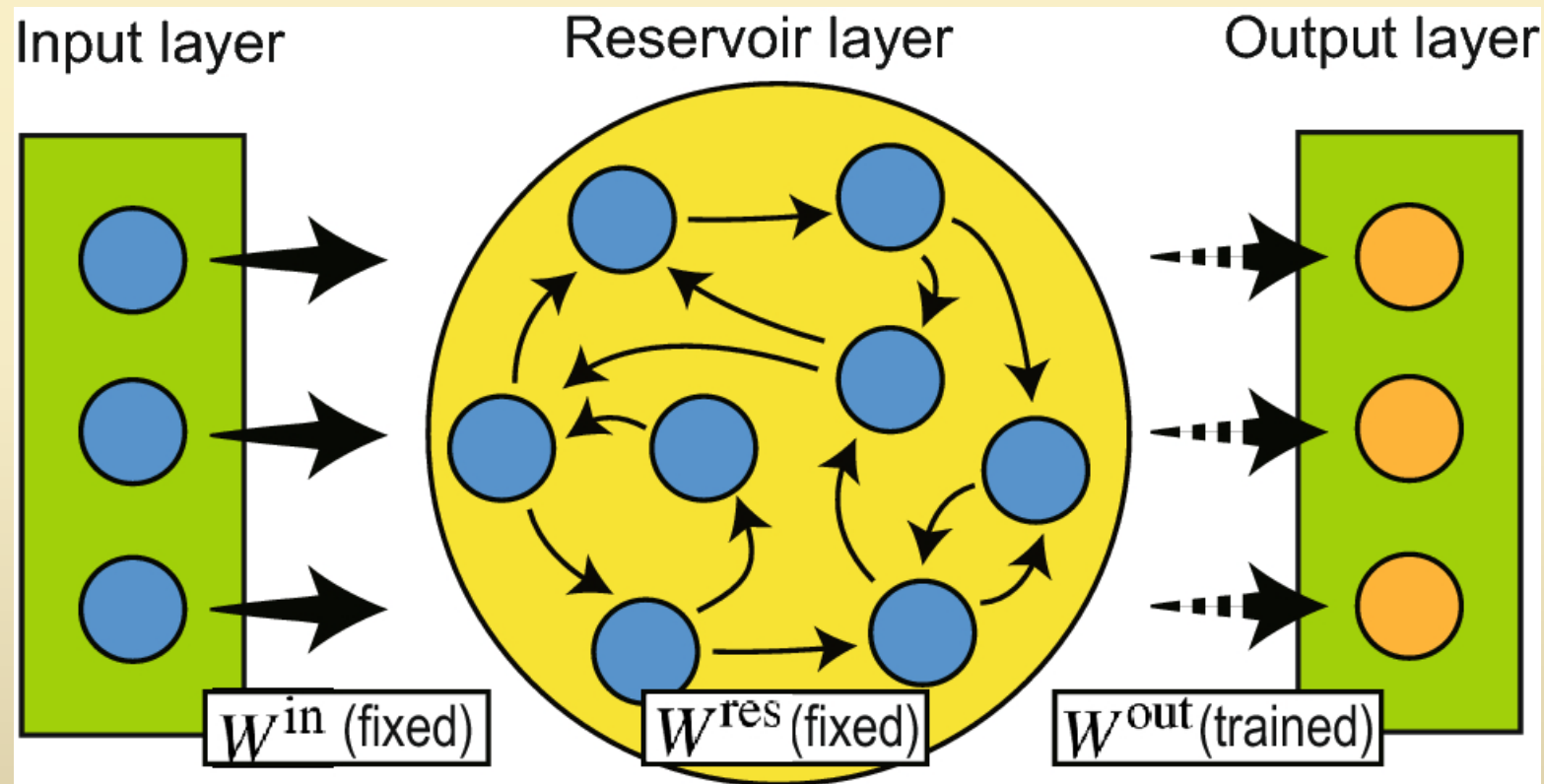




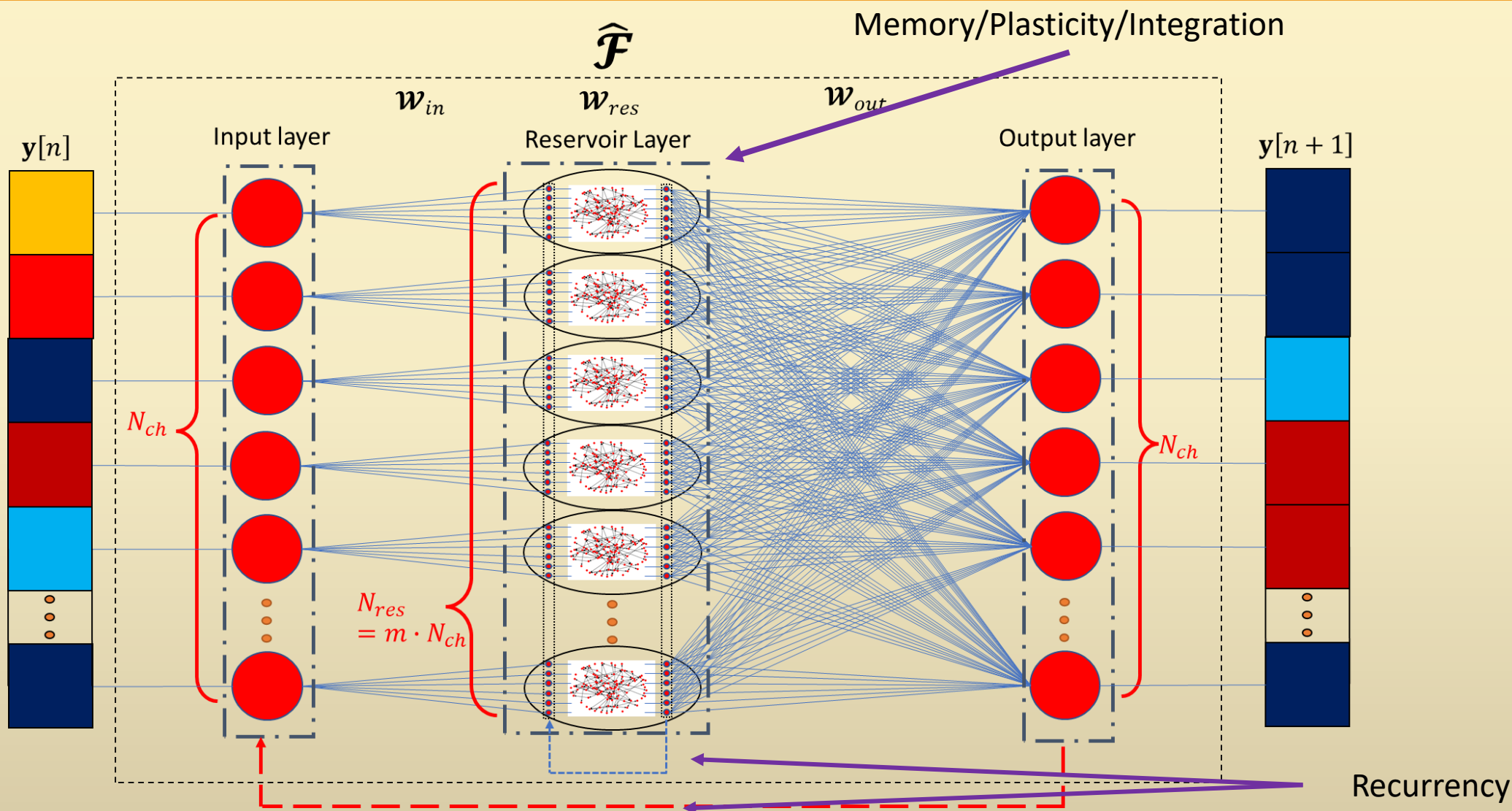
- Neuronal populations-
complex circuits.
- Rate coded information.

Recurrent (Spiking) Neural Network

Reservoir Computing Network



* Taken from: Sakemi, Y., Morino, K., Leleu, T. *et al.* Model-size reduction for reservoir computing by concatenating internal states through time. *Sci Rep* **10**, 21794 (2020). <https://doi.org/10.1038/s41598-020-78725-0>

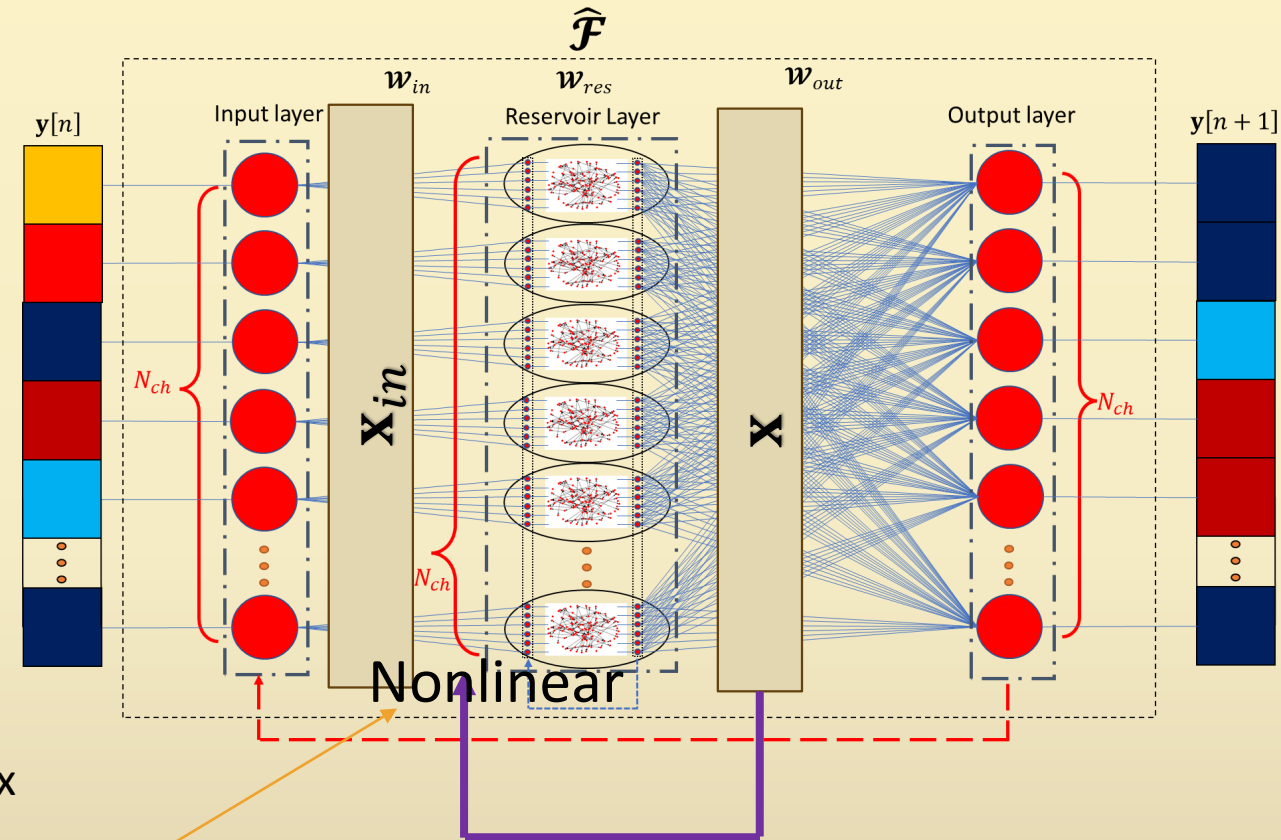


Dynamics

$$\mathbf{x}_{in}[n] = \mathbf{W}_{in}\mathbf{y}[n]$$

$$\mathbf{x}[n] = \mathbf{f}_{NL}(\mathbf{S}(\mathbf{x}_{in}[n] + \alpha\mathbf{W}_{res}\mathbf{x}[n - 1]))$$

$$\mathbf{y}[n + 1] = \mathbf{W}_{out}\mathbf{x}[n]$$

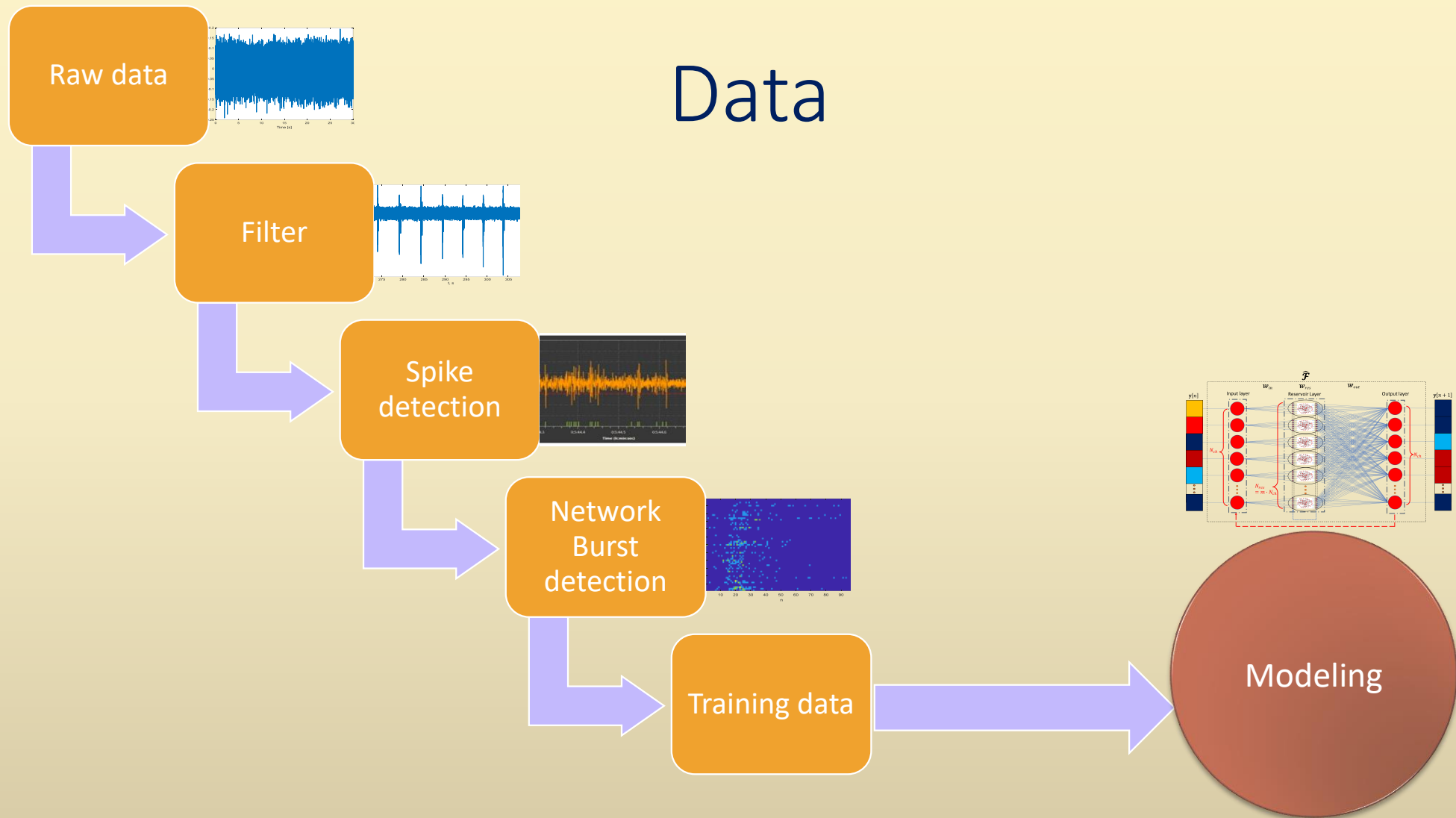


Linear

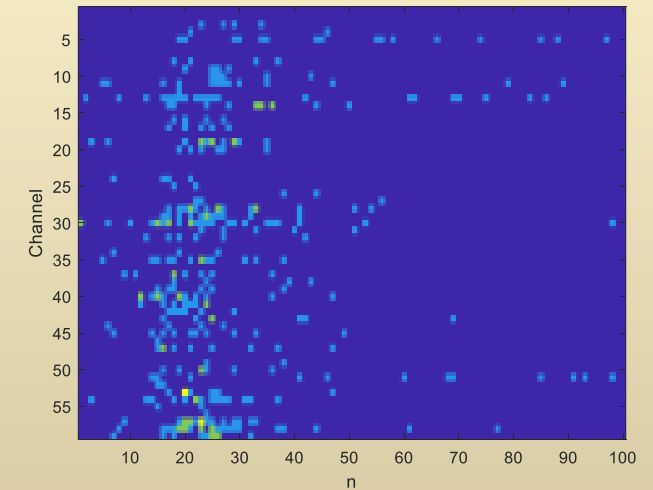
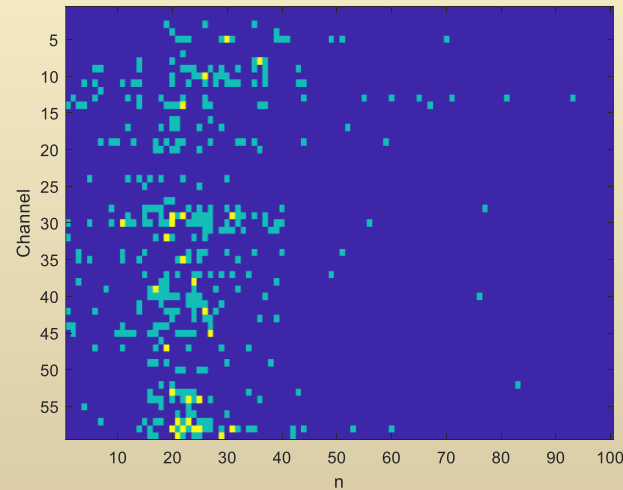
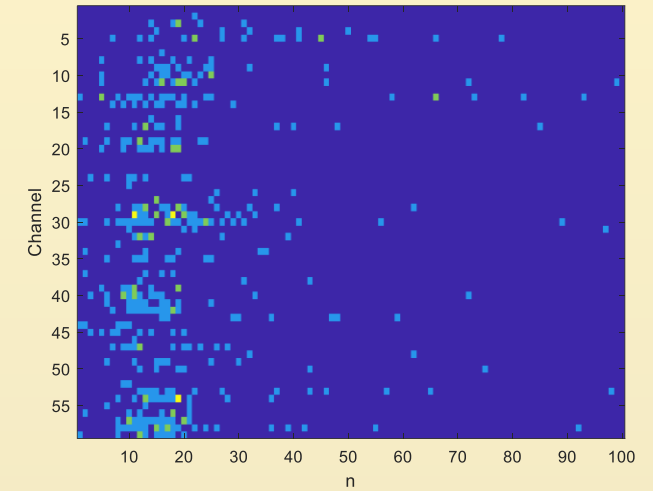
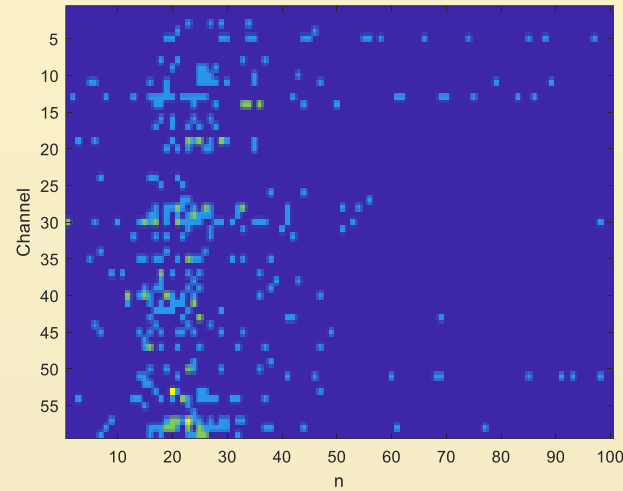
$$\mathbf{T}_0 = \mathbf{W}_{out}\mathbf{S}\mathbf{W}_{in}$$

Intrinsic Conn. Matrix

$$\mathbf{y}[n + 1] = \mathbf{T}_0\mathbf{y}[n] + \mathbf{Q}(\mathbf{x}[n, n - 1, n - 2, n - 3 \dots])$$



Data

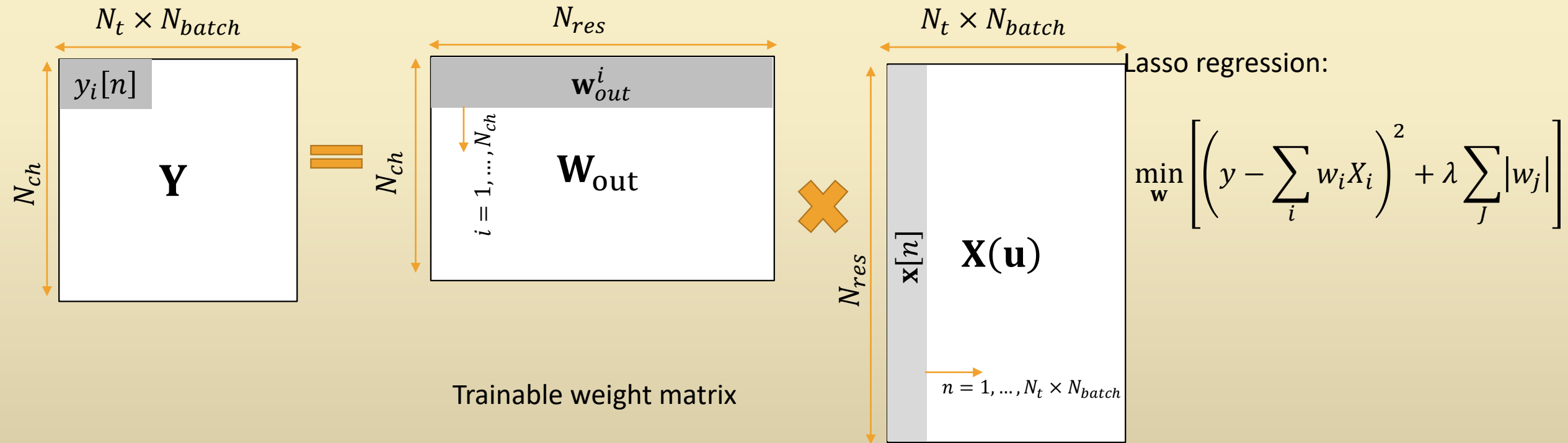


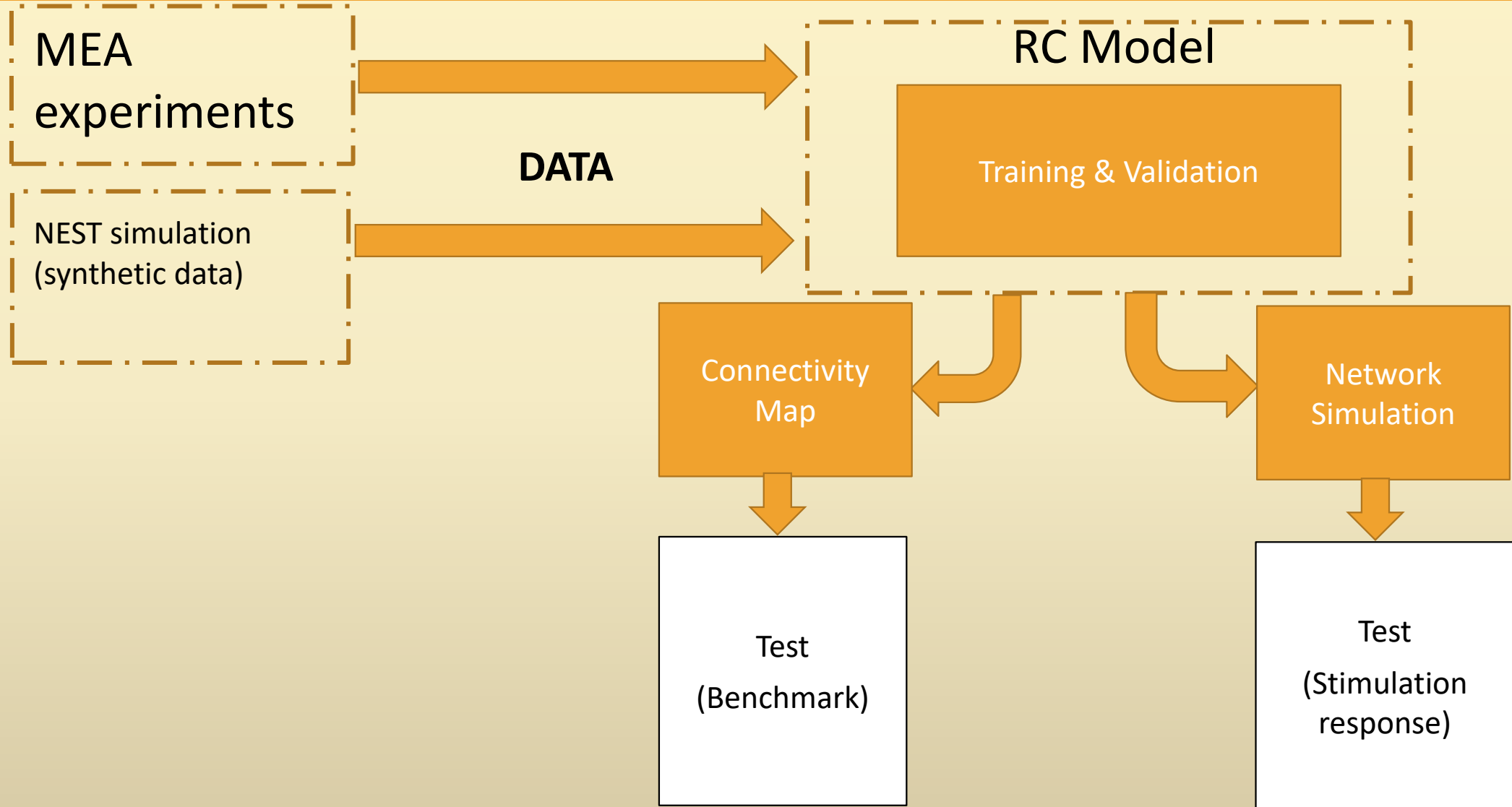
Training

- Only the linear output layer is trained!

Regression problem

$$y_i[n] = \sum_{j=1}^{N_{res}} W_{out}^{i,j} x_j[n], \quad n = 1, \dots, N_t \times N_{batch}$$





Simulation of neuronal culture for benchmarking



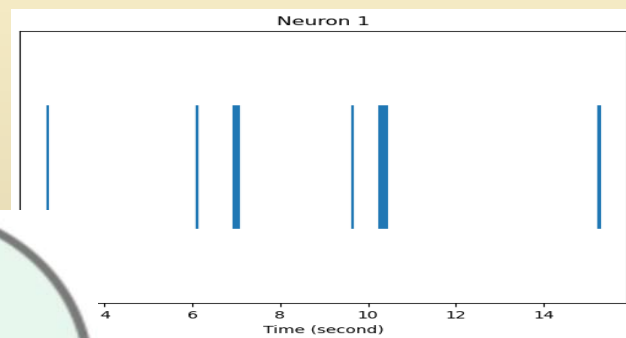
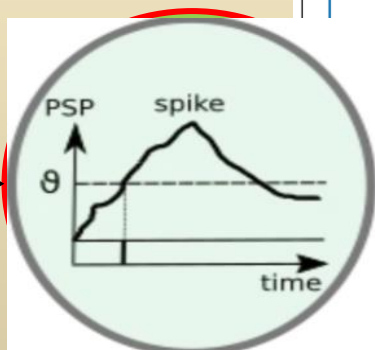
Giorgio Letti

- networks of **point-process** neurons
- Try to replicate the **spiking dynamic** shown by **in-vitro culture**

Point-Process Neuron

- **Simplified neuron** model
- Modelling **basic phenomena**
- No **extracellular potential** can be simulated
- Computationally **cheap**

Background activity



Spiking time

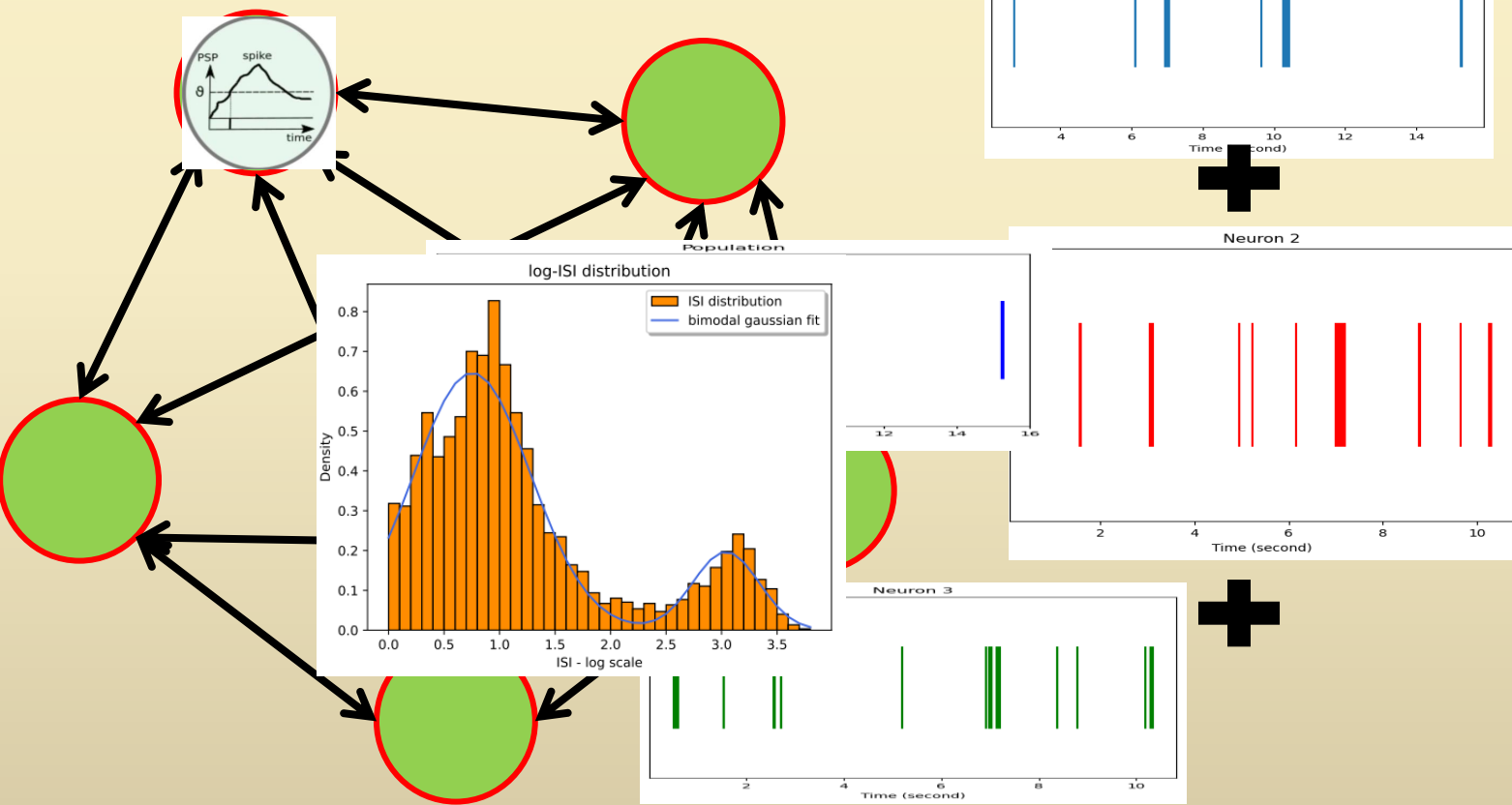


Network dynamic

Simulation of neuronal culture for benchmarking



Giorgio Letti



Population Model

- **Multiple** Izhikevich neuron model
- Collect **Spike train** of each neuron
- **Merge and temporally sort** the Spike trains



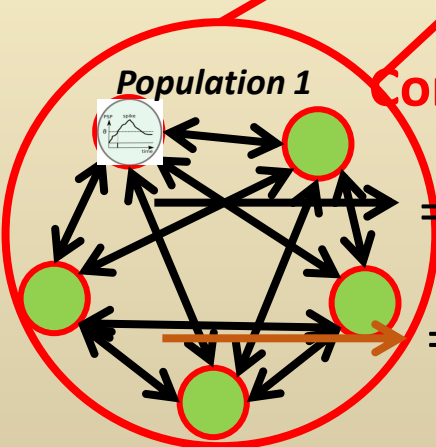
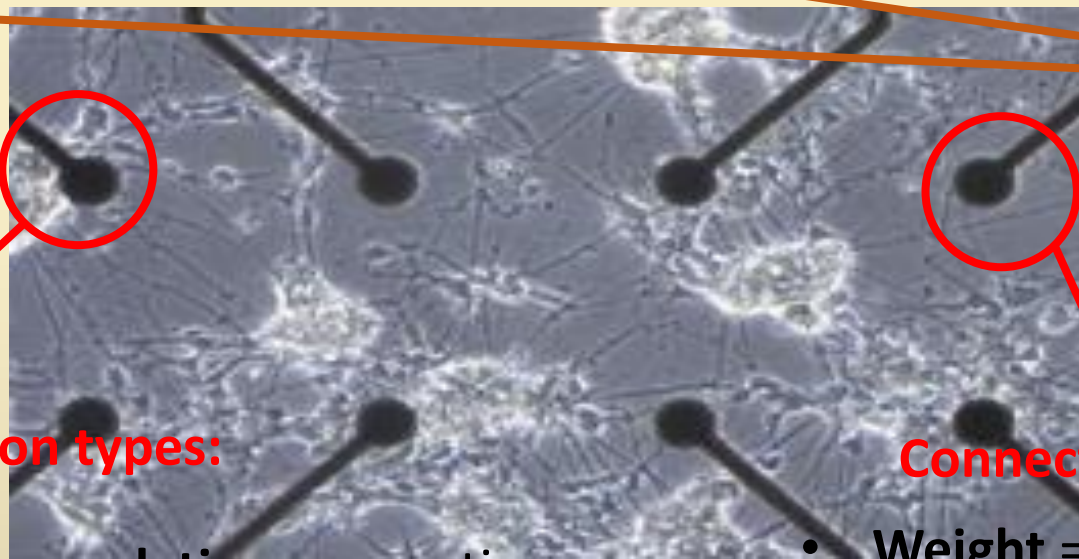
Output:

Spiking time and Inter-spike interval (ISI) distribution of the *Population*

Simulation of neuronal culture for benchmarking



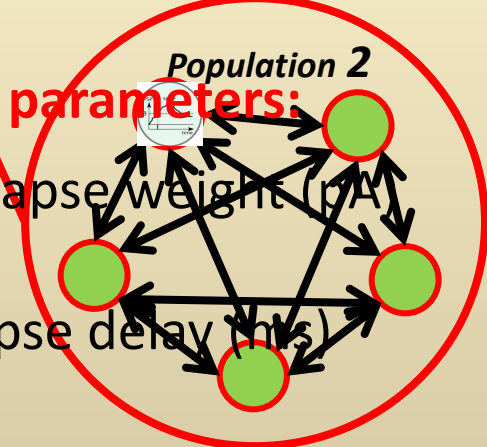
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Connection types:

= Intra-population connections

= Inter-population connections



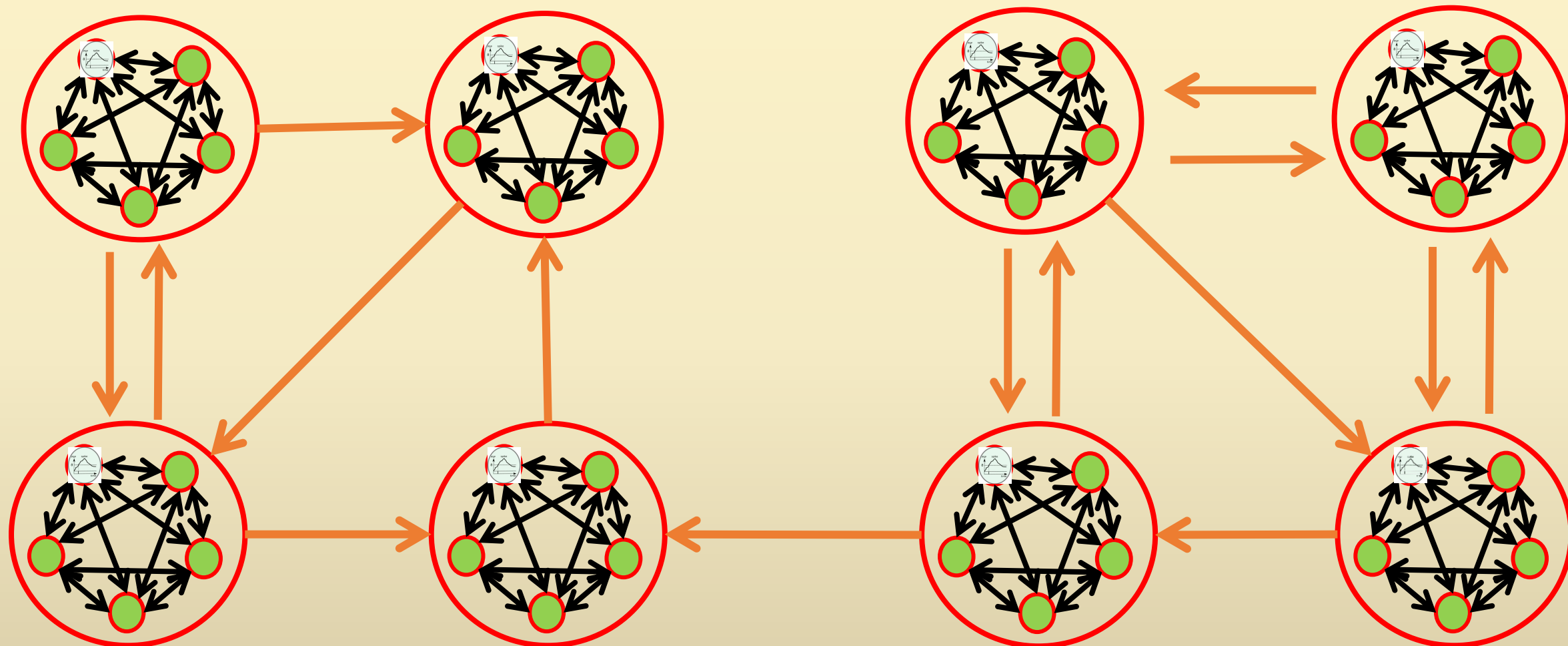
Connection parameters:

• Weight = synapse weight (pA)

• Delay = synapse delay (ms)

Assumptions

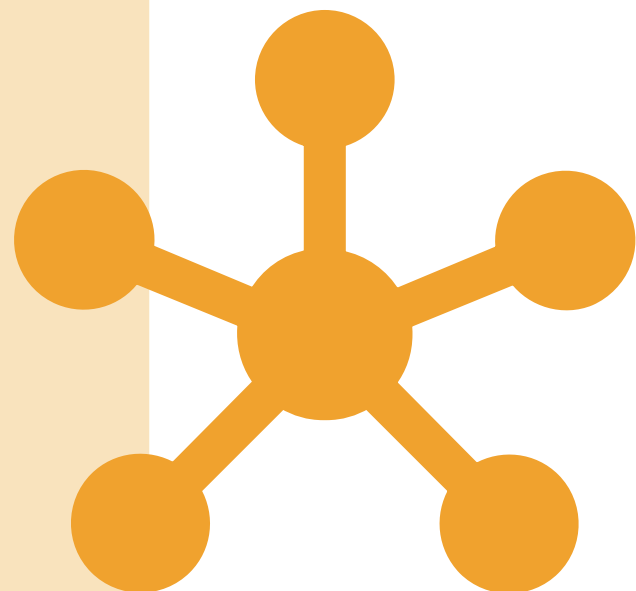
- MEA electrode = Population
- Perfect Electrode



Results

WORK IS STILL IN PROGRESS



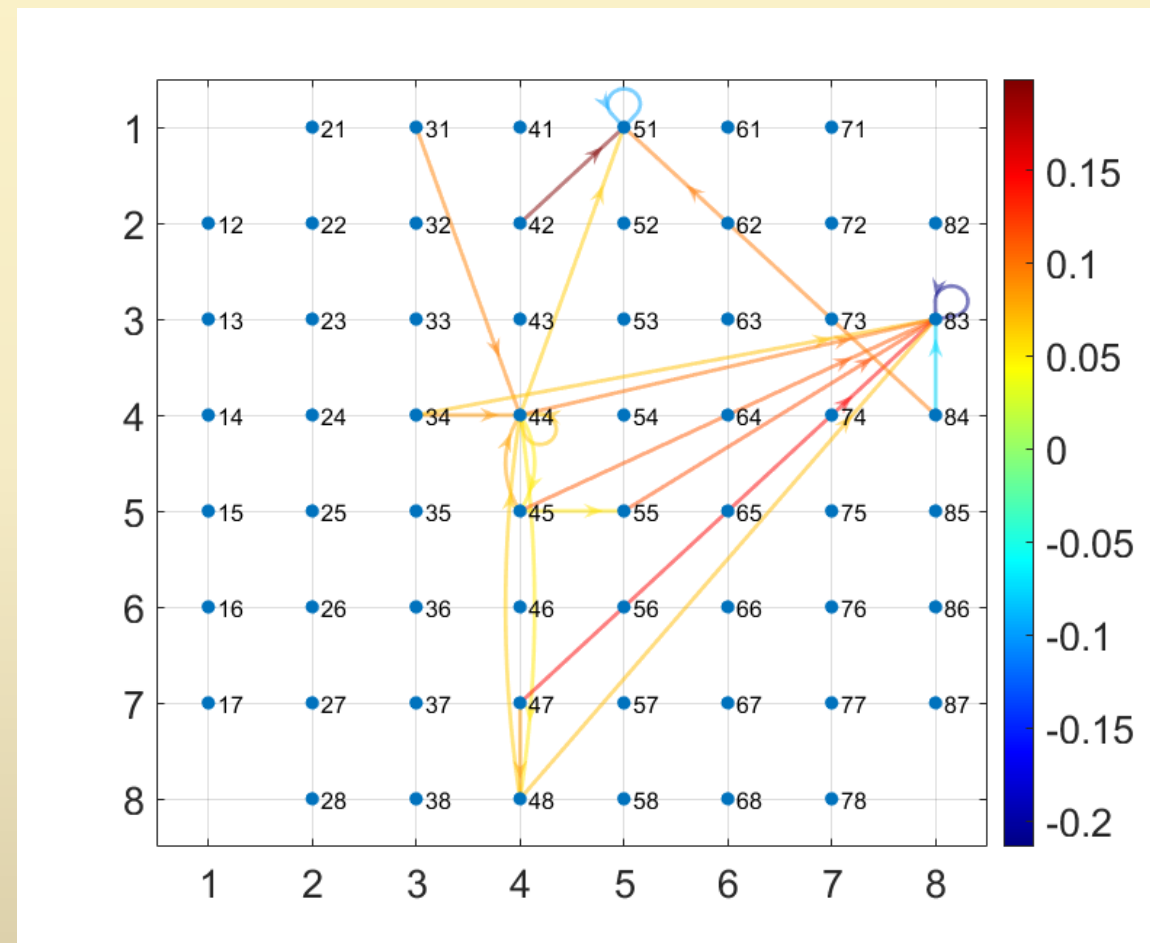


Connectivity Map

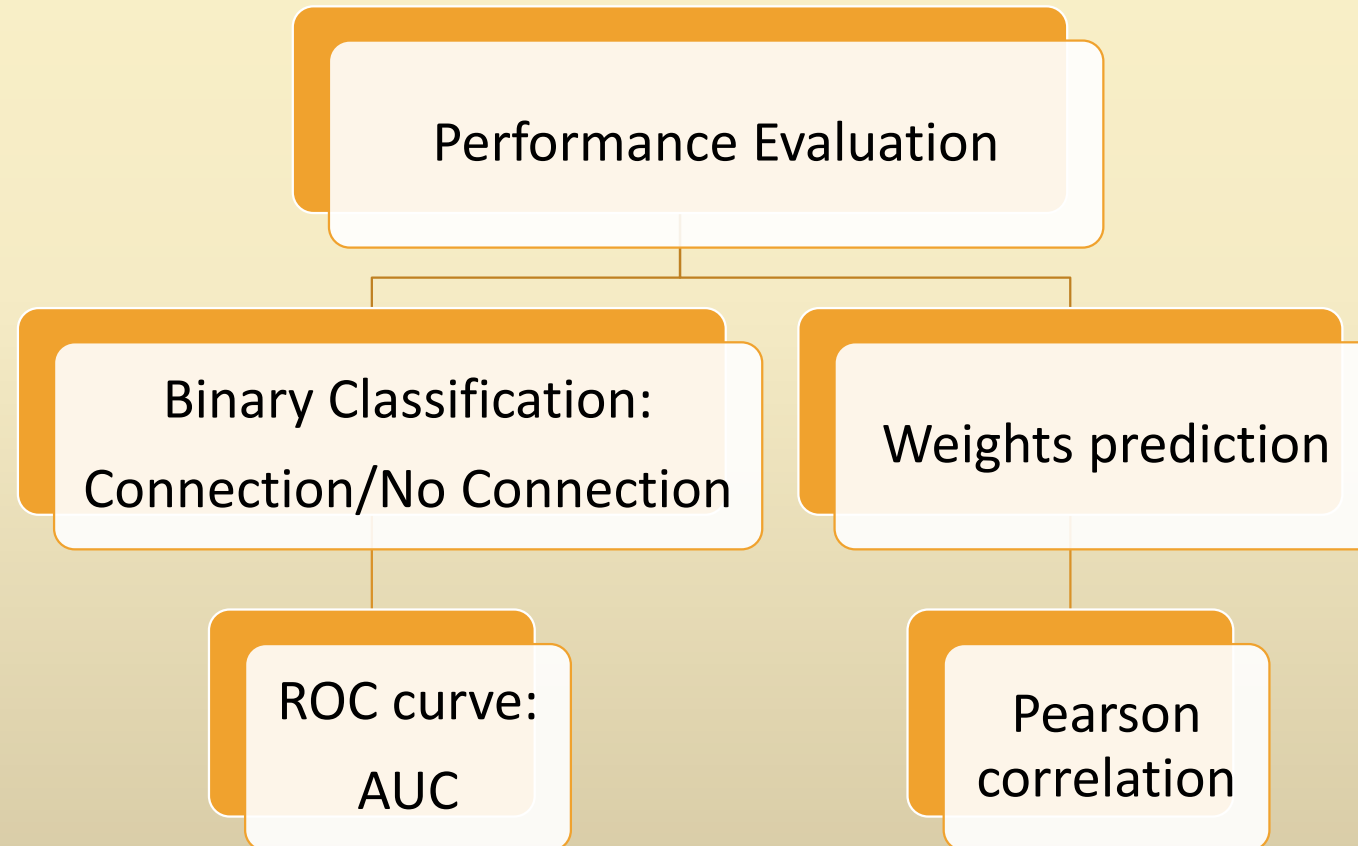


Connectivity Map

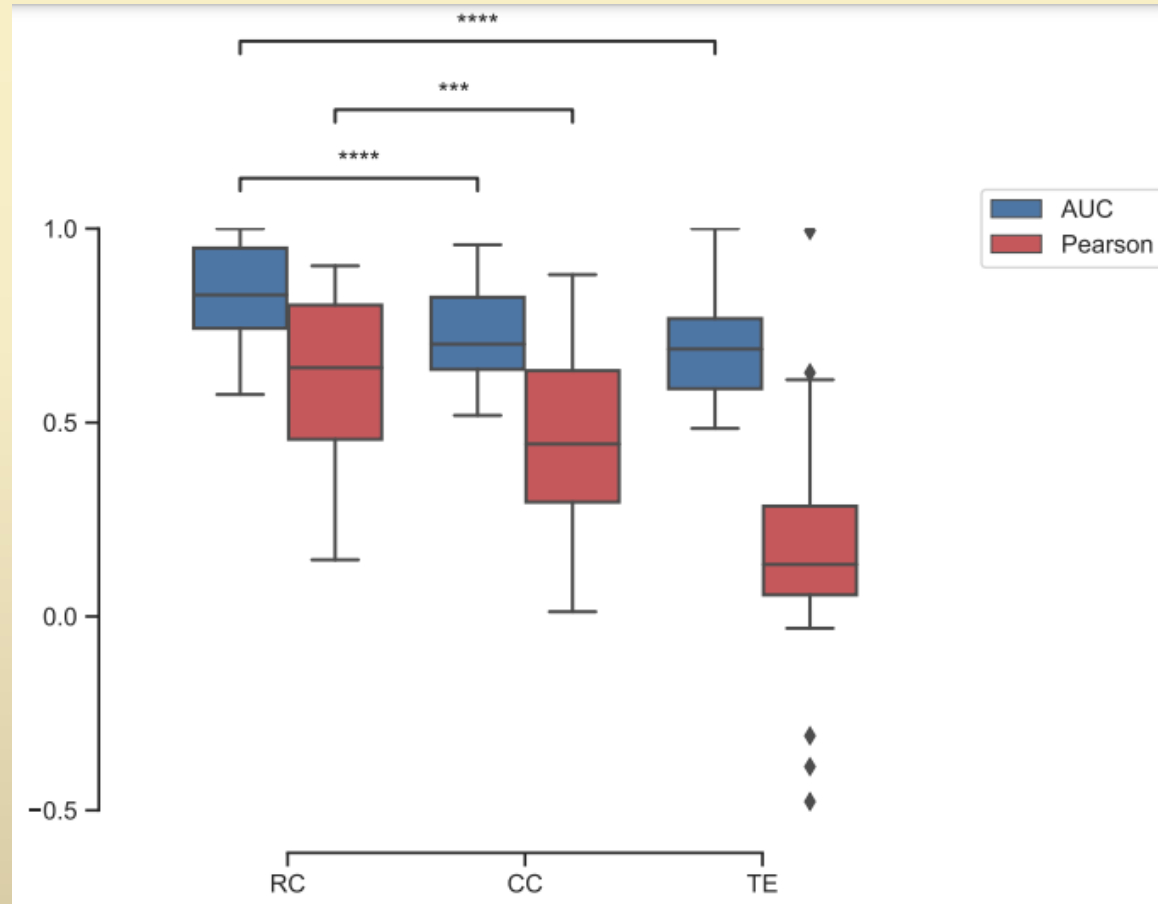
- Weighted connections
- Excitatory/Inhibitory connections



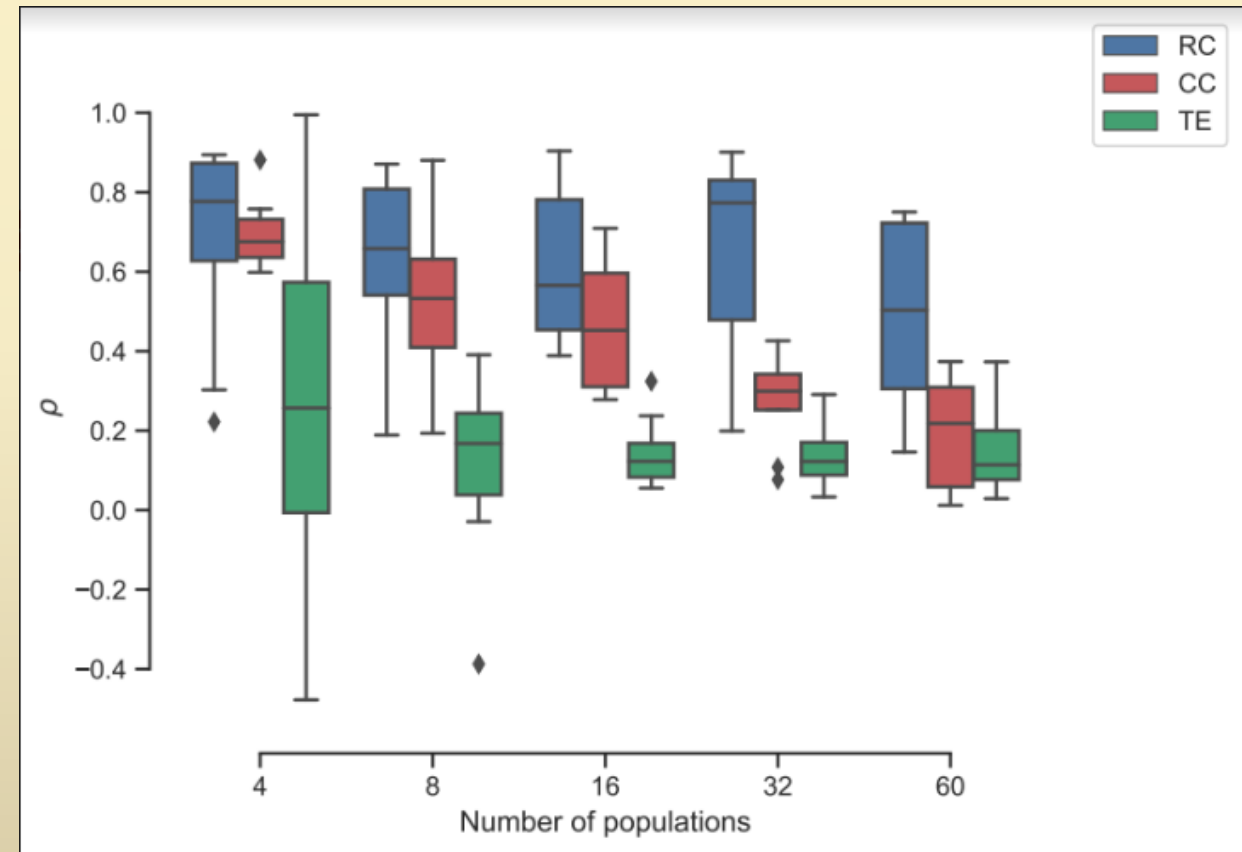
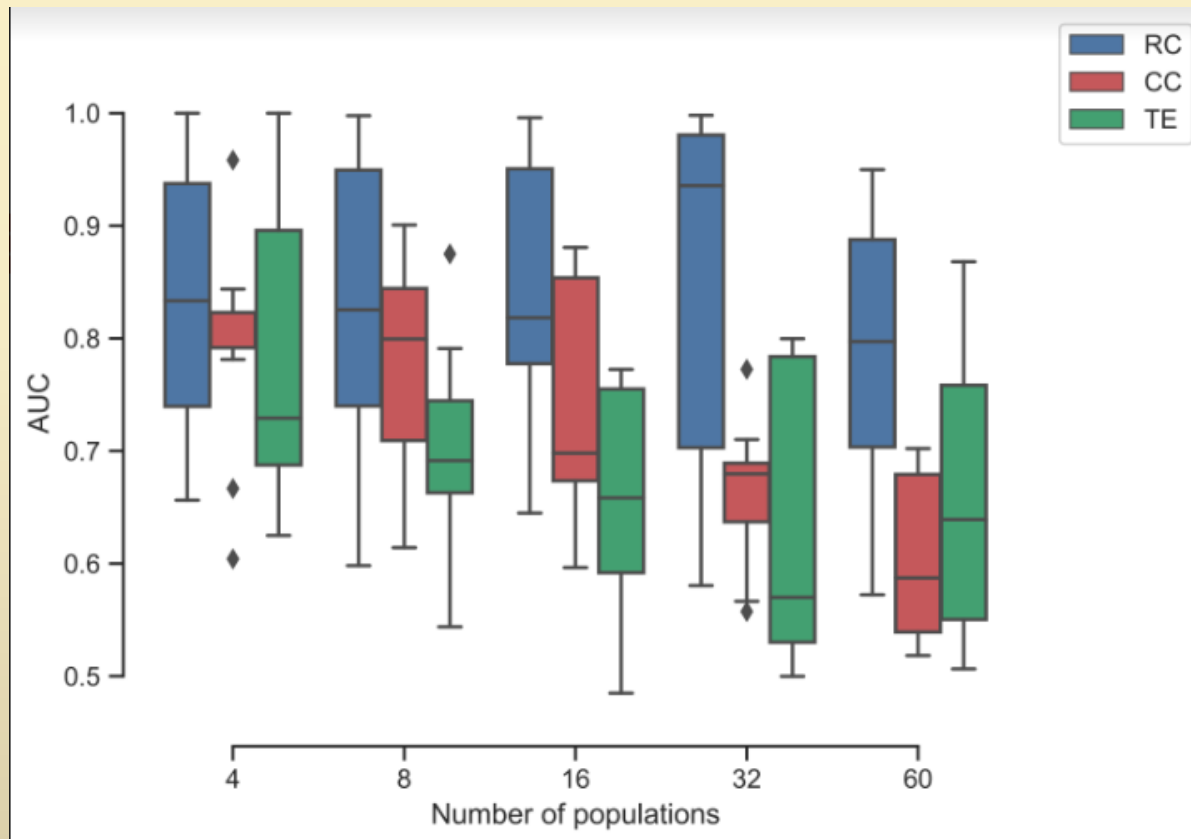
Connectivity



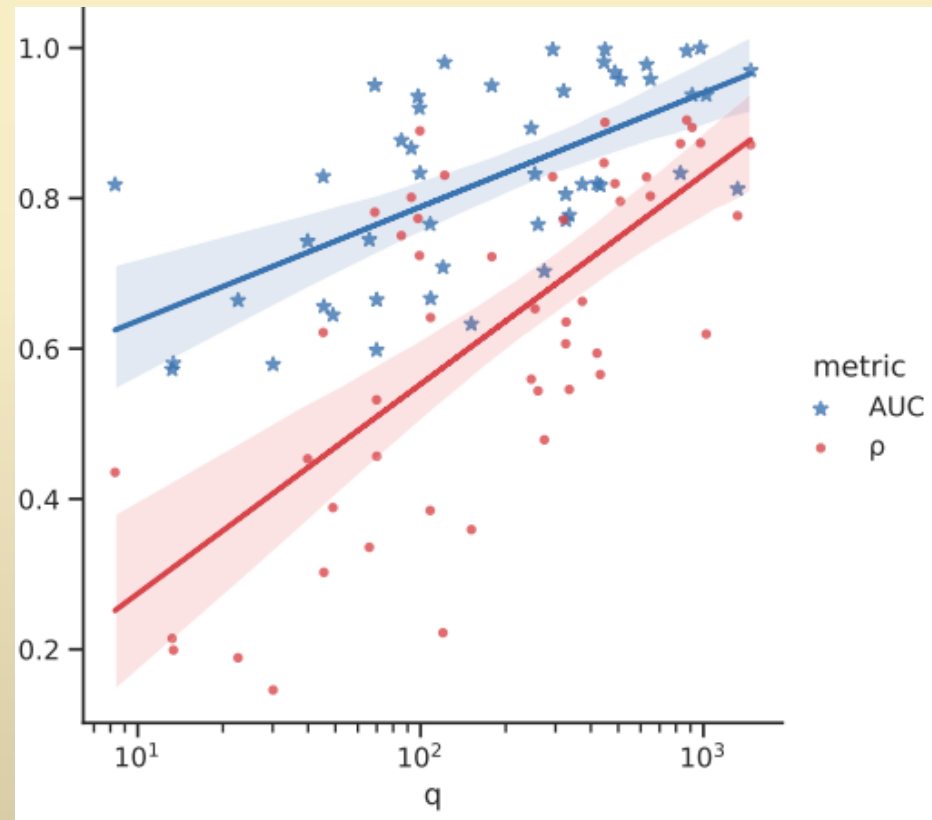
Connectivity- Results



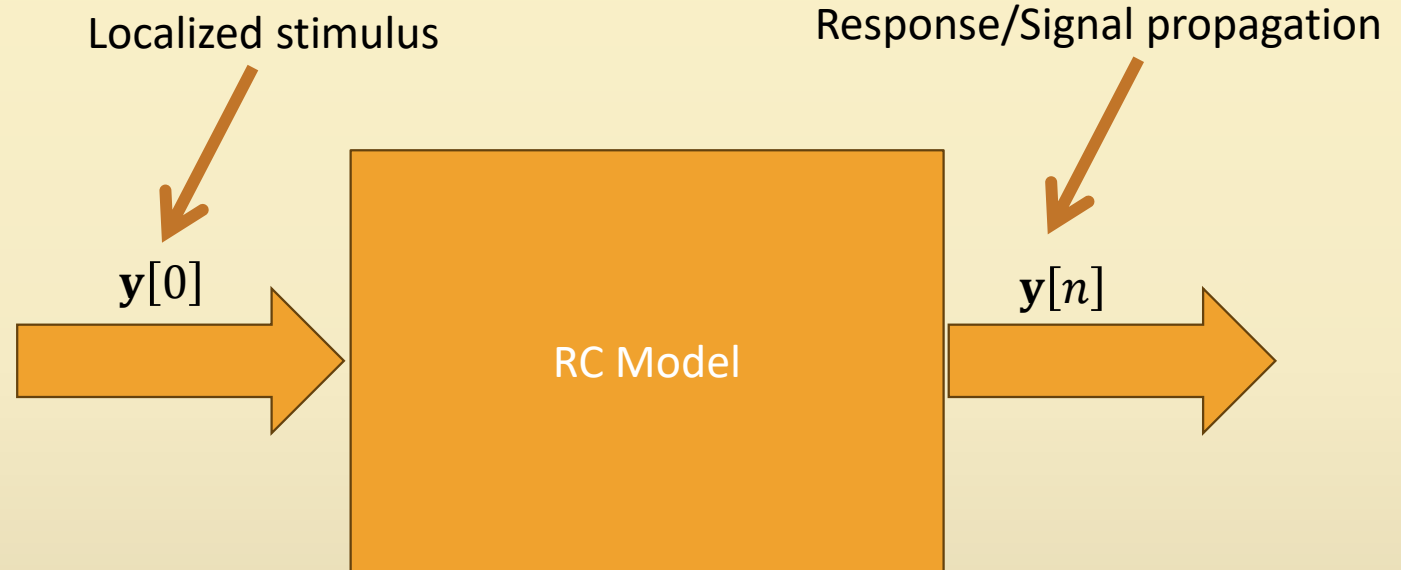
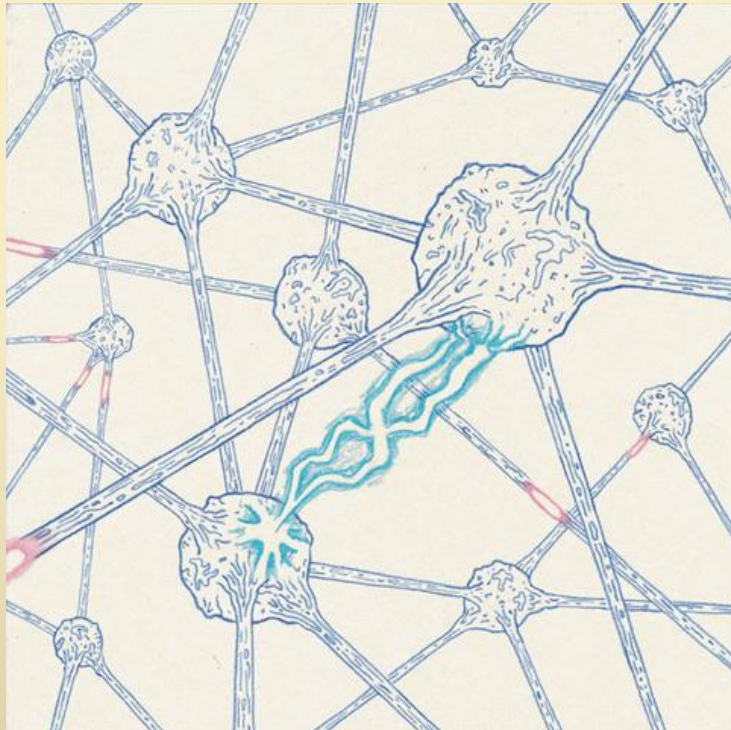
Connectivity- Results



Connectivity- Results

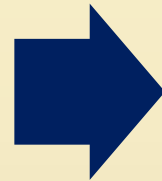


Response test



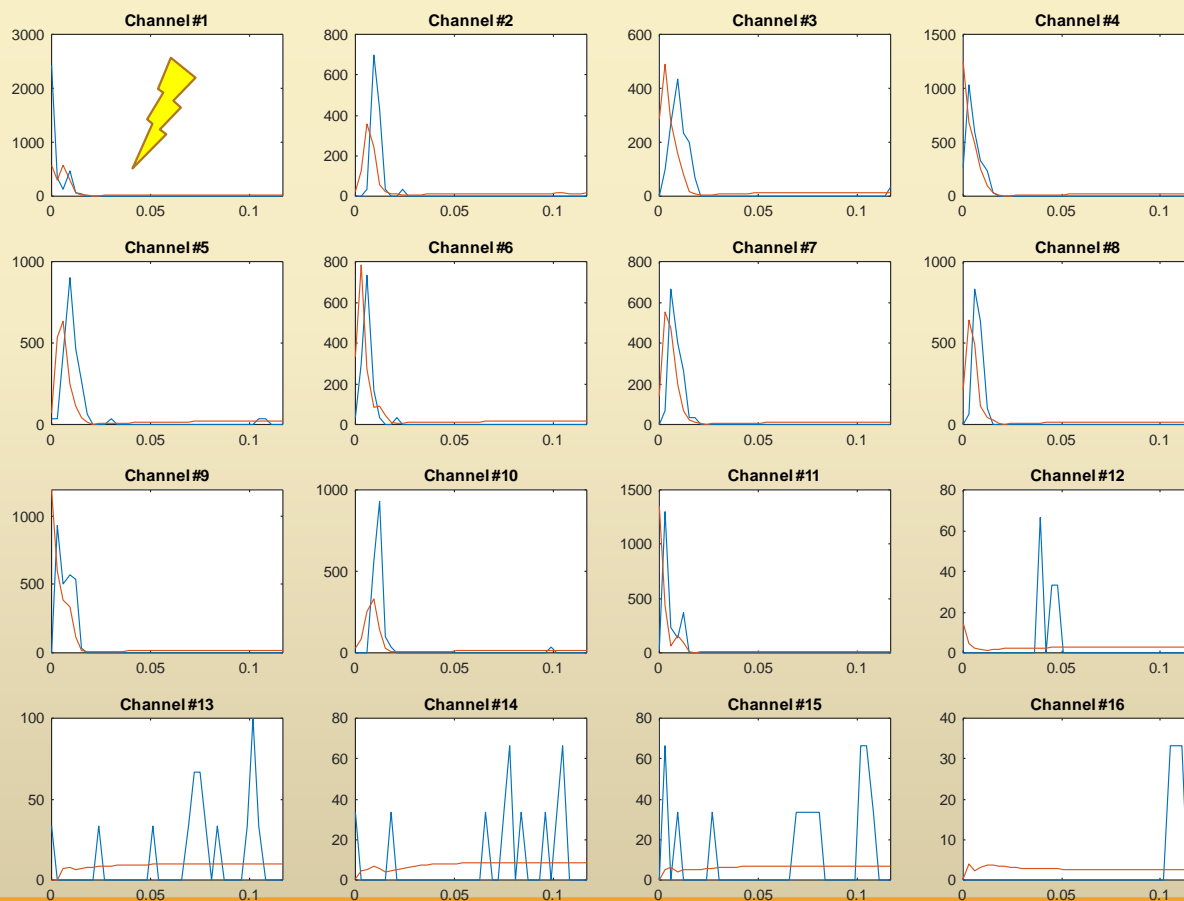
Response test

Training:
Spontaneous
activity



Test:
Stimulus
response

Response test

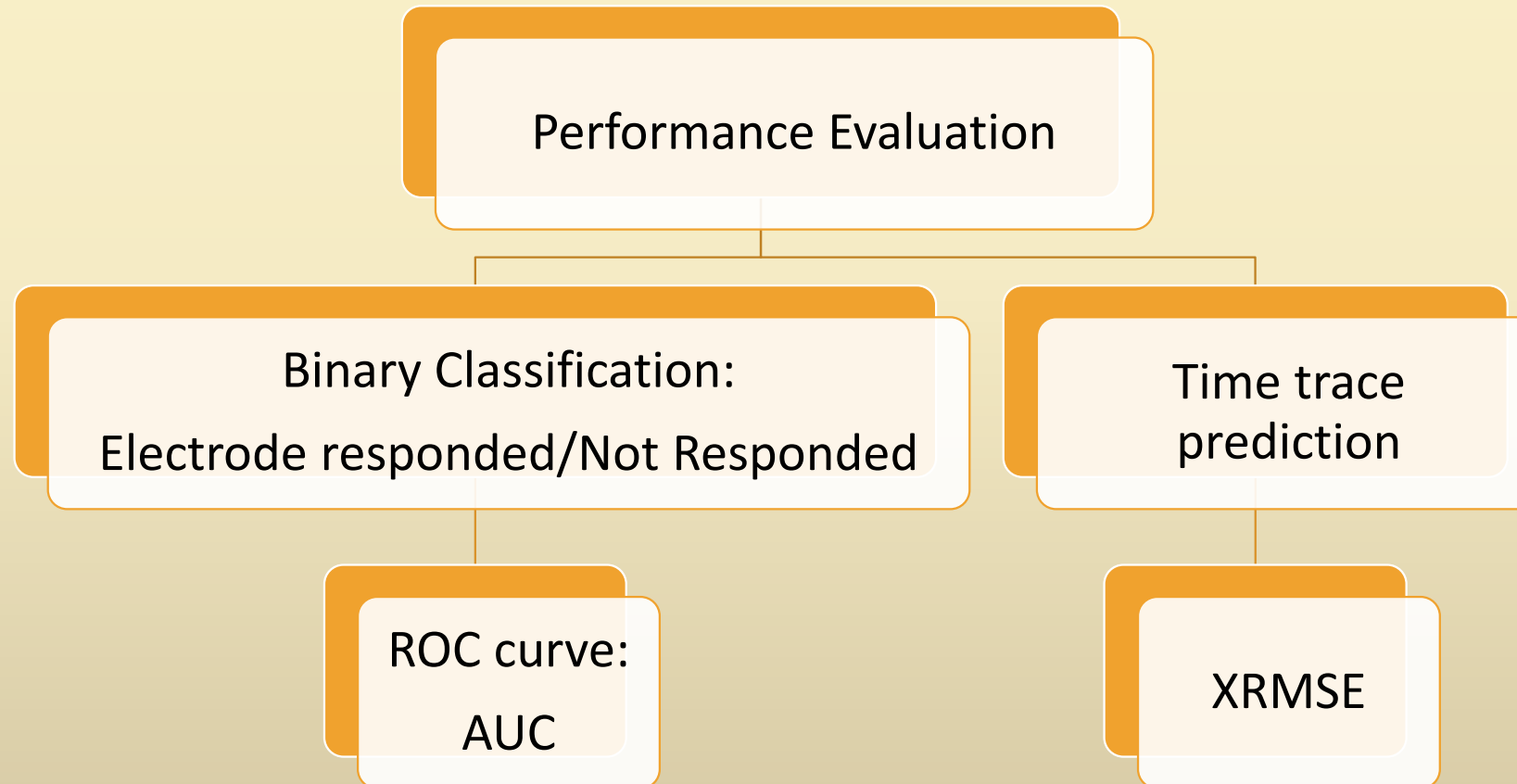


— Experiment
— Model

Spike rate
[Sp/s]

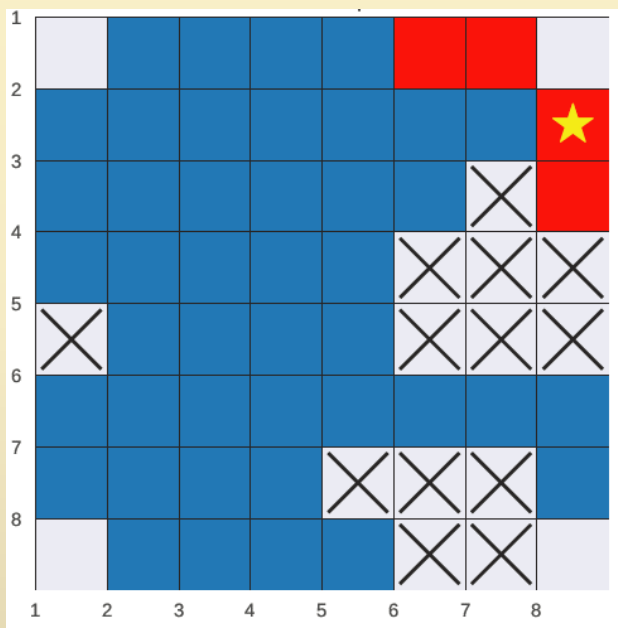
time [sec]

Response test

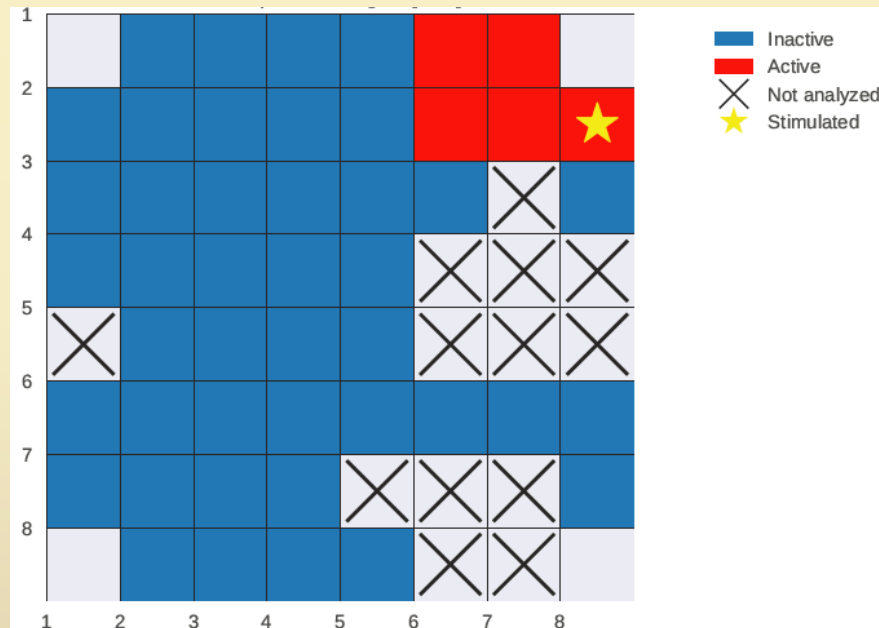


Binary classification

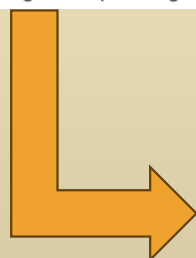
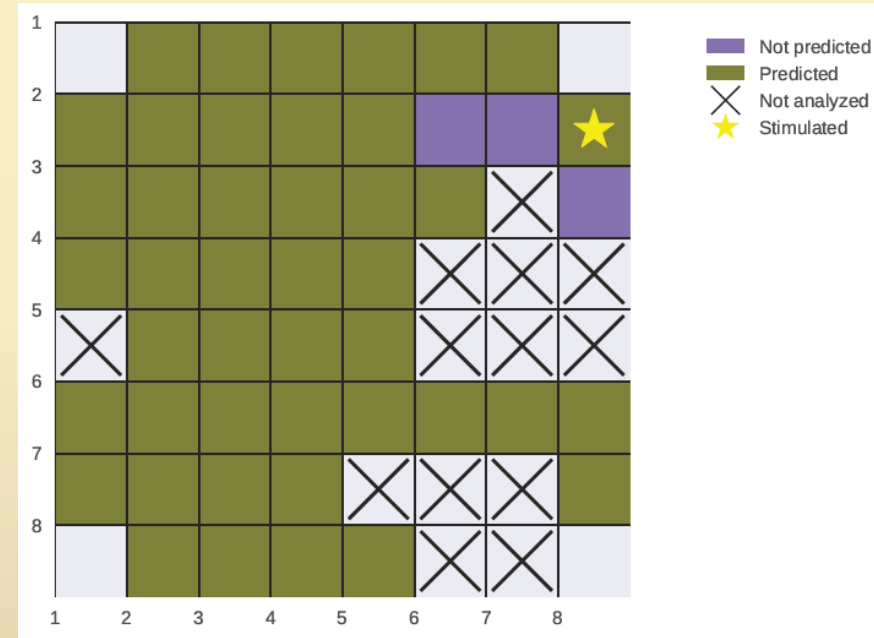
Experiment



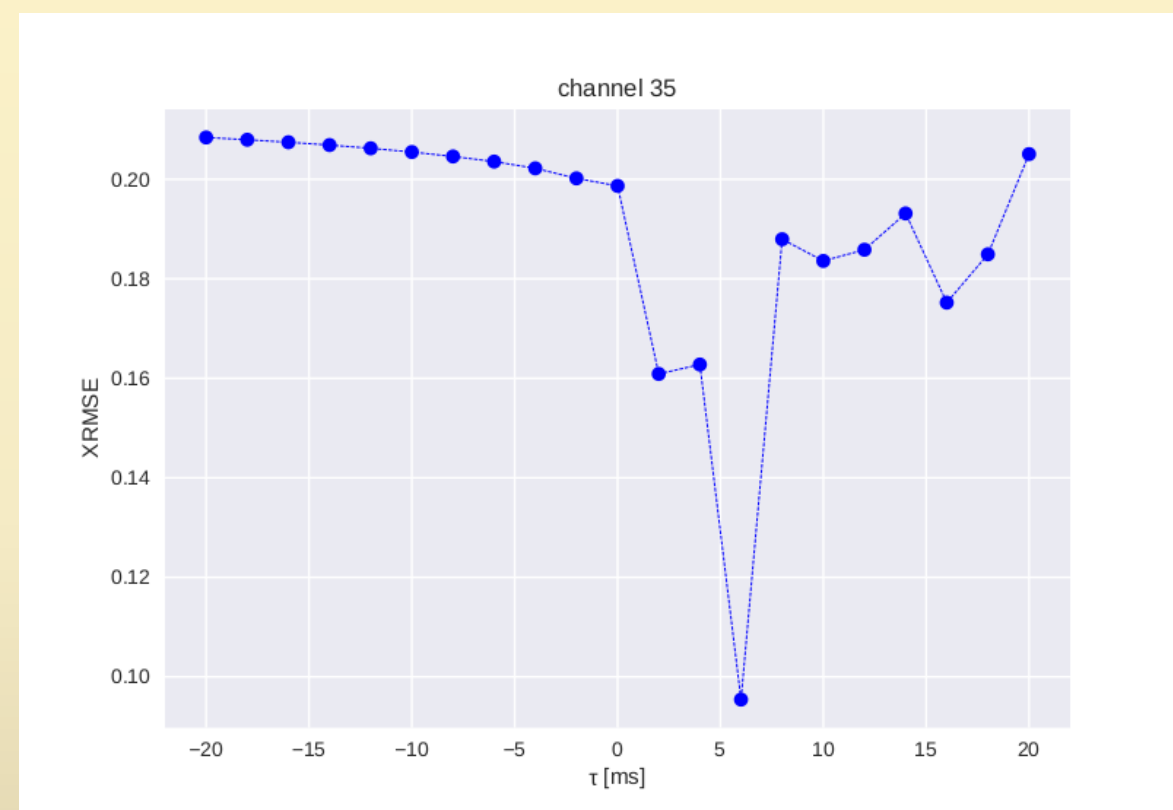
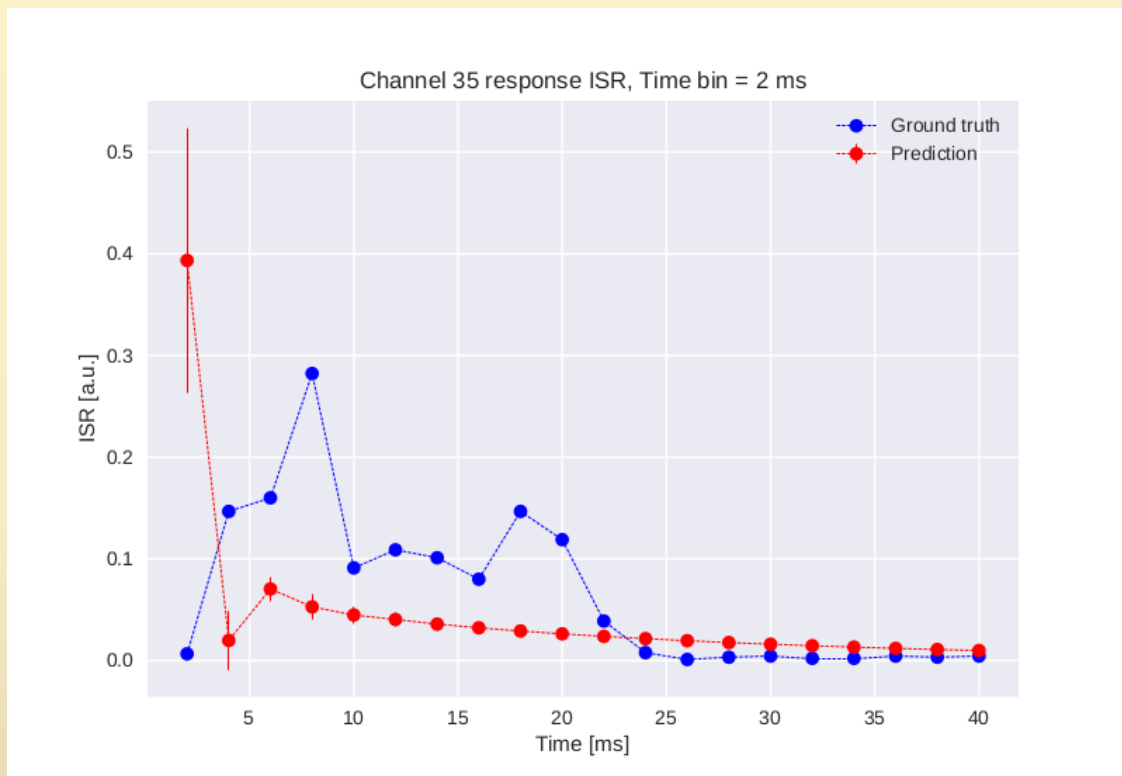
Model Prediction



Performance evaluation

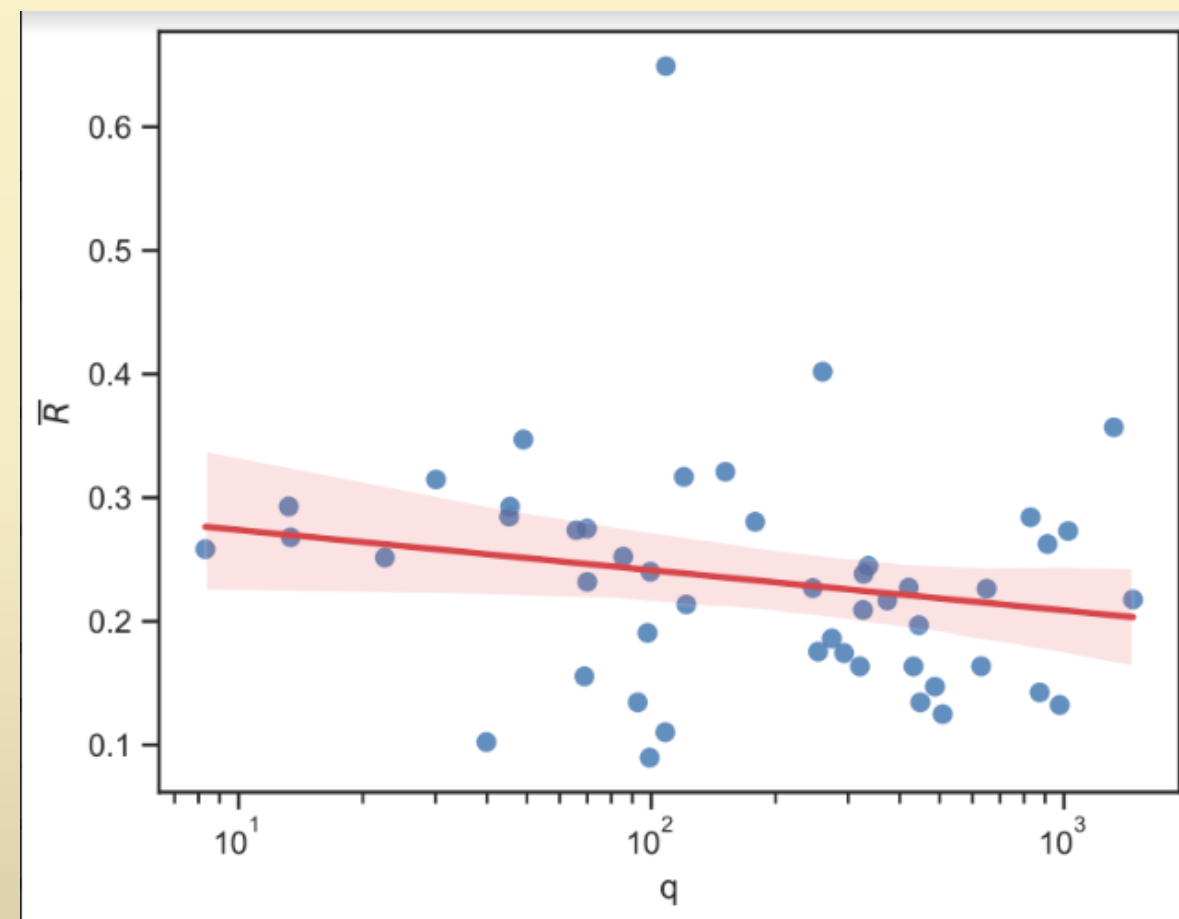
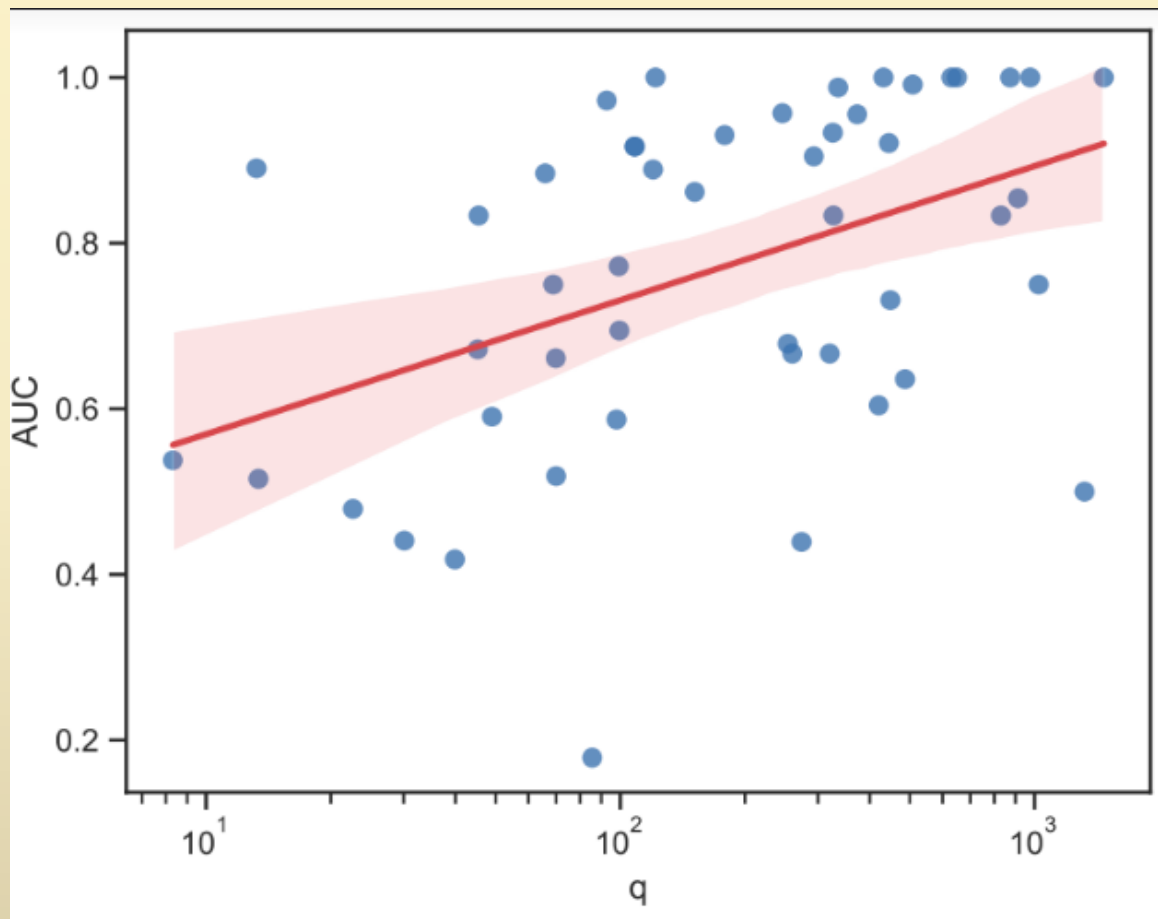


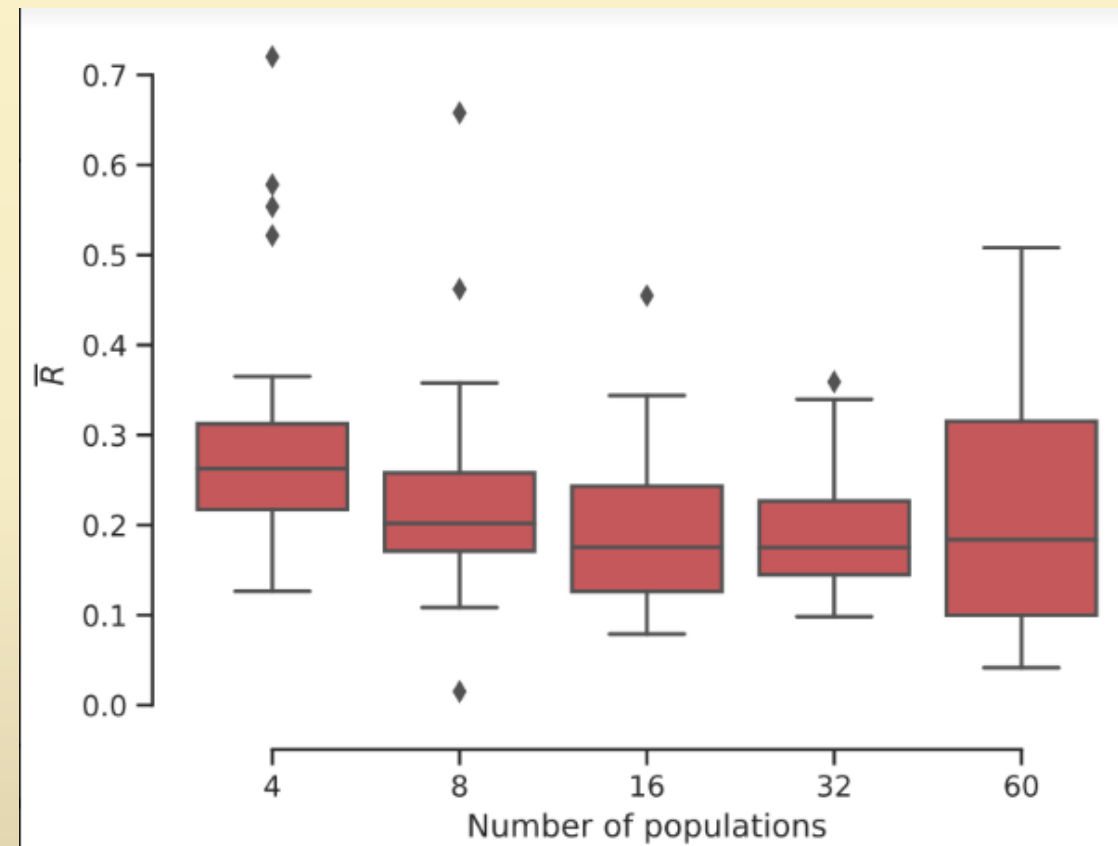
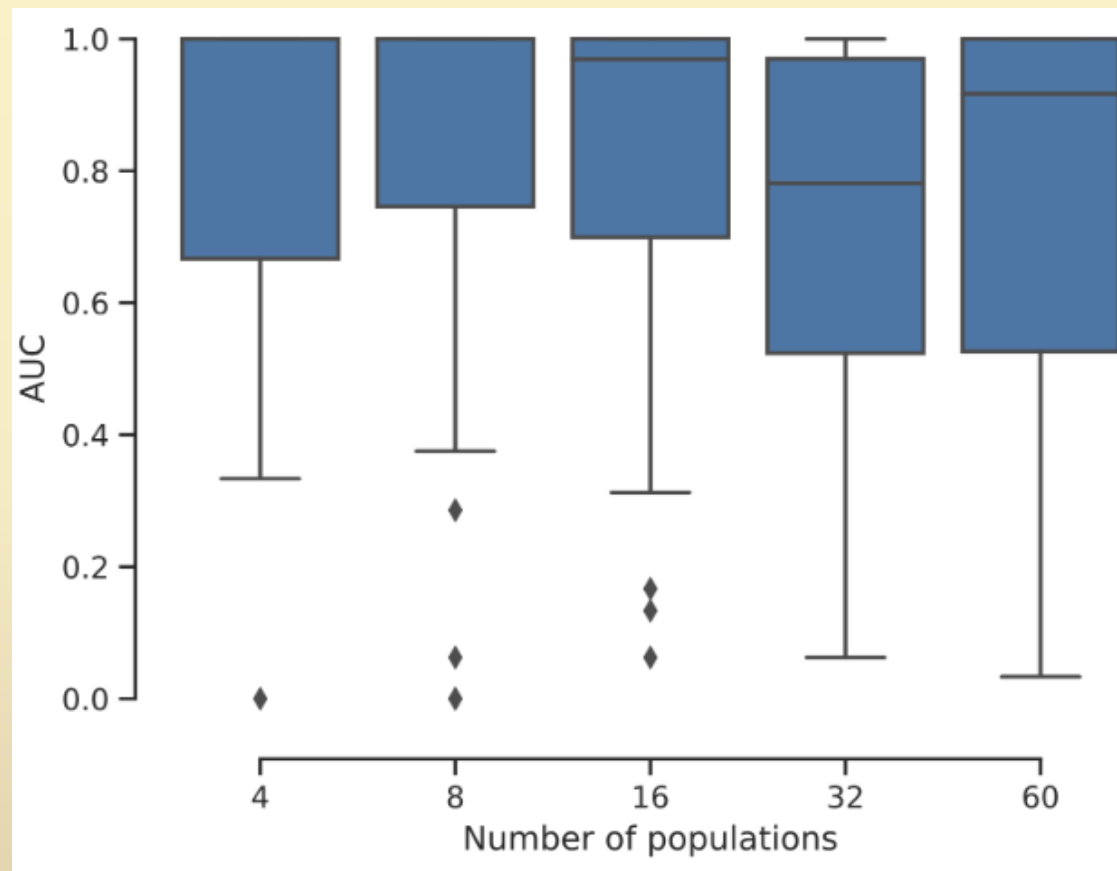
ROC curve - AUC



$$XRMSE(\tau) = \sqrt{\sum_{n=1}^{N_t} w_y[n, \tau] (y_o[n] - y_p[n - \tau])^2}$$

$$\bar{R} = \left\langle \min_{\tau} (XRMSE) \right\rangle$$





Conclusion

- Neuronal dynamics are complex and hard to interpretate.
- We developed a model, based on RCN approach to decode the information stored in time sequences of neuro electrophysiological signals.
- The model can extract the connectivity map on a macroscopic scale with higher accuracy than the existing “classical” methods.
- The model is able to predict the response of the network to a given input (such as localized stimulation).

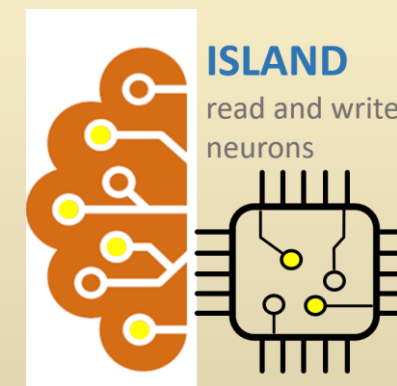
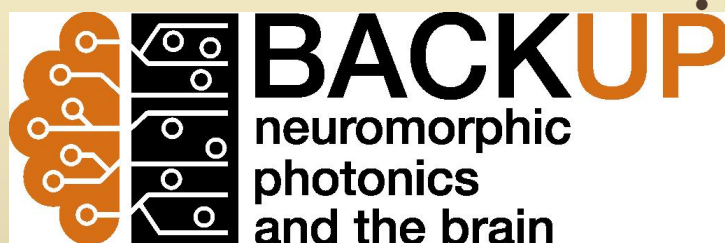


Horizon 2020
European Union Funding
for Research & Innovation



This work has received funding from the European Union's Horizon 2020 research and innovation programme under

- the Marie Skłodowska-Curie grant agreement No 101033260 (project ISLAND).
- the European Research Council (ERC) grant agreement No 788793 (project BACKUP).





Thank you!