Title: "Metricize" the performance of cell-to-cell communication channels with Deep Learning approach

Authors:

*Minh Nguyen[1], Aapo Tervonen[2], Soile Nymark[2], Jyrki Nummenmaa[1], **Huy Tran**[2]*
[1] Faculty of Information Technology and Communication Sciences
[2] Faculty of Medicine and Health Technology

Keywords:
Cell-to-cell communication, Molecular communication, Machine Learning

Abstract
Biological systems are highly complex signal processing systems with many interconnected components, and thus able to exhibit non-linear dynamical responses. However, estimating the performance of these systems remains a challenge, even in the abundance of data and their details. On the technical side, there is no framework to evaluate the mutual information or correlation between the input (e.g. dose and exposure time of a drug) and the recorded time-continuous responses (e.g. reporter genes' fluorescent traces, cell morphology). Analyses, therefore, have been relying on feature reduction, which inadvertently ignores the dynamical aspects and complexity of signaling.

Here, we propose a machine-learning-based approach to estimate the "full" mutual information between the input stimuli and experimental response time series. This is done by finding the prediction accuracy by learning models when decoding the stimuli parameters from the responses. With an optimal learning model (i.e. decoder), this accuracy will inform on the biological systems' (i.e. encoder) transmission capacity.

We test this approach with synthetic data on calcium signaling in 2D tissues (figure 1). We investigate how distant cells can perceive nearby mechanical stimuli, as a function of system noise.
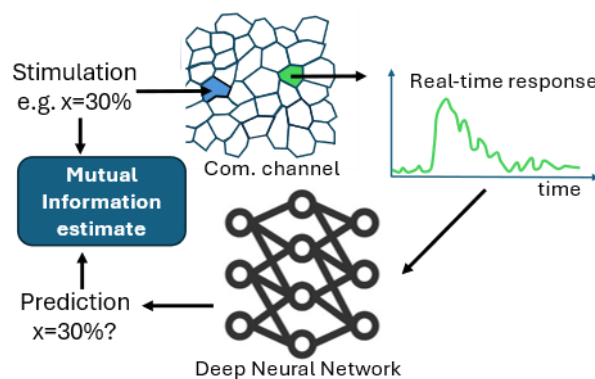
Figure 1. Maching-Learning-assisted Mutual Information estimation