Organoid Intelligence as a Reservoir Computing Paradigm for Time-series Prediction

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(Standard study)

Project Summary

Objective

To significantly advance the state-of-the-art in bio-inspired reservoirs by implementing a compartmentalized, connectome-like, neuronal organoid as a physical reservoir for the prediction of multi-variate chaotic time-series. Building on state-of-the-art results on simple cultures and simulations of entire connectomes, we aim to extend this work to the case of connectome-structured cultures, thereby moving from bio-inspired reservoirs to biological ones.

Target university partner competences

iPSC culture and differentiation, neuronal organoid culture, bioelectronics

ACT provided competences

Reservoir Computing, machine learning and artificial intelligence, chaotic systems

Keywords

Organoid Intelligence, Reservoir Computing, Time-series Prediction

Study Objective

This study will investigate the performance of biological reservoirs for time-series prediction compared against reservoirs built from simulated neurons. It will implement and characterise the biological reservoir in the form of a neuronal organoid interfaced through suitable hardware.

In particular, it will:

- Characterise the echo-state property and intrinsic dynamics of neuronal organoid reservoirs.
- Study how these properties depend on topology and morphology (e.g. degree of compartmentalisation, connectivity patterns, and synaptic-weight distributions).
- Document the role of these features on memory capacity, robustness, and prediction performance.

The overarching goal of this study is to take a fundamental leap in the field of bio-inspired computing, moving from simulated neurons in an artificial neural network to real neurons in a biological neural network, and to showcase how biological reservoirs perform in the task of time-series prediction.

Background and Study Motivation

Reservoir computing is a learning paradigm in which a nonlinear dynamical system is used to increase the dimensionality of an input signal, often a time series, so that future samples can be forecast using a simple (typically linear) readout trained on the expanded signal. The most common implementations are recurrent neural networks (RNNs), usually classified as Echo State Networks (ESNs) [1] or Liquid State Machines (LSMs) [2], depending on what type of neuronal activation function is implemented.

Compared with many advanced machine-learning (ML) models, reservoir computing requires a very small number of trainable parameters, as only the readout layer is typically trained [3–4]. Compared with other nonlinear signal expansion techniques (e.g. radial basis functions [5]), reservoirs are recurrent by construction and thus provide an intrinsic temporal buffer [6–7], a key advantage for time-series prediction [8–9], particularly for chaotic signals [10–11].

In standard practice, ESN reservoirs are randomly initialised, with only a few key hyperparameters carefully tuned: sparsity, spectral radius, and distribution of non-zero weights [12–13]. Under this approach, other important topological features are often overlooked [11,14].

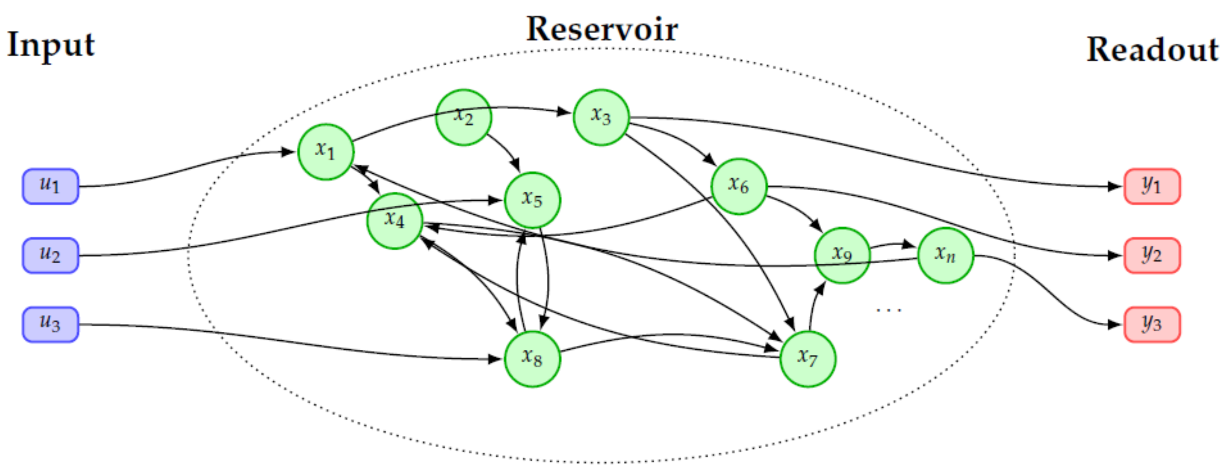

Figure 1: Diagram of an ESN in which a subset of neurons in the reservoir (green) receive the input signal from the input neurons (blue). The readout layer (red), which is usually a fully connected linear layer, extracts activations from another subset of neurons and produces the output.

Nature, by contrast, has evolved extremely large neuronal reservoirs in the form of animal brains over hundreds of millions of years. These systems exhibit complex nonlinear dynamics and support a wide range of behaviours [15–16]. They have been extensively studied to identify features that might inspire improved artificial reservoirs [17]. One prominent line of work maps biological connectomes into reservoir topologies [18]. While complete connectomes are still rare, such work has shown that imposing connectome-inspired constraints on reservoir topology can improve performance [19]. In particular, small-world organisation has been shown to enhance the echo-state property and improve memory capacity and robustness [20]. Recent connectomics advances (e.g. full-brain reconstructions in Drosophila [21] and C. elegans [22]) provide the first complete large-scale biological reservoirs amenable to systematic study.

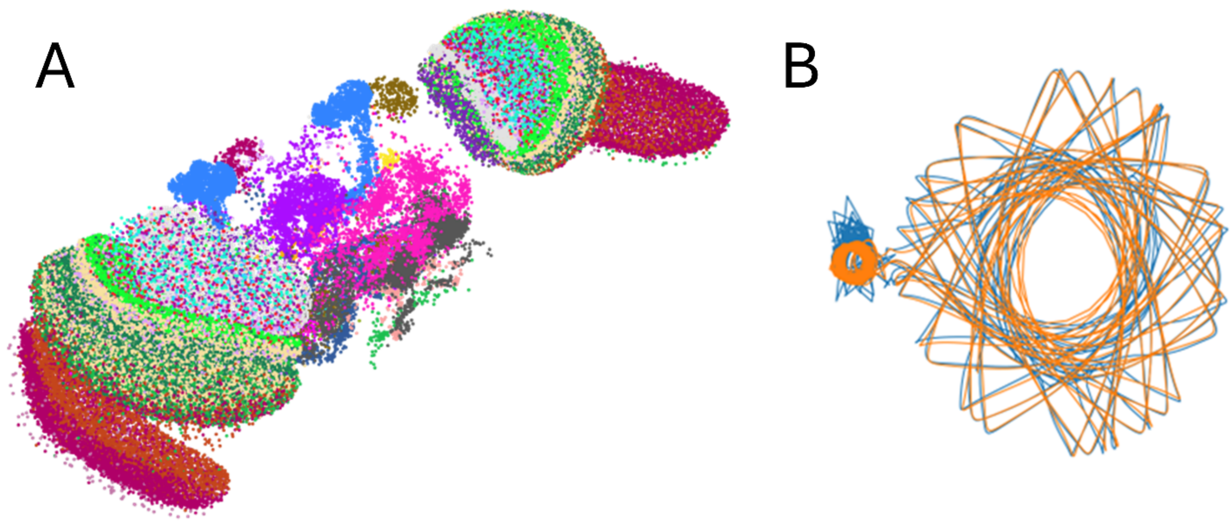

Figure 2: (A) Spatial representation of the Drosophila connectome, in which individual neurons are colour labelled based on the cell type and (B) performance of the connectome-extracted reservoir within an ESN as a time-series prediction tool: the generated ground-truth 3BP trajectory in orange, and the prediction in blue.

Within the ACT, we have investigated the performance of such connectome-based reservoirs, specifically the Drosophila connectome, within the ESN framework for time-series prediction, demonstrating that connectome-derived topology and weight distributions can significantly improve robustness to overfitting compared with standard random reservoirs [23]. However, ESN implementations remain only a coarse abstraction of real neuronal dynamics.

Preliminary work has shown that neuronal cultures can be used as physical reservoirs [24–25]. Building on this, we aim to extend our previous research on multivariate chaotic time-series prediction (e.g. the three-body problem or 3BP) by moving from connectome-based simulations to connectome-inspired neuronal organoids. Our goal is to (i) demonstrate the ability of biological reservoirs to predict complex, multivariate chaotic time series, and (ii) systematically investigate how topological features of such reservoirs affect their dynamics and performance, and how real biolsogical reservoirs differ from artificial bio-inspired ones.

Proposed Methodology

Starting from the ACT current work on bio-inspired reservoir computing, there are currently three challenges to be tackled to achieve our goals:

1. **Stable neuronal cultures with designed topology:** Growing a system of neuronal cultures in which it is possible to have control over the topology of the neurons and the strength of the connecting channels and keeping such cultures alive for the time required to run experiments.
2. **Hardware for stimulation and readout:** Developing hardware that can deliver and receive electrical stimuli from the cell cultures, with the desired time and spatial resolution to be determined after preliminary experiments.
3. **Encoding/Decoding time-series signals:** Starting from our existing pipeline for generating 3BP trajectories and using ESNs, design an encoding of these trajectories into meaningful stimuli for the neuronal cultures. Determine suitable acquisition times and modalities to capture the dynamical state of the reservoir and to implement the readout. Investigate time-series encoding/decoding schemes ensuring compatibility with the chosen hardware and culture constraints.

The ACT implemented a pipeline to generate and test 3BP trajectories on an ESN and is transitioning towards a LSM approach. The encoding for LSMs is already closer to the constraints faced in real spiking systems but will still differ from that required for living neuronal cultures. This mapping must therefore be explored in detail with the partner university, based on the final hardware implementation.

We also plan to explore feedback architectures for generative time-series prediction in the biological setting, expanding our current work on feedback in simulated reservoirs. Feedback to the culture can be the delivered with the same electrical stimuli used for the input signal or through biochemical signalling. The precise specifications will be discussed with the partner university and are also heavily dependent on the final hardware implementation.

With regard to the hardware implementation and the cell culturing facilities, we are open to different solutions, provided they are supported by accompanying arguments and are based on documented scientific results. The overall goal of this study is to transfer a tested setup for reservoir computing for time-series prediction from a simulation environment to the real world. This will lead not only to the verification of hypotheses that have been so far only investigated theoretically but could highlight other important properties of biological reservoirs that have so far been overlooked by the scientific community.

ACT Contribution

The project will be conducted in close scientific collaboration with ACT researchers. ACT researchers will:

- Provide technical expertise in reservoir computing, biomimetics and astrodynamics for the generation of the signal of interest.
- Collaborate with the partner university on the design and the implementation of the software pipeline for experimental trials
- Lead the analysis and evaluation of the reservoir’s dynamics, including measures of the memory capacity and the prediction performance.

- Work closely with the partner university to evaluate preliminary data, ensuring that the system behaves as expected before and during the main experimental campaign, with the aim of minimising experimental overhead and costs while maximising scientific return.

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