A study on the correlation between resting-state functional connectivity and intrinsic neuronal activity of stochastic neural network models

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Main goal

- With the emergence of new stochastic models for biological neuron nets, also comes the need to check whether the proposed models are in same sense “good models” to described the dynamics of biological neural nets.
- For this, we will compare the resting-state functional connectivity and the neuronal connectivity of stochastic neural network models.

Functional connectivity

- Functional connectivity will be considered here as the temporal coherence between neuronal brain signals of anatomically separated brain regions.
- It is experimentally defined by measuring the correlation between resting-state blood oxygen level dependent (BOLD) functional magnetic resonance imaging (fMRI) time-series.
- University Medical Center Utrecht, The Netherlands (Van den Heuvel, M. P. and Stam, C. J. and Boersma, M. and Hulshoff Pol, H. E., 2008)
- They divide the brain into 68 regions.

Functional connectivity

- Recent observations report that resting-state BOLD fMRI time-series show a high correlation with concurrent fluctuations in neuronal spiking, suggesting a direct link between resting-state BOLD fMRI signals and intrinsic neuronal activity (Nir et al., 2008; Shmuel and Leopold, 2008).
- This supports the methodology proposed to validate the stochastic model.

Model - Galves and Löcherbach (2013)

- Consider a stochastic chain $(X_t)_{t\in\mathbb{Z}}$ taking values in $\{0,1\}^{\mathcal{I}}$ for some countable set of neurons $\mathcal{I}$ such that, for each $i \in \mathcal{I}$ and $t \in \mathbb{Z}$,

$$X_t(i) = \begin{cases} 1, & \text{if neuron } i \text{ has a spike at time } t \\ 0, & \text{otherwise.} \end{cases}$$

Model - Galves and Löcherbach (2013)

- For each $i \in \mathcal{I}$ and $t \in \mathbb{Z}$, let

$$L_t^i = \sup\{s < t : X_s(i) = 1\}$$

be the last spike time of neuron i strictly before time t.

- Let $\{W_{j\to i}; i, j \in \mathcal{I}\}$ be a family of "synaptic weights" such that, for $j \neq i$

$$W_{j\to i} \in \mathbb{R}$$

and for all j

$$W_{j\to j} = 0.$$

Model - Galves and Löcherbach (2013)

- At each time t, they consider that

$$P(X_t(i) = 1 | \mathcal{F}_{t-1}) = \phi_i \left(U_t^i, t - L_t^i \right),$$

where

$$U_t^i = \sum_j W_{j \to i} \sum_{s=L_t^i}^{t-1} g_j(t-s) X_s(i).$$

- That is, the probability of a spike of neuron i at time t is given by a function $\phi_i : \mathbb{R} \times \mathbb{N} \to [0, 1]$ that depends on the activities of all neuron such that $W_{j \to i} \neq 0$ until the last spike time of neuron i.

Expanded brain network

- The macroscopic architecture of the brain is a complex network of anatomically segregated regions interconnected by white matter pathways.
- This architecture can be unveiled using diffusion tensor imaging and deterministic streamline tractography.
- University Medical Center Utrecht (de Reus and van den Heuvel, 2013).
- They obtained a 68 by 68 matrix A with the information of strength of connections between regions.

Expanded brain network

The expanded brain network model was generated in the following way:

- Intra-regional connections:
  - In each region of the macroscopic brain network we put N neurons.
  - For each pair of neurons we put an egde between them with probability $d \in (0, 1)$.
- Inter-regional connections:
  - We considered all the pairwise combinations of brain regions and, for each pair, we used the probability given matrix A to generate connections between neurons in the two regions.

Simulation

- We calculate the time-varying mean neuronal activity of each brain region. The time series of this mean neuronal activity was smoothed using zero-phase digital filtering.
- We calculated the correlations between brain region neuronal activities for the simulated model.
- The correlation matrix of the simulated brain region neuronal activities was compared with the correlation matrix of the BOLD fMRI data by measuring the correlation coefficient between the two matrices.

Goal

- Let R_1 the correlation between the matrix only for region that $A_{ij} > 0$.
- For the null model $R_1 = 0.2798$
- For a successful prediction R_1 should then exceed 0.2798.

Simulation

- We used a simplified version of function ϕ_i defined by,

$$\phi_i(U_t) = \frac{1}{1 + \exp\{-2s(U_t - 0.5k)\}} \text{ for all neurons } i, \quad (1)$$

  where $U_t = \sum_{m=L_t^i}^{t-1} \sum_j W_{j \to i} X_m(j)$, k is the density of the graph and s is a parameter that defines the slope of the function.

- Therefore, we did not consider the aging factor of the function ϕ_i and $g_j(t) = 1$ for all $j \in \mathcal{I}$.