

Stochastic dimensional reduction on large biological neural networks

Vincent Painchaud^{1,3}, Nicolas Doyon^{1,3,4} and Patrick Desrosiers^{2,3,4}

¹ Département de mathématiques et de statistique, Université Laval, Québec, Canada

³ Centre interdisciplinaire en modélisation mathématique de l'Université Laval, Québec, Canada

² Département de physique, de génie physique et d'optique, Université Laval, Québec, Canada

⁴ Centre de recherche CERVO, Québec, Canada

Microscopic model

We consider a network of N neurons, whose states evolve stochastically according to a Markov process. The state of a neuron j at time t is a random variable $X_j(t)$ with possible values:

- 0, representing the *sensitive* state,
- 1, representing the *active* state, and
- i , representing the *refractory* state.

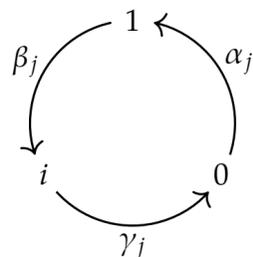


Fig. 1: States and transitions for neuron j .

The allowed transitions and their associated rates are described in Fig. 1. The transition rates β_j and γ_j are both constant, but the activation rate is a nonlinear function of the network's state:

Neuron j activates at a constant rate α_j only if its input exceeds its threshold θ_j .

The evolution of the network's state is governed by 3^N differential equations.

Dimension reduction

We split the network into n populations sharing similar properties, as described in Fig. 2. For each population J , we introduce analogs to the state of a neuron:

- S_J , the sensitive fraction of the population,
- A_J , the active fraction of the population,
- R_J , the refractory fraction of the population.

Since $S_J + A_J + R_J = 1$, only two fractions of each population, A_J and R_J , are needed.

We then see the expected values and covariances (including variances) of the A_J 's and R_J 's as dynamical variables, and obtain a reduced system of $n(2n + 3)$ differential equations.

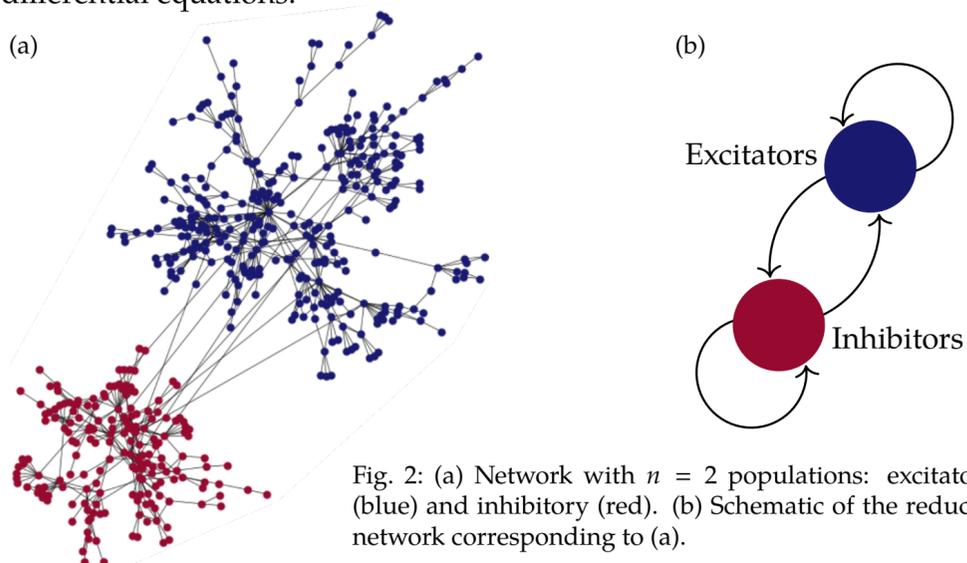


Fig. 2: (a) Network with $n = 2$ populations: excitatory (blue) and inhibitory (red). (b) Schematic of the reduced network corresponding to (a).

Reduced dynamical system

Let B_J be the input in population J and F_{θ_j} be the cumulative distribution function of the thresholds in J , assumed to be three times differentiable. We denote by α_J the mean value of the α_j 's in J , and follow the same pattern for other transition rates.

To simplify notation, let

$$A_J := \mathbb{E}[A_J], \quad R_J := \mathbb{E}[R_J], \quad S_J := \mathbb{E}[S_J], \quad \text{and} \quad B_J := \mathbb{E}[B_J],$$

and let $C_{XY}^{JK} := \text{Cov}[X_J, Y_K]$ with X and Y standing for either A , R , S or B . For any populations J and K (which can be the same), we have

$$\dot{A}_J = -\beta_J A_J + \alpha_J F_{\theta_j}(B_J) S_J + \alpha_J F'_{\theta_j}(B_J) C_{SB}^{JJ} + \frac{1}{2} \alpha_J F''_{\theta_j}(B_J) S_J C_{BB}^{JJ} \quad (1a)$$

$$\dot{R}_J = -\gamma_J R_J + \beta_J A_J \quad (1b)$$

$$\dot{C}_{AA}^{JK} = -(\beta_J + \beta_K) C_{AA}^{JK} + \alpha_K F_{\theta_k}(B_K) C_{AS}^{JK} + \alpha_J F_{\theta_j}(B_J) C_{AS}^{KJ} + \alpha_J F'_{\theta_j}(B_J) S_J C_{AB}^{KJ} + \alpha_K F'_{\theta_k}(B_K) S_K C_{AB}^{JK} \quad (1c)$$

$$\dot{C}_{RR}^{JK} = -(\gamma_J + \gamma_K) C_{RR}^{JK} + \beta_J C_{AR}^{JK} + \beta_K C_{AR}^{KJ} \quad (1d)$$

$$\dot{C}_{AR}^{JK} = -(\beta_J + \gamma_K) C_{AR}^{JK} + \alpha_J F_{\theta_j}(B_J) C_{RS}^{KJ} + \beta_K C_{AA}^{JK} + \alpha_J F'_{\theta_j}(B_J) S_J C_{RB}^{KJ} \quad (1e)$$

where the dot denotes time derivative.

Remarks

- System (1) generalizes Wilson–Cowan's model [3].
- System (1) is defined in $\mathbb{R}^{n(2n+3)}$, but physiologically speaking, the dynamical variables only make sense in a bounded subset of this space, which we call the *physiological domain*.

One population

Here we denote by c the connection coefficient from the population J to itself.

Theorem. System (1) always has a fixed point with zero covariances within the physiological domain, and any such fixed point is stable if $\beta_J > \alpha_J c \sup F'_{\theta_j}$.

Theorem. All fixed points of (1) within the physiological domain have zero covariances if $\beta_J > \alpha_J c \sup F'_{\theta_j}$.

Theorem. System (1) always has a fixed point with non-zero covariances.

Two populations

With a network as in Fig. 2, we observe that considering covariances can change qualitatively the long-term behavior of the system: as shown in Fig. 3, it expands the domain of parameters where limit cycles are possible.

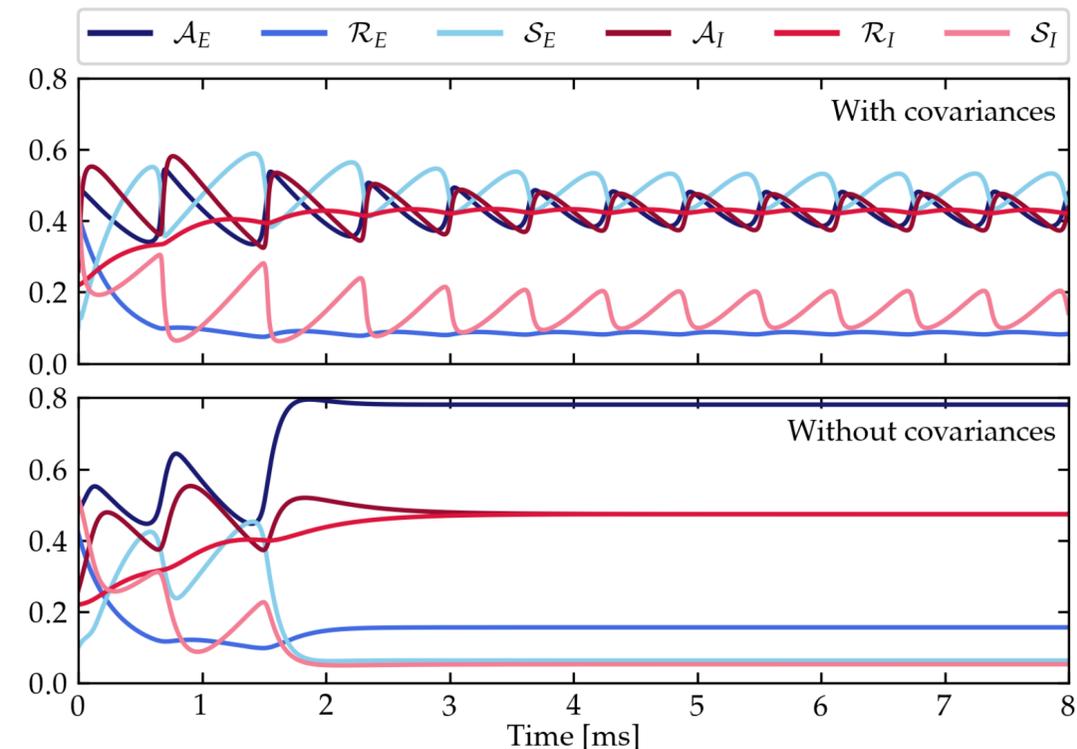


Fig. 3: Two solutions of the reduced dynamical system obtained numerically from the same initial expectations, but considering non-zero covariances for the solution on top, and neglecting them from the start for the solution at the bottom. The same network parameters were used in both cases. The labels E and I mean “excitatory” and “inhibitory”, respectively.

Possible generalizations to more populations

Simulations suggest that regimes as shown in Fig. 3 generalize to more populations. For instance, one can

- weakly connect another population to the network used in Fig. 3, or
- weakly connect two networks identical to that used in Fig. 3, and still observe qualitatively the same behavior, that is, a stable fixed point without covariances, and oscillations with them.

References

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