

Supplementary Material

Simulating a network with SFMs distributed on it

In the Results section, we have elucidated how simple systems could be embedded in larger networks, wherein each node encapsulates information pertaining to the original dynamics. This is achieved through the application of an orthogonal transformation to the simulated time series. Actually, and more correctly, the large-scale brain system, in which the information is distributed, should be the direct result of our simulations, without the help of the orthogonal transformation. To confirm this we arranged the dynamical equations of the systems illustrated to obtain synthetic data in which each time series directly contains inner low-dimensional behavior. Algebraically, the two ways of building such systems are identical. A test was performed using the JiTCSDE package and, having obtained the same results, we decided, for the sake of simplicity and to better present the method, to exhibit only the ones in the Results section.

The transformed system could be constructed as follows. Let $x = [x_1, \dots, x_N]$ be a set of state variables evolving in time according to the differential equation $\dot{x} = f(x)$, in which f is a nonlinear function. If $A = (a_{ij}) \in O(N)$ is an orthogonal matrix, with $AA^T = AA^{-1} = I$, we can then build a new set of state variables $y = [y_1, \dots, y_N] = Ax$, whose evolution is described by the following law

$$\dot{y} = A \dot{x} = Af(x) = Af(A^{-1}y) = Af(A^T y). \quad (A1)$$

Dynamical equations for the single nodes could then be formulated as

$$\dot{y}_i = \sum_{j=1}^N a_{ij} f\left(\sum_{k=1}^N a_{kj} y_k\right) \quad (A2)$$

where use has been made of the orthogonal group properties. From equations (1) and (A1) it turns out that we can simulate network activity in which SFMs are distributed in each node by using the scheme

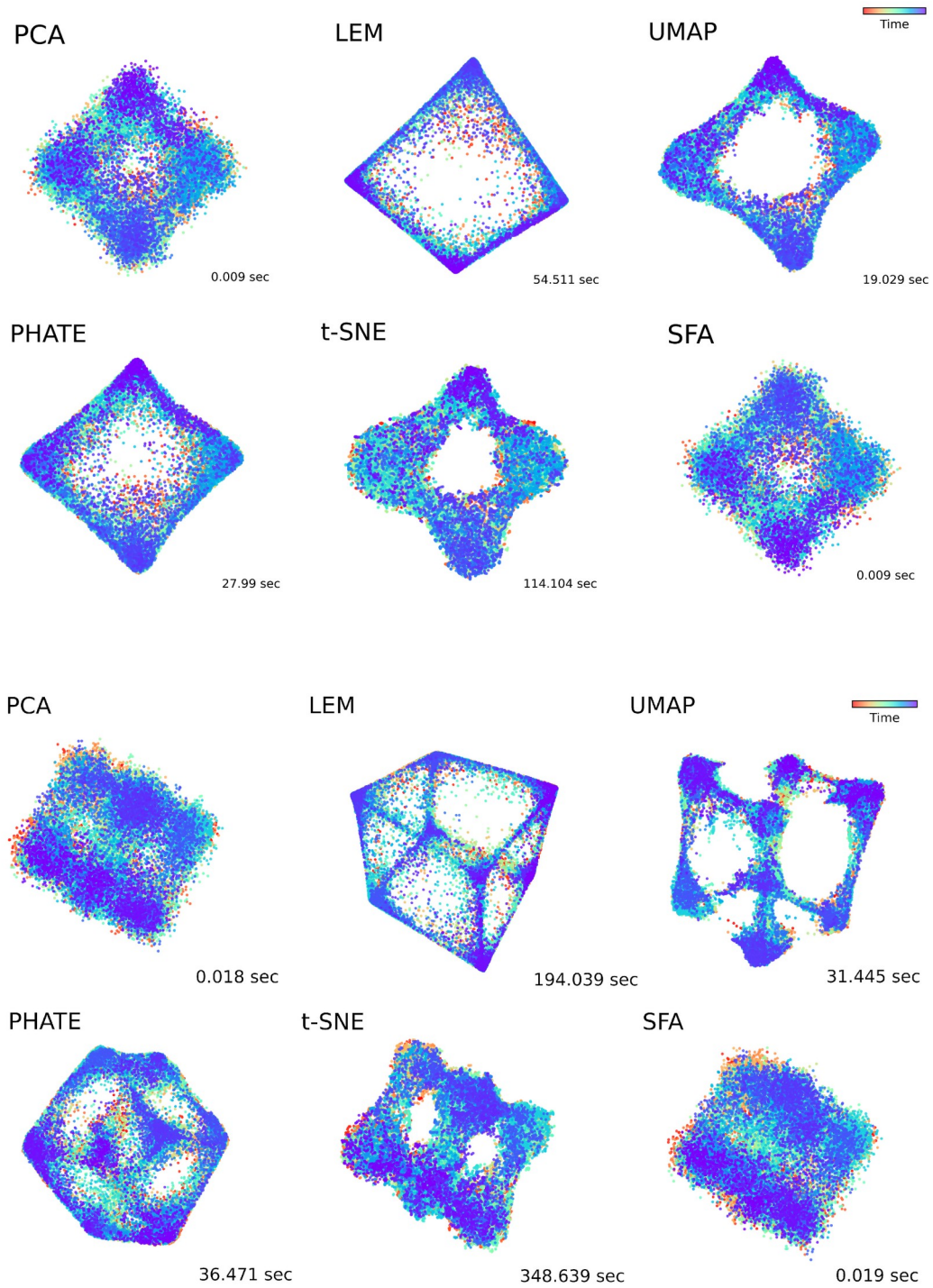
$$\dot{y}_i = \sum_{j=1}^N a_{ij} \left[1 - \left(\sum_{k=1}^N a_{kj} y_k \right)^2 \right] \sum_{k=1}^N a_{kj} y_k + G \sum_{l=1, l \neq j}^N \left(\sum_{k=1}^N a_{kl} y_k \right)^2 \sum_{k=1}^N a_{kj} y_k + \eta_j \quad (A3)$$

where the inner variables behave according to the model described in the Materials and Methods section (a, simple bistable model).

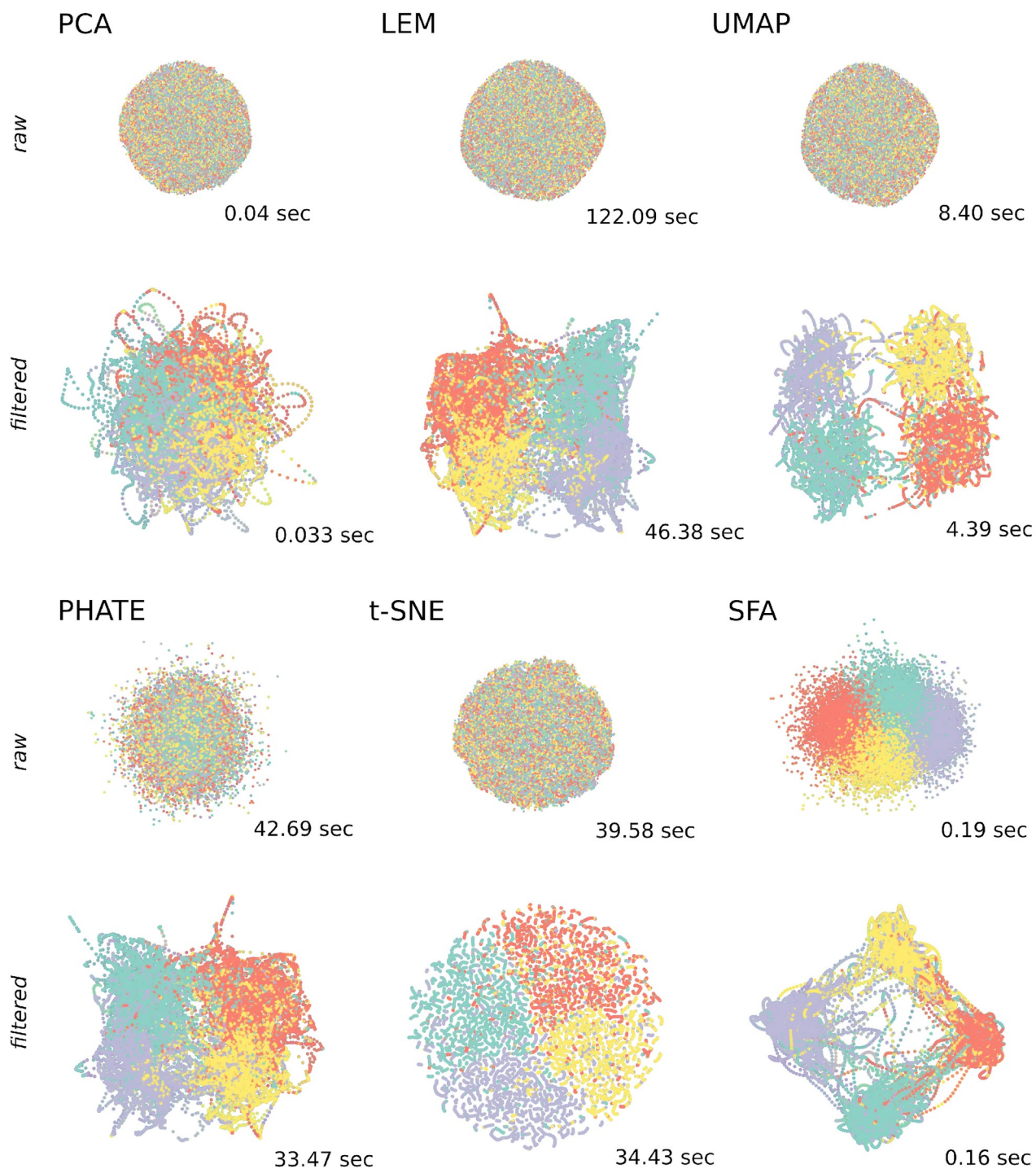
We assume now that our inner dynamics follows the model in the Materials and Methods section (b, large-scale brain model) through variables $x = [x_1, \dots, x_{2N}]$, where $x_i = V_i$, $i = 1, \dots, N$, represents the membrane potential and $x_i = r_{i-N}$, $i = N+1, \dots, 2N$, the firing rate in the Montbrio formulation. We could directly simulate the network activity in which SFMs are distributed using the following scheme for the single node dynamics

$$\begin{aligned} \dot{y}_i = & \sum_{j=1}^N a_{ij} \left[\left(\sum_{k=1}^{2N} a_{kj} y_k \right)^2 + \eta_j + J \sum_{k=1}^{2N} a_{k,j+N} y_k + I - \pi^2 \sum_{k=1}^{2N} a_{k,j+N} y_k + G \sum_{l=1, l \neq j}^{2N} J_{jl} \sum_{k=1}^{2N} a_{k,l+N} y_k \right] \\ & + \sum_{j=1}^N a_{ij+N} \left[\frac{\Delta}{\pi} + 2 \left(\sum_{k=1}^{2N} a_{k,j+N} y_k \sum_{k=1}^{2N} a_{k,j} y_k \right) \right] \end{aligned} \quad (\text{A4})$$

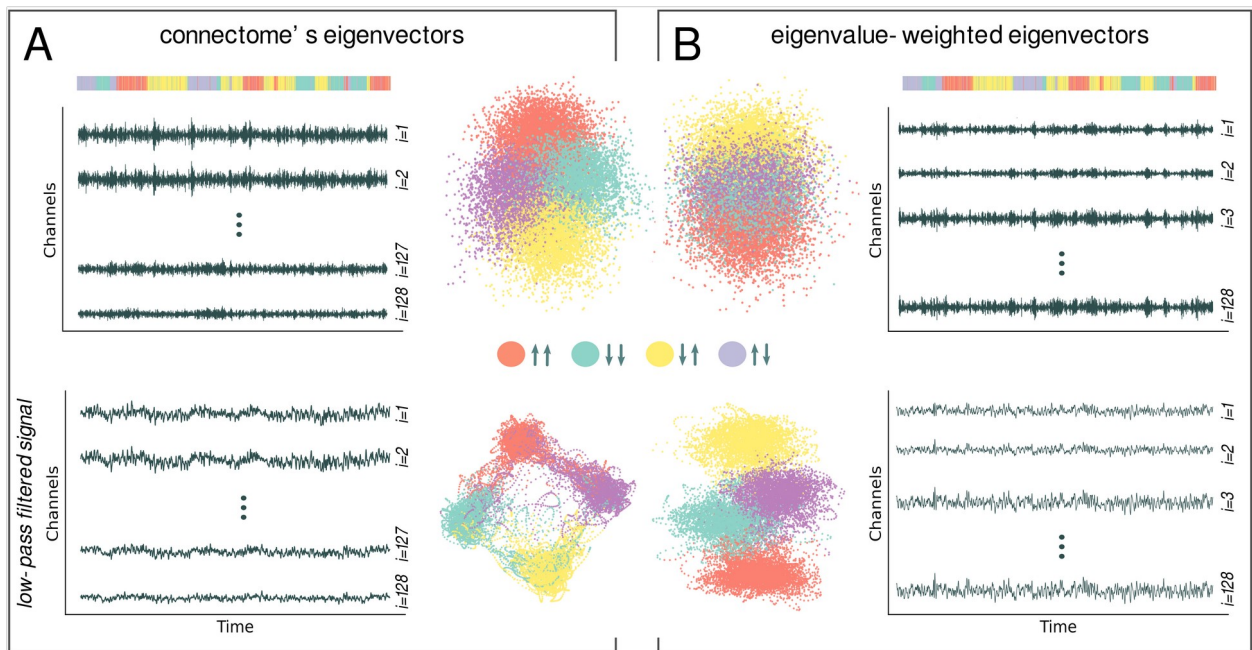
where now a_{ij} is the generic element of the orthogonal matrix $A \in O(2N)$.



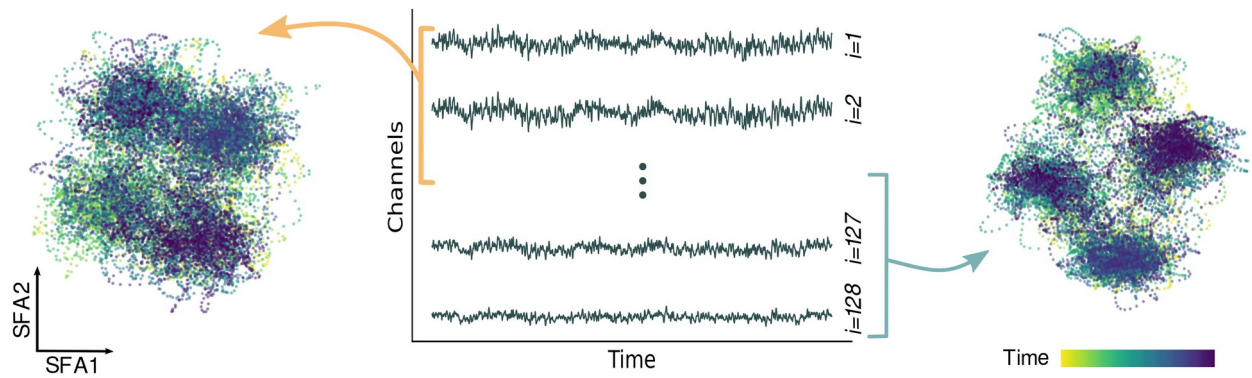
Supplementary Figure 1. Different unfolding techniques comparison (b). We compare the representations obtained when manifold extraction algorithms are performed on the time series obtained in the Results section (a), when $M=2$ (top) and $M=3$ (bottom) for $N=10$.



Supplementary Figure 2. Different unfolding techniques comparison for the EEG-like system. We compare the representations obtained when manifold extraction algorithms are performed on the raw time series (up) and on the low-pass filtered data (bottom) analyzed in Results section (b). The different colors reflect the configurations of the bistable two-modes system.



Supplementary Figure 3. Comparison of dynamics and low-dimensional manifolds derived from eigenvectors of the connectome and eigenvalue-weighted eigenvectors (exponentially decaying). The top row shows the results obtained from the original (non-filtered) EEG-like signals, while the bottom row displays the results after applying low-pass filtering to isolate slow dynamics. In **A**, the signals and manifolds are derived using only the eigenvectors of the connectome, while in **B**, they are derived from eigenvalue-weighted eigenvectors, where the eigenvalues decay exponentially to mimic the fast-decaying eigen-spectrum characteristic of human connectomes. Within each row, the first and fourth columns display the EEG-like time series. In the middle, the low-dimensional manifolds extracted via Slow Feature Analysis (SFA) for each case, allowing direct comparison of the structures resulting from the two transformations. For the non-filtered signals (top row), clustering in the low-dimensional manifold is slightly less distinct in the eigenvalue-weighted case compared to the eigenvector-only approach. After low-pass filtering (bottom row), the manifolds derived from the two transformations exhibit differences but still reveal identifiable patterns and clusters. These results demonstrate that while eigenvalue scaling introduces variations in the raw and filtered dynamics, the low-dimensional structures remain sufficiently robust to capture relevant features.



Supplementary Figure 4. The dynamics are distributed in each node of the system with varying weights. The first two components of SFA performed on the simulated system of Results section, part (b) on two distinct subsets of the EEG-like time series. The first two components of SFA are performed on the simulated system from the Results section, part (b), using two distinct subsets of the EEG-like time series. These subsets capture different proportions of the original latent dynamics, as determined by the weights from the gain matrix, illustrating how the choice of subset influences the resulting low-dimensional representation.