

## A Rosetta Stone for Neural Oscillators: Unifying Computational Models of Brain Dynamics

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Understanding brain dynamics requires models that capture the fundamental mechanisms of neural oscillations. This work aims to mathematically bridge the diverse computational models in neuroscience, elucidating the connections between their parameters and underlying principles. By transitioning from simple single-node oscillators to complex network-level frameworks, we provide a unified perspective that clarifies the relationships among various models.

We begin with single-node analyses to highlight essential oscillator properties. Starting with purely phase-based descriptions, such as phase spinors, we model the temporal evolution of individual oscillators. Progressing to phase-amplitude Hopf models, we incorporate amplitude dynamics, demonstrating how excitation-inhibition interactions influence both amplitude and phase responses. Further enhancing biological realism, single neural-mass equations introduce firing rates and membrane potentials, bridging the gap between abstract mathematical constructs and neuronal behavior.

Extending to network analyses, we explore the Kuramoto model for phase synchronization in large populations and the Stuart-Landau network for coupled amplitude-phase dynamics. More sophisticated neural mass models, including Wilson-Cowan, Jansen-Rit, and NMM2, integrate nonlinear transfer functions and explicit synaptic dynamics, capturing phenomena such as thresholding, saturation, and synaptic delays. These models provide a closer approximation to real neuronal and synaptic processes, facilitating a deeper understanding of collective brain activity.

A crucial aspect of our study is the incorporation of external perturbations—electrical and pharmacological stimuli—into the models. Electrical stimulation is modeled to influence membrane potentials and synaptic currents, while pharmacological agents modify synaptic

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efficacy and neuronal excitability. We demonstrate how these perturbations can shift oscillatory regimes, after synchronization patterns, and affect the stability of neural networks.

By comparing complex-valued and real-valued formulations, we highlight their respective strengths in amthematical elegance and physiological accuracy. This comprehensive mapping serves as a "Rosetta Stone" for population neural models, unifying abstract mathematical representations with biologically detailed frameworks. Our unified approach aims to provide researchers with a clear and elegant foundation for selecting appropriate models, balancing simplicity and realism to advance the understanding of neural processes, disease mechanisms, and therapeutic interventions.