

Building adaptable and reusable pipelines for investigating the features of slow cortical rhythms across scales, methods, and species

Robin Gutzen^{1,4}, Giulia De Bonis², Elena Pastorelli^{2,3}, Cristiano Capone², Chiara De Luca^{2,3}, Sonja Grün^{1,4}, Anna Letizia Allegra Mascaro^{5,6}, Francesco Resta⁵, Francesco Saverio Pavone⁵, Maria V. Sanchez-Vives^{7,8}, Maurizio Mattia⁹, Andrew Davison¹⁰, Pier Stanislao Paolucci², Michael Denker¹

¹ Institute of Neuroscience and Medicine (INM-6) and Institute for Advanced Simulation (IAS-6) and JARA-Institute Brain Structure-Function Relationships (INM-10), Jülich Research Centre, Jülich, Germany

² Istituto Nazionale di Fisica Nucleare (INFN), Sezione di Roma, Rome, Italy

³ Ph.D. Program in Behavioural Neuroscience, "Sapienza" University of Rome, Rome, Italy

⁴ Theoretical Systems Neurobiology, RWTH Aachen University, Aachen, Germany

⁵ European Laboratory for Non-linear Spectroscopy (LENS), University of Florence, Florence, Italy

⁶ Istituto di Neuroscienze, CNR, Pisa, Italy

⁷ Institut d'Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Barcelona, Spain

⁸ Institució Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, Spain

⁹ Istituto Superiore di Sanità, (ISS), Rome, Italy

¹⁰ Unité de Neurosciences, Information et Complexité, Neuroinformatics Group, CNRS FRE 3693, Gif-sur-Yvette, France

Making progress in neuroscience is increasingly a collaborative effort that requires insights obtained across data, methodologies, and models. Individual puzzle pieces must eventually be properly related to one another and integrated to frame the research in a coherent picture. In this process, often three questions arise: How to make results comparable? How to relate complementary, yet different methodological approaches to one another? How to incorporate and validate models based on these findings?

A prominent example of such a scenario is slow cortical waves which are persistently observed in sleeping and anesthetized subjects of various species and across various measurement techniques [1,2], as well as being expressed by various models. While slow waves are a ubiquitous phenomenon with a rich literature basis and have been proposed to be the default activity pattern of the cortical network [3], the diversity of the experimental data and the numerous different analytical methods, tools, and even terminologies makes it difficult to rigorously compare and interrelate results from the various sources to form a coherent understanding.

Here, we present an analysis pipeline for the study of slow wave activity to support quantitative comparisons of analysis results across data sources and algorithms. A key concept of the pipeline is modularity at the correct level of granularity in order to flexibly adapt, reuse, and extend it to a wide range of datasets and research questions. In the spirit of reproducibility, individual analysis blocks are built on a number of community-driven, open-source software tools, e.g., the workflow manager Snakemake (RRID:SCR_003475), the Neo (RRID:SCR_000634) library for data representation [4], the Elephant (RRID:SCR_003833) analysis toolbox, and the pipeline execution can be captured in the EBRAINS Knowledge Graph (<https://kg.ebrains.eu>).

This pipeline design enables multi-scale analyses of measured slow wave activity, which we demonstrate using ECoG [5,6,7] and Calcium Imaging [8,9] data of anesthetized mice. Furthermore, the integration of model data provides a basis for rigorous validation testing [10,11]. While the 'same method - different data' approach enables fair comparisons, the pipeline equally enables 'same data - different methods' benchmarking. Finally, we discuss how the re-usable and adaptable conceptual design helps to derive analysis pipelines for similar research endeavors to amplify collaborative research.

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