PROMEMO
CENTER FOR PROTEINS IN MEMORY

DANDRITE
Danish Research Institute of Translational Neuroscience
Nordic EMBL Partnership for Molecular Medicine

AARHUS UNIVERSITY

PROMEMO / DANDRITE Double Topical Seminar

Tuesday 10 September 2019

at 13:00-15:00

Auditorium 6, room 347, bldg. 1170, Aarhus University

13:00-14:00 Priyanka Rao-Ruiz

Postdoctoral Researcher

Department of Molecular and Cellular Neurobiology,
Center for Neurogenomics and Cognitive Research,
VU University Amsterdam,

Elucidating the Engram-specific Molecular Architecture of Memory Consolidation

Memory consolidation is a time-dependent neurobiological process that includes the stabilization of synapses that were potentiated during learning (synaptic/cellular consolidation) and the transfer of information from the hippocampus to the cortex (systems consolidation). Gene- and protein- dependent alterations are implicated in the synaptic and somatic events that underlie this memory process. These biochemical alterations occur in sparsely distributed and strongly connected networks of neurons spanning multiple brain regions that form a physical trace of memory in the brain, referred to as memory traces or engrams. Although considerable work has been done to causally identify the cellular circuitry of memory, the engram-specific molecular architecture of memory formation and storage remains largely unknown. The overarching aim of my laboratory is to map the transcriptome and proteome of cellular and systems consolidation by combining sensitive cell-sorting, RNA-Seq and Mass-spectrometric techniques of engram cells in the hippocampus and medial pre-frontal cortex.
We have recently demonstrated that memory trace cells in the Dentate Gyrus show a characteristic expression profile for the immediate early gene, Arc, which remains up regulated for several hours after a single conditioning session. This protracted expression of Arc enabled us to examine molecular profiles unique to engram cells after fear conditioning. A sensitive method of full-length transcriptome profiling and RNA- sequencing from as few as 10 engram cells or 10 non-activated neighboring cells revealed gene expression patterns distinctive to memory-trace neurons. Furthermore, engram- specific manipulation of identified molecular networks resulted in a profound memory deficit, indicating that persistent molecular mechanisms in a small percentage of DG granule cells drives the successful consolidation of recent contextual fear memories.

Reference: Rao-Ruiz, P. et al. Engram-specific transcriptome profiling of contextual memory consolidation. Nature communications 10, 2232, doi:10.1038/s41467-019-09960-x (2019).

Host: Marco Capogna, PROMEMO/DANDRITE, Dept. of Biomedicine, Aarhus University

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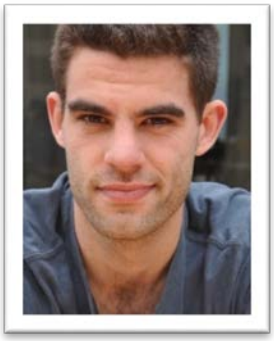

14:00-15:00 Ben Dichter

Lead Data Scientist,
Stanford University
&
Community Liaison, Neurodata Without Borders
Neurophysiology,
Lawrence Berkeley National Laboratory

Using the Neurodata Without Borders: Neurophysiology Standard to Access Tools and Drive Collaboration

Although we are collecting important and valuable neurophysiological data, sharing this data remains difficult. It is far too common for individual laboratories (even individual postdocs and students) to utilize different data formats and descriptions of their experiments. This wastes an extraordinary amount of time, and greatly increases the likelihood of (unintentional) errors in both analysis and description of data that may affect scientific results. Furthermore, the resulting datasets and analyses are difficult to share, presenting a serious barrier to replication and verification. Together, these hinderances can negate the benefit of large-scale collaborations to address the most challenging biomedical problems of our time.

In this talk I will present Neurodata Without Borders: Neurophysiology (NWB:N), a data standard for neurophysiology, providing neuroscientists with a common standard to share, archive, use, and build common analysis tools for neurophysiology data. NWB:N is designed to store a variety of neurophysiology data, including data from intracellular and extracellular electrophysiology experiments, data from optical physiology experiments, and tracking and stimulus data.

As the Community Liaison for NWB:N, my goal is to facilitate adoption and ensure that the NWB:N software ecosystem accelerates scientific discovery for its adopters. Since the official release of NWB:N 2.0 in January, the standard as seen extraordinary growth and adoption. I will report on the labs that have started to adopt the standard, the datasets currently publicly available, the tools that are being developed to create, visualize, analyze and understand NWB:N files, and the plan for the future.

This talk provides a rare opportunity for me to communicate with a European audience. After the talk I would be happy to schedule follow-up meetings to answer specific questions and learn about your data standard needs.

Host: Marco Capogna, PROMEMO/DANDRITE, Dept. of Biomedicine, Aarhus University