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Seminario IDIA/CMM

Speaker: Gonzalo Mena, Department of Statistics and Data Science Carnegie Mellon University, USA.

Título: A Statistical framework for the modeling of continuous phenotypical progression in Alzheimer's Disease.

Abstract: Throughout an organism's life, many biological systems transition through complex biophysical processes. These processes serve as indicators of the underlying biological states. Inferring these latent unobserved states is a key problem in modern biology and neuroscience. Unfortunately, in many experimental setups, we can, at best, obtain snapshots of the system at different times for different individuals, and one major challenge is reconciling those measurements. This formalism is particularly relevant in the study of Alzheimer's Disease (AD) progression, in which we observe in brain donors the aggregation of pathological proteins, but the underlying disease state is unknown. The progression of AD can be modeled by assigning a latent score - termed pseudotime - to each pathological state, creating a pseudotemporal ordering of donors based on their pathological burden.

This paper proposes a hierarchical Bayesian framework to model AD progression using detailed quantification of multiple AD pathological proteins from the Seattle AD Brain Cell Atlas consortium (SEA-AD). Inspired by biophysical models, we model pathological burden as an exponential process. The model's Theoretical properties are studied, using linearization to reveal convergence and identifiability properties. We provide Markov chain Monte Carlo estimation algorithms and show the effectiveness of our approach with multiple simulation studies across data conditions. Applying the methodology to SEA-AD brain data, we infer pseudotime for each donor and order them by pathological burden. Finally, we analyze the information within each pathological feature and utilize it to refine the model by focusing on the most informative pathologies. This lays the groundwork for suggesting future experimental design approaches.

This talk is based on the following papers

https://www.biorxiv.org/content/10.1101/2024.06.10.597236v1
https://www.biorxiv.org/content/10.1101/2023.05.08.539485v3

The main open-source resource is available at

https://sea-ad.org/

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Bio

Gonzalo Mena is an Assistant Professor in the Department of Statistics and Data Science at Carnegie Mellon University. His main research aim is to develop robust, efficient, and theoretically sound statistical methodology for tackling challenging problems involving data in the life sciences.

Before joining CMU he was a Florence Nightingale Bicentennial Fellow and Tutor in Computational Statistics and Machine Learning at the University of Oxford. Before that, he was a Data Science Initiative Postdoctoral Fellow at Harvard University, mentored by Pierre Jacob. Previously, he obtained PhD in Statistics at Columbia University, advised by Liam Paninski. He is originally from Santiago, Chile. There, he obtained a B.Sc. in Mathematical Engineering at Universidad de Chile.

foto: https://gomena.github.io/images/GonzaloLight2.jpg

Fecha:Martes 25 de Junio del 2024 a las 15:00 hrs.
Lugar: Sala de Seminarios Multimedia CMM, sexto piso, torre norte de Beauchef 851.

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