



Life Sciences Seminar

Exploiting data structure: from gene expression to evolution

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Host: Nick Barton

Genome scale molecular datasets are often highly structured, with many correlated observations. This general phenomenon can be related to the underlying data generating process. In gene expression assays, groups of gene are co-regulated through shared transcription factors and signaling pathways. Likewise, for evolutionary data, correlated substitution rates arise due to shared evolutionary pressure. In the first half of the talk we will present a new constrained matrix decomposition approach that directly aligns a lower dimension representation with known biological pathways. Our method provides state-of-the-art accuracy in reconstructing known upstream variables through a biologically interpretable decomposition. In the second half we will discuss a computational approach for modeling the relationship between phenotypes and evolutionary rates and present new results on evolutionary correlates of life-history traits.

Tuesday, March 6, 2018 09:00am - 10:00am

Big Seminar room Ground floor / Office Bldg West (I21.EG.101)



This invitation is valid as a ticket for the ISTA Shuttle from and to Heiligenstadt Station.

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<https://ista.ac.at/en/campus/how-to-get-here/> The ISTA Shuttle bus is marked ISTA Shuttle (#142) and has the Institute Logo printed on the side.