ALMA MATER STUDIORUM
UNIVERSITÀ DI BOLOGNA
DEPARTMENT OF
PHARMACY AND BIOTECHNOLOGY

CMB PhD School Seminars 2022-2023

On **June 15th, 2023**
at **15:00 (Bologna time)/9:00 (New York time)**
online only on Microsoft Teams

https://teams.microsoft.com/l/meetup-join/19%3aN09c0NIyEssBnF7ObCyDOQwkgDWm1qdd9f7F2nJV9fw1%40thread.tacv2/1631519544944?context=%7b%22Tid%22%3a%22e99647dc-1b08-454a-bf8c-699181b389ab%22%2c%22Oid%22%3a%225a941351-ef41-4aa4-8771-fa50a6d62ca1%22%7d

Alexander Lachmann, PhD

RESEARCH ASSISTANT PROFESSOR in the Ma'ayan Laboratory in the Department of Pharmacological Sciences and the **Mount Sinai** Center for Bioinformatics (**New York City**, USA)

will hold a seminar on

"Using big data to propel the prediction of gene function"

The 45-minutes scientific talk by Prof. Lachmann will be followed by a 30-minutes "Meet the speaker" Q&A session with the PhD students.

ABSTRACT

Gene-gene co-expression correlations measured by mRNA-sequencing (RNA-seq) can be used to predict gene annotations based on the co-variance structure within these data. Many approaches yield diminishing returns when increasing the number of available samples. ARCHS4 is a large gene expression repository of over one million uniformly processed RNA-seq samples. With the publicly available data, large portions of the possible gene expression space are accessible for machine learning algorithms. PRediction of gene Insights from Stratified Mammalian gene co-EXPression (**PrismEXP**) uses the Simpsons Paradox for improved gene annotation predictions based on RNA-seq gene-gene co-expression data. Predictions made with PrismEXP outperform predictions made with the global cross-tissue co-expression correlation matrix approach on all tested domains, and training using one annotation domain can be used to predict annotations in other domains.

BIOGRAPHICAL SKETCH

Professor Alexander Lachmann first obtained his *Diplom* in Computer Science in 2008 at the University Aachen (Aachen, Germany) and then his PhD in Biomedical Informatics in 2016 at the Califano Lab, Systems Biology Department, Columbia University (New York, NY, USA). He currently works as a Research Assistant Professor at the Ma'ayan Laboratory in the Department of Pharmacological Sciences and the Mount Sinai Center for Bioinformatics (New York, NY, USA). He is author of more than 50 publications and developed several bioinformatic softwares. His areas of specialization include computa7onal biology, big data analytics and cloud computing.

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