

SEMINAR

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Hosted by Dr Lau On Sun

Supervised learning of gene regulatory networks: from synthetic networks to real-world systems



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Characterization of gene regulatory network (GRN) interactions provides a stepping stone to understanding how genes affect cellular phenotypes. Yet, despite advances in profiling technologies, GRN reconstruction from gene expression data remains a pressing problem in systems biology. Here I present a supervised learning approach, GRADIS, which utilizes support vector machine to reconstruct GRNs based on distance profiles obtained from a graph representation of transcriptomics data. By employing data from *Escherichia coli* and *Saccharomyces cerevisiae* as well as synthetic networks from the DREAM 4 and 5 network inference challenges, we demonstrate that our GRADIS approach outperforms the state-of-the-art supervised and unsupervised approaches. This holds when predictions about target genes for individual transcription factors as well as for the entire network are considered. We employ experimentally verified GRNs from *E. coli* and *S. cerevisiae* to validate the predictions and obtain further insights in the performance of the proposed approach. Our GRADIS approach offers the possibility for usage of other network-based representations of large-scale data, and can be readily extended to help the characterization of other cellular networks, including protein-protein and protein-metabolite interactions.