

Systems Infection Biology Seminar Series

Division of Clinical Microbiology

Contextualization of Molecular Network Models and their Application to Cancer Biology



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Abstract: We develop fast and powerful large-scale data integration methods which enable the reconstruction of context-specific molecular networks, e.g. for a given disease, patient group or individual patient. The fastcore family of algorithms allows the integration of large-scale gene expression data and other data types with generic metabolic reconstructions for producing specific molecular metabolic networks. This is powered by an efficient linear programming approach, which allows to obtain a close-to-optimal minimal network given a core set of metabolic reactions. Largely applied also by other teams, these algorithms have been included in a community-effort toolbox. This has lately been extended with a novel dynamic Flux Balance Analysis approach for multi-tissue metabolic modelling and allows now also for simulating disease-specific metabolic blood level alterations.

Based on these and other state-of-the-art computational biology, data science and machine learning approaches, we developed a variety of fruitful collaborations, notably in cancer research. E.g. we employ the reconstructed cancer specific molecular networks for identifying promising specific targets and to suggest novel treatment strategies. Drug repositioning thereby aims at reorienting approved drugs to novel disease indications. In proof-of-concept studies we used fastcore to predict a number of non-cancer drugs to be effective in colorectal cancer or melanoma, while not harming healthy control tissue. The experimental validation gave superior results compared to large-scale screening efforts.

Date: 01 June 2023

Time: 14:30

Place: Von Behring, ANA Futura, Plan 9

Zoom: <https://ki-se.zoom.us/j/69313579653>

https://wwen.uni.lu/research/fstm/dlsm/people/thomas_sauter



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