

CONFÉRENCE

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Contextualization of Metabolic Network Models and their Application to Drug Repurposing

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Possibilité de participer en visioconférence via Teams :

https://teams.microsoft.com//meetup-join/19%3ameeting_YTcwZjl3ZmMtZjAyZi00MzRjLWFiMjltZDhmNGY2OWZlZGJi%40thread.v2/0?context=%7b%22Tid%22%3a%22158716cf-46b9-48ca-8c49-c7bb67e575f3%22%2c%22Oid%22%3a%2202ba1466-e81f-41ea-9262-be5a2fc4ea14%22%7d

Synopsis

Mathematical modeling of metabolic networks (Constraint-Based Reconstruction and Analysis, COBRA) is a powerful tool to study metabolism on a genome-scale level. It allows to discover the activity of pathways of interests, the amount of produced or exchanged metabolites, and to elucidate essential and specific metabolic genes amongst many other applications. In this talk, Prof. Sauter presents state-of-the-art computational biology, data science, and machine learning approaches and their applications in cancer research. His group has developed 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, and increase the predictive power of such metabolic models. For instance, cancer specific molecular networks have enabled identifying promising specific targets and to suggest novel treatment strategies. Drug repurposing thereby aims at reorienting approved drugs to novel disease indications. In proof-of-concept studies, several non-cancer drugs were predicted to be effective in colorectal cancer, melanoma, or glioblastoma, while less harmful to healthy control tissue. The experimental validation gave superior results compared to large-scale screening efforts. It was also shown that synergistic effects of such metabolic drugs in combination with state-of-the-art targeted signaling drugs are possible.

Organisation et contact

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