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INTEGRATIVE APPROACHES AND WORKFLOWS TO IDENTIFY DISEASE SPECIFIC BIOMARKERS AND THERAPEUTIC CANDIDATES

ABSTRACT

Unravelling mechanisms underlying diseases for the prediction of disease markers has motivated the development of various systems biology approaches. Key challenges for the development of mathematical models to mimic the real biological scenario is (i) the size of interacting biological components, (ii) the nonlinear nature of spatio-temporal interactions and (iii) feedback loops in the structure of interaction networks.

Exploring large scale networks is an art where several analytic tools are integrated in a computational workflow to identify disease specific small regulatory modules. These small modules are subjected to a more detailed analysis using mathematical modeling for the prediction of disease signatures, i.e. set of network derived diagnostic/prognostic biomarkers.

I shall discuss an integrative workflow to study large-scale biochemical disease networks by combining techniques from bioinformatics and systems biology in the context of tumor metastasis. In particular, I will highlight methodology using an algorithm employing multiobjective optimization concepts to rank and select key regulatory motifs mainly responsible for network dynamics and helps in generating process specific hypotheses on which a systems biology model can be constructed for the excellent guesswork of disease markers and therapeutic candidates.