

Algorithmic Challenges in Mass Spectrometry and Systems Biology

Benno Schwikowski
The Institute for Systems Biology, Seattle, USA

Abstract: Cell biology is in the middle of a paradigm change where approaches focusing on the biochemically oriented understanding of single genes are slowly replaced by the systems approach that views systems of genes and proteins in their network context [1]. In this talk we will examine a number of new computational challenges associated with this approach, from various aspects of interpreting peptide mass spectra, to the visualization and integration of heterogenous data types in the molecular network context [2-5].

References:

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