

INVITED LECTURE H12

Identifying protein complexes from protein interactome maps

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Protein complexes are fundamental for understanding principles of cellular organizations. However, most protein interactome maps are still essentially an in vitro scaffold. Furthermore, these protein interactome maps contain a significant amount of noise interactions, as well as missing many real interactions. It is thus an important challenge to reliably deduce in vivo protein interactions and to identify membership in the same protein complexes. In this talk, we describe our recent work on computational techniques for protein complex prediction from noisy incomplete protein interaction network data. Here, we first develop an effective and efficient approach to remove false-positive protein interactions and recover missing protein interactions. The approach relies on a common neighbourhood expectation maximization. Then we show that all popular methods for identifying protein complex prediction from protein interaction networks benefit significantly from the cleansed networks by our approach. In particular, even simple-minded method such as predicting maximum cliques as complexes yields over 40% recall at over 90% precision on cleansed networks.