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Identifying Protein Interaction Subnetworks by A Bootstrapping Markov Random Field-based Method

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Abstract

Identification of protein-protein interaction (PPI) networks has become increasingly important to our global understanding of the molecular mechanisms that drive cancer. We present a new method, based on a bootstrapping Markov random field (BMRF) framework, to improve subnetwork identification for mechanistic studies of breast cancer. The method follows a maximum-a-posteriori (MAP) principle to form a novel network score that explicitly considers pairwise gene interactions in PPI networks, and searches for subnetworks with maximal network scores. To improve their robustness across data sets, a bootstrapping scheme is implemented to statistically select high confidence subnetworks. We first compared the BMRF-based method with existing methods on simulation data to demonstrate its improved performance. We then applied our method to breast cancer data to identify PPI subnetworks associated with breast cancer progression and/or tamoxifen resistance. The experimental results show that not only an improved prediction performance can be achieved by the BMRF approach when tested on independent data sets, but biologically meaningful subnetworks can also be revealed that are relevant to breast cancer and tamoxifen resistance.

Biography

Li (Lily) Chen is a research associate in the Department of Pathology at The Johns Hopkins University, School of Medicine. She received a PhD in Electrical Computer Engineering from Virginia Tech in 2010. Her research interests include developing mathematical algorithms and statistical approaches to analyze variety of biological data using machine learning and data mining techniques, and integrating multiple biological data sources/types to understand cancer related biological mechanism for biomarker identification.