

Constructing Tumor-Specific Gene Regulatory Networks Based on Samples with Tumor Purity Heterogeneity

Pei Wang, PhD

Associate Professor

**Department of Genetics and Genomic Sciences
Icahn School of Medicine at Mount Sinai**

ABSTRACT

Tumor tissue samples often contain an unknown fraction of normal cells. This problem well known as tumor purity heterogeneity (TPH) was recently recognized as a severe issue in omics studies. Specifically, if TPH is ignored when inferring co-expression networks, edges are likely to be estimated among genes with mean shift between normal and tumor cells rather than among gene pairs interacting with each other in tumor cells. To address this issue, we propose TSNet a new method which constructs tumor-cell specific gene/protein co-expression networks based on gene/protein expression profiles of tumor tissues. TSNet treats the observed expression profile as a mixture of expressions from different cell types and explicitly models tumor purity percentage in each tumor sample. The advantage of TSNet over existing methods ignoring TPH is illustrated through extensive simulation examples. We then apply TSNet to estimate tumor specific co-expression networks based on breast cancer expression profiles. We identify novel co-expression modules and hub structure specific to tumor cells.

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LEPH 115, 60 College Street

Lunch at 11:45 AM in LEPH 108