Systems Biology Approach to Analysis of Cancer Heterogeneity

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We consider exhibiting cancer characteristics as diversity of molecular networks. Recently, we developed probabilistic graphical model-based computational method termed NetworkProfiler for estimating gene regulatory networks of each patient sample from RNA expression profile data. Based on NetworkProfiler, we succeeded in finding sub-networks whose structure is changed according to cell (patient) status such as Epithelial-Mesenchymal Transition (EMT), relapse free survival time or drug sensitivity; those are called modulator and must be given prior to the gene network construction. On the other hand, by focusing on a specific sub-network, we can explore potential modulators that strongly affect activity of the sub-network. However, the computation of this task is very hard and requires the use of super-computer. In this talk, we introduce the algorithm of NetworkProfiler together with representative examples and show the results of modulator search related to cancer malignancy or drug sensitivity by RNA expression data of various types of cancer cells.

Key Words: RNA expression data, gene network, variant coefficient model, sparse learning