AJ0947

がん多様性の理解を目指したゲノムビッグデータ解析

Genomic Big Data Analysis towards Understanding 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 cells' (patients') 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. Also, because we have huge number of estimated gene networks, each gene network consists of about ten thousands of genes, more than the input RNA expression data, the output, i.e., gene networks, seems a big data set. 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. We used over 700 microarray gene expression data and over 100 drug sensitivities, over estimated 70,000 gene networks were obtained. We further analyze this network dataset to elucidate the sub gene networks defining the sensitivities of cancer cells against each of drugs.

Cancer Heterogeneity, Gene Network, RNA expression, Statistical Modeling, High Performance Computing

ご注意

ここで表示されている改行位置などのレイアウトは、抄録集編集時に変更させて頂くことがございますこと、予めご了承ください。