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Detection of molecular candidates responsible for phenotype changes by computational analysis of omics data

オミックスデータ数理解析による表現型変化の要因となる分子候補の検出

Katsuhisa Horimoto / 堀本　勝久
Computational Biology Research Center (CBRC)
National Institute of Advanced Industrial Science and Technology (AIST)
産業技術総合研究所　生命情報工学研究センター

Recently, we proposed a new approach for analyzing omics data. Our approach is distinctive from previous ones. In contrast to previous approaches in which molecular data are unified by several mathematical ways to describe phenotype data, from “bottom-up” view point, we adopt a “top-down” approach, by focusing on the phenotype difference between samples, rather than those between molecular data. The performance of our approach was examined for the progression data from diabetes rats and the proteomics data from lung cancer cell lines, and these analyses revealed a set of molecular functions more clearly, in comparison with those by a standard “bottom-up” approach.

Keywords : phenotype, omics data, computational systems biology