

# Data integration matters to explore (epi)omics data derived from human diseases

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## Abstract

Recently, several 'omics' technologies enable quantitative measuring of the abundance of various biological entities in a large-scale, and thus allow comparison of their variation between different physiological states on a genomic scale. Popular 'omics' platforms include as follows: transcriptomics, which measures mRNAs or miRNAs; methylomics, which measures levels of global methylation, and proteomics which measures global abundance of protein expression, etc.. No single 'omics' analysis can fully reveal the complexities of fundamental biology, and thus integration of multiple layers of information, the multi-'omics' approach, is required to acquire a precise picture. Some attempts have already been made recently to integrate 'multi-omics' datasets in various biological systems and the results have indicated that the approach is a powerful tool for understanding the functional dynamics of total cellular systems. Bioinformatics has thus essential roles in the analyses of all areas of omics studies. I'm going to introduce part of our efforts for integrating microbiome, transcriptome, and methylome data by Bioinformatics for understanding underlying mechanisms of human diseases such as cancers and heart disease.