Life Sciences

Unlocking Cellular Mysteries: Advancements in Single-Cell Omics Analysis with Genome-Scale Metabolic Modeling

The widespread applications of single-cell technologies have generated a large amount of single-cell data, resulting in a growing need for single-cell data analysis and interpretation methods. While methods such as machine learning allow for single-cell data analysis, they cannot interpret the data very well.

Genome-scale metabolic models (GEMs) contain a priori metabolic network knowledge and have become a powerful tool for integrating and interpreting omics data from bulk samples. Therefore, GEMs may also be used to analyze single-cell data, and this field is indeed emerging. Integrative analysis of single-cell data with GEMs is expected to reveal discoveries in cell metabolism and explore metabolic differences between cell types, even within complex tissues.

Recently, Dr. CHEN Yu from the Shenzhen Institute of Advanced Technology (SIAT) of the Chinese Academy of Sciences and his collaborator Dr. Eduard J Kerkhoven from Chalmers University of Technology, Gothenburg, Sweden, retrospectively examined the methods developed for integrating bulk omics data with GEMs.

The result was published in the *Current Opinion in Biotechnology* on February 15, entitled "*Single-cell omics analysis with genome-scale metabolic modeling*."

Integrating single-cell data into GEMs appears to be quite simple at first sight since methods developed for bulk data only need to be adapted to single-cell data. Therefore, this article first introduces two categories of standard methods for integrating bulk omics data with GEMs. The first one is model extraction, which removes inactive reactions from the reference GEM, including the complete metabolic reaction set annotated by the genome, based on omics data to generate context-specific models, such as tissue or organ-specific models. The second one is to use omics data as constraints to improve metabolic flux prediction. Subsequently, researchers introduce current methods of using GEMs to analyze single-cell data, similar to those used for analyzing bulk data.

"We summarize the challenges, mainly stemming from the limitations of single-cell technologies themselves," said Dr. CHEN, the first author of this paper.

While GEMs are mainly used to analyze single-cell RNAseq data, with the development of single-cell proteomics and metabolomics, it is believed that GEM-aided analysis of multi-omics of single cells will come true soon.

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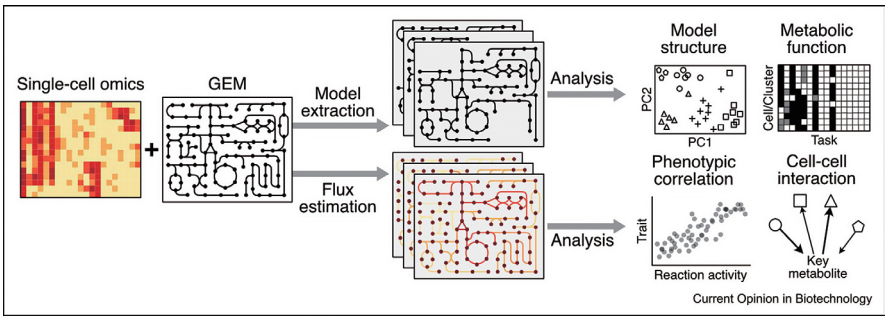

Single-cell omics analysis with GEMs. (Image by SIAT)

(Source: SIAT)