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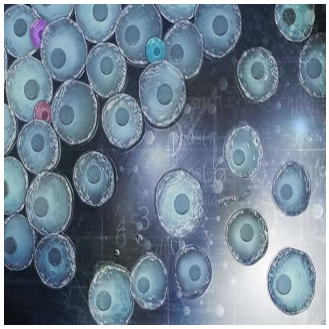
New Method Improves Genomics Analyses



A novel technique developed by scientists at The European Molecular Biology Laboratory's European Bioinformatics Institute (EMBL-EBI) allows the analysis of RNA sequence data enabling researchers to identify new subtypes of cells.

Single-cell RNA-sequencing technology is relatively new and helps scientists understand how genes are expressed in different types of healthy tissue and in cancers. Researchers can get data on the gene-expression profiles of hundreds of individual cell types. However, the single-cell transcriptome profiles are fairly complex making it a challenge to make sense of the data.

Till now, there wasn't a robust method that would not only identify subtypes but also deal with confounding factors. This new single-cell latent variable method (scLVM) allows researchers to detect hidden sub-structures and enables them to identify relevant biological signals.

"We've defined how factors such as cell-cycle stage, measurement noise or biological processes can be taken into account, making it possible to create a more accurate picture of gene expression in different cell types and subtypes," says Florian Büttner, who led the research at EMBL-EBI as an EMBO Visiting Scientist from the Institute of Computational Biology at Helmholtz Zentrum München. "Combining single-cell analyses with statistical methods lets us identify cell types that would otherwise remain undetected."

According to Oliver Stegle, Research Group Leader at EBML-EBI, the actual goal is not to just to have gene expression data from cells but to also have a way to identify and correct the underlying factors that differentiate individual cells. This new model accounts for relatedness between cells, identifies potentially confounding variables and removes them. It also helps in finding new sub-types and identifies variables that were previously unknown.

The ability to do such an analysis is critical for medical research and can enable scientists to explore the pathogenesis of various diseases. With this novel technique, it is now possible to create detailed cell profiles using single-cell genomics.

Source: European Bioinformatics Institute EMBL-EBI

Image Credit: Spencer Phillips, EMBL-EBI

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