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Singapore elevates analysis of genomic data with breakthrough mathematical technique

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Harnessing manifold fitting techniques to overcome hurdles in data analysis



A novel approach for analysing single-cell RNA sequencing (scRNA-seq) data has been unveiled by researchers at the National University of Singapore (NUS). This method promises to enhance both the precision and speed of data interpretation, potentially accelerating progress in numerous areas of biomedical investigation, including studies on cancer and Alzheimer's disease.

The innovative framework, dubbed scAMF (Single-cell Analysis via Manifold Fitting), was developed by a team of scientists led by Associate Professor Zhigang Yao from the Department of Statistics and Data Science at the NUS Faculty of Science.

The framework employs advanced mathematical techniques to fit a low-dimensional manifold within the high-dimensional space where the gene expression data are measured. By doing so, scAMF effectively reduces noise while preserving crucial biological information. This allows for more accurate characterisation of cell types and states.

This research was done in collaboration with Professor Yau Shing-Tung at Tsinghua University, China.

Building on the success of scAMF, the research team is now developing a novel framework for constructing high-resolution, multiscale cell atlases. This new approach aims to overcome current methodological limitations in cell atlas construction, such as challenges in identifying small cell populations and outdated unsupervised learning techniques.

This ongoing research promises to push the boundaries of single-cell analysis even further, potentially revolutionising our understanding of cellular diversity and function across various biological systems.