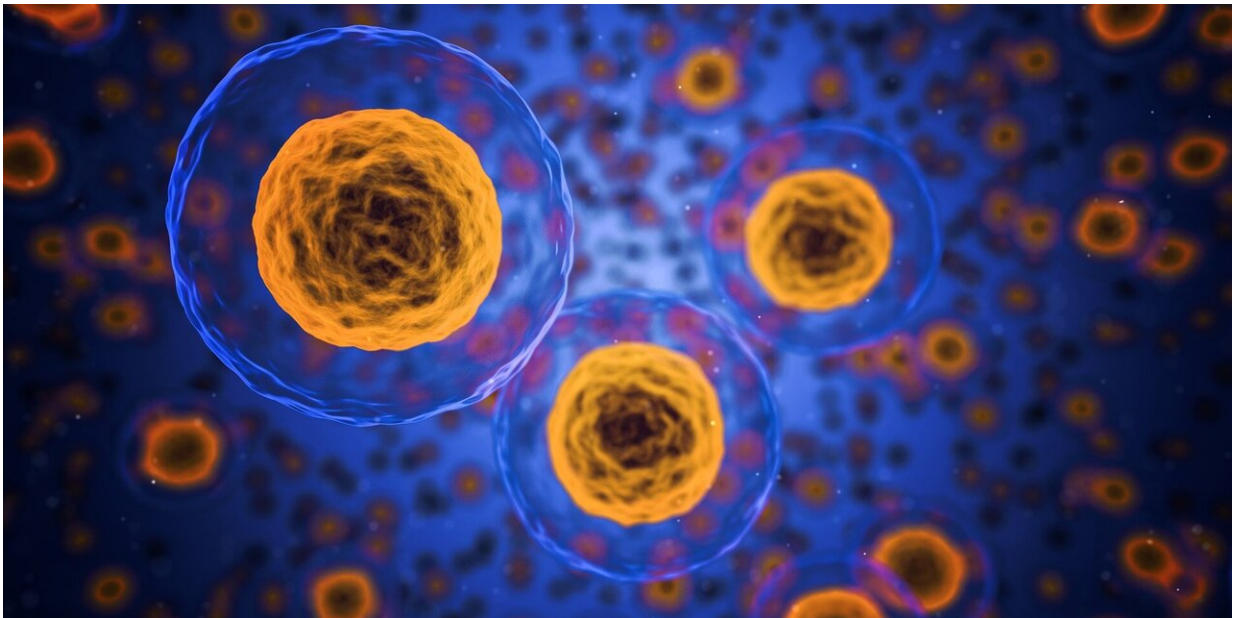


# New tool for understanding cells in health and disease

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A first-of-its-kind data analysis platform is enabling researchers to select the best tool for interpreting the overwhelming amounts of data generated by single-cell research.

Accurately making sense of these datasets will help to explain the vital and varied roles cells play in health and disease. The platform, CellBench, was published today in *Nature Methods*.

The freely accessible platform, which includes [software](#) and several gold standard datasets compares the performance of thousands of different [single-cell](#) analysis options, enabling researchers to identify the best method for the questions they wish to answer.

The project was led by Associate Professor Matthew Ritchie and Mr Luyi Tian from the Walter and Eliza Hall Institute of Medical Research, along with Dr. Kim-Anh Lê Cao and Mr Al J Abadi at the University of Melbourne.

## **Making sense of mass data**

Much is still unknown about the trillions of cells in the human body. In the quest to better understand cells and the role they play in health and disease, a technique called single-cell sequencing has become a hot research field.

Over the past five years there has been an explosion of new analysis tools for interpreting single-cell data. This has left researchers with hundreds of options to choose between in the challenging task of interpreting large and complex biological datasets.

Associate Professor Ritchie said the ability to identify and define each cell and its activity was invaluable for preventing and treating disease.

"The challenge is that a colossal amount of complex biological data is generated from single-cell studies. Our platform offers a solution to this by helping researchers accurately and efficiently make sense of the overwhelming amounts of information from their studies," he said.

## **Ensuring gold standard analysis**

Dr. Kim-Anh Lê Cao said choosing the right data analysis tool is crucial for avoiding misleading results or the incorrect biological interpretation of data.

"One of the biggest challenges we face in this area of research is our ability to compare the efficiency of all analysis methods currently available. This can only be done if we have good data like CellBench to do this benchmarking.

"CellBench is already enabling researchers to choose the right analysis method and generate meaningful and accurate conclusions from their data," she said.

Associate Professor Ritchie said it was clear there was a real demand for a single-cell analysis benchmarking tool because the team's study had already been downloaded more than 3,000 times on a preprint server for biology called bioRxiv and that their data had already featured in five other research studies.

"We're really pleased to see the rapid uptake and use of the data from our CellBench project," he said.

The researchers hope the platform will serve to encourage more rigorous testing, leading to better quality data [analysis](#) methods being developed in the future. Ultimately, their hope is that the [platform](#) will assist researchers in making new discoveries and developing more effective therapies for the major health challenges of our time.

**More information:** Luyi Tian et al. Benchmarking single cell RNA-sequencing analysis pipelines using mixture control experiments, *Nature Methods* (2019). [DOI: 10.1038/s41592-019-0425-8](https://doi.org/10.1038/s41592-019-0425-8)

Provided by Walter and Eliza Hall Institute of Medical Research

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