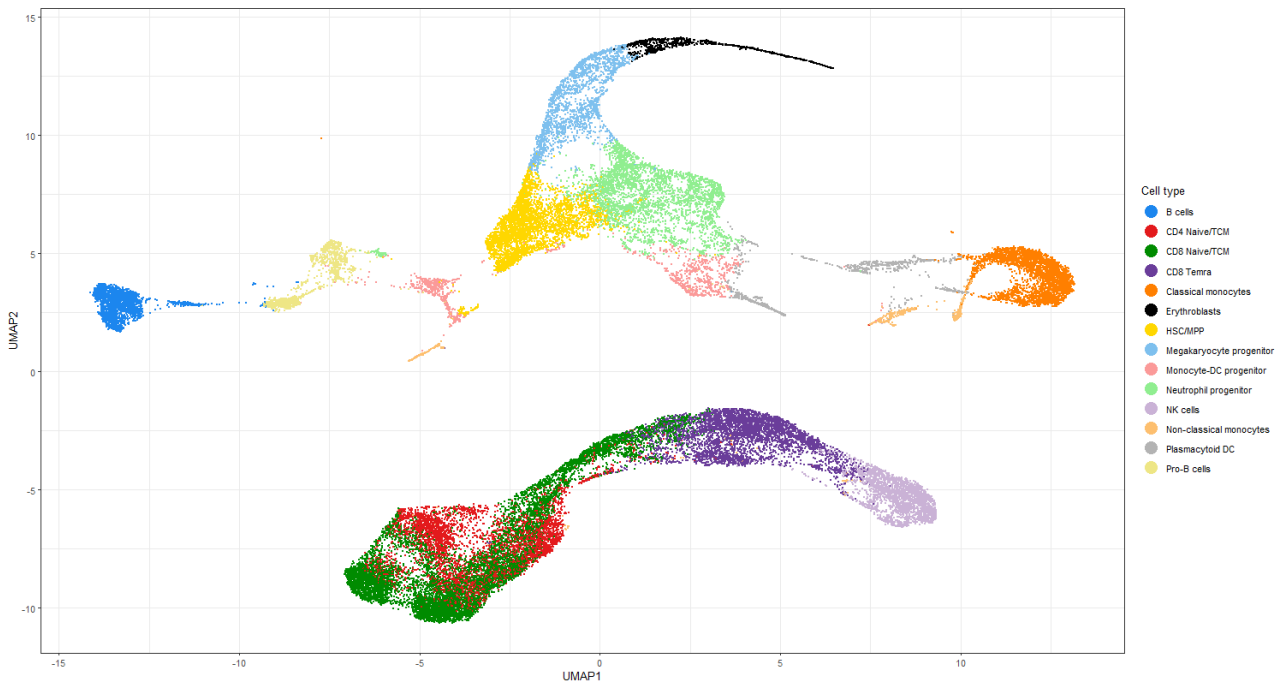


RCA2: A SCALABLE SUPERVISED CLUSTERING ALGORITHM THAT REDUCES BATCH EFFECTS IN SCRNA-SEQ DATA



Uniform Manifold Approximation and Projection (UMAP) of human bone marrow single cell data generated with RCA2.

Single-cell technologies allow researchers to analyse the activities of genes, known as gene-expression, across different cell-types at an unprecedented level in a single experiment. However, analysing single-cell data using established “unsupervised” methods have shown to be prone to technical variations.

To resolve these problems, GIS scientists developed a scalable and robust algorithm for the supervised clustering of single-cell RNA-seq data that can be easily integrated into existing workflows – [RCA2](#). It is the first integration of reference-based single-cell data analysis with state-of-the-art data structures and clustering algorithms. Its robustness to technical variation and batch effects is demonstrated on multiple data sets, including human bone marrow as well as blood samples from COVID-19 patients.

RCA2 provides a user-friendly framework incorporating multiple commonly used downstream analysis modules and can be easily applied to analyse both human and mouse data. Its scalable supervised clustering methods will facilitate a unified analysis of cohort-scale single-cell data sets that are produced in several international projects.

Access RCA2 here: <https://github.com/prabhakarlab/RCAv2>

“RCA2 significantly speeds up the rate of data analysis. Results obtained are also more robust and easier to interpret.”



*Dr Shyam Prabhakar, Associate Director,
Laboratory of Systems Biology & Data Analytics, GIS*



“Single-cell data is key to advance our knowledge on diseases such as cancer. Helping to analyse such data efficiently and accurately can help in many ongoing projects. For instance, RCA2 was used in all of our research groups’ single-cell projects investigating chronic myeloid leukemia, colorectal cancer, and COVID-19.”

Prof Patrick Tan, Executive Director, GIS