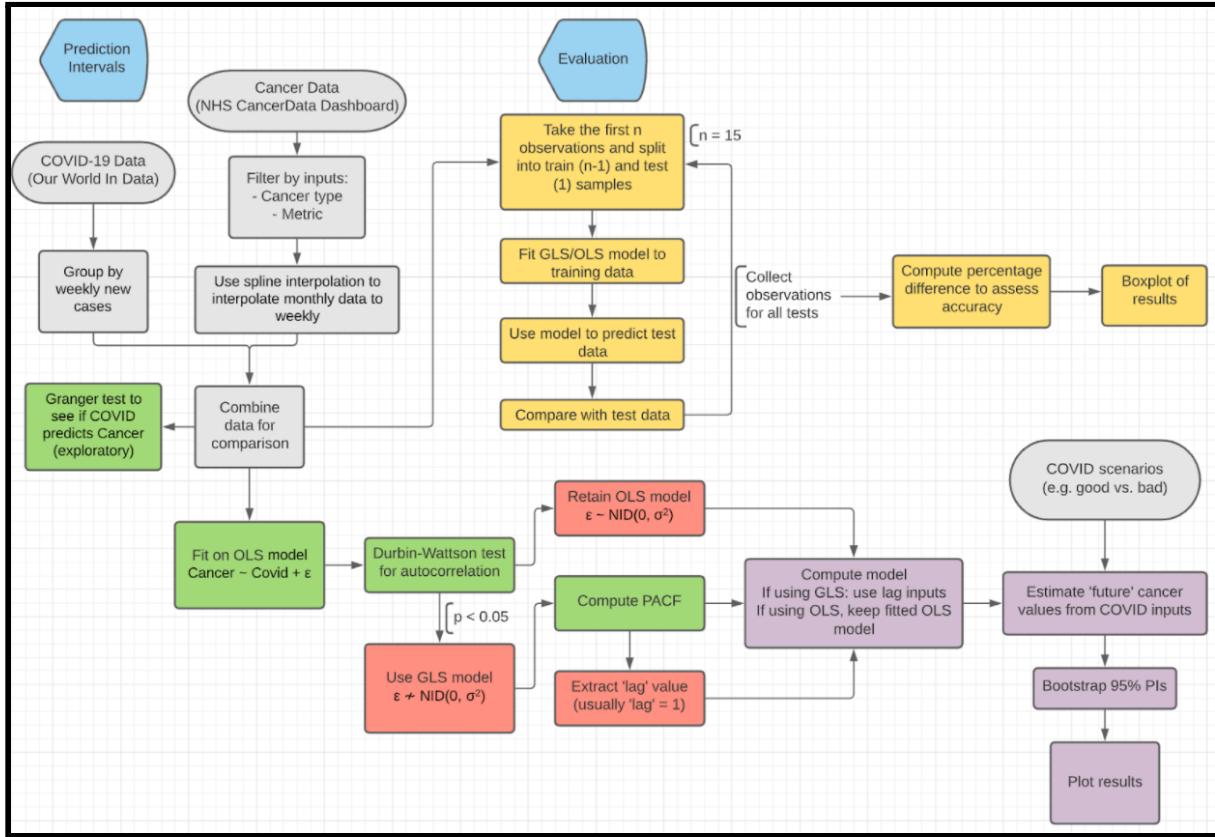


## Selection of Figure 1 examples



## Example from COVID project

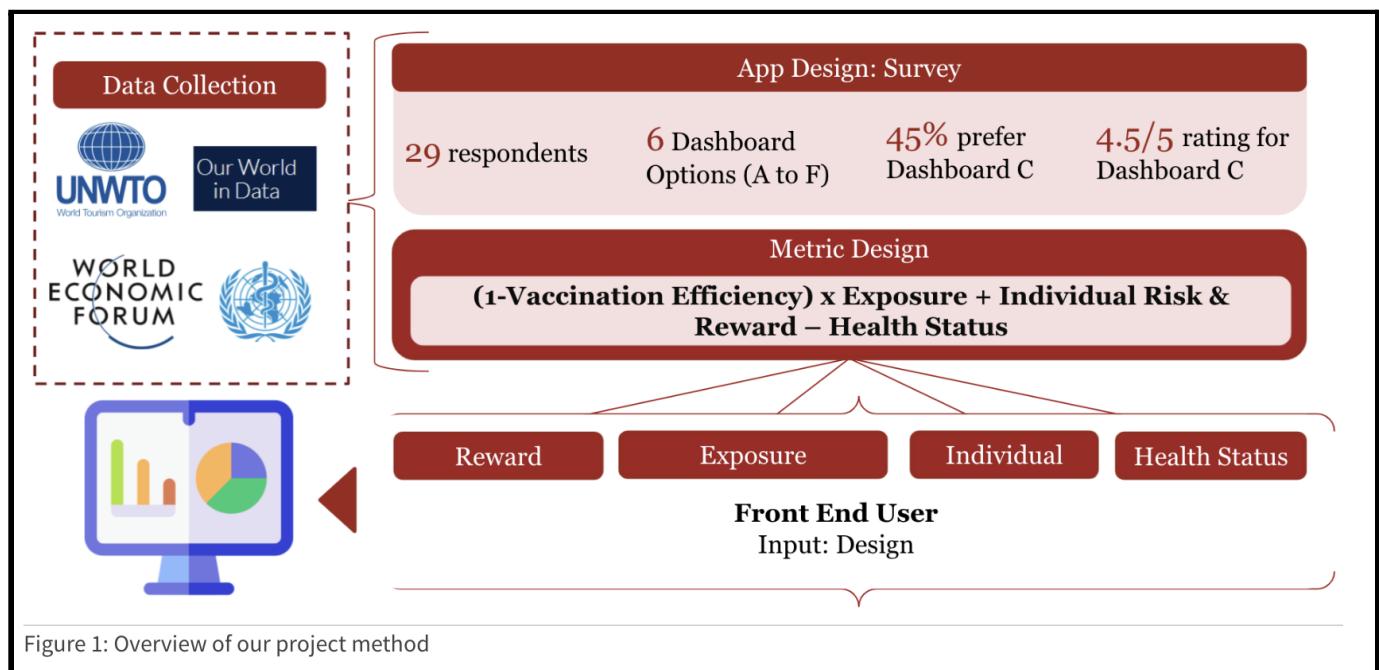
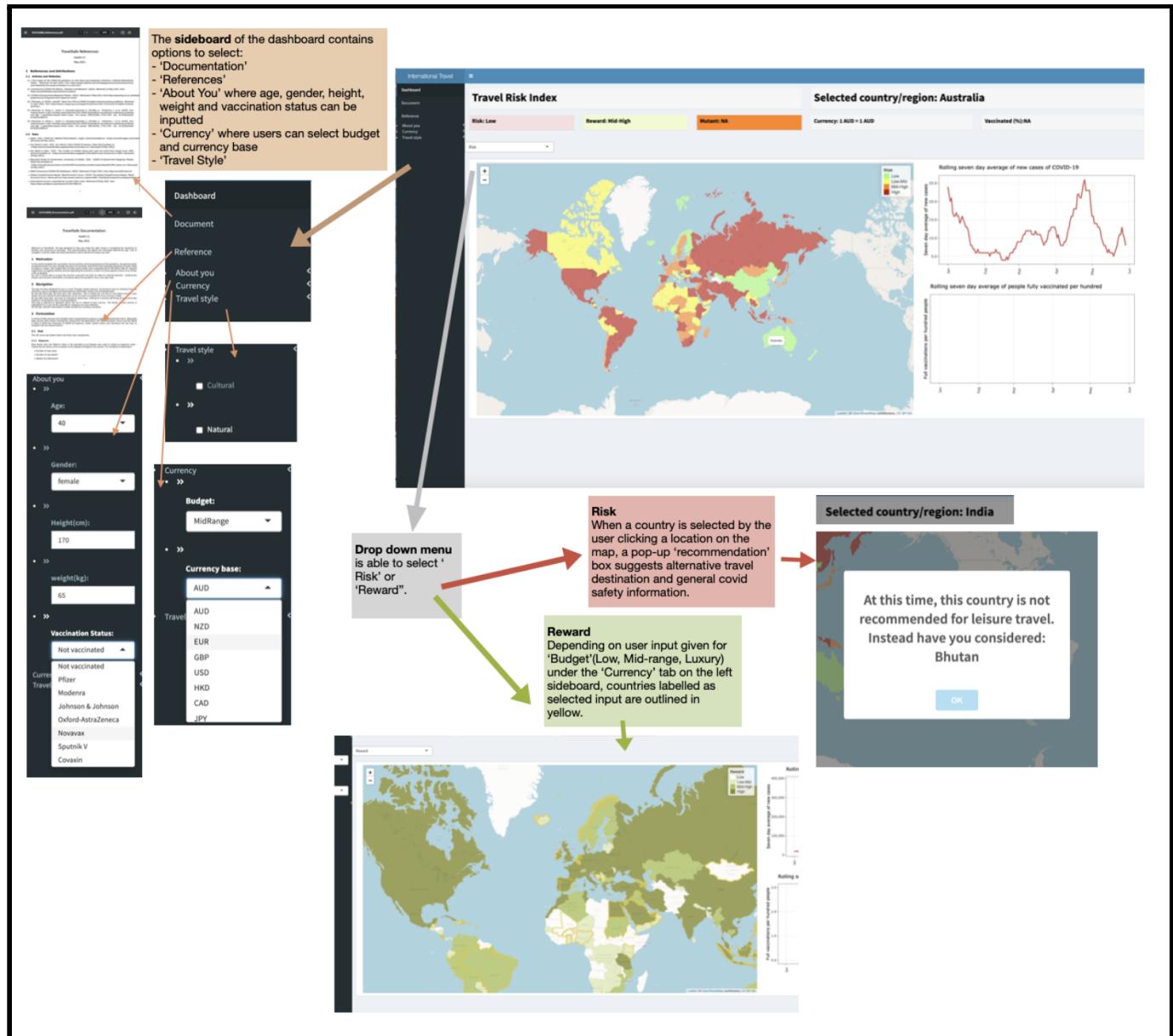
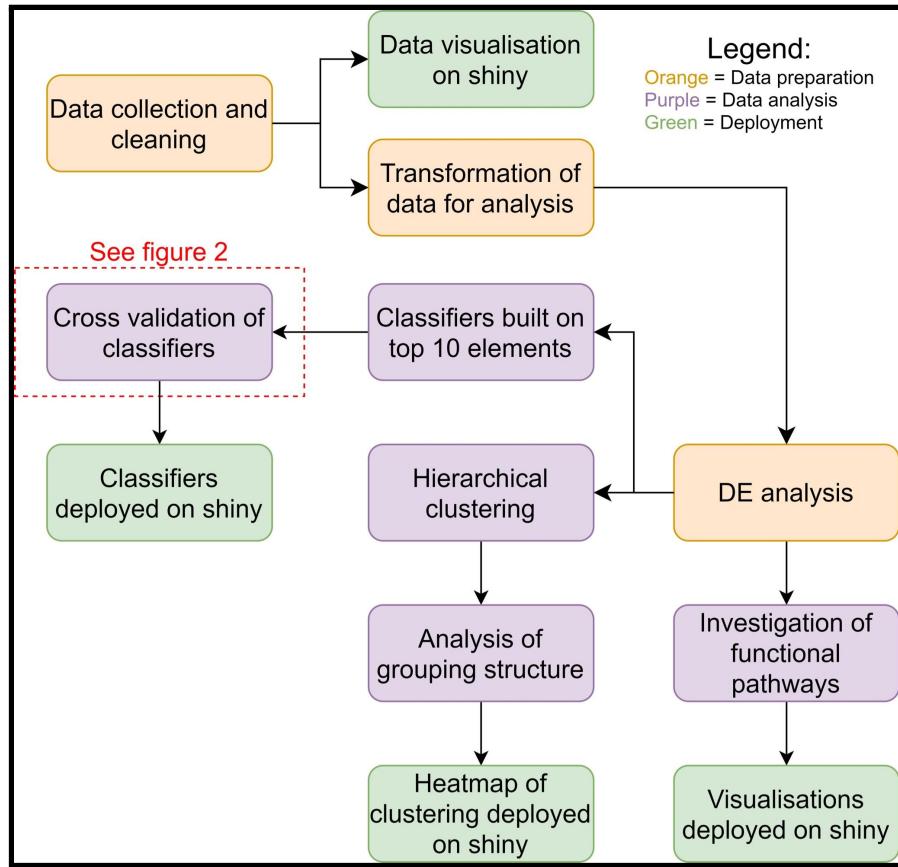
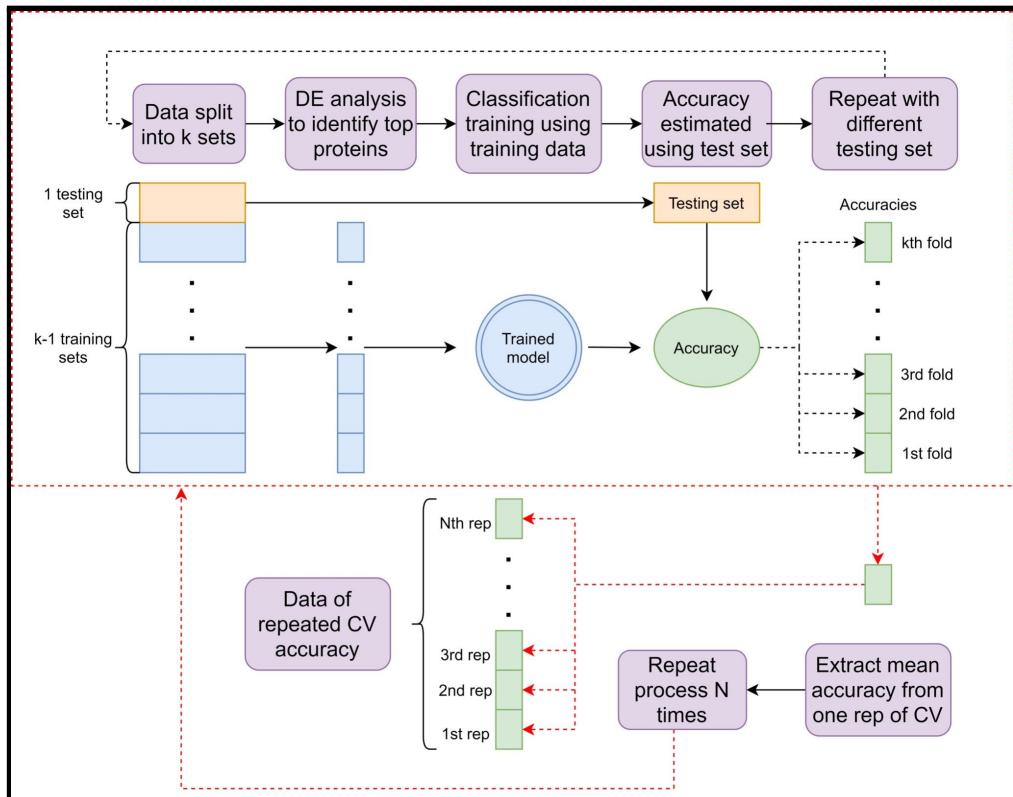


Figure 1: Overview of our project method

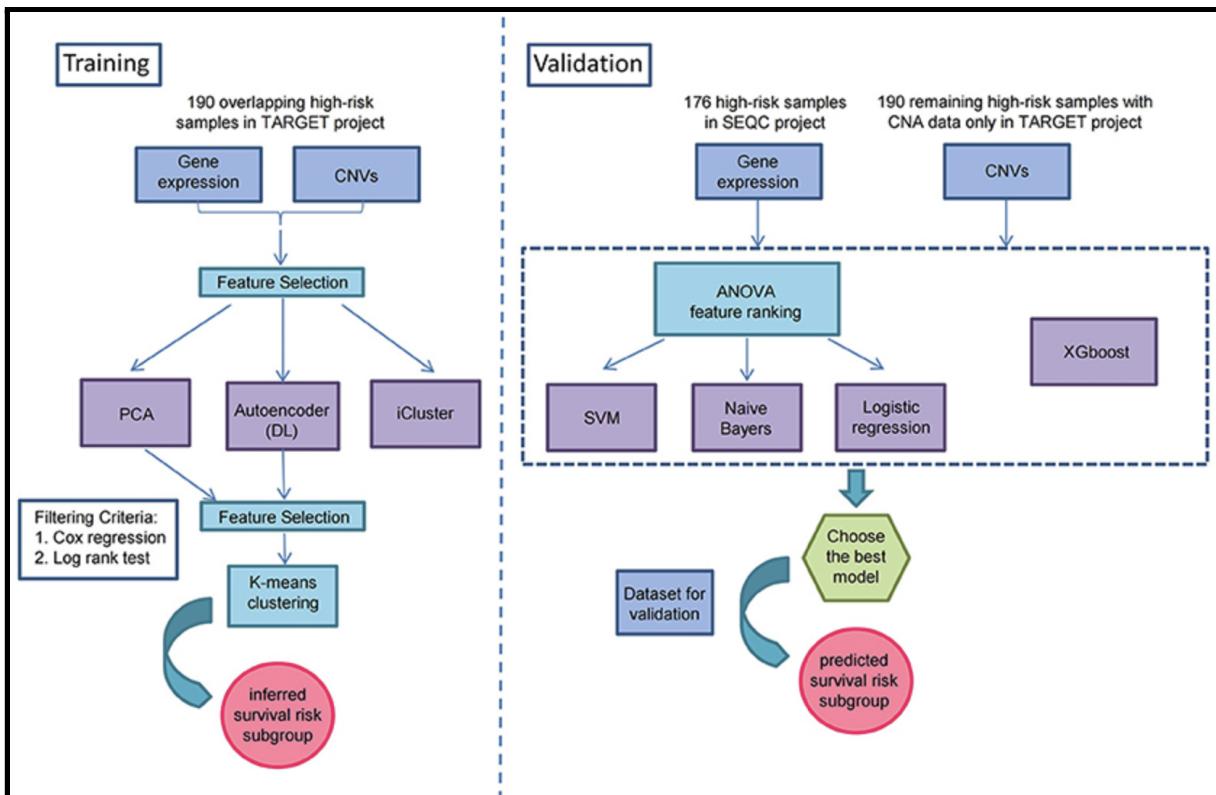
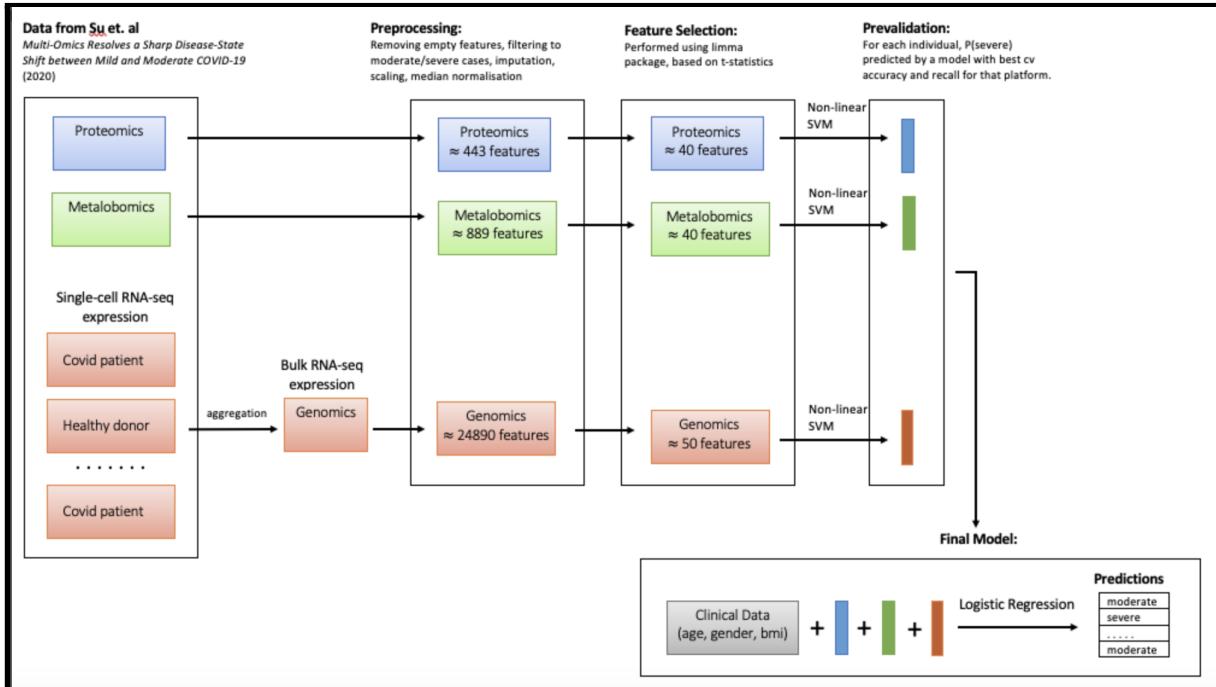
Farhan's group Figure 1 and Figure 2 (CV figure) for the Kidney project:



Farhan's group Figure 2 (CV figure) for the Kidney project:

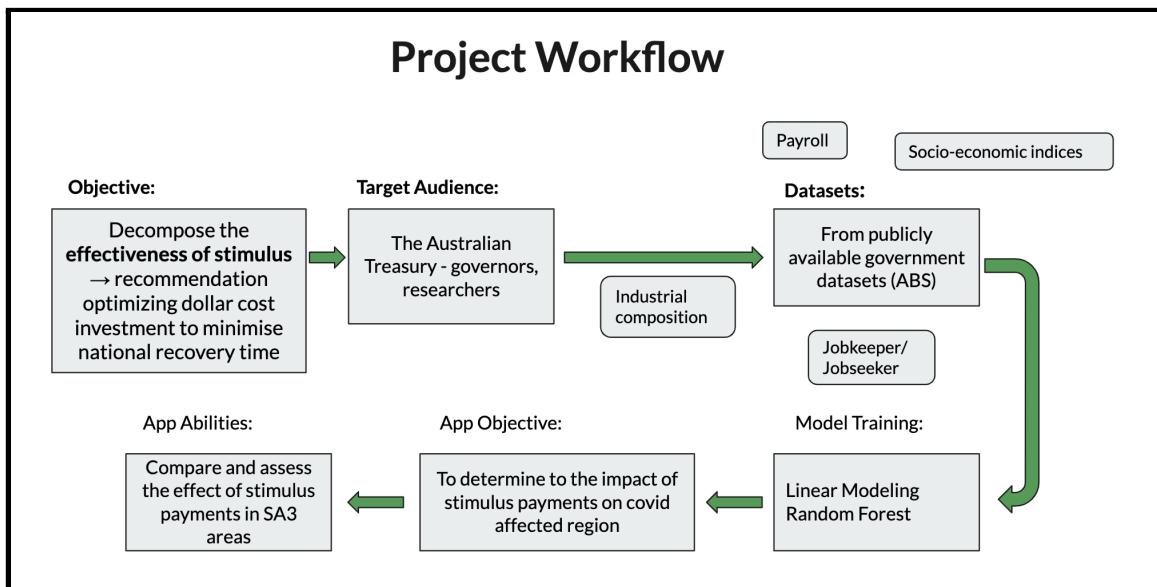
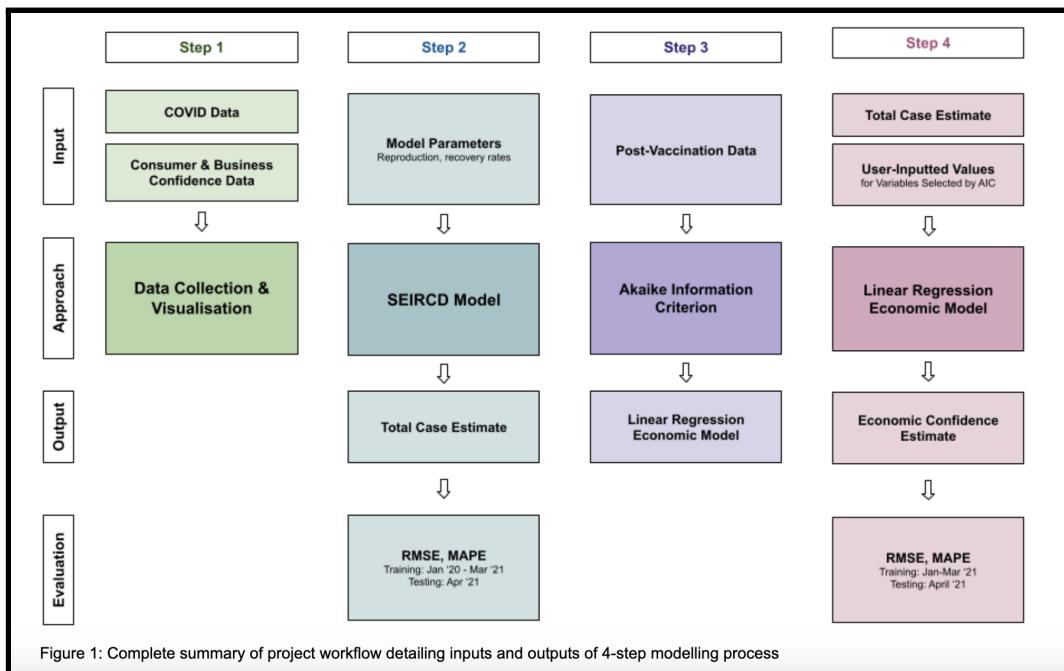
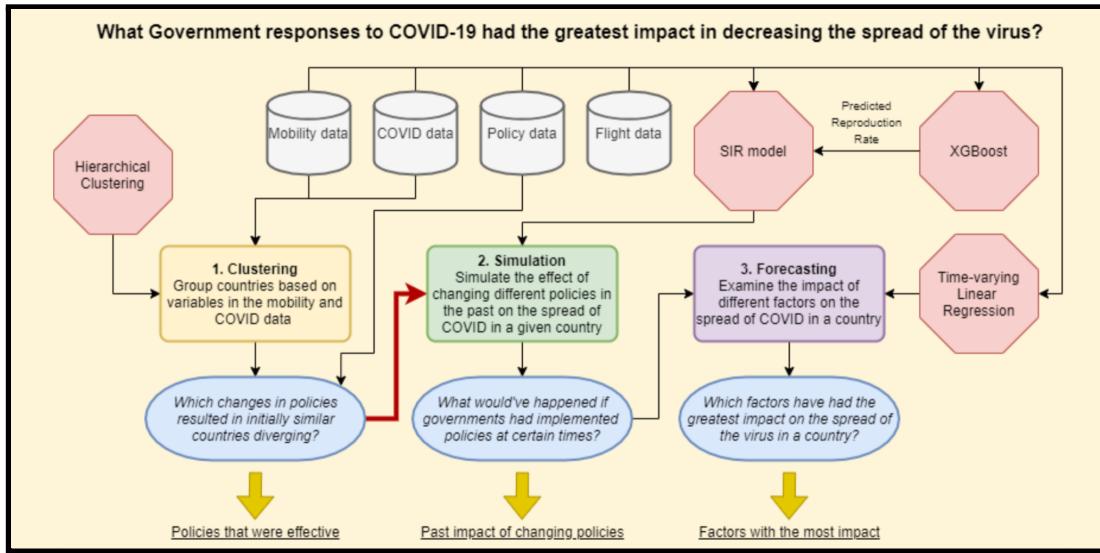


## 2021 covid multi-omics projects

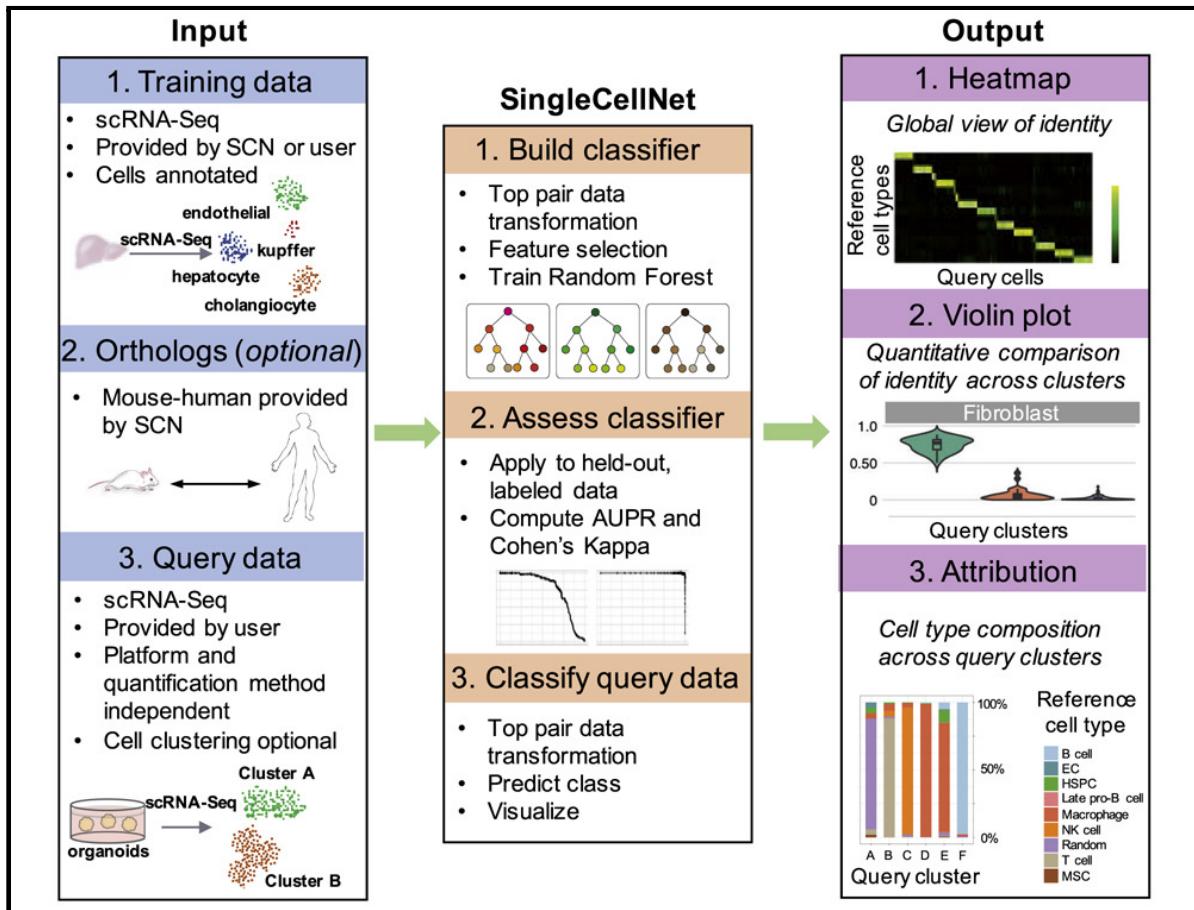


## 2021 health group workflow (similar to this year's covid projects)

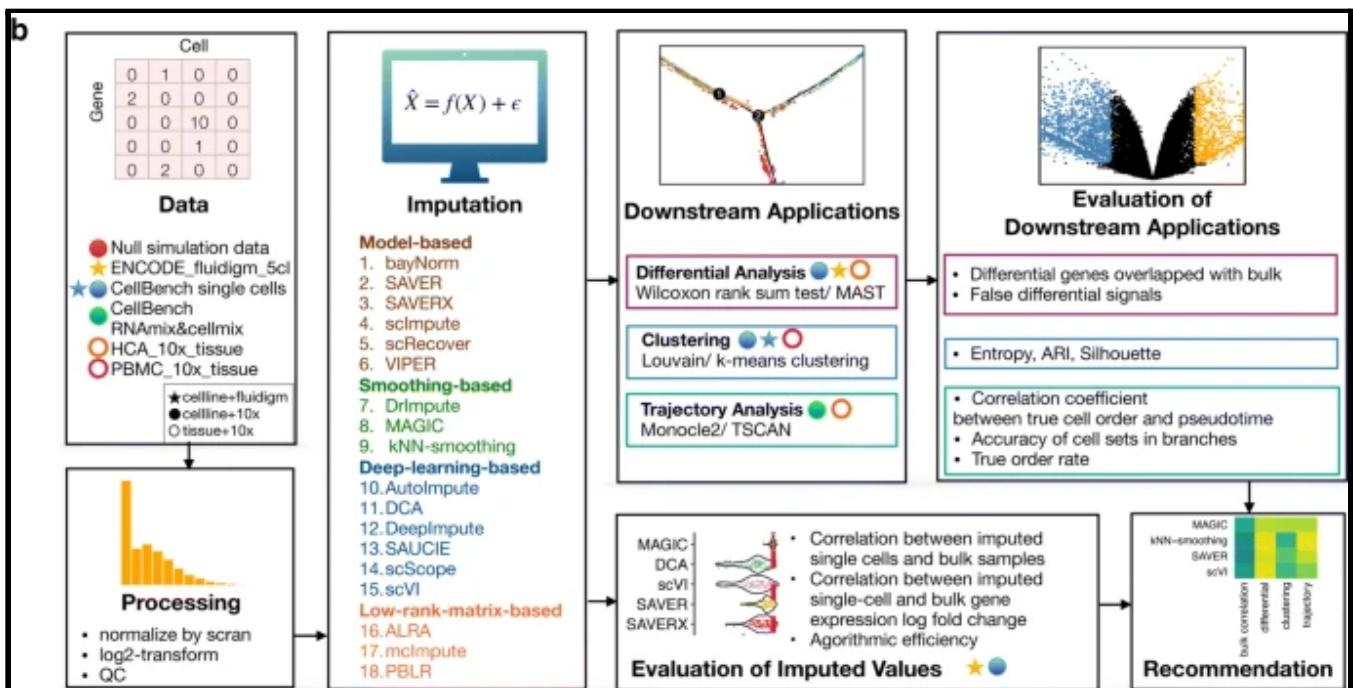
1. Data details and method details are included and the process is clear.
2. Process is clear
3. Story telling way



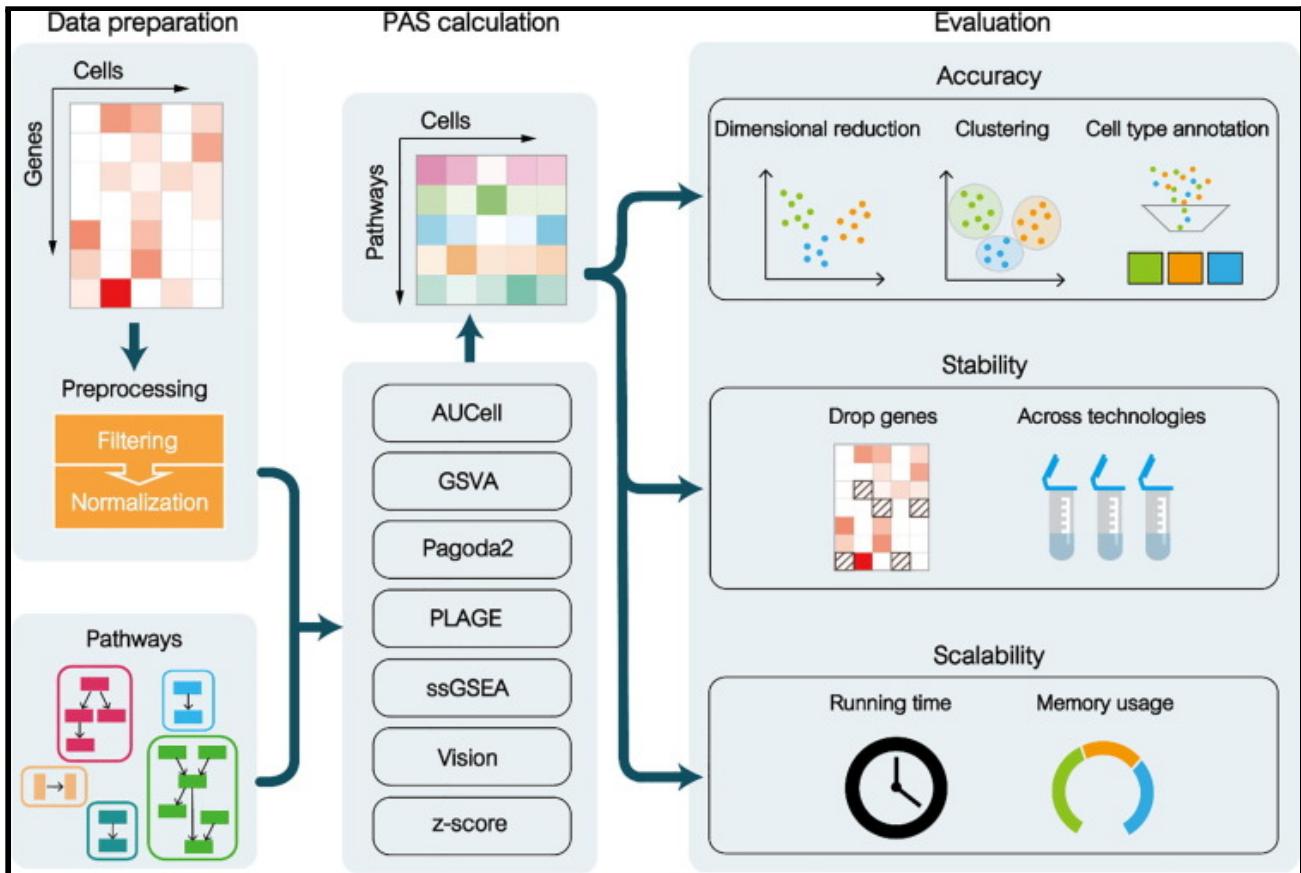
## Selected examples from current literatures



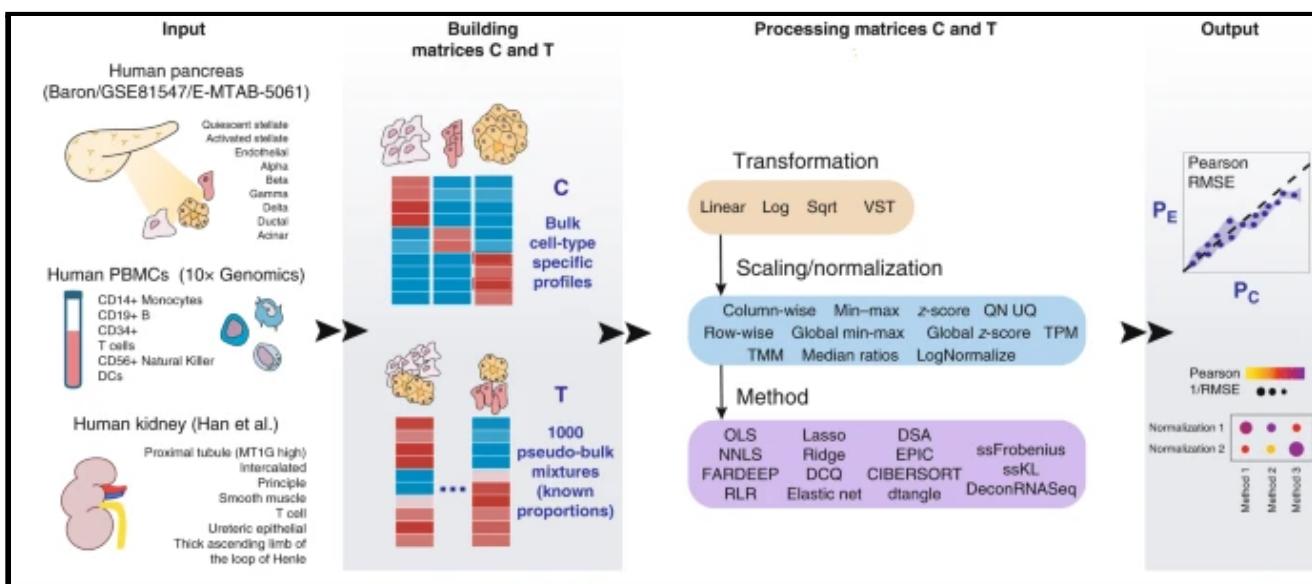
Ref: [SingleCellNet: A Computational Tool to Classify Single Cell RNA-Seq Data Across Platforms and Across Species - ScienceDirect](#)



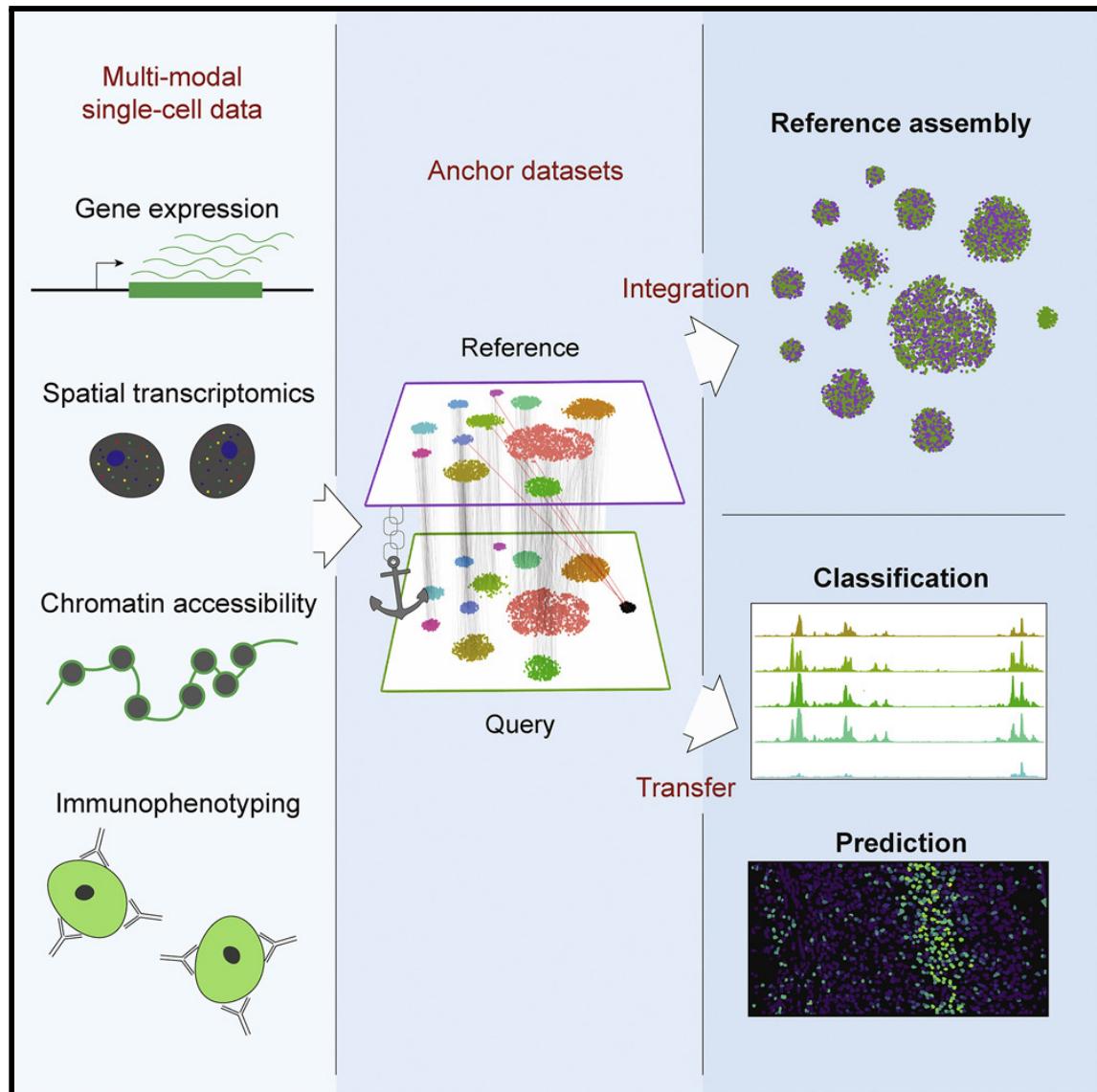
Ref: [A systematic evaluation of single-cell RNA-sequencing imputation methods | Genome Biology | Full Text](#)



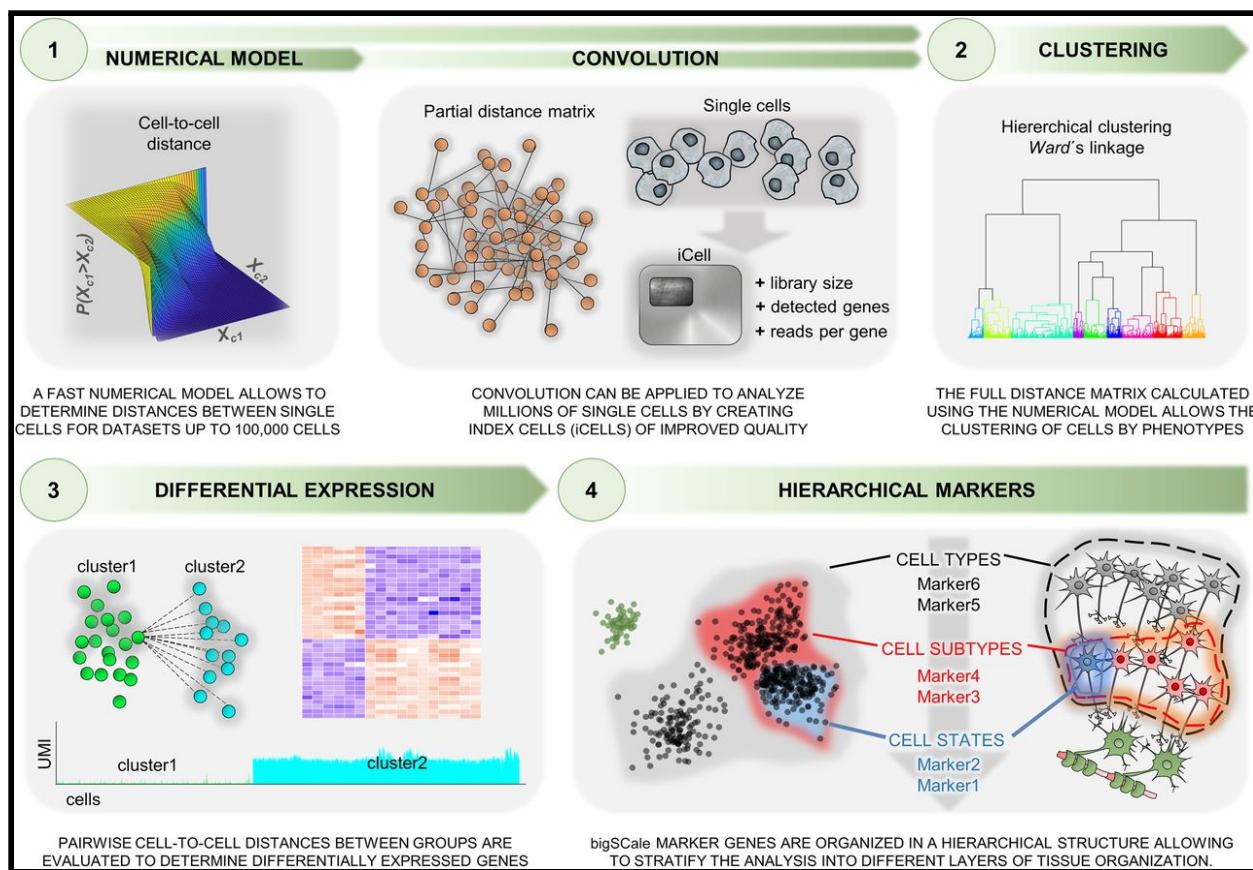
Ref: [Benchmarking algorithms for pathway activity transformation of single-cell RNA-seq data - ScienceDirect](#)



Ref: [Benchmarking of cell type deconvolution pipelines for transcriptomics data | Nature Communications](#)



Ref: [Comprehensive Integration of Single-Cell Data - ScienceDirect](#)



Ref: [bigSCale: an analytical framework for big-scale single-cell data](#)