## CellID: A Brief story about single cell data analysis and methods development; its joy and its frustration from the perspective of a 3rd year PhD Student

Akira Cortal $^{*1}$ 

<sup>1</sup>Imagine Institute of Genetic Disease – Imagine – France

## Résumé

The past few years, single cell RNASeq and more generally single cell omics has revolutionised the next generation sequencing and omics data by providing further resolution to the data and hence allowing a better investigation of the heterogeneity present in a biological sample and leading to major discovery such as the characterisation of new rare subpopulations. However single cell omics data suffer from a lot of technical and statistical challenges that can be solved using different and numerous tools and software created by the single cell community. Here we propose a quick and a **very subjective** overview about single cell data analysis based on our experience. We will go through the difficulty encountered in single cell, a non-exhaustive list of methods to deal with it, some recommendations, exciting new tools and finally a preview of our ongoing work CellID; a new method developed by our lab that enables extraction of gene signatures at a single cell level.

<sup>\*</sup>Intervenant