Computationally Sorting Immune Cells From Single-Cell Epigenomics Data

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SCAN ME

Motivation/Introduction

It has become possible to obtain single-cell data for thousands or even millions of cells, providing whole-transcriptome and/or whole-epigenome measurements. In application to tumour tissue, this provides the opportunity to profile the complement of immune cell types and to analyse their molecular state such as, for example, activation vs suppression. However, the immune system features a range of cell types and immune cells exhibit a high degree of plasticity in different tissues, creating a challenge of comprehensively and accurately classifying the cells and their states in such data. I will present my work addressing this issue using a decision tree approach.

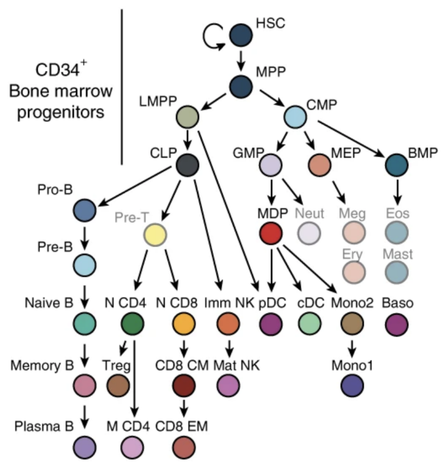

Figure 1. Hema Caption and [1]

Why ATAC-Seq

ATAC-Seq analysis makes it possible to identify open chromatin regions with a low number of cells and mostly active genes.

ATAC-Seq is an simply way to examine chromatin state, however bulk ATAC-Seq provides a standard overview of the open chromatin without distinguishing the cell type/stage. The principal benefit of the single cell ATAC-Seq method is that this approach enables the idendification and recognition of open chromatin in diverse or complicated tissue and cell samples. Numerous biological samples, like tumours and tissues in different developmental states, contain multiple sub-populations of cells that potentially have different epigenomic profiles. Single cell ATAC-Seq provides the most precise description of chromatin state in these dynamic processes. We are able to identify cell subpopulation using scATAC-seq.

open region atac-seq fotosu ekle

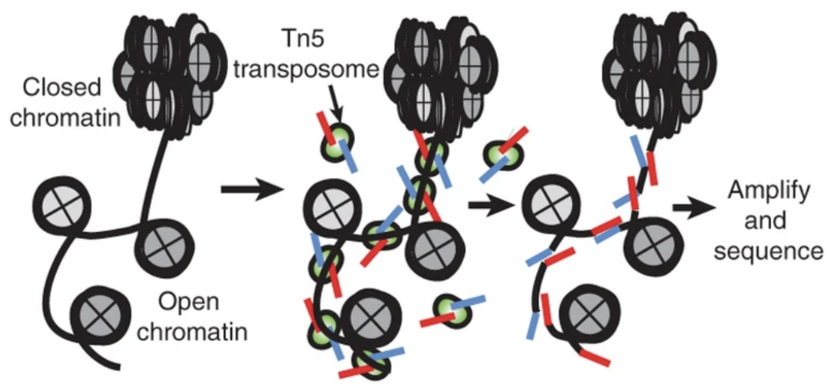

Figure 2. ATAC and (CITE)

what we think....

scClassifR

it was designed using RNA seek data and we know you're using it like

Figure 3. ATAC and (CITE)

Methods

We have some evolution some p....s

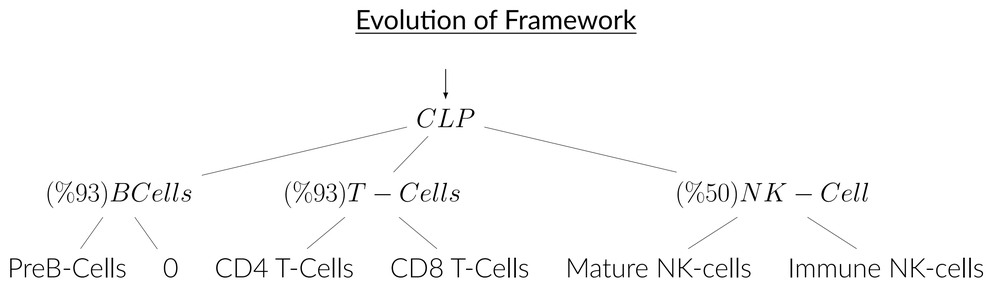

Figure 4. ATAC and (CITE)

We apply scATAC-seq to obtain chromatin profiles of more than 60,000 single cell in human blood. Immune cell come out of the blood and find marker and create classifier and apply with tumour data

Decision Tree

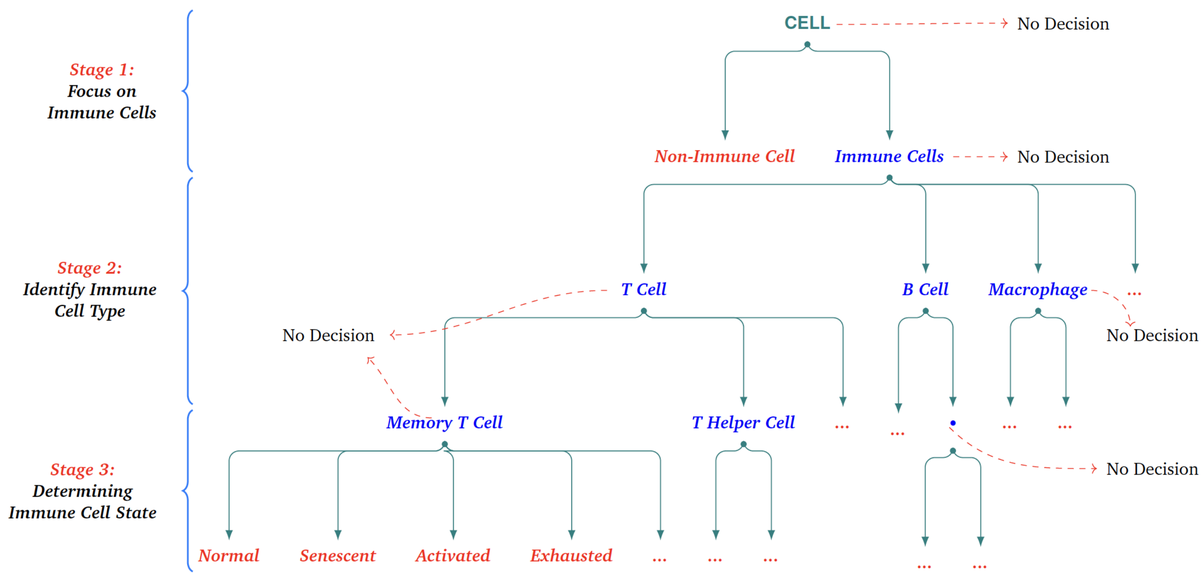

Figure 5. Decision Tree

- **The classification** of cells into known cell-types or simply cell sorting is one of the important parts of this research.
  - We aim to generate a more tailor made method that is even more reliable and potentially more reproducible across a large set of samples for the immune cells specifically.
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Future Direction of Research

Having reached the exact type of each immune cell, then we will inquire about the cell states. The main question is that we will deal with in this section is what exactly we can say about each of the immune cell states.

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2. **Cras vehicula blandit urna ut maximus**. Aliquam blandit nec massa ac sollicitudin. Curabitur cursus, metus nec imperdiet bibendum, velit lectus faucibus dolor, quis gravida metus mauris gravida turpis.
3. **Vestibulum et massa diam**. Phasellus fermentum augue non nulla accumsan, non rhoncus lectus condimentum.

References

[1] Ansuman T Satpathy, Jeffrey M Granja, Kathryn E Yost, Yanyan Qi, Francesca Meschi, Geoffrey P McDermott, Brett N Olsen, Maxwell R Mumbach, Sarah E Pierce, M Ryan Corces, et al. Massively parallel single-cell chromatin landscapes of human immune cell development and intratumoral t cell exhaustion. *Nature biotechnology*, 37(8):925–936, 2019.

[2] Claude E. Shannon. A mathematical theory of communication. *Bell System Technical Journal*, 27(3):379–423, 1948.