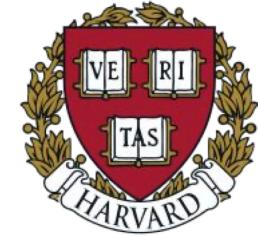




Discovery of hematopoietic stem cell subtype through Single Cell VR- a python-based application for genome-wide data visualization



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ABSTRACT

The technology to monitor global gene regulation in individual cells represents a significant turning point in cell biology. For the first time, we can determine the expression level of every gene across thousands of individual cells in a single experiment. This data can generate classification of new cell types and states as well as comprehensive models that predict cell behaviour during aging. Under the Pinello Lab, our task was to take published single-cell genomics data and process it using their platform SingleCellVR.com, so anyone can explore the models using cardboard VR visors.

BACKGROUND

Before attempting STREAM/PAGA tutorials found on the Pinello Lab GitHub, it was important to explore the website (Fig. 1) and read recent literature either covering the uses of single-cell genomics or for finding a potential dataset to process.

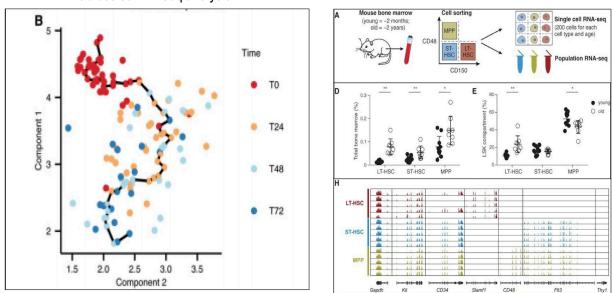
The Winsor Science Internship group first read a 2015 publication in Genomics Research titled "Defining cell types and states with single-cell genomics" by Cole Trapnell (Genome Research, 2015, 1491–1498). It explained how the variation in the gene expression profile of a single cell type can be effectively visualized using dimensionality reduction, a transformation that reduces the number of input variables so that data can be represented by a 2D or 3D graph (Fig. 2).

Weeks later, a promising scRNA-seq dataset was found in a paper published under the Regev Lab titled "Single-cell RNA-seq reveals changes in cell cycle and differentiation programs upon aging of hematopoietic stem cells" (Genome Research, 2015, 1860–72). The remarkable capacity of blood cell production by multipotent hematopoietic stem cells (HSCs) declines with age, indicated by the accumulation of HSCs in the bone marrow, and increased incidence of myeloid diseases like leukemia. ScRNA-seq analysis reveals a six-fold increase in CD48-/CD150+ long-term (LT) HSCs in the bone marrow (Fig. 3). SingleCellVR.com can be used to determine whether this correlates with the emergence of an LT-HSC subtype.



Figure 1:
SingleCellVR.com

Figure 2: Fig. B from Trapnell et al., 2015 (pg. 5): example of dimensionality reduction present in graphs across scRNA-seq analysis.



Time
● T0
● T24
● T48
● T72

METHODS

Standard 2D analysis

1 | Simple data conversion

2 | singlecellvr.com

3 | Flexible and affordable UX

The point of processing scRNA-seq data through STREAM or SCANPY is to eliminate insignificant data and graph gene expression in cells before uploading to SingleCellVR.com. Figures from Stein et al., 2020.

A. Step 1 | Select or upload your data

B. Step 2 | Scan the QR code with your phone and explore your data in the VR world!

