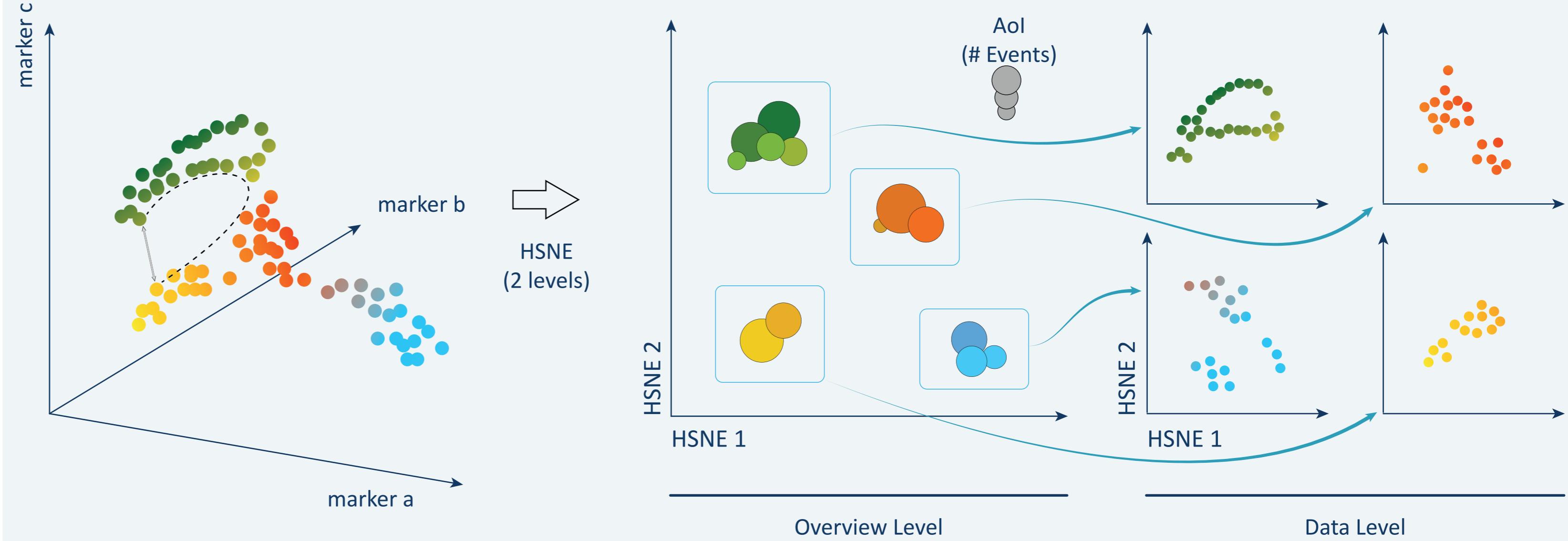


Interactive Visual Analysis of Mass Cytometry Data by Hierarchical Stochastic Neighbor Embedding

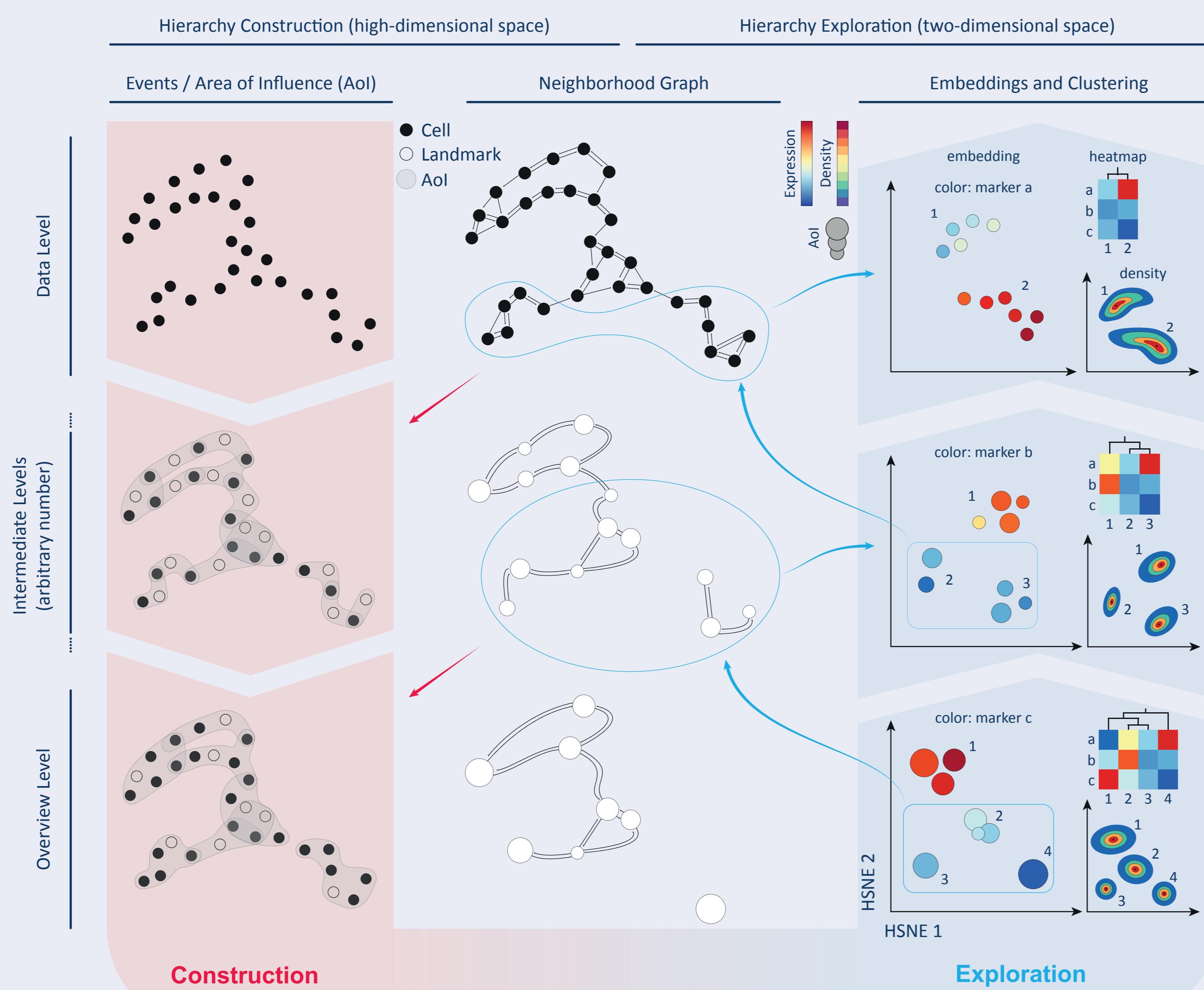
Introduction

Immunesystem-wide CyTOF studies^[1] produce millions of cells, which most computational tools cannot handle without downsampling, potentially leading to data loss. HSNE^[2] builds a hierarchy of non-linear similarities, allowing exploration of large scale datasets at full resolution interactively and, through that, efficient discovery of rare cell populations.

Concept: Non-Linear Hierarchy (Abstract to Single-Cell)



Hierarchy Construction and Exploration

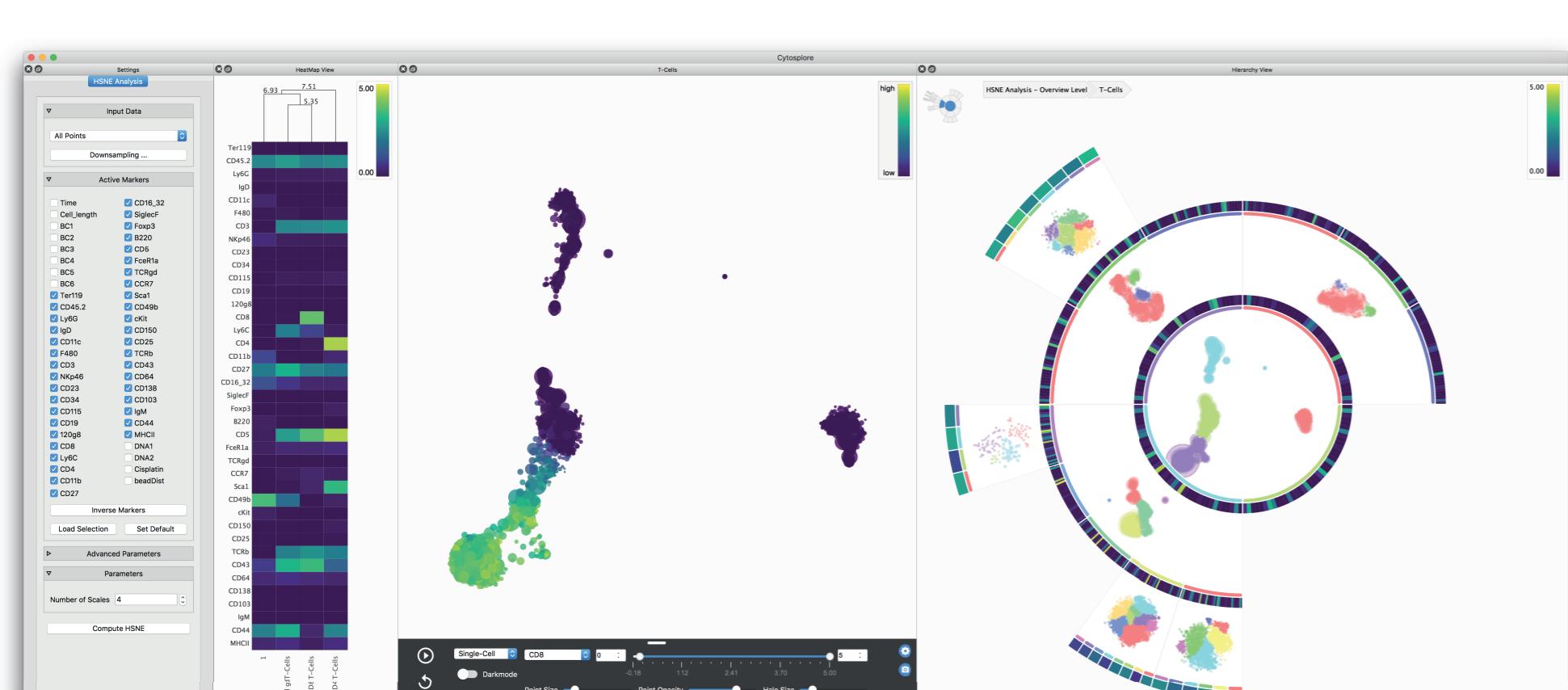
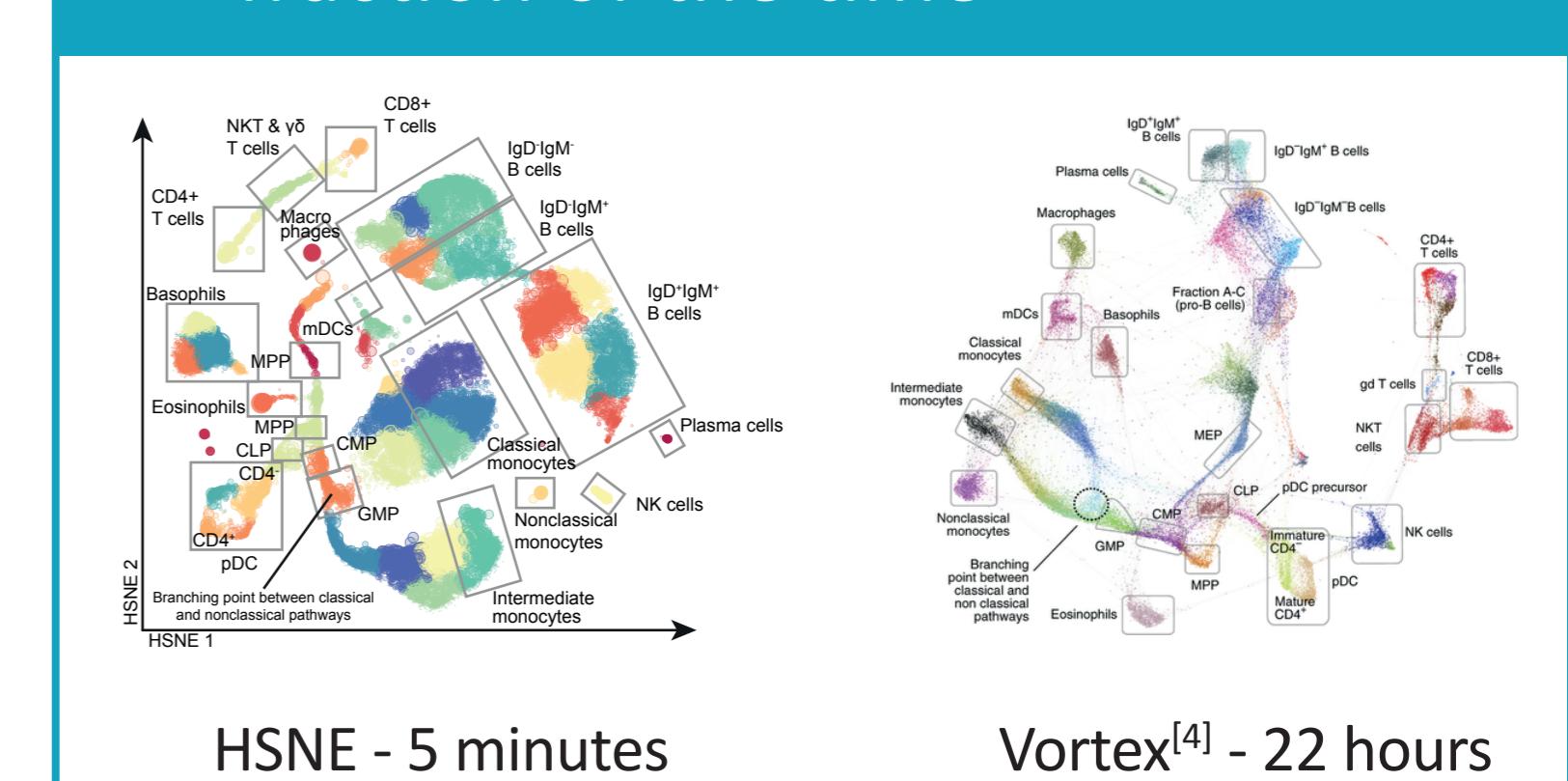


Advantages

- Millions(!) of cells
- Non-linear distances, based on single cell resolution throughout the hierarchy
- Full data access, zoom into single-cell resolution
- Interactive, integrated software Cytosplore^[3]

Results

- State-of-the-art precision in a fraction of the time



References

- [1] van Unen, et al. Mass Cytometry of the Human Mucosal Immune System Identifies Tissue- and Disease-Associated Immune Subsets. *Immunity* 44, 1227–1239 (2016).
- [2] Pezzotti et al. Hierarchical Stochastic Neighbor Embedding. *Comput. Graph. Forum* 35, 21–30 (2016).
- [3] Höllt, et al. Cytosplore: Interactive Immune Cell Phenotyping for Large Single-Cell Datasets. *Comput. Graph. Forum* 35, 171–180 (2016).
- [4] Samusik et al. Automated mapping of phenotype space with single-cell data. *Nat. Methods* 13, 493–496 (2016).

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