

POSTER NUMBER: 2017

Interactive Visual Analysis of Mass Cytometry Data by Hierarchical Stochastic Neighbor Embedding Reveals Rare Cell Types

Thomas Höllt^{1,2}, Vincent van Unen³, Nicola Pezzotti¹, Na Li³, Marcel Reinders⁴, Elmar Eisemann¹, Frits Koning³, Anna Vilanova¹, Boudewijn Lelieveldt^{4,5}

¹Computer Graphics and Visualization Group, TU Delft, the Netherlands; ²Computational Biology Center, Leiden University Medical Center, the Netherlands; ³Department of Immunohematology and Blood Transfusion, Leiden University Medical Center, the Netherlands

⁴Pattern Recognition and Bioinformatics Group, TU Delft, the Netherlands; ⁵Division of Image Processing, Department of Radiology, Leiden University Medical Center, the Netherlands

Mass cytometry allows high-resolution dissection of the cellular composition of the immune system. However, the high-dimensionality, large size, and non-linear structure of the data poses considerable challenges for data analysis.

We introduce Hierarchical Stochastic Neighbor Embedding (HSNE) for single-cell analysis, a computational approach that constructs a hierarchy of non-linear similarities, allowing the analysis of millions of cells via different levels of detail up to single-cell resolution within minutes. We integrated HSNE into the Cytosplore+HSNE framework to facilitate interactive exploration and analysis of the hierarchy by a set of corresponding two-dimensional plots with stepwise increase in detail up to the single-cell level. This divide and conquer approach minimizes computation time and, thereby, allows efficient and interactive visualization.

We validated the discovery potential of Cytosplore+HSNE by re-analyzing a recent study on gastrointestinal disorders as well as two other publicly available mass cytometry datasets. We found that Cytosplore+HSNE efficiently identifies both abundant and rare cell populations, without resorting to downsampling of the data, including rare cell populations that were missed in a previous analysis due to downsampling. Taken together, Cytosplore+HSNE offers unprecedented possibilities for visual exploration and analysis of millions of cells measured in mass cytometry studies.

This work was supported by the STW Project 12720.