Leiden
Computational Biology Center

INTEGRATING & COMPARING UMAP IN CYTOSPLORE

Contact: Thomas Höllt — t.hoellt@lumc.nl

Focus: Practical

Duration: 3–6 Months

Requirements: Programming skills in C++ are required. Implementation will be in the Cytosplore platform, based on C++, Qt, OpenGL, and javascript. Minimal interaction with OpenGL and javascript code might be necessary.

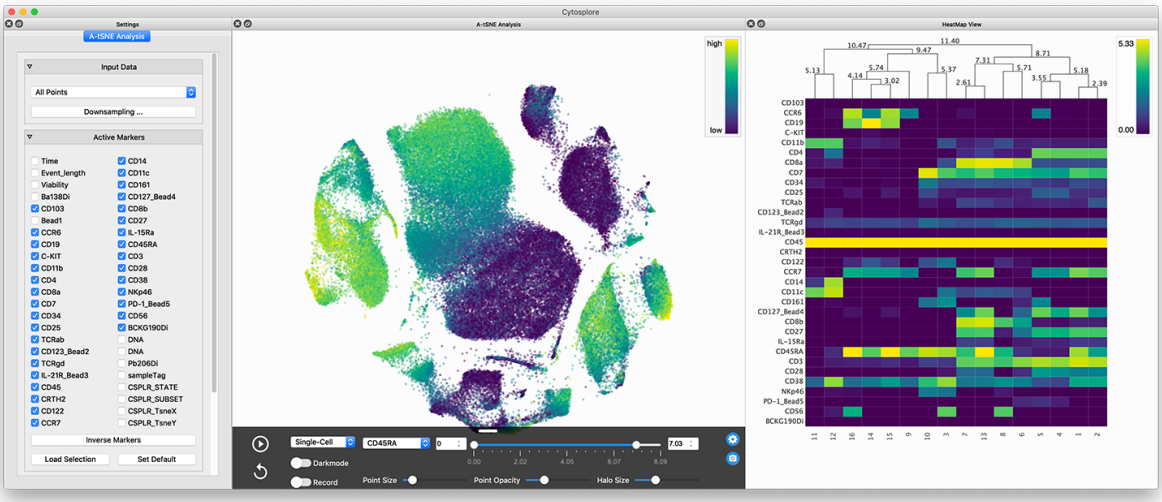

Figure 1: **Screenshot of Cytosplore.**

To understand how the immune system works, one needs to have a clear picture of its cellular compositon and the cells' corresponding properties and functionality. Mass cytometry is a novel technique to determine the properties of single-cells with unprecedented detail. This amount of detail allows for much finer differentiation but also comes at the cost of more complex analysis [vULM*16, LvUH*18].

Cytosplore [HPvU*16, vUHP*17] , implements an interactive workflow to analyze mass cytometry data in an integrated system, providing multiple linked views, showing different levels of detail and enabling the rapid definition of known and unknown cell types. The main visual analysis of the data in Cytosplore is done by inspecting embeddings computed using t-SNE or HSNE.

Recently an alternative to these techniques called UMAP [MH18] gained traction and has been shown effective for single-cell analysis [BMH*18]. The goal of this project is to implement UMAP in Cytosplore and compare it to HSNE.

REFERENCES

[BMH*18] BECHT E., MCINNES L., HEALY J., DUTERTRE C.-A., KWOK I. W. H., NG L. G., GINHOUX F., NEWELL E. W.: Dimensionality reduction for visualizing single-cell data using umap. *Nature Biotechnology* (2018). doi:10.1038/nbt.4314.

[HPvU*16] HÖLLT T., PEZZOTTI N., VAN UNEN V., KONING F., EISEMANN E., LELIEVELDT B. P. F., VILANOVA A.: Cytosplore: Interactive immune cell phenotyping for large single-cell datasets. *Computer Graphics Forum (Proceedings of EuroVis) 35*, 3 (2016), 171–180. doi:10.1111/cgf.12893.

[LvUH*18] LI N., VAN UNEN V., HÖLLT T., THOMPSON A., VAN BERGEN J., PEZZOTTI N., EISEMANN E., VILANOVA A., CHUVA DE SOUSA LOPES S. M., LELIEVELDT B. P., KONING F.: Mass cytometry reveals innate lymphoid cell differentiation pathways in the human fetal intestine. *Journal of Experimental Medicine 215*, 5 (2018), 1383–1396. doi:10.1084/jem.20171934.

[MH18] MCINNES L., HEALY J.: UMAP: Uniform manifold approximation and projection for dimension reduction. *arXiv* (2018). arXiv:1802.03426.

[vUHP*17] VAN UNEN V., HÖLLT T., PEZZOTTI N., LI N., REINDERS M. J. T., EISEMANN E., KONING F., VILANOVA A., LELIEVELDT B. P. F.: Visual analysis of mass cytometry data by hierarchical stochastic neighbor embedding reveals rare cell types. *Nature Communications 8*, 1740 (2017), 1–10. doi:10.1038/s41467-017-01689-9.

[vULM*16] VAN UNEN V., LI N., MOLENDIJK I., TEMURHAN M., HÖLLT T., VAN DER MEULEN-DE JONG A. E., VERSPAGET H. W., MEARIN M. L., MULDER C. J., VAN BERGEN J., LELIEVELDT B. P. F., KONING F.: Mass cytometry of the human mucosal immune system identifies tissue- and disease-associated immune subsets. *Immunity 44*, 5 (2016), 1227–1239. doi:10.1016/j.immuni.2016.04.014.