From algorithms to applications

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For high-dimensional cytometry data, it becomes more and more difficult to get a comprehensive overview of the data when using only manual gating. In this talk, I will highlight some of the computational tools developed in the SaeysLab that can help, such as FlowSOM for population discovery, CytoNorm for batch effect correction and PeacoQC for quality control. Next to algorithm development, we also have a strong focus in the lab on applying these tools in clinical collaborations, where machine learning algorithms can help for further downstream analysis. I will showcase some pipelines developed for different diseases, such as diagnosis prediction for CVID, survival time analysis in non-small cell lung cancer, and the characterization of immunophenotypic heterogeneity in acute myeloid leukemia.