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HIGH DIMENSIONAL CHARACTERISATION OF CELLULAR FEATURES BY SINGLE CELL MASS CYTOMETRY

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High resolution measurement characterizing the large number of cellular features is in the focus of recent cell biological research. To achieve these goals single cell mass cytometry combines advantages of the single cell resolution of traditional fluorescence-based flow cytometry with the multiplexicity of inductively coupled plasma-mass spectrometry. Instead of fluorophores detection for mass cytometry is based on stable heavy-metal isotope labeled antibodies. Thus, the autofluorescence and spectral overlapping are eliminated. The current state-of-the-art mass cytometer is capable of measuring up to 135 different stable isotopes of rare earth metals, although the current availability of these tags in high purity limits the usage to around 45 different rare earth metal tags. This unique feature enables researchers to multiplex up to 45 different antibodies in one single tube.

Extensive mapping of signaling networks in single cells, cell surface receptor quantification has been also achieved by single cell mass cytometry. Sample multiplexing is also possible by barcoding prior the antibody labeling which enables the combination of 20 different samples in one single tube. Cell types, cellular populations of interest can be visualized on dot plots and the protein expression levels are demonstrated by histograms. Furthermore, gating hierarchy above 10–12 level is also manageable. Mass cytometry deeply reveals cellular heterogeneity on the basis of highly multiplex phenotypical and functional characterization. There are several novel algorithmic approaches to process large datasets such as: SPADE, viSNE, Citrus.

The monitoring of the complex immunophenotype is highly relevant in several human diseases which have been previously restricted to limited number of markers with flow cytometry compared to single cell mass cytometry. Human systemic autoimmune diseases (rheumatoid arthritis, systemic lupus erythemathosus and systemic sclerosis) are under investigation. The cellular complexity and functional heterogeneity of solid tumors, inflammatory diseases and animal models (tumor, bone marrow, spleen, lymph nodes) will be also analyzed in our laboratory by single cell mass spectrometry.

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