



**University of
Zurich^{UZH}**

Introduction: High-dimensional cytometry data analysis

STA426 lecture materials

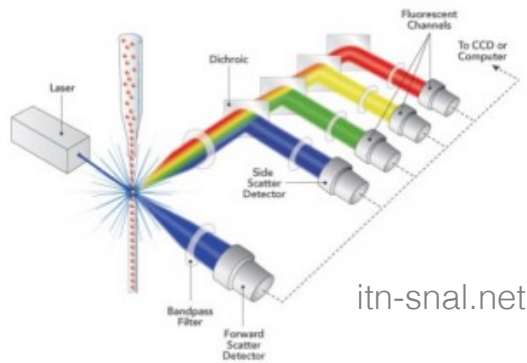
Lukas M. Weber

11 Dec 2017

High-dimensional cytometry

- antibody-based
- protein expression levels in single cells

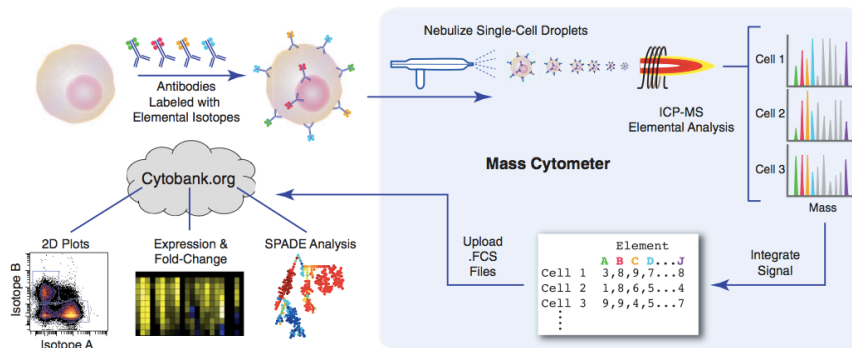
(A)



Fluorescent flow cytometry / FACS

~5–20 proteins/cell; 1000s cells/sec

(B)



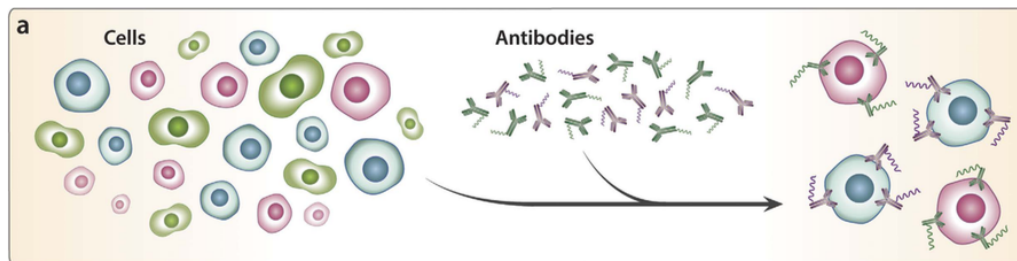
Mass cytometry / CyTOF

~30–50 proteins/cell; 100s cells/sec

Bendall et al. (2011), Fig. 1A

Future developments...

(C)

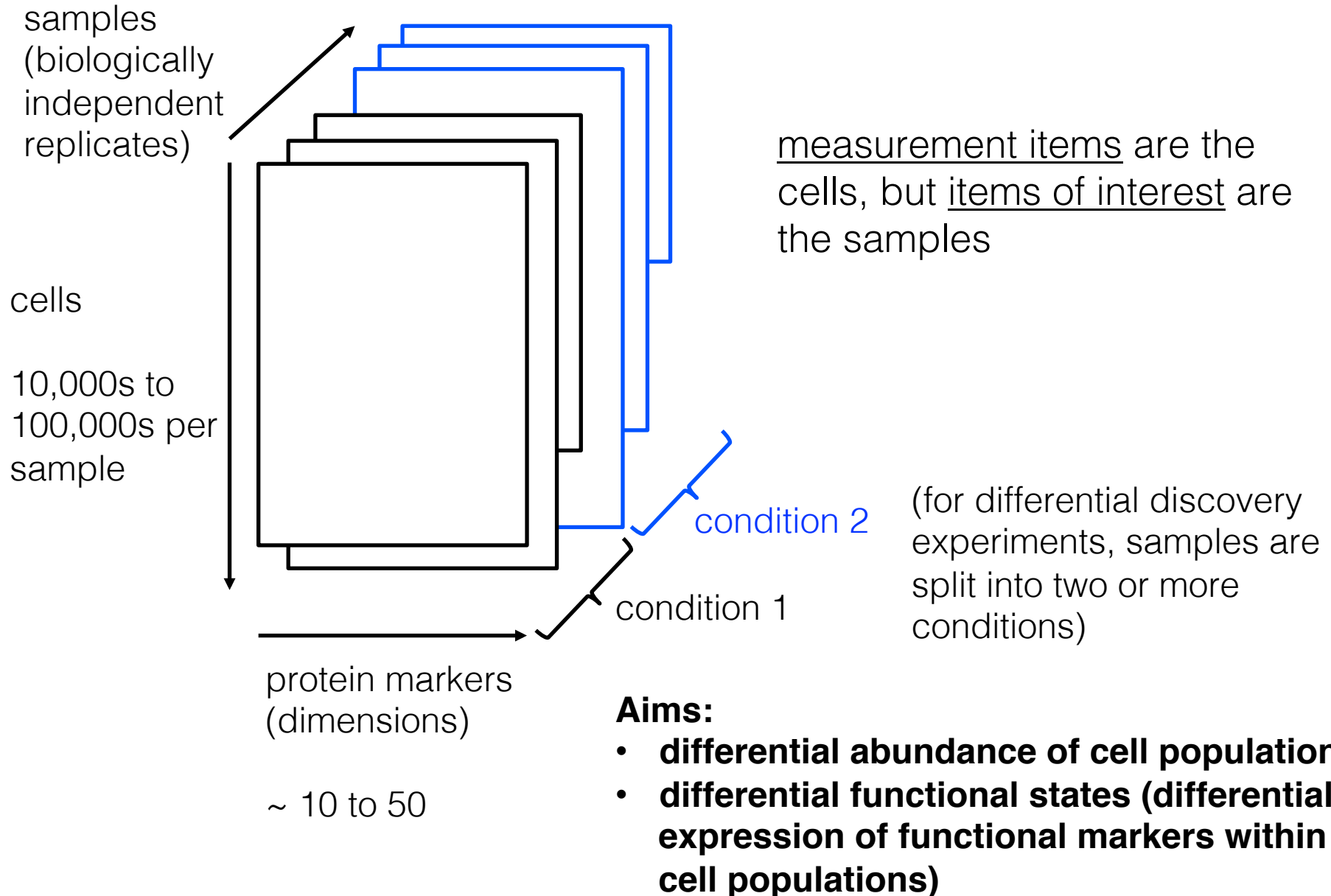


DNA-tagged cytometry

>100 proteins/cell
(limit: number of antibodies)

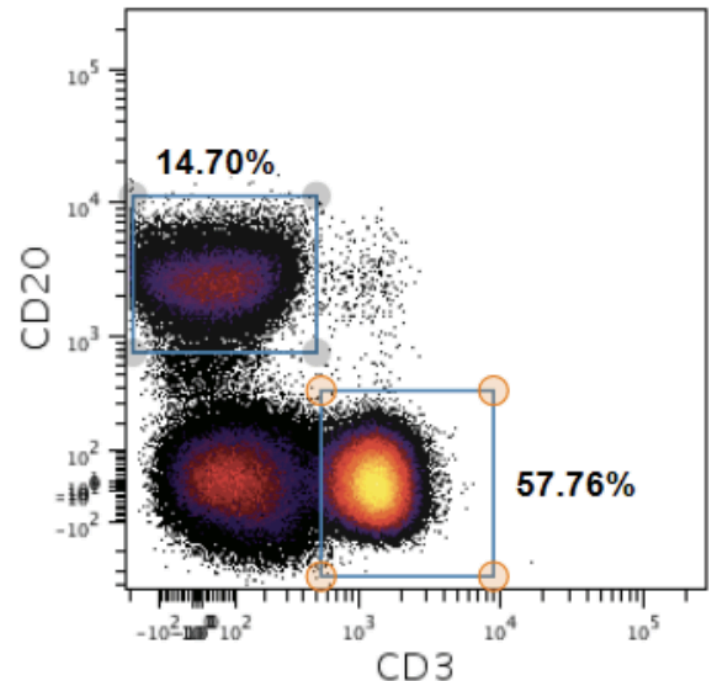
Shahi et al. (2017), Fig. 1A

Differential analysis for high-dim. cytometry



Automated analysis methods

- Manual gating
 - visual inspection of 2D scatterplots to detect known cell populations
- High-dimensional data
 - too many possible 2D scatterplots; subjective; difficult to reproduce; difficult to detect unknown populations
 - $n = 40$ dimensions:
 $n(n - 1) / 2 = 780$ scatterplots
- Require automated analysis methods



manual gating example: Cytobank
<https://www.cytobank.org/>

CyTOF workflow: Nowicka et al. (2017)

(1) Paper

F1000Research



METHOD ARTICLE

REVISED CyTOF workflow: differential discovery in high-throughput high-dimensional cytometry datasets [version 2; referees: 2 approved]

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Open Peer Review

Referee Status:

(2) Bioconductor workflow

CyTOF workflow: differential discovery in high-throughput high-dimensional cytometry datasets

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Exercise

- Perform a “null comparison” using code and data from the CyTOF workflow
 - e.g. 4 vs. 4 comparison of “Reference” samples only
 - modify inputs to the differential testing / plotting functions and re-run the analysis
 - what do we expect? what do the results show?