Mass Cytometry (Cytometry by Time-Of-Flight)



How many markers do you need to define a T cell population?

1	3	5		11	18	~21-c	olours
1977	1984	1995		2001	2006	2015	
T cells lineages	CD4 T cell subsets		Phenotypic markers	Memor	y Activa	tion H	oming
CD3 CD4 CD8 TCRγδ-Vd1 TCRγδ-Vd2 MAIT (Va7.2.CD161)	Tregs CTLA4 Th1 IFNg, GZB Th2 IL4, IL13 Tfh IL21 Th17 IL17, TNF	, TNF	CD25 FOXP3 CD127 CCR4 CXCR3 CCR6	CD45RA CD45RC CCR7 CD27	ICOS Ki67 Bcl2 PD1 HLAD	DR (ntb7 CD49a CD49d CLA CCR2 CX3CR1

CCR10

CXCR5

CXCR5

CD103

CCR9

NKT (CD1d-GalCer)

Th9 IL9

Spectral overlap hinders the expansion of multicolour flow cytometry





Cytometry by Time-Of-Flight - CyTOF



Bendall et al, 2012

CyTOF measures only metals					
Cells identification:	Iridium as DNA intercalato				
Live Dead:	Cisplatin				
Markers:	Heavy metals isotopes				
S-phase:	lodine (IdU)				
In vivo tracking:	Gold nanoparticles				
Barcoding:	Palladium				

Osmium

Size:

Before you start your project

- Does Mass Cytometry help to answer my question?
- Well defined cohort/dataset
- Spend time in designing your panel (spillover, don't forget any marker)
- Need bioinformatics support?

Expensive (?)
Low Throughput
Takes time

Your Mass Cytometry project

Hope Reality







Standard manual gating using bivariate plots



N Markers= NxN/2 bivariate plots

1 1 1.1 k k 176Yb_CLA 1 11 1 6 4 E -. 2 V 4 -. 1 . . 1 6 6.1 . 2 .. 100 1 . . . 1 6 12

Multidimensionality reduction



Nature Biotechnology **volume 31**, pages 545–552 (2013)

The power of high dimensional analysis



Nature Immunology volume 17, pages 890–895 (2016)

Defining distinct populations on viSNE plots

Manual-gating on a bi-dimensional map



Unsupervised clustering (ACCENSE, DensVM, ClusterX)



Define the features of the different clusters

- Visualization of marker expression (viSNE)
- Heatmaps (Cytofkit, Cytobank)
- MEM (marker enrichment model)





Data analysis workflow









Software



- heavily down-sampled
- SPADE
- viSNE
- Citrus
- flowSOM



Cytofkit

- Phenograph
- UMAP
- Cluster X
- DensVM
- t-SNE
- Isomap
- PCA



- Phenograph
- UMAP
- t-SNE
- PCA
- SPADE
- FlowSOM
- downsampler

Issues in data analysis

Batch effects

Computationally heavy

Kinetics, longitudinal studies, biological models, etc.

Need for bioinformatics support

nature methods Highly multiplexed simultaneous detection of RNAs and proteins in single cells

Andreas P Frei^{1,5}, Felice-Alessio Bava^{1,5}, Eli R Zunder^{1,2}, Elena W Y Hsieh^{1,3,4}, Shih-Yu Chen¹, Garry P Nolan¹ & Pier Federico Gherardini¹



publications

Resource

Cell

Data-Driven Phenotypic Dissection of AML Reveals Progenitor-like Cells that Correlate with Prognosis



16-phenotypic markers 15-phospho-proteins

Levine JH et al, 2015

Hyperion Imaging System

RUDGM

nature methods

Highly multiplexed imaging of tumor tissues with subcellular resolution by mass cytometry

Charlotte Giesen^{1,8}, Hao A O Wang^{2,3,8}, Denis Schapiro^{1,4}, Nevena Zivanovic^{1,5}, Andrea Jacobs¹, Bodo Hattendorf², Peter J Schüffler⁶, Daniel Grolimund³, Joachim M Buhmann⁶, Simone Brandt⁷, Zsuzsanna Varga⁷, Peter J Wild⁷, Detlef Günther² & Bernd Bodenmiller¹



FACS vs CyTOF





Parameters

4-10 easy10-20 hard20-30 very hard

<35 easy 42-48 hard (Limit 135)

Auto-fluorescence

Yes

Sorting

Yes

No

No

Acquisition speed

10000-20000/s

150-500/s

Competing technologies

Mass Cytometry

Multi Colour Flow Cytometry

Cite-Seq (DNA Tags)

45-60 (Limit 135)

30-50 Fluorochromes

No limits in number of antibodies

Difficult to build panel Custom made conjugations Limited Flexibility Low Throughput Low number of cells Sensitivity? \$\$\$\$\$

High Throughput
Cell isolation
High sensitivity

Protein detection+ scRNA sequencing

WIMM Mass Cytometry Facility

https://www.imm.ox.ac.uk/research/facilities/mass-cytometry-facility



Panels available:

Human:

- T cell phenotyping
 - T cell functional
 - Myeloid
- Phospho-proteins, fixed cells

<u>Mouse</u>:

General phenotyping