

Multiparametric Cytometry Data Analysis: Stairway to High-Content



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High-content cytometry enables large-scale, single-cell proteomics with 40+ markers. We will cover key data processing steps—QC, normalization, batch correction, dimensionality reduction, clustering, annotation, and integration—through expert talks, round-tables, and software solutions with the aim to build a collective consensus and knowledge around high-content cytometry data analysis.



Deadline: **July 3, 2026**

PHASE I THEORETICAL



October
5-7, 2026



Montpellier

CYTOMETRY DATA PRE-PROCESSING

Annelies EMMANEEL (VIB, BEL), Raphael GOTTARDO (University of Lausanne, CHE) and Sofie van GASSEN (VIB, BEL)

CYTOMETRY DATA UNSUPERVISED ANALYSIS

Anna BELKINA (Boston University, USA), Yvan SAEYS (VIB, BEL) and Jonathan IRISH (Vanderbilt University, USA)

AUTOMATED GATING AND MACHINE LEARNING

Martin MESTDAGH (Institut Curie, FRA), Can PINAR (Cytolytics, DEU), Benjamin TAST (LMU-BMC, DEU), Vincent PETIT (METAFlow, FRA), Mar NARANJO-GOMEZ (IRMB, FRA), Arielle GINSBERG (TerraFlow, USA) and Sonia GAVASSO (University of Bergen, NOR)

CELL ANNOTATION

Alexia ALFARO (Institut Gustave Roussy, FRA), Ryan BRINKMAN (BC Cancer Agency, CAN) and Antonio COSMA (Luxembourg Institute of Health, LUX)

BIOLOGICAL AND CLINICAL CYTOMETRY DATA INTEGRATION

Sarah BONTE (VIB, BEL), Thomas ASHHURST (University of Sydney, AUS) and Samuel GRANJEAUD (CRCM, FRA)

Inserm
Workshop

291



PHASE II PRACTICAL



November
16-18, 2026



Luxembourg,
Lille, Paris &
Marseille

The aim of the practical workshops will be to explore different aspects of high-content cytometry data analysis with experts in the field, and to train young researchers for future implementation in their practice. The principle, the workflow, interpretation and comparison of each process/tool will be discussed.

- Control and push the limits of unsupervised analysis ¹
- Dimension reduction and clustering pipelines and available tools ²
- Automated supervised pipelines with OpenCyto and FowDensity ²
- Full analysis pipeline supported by Business Intelligence tools ¹

¹ experience in conventional data analysis required;
² minimal experience in R required.

SELECTION: 44 trainees (8 for Luxembourg, 12 for Lille, 12 for Paris & 12 for Marseille) will be selected among Phase I participants.

INFORMATION &
REGISTRATION [CLICK HERE](#)



Inserm Workshop 291

Analyse des Données Multiparamétriques de Cytométrie : en chemin vers le haut-contenu **Multiparametric Cytometry Data Analysis: Stairway to High-Content**

5-7 octobre 2026 / October 5-7, 2026 ■ Montpellier, France

Lundi 5 octobre 2026 ■ **Monday October, 5th 2026**

14:30 - 15:00	Reception of participants
15:00 - 15:15	Welcome and presentation by the organizers
SESSION I	Cytometry data pre-processing
15:15 - 16:00	Selection of high-quality cytometry data Annelies Emmaneel (VIB, Ghent, Belgium)
16:00 - 16:30	Coffee Break & Posters Session
16:30 - 17:15	Normalization, transformation and scaling of cytometry data Raphael Gottardo (University of Lausanne, Switzerland)
17:15 - 18:00	Experimental design, quality controls and batch correction Sofie van Gassen (VIB, Ghent, Belgium)
18:00 - 19:00	Panel discussion
19:00 - 19:15	Posters Presentation
19:15	Cocktail Dinner & Posters Session

Mardi 6 octobre 2026 ■ **Tuesday October, 6th 2026**

06:30 - 08:30	Breakfast
SESSION II	Cytometry data unsupervised analysis
08:30 - 09:15	Dimension Reduction: how to use it properly. Anna Belkina (Boston University, USA)
09:15 - 10:00	Clustering: use, limits and control. Yvan Saeys (VIB, Ghent, Belgium)
10:00 - 10:30	Coffee Break & Posters Session
10:30 - 11:15	Clustering & Dimension Reduction: making most of them. Jonathan Irish (Vanderbilt University, Nashville, USA)
11:15 - 12:00	Panel discussion
12:00 - 13:00	Lunch

SESSION III	Automated gating and machine learning
13:00 - 13:45	StarGate, rigorous repetitive analyses with standardized gating strategies Martin Mestdagh (Institut Curie, Paris, France)
13:45 - 14:30	Cytolytic: One stream automatic solution for your analysis Can Pinar (Cytolytics, Berlin Germany) Benjamin Tast (LMU-BMC, Munich, Germany)
14:30 - 15:15	METAFlow: Augmented intelligence-driven analysis solution Vincent Petit (METAFlow, Paris, France) Mar Naranjo-Gomez (IRMB INSERM, Montpellier, France)
15:15 - 16:00	TerraFlow: Supervised analysis from the FCS to the scientific report Arielle Ginsberg (TerraFlow, New York, USA) Sonia Gavasso (University of Bergen, Norway)
16:00 - 16:45	Round Table
16:45 - 17:15	Coffee Break & Posters Session
SESSION IV	Cell annotation
17:15 - 17:30	Introduction to cell annotation Alexia Alfaro (Institut Gustave Roussy, Paris, France)
17:30 - 18:15	Global Standardization of Immune Cell Population Identification and Semantic Annotation Ryan Brinkman (BC Cancer Agency, Vancouver, Canada)
18:15 - 19:00	Global Standardization by arithmetization Antonio Cosma (Luxembourg Institute of Health, Esch-sur-Alzette, Luxembourg)
19:00 - 19:30	Panel discussion
20:15	Dinner

Mercredi 7 octobre 2026 ■ **Wednesday October, 7th 2026**

06:30 - 08:30	Breakfast
SESSION V	Biological and clinical cytometry data integration
08:30 - 09:15	Cytometry / Omics / Clinics: how to perform integration? Sarah Bonte (VIB, Ghent, Belgium)
09:15 - 10:00	Application of cytometry data integration in multiomics analysis Thomas Ashhurst (University of Sydney, Australia)
10:00 - 10:30	Coffee Break & Posters Session
10:30 - 11:15	Machine learning for integrating clinical and biological data Samuel Granjeaud (CRCM, Marseille, France)
11:15 - 12:00	Panel discussion
12:00 - 14:00	Lunch
14:00	Departure