

# 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

Sofie van GASSEN (VIB, BEL), Raphael GOTTARDO (University of Lausanne, CHE) and Katrien QUINTELIER (VIB, BEL)

### CYTOMETRY DATA UNSUPERVISED ANALYSIS

Anna BELKINA (Boston University, USA), Yvan SAEYS (VIB, BEL) and Jonathan IRISH (University of Colorado, 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 (Dotmatics, USA) 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)

## 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 <sup>1</sup>
- Dimension reduction and clustering pipelines and available tools <sup>2</sup>
- Automated supervised pipelines with OpenCyto and FowDensity <sup>2</sup>
- Full analysis pipeline supported by Business Intelligence tools <sup>1</sup>

<sup>1</sup> experience in conventional data analysis required;  
<sup>2</sup> 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**