Publishing Flow Cytometry Data

User guidelines

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Policy, purpose and responsibilities

- The goal of this document is to ensure a proper preparation of your data and information to publish flow cytometry data following MIFlowCyt guidelines
- Instrument configuration tables as well as other templates can be requested from the CAF. Please contact:

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or

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026/300.85.79

What information should I provide about my flow cytometry experiments to include them in my manuscript?

- To ensure that you have submitted all relevant information, this guide will provide you with best practices in information to provide. The basis of this document has been prepared in conformity with the "Minimum Information About a Flow Cytometry Experiment (MIFlowCyt)" paper, published in 2008 in Cytometry part A (DOI: 10.1002/cyto.a.20623)
- It has been assumed that your manuscript will content standard information, such as the purpose of the experimentations, what are the type of samples used, how they have been performed in terms of groups and biological variables observed, treatment of the samples, what are the conclusion from these experimentations, and how flow cytometry experiments are included in the overall protocol of preparation of the sample.
- On top of all the relevant experimental information's, that might be englobed in a more general description of the overall project, some points must be included regarding the flow cytometry data them-selves:

1. Instrument details:

- Several information regarding the instrument itself have to be provided: name and model of the instrument, manufacturer, instrument optical configuration (lasers + filters), running sheath fluid. **Such documents-tables are prepared by the CAF for each instrument, please request them upon needs.**
- The acquisition settings mut be provided, meaning the voltages/gain used for each channel with corresponding fluorochrome, as well as the type of data recorded (A-H-W).

- A sentence explaining how the instrument is standardized long-term: ***"The flow cytometer was quality-controlled at least weekly using manufacturer-recommended procedures and an internal 8-peak bead protocol. Instrument maintenance and performance monitoring were conducted by the core facility, with documented long-term stability."***

2. Samples details:

- The exact protocol of sample preparation must be provided: *the number of cells, timing, volumes, temperature and all buffer used (Fix/Perm, brilliant staining buffer, Fc block…)*
- The panel used must be fully documented:
  a. Using a table showing all information: *AB specificity (e.g. CD4), alternative protein names (if applicable), clone used, vendor, fluorescent dye, concentration (in ug/ml), and purpose (dump, viability, specific cellular sub-type gating, etc.).* ***Such template-table is available by the CAF, please request it upon needs.***
  b. Explaining how the panel has been checked: *controls used during experiment (pos-neg-FMOs-standardization samples), titration performed*
- State about the sample acquisition: *flow rate, timing after staining if delayed, tube or plate, fresh filtering or not.*

3. Analysis details:

- Include how the compensation/unmixing was performed: *beads and/or cells, software used*
- State the data transformation used: *usually it's bi-exponential scaling (to better resolve the data close to 0 and the fluorescence that has a much higher dynamic range), but could be linear for cell cycle analysis, or some others.*
- Explain the gating details of your analysis:
  a. Explain the cleaning steps, full gating strategy used, statistical values obtained (%, MFI, CV…)
  b. Explain how the gates were places (based on FMO or negative or nice separation), if they have been adapted for each sample or not
  c. Include a figure representing the full gating on a sample with arrows and gates
- What was the software used for the analysis, if it was performed manually or unsupervised. If unsupervised, cite the algorithms used for clustering, also for any visual dimensionality reduction (tSNE, UMAP…) used and how the clusters have been annotated.

4. Data accessibility & representation:

- If you represent graphically some flow cytometry data, please include:
  a. Correct axes legend: *laser, filter, analyte, dye*
  b. Scaling of each axis
  c. Type of sample-gate represented on each graph in the direct legend

- The raw data, meaning FCS files, must be made available in a public repository (fair science principle) as much as possible, or at least made available upon request.
  a. No specific public flow cytometry database exists (don't use "flowrepository", it's not working anymore), but you can use for example "Zenodo" for your data.
  b. Your FSC files should contain *correct channel annotation, correct sample name*. ***These information's MUST be well entered on the software of analysis before exportation of the data!***

SOP revision (annually at minimum)

Revision	Date	Description of Changes	Reviewed By
V1	09.07.2026	Initial Release	Sarah Cattin