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Title: "New Flow Cytometry Data Standards and Data Analysis with Bioconductor"

The Flow Informatics and Computational Cytometry Society (FICCS) (<http://www.ficcs.org>) and the International Society for Analytical Cytology (ISAC) Data Standards Task Force (DSTF) (<http://www.isac.net>) have been cooperating on the development of new flow cytometry data standards (<http://flowcyt.sourceforge.net/>). While FCS will continue to be supported by ISAC, the DSTF has been looking for a more flexible solution that would reuse existing standards (formats) to store binary analytical cytology data. A focus has been on developing a methodology to standardize the recording of metadata (e.g., gating descriptions), while both simplifying the data standard and facilitating the incorporation of data from other platforms (e.g., image and Raman spectrophotometry data)

The general strategy for development of new cytometry data file format standards has been to:

- (i) Define the information required to be in the data file;
- (ii) Prepare a requirements document to focus the development process;
- (iii) Apply (i) and (ii) to guide the development and review of new data standards.

This effort has resulted in the Minimum Information about a Flow Cytometry Experiment (MIFlowCyt) criteria, which has been recently adopted by ISAC, Proposals for encoding gating/transformations and compensation (Gating-ML), raw data (netCDF) and a data/metadata container (Analytical Cytometry Standard; ACS) are under consideration as ISAC DSTF Working Drafts.

In parallel with data standards efforts, there has been a drive to develop open source software tools to facilitate high-throughput flow cytometry data analysis. Quality control and quality assessment are critical when developing new high-throughput technologies and their associated information services. A variety of exploratory data analytic tools for analyzing flow cytometry data have been implemented in the Bioconductor open source and open development software project for bioinformatics (<http://www.bioconductor.org/>). Examples of how these tools can be used in the context of analyzing clinical FCM data will be presented.