

Bioinformatics Data Standards
for
Flow Cytometry

Why Bioinformatics Standards for Flow Cytometry?

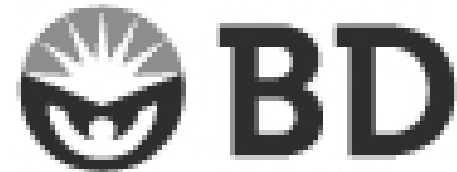
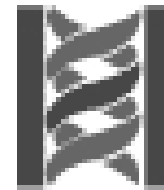
- Flow cytometry is a widely used clinical and research technology
 - Cancer, HIV, stem cells, vaccine development, cell types
- Data gathering step is increasing throughput...
 - Technology is data intensive
 - 300,000 cells/minute
 - 6 parameters/cell
 - Now high throughput FCM
 - 1,000 samples/day

Why Bioinformatics Standards for Flow Cytometry?

- Data (information) processing now has to increase
- Data analysis is currently:
 - slow
 - error prone
 - not standardized
 - most limiting aspect of technology
- Need to simplify extraction of statistical information for end users (scientists)

Collaborative Group

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- Dr. Perry Haaland
- Adam Treister
- International Society of Analytical Cytology



Bioinformatics Standards for Flow Cytometry

1. Non-technical description of important experimental parameters to be captured
2. Ontology for standardizing scientists' experimental descriptions
3. Encapsulate experimental descriptions in ways that are computationally tractable (e.g., UML)
4. Capture experimental descriptions within data exchange standard (e.g., RDF, XML)
5. Provide standardized way to store information (e.g., SQL schema)
6. Reference implementations of above

Implications of FCM Standards

- Facilitate basic and clinical research
 - Once standards are in place more complex bioinformatics analyses can begin
- Exchange of data both within collaborations and between scientific groups
- Facilitate automated, traceable and flexible methods for processing the data