

REPRESENTING FLOW CYTOMETRY EXPERIMENTS WITHIN FUGE

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Objective

The lack of bioinformatics standards in flow cytometry (FCM) prevents collaborative opportunities to recreate experimental methods and results. Flow cytometry data file standard (FCS) has been adopted as the common representation of FCM data without major compatibility issues for fluorescence values that FCS captures. However, experimental metadata and analysis components are not recorded in a standardized fashion for use by independent parties. Flow cytometry community has identified the need of a shared object model to capture experimental workflow including data and metadata in broad context.

Materials & Method

Flow Informatics and Computational Cytometry Society (FICCS) Object Model Working Group (FICCS OMWG) has been established during the FICCS meeting in Seattle, WA, USA, in September 2006. The group committed to evaluate possibilities of building an FCM-specific object model based on existing technologies and models; possibly reusing and sharing common concepts with other 'omics' sciences. Representatives of the working group met for a development workshop in Dallas, TX, USA, in October 2006. The main purpose of the workshop was to closely evaluate whether the Functional Genomics Experiment (FuGE) Object Model is useful as the core for the FCM object model, and, based on the results, specify methodology and strategy to develop the first initial draft of the model. The timeline and resulted action items were specified aiming to present an initial draft solution at the FICCS meeting in Seattle, WA, USA, in November 2006.

Results & Conclusions

FICCS OMWG chose FuGE as the core for the FCM object model. The main areas to start extending FuGE were identified as:

- (i) *Flow cytometry protocol package.* FCM-specific classes shall be extended from FuGE to support FCM-specific actions including computational and data processing actions.
- (ii) *Data package.* Event though FCS is supposed to represent FCM data, an FCM-specific data class was identified as essential to capture associations between parameters (FCS) and conceptual molecules (FuGE).
- (iii) *Material package.* Physical characteristics of material used as FCM sample are describable using general FuGE concepts. FCM extension mainly captures the role of various subcomponents in conjugated samples (i.e., reporter and detector), which is crucial to associate detected fluorescence values with properties of biological interests.

Several FCM use cases will be modeled within the FCM-extended FuGE in order to provide immediate feedback and validation.