Flow Cytometry: Critical Assessment of Population Identification Methods (FlowCAP)
To advance the development of computational methods for the identification of cell populations of interest in flow cytometry data

http://flowcap.flowsite.org

FlowCAP Organizing Committee
- Ryan Brinkman, British Columbia Cancer Agency
- Raphael Gottardo, Fred Hutchison Cancer Research Center
- Richard Scheuermann, University of Texas Southwestern Medical Center
- Jill Schoenfeld, Tree Star, Inc.

Sponsored by the National Institute of Allergy and Infectious Diseases
FlowCAP Summit 2010

Date: September 21st & 22nd, 2010
Time: 8:30AM-5:50 PM (Tuesday) and 9:00AM-3:30 PM (Wednesday)
Location: Natcher Conference Center, NIH Campus
45 Center Drive
Bethesda, Maryland 20892

AGENDA

DAY ONE (Tuesday):

8:30-9:00AM  Registration

9:00-9:10AM  Importance of FlowCAP from the DAIT Perspective
Dan Rotrosen
Division of Allergy Immunology and Transplantation, NIAID

9:10-9:40AM  FlowCAP: history, goals and design of FlowCAP-I
Richard H. Scheuermann
U.T. Southwestern Medical Center

9:40-10:10AM  Rapid Cell Population Identification in Flow Cytometry Data
Nima Aghaeepour
British Columbia Cancer Agency

10:10-10:40AM  Automatic determination of the number of mixture components in Flow
Cytometry with Variational Bayes
Hannes Bretschneider
University of British Columbia

10:40-11:00AM  BREAK

11:00-11:30AM  GPU accelerated Bayesian mixture models for FCM analysis
Cliburn Chan
Duke University

11:30-12:00PM  flowMerge: Merging mixture components for automated gating of flow
cytometry data
Greg Finak
Clinical Research Institute of Montreal

12:00-12:30PM  Flow Cytometry Data Assessment with L2 Discrepancy Learning Process:
Analysis and Visualization
Faysal Khettabi
British Columbia Cancer Agency

12:30-1:30PM  LUNCH
1:30-2:00PM  On the use of NMF and curvHDR to cluster flow cytometry data
Joe Maisog
Medical Numerics, Inc. / Georgetown University Medical Center

2:00-2:30PM  TBD (FLAME)
Geoff McLauchlan
University of Queensland

2:30-3:00PM  SWIFT: Scalable Weighted Iterative Flow-clustering Technique
Iftekhar Naim
University of Rochester

3:00-3:30PM  Self-organizing Maps for Flow Cytometry Data Analysis
Radina Nikolic
British Columbia Institute of Technology (BCIT)

3:30-3:50PM  BREAK

3:50-4:20PM  FLOCK: a density-based clustering method for automated identification
and comparison of cell populations in high-dimensional flow cytometry data
Yu Qian
U.T. Southwestern Medical Center

4:20-4:50PM  Support Vector Machines for classification of flow data
John Quinn
TreeStar, Inc

4:50-5:20PM  Misty Mountain - A Parallel Clustering Method. Application to Fast
Unsupervised Flow Cytometry Gating
Istvan Sugar
Mt. Sinai School of Medicine

5:20-5:50PM  SamSPECTRAL: Efficient spectral clustering on flow cytometry data
Habil Zare
British Columbia Cancer Agency

5:50PM  ADJOURN

DAY TWO (Wednesday):

9:00-10:00AM  KEYNOTE ADDRESS
Coherent Single Cell Analysis in the 21st Century: ROFLMAO
Mario Roederer
National Institutes of Health

10:00-10:20AM  BREAK

10:20-11:20AM  FlowCAP-I Results
Ryan Brinkman
11:20-12:00PM  FlowCAP-I Debrief: What worked and what didn’t work
Richard H. Scheuermann
U.T. Southwestern Medical Center

12:00-1:00PM  LUNCH

1:00-1:30PM  Comparative Metrics: Measuring the quality of a classification method without a known ground truth
Adam Triestar
TreeStar, Inc

1:30-1:50PM  FlowCAP-II: comparative metrics
Jill Schoenfeld
TreeStar, Inc

1:50-2:20PM  FlowCAP-II: Dataset classification and identification of important gaps in datasets used for FlowCAP-I
Richard H. Scheuermann
U.T. Southwestern Medical Center

2:20-2:40PM  FlowCAP-II: Beyond classification – other opportunities for FCM data analysis
Ryan Brinkman
British Columbia Cancer Agency

2:40-3:00PM  FlowCAP-II: design, funding
Ryan Brinkman
British Columbia Cancer Agency

3:00-3:30PM  Wrap up
Richard H. Scheuermann
U.T. Southwestern Medical Center

3:30PM  ADJOURN