

# FlowCAP2 Results: Challenges 1, 2, and 3

Nima Aghaeepour

CIHR/MSFHR Strategic Training Program in Bioinformatics for Health Research,  
University of British Columbia

*Sep.22.2011*

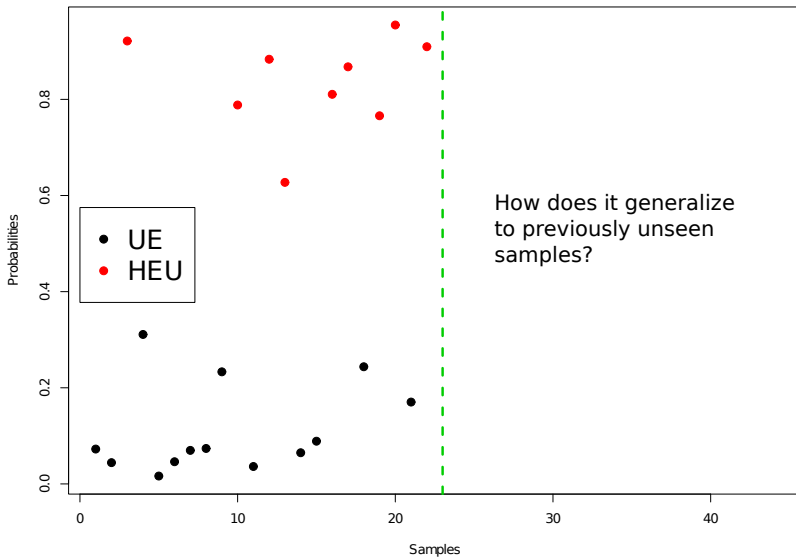


CIHR/MSFHR Strategic Training Program in  
**BIOINFORMATICS**

## Binary Classification

- Goal: evaluate the ability of computational pipelines in finding cell populations that can discriminate between two classes:
  - **1:** HEU vs UE
  - **2:** AML vs normal
  - **3a:** ENV vs GAG
  - **3b:** Responders vs non-responders
- Participants identify the cell populations that are different across the two classes.

# Problem Statement



## Binary Classification

- Two classes.
  - ① HEU vs UE
  - ② AML vs normal
  - ③ ENV vs GAG
  - ④ Responders vs non-responders
- Participants identify the cell populations that are different across the two classes.
- **Results will be tested on independent samples.**

# Evaluation Metrics (e.g., for AML)

## True(T), False(F), Positive(P) Negative(N)

- **TP:** An AML case marked as AML by a participants.
- **FP:** A normal case marked as AML by a participants.
- **FN:** An AML case marked as normal by a participants.
- **TN:** A normal case marked as normal by a participants.

## Accuracy

- **Accuracy:**  $(TP + TN)/(TP + TN + FP + FN)$

## Sensitivity and Specificity

- **Sensitivity:**  $TP/(TP + FN)$
- **Specificity:**  $TN/(FN + FP)$

## F-measure

- **F-measure:**  
 $2 * Sensitivity * Specificity / (Sensitivity + Specificity)$ 
  - Should not be mistaken with FlowCAP1's F-measure.

# **Challenge 1:** HIV Exposed Uninfected vs UnExposed Infants

# Challenge 1: HEU vs UE

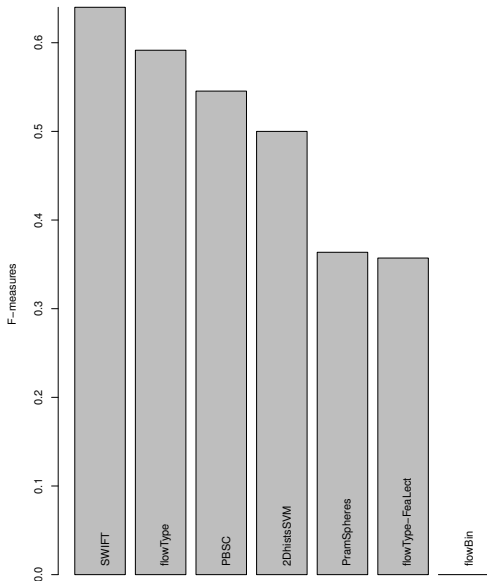
Table 1: Challenge 1: HEUvsUE

|                  | Sensitivity | Specificity | Accuracy | F-measure |
|------------------|-------------|-------------|----------|-----------|
| 2DhistsSVM       | 0.50        | 0.50        | 0.50     | 0.50      |
| flowBin          | 0.00        | 0.48        | 0.45     | 0.00      |
| flowType         | 0.58        | 0.60        | 0.59     | 0.59      |
| flowType-FeaLect | 0.33        | 0.38        | 0.36     | 0.36      |
| PBSC             | 0.55        | 0.55        | 0.55     | 0.55      |
| PramSpheres      | 0.36        | 0.36        | 0.36     | 0.36      |
| SWIFT            | 0.67        | 0.62        | 0.64     | 0.64      |

Note: FLOCK has been renamed to PBSC.

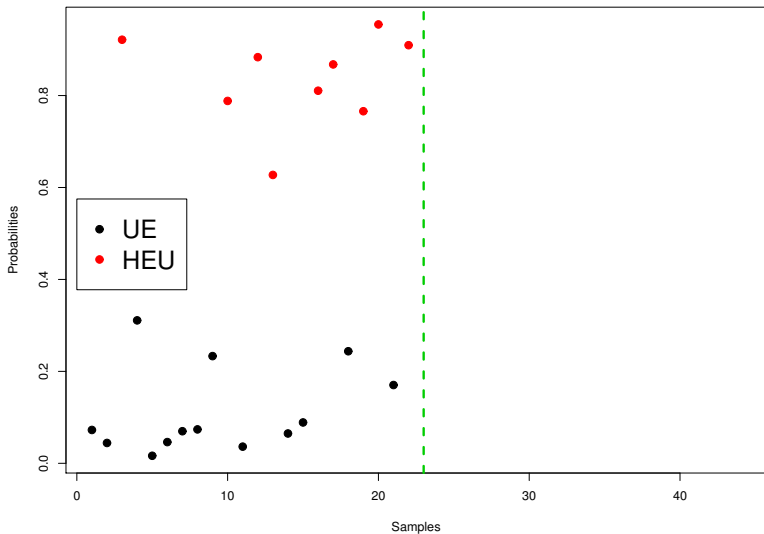
## HEU vs UE

- Random: 0.5
- How can some of them be worst than random?
- Have we been able to find something meaningful?
  - Cross-validation
  - Holdout validation (using other time points).

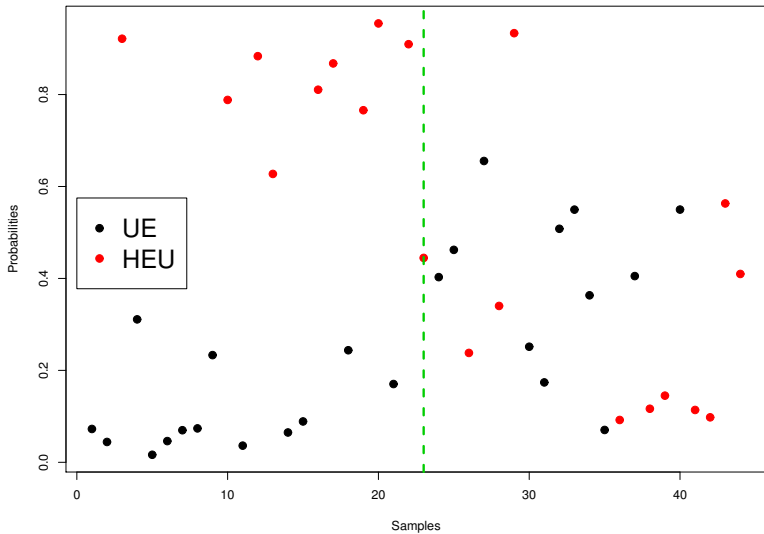




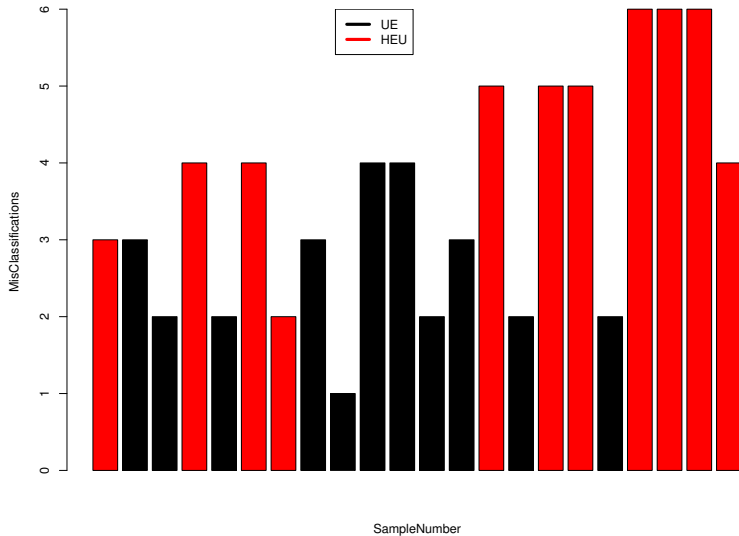
# Challenge 1: HEU vs UE



# Challenge 1: HEU vs UE



# Challenge 1: HEU vs UE



# Challenge 2: AML vs normal subjects

## AML

- Three perfect classification of 360 patients.

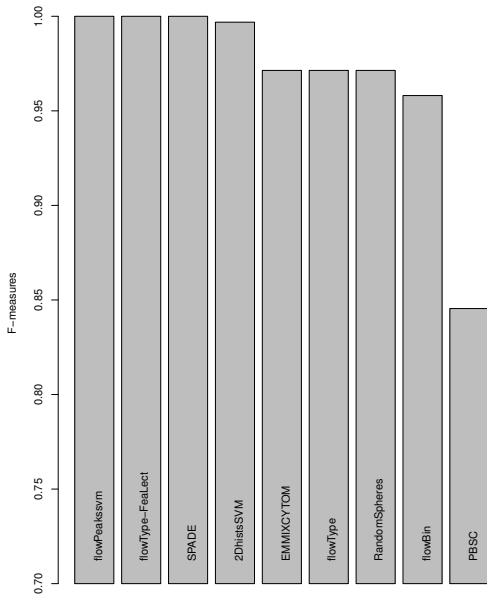
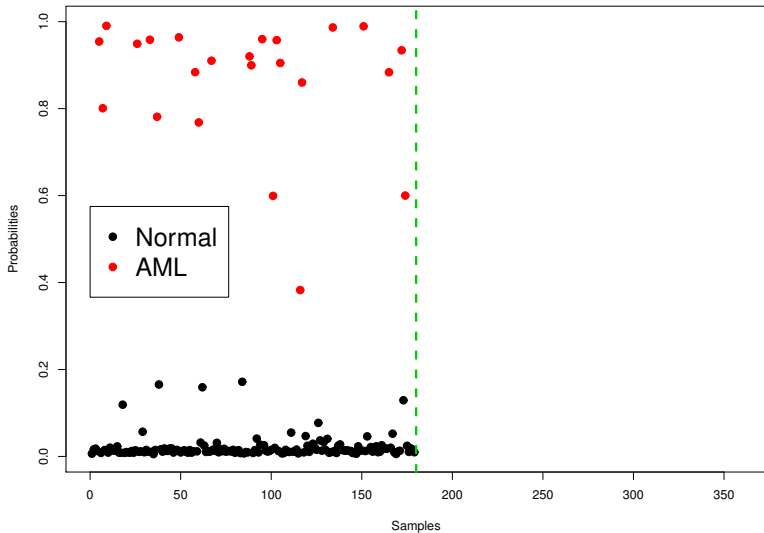


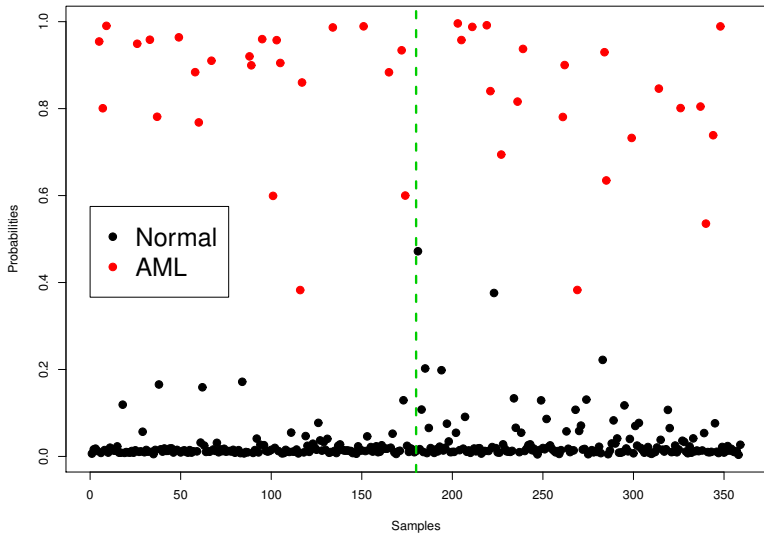
Table 2: Challenge 2: AML

|                  | Sensitivity | Specificity | Accuracy | F-measure |
|------------------|-------------|-------------|----------|-----------|
| 2DhistsSVM       | 1.00        | 0.99        | 0.99     | 1.00      |
| EMMIXCYTOM       | 0.95        | 0.99        | 0.99     | 0.97      |
| PBSC             | 0.75        | 0.97        | 0.94     | 0.85      |
| flowBin          | 1.00        | 0.92        | 0.92     | 0.96      |
| flowPeakssvm     | 1.00        | 1.00        | 1.00     | 1.00      |
| flowType         | 0.95        | 0.99        | 0.99     | 0.97      |
| flowType-FeaLect | 1.00        | 1.00        | 1.00     | 1.00      |
| RandomSpheres    | 0.95        | 0.99        | 0.99     | 0.97      |
| SPADE            | 1.00        | 1.00        | 1.00     | 1.00      |

## Challenge 2: AML

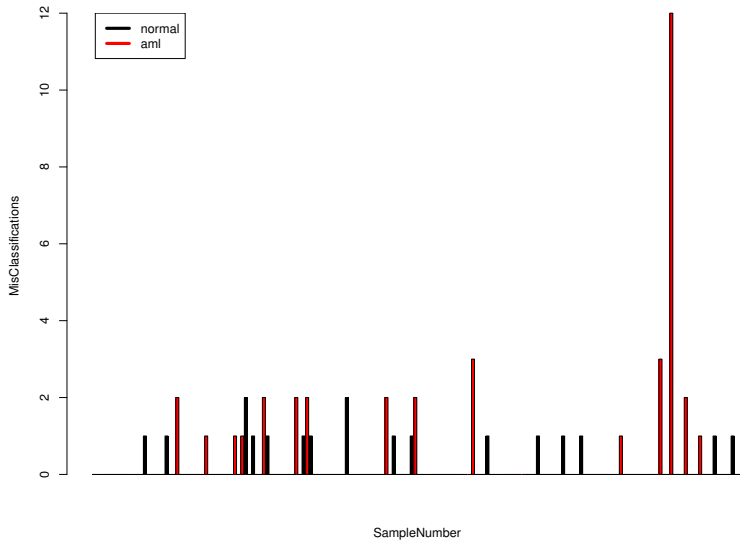


# Challenge 2: AML

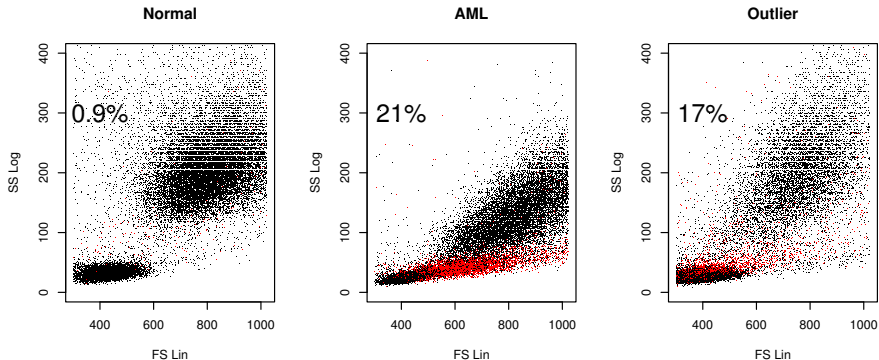




# Challenge 2: AML



## Challenge 2: AML



This dataset, perhaps, requires analysis of one marker at a time. Potential challenge for FlowCAP3: a dataset in which multiple markers should be used to find a rare cell populations.

# Challenge 3a: Identification of Antigen Stimulation Group

## HVTNa

- Six perfect classifiers for 40 patients.

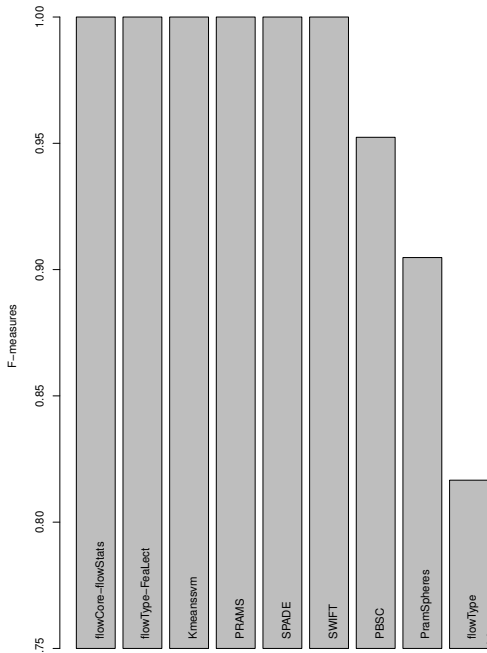
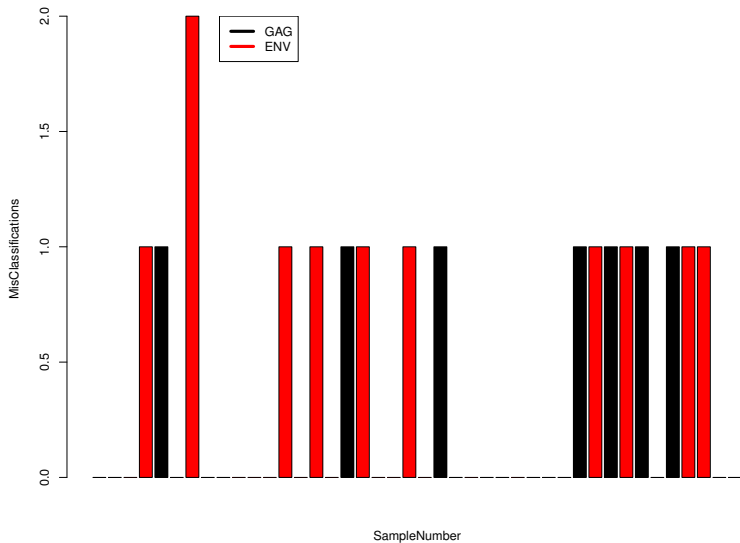


Table 3: Challenge 3: HVTNa

|                    | Sensitivity | Specificity | Accuracy | F-measure |
|--------------------|-------------|-------------|----------|-----------|
| PBSC               | 0.95        | 0.95        | 0.95     | 0.95      |
| flowType           | 0.88        | 0.76        | 0.81     | 0.82      |
| flowType-FeaLect   | 1.00        | 1.00        | 1.00     | 1.00      |
| flowCore-flowStats | 1.00        | 1.00        | 1.00     | 1.00      |
| Kmeanssvm          | 1.00        | 1.00        | 1.00     | 1.00      |
| PRAMS              | 1.00        | 1.00        | 1.00     | 1.00      |
| PramSpheres        | 0.90        | 0.90        | 0.90     | 0.90      |
| SPADE              | 1.00        | 1.00        | 1.00     | 1.00      |
| SWIFT              | 1.00        | 1.00        | 1.00     | 1.00      |

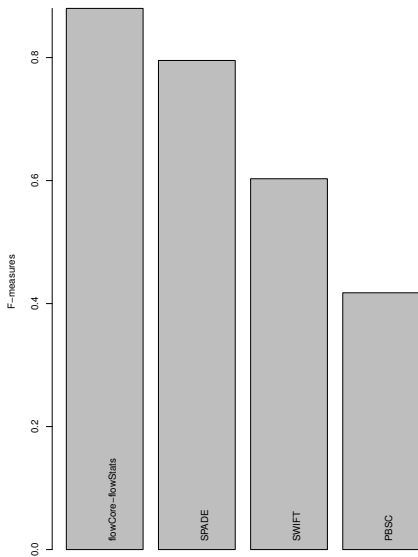
# Challenge 3: HVTNa



**Challenge 3b:** Identification of Responders and Non-Responders in Intracellular Cytokine Staining of Post-HIV Vaccine Antigen Stimulated T-cells

## HVTNb

- Maximum of 0.8 F-measure against cytokine repos measured by a human across 80 samples. Has the human been wrong?



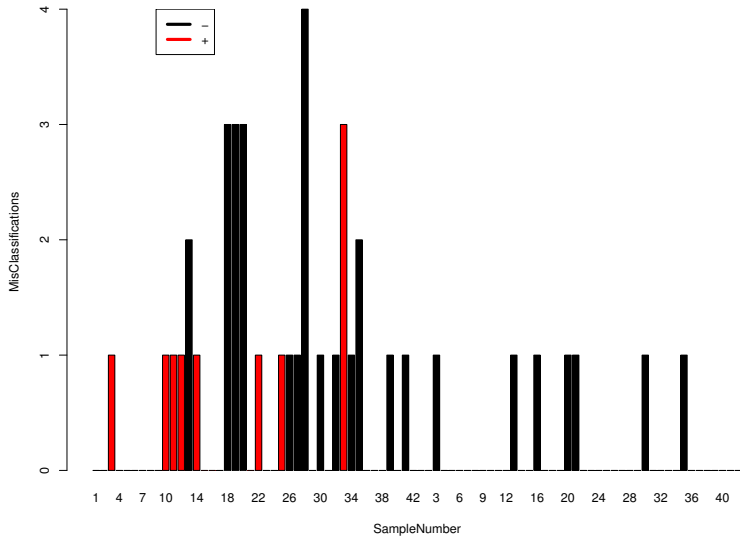
Algorithms



Table 4: Challenge 3: HVTNb

|                    | Sensitivity | Specificity | Accuracy | F-measure |
|--------------------|-------------|-------------|----------|-----------|
| PBSC               | 0.27        | 0.89        | 0.81     | 0.42      |
| flowCore-flowStats | 0.79        | 1.00        | 0.96     | 0.88      |
| SPADE              | 0.67        | 0.99        | 0.93     | 0.80      |
| SWIFT              | 0.43        | 0.98        | 0.83     | 0.60      |

# Challenge 3: HVTNb



# Acknowledgements

**FlowCAP CC** Ryan Brinkman, Raphael Gottardo, Tim Mosmann, Richard Scheuermann

**Upenn** Wade Rogers

**CFRI** Tobias Kollman

**FHCRC** Steve De Rosa

**UBC** Holger Hoos

## FlowCAP Participants

**Funding** FlowCAP is supported by NIH/NIBIB grant (EB008400).  
The FlowCAP summits are supported by NIH/NIAID.