



BC Cancer Agency

CARE & RESEARCH

An agency of the Provincial Health Services Authority



Lymphoma Diagnosis

Based on Automated analysis of Flow Cytometry Data

Habil Zare

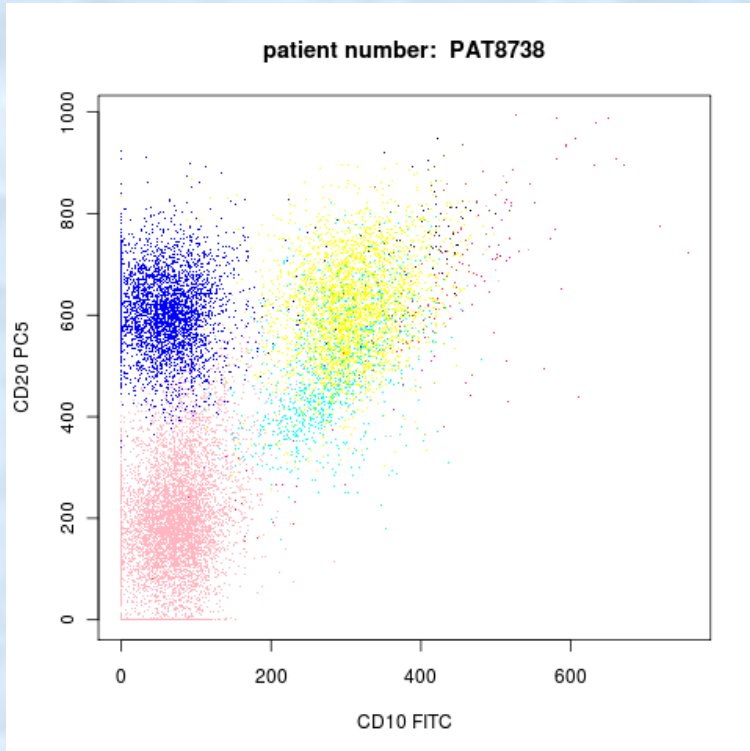
and

Ali Bashashati, Andrew Weng, Randy Gascoyne, Arvind
Gupta, Ryan Brinkman

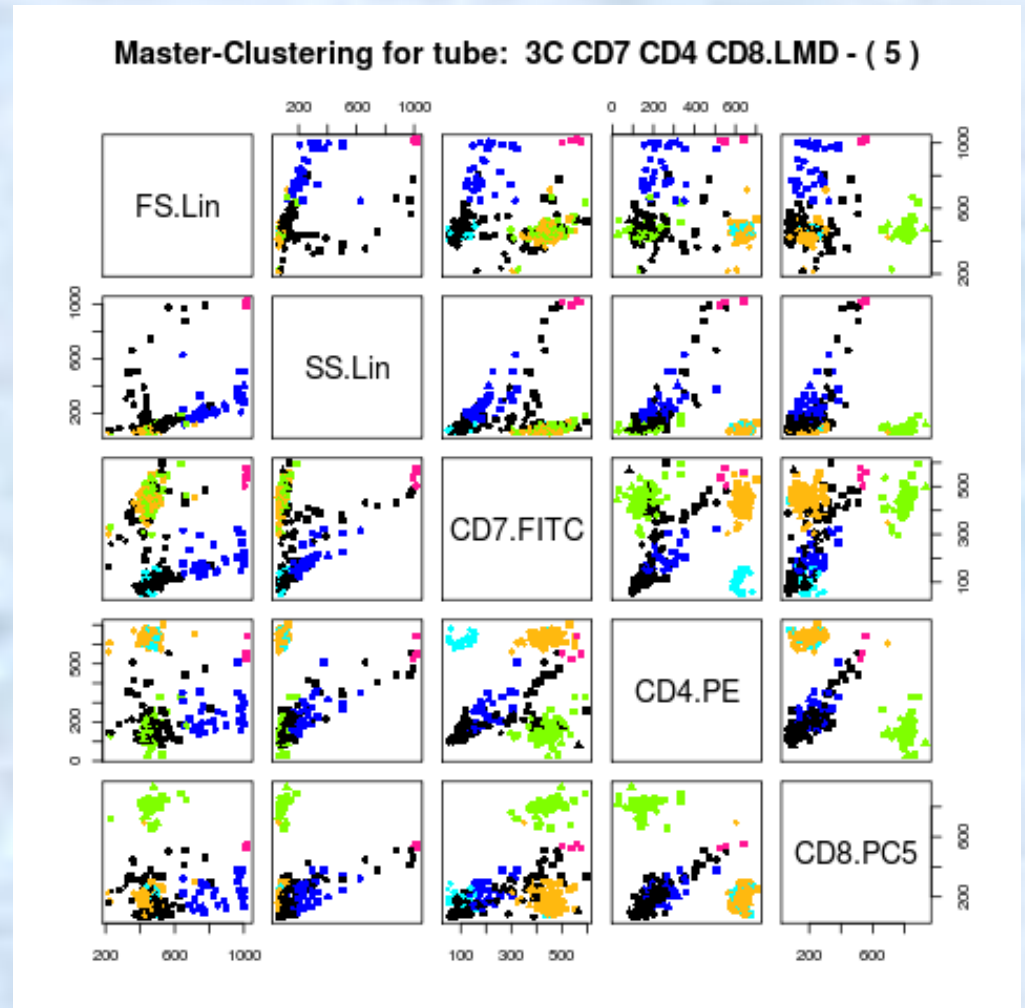
British Columbia Cancer Agency and University of British Columbia, Canada

Cancer Bioinformatics Workshop
Cambridge Research Institute
2nd - 4th September 2010

Flow Cytometry



Clustered by **SamSPECTRAL**



multi-dimensional

Method:

Challenge: Over 200 features with only samples → LASSO

$$\|Ax - y\|^2 + \lambda \|x\|_1$$

Result:

Table 1. Preliminary results of lymphoma classification of 100 random patients

			<i>Predicted</i>					
	type	Total	DLBC	follicular ¹	class_M ²	SLL ³	undetermined ⁴	misclassified ⁵
<i>Actual</i>	DLBC	28	25 (89%)	0	0	0	3 (11%)	4
	follicular	49	2 (4%)	46 (94%)	0	0	1 (2%)	0
	class_M	8	2(4%)	0	5(63%)	0	1(12%)	0
	SLL	15	0	0	0	14(93%)	1(12%)	0
	other	20	-	-	-	-	20	-

¹follicular = {FOLL1, FOLL2, FOLL3A, FOLL33B, FSC-FOLL1, FM-FOLL2}

²class_M = {MALT, MCL, MCLD, MCLMZ, MCLN, MZLN, MZLS}

³SLL = {SLL, SLLV}

⁴undetermined: Patient did not score high enough in any category

⁵Misclassified for a group of diagnosis is the number of patients who are predicted to be in this group incorrectly. Except for DLBC, no patients were misclassified.

BOLD: The number of correctly diagnosed patients are bold numbers on the diagonal.