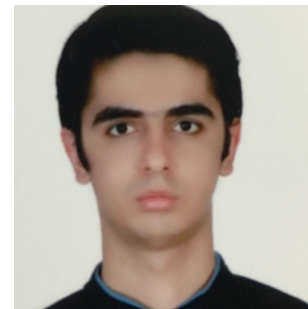


Amirreza Rouhi– Master student  
Thesis submission: April 2020  
Adv: Prof. Stefano Ceri



# Ensemble Feature Selection for Single Cell Hi-c data



**POLITECNICO**  
MILANO 1863

# Introduction to single-cell Hi-C data

## ➔ 1. Introduction to single-cell Hi-C data

## 2-What is the Goal?

## 3. Proposed Method

## 4. Experimental Results

## 5- Future works

Hi-C  Chromatin conformation capture method

**Hi-C data** is often used to *analyze genome-wide chromatin organization*

Single-cell Hi-C is a modification of the original [Hi-C](#) protocol

Allows us to determine **proximity of different regions** of the *genome* in a single cell

*Single-cell* assays introduce a new axis of **variation— cell-to-cell variability**—that *is not directly observable in data derived from a bulk sequencing*

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# Single Cell Hi-C Data

## 1. Introduction to single-cell Hi-C data

## 2-What is the Goal?

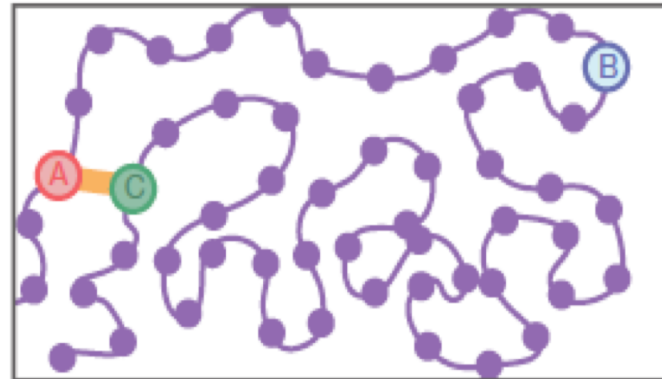
## 3. Proposed Method

## 4. Experimental Results

## 5- Future works

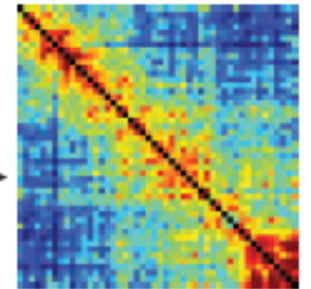
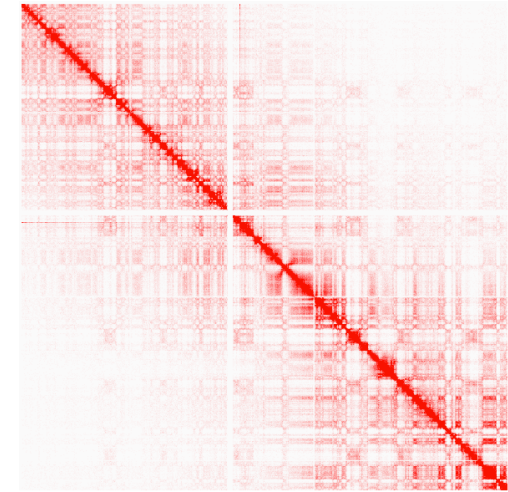
Single Cell Hi-C data is represented as **two-dimensional contact matrices**

Genomic distance between loci:  
Nuclear distance between loci:



**Contact Matrix**

	A	B	C
A	-	0.01	0.09
B	0.01	-	0.02
C	0.09	0.02	-

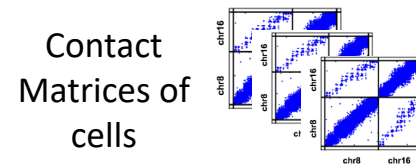
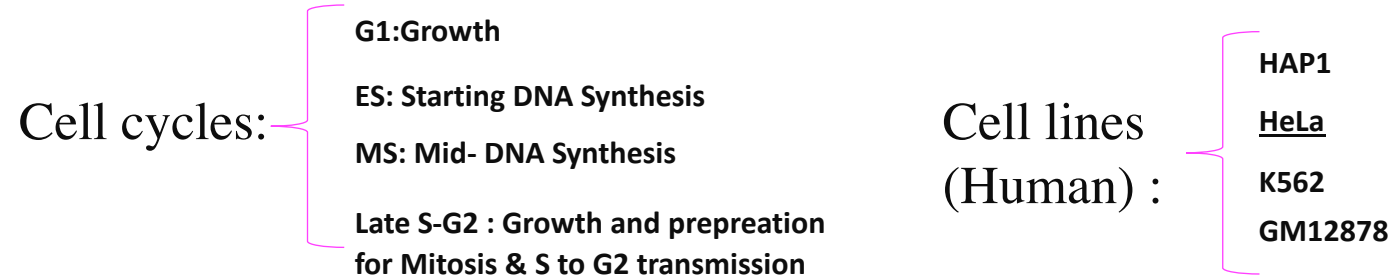


**The sparsity of single-cell Hi-C data is higher than most other types of single-cell data.**

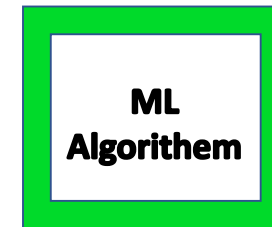
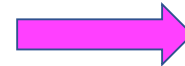
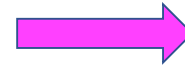
**Main Problem : The Sparsity of Single Cell Hi-C data**

# What is the Goal?

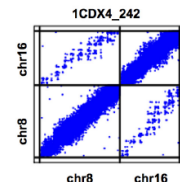
Design a **Unique method** to use in two different problems:  
Determine the 1-Cell Cycle and 2-Cell line of **each cell**



Labels **G1 ES MS**



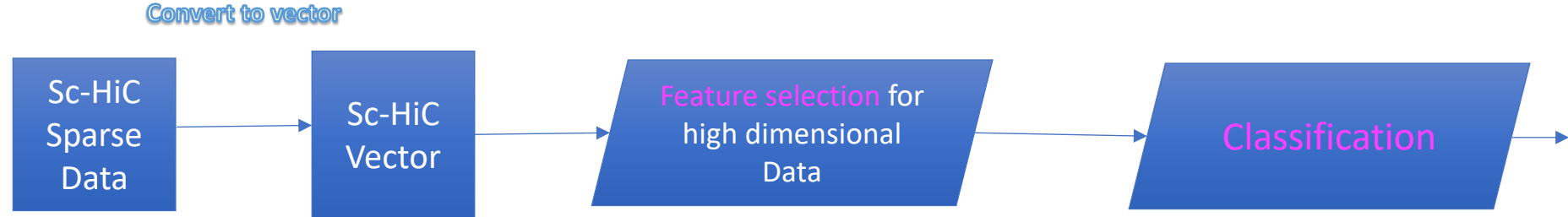
unseen data



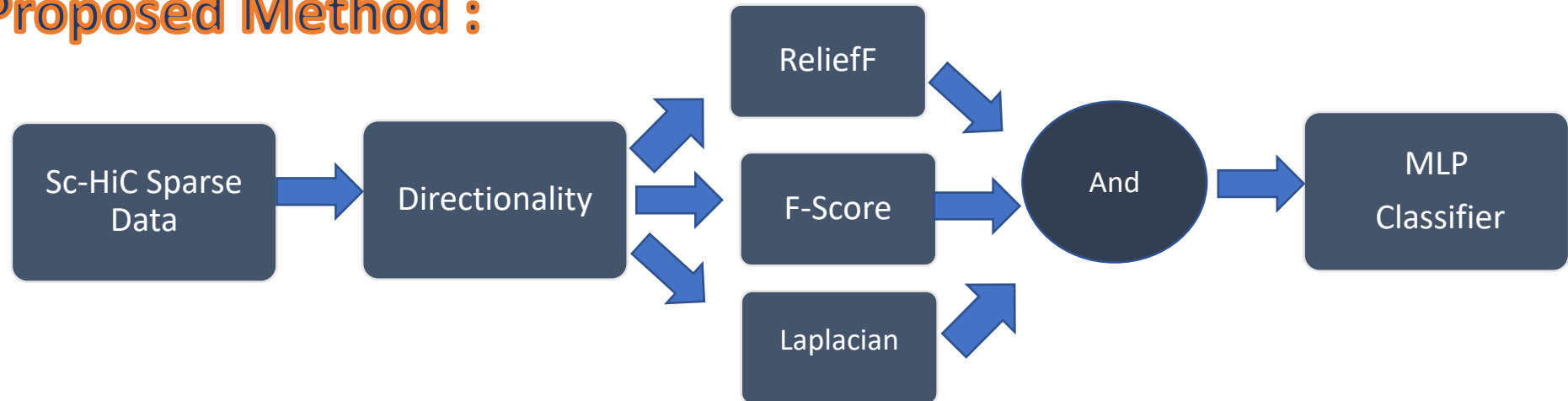
Stage Prediction

**96%G1**  
**2%ES**  
**1%MS**  
**1%G2**

## Proposed framework



## Proposed Method :



# Directionality :

If in a sparse matrix X for diagonal cell (i,i) we have:

$$X(i,j) = \begin{pmatrix} 0 & 3 & 1 & 0 & 2 & 3 & 8 & 1 & 1 & 3 \\ 1 & 1 & 0 & 0 & 7 & 1 & 2 & 2 & 3 & 3 \\ 1A4 & 2 & 2 & 0 & 0 & 6 & 7 & 1 & 2B4 & 2 \\ 1 & 2 & 3 & 10 & 0 & 4 & 6 & 1 & 0 & 5 \\ 3 & 2 & 2 & 1 & 4 & 3 & 2 & 1 & 6 & 0 \\ 7 & 4 & 4 & 5 & 3 & 9 & 6 & 1 & 6 & 1 \\ 7 & 1 & 1 & 5 & 2 & 8 & 9 & 1 & 3 & 6 \\ 5 & 0 & 1 & 6 & 2 & 0 & 0 & 0 & 1 & 5 \\ 1 & 6 & 3 & 3 & 4 & 6 & 2 & 0 & 1 & 1 \\ 1 & 2 & 2 & 4 & 1 & 1 & 3 & 0 & 8 & 2 \end{pmatrix}$$

$A_i = \sum_{j=n}^i X(i,j)$  Summation of contacts between bin i and previous bins

$B_i = \sum_{k=i}^{i+n} X(i,k)$  Summation of contacts between bin i and next bins

Where n is a boundaries variable. Then we can assign a score (Directionality Score) to each bin as:

$$\text{Directionality\_Score} = \frac{B-A}{|B-A|}$$

Now we were able to convert the matrix into vectors (for each column we have a score) .

1. Introduction to single-cell  
Hi-C data

2-What is the Goal?

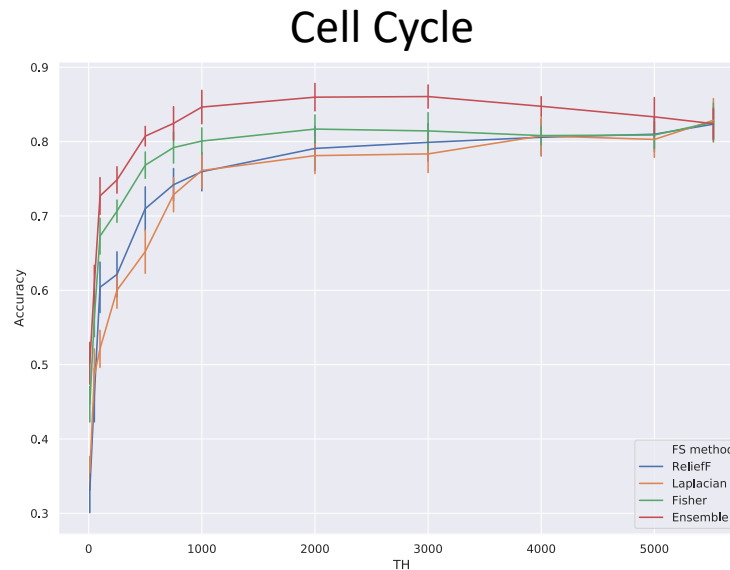
➔ 3. Proposed Method

4. Experimental Results

5- Future works

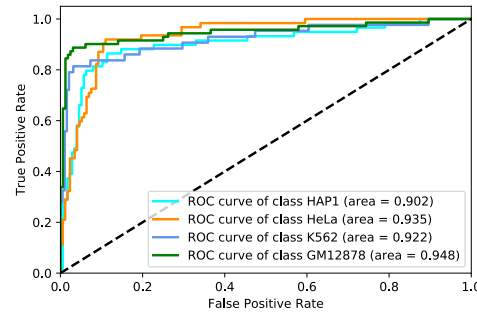
# Experimental Results- Accuracy

Comparison between the accuracy rate of the proposed Ensemble method and single methods using MLP classifier (10 CV)

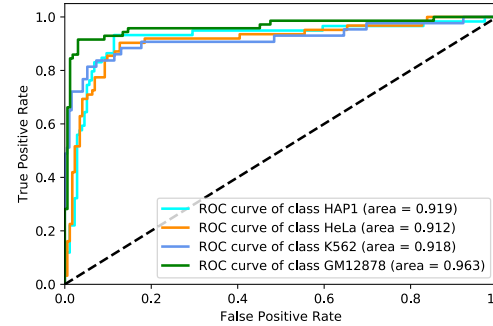


# Experimental Results- ROC

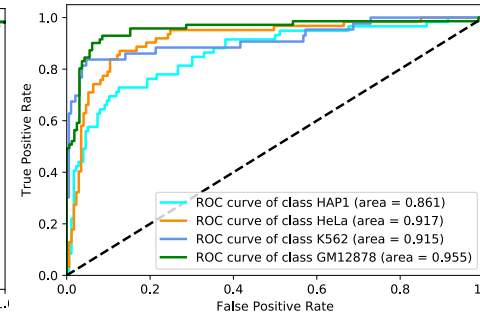
## Cell Cycle:



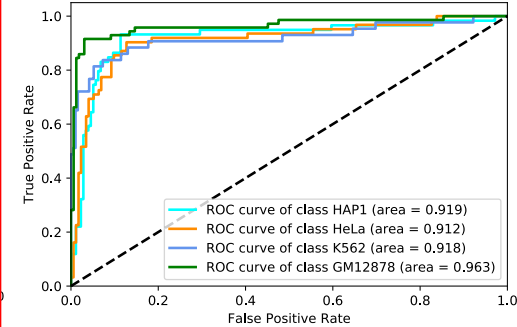
ROC Curve for applying Fscore method



ROC Curve for applying Laplacian score method

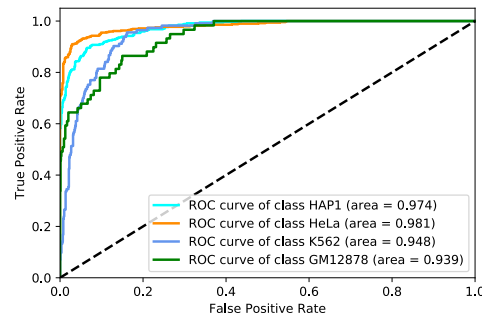


ROC Curve for applying ReliefF method

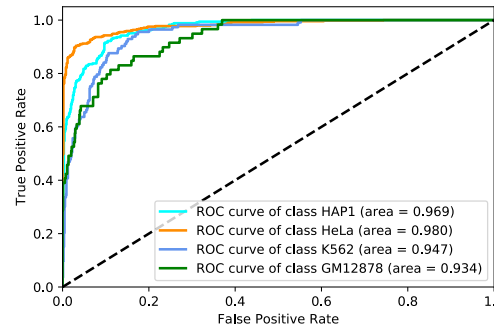


ROC Curve for applying Ensemble method

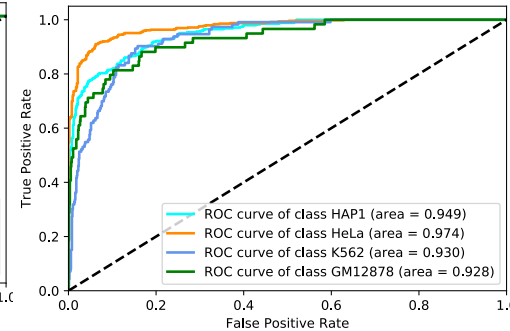
## Cell Line:



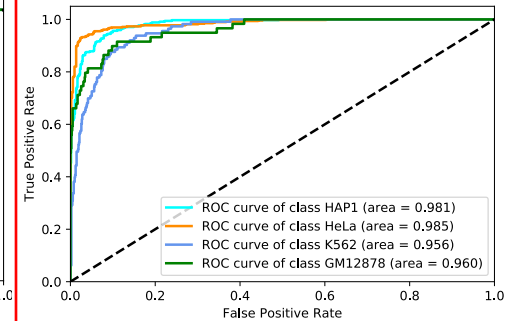
ROC Curve for applying Fscore method



ROC Curve for applying Laplacian score method



ROC Curve for applying ReliefF method

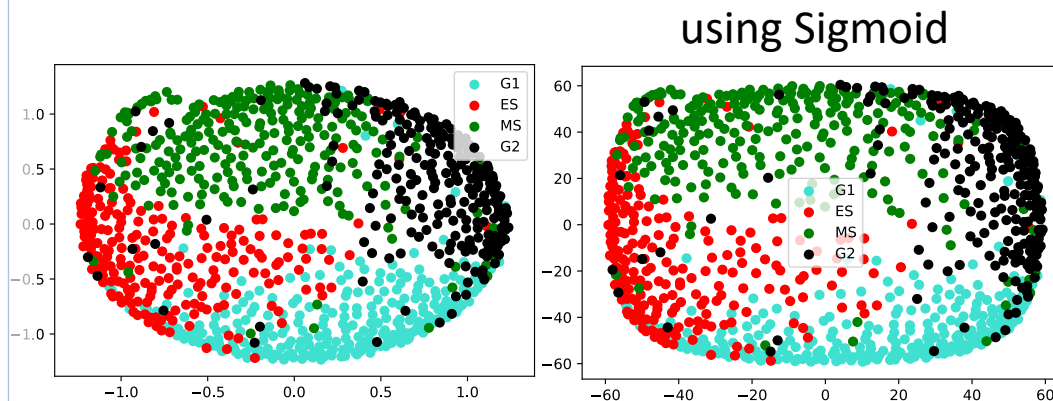


ROC Curve for applying Ensemble method

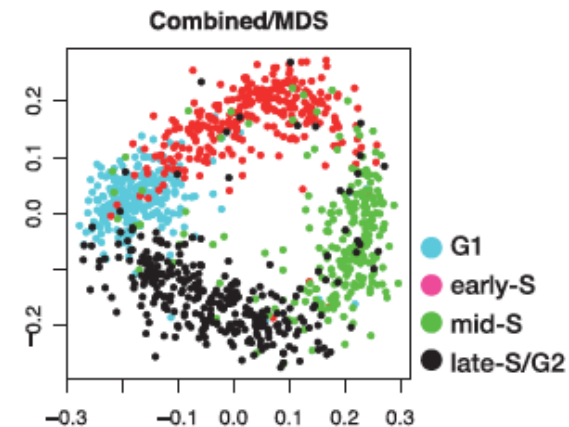


# Experimental Results- Cell Cycle

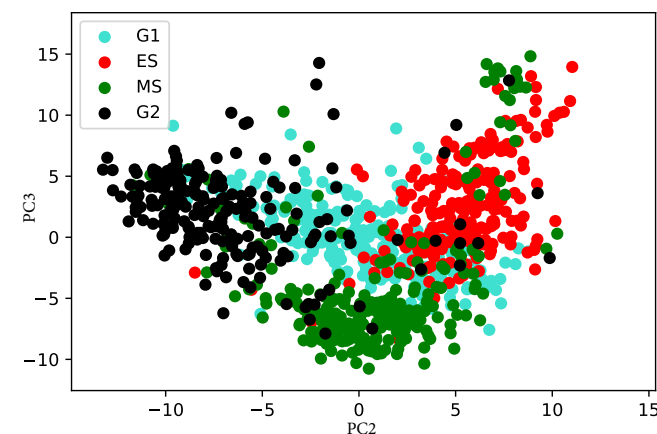
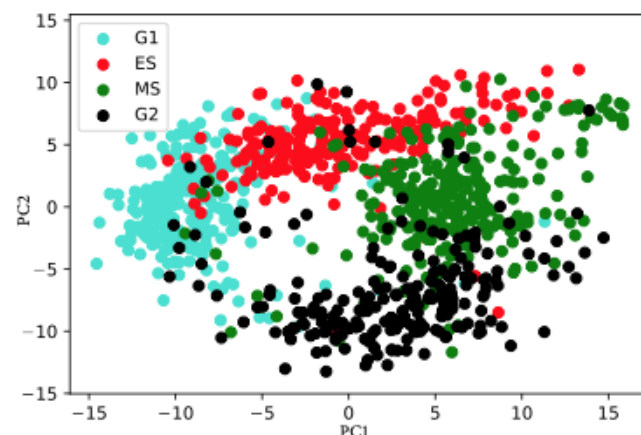
MDS projections from the four cell-cycle phases when the Distance measure is calculated using cosine



Compare with result from Li et al. :

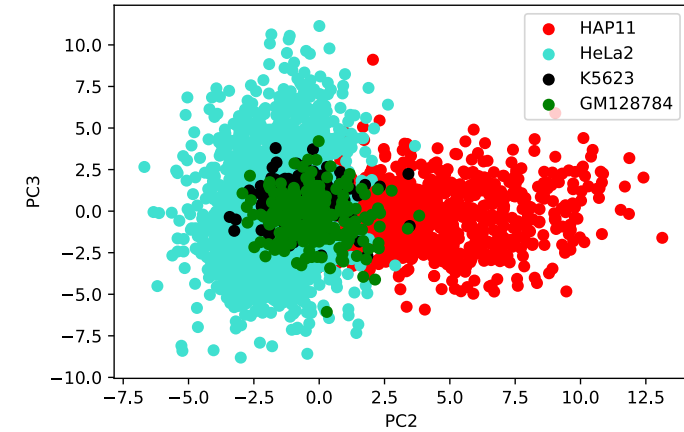
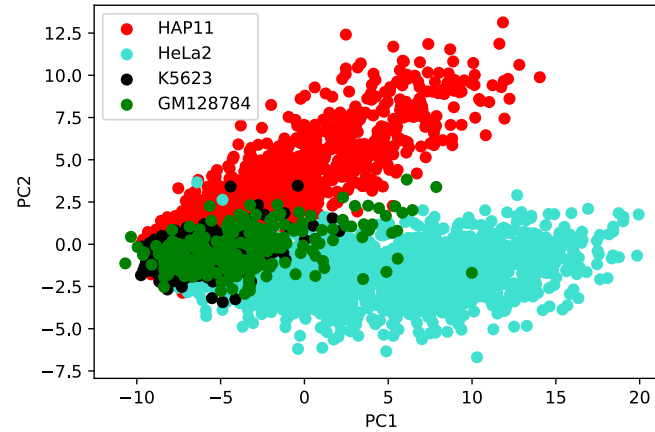


PCA projections from the four cell-cycle phases :

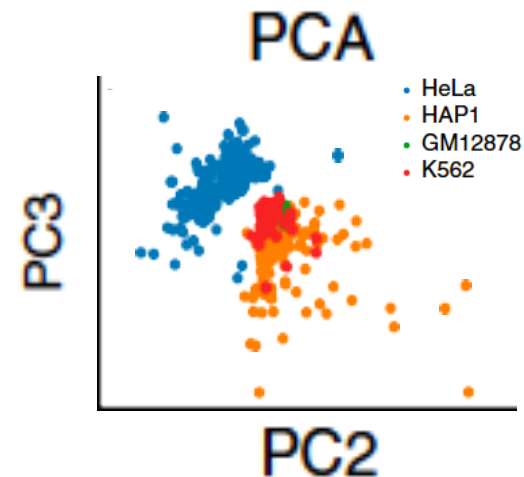


# Experimental Results- Cell Line

PCA projections from the four lines

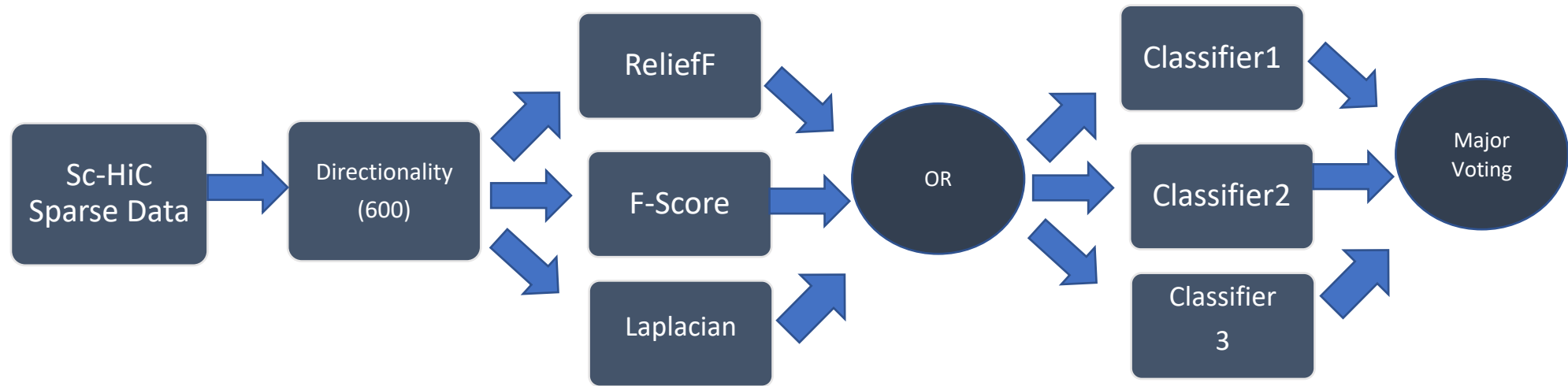


Compare with result from Zhou et al. :



## Future works

### Applying Ensemble Classification

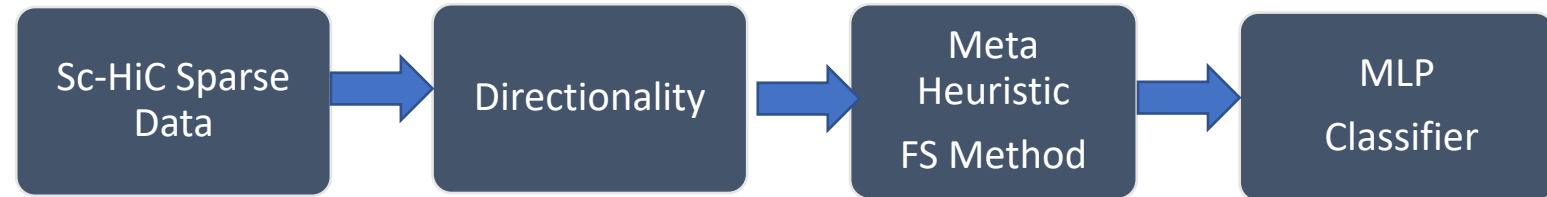


Benefit:

\*Increase the classification accuracy by using ensemble technique and aggregate the results

## Future works

Applying meta-Heuristic Feature Selection methods



\*Increase the performance of selecting the effective bins

**Thank you for your attention**