A Time Series Based Approach for Classifying Mass Spectrometry Data

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joint work with:

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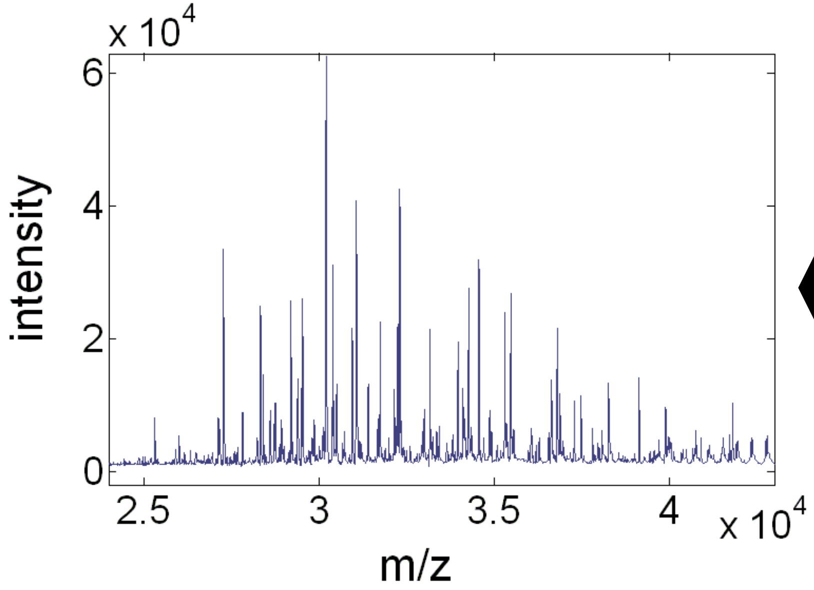
Introduction

A typical *Mass Spectrum*



m/Z	intensity
....	...
799.976004	135.864
800.004478	156.232
800.032953	140.765
800.061429	152.13
800.089905	137.15
800.118381	132.145
800.146858	131.137
800.175336	122.761
800.203814	124.499
800.232292	125.993
...	...

Mass Spectrometry (MS)

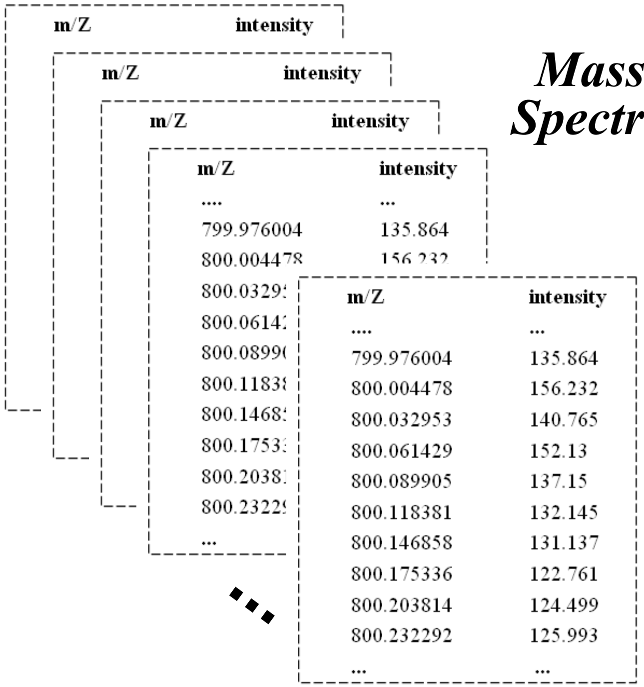
⇓

MS-based Proteomics

Focus in MS-based Proteomics:

identify discriminating values in the spectra (i.e. (m/z, intensity) couples corresponding to biomarkers) that are indicators of biological states (e.g. disease).

Introduction



Mass Spectra

PROBLEMS:

HIGH dimensionality

HUGE datasets

Mandatory requirement:

AUTOMATIC DATA MANAGEMENT

Introduction

Traditional data mining tasks directly applied on raw spectra may not reach satisfying results

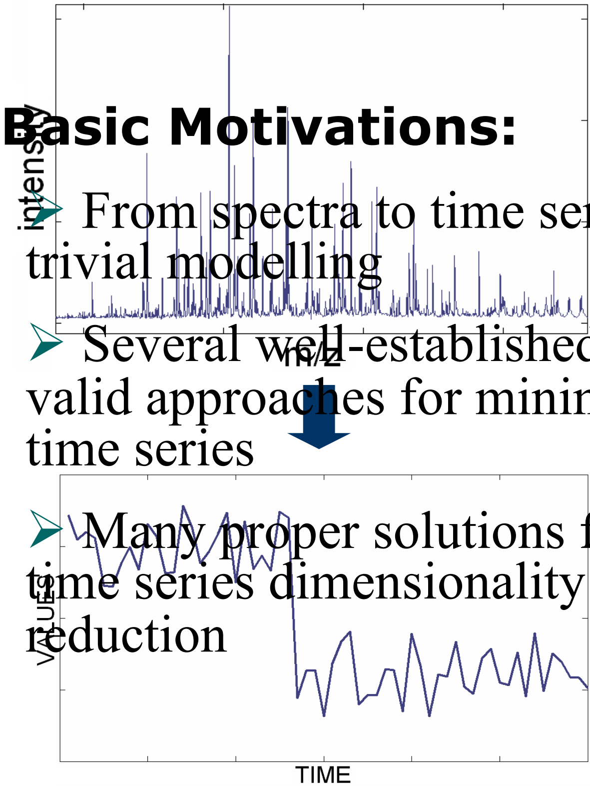
Need for a proper mass spectra representation

IDEA:

Mass Spectra modelled as **TIME SERIES**

Basic Motivations:

- From spectra to time series: trivial modelling
- Several well-established and valid approaches for mining of time series
- Many proper solutions for time series dimensionality reduction



Introduction

Our idea allowed us to reach
excellent results
in classifying mass spectra:

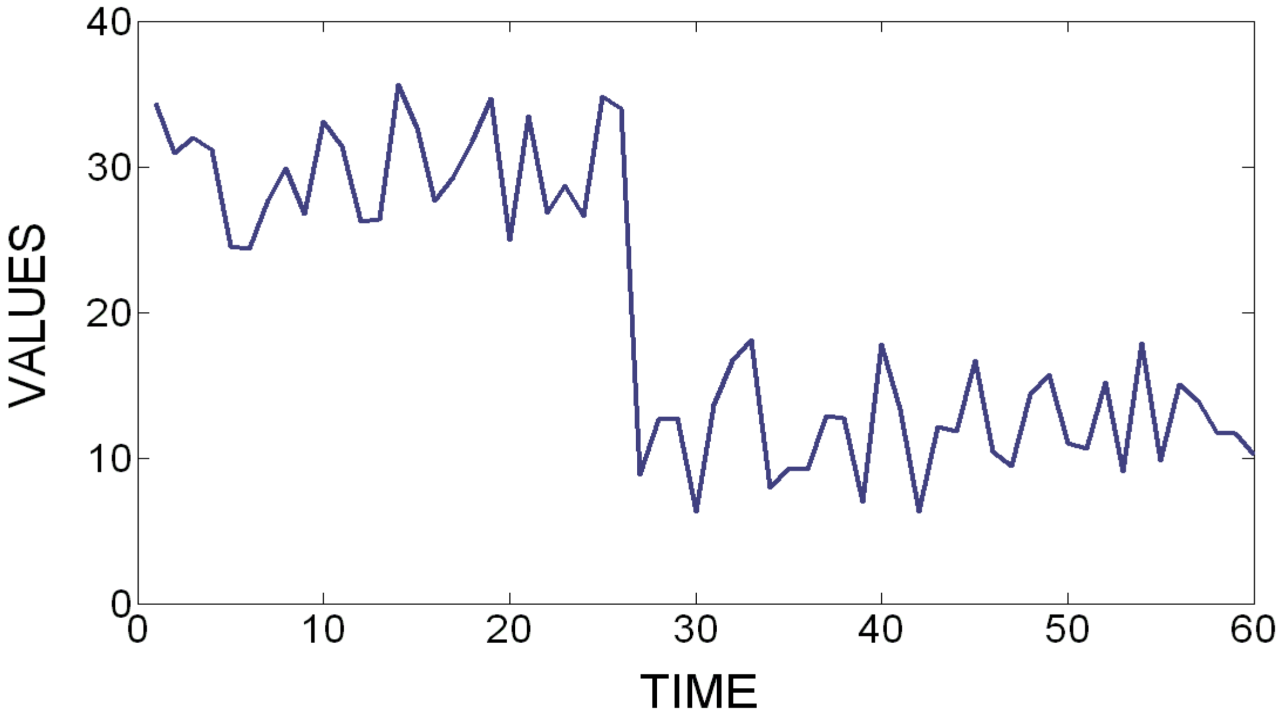
Ovarian Cancer dataset ➡ **classification accuracy: 87%**

MALDI UNICZ dataset ➡ **classification accuracy: 96%**

Outline

- Introduction
- Overview of time series data management
    - The DSA model
- A Time Series based Framework for Mass Spectrometry Data
- Experimental results
- Conclusions

Time Series data



Traditional time series form:

$$T = [(x_1, t_1), \ldots, (x_n, t_n)]$$

Time series form under condition of fixed sampling period:

$$T = [x_1, \ldots, x_n]$$

Time Series Data Mining

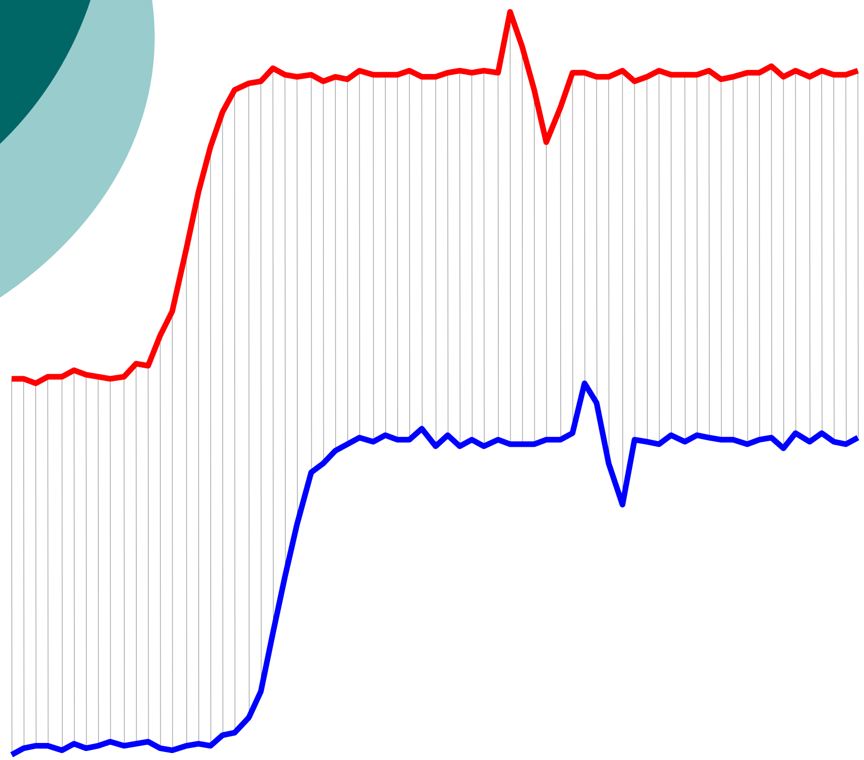
Automatic management of time series data
is typically accomplished
by applying data mining tasks.

Two main issues:

- **Distance Measures**
  - One-to-one alignment (euclidean distance)
  - Warping time axis
  - String matching
- **Dimensionality Reduction**
  - Piecewise discontinuous functions
  - Low-order continuous functions

Time Series Distance Measures:
Dynamic Time Warping

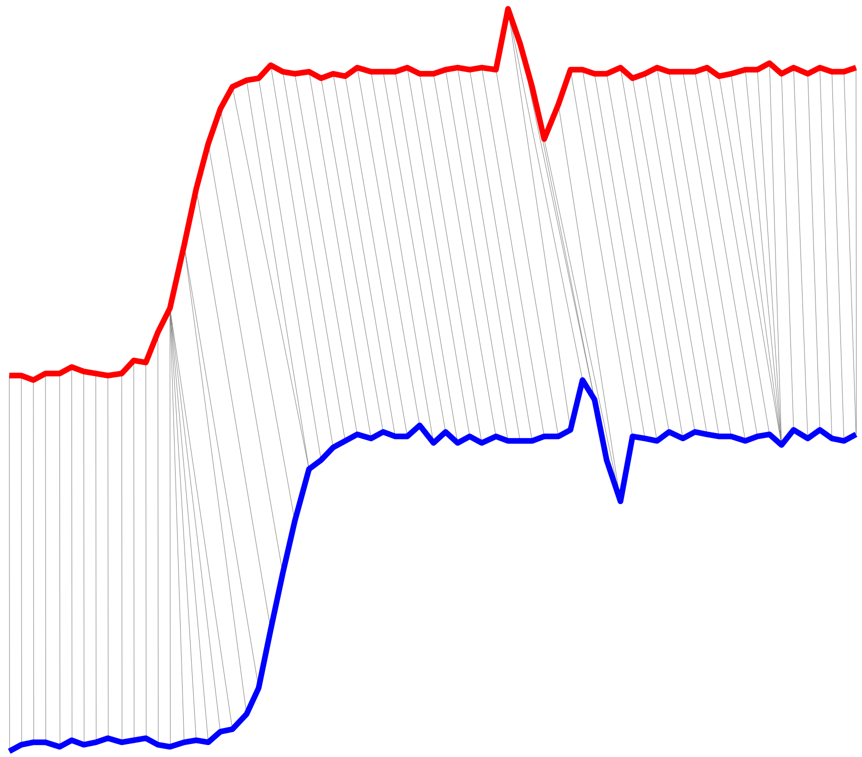
Euclidean



Fixed Time Axis

Sequences are aligned "one to one"

Dynamic Time Warping



"Warped" Time Axis

Nonlinear alignments are possible

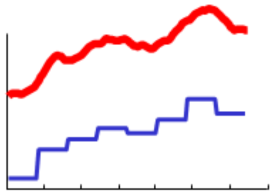
figures borrowed from tutorial "Data Mining and Machine Learning in Time Series Databases" (2006), Dr. Eamonn Keogh, University of California

Time Series Dimensionality Reduction

Approximation via piecewise discontinuous functions

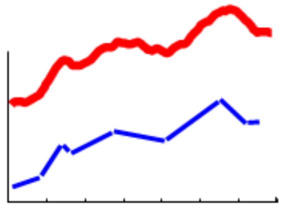
DWT

Discrete Wavelet Transform



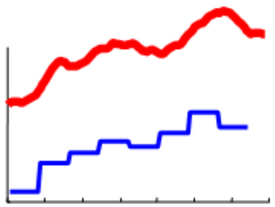
PLA

Piecewise Linear Approximation



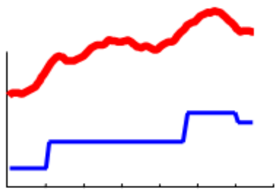
► PAA

Piecewise Aggregate Approximation



► APCA

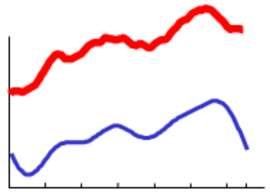
Adaptive Piecewise Constant Approximation



Approximation via low-order continuous functions

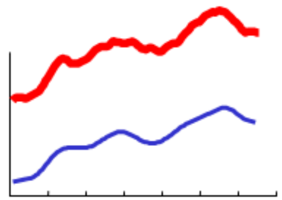
DFT

Discrete Fourier Transform

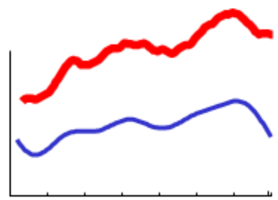


SVD

Singular Value Decomposition



► Chebyshev Polynomials



figures borrowed from tutorial "Data Mining and Machine Learning in Time Series Databases" (2006), Dr. Eamonn Keogh, University of California

Time Series Dimensionality Reduction: *DSA model*

DSA (***D****erivative time series* ***S****egment* ***A****pproximation*) – CIKM’06

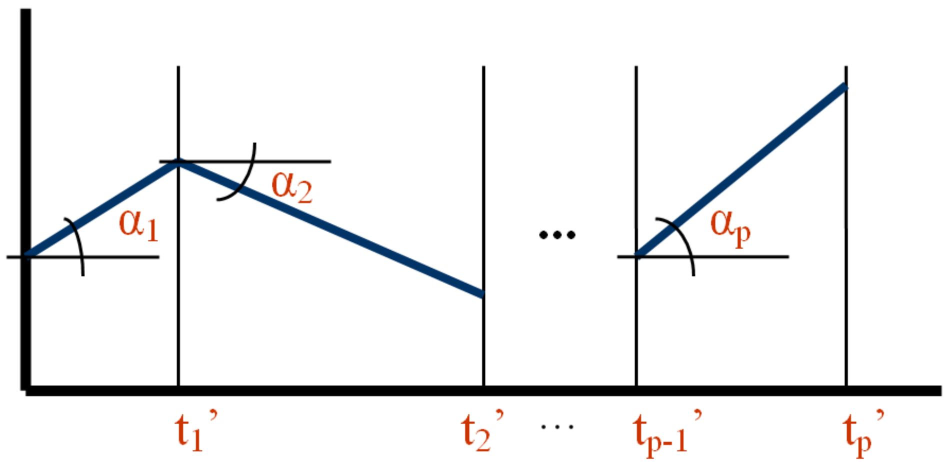
- High rate data compression
- Feature-reach representations
- Best trade-off between effectiveness and efficiency

$$T = \left[(x_1, t_1), (x_2, t_2), \ldots, (x_n, t_n)\right] \Rightarrow \tau = \left[(\alpha_1, t'_1), (\alpha_2, t'_2), \ldots, (\alpha_p, t'_p)\right]$$

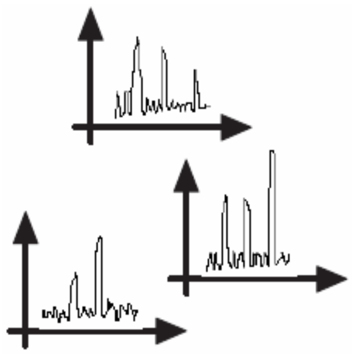
Time Series **DSA sequence**

DSA steps:

1. *Derivation*
2. *Segmentation*
3. *Segment Approximation*

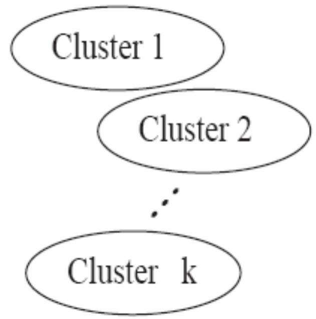


Classification of MS data: *our proposal*



raw mass spectra

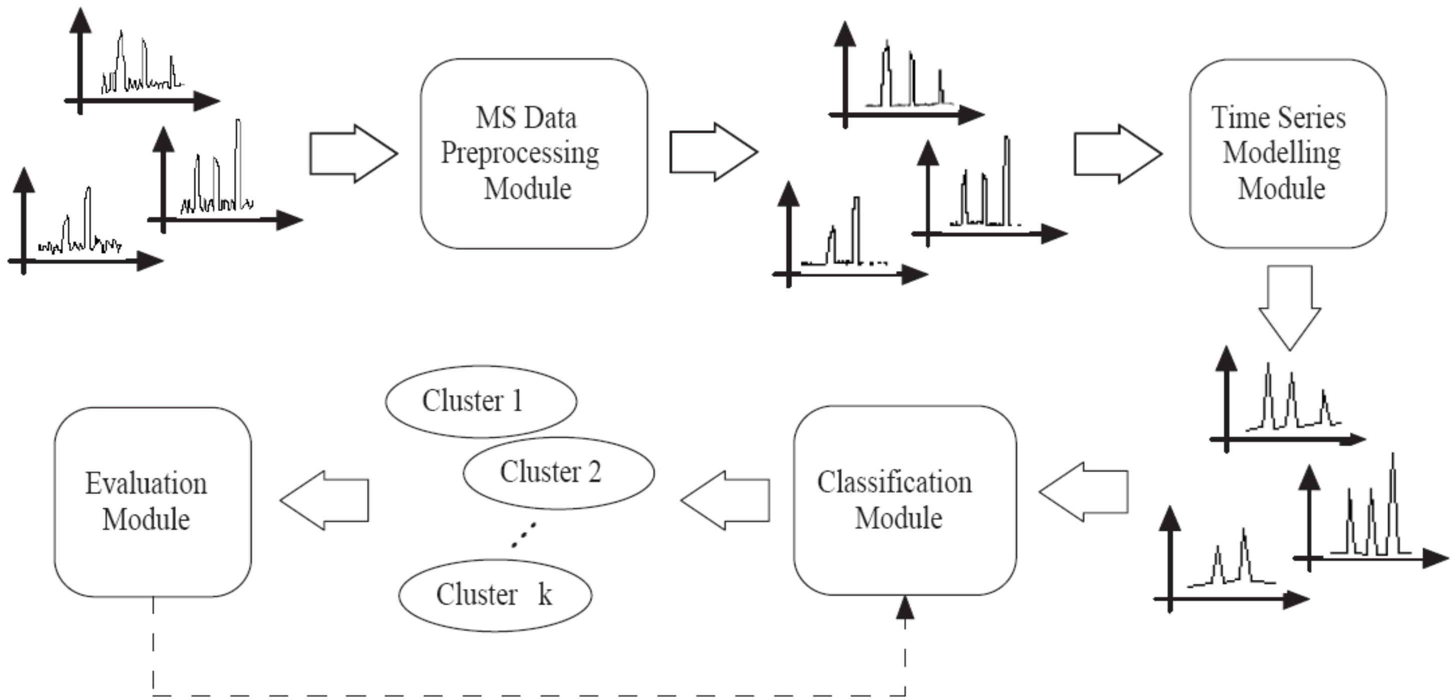
Framework
for Classifying
Mass Spectrometry Data



classified mass spectra

Novelty:
Time Series based representation for Mass Spectra

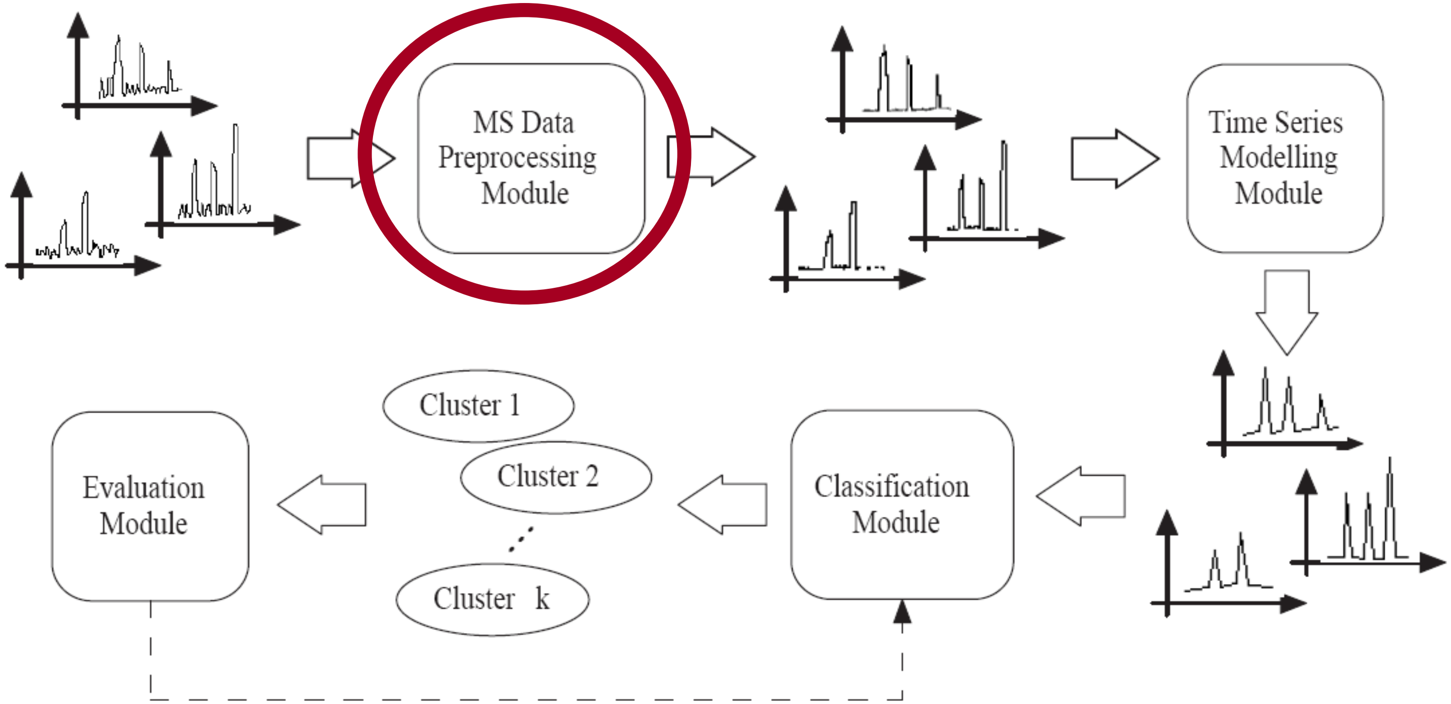
The proposed framework



Three main parts:

1. *MS Data Preprocessing*
2. *Time Series Modelling*
3. *Classification and Evaluation*

The proposed framework:
MS data preprocessing



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The proposed framework:
MS data preprocessing

The *MS Data Preprocessing Module* performs a set of preliminary steps on the original raw spectra.

Three main steps:

- Noise reduction
- Identification of valid peaks
- Quantization

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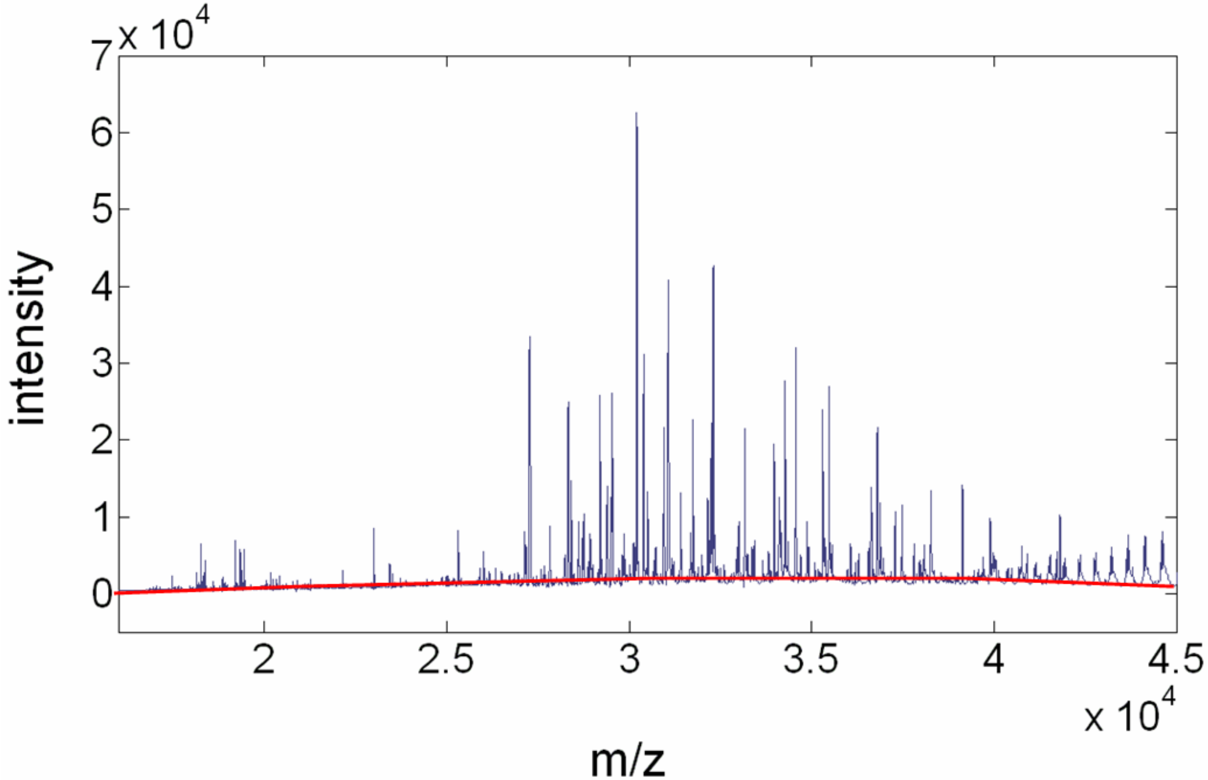

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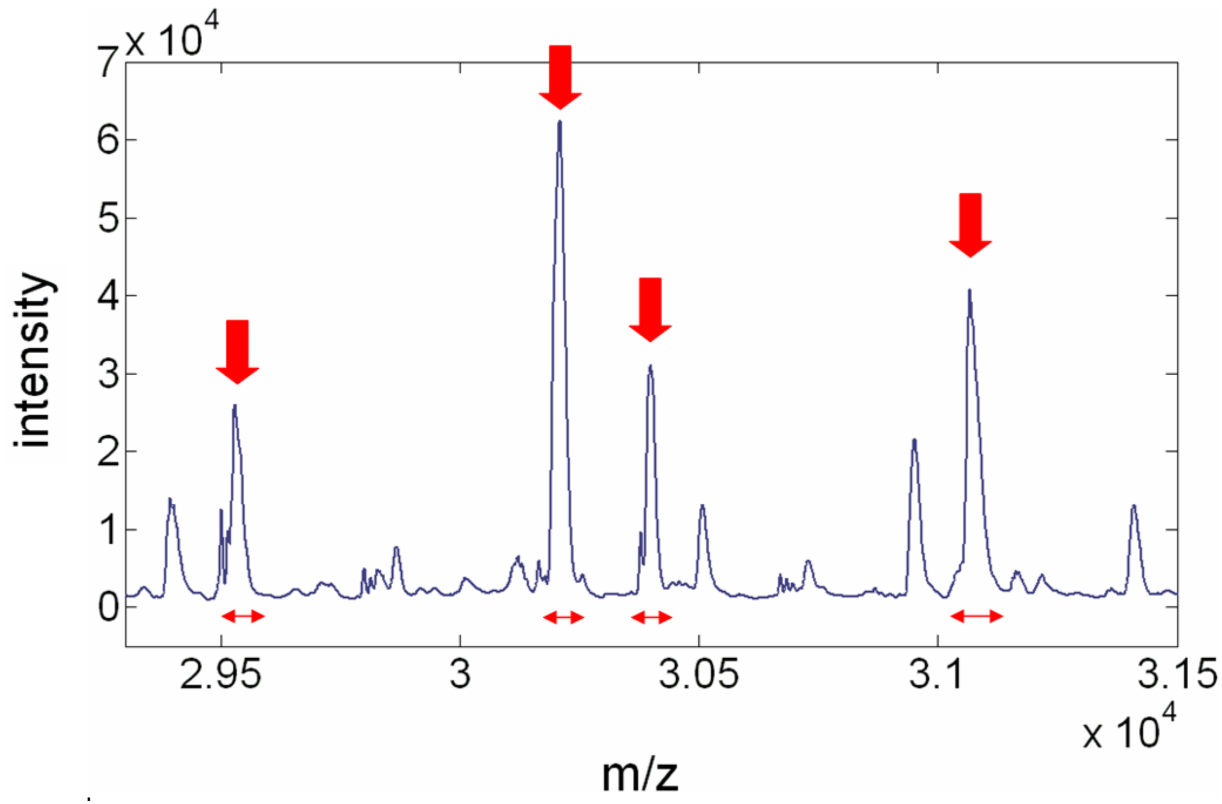

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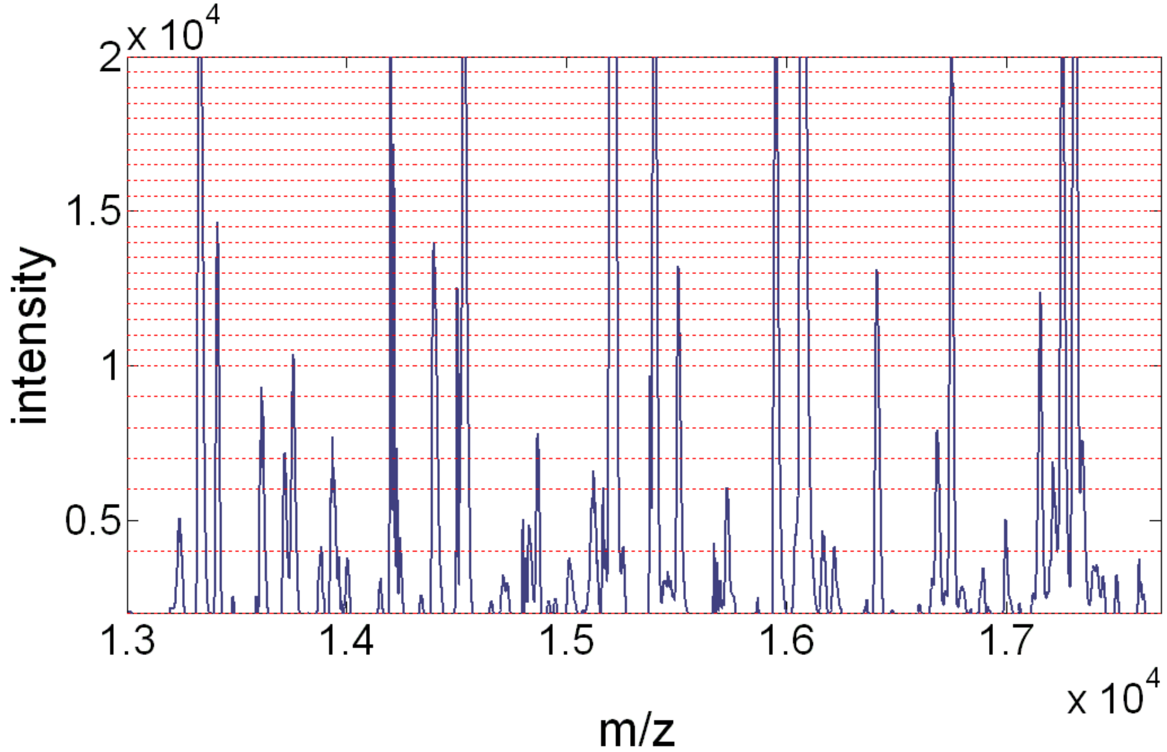
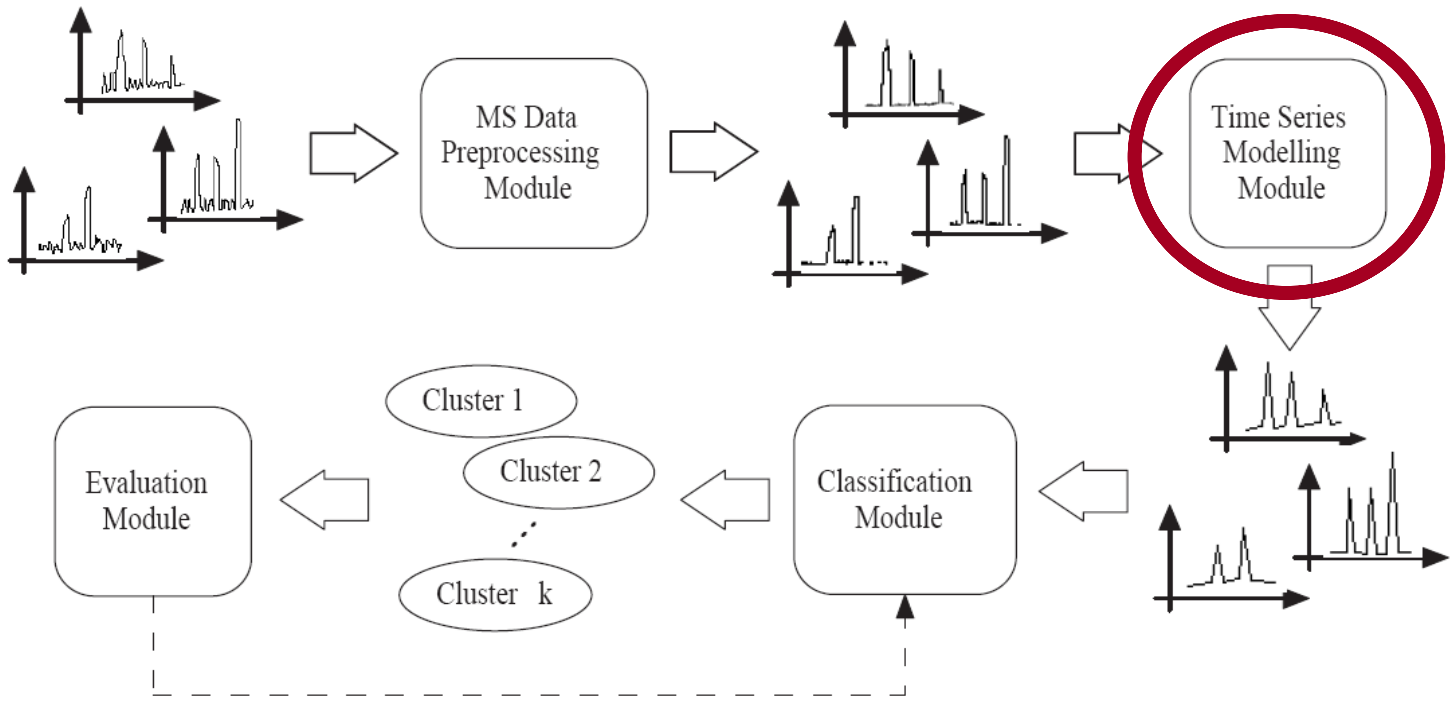


The proposed framework:
time series modelling



Three main parts:

1. *MS Data Preprocessing*
2. *Time Series Modelling*
3. *Classification and Evaluation*

The proposed framework:
time series modelling

The *Time Series Modelling Module* represents the preprocessed spectra into a time series based model.

$$S = \left[\left(I_1, (m/z)_1\right), \left(I_2, (m/z)_2\right), \ldots, \left(I_n, (m/z)_n\right)\right]$$ **Mass Spectrum**

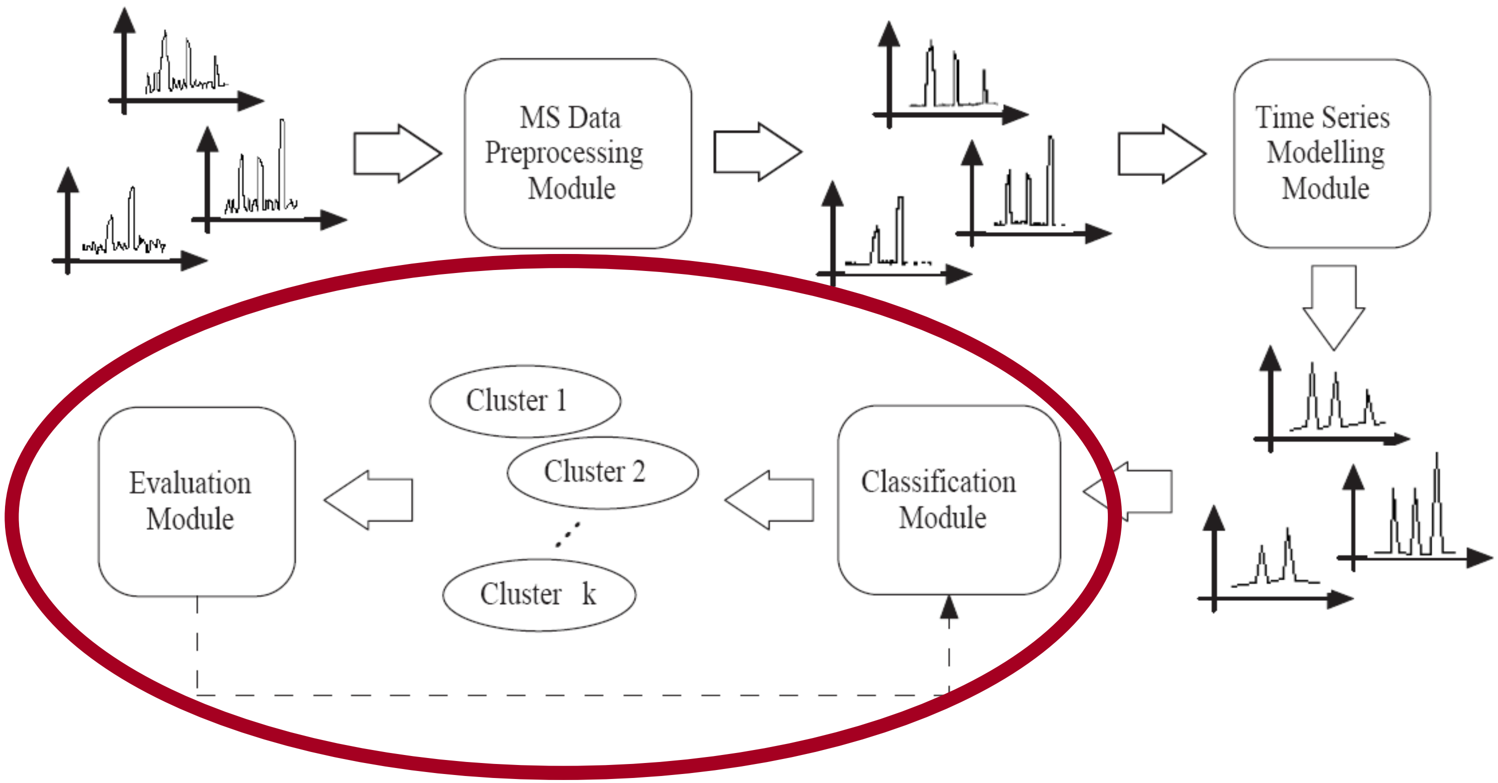
$\Downarrow$

$$T = \left[(x_1, t_1), (x_2, t_2), \ldots, (x_n, t_n)\right]$$ **Time Series**

$\Downarrow$

$$\tau = \left[(\alpha_1, t'_1), (\alpha_2, t'_2), \ldots, (\alpha_p, t'_p)\right]$$ **DSA sequence**

The proposed framework:
classification and evaluation



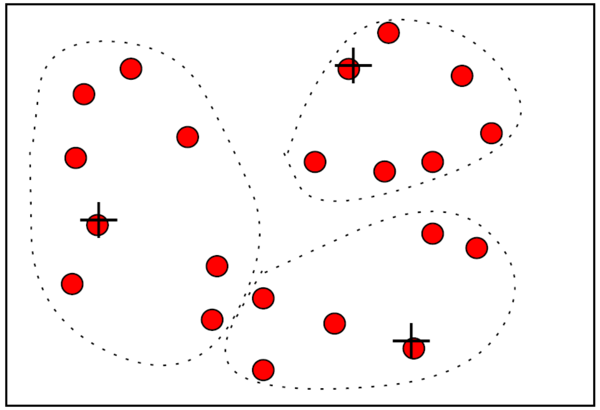
Three main parts:

1. *MS Data Preprocessing*
2. *Time Series Modelling*
3. *Classification and Evaluation*

The proposed framework: *classification and evaluation*

The *Classification Module* performs a task of ***clustering*** (i.e. *unsupervised classification*) on mass spectra

- High intra-cluster similarity
- Low inter-cluster similarity



The *Evaluation Module* is in order to assess the accuracy of the output classification w.r.t. the desired classification.

$$\Gamma = \{\Gamma_1, \ldots, \Gamma_k\}$$

desired classification

$$C = \{C_1, \ldots, C_k\}$$

output classification

$$P = \frac{1}{k}\sum_{i=1}^{k}\frac{|C_i \cap \Gamma_i|}{|C_i|}$$ ***precision***

$$R = \frac{1}{k}\sum_{i=1}^{k}\frac{|C_i \cap \Gamma_i|}{|\Gamma_i|}$$ ***recall***

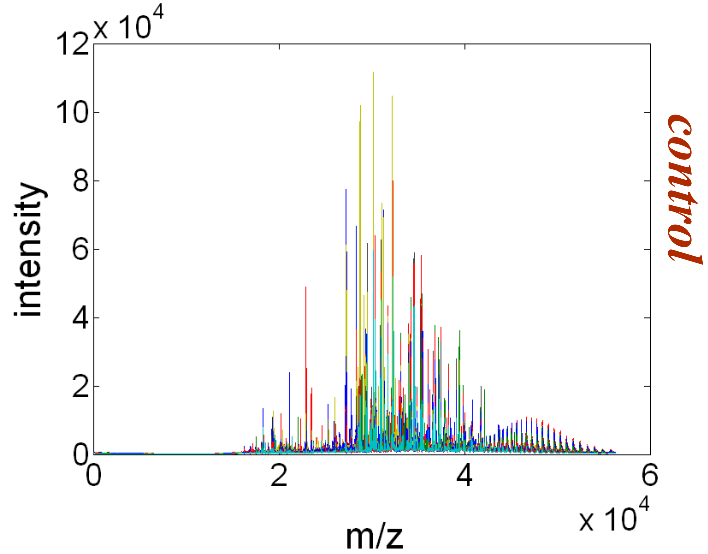
$$F = \frac{2PR}{P+R}$$ ***f-measure***

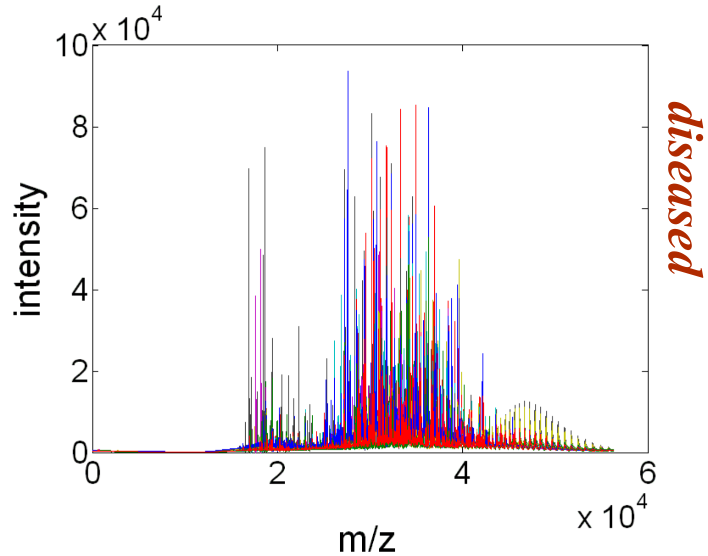
Experimental Results

Ovarian Cancer(*)

SELDI dataset

- ***50*** *spectra*
- ***2*** *classes (control - diseased)*
- ***56,384*** *(m/z, intensity) couples*





Classification Results:

$P = 0.88$

$R = 0.86$

$F = 0.87$

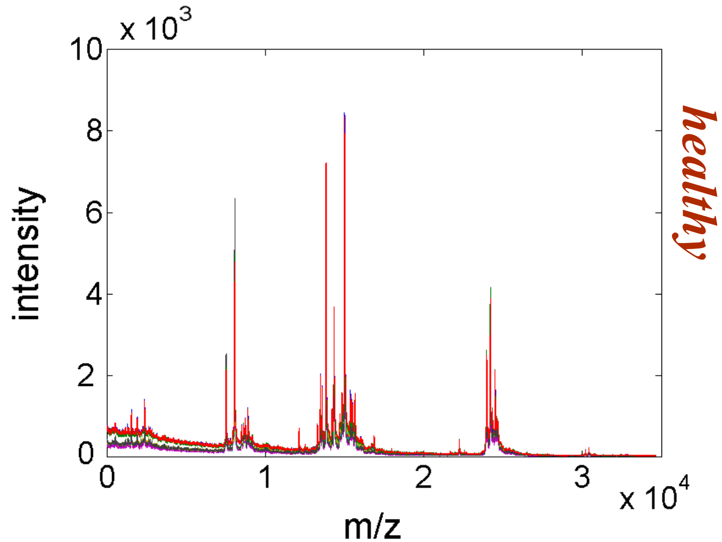
(*) Available at: http://sdmc.lit.org.sg/GEDatasets/Datasets.html

Experimental Results

MALDI
UNICZ

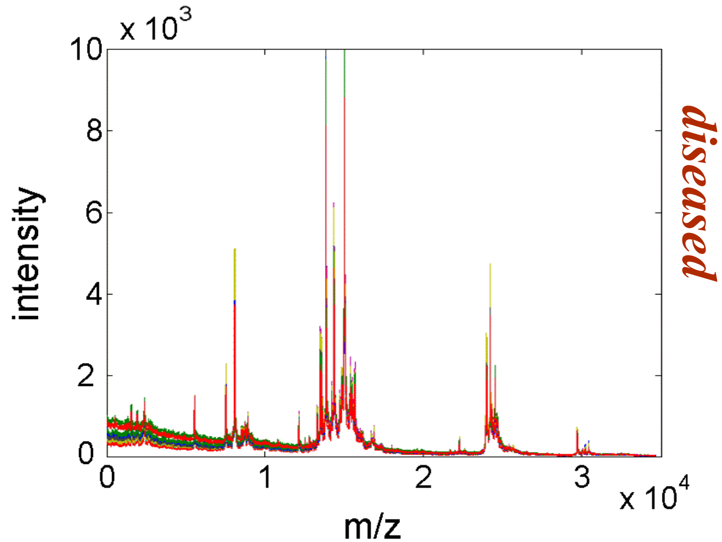
MALDI dataset

- *20 spectra*
- *2 classes (healthy - diseased)*
- *34,671 (m/z, intensity) couples*



Classification Results:

***P* = 0.99**
***R* = 0.93**
***F* = 0.96**



Conclusions

- Mass Spectrometry meets Time Series:
  a new framework
  for classifying MS data
- High capability in classifying
  and discriminating mass spectra

Thanks...