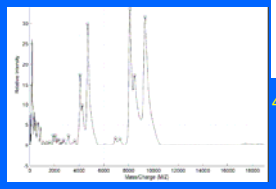
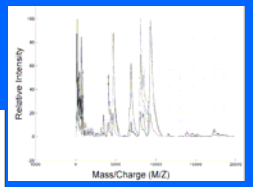
PROTEOMICS SIGNAL PROCESSING II

3. Peak alignment





4. Peak detection

PROTEOMICS SIGNAL PROCESSING III

5. Potential biomarkers detection

FEATURES EXTRACTED FROM THE PROSTATE CANCER DATA SET BY THE PROPOSED METHOD. COLUMN 1 SHOWS THE NUMBER OF SIGNIFICANT FEATURES. COLUMN 2 PROVIDES THE FEATURES EXTRACTED FROM THE PRESENT WORK. THE LAST THREE COLUMNS PRESENT FEATURES FOUND IN PREVIOUS STUDIES [5, 6, 19].

Number of features	M/Z	Adam et al.	Qu et al.	Petricoin et al.
1	28	4475	3486	3080
2	47	5074	3963	4819
3	96		4071	5439
4	194		4080	
5	234		5289	
6	252			
7	299			
8	342			
9	368			
10	4077			

CLASSIFICATION RESULTS FOR 26 SPECTRA OF PROSTATE CANCER WITH ELEVATED PSA LEVEL AGAINST 43 SPECTRA OF PROSTATE CANCER WITH PSA LEVEL GREATER THAN TEN

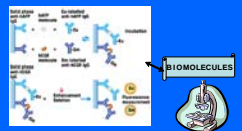
No. Spectra / PSA level	PSA<1	PSA≥4	accuracy
63 / PSA<1	23	3	88%
69 / PSA≥4	2	41	95%
Overall accuracy			93%

6. Classification

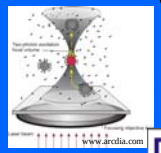
3. Biomolecules recognition for in vitro diagnostics

BIOINFORMATICS: BIOMOLECULES DETECTION EXPERIMENTAL PROCEDURE

Immunoassay techniques yield estimates of concentrations of analytes

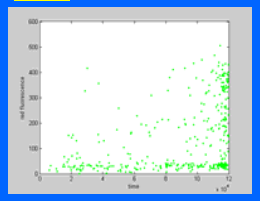


1. The target molecules are recognized and bind by specific fluorescent labelled antibodies
2. By measuring the fluorescent emission of the labelling dyes, information can be obtained concerning the type and amount of the target molecules
3. Measuring is performed by exciting and counting the fluorescence induced by each microparticle using a Laser induced

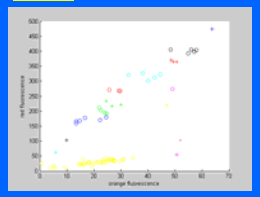


ROBUST ESTIMATION OF BIOMOLECULES SIGNALS I

Raw data



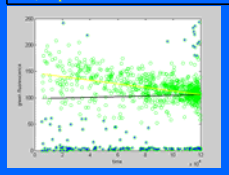
Clustering



ROBUST ESTIMATION OF BIOMOLECULES SIGNALS II

Outliers and robust estimation

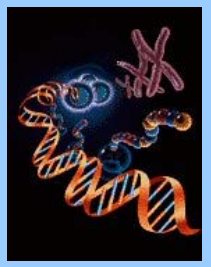
Dataset	class1	class2	class3
All 0 hAFP 0 bhCG	24.98	169.03	366.05
All 0 hAFP 100 bhCG	26.26	172.63	351.44
All 0 hAFP 1000 bhCG	25.96	167.06	364.77
1 cuv, 5 rep meas. 0 hAFP 0 bhCG	18.35	174.84	376.22
1 cuv, 5 rep meas. 0 hAFP 100 bhCG	25.78	178.45	359.42
1 cuv, 5 rep meas. 0 hAFP 1000 bhCG	22.56	170.60	358.35



TECHNOLOGICAL EDUCATIONAL INSTITUTE OF ATHENS
Dept. of Medical Instruments Technology

medisp Lab
MEDICAL IMAGE & SIGNAL PROCESSING LABORATORY

BIOINFORMATICS



Medical Image and Signal Processing Lab.,
Dept. of Medical Instruments Technology,
Technological Educational Institution of Athens, Ag. Spyridonos Street,
Egaleo, GR-122 10, Athens, Greece.

Director: Prof. D. Cavouras, Ph.D.,
E-mail: cavouras@teiath.gr
URL: http://www.teiath.gr/stef/tio/medisp/index.htm

MEDISP'S INVOLVEMENT TO STATE OF ART BIOINFORMATICS TECHNOLOGIES

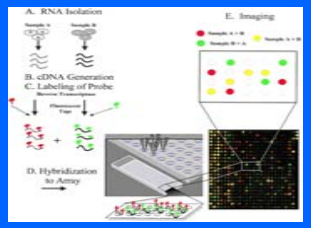
1. Microarrays image processing for gene expression systematic analysis
2. Proteomics signal processing for identification of biomarkers and diagnosis of cancer
3. Biomolecules recognition for in vitro diagnostics

1. Microarrays image processing for gene expression analysis

MICROARRAYS EXPERIMENTAL PROCEDURE

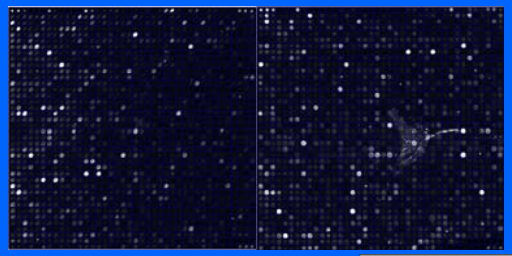
The basic microarray experimental procedure involves

1. Sampling of DNA and cDNA molecules (targets) from the test subjects.
2. Isolation of targets messenger RNA in a solid substrate.
3. Printing of targets using metallic pin or inkjet based systems (spots)
4. Labeling of printed targets using fluorescent dyes (Green and Red).
5. Hybridization of fluorescent targets.
6. "Reading", of the hybridized fluorescent targets (confocal microscopy)



MICROARRAYS IMAGE PROCESSING I

1.Gridding for facilitating spot detection



MICROARRAYS IMAGE PROCESSING II

2. Restoration for noise removal

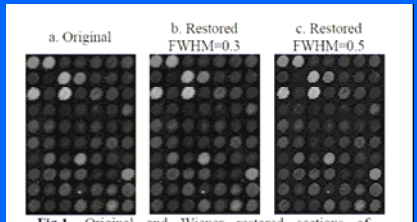
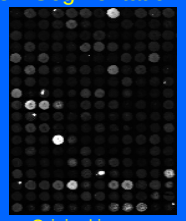


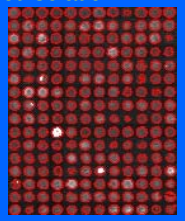
Fig.1. Original and Wiener restored sections of microarray images for two different choices of Gaussian PSF kernel

MICROARRAYS IMAGE PROCESSING III

3. Segmentation for spot isolation



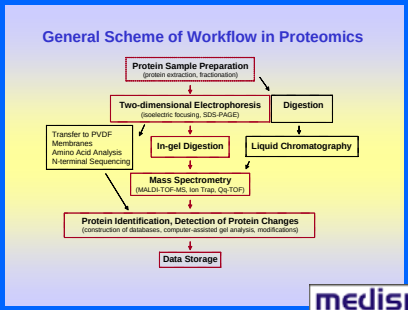
Original image



Segmented image

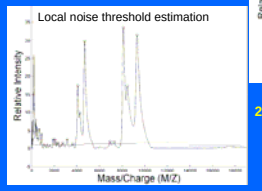
2. Proteomics signal processing for identification of biomarkers and diagnosis of cancer

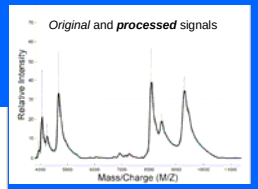
BIOINFORMATICS: PROTEOMICS EXPERIMENTAL PROCEDURE



PROTEOMICS SIGNAL PROCESSING I

1. Baseline subtraction – Normalization – Smoothing





2. Noise estimation