

Postgraduate student: **Dimitrios Siderakis**

Thesis Title:

Design and development of a Pattern Recognition system for discriminating amongst healthy, benign and malignant prostate tumors, employing proteomic mass spectroscopy (MS) samples

Abstract:

The aim of this thesis was to implement a pattern recognition system for the discrimination amongst healthy, benign and malignant prostate tumors from proteomic mass spectroscopy samples and to identify m/z intervals of potential biomarkers associated with prostate cancer. For this reason, we used two different data sets, one from the National Cancer Institute of America and one from the East Virginia Medical School, which have been repeatedly used in studies of prostate cancer.

Due to the specificity of tested spectra, initially there was a demand of pre-processing (smoothing, noise assessment, finding and peak alignment) to make them suitable for further analysis. At this stage we experimented thoroughly so as to find the optimal parameters for pre-processing of spectra. We then developed five different classifiers (MDC, KNN, Bayesian, PNN, SVM) and a system combining these so as to achieve maximum performance. For finding the optimal combination of features we implemented the exhaustive search, sequential forward selection (SFS), sequential backward selection (SBS), sequential forward floating selection (SFFS) and sequential backward floating selection (SBFS).

After experimentation with these techniques and models of machine learning we achieved accuracy of 95-98% for the first set of data and of 92-93% for the second data set. Furthermore, based on the features the classifiers used when they achieved their optimal performance, we concluded at 6 different intervals of m/z as probable to contain biomarkers related to prostate cancer. After correlation with previous studies, biomarkers proposed by other research groups were found to be within our proposed intervals of m/z .

Examining Committee

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