



Working Group on Statistical Learning Seminar

Title: A Proteomics and Bioinformatics Approach towards Biomarker Panel Identification in Prostate Cancer: From Discovery to T

Speaker: Yue Fan

Date: Fri 29th April 2011 at 1:00PM

Location: Statistics Seminar Room- L550 Library building

Abstract: Prostate cancer (PCa) remains the most common form of male cancer (20

Preclinical serum samples were collected from men with different grades and stages of PCa, benign prostate hyperplasia and age matched health controls as part of the Irish prostate cancer research consortium bioresource and Innsbruck Prostate cancer bioresource. After removing 6 most abundant serum proteins, proteomics profiling of these serum samples was carried out using 2D-DIGE and label-free LC-MS/MS experiments. Biomarker panels were identified and assessed by feature selection and classification using Random Forests method. The prediction performance of the selected biomarker panel was assessed using 10 fold cross validation and AUC values were calculated. The BPH and PCa panel gives an AUC value of 0.926, and the panel for predicting disease stages achieved AUC value of 0.742, which provide improved prediction accuracies than current standard clinical tools. The validation of two proteins Haptoglobin and Glutathione Peroxidase 3 using western blotting on independent samples ($n=80$) confirmed the 2D-DIGE results. MRM was designed and optimized for the identified biomarker panel and potential biomarkers from the literature and we are currently undergoing validations. With carefully validation,

these panels in combination with current clinical tools could improve diagnosis and thus patient outcome through the selection of appropriate treatment options.