Andreas Kryger Jensen, M.Sc

Statistical methods for analyzing serum proteome data with applications in early detection of breast and ovarian cancer and as prognostic tools

Background: Breast cancer and ovarian cancer both dramatically affect female health. Breast cancer is the most common malignant disease in women in Denmark, comprising approximately 25% of all cancers [1]. Ovarian cancer is a serious malignancy and with a five-year survival rate of 32% ovarian cancer has the highest mortality rate among the gynaecologic malignancies [1]. Despite advances in understanding the biology and pathology of cancer diseases, early diagnosis and intervention are the most important factors positively affecting survival. In addition, with the advent of novel effective targeted therapies, predictive and prognostic tests are needed, which can assist in tailoring individualized treatment regimens and save patients from serious side effects.

There has been great interest from the clinical community in exploiting simple mass spectrometry (MS) protein profiling for the analysis of biomarkers from easily available body fluids such as blood serum as a potentially valuable alternative to other diagnostic and prognostic tools. A method utilizing a pattern of biomarkers specific to the pathological process is expected to cover the heterogeneity of cancer and ensure valuable diagnostic, predictive and prognostic information of the disease.

Aim: The overall objective and vision of this PhD project is to develop, validate and apply statistical methods for the analysis of data derived from mass spectrometric analysis of blood samples obtained from women with breast or ovarian cancers matched with healthy controls in order to distinguish neoplastic from non-neoplastic disease-

Methods: We focus on the Matrix Assisted Laser Desorption/Ionization Mass Spectrometry (MALDI MS) technique for serum protein profiling. Several different data sets are analyzed with state-of-the-art statistical methods with the purpose of predicting tumor stages based of subject specific protein profiles.

Results: During the project we have developed a novel statistical methodology for classifying MALDI spectrometry data. The method has been applied to a data set of Danish ovarian cancer patients and validated on an independent data. The results will be published in a forthcoming article.

Primary supervisor: **Jacob Hjelmborg** , Ass. professor, University of Southern Denmark
Co-supervisors: **Torben Martinussen**, Professor, University of Copenhagen
                    Ole Mogensen, Professor, DMSci
                    Jonna Skov Madsen, Consultant, PhD., Hospital Lillebælt, Vejle
                    Anne Kjærgaard Øgendahl, PhD, University of Southern Denmark