An Investigation of Spectral Pre-Processing of FTIR Images from Prostate Cancer Tissue

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Fourier Transform Infrared (FTIR) spectroscopy coupled with advanced computational methods has been widely shown to detect many forms of cancer from tissue biopsies. The advent of FTIR-Imaging allows the concurrent collection of numerous spectra from tissue samples, corresponding to a visual image.

Raw chemical images obtained using FTIR-Imaging are influenced by physical contributions, including light scattering effects, sample thickness and changes in the surrounding environment. Scattering is particularly strong at edges of tissue which is most evident in highly glandular prostate tissue. To accurately interpret the raw data and account for these variables, a number of pre-processing methods can be employed. These include vector normalisation, linear derivatisation and RMieS-EMSC to specifically address the scattering problems (1). Hierarchical cluster analysis (HCA) is commonly employed to cluster spectra forming an image map, based on biochemical differences and similarities between them. Regions corresponding to these clusters thus represent biochemically different components of tissue.

H&E stained and HCA images of prostate cancer tissue are shown in Figure 1. A histopathologist was consulted in order to evaluate which pre-processing method gives the most accurate representation of the true histopathology. The best agreement between images after applying RMieS-EMSC to the data was found to be a combination of vector normalisation and second derivative techniques.

![Figure 1. The H&E stained image of a section of prostate cancer tissue biopsy(a) and its corresponding HCA imaging (b) after RMieS-EMSC, vector normalisation and second derivative.](image)

(1) Bassan et al, "Resonant Mie Scattering (RMieS) correction of infrared spectra from highly scattering samples". Analyst, 135, 268-277 (2010)