Analysis of the spectral changes between normal and abnormal individual cells

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In two recent publications,[1,2] we have reported the distinction between normal, atypical/dysplastic and cancerous individual squamous cells both from the oral cavity as well as the cervix. This distinction was accomplished via covariance-based methods, such as principal component analysis (PCA) or soft independent modeling of class analysis (SIMCA), of about 100,000 infrared spectra of individual cells.

In order to assess whether or not the spectral changes between normal and diseased states of cervical and oral cells are similar, we have undertaken a study[3] in which we have extracted the spectral pattern that is used by the multivariate methods to distinguish normal from diseased cells. We refer to this spectral pattern as the "spectral signature of disease". These signatures of disease spectra reveal large changes in protein spectral features, along with smaller, concomitant changes in the "phosphate" regions (ca. 1235 and 1090 cm^{-1}) of DNA, RNA, phospholipids and – possibly – phosphorylated proteins.

In this presentation, we briefly review data acquisition strategies, data pre-processing, as well as the signature of disease spectra for viral infections and cancerous/pre-cancerous changes in cellular spectra.

References:
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[2]   K. Papamarkakis, J. M. Schubert, B.Bird, M. Miljković, K. Bedrossian, N. Laver, and M. Diem, "Cytopathology by Optical Methods: Spectral Cytopathology of the Oral Mucosa", (2009) *Laboratory Investigations*, submitted
[3]   M. Diem, K. Papamarkakis, J. Schubert, B. Bird, M. Romeo and M. Miljković, "The Infrared Spectral Signatures of Disease: Extracting the Distinguishing Spectral Features between Normal and Cancerous States", (2009) *Appl.Spectrosc.*, in press (Focal point article, Nov 2009)