Statistical image analysis in medicine and biology

Tuesday 23rd May 2017

Imaging techniques play an increasingly important role across medicine and almost all biological sciences. As the variety of methods for capturing images of biological structures has increased, so too has the scale of data sets in terms of resolution and speed of capture. Novel statistical methodology is required to analyse these complex data sets. This meeting brings together four eminent speakers to present a mixture of methodology and applications in statistical image analysis.

Venue: Room 3B, Student Central, Malet Street, London WC1E 7HY

Programme

13:30 - 14:15	**John Aston (Cambridge)** **Using geometry and registration in population image analysis** In many applications, a population of images is available and it is important to understand the underlying information and variation in such data. However, often the images have some intrinsic geometry associated with them (for example, they are surfaces embedded in 3-D) and this should be included in the analysis. Furthermore, often the images need to be aligned before analysis, but rather than throwing this registration information away, it is often vital that it is further incorporated into the subsequent modelling. We will develop some techniques that help build these effects into the statistical analysis of medical image data such as brain images or musculoskeletal images.
14:15 - 15:00	**Adrian Bowman (Glasgow)** **Surfaces, shapes and anatomy** Three-dimensional surface imaging, through laser-scanning or stereo-photogrammetry, provides high-resolution data defining the surface shape of objects. In an anatomical setting this can provide invaluable quantitative information, for example on the success of surgery. Two particular applications are in the success of facial surgery and in developmental issues with associated facial shapes. An initial challenge is to extract suitable information from these images, to characterise the surface shape in an informative manner. Landmarks are traditionally used to good effect but these clearly do not adequately represent the very much richer information present in each digitised images. Curves with clear anatomical meaning provide a good compromise between informative representations of shape and simplicity of structure, as well as providing guiding information for full surface representations. Some of the issues involved in analysing data of this type will be discussed and illustrated. Modelling issues include the measurement of asymmetry and longitudinal patterns of growth.
15:00 - 15:30	**Tea break**

15:30 - 16:15

Ian Dryden (Nottingham)

Sparsity and measurement error in the statistical analysis of magnetoencephalography (MEG) data

We consider statistical methodology for the analysis of Magnetoencephalography (MEG) data which is a functional neuroimaging technique. MEG focuses on the small magnetic fields resulting from the naturally occurring electrical currents during brain activity. By recording the brain's magnetic fields at a number of reference points around the head using an array of SQUIDs (superconducting quantum interference devices), the aim is to estimate which brain areas are active. MEG has very high temporal resolution and directly measures the actual activity itself rather than the secondary effects of brain activity such as blood oxygenation levels in fMRI. We model the sources as equivalent current dipoles (ECD) which group together the current from many neurons with the same direction as one dipole. We represent current dipoles as vectors with a strength and orientation, and the estimation can be formulated as an inverse problem with many more parameters than data measurements. We use various sparse regression methods, including the LASSO, Elastic Net, Square Root Lasso and Penalized Euclidean Distance, and compare source estimates with the more commonly used Minimum Norm and Beamformer approaches. The method requires specification of the design (leadfield) matrix from physical considerations, and we also consider estimation in the presence of measurement error in that matrix.

This is joint work with Jonathan Davies, Chris Brignell and Matt Brookes at the University of Nottingham.

16:15 - 17:00

Ian Jermyn (Durham)

Accurate morphology preserving segmentation of multiple, overlapping cells

The identification of fluorescently stained cell nuclei is the basis of cell detection, segmentation, and feature extraction in high content microscopy experiments. The nuclear morphology of single cells is also one of the essential indicators of phenotypic variation. However, the cells used in experiments can lose their contact inhibition, and can therefore pile up on top of each other, making the detection of single cells extremely challenging using current segmentation methods. The model we present here can detect cell nuclei and their morphology even in high confluency cell cultures with many overlapping cell nuclei. We combine the “gas of near circles” active contour model, which favors circular shapes but allows slight variations around them, with a new data model. This captures a common property of many microscopic imaging techniques: the intensities from superposed nuclei are additive, so that two overlapping nuclei, for example, have a total intensity that is approximately double the intensity of a single nucleus. We demonstrate the power of our method on microscopic images of cells, comparing the results with those obtained from a widely used approach, and with manual image segmentations by experts.