



MCMC in statistical genomics practise

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This talk will be concerned with some of the issues that arise when attempting to use Bayesian modelling strategies and MCMC computation for large scale genomics analyses. In the first part of the talk, strategies that we have been implementing in high dimensional genomics regressions with small n and large p to perform variable selection and explore large model spaces will be reviewed and illustrated in a range of genomics applications.

The increased availability of summary genome wide data from genetics consortia assembling very large collections of samples leads to the challenging large n and large p framework, but with missing information. In the second part of the talk, we will turn to discussing how to implement approximate multivariate Bayesian model exploration when the available data does not allow the computation of the joint likelihood.

This is joint work is with L Bottolo (Imperial College), P Newcombe (MRC Biostatistics Unit) and D Conti (University of Southern California).

Keywords: variable selection; high dimensional regression; genomics, GWAS.