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## BAYESIAN METHODS FOR GENOMICS

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The analysis of the high-dimensional Genomics data generated by modern technologies, such as DNA microarrays, poses challenge to standard statistical methods. In this talk I will describe how Bayesian methodologies can be successfully employed in the analysis of such data. In particular, I will look at ways to incorporate spike and slab priors into various kinds of models. In linear regression models, this will allow the selection of the important variables (genes). Models and algorithms are quite flexible and allow the incorporation of additional information, such as data substructure and/or knowledge on gene functions and gene interactions. If time allows, I will then show how mixture priors can be employed in a Bayesian nonparametric model which exploits clustering for increased sensitivity in multiple hypothesis testing. The model permits inference on differential expression while at the same time clustering genes having similar patterns of expression. I will assess performances on simulated data and then show applications to DNA microarray studies.