

UNIVERSITY OF SYDNEY

SCHOOL OF MATHEMATICS AND STATISTICS

Statistics Seminar

Friday April 6, 2.00pm., Carslaw Lecture Room 173 (Level 1)

Comparative Genomics in a Post-Genomic Era

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Abstract

Recent advances in DNA sequencing techniques have produced a wealth of genomic sequence data and we now face the daunting task of analyzing this increasingly large and complex body of data. When this involves comparison of data from different genomes it is important to realize that the comparisons must be done in the context of the evolutionary history. This is the only statistically sound method for comparisons of data from more than two genomes. There are many phylogenetic and tree-dependent comparative methods available for such analyses. Usually, the methods are based on assumptions. For the methods to be applicable, the assumptions must not be violated by the data. Therefore, it is important that data surveying methods are used to determine whether the data set violates the assumptions of phylogenetic and tree-dependent comparative methods. However, methods for surveying sequence data are either not available or may give misleading results and if discrepancies exist between the assumptions of phylogenetic methods and the data, the user is left with few choices. He or she may (a) assume that the violation is not sufficient to confound the ensuing phylogenetic analysis; (b) abandon the data set and choose another one; or (c) apply a phylogenetic method that is not confounded to the same degree by the data's complexity. None of these options are satisfactory when the aim is to compare completely sequenced genomes.

In this seminar, I will focus on some problems that need to be addressed when completely sequenced genomes are to be compared. In particular, I will focus on compositional heterogeneity, exploration of tree-space, model uncertainty and model averaging, and concatenation of different sequences.

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