UNIVERSITY OF SYDNEY

SCHOOL OF MATHEMATICS AND STATISTICS

Statistics Seminar

Friday, 10th October, 2008. 2.00pm, Carslaw 173

Protein Folding - going in the right direction

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Abstract

An aim of bioinformatics is to assist in determining the role of gene products. A first step in this task is to move from the one dimension of the gene to the three dimensional structure of the protein which it produces - one of the sizeable scientific challenges of our time.

Proteins are produced sequentially in a cellular device called the ribosome, a process known as "translation", well-acknowledged by experimentalists. Triplets of nucleotides, known as codons, enter the ribosome and a single amino acid is produced; the resulting string of amino acids folds to the native, lowest energy structure in a process termed "cotranslational folding".

In this seminar three aspects of such folding will be discussed. First, the cotranslational folding of simple models will be considered and the properties of cotranslationally folded proteins examined. Second, evidence for cotranslational folding of real proteins will be investigated and thirdly, a cotranslational protein fold prediction algorithm will be introduced.

And if you know nothing about proteins, that's fine. All you need to know will be introduced in the seminar.

Enquiries about the Statistics Seminar should be directed to
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