Hamilton Institute

Multiple Alignments, Microarrays and Multivariate Analysis

Prof. Des Higgins
Conway Institute, UCD

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Abstract

I will describe two bioinformatics research topics from my lab.

1) Multiple alignment is where you take sets of related DNA or protein sequences and line them up so as to maximise their similarities. This is a computationally difficult but important problem. Traditional approaches are entirely algorithmic although more recent advances have been at least partly probabilistic in nature.

2) Microarrays are high throughput devices for simultaneously measuring levels of expression for many genes in biological samples. I will describe the application of some multivariate analysis techniques to some simple problems in microarray data analysis. These include the case of sample classification where microarrays are used to diagnose disease.

In this case we use a method called Between Group Analysis which can be used to give a kind of supervised PCA or correspondence analysis (CA). A second application is in the area of data integration where we use Co-Inertia Analysis to carry out multiple PCA or CA on multiple data sets.

Venue: Seminar Room, Hamilton Institute, Rye Hall, NUI Maynooth

Time: 1.00 - 2.00pm (followed by tea/coffee)

Travel directions are available at www.hamilton.ie

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