



Colloquium

The Institute Colloquium: Natural selection and the genome

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Host:

Natural selection is usually thought of as causing the evolution of properties of organisms like their structure, physiology and behaviour, which are controlled by the instructions encoded in their genomes. However, genomes themselves are the product of evolution, and natural selection must play a major role in shaping their organization. Detecting and quantifying this aspect of selection and its interactions with other evolutionary factors, such as mutation and random sampling effects due to finite population size, is a major challenge for biologists, especially as the intensity of selection on many genomic features is probably so small as to be inaccessible to experimental measurement. It is increasingly recognised that patterns of DNA sequence variation within populations offer considerable power to detect and estimate selective effects of the order of one in a million or less, if these patterns are compared with the predictions of models of the evolutionary processes involved. The utility of approaches based on such model-based analyses of sequence data is illustrated with two examples from *Drosophila* population genetic studies. One concerns selection on codon usage bias, the non-random use of alternative codons for the same amino-acid, and the related problem of the GC content of sequences. The other concerns selection on the size of non-coding sequences, especially introns. The evidence for pervasive selection on these and other features of genomes raises the old problem of the genetic load; how can a population survive the action of selection at tens or hundreds of millions of sites throughout the genome? Two alternative resolutions of this problem are presented.

Monday, November 19, 2012 04:30pm - 05:30pm

Raiffeisen Lecture Hall, Central Building



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