VICTORIAN CENTRE FOR BIOSTATISTICS

ViCBiostat

Victorian Centre for Biostatistics

Seminar

Thursday 21st August 2014
9.30am to 10.30am
Melbourne School of Population and Global Health, Melbourne University
Room 515, Level 5,
207 Bouverie Street, Carlton

Exploring the structure of whole-genome conservation profiles using Bayesian segmentation

Dr Jonathan Keith
Monash University

Conservation is a key indicator of function in genomes, and can potentially be used to discover novel functional non-protein-coding RNAs and regulatory sequences. However, recent investigations have demonstrated that a simple dichotomy between conserved and non-conserved sequence is too naïve a distinction to reflect the full complexity of the numerous types of structural and functional constraints acting on genomes. This presentation will discuss recent investigations into the detailed structure of whole-genome conservation profiles, using Bayesian segmentation techniques to identify multiple classes of conservation level. By integrating information about conservation with profiles of other properties indicative of function, including GC content and transition/ transversion ratios, a much finer level of structure can be detected. The method has been applied to a range of species including Drosophila, zebrafish, malaria and bacterial genomes, and results from each of these will be presented. One key implication of these results is that the proportion of functionally constrained sequence in eukaryotic genomes may be very much larger than previously supposed. Another key implication is that genomic sequences may be subject to ephemeral functional constraints that act on too short a time scale to be detected in most comparative genomic studies. The functional content of various classes of conserved sequence will also be discussed.

Dr Jonathan Keith works in the School of Mathematical Sciences at Monash University as a Senior Lecturer. He is a researcher in Bayesian methods, bioinformatics and genetic epidemiology. His current main research interest is in statistical methods for the detection of novel non-protein-coding functional elements in genomes. He also has current and recent projects in phylogenetics, whole genome association studies and identification of quantitative trait loci.

He is currently a chief investigator on two ARC Discovery grants: Statistical methods for detection of non-coding RNAs in Eukaryote Genomes and Statistical methods for discovering RNAs contributing to human diseases and phenotypes.

www.vicbiostat.org.au

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