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

Abstract:
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.