

Contributed Talks – additions

Whole genome linkage mapping with Lep-MAP3

Pasi Rastas

Linkage mapping is a very powerful genomics tool that enables very comprehensive validation and refinement of de novo genome assemblies, especially on data generated on high-throughput sequencing (up to >1,000,000 variants on >1,000 individuals). Moreover, family-based linkage and association studies, quantitative trait locus mapping, analysis of genome synteny and other genomic data analyses require and benefit from dense and accurate maps. However, the tools that are currently available for constructing linkage maps are not well suited for such large datasets.

I will give a general overview of linkage map construction software Lep-MAP3 for large datasets, and explain how to scale linkage mapping models and algorithms to the case where the number of markers is orders of magnitude larger than the number of individuals (and thus number of recombinations). Lep-MAP3 can produce very dense and accurate maps even on low coverage sequencing and utilize data simultaneously on multiple families. It can model achiasmatic meiosis (recombination in only one sex) as well as sex-specific or sex-averaged recombination.

Mapping results are presented on real and simulated data as well as comparisons to other software to prove that Lep-MAP3 is the state-of-the-art in linkage mapping. A preliminary version Lep-MAP3 is publicly available from <http://sourceforge.net/projects/lep-map3/>

Sink or Sail: Behavioural adaptations on water in aerially dispersing species

Sara Goodacre

Long-distance dispersal events have the potential to shape species distributions and ecosystem diversity, and to influence processes such as population persistence and the pace and scale of invasion. We have studied dispersal in terrestrial spiders that persist in disturbed environments through their ability to re-colonise vacant habitat by long-distance aerial dispersal (“ballooning”). Individuals have no control over where they land once airborne and their tendency to spread has previously been thought to be limited by the costs of encountering water. However, in our study we show that aerial dispersal is associated with behavioural adaptations that allow individuals to survive encounters with water. The potential for genetic connectivity between populations, which can influence the rate of localized adaptation, thus exists over much larger geographic scales than previously thought. Newly available habitat may be particularly influenced given the degree of ecosystem disturbance that is known to follow new predator introductions.

Understanding the evolution of a social chromosome: A gene expression approach

Carlos Martínez-Ruiz (S), Richard A. Nichols and Yannick Wurm

Supergenes may play a key role in the evolution and maintenance of complex phenotypes such as social behaviour, by reducing the recombination which would break up haplotypes having beneficial epistatic interactions. A recently characterised example is the supergene that controls a polymorphism in the social structure of red fire ant (*Solenopsis invicta*) colonies. This species displays two social phenotypes: colonies can either have single or multiple queens. A suite of phenotypic differences between the social forms is perfectly correlated with the presence of an inversion in a region referred to as the 'social chromosome'. The effect of the inversion is dominant, and homozygotes appear not to be viable; hence the inversion is effectively non recombining, which means its evolutionary history has similarities with Y and W sex chromosomes. However, there are also some differences to sex chromosomes, so this system provides an interesting test for theories describing the evolution of sex chromosomes and of supergenes. I use transcription patterns in workers and queens of both social forms in *S.invicta* to understand the nature of the selection that has shaped the evolution of the social chromosome. These results will help understand whether social chromosomes have evolved under a scenario of evolutionary conflict, in a similar way to sexual chromosomes.