Centre for Bioinformatics and Computational Genetics

Most of the Centre's work has applications in agricultural livestock, but also yields insight into mammalian genome evolution.

In addition, there has been a database developed of public domain bovine Quantitative Trait Loci (QTL) and have coupled this to an easily navigated web interface that allows researchers to compare QTL locations for varied QTL within the bovine genome. We have recently linked this to a genome browser (Gbrowse) in order to allow researchers to be able to transition directly from QTL data to SNP locations, gene locations and annotations.

Research in the Centre for Bioinformatics and Computational Genetics has two foci:

- Creating new software tools for biologists to analyse genomic data
- Analysing genome data using computational methods

The first aim is currently served by improving our bovine Quantitative Trait Locus database, and implementing a Java based object oriented framework for genomic data.

The second aim currently involves analysing the bovine, equine, elephant, armadillo and sheep genome sequence assemblies for repeated sequence elements using a de novo repeat identification tool developed by and in collaboration with Bob Edgar that has only been used for dipteran repeat analysis to date.

Biological mechanisms underlying genome evolution are believed to originate with retrotransposon insertions that ultimately lead to segmental (gene) duplications/deletions, incorporation of retrotransposons into protein coding genes (exaptation) or gene duplication via retro-gene formation. The resulting “churning” of both non-protein coding regions and protein domains are two of the major forces that drive adaptation and speciation. Our primary research aim is to identify associations of RTE derived repeats that are conserved across mammalian genomes or species specific. Because evolutionary conservation is a hallmark of functional importance, these associations will uncover novel, functionally important aspects of genome structure. Whilst the main focus of this work is directed at evolutionary questions, retrotransposon insertions are believed to be frequent events that give rise to novel mutations.

This is an important research problem both in terms of our understanding of evolutionary mechanisms and processes but also due to the fact that these processes frequently give rise to mutations or structural variation affecting gene regulation and function which can result in disease or alter economically important agricultural traits.

The current model for mammalian genome evolution is centred upon identifying evolutionarily conserved sequences (genes) and breakpoints that allow the reconstruction of an ancestral mammalian karyotype from syntenic relationships and breakpoint mapping. We expect to contribute a novel methodology for identifying conserved regions based on retrotransposons that will identify ancient mammalian genome territories. This

will lead to an improved understanding of how genomes have evolved, in particular with respect to constraints on non-protein coding regions.

This is an important outcome because our understanding of gene regulation is currently limited by our ability to identify regulatory regions in silico. We also expect to identify species-specific genomic regions that have been preferentially invaded by newly evolved retrotransposons. This will identify genomic regions that have contributed to speciation by disruption of synteny and are likely responsible for the phenotypic differences associated with speciation.

Honours Projects

Honours projects in either area, or related to these areas are available in my lab. It would be helpful (but not required) if students already had some familiarity with either Unix/Linux or Perl or Java. All that is really required is curiosity and an interest in Bioinformatics.

Contact Details:

Centre for Bioinformatics and Computational Genetics

Address
Room 2.10, The Braggs Building
The University of Adelaide
SA 5005
AUSTRALIA
North Terrace Campus

Contact
Prof. David Adelson
Room 1.27, Molecular Life Science Building
T: +61 8 8313 7555
F: +61 8 8313 5338
email: david.adelson@adelaide.edu.au