SEMINAR ANNOUNCEMENT

We would like to invite you to attend this seminar hosted by A/Prof. Sudipto Roy:

Date: 24 June 2014, Tuesday
Time: 3:00PM – 4:00PM
Venue: Level 3, IMCB Seminar Room 3-46, Proteos, Biopolis

Speaker: Dr Gos Micklem, Director, Cambridge Computational Biology Institute, Department of Genetics, University of Cambridge, United Kingdom
Title: Horizontal gene transfer in Bdelloid rotifers and beyond; Model organism data integration in InterMine

Part 1:
Bdelloid rotifers are small water-dwelling invertebrates that are found worldwide. They have a number of unusual features including desiccation resistance, ionizing radiation resistance and the fact that they have been asexual for millions of years in spite of evolutionary theory suggesting they should have become extinct as a result. We have surveyed the transcriptome of the bdelloid Adineta ricciae and find a remarkable level of horizontal gene transfer (HGT). It appears that at least ~8-9% of all UniProt-matching transcripts may have been horizontally acquired, mainly from eubacteria but also fungi, protists and algae and ~80% of the genes acquired are enzymes. Bdelloid rotifers therefore express horizontally acquired genes on a scale unprecedented in animals, and it is likely that foreign genes make a profound contribution to their metabolism. This represents a potential mechanism for ancient asexuals to adapt rapidly to changing environments and thereby persist over long evolutionary time periods in the absence of sex. Recent work in a similar vein examines evidence for HGT more widely across the animal kingdom.

Part 2:
Model organisms are important for biomedical research in two main ways: 1) they allow experiments to be carried out that would be difficult or impossible in humans and so allow us to find out about basic biological processes; 2) they can assist biomedical research more directly by providing models for human diseases. Model organism databases provide access to high quality curated data but large scale data integration is still a challenge in modern biology. The open source InterMine data integration platform addresses this challenge. InterMine will be described, as well as a collaboration in which almost all the major animal model organism databases have built interMine databases. The object of the collaboration is to provide better tools for the model organism communities as well as improved interoperation between the different databases. To complement the above we have built a pilot human database, metabolicMine, and will soon start building a general human database. By allowing these different databases to interoperate we hope to improve the ease with which biomedical researchers can exploit model organisms.

Biography:
Gos Micklem carried out PhD and postdoctoral research in budding yeast and Drosophila molecular genetics before switching to computational research at the Wellcome Trust Sanger Institute. His work on human genomic sequence annotation was the basis for the ENSEMBL annotation pipeline. After three years he joined a biotech start-up company to head bioinformatics and four years after that joined the University of Cambridge Genetics Department, where his group develops the InterMine data integration platform. Other current research interests include genome sequencing and analysis, synthetic biology and Toxoplasma genomics. In 2004 he was made Director of the Cambridge Computational Biology Institute (CCBI) and since 2005 he has co-organised the Cambridge team for the International Genetically Engineered Machines (iGEM) undergraduate summer competition in synthetic biology.

ALL ARE WELCOME *(No registration required)*