

Ryan Lower

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Education

2005 - 2006

MRes in Bioinformatics at the University of York.

Topics include: Python, Perl & Java programming, Structural Bioinformatics, Systems Biology, Machine Learning and Molecular Sequence Analysis. Skills reinforced over 3 research projects, the last of which was a three-month external research placement.

2002 - 2005

BSc (Hons) 2.2 in Genetics at the University of York

1995 - 2005

Loughborough Grammar School

5 GCE A Levels: Mathematics, Further Mathematics, Biology, Chemistry and General Studies.

9 GCSEs including Mathematics [A*] and English [B]

Research

2006 - 2010

PhD: Evolution of bacterial genome composition

Investigating evolutionary processes over differing genome components using large scale analysis of all fully sequenced bacterial genomes. Work primarily focused on sequence signature directionality of predicted orthologous gene sets. Bioinformatic analysis of 84 *Rhizobial* 454 sequenced genomes from within an small geographical area (1m²). Investigation of the definition of core / accessory gene components and rates of gene exchange

2006

Investigating patterns of *cis*-regulatory elements within human genes and their putative orthologs

Bioinformatic investigation of trends across orthologous sets of genes sharing computationally predicted transcription factor sites. Implemented pipelines to test promoter conservation, evolutionary rates, binding site specificity, gene ontology and human-ortholog motif intersections with the aim of improving the original prediction program.

(Department of Computer Science, University of Illinois)

2006 **RepSeq: Identification of amino acid repeats**
Repeat containing proteins have been implicated in parasite pathogenesis. To further investigation of such proteins, a perl algorithm was designed to identify sequence repeat regions (SRRs), tandem repeat regions (TRRs) and single amino acid repeats (SAARs) from a complete proteome. Such regions are stored in a MySQL database which is accessible via a simple PHP based interface.
(Centre for Immunology and Infection, University of York)

2005 **Computational comparisons of *Rhizobium etli* and *Rhizobium leguminosarum* annotations**
Group project aimed at improving the two annotations before publication in early 2006. Wrote an algorithm / program to identify homologous gene pairs with differing annotated start sites and, where possible, reconciled them using evidence from the annotations and related genomes.
(Department of Biology, University of York)

2005 **Bacterial conjugation: Is the probability of recombination dependent on location of the gene?**
Final year research project: Investigated recombination events between 14 antibiotic resistance and metabolism marker genes using the model organism *E. coli*. Involved the production of specific mutants, designing efficient recombination experiments and analysis of large data sets.
(Department of Biology, University of York)

Papers

2010 **Introducing the bacterial 'chromid': not a chromosome, not a plasmid.** Trends Microbiol

2009 **The NfeD protein family and its conserved gene neighbours throughout prokaryotes: functional implications for stomatin-like proteins.** J Mol Evol

2008 **RepSeq - A database of amino acid repeats present in lower eukaryotic pathogens.** BMC Bioinformatics

Other experience

2007 onwards **School Assessment Management System**
Devised and implemented (in Ruby on Rails) a web-based assessment system to track and analyse pupil's achievement progression. Recent updates include SMS communication with parents. Rated very highly by Ofsted.
(Merrydale Infant School, Leicester)