Kim RUTHERFORD
Software Development and Bioinformatics

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⧉ http://kimrutherford.github.io
Dunedin New Zealand

Profile

Bioinformatics, genomics and programming.

Education

Bachelor of Science with Honours in Computer Science and Mathematics. Victoria University, Wellington, New Zealand

Skills and Experience

- Genome annotation and analysis tool development
- Development and maintenance of data warehousing software for genomics and proteomics
- Data processing, data management and analysis of next generation sequencing results
- Web application development
- SQL database administration and maintenance
- Systems administration including software and database installation, configuration and deployment

Work experience

Sept 2012 – Present **Scientific Officer** *Gemmell lab*
Department of Anatomy, University of Otago

Tasks bioinformatics support for the group
genome and transcriptome assembly and analysis
mentoring / training of group members in bioinformatics

June 2010 – Present **Programmer** *S. pombe genome database (PomBase)*
Department of Biochemistry, University of Cambridge

Tasks web and database programming
system adminstration for curation.pombase.org

Feb 2009 – June 2010 **Computer Associate** *Baulcombe Group*
Department of Plant Sciences, University of Cambridge

Tasks bioinformatics support
creation of a short read analysis pipeline

Sept 2007 – Feb 2009 **Programmer** *modENCODE Data Coordination Center*
Cambridge Systems Biology Centre

Tasks helped create the data warehouse for the data from modENCODE:
⧉ modMine

Feb 2004 – Sept 2007 **Programmer** *FlyMine/InterMine group*
Department of Genetics, University of Cambridge

Tasks Java programming for the InterMine project

Sept 1998 – Feb 2004 **Principal Computer Programmer** *Pathogen Sequencing Unit*
The Sanger Institute

Tasks programming and bioinformatics support
Major projects ⧉ Artemis - a genome analysis and annotation tool
⧉ ACT - a genome comparison viewer

Publications

⧉ Scopus profile

Feb 2000 **The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hypervariable sequences.**
J. Parkhill et al.
Nature. 2000 Feb 10;403(6770):665-8.

Mar 2000 **Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.**
J. Parkhill et al.
Nature. 2000 Mar 30;404(6777):502-6.

Oct 2000 **Artemis: sequence visualisation and annotation.**
K. Rutherford, J. Parkhill, J. Crook, T. Horsnell, P. Rice, M-A. Rajandream and B. Barrell
Bioinformatics. 2000 Oct;16(10):944-5.

Feb 2001   **Massive gene decay in the leprosy bacillus.**
S. Cole et al.
Nature. 2001 Feb 22;409(6823):1007-11.

June 2001   **A Re-annotation of the Saccharomyces *cerevisiae Genome*.**
V. Wood, K. M. Rutherford, A. Ivens, M-A Rajandream and B. Barrell
Comp Funct Genomics. 2001 June; 2(3): 143–154.

Oct 2001   **Genome sequence of *Yersinia pestis*, the causative agent of plague.**
J. Parkhill et al.
Nature. 2001 Oct 4;413(6855):523-7.

Oct 2001   **Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.**   J. Parkhill et al.
Nature. 2001 Oct 25;413(6858):848-52.

Feb 2002   **The genome sequence of *Schizosaccharomyces pombe*.**
V. Wood et al.
Nature. 2002 Feb 21;415(6874):871-80.

May 2002   **Complete genome sequence of the model actinomycete *Streptomyces coelicolor* A3(2).**
S. Bentley et al.
Nature. 2002 May 9;417(6885):141-7.

Oct 2002   **Sequence of Plasmodium falciparum chromosomes 1, 3–9 and 13.**
N. Hall et al.
Nature. 2002 Oct 3;419(6906):527-31.

Oct 2002   **Genome sequence of the human malaria parasite Plasmodium falciparum.**
J. Malcolm et al.
Nature. 2002 Oct 3;419(6906):498-511.

June 2003   **Viewing and annotating sequence data with Artemis.**
M. Berriman and K. Rutherford
Brief Bioinform. 2003 Jun;4(2):124-32.

Aug 2003   **The DNA sequence of chromosome I of an African trypanosome: Gene content, chromosome organisation, recombination and polymorphism**
N. Hall et al.
Nucl. Acids Res. (2003) 31 (16): 4864-4873.

Nov 2003   **The complete genome sequence and analysis of *Corynebacterium diphtheriae* NCTC13129.**
A. Cerdeño-Tárraga et al.
Nucleic Acids Res. 2003 Nov 15;31(22):6516-23.

Jan 2004   **GeneDB: a resource for prokaryotic and eukaryotic organisms.**
Hertz-Fowler C et al.
Nucleic Acids Res. 2004 Jan 1;32(Database issue):D339-43.

June 2004   **Complete genomes of two clinical *Staphylococcus aureus* strains: Evidence for the rapid evolution of virulence and drug resistance.**
M. Holden et al.
*Proc Natl Acad Sci U S A. 2004 Jun 29;101(26):9786-91*a

Sep 2004   **Genomic plasticity of the causative agent of melioidosis, *Burkholderia pseudomallei*.**
M. Holden et al.
Proc Natl Acad Sci U S A. 2004 Sep 28;101(39):14240-5.

Jan 2005   **A comprehensive survey of the *Plasmodium* life cycle by genomic, transcriptomic, and proteomic analyses**
N. Hall
Science 07 Jan 2005: Vol. 307, Issue 5706, pp. 82-86

June 2005   **A Human-Curated Annotation of the *Candida albicans* Genome**
Braun et al.
PLoS Genet. 2005 Jul;1(1):36-57. Epub 2005 Jun 17

Aug 2005   **ACT: the Artemis comparison tool.**
T. Carver, K. Rutherford, M. Berriman, M-A. Rajandream, B.. Barrell and J. Parkhill
Bioinformatics. 2005 Aug 15;21(16):3422-3

Sep 2005   **WebACT - An online companion for the Artemis Comparison Tool**
J. Abbott, D. Aanensen, K. Rutherford, S. Butcher and B. Spratt
Bioinformatics. 2005 Sep 15;21(18):3665-6. Epub 2005 Aug 2

July 2007 **FlyMine: an integrated database for *Drosophila* and *Anopheles* genomics.**
R. Lyne et al.
Genome Biol. 2007;8(7):R129.

Dec 2010 **Integrative Analysis of the *C. elegans* Genome by the modENCODE Project.**
The modENCODE Consortium
Science. 2010 Dec 24;330(6012):1775-87.

Dec 2010 **Identification of Functional Elements and Regulatory Circuits by *Drosophila* modENCODE.**
The modENCODE Consortium
Science. 2010 Dec 24;330(6012):1787-97.

Nov 2011 **The Gene Ontology: enhancements for 2011.**
Gene Ontology Consortium. *Nucleic Acids Res. 2012 Jan;40(Database issue):D559-64. Epub 2011 Nov 18.*

Jan 2012 **PomBase: a comprehensive online resource for fission yeast.**
Wood V et al.
Nucleic Acids Res. 2012 Jan;40(Database issue):D695-9.

Jan 2012 **modMine: flexible access to modENCODE data.**
S. Contrino et al.
Nucleic Acids Res. 2012 Jan;40(Database issue):D1082-8.

Sep 2012 **InterMine: a flexible data warehouse system for the integration and analysis of heterogeneous biological data** R. Smith et al.
Bioinformatics. (2012) 28 (23):3163-3165.

Jan 2013 **Gene ontology annotations and resources.**
Gene Ontology Consortium
Nucleic Acids Res. 2013 Jan;41(Database issue):D530-5. doi: 10.1093/nar/gks1050

Feb 2014 **Canto: An online tool for community literature curation**
K. Rutherford, M. A. Harris, A. Lock, S. G. Oliver and V. Wood
Bioinformatics (2014) doi: 10.1093/bioinformatics/btu103

June 2014 **Improving functional annotation for industrial microbes: A case study with *Pichia pastoris***
D. Dikicioglu, V. Wood, K. Rutherford, M. McDowall, S. Oliver
Trends in Biotechnology (2014) 10.1016/j.tibtech.2014.05.003

Oct 2014 **PomBase 2015: updates to the fission yeast database**
M. McDowall, M. Harris, A. Lock, K. Rutherford, D. Staines, J. Bähler, P. Kersey, S. Oliver and V. Wood
Nucl. Acids Res. (2014) doi: 10.1093/nar/gku1040

Dec 2014 **Molecular evolution of Dmrt1 accompanies change of sex-determining mechanisms in reptilia**
D. E. Janes et al.
Biol Lett. 2014 Dec; 10(12): 20140809.

Jan 2015 **Gene Ontology Consortium: going forward**
The Gene Ontology Consortium
Nucl. Acids Res. (28 January 2015) 43 (D1): D1049-D1056.

Nov 2015 **Large-scale transcriptome sequencing reveals novel expression patterns for key sex-related genes in a sex-changing fish**
H. Liu, M. Lamm, K. Rutherford, M. Black, J. Godwin and N. Gemmell
Biology of Sex Differences (2015) 6:26

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