Kim RUTHERFORD
Software Development and Bioinformatics

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Profile

I am a software developer and bioinformatician. For the last 18 years I have been helping biologists to capture, analyse and interpret genomic data.

Skills and Experience

- Software development: web, desktop and server
- Database administration and maintenance
- Genome annotation and analysis
- Processing, management and analysis of next generation sequencing data
- Systems administration including software and database installation and configuration

Work experience

June 2010 – Present	**Programmer** *S. pombe genome database (PomBase)* Department of Biochemistry, University of Cambridge
Tasks	web and database programming system administration for curation.pombase.org
Major projects	⬈ Canto - a community curation tool ⬈ PomBase v2

Sept 2012 – Dec 2016	**Scientific Officer** (part time) *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 ⬈ tuatara ⬈ genome project

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 modENCODE project: ⬈ 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 ● ⬈ Google Scholar ● ⬈ ORCID ● ⬈ Europe PMC

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.**
V. Wood, M.A. Harris, M.D. McDowall, K. Rutherford, B.W. Vaughan, D.M. Staines, M. Aslett, A. Lock, J. Bähler, P.J. Kersey, S.G. Oliver
Nucleic Acids Res. 2012 Jan;40(Database issue):D695-9.

Jan 2012 | **modMine: flexible access to modENCODE data.**
S. Contrino, R.N. Smith, D. Butano, A. Carr, F. Hu, R. Lyne, K. Rutherford, A. Kalderimis, J. Sullivan, S. Carbon, E.T. Kephart, P. Lloyd, E.O. Stinson, N.L. Washington, M.D. Perry, P. Ruzanov, Z. Zha, S.E. Lewis, L.D. Stein, G. Micklem
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.N. Smith, J. Aleksic, D. Butano, A. Carr, S. Contrino, F. Hu, M. Lyne, R. Lyne, A. Kalderimis, K. Rutherford, R. Stepan, J. Sullivan, M. Wakeling, X. Watkins, G. Micklem
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

Feb 2016   **Uncovering the pathways underlying whole body regeneration in a chordate model, *Botrylloides leachi* using de novo transcriptome analysis**
L. Zondag, K. Rutherford, N. Gemmell and M. Wilson
BMC Genomics (2016) 17:114 DOI 10.1186/s12864-016-2435-6

Jan 2017   **PHI-base: A new interface and further additions for the multi-species pathogen-host interactions database.**
Urban, M., Alayne Cuzick, A., Rutherford, K., Irvine, A., Pedro, H., Pant, R., Sadanadan, V., Khamari, L., Billal, S., Mohanty S., and. Hammond-Kosack, K.E.
Nucleic Acids Research (2017) doi: 10.1093/nar/gkw1089

2017   **Male-female relatedness at specific SNP-linkage groups influences cryptic female choice in Chinook salmon (*Oncorhynchus tshawytscha*)**
C. Gessner, S.L. Johnson, P. Fisher, S. Clarke, K. Rutherford, J. Symonds, N.J. Gemmell
(In press)

2017   **Identification of sex differences in zebrafish brain during early sexual differentiation and masculinisation using methyltestoterone**
S.L.J. Lee, J.A. Horsfield, M.A. Black, K. Rutherford, N.J. Gemmell
(In press)

2017   **Analysis of the genome of the New Zealand giant Collembola (Holacanthella duospinosa) sheds light on hexapod evolution**
C. Wu, M.D. Jordan, R.D. Newcomb, N.J. Gemmell, S. Bank, K. Meusemann, P.K. Dearden, E.J. Duncan, S. Grosser, K. Rutherford, P.P. Gardner, R.N. Crowhurst, B. Steinwender, L. Tooman, M.I. Stevens, and T.R. Buckley
(In press)