

Kim RUTHERFORD

Software Development and Bioinformatics

☎ +64 212508293
✉ kmr@bioinformatics.nz
🔗 <https://kmr.bioinformatics.nz>
Dunedin, New Zealand

Profile

I am a software developer and bioinformatician. For the last 20 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 assembly, 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.
- Sep 2000 **Analysis of 114 kb of DNA sequence from fission yeast chromosome 2 immediately centromere-distal to *his5*.**
Z. Xiang et al.
Yeast 16: 1405-1411.
- 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):9786-91a
- 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

Nov 2016 **The Gene Ontology Consortium; Expansion of the Gene Ontology knowledgebase and resources.**

The Gene Ontology Consortium

Nucleic Acids Res 2017; 45 (D1): D331-D338. doi: 10.1093/nar/gkw1108

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

June 2017 **PomBase - the scientific resource for fission yeast**

V. Wood, A. Lock, K. Rutherford, M.A. Harris

Methods in Molecular Biology doi: 10.17863/CAM.12124

July 2017

Histological and transcriptomic effects of 17 α -methyltestosterone on zebrafish gonad development

S.L.J. Lee, J.A. Horsfield, M.A. Black, K. Rutherford, A. Fisher, N.J. Gemmell
BMC Genomics (2017) 18:557 doi: 10.1186/s12864-017-3915-z

- July 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
Proc. R. Soc. B 2017 284 20170853; DOI: 10.1098/rspb.2017.0853.
- Nov 2017 **Female mimicry by sneaker males has a transcriptomic signature in both the brain and gonad in a sex changing fish**
E.V. Todd, H. Liu, M.S. Lamm, J.T. Thomas, K. Rutherford, K.C. Thompson, J.R. Godwin, N.J. Gemmell
Molecular Biology and Evolution, doi: 10.1093/molbev/msx293
- Dec 2017 **Identification of sex differences in zebrafish (*Danio rerio*) brains during early sexual differentiation and masculinisation using 17 α -methyltestosterone**
S.L.J. Lee, J.A. Horsfield, M.A. Black, K.M. Rutherford, N.J. Gemmell
Biology of Reproduction, doi: 10.1093/biolre/iox175
- Dec 2017 **Analysis of the genome of the New Zealand giant collembolan (*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.K. Tooman, M.I. Stevens, T.R. Buckley
BMC Genomics. 2017 Oct 17;18(1):795. doi: 10.1186/s12864-017-4197-1.
- Feb 2018 **Genetic sex assignment in wild populations using GBS data: a statistical threshold approach**
W. Stovall, H.R. Taylor, M. Black, S. Grosser, K. Rutherford, N.J. Gemmell
Molecular Ecology Resources. doi: 10.1111/1755-0998.12767
- Apr 2018 **De novo draft assembly of the *Botrylloides leachii* genome provides further insight into tunicate evolution**
S. Blanchoud, K. Rutherford, L. Zondag, N. Gemmell, M. Wilson
Sci Rep. 2018 Apr 3;8(1):5518. doi: 10.1038/s41598-018-23749-w.
- Apr 2018 **Adipose Transcriptome Analysis Provides Novel Insights into Molecular Regulation of Prolonged Fasting in Northern Elephant Seal Pups**
B. Martinez, J. Khudyakov, K. Rutherford, D. Crocker, N. Gemmell, R. Ortiz
Physiological Genomics. doi: 10.1152/physiolgenomics.00002.2018
- Aug 2018 **Reduced representation sequencing detects only subtle regional structure in a heavily exploited and rapidly recolonizing marine mammal species**
N. Dussex, H.R. Taylor, W.R. Stovall, K. Rutherford, K.G. Dodds, S.M. Clarke, N.J. Gemmell
Ecology and Evolution. doi: 10.1002/ece3.4411
- Aug 2018 **Evolutionary history of the podoplanin gene**
J. Renart, D. San Mauro, A. Agorreta, K. Rutherford, N. J. Gemmell, M. Quintanilla
Gene Reports. doi: 10.1016/j.genrep.2018.08.005
- Oct 2018 **PomBase 2018: user-driven reimplementations of the fission yeast database provides rapid and intuitive access to diverse, interconnected information**
A. Lock, K. Rutherford, M.A. Harris, J. Hayles, S.G. Oliver, J. Bähler, V. Wood
Nucleic Acids Research. <https://doi.org/10.1093/nar/gky961>

Apr 2018

PomBase: The Scientific Resource for Fission Yeast

"Eukaryotic Genomic Databases : Methods and Protocols"

A Lock, K Rutherford, M.A. Harris, V. Wood

[✂](#) *Methods in Molecular Biology*, vol 1757. doi: 10.1007/978-1-4939-7737-6_4

● [✈](#) kim_rutherford ● [🌐](#) kimrutherford ● [✂](#) kmr.bioinformatics.nz ● [✂](#) keybase.io/kmr ● Skype:
kim_rutherford