Kim RUTHERFORD

Software Development and Bioinformatics

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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
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

Oct 2001 – 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

Apr 1999 – Oct 2001
Senior Computer Programmer *Pathogen Sequencing Unit*
The Sanger Institute

Sept 1998 – Apr 1999
Computer Programmer *Pathogen Sequencing Unit*
The Sanger Institute

Publications

Google Scholar ● ORCID ● Europe PMC ● ResearcherID ● Scopus profile

Dec 2019
The tuatara genome: insights into vertebrate evolution from the sole survivor of an ancient reptilian order
N. Gemmell, K. Rutherford, S. Prost, M. Tollis, D.J. Winter, J.R.Macey, D.L. Adelson, A. Suh, T. Bertozzi, J. Grau, C. Organ, P. Gardner, *et al.*
bioRxiv preprint *10.1101/867069*

Nov 2019
PHI-base: the pathogen–host interactions database
M. Urban, A. Cuzick, J. Seager, V. Wood, K. Rutherford, S. Yagwakote Venkatesh, N. De Silva, M. Carbajo Martinez, H. Pedro, A.D. Yates, K. Hassani-Pak, K.E. Hammond-Kosack
Nucleic Acids Research. *10.1093/nar/gkz904*

Mar 2019
Molecular structure of sauropsid β-keratins from tuatara (*Sphenodon punctatus*)
D. Parry, R. Fraser, L. Alibardi, K. Rutherford, N. Gemmell
J. Struct. Biol. 207, 21-28. *10.1016/j.jsb.2019.04.008*

Jan 2019
PomBase 2018: user-driven reimplementation 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. *10.1093/nar/gky961*

Dec 2018

Stress, novel sex genes and epigenetic reprogramming orchestrate socially-controlled sex change
E.V. Todd, O. Ortega-Recalde, H. Liu, M.S. Lamm, K.M. Rutherford, H. Cross, M.A. Black, O. Kardailsky, J.A. Graves, T.A. Hore, J.R. Godwin, N.J. Gemmell
Science Advances Vol. 5, no. 7 10.1126/sciadv.aaw7006

Nov 2018 **Hidden in plain sight: What remains to be discovered in the eukaryotic proteome?**
V. Wood, A. Lock, M. Harris, K. Rutherford, J. Bahler, S Oliver
Open Biology. 10.1098/rsob.180241

Oct 2018 **RNAcentral: a hub of information for non-coding RNA sequences**
The RNAcentral Constortium
Nucleic Acids Research. 10.1093/nar/gky1034

Oct 2018 **The Gene Ontology Resource: 20 years and still GOing strong**
The Gene Ontology Consortium
Nucleic Acids Research. 10.1093/nar/gky1055

Aug 2018 **Evolutionary history of the podoplanin gene**
J. Renart, D. San Mauro, A. Agorreta, K. Rutherford, N. J. Gemmell, M Quintanill
Gene Reports. 10.1016/j.genrep.2018.08.005

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. 10.1002/ece3.4411

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. 10.1152/physiolgenomics.00002.2018

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. 10.1038/s41598-018-23749-w.

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. 10.1111/1755-0998.12767

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. 10.1186/s12864-017-4197-1.

Dec 2017 **Identification of sex differences in zebrafish (*Danio rerio*) brains during early sexual differentiation and masculinisation using 17α-methyltestoterone**
S.L.J. Lee, J.A. Horsfield, M.A. Black, K.M. Rutherford, N.J. Gemmell
Biology of Reproduction, 10.1093/biolre/iox175

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, 10.1093/molbev/msx293

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; 10.1098/rspb.2017.0853.

July 2017 **Histological and transcriptomic effects of 17α-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 10.1186/s12864-017-3915-z

June 2017 **PomBase – the scientific resource for fission yeast**
V. Wood, A. Lock, K. Rutherford, M.A. Harris
Methods in Molecular Biology 10.17863/CAM.12124

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) 10.1093/nar/gkw1089

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. 10.1093/nar/gkw1108

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 10.1186/s12864-016-2435-6

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 10.1186/s13293-015-0044-8

Jan 2015 **Gene Ontology Consortium: going forward**
The Gene Ontology Consortium
Nucl. Acids Res. (28 January 2015) 43 (D1): D1049-D1056. *10.1093/nar/gku1179*

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. *10.1098/rsbl.2014.0809*

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) *10.1093/nar/gku1040*

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*

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) *10.1093/bioinformatics/btu103*

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

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. *10.1093/bioinformatics/bts577*

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. *10.1093/nar/gkr921*

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. *10.1093/nar/gkr853*

Nov 2011 **The Gene Ontology: enhancements for 2011.**
Gene Ontology Consortium.
Nucleic Acids Res. 2012 Jan;40(Database issue):D559-64. *10.1093/nar/gkr1028*

Dec 2010 **Identification of Functional Elements and Regulatory Circuits by *Drosophila* modENCODE.**
The modENCODE Consortium
Science. 2010 Dec 24;330(6012):1787-97. *10.1126/science.1198374*

Dec 2010 **Integrative Analysis of the *C. elegans* Genome by the modENCODE Project.**
The modENCODE Consortium
Science. 2010 Dec 24;330(6012):1775-87. *10.1126/science.1196914*

July 2007 **FlyMine: an integrated database for *Drosophila* and *Anopheles* genomics.**
R. Lyne *et al.*
Genome Biol. 2007;8(7):R129. *10.1186/gb-2007-8-7-r129*

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. *10.1093/bioinformatics/bti601*

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 *10.1093/bioinformatics/bti553*

June 2005 **A Human-Curated Annotation of the *Candida albicans* Genome**
Braun *et al.*
PLoS Genet. 2005 Jul;1(1):36-57. *10.1371/journal.pgen.0010001*

Jan 2005 **A comprehensive survey of the *Plasmodium* life cycle by genomic, transcriptomic, and proteomic analyses**
N. Hall *et al.*
Science 07 Jan 2005: Vol. 307, Issue 5706, pp. 82-86 *10.1126/science.1103717*

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. *10.1073/pnas.0403302101*

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 *10.1073/pnas.0402521101*

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. *10.1093/nar/gkh007*

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. *10.1093/nar/gkg874*

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. PMC169939

June 2003 **Viewing and annotating sequence data with Artemis.**
M. Berriman and K. Rutherford
Brief Bioinform. 2003 Jun;4(2):124-32. PMID:12846394

Oct 2002 **Genome sequence of the human malaria parasite *Plasmodium falciparum*.**
J. Malcolm *et al.*
Nature. 2002 Oct 3;419(6906):498-511. 10.1038/nature01097

Oct 2002 **Sequence of *Plasmodium falciparum* chromosomes 1, 3–9 and 13.**
N. Hall *et al.*
Nature. 2002 Oct 3;419(6906):527-31. 10.1038/nature01095

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. 10.1038/417141a

Feb 2002 **The genome sequence of *Schizosaccharomyces pombe*.**
V. Wood *et al.*
Nature. 2002 Feb 21;415(6874):871-80. 10.1038/nature724

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. 10.1038/35101607

Oct 2001 **Genome sequence of *Yersinia pestis*, the causative agent of plague.**
J. Parkhill *et al.*
Nature. 2001 Oct 4;413(6855):523-7. 10.1038/35097083

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. 10.1002/cfg.86

Feb 2001 **Massive gene decay in the leprosy bacillus.**
S. Cole *et al.*
Nature. 2001 Feb 22;409(6823):1007-11. 10.1038/35059006

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. 10.1093/bioinformatics/16.10.944

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. full text

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. 10.1038/35006655

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. 10.1038/35001088

Book Chapters

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. 10.1007/978-1-4939-7737-6_4

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