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

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

Mar 2019	**DNA from mollusc shell - a valuable and underutilised substrate for genetic analyses** S. Ferreira, R. Ashby, G.-J. Jeunen, K. Rutherford, C. Collins, E. Todd, N. Gemmell *In review*

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_