

Profile

I am a software developer and bioinformatician. For the last 25 years I have been helping biologists to capture, analyse and interpret genomic data.

Skills and Experience

- Software development
- 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*
- full stack development
 - bioinformatics support
 - system administration
- Major projects*
- [Canto](#) - a community curation tool
 - [PomBase v2](#)
 - [JaponicusDB](#)
- Secondments*
- FlyBase - 3 months customising [Canto](#) for drosophila phenotypes
 - PHI-base - 6 months adapting Canto for pathogen-host interaction phenotype curation
- Sept 2012 – Dec 2016 **Scientific Officer** (part time) *Gemmell Group*
Department of Anatomy, University of Otago
- Tasks*
- bioinformatics support
 - genome and transcriptome assembly and analysis
 - bioinformatics mentoring and training
 - [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

Oct 2023	Revised fission yeast gene and allele nomenclature guidelines for machine readability M. Lera-Ramírez, J. Bähler, J. Mata, K. Rutherford, C.S. Hoffman, S. Lambert, S. Oliferenko, S.G. Martin, K.L. Gould, L-L. Du, S.A. Sabatinos, S.L. Forsburg, O. Nielsen, P. Nurse, V. Wood <i>GENETICS</i> , <i>iyad143</i> ↗ DOI: 10.1093/genetics/iyad143
July 2023	A framework for community curation of interspecies interactions literature A. Cuzick, J. Seager, V. Wood, M. Urban, K. Rutherford, K.E. Hammond-Kosack <i>eLife</i> . ↗ DOI: 10.7554/eLife.84658
March 2023	The Gene Ontology knowledgebase in 2023 The Gene Ontology Consortium <i>GENETICS</i> . ↗ DOI: 10.1093/genetics/iyad031
Dec 2021	JaponicusDB: Rapid deployment of a model organism database for an emerging model species K. Rutherford, M. Harris, S. Oliferenko, V. Wood <i>GENETICS</i> . ↗ DOI: 10.1093/genetics/iyab223
Dec 2021	Fission stories: Using PomBase to understand <i>Schizosaccharomyces pombe</i> biology M. Harris, K. Rutherford, J. Hayles, A. Lock, J. Bähler, S. Oliver, J. Mata, V. Wood <i>GENETICS</i> . ↗ DOI: 10.1093/genetics/iyab222
Nov 2021	PHI-base in 2022: a multi-species phenotype database for Pathogen-Host Interactions M. Urban <i>et al.</i> <i>NAR</i> ↗ DOI: 10.1093/nar/gkab1037
Dec 2020	The Gene Ontology resource: enriching a GOLD mine The Gene Ontology Consortium <i>Nucleic Acids Research</i> . ↗ DOI: 10.1093/nar/gkaa1113
Dec 2020	A genome-wide investigation of adaptive signatures in protein-coding genes related to tool behaviour in New Caledonian and Hawaiian crows N. Dussex <i>et al.</i> <i>Molecular Ecology</i> . ↗ DOI: 10.1111/mec.15775
Nov 2020	Dense sampling of bird diversity increases power of comparative genomics S. Feng <i>et al.</i> <i>Nature</i> . ↗ DOI: 10.1038/s41586-020-2873-9
Sep 2020	Term Matrix: A novel Gene Ontology annotation quality control system based on ontology term co-annotation patterns V. Wood <i>et al.</i> <i>Open Biology</i> . ↗ DOI: 10.1098/rsob.200149
Aug 2020	The tuatara genome reveals ancient features of amniote evolution N. Gemmell, K. Rutherford, <i>et al.</i> <i>Nature</i> . ↗ DOI: 10.1038/s41586-020-2561-9
July 2020	DNA from mollusc shell: a valuable and underutilised substrate for genetic analyses S. Ferreira, R. Ashby, G-J. Jeunen, K. Rutherford, C. Collins, E.V. Todd, N.J. Gemmell <i>PeerJ</i> . ↗ DOI: 10.7717/peerj.9420
Apr 2020	Community curation in PomBase: enabling fission yeast experts to provide detailed, standardized, sharable annotation from research publications A. Lock, M. Harris, K. Rutherford, J. Hayles, V. Wood <i>Database</i> . ↗ DOI: 10.1093/database/baaa028
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 <i>Nucleic Acids Research</i> . ↗ DOI: 10.1093/nar/gkz904
July 2019	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 <i>Science Advances</i> . ↗ DOI: 10.1126/sciadv.aaw7006
July 2019	Molecular structure of sauropsid β-keratins from tuatara (<i>Sphenodon punctatus</i>) D. Parry, R. Fraser, L. Alibardi, K. Rutherford, N. Gemmell <i>Journal of Structural Biology</i> . ↗ DOI: 10.1016/j.jsb.2019.04.008
Feb 2019	Hidden in plain sight: What remains to be discovered in the eukaryotic proteome? V. Wood, A. Lock, M. Harris, K. Rutherford, J. Bähler, S. Oliver <i>Open Biology</i> . ↗ DOI: 10.1098/rsob.180241
Nov 2018	RNAcentral: a hub of information for non-coding RNA sequences The RNAcentral Consortium <i>Nucleic Acids Research</i> . ↗ DOI: 10.1093/nar/gky1034
Oct 2018	PomBase 2018: user-driven reimplementaion 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 <i>Nucleic Acids Research</i> . ↗ DOI: 10.1093/nar/gky961

- Oct 2018 **The Gene Ontology Resource: 20 years and still GOing strong**
The Gene Ontology Consortium
Nucleic Acids Research. [DOI: 10.1093/nar/gky1055](#)
- Aug 2018 **Evolutionary history of the podoplanin gene**
J. Renat, D. San Mauro, A. Agorreta, K. Rutherford, N. J. Gemmell, M Quintanill
Gene Reports. [DOI: 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. [DOI: 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. [DOI: 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
Scientific Reports. [DOI: 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. [DOI: 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. [DOI: 10.1186/s12864-017-4197-1](#).
- 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](#)
- 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](#)
- 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. [DOI: 10.1098/rspb.2017.0853](#).
- 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. [DOI: 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. [DOI: 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. [DOI: 10.1093/nar/gkw1089](#)
- Nov 2016 **The Gene Ontology Consortium; Expansion of the Gene Ontology knowledgebase and resources.**
The Gene Ontology Consortium
Nucleic Acids Research. [DOI: 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. [DOI: 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. [DOI: 10.1186/s13293-015-0044-8](#)
- Jan 2015 **Gene Ontology Consortium: going forward**
The Gene Ontology Consortium
Nucleic Acids Research. [DOI: 10.1093/nar/gku1179](#)
- Dec 2014 **Molecular evolution of Dmrt1 accompanies change of sex-determining mechanisms in reptilia**
D. E. Janes *et al.*
Biology Letters. [DOI: 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
Nucleic Acids Research. [DOI: 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. [DOI: 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. [DOI: 10.1093/bioinformatics/btu103](#)
- Jan 2013 **Gene ontology annotations and resources.**
Gene Ontology Consortium
Nucleic Acids Research. [DOI: 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. [DOI: 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 Research. [DOI: 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 Research. [DOI: 10.1093/nar/gkr853](#)
- Nov 2011 **The Gene Ontology: enhancements for 2011.**
Gene Ontology Consortium.
Nucleic Acids Research. [DOI: 10.1093/nar/gkr1028](#)
- Dec 2010 **Identification of Functional Elements and Regulatory Circuits by *Drosophila* modENCODE.**
The modENCODE Consortium
Science. [DOI: 10.1126/science.1198374](#)
- Dec 2010 **Integrative Analysis of the *C. elegans* Genome by the modENCODE Project.**
The modENCODE Consortium
Science. [DOI: 10.1126/science.1196914](#)
- July 2007 **FlyMine: an integrated database for *Drosophila* and *Anopheles* genomics.**
R. Lyne *et al.*
Genome Biology. [DOI: 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. [DOI: 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. [DOI: 10.1093/bioinformatics/bti553](#)
- June 2005 **A Human-Curated Annotation of the *Candida albicans* Genome**
B.R. Braun *et al.*
PLoS Genetics. [DOI: 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. [DOI: 10.1126/science.1103717](#)
- Sep 2004 **Genomic plasticity of the causative agent of melioidosis, *Burkholderia pseudomallei*.**
M. Holden *et al.*
Proc Natl Acad Sci. [DOI: 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. [DOI: 10.1073/pnas.0402521101](#)
- Jan 2004 **GeneDB: a resource for prokaryotic and eukaryotic organisms.**
Hertz-Fowler C *et al.*
Nucleic Acids Research. [DOI: 10.1093/nar/gkh007](#)
- Nov 2003 **The complete genome sequence and analysis of *Corynebacterium diphtheriae* NCTC13129.**
A. Cerdño-Tárraga *et al.*
Nucleic Acids Research. [DOI: 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.*
Nucleic Acids Research. [DOI: 10.1093/nar/gkg674](#)
- June 2003

Viewing and annotating sequence data with Artemis.

M. Berriman and K. Rutherford

Briefing in Bioinformatics. [DOI: 10.1093/bib/4.2.124](#)

- Oct 2002 **Genome sequence of the human malaria parasite *Plasmodium falciparum*.**
J. Malcolm *et al.*
Nature. [DOI: 10.1038/nature01097](#)
- Oct 2002 **Sequence of *Plasmodium falciparum* chromosomes 1, 3–9 and 13.**
N. Hall *et al.*
Nature. [DOI: 10.1038/nature01095](#)
- May 2002 **Complete genome sequence of the model actinomycete *Streptomyces coelicolor* A3(2).**
S. Bentley *et al.*
Nature. [DOI: 10.1038/417141a](#)
- Feb 2002 **The genome sequence of *Schizosaccharomyces pombe*.**
V. Wood *et al.*
Nature. [DOI: 10.1038/nature724](#)
- Oct 2001 **Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.**
J. Parkhill *et al.*
Nature. [DOI: 10.1038/35101607](#)
- Oct 2001 **Genome sequence of *Yersinia pestis*, the causative agent of plague.**
J. Parkhill *et al.*
Nature. [DOI: 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
Comparative and Functional Genomics. [DOI: 10.1002/cfg.86](#)
- Feb 2001 **Massive gene decay in the leprosy bacillus.**
S. Cole *et al.*
Nature. [DOI: 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. [DOI: 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. [PMID:11054821](#)
- Mar 2000 **Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.**
J. Parkhill *et al.*
Nature. [DOI: 10.1038/35006655](#)
- Feb 2000 **The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hypervariable sequences.**
J. Parkhill *et al.*
Nature. [DOI: 10.1038/35001088](#)

Book Chapters

- May 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. [DOI: 10.1007/978-1-4939-7737-6_4](#)