

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

- 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

- › [🔗 PomBase](#)
- › [🔗 JaponicusDB](#)
- › [🔗 Canto](#) - a community curation tool

Secondments

- › PHI-base - 6 months adapting Canto for pathogen-host interaction phenotype curation
- › FlyBase - 3 months customising [🔗 Canto](#) for *Drosophila* phenotypes

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:
[↗ NAR publication](#)

Feb 2004 – Sept 2007 **Programmer** *FlyMine/InterMine group*
Department of Genetics, University of Cambridge

Tasks

- › Software engineering for the InterMine data warehouse project:
[↗ Bioinformatics publication](#)

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 2025 **RNAcentral in 2026: Genes and literature integration**
A.F. Green *et al.*
preprint [↗ DOI: 10.1101/2025.09.19.677274](#)

Feb 2025 **A compendium of human gene functions derived from evolutionary modelling**
The Gene Ontology Consortium
Nature (2025) [↗ DOI: 10.1038/s41586-025-08592-0](#)

Feb 2024 **PomBase: a Global Core Biodata Resource — growth, collaboration, and sustainability**
K.M. Rutherford, M. Lera-Ramírez, V. Wood
Genetics, iyae007 [↗ DOI: 10.1093/genetics/iyae007](#)

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
Genetics, iyad143 [↗ 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
eLife. [↗ DOI: 10.7554/eLife.84658](#)

March 2023 **The Gene Ontology knowledgebase in 2023**
The Gene Ontology Consortium
Genetics. [↗ 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
Genetics. [DOI: 10.1093/genetics/iyab223](#)
- Dec 2021 **Fission stories: Using PomBase to understand *Schizosaccharomyces pombe* biology**
M. Harris, K. Rutherford, J. Hayles, A. Lock, J. Bähler, S. Oliver, J. Mata, V. Wood
Genetics. [DOI: 10.1093/genetics/iyab222](#)
- Nov 2021 **PHI-base in 2022: a multi-species phenotype database for Pathogen-Host Interactions**
M. Urban *et al.*
NAR [DOI: 10.1093/nar/gkab1037](#)
- Dec 2020 **The Gene Ontology resource: enriching a GOld mine**
The Gene Ontology Consortium
Nucleic Acids Research. [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 *et al.*
Molecular Ecology. [DOI: 10.1111/mec.15775](#)
- Nov 2020 **Dense sampling of bird diversity increases power of comparative genomics**
S. Feng *et al.*
Nature. [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 *et al.*
Open Biology. [DOI: 10.1098/rsob.200149](#)
- Aug 2020 **The tuatara genome reveals ancient features of amniote evolution**
N. Gemmell, K. Rutherford, *et al.*
Nature. [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
PeerJ. [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
Database. [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
Nucleic Acids Research. [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
Science Advances.  DOI: 10.1126/sciadv.aaw7006

- July 2019 **Molecular structure of sauropsid β -keratins from tuatara (*Sphenodon punctatus*)**
D. Parry, R. Fraser, L. Alibardi, K. Rutherford, N. Gemmell
Journal of Structural Biology.  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. Bahler, S Oliver
Open Biology.  DOI: 10.1098/rsob.180241
- Nov 2018 **RNAcentral: a hub of information for non-coding RNA sequences**
The RNAcentral Consortium
Nucleic Acids Research.  DOI: 10.1093/nar/gky1034
- Oct 2018 **PomBase 2018: user-driven reimplemention 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.  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. Renart, 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 (*Holcanchella 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., Sadanandan, 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**

- 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. Beriman, 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. Cerdeño-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. Beriman 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).**

- 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