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- [↗ ORCID](https://orcid.org/0000-0002-1072-009X)
- [↗ Google Scholar](https://scholar.google.com/citations?user=000000021072009X&hl=en)

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

- [↗ PomBase](https://pombase.org)
- [↗ JaponicusDB](https://japonicusdb.org)
- [↗ Canto](https://canto.pombase.org) - a community curation tool

Secondments

- PHI-base - 6 months adapting Canto for pathogen-host interaction phenotype curation
- FlyBase - 3 months customising [↗ Canto](https://canto.pombase.org) 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](https://tuatara.genomeproject.org)

Feb 2009 – June 2010

Publications

	Computer Associate <i>Baulcombe Group</i> Department of Plant Sciences, University of Cambridge <i>Tasks</i> <ul style="list-style-type: none">› bioinformatics support› creation of a short read analysis pipeline
Sept 2007 – Feb 2009	Programmer <i>modENCODE Data Coordination Center</i> Cambridge Systems Biology Centre <i>Tasks</i> <ul style="list-style-type: none">› helped create the data warehouse for the modENCODE project: ↗ NAR publication
Feb 2004 – Sept 2007	Programmer <i>FlyMine/InterMine group</i> Department of Genetics, University of Cambridge <i>Tasks</i> <ul style="list-style-type: none">› Software engineering for the InterMine data warehouse project: ↗ Bioinformatics publication
Oct 2001 – Feb 2004	Principal Computer Programmer <i>Pathogen Sequencing Unit</i> The Sanger Institute <i>Tasks</i> <ul style="list-style-type: none">› programming and bioinformatics support <i>Major projects</i> <ul style="list-style-type: none">› ↗ Artemis - a genome analysis and annotation tool› ↗ ACT - a genome comparison viewer
Apr 1999 – Oct 2001	Senior Computer Programmer <i>Pathogen Sequencing Unit</i> The Sanger Institute
Sept 1998 – Apr 1999	Computer Programmer <i>Pathogen Sequencing Unit</i> The Sanger Institute
<ul style="list-style-type: none">● ↗ Google Scholar● ↗ ORCID● ↗ Europe PMC● ↗ ResearcherID● ↗ Scopus profile	
Oct 2025	RNAcentral in 2026: Genes and literature integration A.F. Green <i>et al.</i> <i>preprint</i> ↗ DOI: 10.1101/2025.09.19.677274
Feb 2025	A compendium of human gene functions derived from evolutionary modelling The Gene Ontology Consortium <i>Nature</i> (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 <i>Genetics</i> , <i>iyaе007</i> ↗ DOI: 10.1093/genetics/iyaе007
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

- 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 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.  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 (*Holocanthella 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
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.*

- 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. Berrieman 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