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Software Development and Bioinformatics

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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

(In press)

2017

Identification of sex differences in zebrafish brain during early sexual differentiation and masculinisation using methyltestosterone

S.L.J. Lee, J.A. Horsfield, M.A. Black, K. Rutherford, N.J. Gemmell

(In press)

2017

Analysis of the genome of the New Zealand giant Collembola (*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. Tooman, M.I. Stevens, and T.R. Buckley

(In press)

Profile

I am a software developer and bioinformatician. For the last 18 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 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 for curation.pombase.org

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

Sept 1998 – 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

Publications

● [Scopus profile](#) ● [Google Scholar](#) ● [ORCID](#) ● [Europe PMC](#)

- 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.
- 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.
- 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.
- Feb 2001 **Massive gene decay in the leprosy bacillus.**
S. Cole et al.
Nature. 2001 Feb 22;409(6823):1007-11.
- 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.
- Oct 2001 **Genome sequence of *Yersinia pestis*, the causative agent of plague.**
J. Parkhill et al.
Nature. 2001 Oct 4;413(6855):523-7.
- 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.
- Feb 2002 **The genome sequence of *Schizosaccharomyces pombe*.**
V. Wood et al.
Nature. 2002 Feb 21;415(6874):871-80.
- 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.
- Oct 2002 **Sequence of *Plasmodium falciparum* chromosomes 1, 3-9 and 13.**
N. Hall et al.
Nature. 2002 Oct 3;419(6906):527-31.
- Oct 2002 **Genome sequence of the human malaria parasite *Plasmodium falciparum*.**
J. Malcolm et al.
Nature. 2002 Oct 3;419(6906):498-511.
- June 2003 **Viewing and annotating sequence data with Artemis.**
M. Berriman and K. Rutherford
Brief Bioinform. 2003 Jun;4(2):124-32.
- 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.
- 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.
- 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.
- 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):9786-91a
- 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.
- Jan 2005 **A comprehensive survey of the *Plasmodium* life cycle by genomic, transcriptomic, and proteomic analyses**
N. Hall
Science 07 Jan 2005: Vol. 307, Issue 5706, pp. 82-86
- June 2005 **A Human-Curated Annotation of the *Candida albicans* Genome**
Braun et al.
PLoS Genet. 2005 Jul;1(1):36-57. Epub 2005 Jun 17
- 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
- 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. Epub 2005 Aug 2
- July 2007 **FlyMine: an integrated database for *Drosophila* and *Anopheles* genomics.**
R. Lyne et al.
Genome Biol. 2007;8(7):R129.
- Dec 2010 **Integrative Analysis of the *C. elegans* Genome by the modENCODE Project.**
The modENCODE Consortium
Science. 2010 Dec 24;330(6012):1775-87.
- Dec 2010 **Identification of Functional Elements and Regulatory Circuits by *Drosophila* modENCODE.**
The modENCODE Consortium
Science. 2010 Dec 24;330(6012):1787-97.
- Nov 2011 **The Gene Ontology: enhancements for 2011.**
Gene Ontology Consortium. *Nucleic Acids Res.* 2012 Jan;40(Database issue):D559-64. Epub 2011 Nov 18.
- 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.

- 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.
- 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.
- Jan 2013 **Gene ontology annotations and resources.**
Gene Ontology Consortium
Nucleic Acids Res. 2013 Jan;41(Database issue):D530-5. doi: 10.1093/nar/gks1050
- 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) doi: 10.1093/bioinformatics/btu103
- 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
- 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) doi: 10.1093/nar/gku1040
- 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.
- Jan 2015 **Gene Ontology Consortium: going forward**
The Gene Ontology Consortium
Nucl. Acids Res. (28 January 2015) 43 (D1): D1049-D1056.
- 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
- 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 DOI 10.1186/s12864-016-2435-6
- 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) doi: 10.1093/nar/gkw1089