

Curriculum Vitae - Bioinformatics

Dr. Jeremy D. Parsons

Personal Details

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Marital Status:	Single		
Nationality:	British		

Academic Qualifications

- University of Cambridge, Department of Medicine Ph.D.
- University of Kent at Canterbury, Computer Science MSc.
- Sheffield University Special Honours Microbiology BSc. class 2:1

Technical Skills

- **Languages:** Java, 'C', Perl, Python, PostScript, Bash UNIX shell script, occam2, Motorola 68000 assembler, C++, NewtonScript, R
- **Libraries and Patterns:** Parallel processing and multi-threading, Swing, RMI, CORBA, regular expressions, XML, JMF, image processing, Standard design patterns J2SE
- **Web Programming:** Servlets, JSP, JSTL, applets, PHP, Apache and Tomcat maintenance
- **Databases:** JDBC Programming, PostgreSQL, MySQL, and Oracle.
- **System Administration:** Unix (15+ years with Linux and Solaris), Macs (infrequently over 10 years), Firewall, LDAP
- **Bioinformatics:** Genome & RNA assemblers & editors, Next Gen. mappers, functional, variant & network analyses

Career

2015 - 2016 Garvan Institute of Medical Research, Immunology Dept., Australia

- Differential Expression Analyses in mice. RNAseq pipelines.
- Endogenous Retrovirus (ERV) expression
- Transcriptional control of Immune Response (IR) genes by ERV TFBS motifs.

- R presentation graphics and signal compression for heatmaps.

2011 - University of Queensland Bioinformatics with QFAB and Phil
2014 Hugenholtz, Brisbane, Australia

- Metagenomic analyses of mouse and sheep digestion
- Bacterial genome assembly including difficult 16S repeat regions
- Initial Macadamia and Koala genome assemblies and analyses.
- Transcriptomics and Differential Expression analyses in Sugar Cane and bacteria
- Web databases, Bioinformatics support and analysis, pipeline scripting and Java Programming
- BRAEMBL project and many others

2010 - Bioinformatics research & genome comparisons: Byrappa
2011 Venkatesh, Singapore

- DNA Assembly and analysis, pipeline scripting and Java Programming
- Studying Vertebrate evolution using Elephant Shark as a reference genome
- NGS Roche 454 Linker and adapter removal via sensitive parallel alignments

2008 - Cheminformatics at European Patent Office (EPO Den Haag) with
2009 Stephane Nauche

- Java Programming and Natural Language Parsing
 - Discovering new chemicals in EPO patent images and text
 - Parsing scientific literature using OSCAR 3
 - XML handling, databases and Java servlets

2007 ACI Worldwide

- Java Programming
 - Introduction to electronic payments
 - User interface design in Java

2006 - Reuters
2007

- JRisk Programmer
 - Financial software training
 - Java J2EE bugfixing

2006 - Building Research Establishment
Contract

- Analyst and Programmer
 - Image processing applications for visual analysis of timber

- Multi-threaded Java analysis pipeline and GUI

2003 -
2005

Paradigm Therapeutics

- Senior Bioinformatician (analyst/programmer) with a special focus on phenotype database development.
 - - Flexible data collection, querying and MIS report generation
 - - PostgreSQL DB with Java Beans, JSP, JSTL, and servlets
- Systems support including networking and centralized Linux servers for Macs and Linux desktops

2002 -
2003

Bioinformatics consulting at littlest.co.uk

- General bioinformatics support
- Development of parallel text indexing and publishing tools - Java, AWT, Swing, Regular Expressions, PVM, C

2001 -
2002

Bioinformatics at Lion Bioscience Ltd, Cambridge, UK. with Thure Etzhold

- Analyst and programmer for client/server systems including a graphical SRS PRISMA viewer - Java, Swing (large canvas component), XML specifications, Icarus
- Bioinformatics support and documentation

1999 -
2000

Bioinformatics at Cereon Genomics, Boston, MA, USA. with Stan Letovsky & David Bush

- Positional cloning and analysis of plant disease resistance genes - Databases, Perl, UNIX scripting, regular expressions
- Analysis database support, user training - Java, servlets

1997- 1999 Post-doctoral research at European Bioinformatics Institute with Tom Flores, Geoff Barton and Patricia Rodriguez-Tomé

- Sequence chromatogram (DNA trace file) browsing client/server systems
 - - Analyst and programmer: Java parsing, communication and graphics on scrolling canvas
- Linking Biological Databases using CORBA leading a five nation European consortium.
- Architect and programmer for a parallel distributed incremental DNA sequence alignment system that worked across 2-40 processors - 'C' and PVM
- Java client applications combining multiple data sources into graphical data summaries
- C++ server and CORBA wrapper for EST alignments and CORBA supercluster application

- 1996-1997 Bioinformatics research and support for Zeneca Pharmaceuticals with Rakesh Anand and David Pioli
- Positional cloning support for arthritis research
 - Bioinformatics programming including an email and web-based sequence alert system - Perl
 - System support - Solaris and Linux
 - Graphical client interfaces and general bioinformatics - Java
- 1993 - 1995 Post-doctoral research at Bob Waterston's Genome Sequencing Center, Washington University St. Louis. with LaDeana Hillier
- Development of sequence analysis and visualisation tools including ESTCluster and Miropeats(PrintRepeats)
 - - C, Perl and PostScript programming
 - Managing and training new programmers for a joint project with David States' group at IBC
 - System administration - Solaris and MacOS
 - Studies of variables in DNA sequence production efficiency - Postgres DBMS and SQL querying
 - Image analysis of sequence gels and lane tracking algorithms, EST clustering, DNA sequence assembly - 'C', and X11 graphics
- 1989-1993 Ph.D. in University of Cambridge Dept. of Medicine, lead by Sydney Brenner (Nobel Laureate)
- Ph.D. Thesis title is "Computer Analysis of Molecular Sequences" supervised by Martin Bishop
 - Clustering partially sequenced cDNA sequences (ESTs) - 'C'
 - Visualisation of dipeptide frequencies. - UNIX shell and PostScript
- 1989 University of Cambridge Computing Service Research Associate: Colleges Project Officer.
- 1987-88 University of Kent at Canterbury - Two years of computer science including a parallel processing research project in communications entitled "Implementing the X-25 Data Link Protocol in Occam 2"
- 1984-1987 University of Sheffield studying microbiology, chemistry and basic computing
- 1984 Self-employed: writing graphical computer games in 6809 assembly language: one sold over 4000 copies.

Publications

- 2016 Paungfoo-Lonhienne, Chanyarat; Lonhienne, Thierry G. A.; Yeoh, Yun Kit; Donose, Bogdan C.; Webb, Richard I.; Parsons, Jeremy; Liao, Webber; Sagulenko, Evgeny; Lakshmanan, Prakash; Hugenholtz, Philip; Schmidt, Susanne; Ragan, Mark A.; Crosstalk between sugarcane and a plant-growth promoting Burkholderia species, *Nature Scientific Reports*

6:37389 DOI: 10.1038/srep37389

- 2016 Kate L. Ormerod, Jeremy D. Parsons, Philip Hugenholtz et al., Genomic characterization of the uncultured Bacteroidales family S24-7 inhabiting the guts of homeothermic animals *Microbiome* **4:36** DOI: 10.1186/s40168-016-0181-2
- 2013 Mohammad Tawhidul Islam, Jeremy Parsons et al., Unlocking the Puzzling Biology of the Black Périgord Truffle Tuber *melanosporum*, J. Proteome Res., **12**, pp 5349-5356., DOI: 10.1021/pr400650c
- 2000 Parsons, J.D. and Rodriguez-Tomé P., JESAM: CORBA software components to create and publish EST alignments and clusters, *Bioinformatics*, **16**, 313-325.
- 1999 Parsons, Jeremy D., Buehler, Eugen, and Hillier, LaDeana, DNA Sequence Chromatogram Browsing Using JAVA and CORBA., *Genome Res.*, **9**, 277-281.
- 1996 Hillier, L, Parsons, J.D., et al., Generation and Analysis of 280,000 Human Expressed Sequence Tags, *Genome Research*, **6**, 807-828.
- 1996 Cooper, Matthew L., Maffitt, David R., Parsons, Jeremy.D., Hillier, LaDeana, and States, David J., Lane Tracking Software for Four-color Fluorescence-based Electrophoretic Gel Images, *Genome Res*, **6**, 1110-1117.
- 1995 Berks, M., and the *C. elegans* Genome Mapping and Sequencing Consortium, The *C. elegans* Genome Sequencing Project, *Genome Res.*, **5**,99-104.
- 1995 Parsons, J.D., Miropeats: Graphical DNA Sequence Comparisons, *Comput. Applic. Biosci.*, **11**, 615-619.
- 1995 Parsons, J.D., Improved Tools for DNA Comparison and Clustering, *Comput. Applic. Biosci.*, **11**, 603-613
- 1994 Johnston,M., Parsons,J., et al., Complete Nucleotide Sequence of *Saccharomyces Cerevisiae* Chromosome VIII. *Science*, **265**, 2077-2082
- 1992 Duff, K., Parsons J., and Hodgeman, T.C., Secondary structure analysis identifies a putative mouse protein demonstrating similarity to the repeat units found in CDC4, the G protein *B* subunits and related proteins., *J. DNA Seq. and Map.*, **3**, 213-220.
- 1992 Parsons, J.D., Brenner, S. and Bishop, M.J., (1992), Clustering cDNA Sequences, *Comput. Applic. Biosci.*, **8**, 461-466
- 1991 Poster at Cold Spring Harbor - Clustering DNA Sequences

Other Qualifications

- AO Level: Statistics.
- A Levels: Biology, Chemistry, Physics
- O Levels: English Language, Mathematics, Physics, Chemistry, Biology, French, Geography. AO Level: Statistics.
- British and Australian driving licences

Interests and Activities

- Tourist-level German, and Spanish

- International travel and travel writing, hang gliding, cycletouring, hillwalking, skiing, sailing
- Renewable energy development, aircraft and rocket engineering.
- Photography and open source photographic software development