

Curriculum Vitae - Bioinformatics

Dr. Jeremy D. Parsons

Personal Details

Name:	Jeremy David Parsons	Home Address:	5 Roughdown Villas Road, Hemel Hempstead, Herts. HP3 0AX England
Phone:	+44 7913 024857 +63 945 1940 708		
Personal email:	jp @ jeremyparsons .com		
Consulting website:	http://www.littlest.co.uk/		
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, regular expressions, XML, JMF, image processing, Standard design patterns J2SE, RMI, CORBA
- **Web Programming:** Servlets, JSP, Spring, JSTL, 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), Firewalls, LDAP
- **Bioinformatics:** Genome & RNA assemblers & editors, Metagenomics, Next Gen. mappers, functional, variant & network analyses

Career

- 2020 - Rothamsted Research, Harpenden, England with Keywan Hassani-Pak
- Senior Bioinformatician - DFW project
 - Python programming and knowledge networks - KnetMiner
- 2017 - 2019 Solar Power Developer and investor, Australia and Asia. www.filsolar.com
- Promotion and financing of cheap distributed renewable energy.
- 2015 - 2016 Garvan Institute of Medical Research, Immunology Dept., Australia
- Differential Expression Analyses in mice. UNIX scripting and RNAseq pipelines.
 - Big data processing, R presentation graphics and signal compression for heatmaps.
 - Endogenous Retrovirus (ERV) expression
 - Transcriptional control of Immune Response (IR) genes by ERV TFBS motifs.
- 2011 - 2014 University of Queensland Bioinformatics with QFAB and Phil Hugenholtz, Brisbane, Australia
- SQL and Java Web databases, Bioinformatics support and analysis, pipeline scripting and Java Programming
 - 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
 - BRAEMBL project and many others
- 2010 - 2011 Bioinformatics research & genome comparisons: Byrappa 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 - 2009 Cheminformatics at European Patent Office (EPO Den Haag) with 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 - 2007 Reuters - Java JRisk Programmer
- Financial software training
 - Java J2EE bugfixing
- 2006 - Contract Building Research Establishment - Analyst and Programmer
- Image processing applications for visual analysis of timber
 - Multi-threaded Java image analysis pipeline and GUI
- 2003 - 2005 Paradigm Therapeutics - Senior Bioinformatician (analyst/programmer)
- 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 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, MGU 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: Scopus: 7402708504 , ORCID: 0000-0003-1716-731X

2021 Keywan Hassani-Pak, Ajit Singh, Marco Brandizi, Joseph Hearnshaw, Jeremy D. Parsons, Sandeep Amberkar, Andrew L. Phillips, John H. Doonan and Chris Rawlings; KnetMiner: a comprehensive approach for supporting evidence-based gene discovery and complex trait analysis across species, *Plant Biotechnology Journal*, **19**, pp. **1670-1678** DOI: [10.1111/pbi.13583](https://doi.org/10.1111/pbi.13583)

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](https://doi.org/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](https://doi.org/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](https://doi.org/10.1021/pr400650c)

2001 Perret X., Parsons J., Viprey V., Reichwald K., Broughton W.J.; IRepeat sequences of genomes of Rhizobium and Sinorhizobium meliloti: a comparative analysis.; *Canadian Journal of Microbiology* (2001), **47(6)**, 548-558, DOI: [10.1139/cjm-47-6-548](https://doi.org/10.1139/cjm-47-6-548)

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

- A Levels: Biology, Chemistry, Physics
- AO Level: Statistics.
- O Levels: English Language, Mathematics, Physics, Chemistry, Biology, French, Geography
- 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