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, 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.
- Endogenonous 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 handlling, 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 asssembly - '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

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

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

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 Electorphoretic 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