

NICHOLAS JAMES DICKENS

DPhil BSc ARCS
dickensn@fau.edu

Research Experience

- Nov 2009 – Sept 2016* Wellcome Trust Centre for Molecular Parasitology (WTCMP), University of Glasgow, B6-28 SGDB, 120 University Place, Glasgow, G12 8TA, UK.
Bioinformatics research, service, support and training for 12 PIs across a Wellcome Trust Centre for Excellence. Research in bioinformatics and ‘-omics’.
- Oct 2014 onwards* **Bioinformatics and Experimental Sequencing Team Leader** (Grade 8, lecturer grade/assistant professor equivalent). Moved from *de facto* head of the team to official management of the core bioinformatics team. In addition to leading this team, I also established a new experimental sequencing initiative in Centre specializing in the use of new sequencing technologies and the development of organism-specific techniques for ‘-omic’ analysis; for example, low DNA/RNA in mixed host/parasite samples through custom target enrichment. Continued to develop my independent research projects in the application of machine learning to understand parasite genomes.
Research collaboration highlights: Laouini group (Pasteur Institute Tunis, Tunisia), Mottram group (University of York), McCulloch group (WTCMP, University of Glasgow, UK), David Roos, Omar Harb and EuPathDB team (University of Pennsylvania, Philadelphia, USA), Christiane Hertz-Fowler (Centre for Genomic Research, Liverpool), Cupolillo group (Fiocruz, Rio de Janeiro, Brazil), Miguel Navarro (IPB, Granada, Spain), Parasite Biology group (Sanger, UK) and Liam Morrison (Roslin Institute, Edinburgh UK)
- Nov 2012 - Oct 2014* **Senior Bioinformatician** (Grade 8, lecturer grade/assistant professor equivalent). Promoted as lead in the core bioinformatics team. Driving the provision of analysis pipelines and tools for WTCMP members and collaborators; including management of their data and centralizing code and training resources. Analysis experience with data from Illumina, Life Technologies and Pacific Biosystems platforms. Development of University of Glasgow cloud-based (Amazon Web Services) high-throughput sequence data analysis platform (e.g. custom clusters and cloud-based Galaxy resources) and novel analysis workflows. I also developed a small portfolio of independent computational parasitology research in the use of machine learning for data integration and genome analysis, which is now the basis for my group. Formalized code versioning and data repository for the WTCMP.
- Nov 2009 - Nov 2012* **Genome and Data Analyst** (Grade 7, senior post-doc grade/assistant professor equivalent). High-throughput sequencing genomics, transcriptomics and systems approaches in parasite genomes. Reference-based and *de novo* assemblies of genomes, gene copy number variation methods, chromosome aneuploidy and sequence variation in comparative genomics. Integration of clinical metadata. Also microarray data analysis. Development experience on many platforms and in many languages, especially Python, Perl and R. Some Java and C tool development. Created training programmes for students, post-docs and PIs. Other domain-specific languages including Matlab, MySQL and postgresql development.

- Oct 2006 – Oct 2009* **Bioinformatician and Data Analyst** (higher scientific officer, post-doc grade). The Institute of Cancer Research (ICR), 15 Cotswold Way, Sutton, Surrey, SM2 5NG, UK.
Close work with experimental researchers. Development of databases and analysis software. Responsible for clinical & biological data organization and quality control. Multiple collaborations in both research & clinical trials. Prognostic and predictive biomarkers (clinical & experimental), risk analysis, genome-wide association, database design, biostatistics, network analysis, systems biology, experimental design and translational medicine. Perl, R, Matlab, MySQL, web scripting, e.g. Javascript and PHP.
- May 2005 – Oct 2006* **Bioinformatics Research Associate** (post-doc grade) MRC Clinical Sciences Centre, Imperial College, London W12 0NN, UK.
Large-scale data analysis and provision of tools for a research group and research consortium.
Microarray analysis, SNP and QTLs in type-2 diabetes, heart disease and obesity. Animal models and clinical trial data. Published software development in Java, research and data analysis, publications and collaborations. Perl, MySQL and Oracle.
- Jan 2001 – Jan 2002* **Research Associate** (research assistant grade) MRC Functional Genetics Unit, Department of Human Anatomy and Genetics, South Parks Road, Oxford, OX1 3QX, UK.
Published software development in Perl/PHP/MySQL, Python, PostgreSQL, Matlab. Systems administration Beowulf cluster and running SMART database and website mirror in Oxford.
- Oct 2000 – Dec 2000* **Bioinformatics Internship.** N.V. Organon, PO Box 20, 5340 BH Oss, The Netherlands. Fixed term research and software development project. Perl, PHP, MySQL, C.

Education and Qualifications

- 2002 –2006*
University of Oxford,
Christ Church College.
MRC Studentship. **PhD Computational Biology. “Comparisons of Proteins and Genomes by Integrating Bioinformatics Data”.**
Investigating the evolution of human disease genes by comparing them with the genomes of mouse and chicken. Contributed to the initial analysis of mouse and chicken genomes, beginning a career in genomics spanning many eukaryotes.
- 1996 - 2000*
Imperial College,
London **BSc Honors Applied Biology (2i) with a year in research. Associate of the Royal College of Science.**
Specialized in neuroscience, genetics, animal behavior and evolution & development. Honors research project in bioinformatics human endogenous retroviruses.

International Research Meetings (Recent Highlights)

University Federal Rio de Janeiro 2015. Invited presentation in a workshop on *Leishmania* genome analysis and research seminar on the computational filtering of *Leishmania* genomic data and integration with other data. **LeiSHield, Tunis 2014.** Invited to deliver a one day workshop on good practice in *Leishmania* genomic analysis. Have forged two new collaborations from this with members of LeiSHield and will lead exemplar genome analysis in forthcoming training workshop in Oct 2016. **EuPathDB, U Penn, Philadelphia, 2013.** Invited to contribute to ongoing work in EuPathDB and since this meeting two of my workflows have been incorporated into TriTrypDB. **Leishmania Genome Plasticity, 2012.** Society for General Microbiology Autumn Conference 2012, University of Warwick, UK September 2012. Invited speaker on the theme of the Dynamic Genome. **Leishmania Genomics, Leishmania Network, 2011.** Lausanne. Presented gene and chromosome copy number variation analysis to a group of Leishmania genome experts. Invited speaker.

Supervision, Teaching and Public Engagement (Recent Highlights)

Post-graduate Training for PhD students 2015/16. Ran introduction to NGS analysis for PhD students in the Institute of Infection, Immunity and Inflammation, University of Glasgow.

Fiocruz and University Federal Rio de Janeiro 2014/15. Ran introduction to genomic and transcriptomics analysis for PhD students and Post-Doc researchers.

PhD (2014-) and Masters (2012-) Student Supervision 2 PhD students and 5 Masters students.

PhD and Post-doc week training course in Parasite Bioinformatics 2015. Fundação Oswaldo Cruz (Fiocruz) Brazil. Designed and delivered the training.

MSc Module BIOL 5197 Omics for Biomedical Sciences, 2015-2016. Genomics technology lectures, contributed to course design in a module that spans 6 MSc courses. **MSc Bioinformatics, University of Glasgow, 2011-2015.** Designed and taught genomics module on MSc course. Supervised final project students. Project assessor, student viva examination. Designed two new modules for 2015 and helped with course redesign. **MRes Infection and Immunity, 2012-2014.** Introduction to Bioinformatics module. Examiner and assessor for the course.

UK STEMNET Ambassador, 2005-2012. “I’m a scientist, get me out of here”, 2008. Won a national online communication competition for scientists with high school students.

NESTA Famelab, 2007. National science communication competition. Winner of the Glasgow heat and finalist. Received media training in TV, radio and the web including podcasts and video cast.

Funding, Patents and Publications

Grants & Other Funding

Wellcome Trust Institute Strategic Support Funding (WT ISSF) Comparative transcriptomic analysis of central nervous system and bloodstream-resident trypanosomes in a murine model of human African sleeping sickness, £25k co-investigator. Sept 2015.

CRACK-IT A multiscale model to minimise animal usage in leishmaniasis drug development. (NC3R UK funded), £230k co-investigator. Jan 2015.

EPSRC DTP PhD Studentship ‘Machine learning approaches to understand mechanisms of diversity in kinetoplastid genomes’, £68k lead supervisor. Oct 2014.

WT DTP PhD Studentship “, £90k co-supervisor. Sept 2014.

LeiSHield: a new collaborative action to determine prevalence anticipate emergence and assess urbanisation of cutaneous and visceral leishmaniasis in partner countries, £4,500 co-investigator. July 2014.

WT ISSF Pilot Award, PI £3,500, pump-priming matched by £3,500 WTCMP Director’s discretionary fund to fund a research technician for 3 month method development research project. June 2014.

WT ISSF Catalyst Award, 18 months pump-priming to expand pilot study. PI £15,000 “*Leishmania* genome sequence diversity and disease tropism in the Sudan”. July 2012.

Patent

US Patent Application WO2010064016 “Methods for Determining a Prognosis in Multiple Myeloma”, filed December 2009, Published 2010. Primary Inventor. Identified a prognostic gene expression signature and designed a molecular test that could be used independently based on the signature.

Publications (* = Equal Contribution, PMID = Pubmed Identifier)

- Devlin R, Marques CA, Paape D, Prorocic M, Zurita-Leal AC, Campbell SJ, Lapsley C, **Dickens N**, McCulloch R. Mapping replication dynamics in *Trypanosoma brucei* reveals a link with telomere transcription and antigenic variation. *Elife* 2016 PMID: 27228154.
- Marques CA*, **Dickens NJ***, Paape D, Campbell SJ & McCulloch R. Genome-wide mapping reveals single-origin chromosome replication in *Leishmania*, a eukaryotic microbe. *Genome Biology* 2015 PMID: 26481451.
- Tschoeke DA, Nunes GL, et al., The Comparative Genomics and Phylogenomics of *Leishmania amazonensis* Parasite. *Evol Bioinform* 2014 PMID: 25336895.
- Sinha A, Hughes KR, Modrzynska K, Otto TD, Pfander C, **Dickens NJ**, Religa AA, Bushell E, Graham AL, Orr R, Kafsack B, Williams A, Llinas M, Berriman M, Billker O, Waters AP. Identification of a cascade of related proteins central to commitment and development of gametocytogenesis in *Plasmodium*. *Nature* 2014 PMID: 24572359.
- Porcel BM, Denoed F, Opperdoes F, Noel B, Madoui M, Hammarton TC, Field MC, Da Silva C, Couloux A, Poulain J, Katinka M, Jabbari K, Aury J-M, Campbell DA, Cintron R, **Dickens NJ**, Docampo R, Sturm NR, Koumandou VL, Fabre S, Flegontov P, Lukeš J, Michaeli S, Mottram JC, Szöör B, Zilberstein D, Bringaud F, Wincker P, Dollet M. The streamlined genome of *Phytomonas* spp. relative to human pathogenic kinetoplastids reveals a parasite tailored for plants. *PLOS Genetics* 2013 PMID: 24516393.
- Jones NG, Thomas EB, Brown E, **Dickens NJ**, Hammarton TC, Mottram JC. Regulators of *Trypanosoma brucei* cell cycle progression and differentiation identified using a kinome-wide RNAi screen. *PLOS Pathogens* 2014. PMID: 24453978.
- Tiengwe C, Marcello L, Farr H, **Dickens N**, Kelly S, Swiderski M, Vaughan D, Gull K, Barry JD, Bell SD, McCulloch R. Genome-wide analysis reveals extensive functional interaction between DNA replication initiation and transcription in the genome of *Trypanosoma brucei*. *Cell Rep* 2012 PMID: 22840408.
- **Rogers MB***, **Hilley JD***, **Dickens NJ***, Wilkes J, Bates PA, Depledge DP, Harris D, Her Y, Herzyk P, Imamura H, Otto TD, Sanders M, Seeger K, Dujardin JC, Berriman M, Smith DF, Hertz-Fowler C, Mottram JC. Chromosome and gene copy number variation allow major structural change between species and strains of *Leishmania*. *Genome Res.* 2011 PMID: 22038252.
- Johnson DC, Corthals SL, Walker BA, Ross FM, Gregory WM, **Dickens NJ**, Lokhorst HM, Goldschmidt H, Davies FE, Durie BG, Van Ness B, Child JA, Sonneveld P, Morgan GJ. Genetic factors underlying the risk of thalidomide-related neuropathy in patients with multiple myeloma. *J Clin Oncol.* 2011 PMID: 21245421.

- Walker BA, Leone PE, Chiecchio L, **Dickens NJ**, Jenner MW, Boyd KD, Johnson DC, Gonzalez D, Dagrada GP, Protheroe RK, Konn ZJ, Stockley DM, Gregory WM, Davies FE, Ross FM, Morgan GJ. A compendium of myeloma-associated chromosomal copy number abnormalities and their prognostic value. *Blood* 2010 PMID: 20616218.
- Bagratuni T, Wu P, Gonzalez de Castro D, Davenport EL, **Dickens NJ**, Walker BA, Boyd K, Johnson DC, Gregory W, Morgan GJ, Davies FE. XBP1s levels are implicated in the biology and outcome of myeloma mediating different clinical outcomes to thalidomide-based treatments. *Blood* 2010 PMID: 20421453.
- **Dickens NJ***, Walker BA*, Leone PE, Johnson DC, Brito JL, Zeisig A, Jenner MW, Boyd KD, Gonzalez D, Gregory WM, Ross FM, Davies FE, Morgan GJ. Homozygous deletion mapping in myeloma samples identifies genes and an expression signature relevant to pathogenesis and outcome. *Clin Cancer Res.* 2010 PMID: 20215539.
- Brito JL, Walker B, Jenner M, **Dickens NJ**, Brown NJ, Ross FM, Avramidou A, Irving JA, Gonzalez D, Davies FE, Morgan GJ. MMSET deregulation affects cell-cycle progression and adhesion regulons in t(4;14) myeloma plasma cells. *Haematologica* 2009 PMID: 19059936.
- Johnson DC, Corthals S, Ramos C, Hoering A, Cocks K, **Dickens NJ**, Haessler J, Goldschmidt H, Child JA, Bell SE, Jackson G, Baris D, Rajkumar SV, Davies FE, Durie BG, Crowley J, Sonneveld P, Van Ness B, Morgan GJ. Genetic associations with thalidomide mediated venous thrombotic events in myeloma identified using targeted genotyping. *Blood* 2008 PMID: 18805967.
- Leone PE, Walker BA, Jenner MW, Chiecchio L, Dagrada G, Protheroe RK, Johnson DC, **Dickens NJ**, Brito JL, Else M, Gonzalez D, Ross FM, Chen-Kiang S, Davies FE, Morgan GJ. Deletions of CDKN2C in multiple myeloma: biological and clinical implications. *Clin Cancer Res.* 2008 PMID: 18829482.
- Grieve IC, **Dickens NJ**, Pravenec M, Kren V, Hubner N, Cook SA, Aitman TJ, Petretto E, Mangion J. Genome-wide co-expression analysis in multiple tissues. *PLoS One* 2008 PMID: 19112506.
- Jenner MW, Leone PE, Walker BA, Ross FM, Johnson DC, Gonzalez D, Chiecchio L, Dachs Cabanas E, Dagrada GP, Nightingale M, Protheroe RK, Stockley D, Else M, **Dickens NJ**, Cross NC, Davies FE, Morgan GJ. Gene mapping and expression analysis of 16q loss of heterozygosity identifies WWOX and CYLD as being important in determining clinical outcome in multiple myeloma. *Blood* 2007 PMID: 17609426.
- Petretto E, Mangion J, **Dickens NJ**, Cook SA, Kumaran MK, Lu H, Fischer J, Maatz H, Kren V, Pravenec M, Hubner N, Aitman TJ. Heritability and tissue specificity of expression quantitative trait loci. *PLoS Genet.* 2006 PMID: 17054398.
- Mueller M, Goel A, Thimma M, **Dickens NJ**, Aitman TJ, Mangion J. eQTL Explorer: integrated mining of combined genetic linkage and expression experiments. *Bioinformatics* 2006 PMID: 16357031.
- International Chicken Genome Sequencing Consortium (Hillier, LW et al, 182 authors). Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature* 2004 PMID: 15592404.
- Allen M, Heinzmann A, Noguchi E, Abecasis G, Broxholme J, Ponting CP, Bhattacharyya S, Tinsley J, Zhang Y, Holt R, Jones EY, Lench N, Carey A, Jones H, **Dickens NJ**, Dimon C, Nicholls R, Baker C, Xue L, Townsend E, Kabesch M, Weiland SK, Carr D, von Mutius E, Adcock IM, Barnes PJ, Lathrop GM, Edwards M, Moffatt MF, Cookson WO. Positional cloning of a novel gene influencing asthma from chromosome 2q14. *Nature Genetics* 2003 PMID: 14566338.
- Maurer-Stroh S, **Dickens NJ**, Hughes-Davies L, Kouzarides T, Eisenhaber F, Ponting CP. The Tudor domain 'Royal Family': Tudor, plant Agenet, Chromo, PWWP and MBT domains. *Trends Biochem Sci.* 2003 PMID: 12575993.

- **Dickens NJ**, Ponting CP. THoR: a tool for domain discovery and curation of multiple alignments. *Genome Biol.* 2003 PMID:12914660.
- Mouse Genome Sequencing Consortium (Waterston RH et al, 222 authors). Initial sequencing and comparative analysis of the mouse genome. *Nature* 2002 PMID: 12466850.
- **Dickens NJ**, Beatson S, Ponting CP. Cadherin-like domains in alpha-dystroglycan, alpha/epsilon-sarcoglycan and yeast and bacterial proteins. *Curr Biology* 2002 PMID: 11909544.
- Letunic I, Goodstadt L, **Dickens NJ**, Doerks T, Schultz J, Mott R, Ciccarelli F, Copley RR, Ponting CP, Bork P. Recent improvements to the SMART domain-based sequence annotation resource. *Nucleic Acids Res* 2002 PMID: 11752305.
- Ponting CP, **Dickens NJ**. Genome cartography through domain annotation. *Genome Biology* 2001. PMID: 11521679.