CHRIS HUNTER

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EXPERIENCE

Director, GigaDB | BGI-Hong Kong Co Ltd (Remote from UK)
April 2013 – Present
Promoted from Lead BioCurator, January 2021
Initially employed as the lead biocurator for GigaDB, I was promoted to director in 2021. I manage the operations of GigaDB, the data repository component of GigaScience Press. The press publishes two open-access journals pioneering the integration of manuscript publication with comprehensive data archiving. My team are responsible for enhancing research transparency and reproducibility through rigorous data audits prior to publication.
Key responsibilities include:
   • Overseeing data organisation and deposition protocols for researchers, ensuring compliance with both GigaDB and external repository standards
   •Coordinating stakeholder engagement to facilitate GigaDBs' strategic expansion
   •Conceptualising and implementing advanced search and visualisation tools to optimise data accessibility and utility
   •Managing diverse scientific datasets across multiple research domains
   •Facilitating DataCite DOI assignment for datasets to ensure proper citation and attribution of datasets
   •International conference presentations and community engagement

Board Member | Genomic Standards Consortium (GSC) *(Voluntary)*
May 2018 – Present | *Active Involvement: 2008 – Present*
The Genomic Standards Consortium (GSC) is an open-membership working body formed in September 2005. The aim of the GSC is making genomic data discoverable. The GSC enables genomic data integration, discovery and comparison through international community-driven standards. I have been involved with the GSC since 2008, becoming a board member in 2018, and the secretary of the board in 2023.
I contribute expertise to the working groups focused on terminology standardisation and tool development for the genomic and metagenomic research community. I leverage my extensive experience with the GSC standards to inform the development of comprehensive and practical new checklists for genome sequencing initiatives.

Bioinformatician, InterPro-Metagenomics | EMBL-EBI
September 2009 – September 2012
I led the development and implementation of the EBI Metagenomics Portal (subsequently rebranded as MGnify), integrating multiple EMBL-EBI resources including InterPro, ENA, UniProt/MES, GO, and Ensembl. Provided global research community access to sophisticated metagenomics analysis pipelines.
Responsibilities encompassed:
   • Web interface design and usability optimisation
   • User data acquisition and integration protocols
   • Regular stakeholder reporting and project management
   • International conference presentations and community engagement

Database Curator, ENA Nucleotide Sequence Database | EMBL-EBI
September 2007 – September 2009

The European Nucleotide Archive (ENA) is Europe's primary nucleotide sequence resource. DNA and RNA sequences are submitted from individual researchers, genome sequencing projects and patent applications. I maintained data integrity and searchability for Europe's primary nucleotide sequence resource. Served as primary liaison for data submitters, ensuring compliance with minimum standards while maintaining positive user relationships. Key contributions included:

- Development of submission protocols for next-generation sequencing data (Short Read Archive)
- Implementation of quality control measures using Unix-based command-line tools
- Customer relationship management and technical support for international research community

Postdoctoral Researcher, Cancer Genome Project | Sanger Institute
February 2004 – September 2007
Conducted comprehensive somatic variant analysis in cancer tissues to advance understanding of oncological mechanisms. Managed complete analytical workflows from primer design through data interpretation, utilising specialised software including Mutation Surveyor, Chromas, and OncoCSA.

Postdoctoral Researcher | MRC UK HGMP Resource Centre
July 2002 – January 2004
Established and optimised Dual Luciferase assay protocols for identifying regulatory regions within gene 3'UTRs. Developed and implemented web-based workflow tracking systems to enhance laboratory efficiency. Core duties encompassed literature-based target identification, computational analysis, primer design, and staff training coordination.

Scientific Researcher | Cylcacel Ltd, Polgen Division
January 2002 – June 2002
Conducted molecular biology research including DNA/RNA preparation, PCR, gene cloning, transient transfections, FACS analysis, and dsRNA synthesis. Specialised in laboratory automation enhancement through MWG liquid handling robot optimisation.

EDUCATION

Doctor of Philosophy (PhD) | Darwin College, Cambridge University
1999 – 2003
Thesis: "Identification, Cloning and Characterisation of the Alpha2 Adrenergic Receptor Gene Family in the Japanese Pufferfish *Fugu rubripes*"
Submitted: May 10, 2003
Research Locations: MRC UK HGMP Resource Centre (Fugu Genomics Group); Pfizer Global R&D, Sandwich, Kent
Funding: BBSRC Industrial Case Award in partnership with Pfizer Global R&D
Research Focus: DNA extraction, manipulation, and sequencing; computational analysis of gene families

Bachelor of Science (Honours) Applied Biology, 2:1 | Nottingham Trent University
1994 – 1998

CORE COMPETENCIES

Technical Skills
- **Bioinformatics:** Advanced Unix command-line proficiency, Galaxy platform, GitHub version control
- **Programming:** Python scripting, web development using GitHub Pages, Markdown, and HTML
- **Database Management:** Ontology development and implementation, data curation protocols
- **Laboratory Techniques:** Comprehensive molecular biology methodologies (historical experience)

Professional Skills
- **Leadership:** Team management and strategic planning
- **Communication:** Technical writing, public speaking, and stakeholder engagement
- **Project Management:** Multi-stakeholder coordination and international collaboration

PROFESSIONAL DEVELOPMENT

Training & Certifications
- Management Fundamentals
- Advanced Unix Systems Administration
- Scientific Writing and Presentation Skills
- Phylogenetic Analysis (Staden Package)
- Programming Languages: Perl,Python and SQL
- XML Data Processing
- Robotic Liquid Handling Systems (MWG)

Conference Participation
- Genomic Standards Consortium Meetings (almost every year since 2008)
- Intelligent Systems for Molecular Biology (almost every year since 2013)
- International Metagenomics Conferences (multiple)
- Public Engagement: Educational presentations to secondary schools and public audiences

SELECTED PUBLICATIONS *Complete publication list available via ORCID: 0000-0002-1335-0881*

Eloe-Fadrosh, E.A., ... Hunter, C.I., ... et al. (2024). A Practical Approach to Using the Genomic Standards Consortium MIxS Reporting Standard for Comparative Genomics and Metagenomics. In: Setubal, J.C., Stadler, P.F., Stoye, J. (eds) *Comparative Genomics. Methods in Molecular Biology*, vol 2802. Humana, New York, NY.

Armit, C., Tuli, M.A., Hunter, C.I. (2022). A Decade of GigaScience: GigaDB and the Open Data Movement. *GigaScience*, 11, giac053.

Mirzayi, C., ... Hunter, C.I., ... et al. (2021). Reporting guidelines for human microbiome research: the STORMS checklist. *Nature Medicine*, 27, 1885–1892.

Hunter, C.I., Mitchell, A., Jones, P., McAnulla, C., Pesseat, S., Scheremetjew, M., & Hunter, S. (2012). Metagenomic analysis: the challenge of the data bonanza. *Briefings in Bioinformatics*, 13(6), 743–746.

Hunter, C., Cochrane, G., Apweiler, R., & Hunter, S. (2011). The EBI Metagenomics Archive, Integration and Analysis Resource. In *Handbook of Molecular Microbial Ecology I: Metagenomics and Complementary Approaches* (ed F. J. de Bruijn), John Wiley & Sons.

Leinonen, R., Akhtar, R., Birney, E., ... Hunter, C., ... Cochrane, G. (2010). Improvements to services at the European Nucleotide Archive. *Nucleic Acids Research*, 38(Database issue), D39–D45.

Stephens, P., Hunter, C., Bignell, G., Futreal, P.A., Wooster, R., Stratton, M.R., et al. (2004). Lung cancer: intragenic ERBB2 kinase mutations in tumours. *Nature*, 431(7008), 525–526.

PERSONAL INTERESTS

Competitive swimming with Team Anglia Masters, including participation in British Championships. Additional interests include outdoor activities (hiking, cycling), gardening, and home improvement projects. Former rugby player at county and club levels.

References available upon request