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Overview

Computational biologist with 20 years' experience developing and applying quantitative image analysis and machine learning methods to cell biology. Engineering background combined with extensive wet-lab experience in cell biology, virology and microbiology. Lead the bioimage analysis team at the Francis Crick Institute, supporting 100+ research groups and 17 science technology platforms (STPs). Research focus on reproducibility, statistical rigour and FAIR practice in image analysis (30+ publications, 1,800+ citations).

Current Position

since 2021 **Image Analysis Lead & Deputy Head,** Advanced Light Microscopy, Francis Crick Institute.

- Built and lead team of image analysts, supporting 100+ research groups and 17 technology platforms with analytical solutions.
- Mentor researchers and develop team members in machine learning deployment, leveraging open-source software and high-performance computing.
- Lead a cross-STP bioimage analysis working group, connecting imaging with spatial omics, software engineering and AI.
- Co-leading the establishment of a Spatial Biology Consortium to track and manage spatial biology/omics projects across STP boundaries.
- Established institute-wide training programmes reaching 600+ researchers, creating the foundation for a Royal Microscopical Society-supported international workshop.
- Co-founded and lead the Crick BioImage Analysis Symposium, an annual international event attracting 150+ participants and driving industry-academic partnerships.
- Developing prototype agentic AI systems, largely with LLM coding assistants, including multi-agent pipelines that generate and validate analysis code.

Selected Publications

1. Marcotti, S., Gerontogianni, L., Kelly, G., & **Barry**, **D. J.** (2026). Practical statistics for bioimage analysis – a guide to experimental design and data interpretation. *J Cell Sci*, *139*(10), jcs264367.
2. Jones, R. A., Renshaw, M. J., & **Barry**, **D. J.** (2024). Automated staging of zebrafish embryos with deep learning. *Life Sci Alliance*, *7*(1).
3. Sivagurunathan, S., Marcotti, S., Nelson, C. J., Jones, M. L., **Barry**, **D. J.**, Slater, T. J. A., … Cimini, B. A. (2024). Bridging imaging users to imaging analysis – a community survey. *J Microsc*, *296*(3), 199–213.
4. **Barry**, **D. J.**, Gerri, C., Bell, D. M., D'Antuono, R., & Niakan, K. K. (2022). GIANI – open-source software for automated analysis of 3D microscopy images. *J Cell Sci*, *135*(10).
5. Abella, J. V. G., Galloni, C., Pernier, J., **Barry**, **D. J.**, Kjær, S., Carlier, M.-F., & Way, M. (2016). Isoform diversity in the Arp2/3 complex determines actin filament dynamics. *Nat Cell Biol*, *18*(1), 76–86.
6. **Barry**, **D. J.**, Durkin, C. H., Abella, J. V. G., & Way, M. (2015). Open source software for quantification of cell migration, protrusions, and fluorescence intensities. *J Cell Biol*, *209*(1), 163–180.

Previous Experience

2017 – 2021 **Bioimage Data Analyst,** Advanced Light Microscopy Facility, Francis Crick Institute.

- Designed and implemented image analysis tools and deep/machine learning workflows for diverse biomedical research projects, contributing to high-impact publications across multiple disease areas.
- Deployed machine learning algorithms for analysis of multi-dimensional microscopy data, establishing best practices for reproducible pipelines.
- Mentored early-career researchers in computational methods and data visualisation, translating complex analytical approaches for non-technical audiences.

2010 – 2016 **Postdoctoral Fellow, Quantitative Imaging & Cell Biology,** Cancer Research UK London Research Institute.

- Conducted wet-lab microscopy experiments studying viral infections and cellular processes, combining hands-on experimental work with computational analysis.
- Developed software tools for quantitative analysis of multi-dimensional datasets, bridging experimental biology and computational approaches.
- Collaborated with molecular biologists and biochemists to integrate computational methods into experimental workflows and advance mechanistic understanding.

Stakeholder & Community Engagement

since 2020 **CBIAS:** Co-founder and lead organiser of the Crick BioImage Analysis Symposium, 150+ annual attendees, bringing together researchers, analysts, funders, and industry.

since 2021 **RMS-DAIM:** Founding committee member, Royal Microscopical Society's Data Analysis in Imaging Section, designed and delivered international training programme across four institutions in UK and Ireland.

since 2025 **UK-BIAS:** Leading the establishment of the UK Network of BioImage Analysts, a component of the Euro-BioImaging UK Node, with 13 analysts across 10 UK institutions.

since 2026 **BioFAIR:** Appointed to BBSRC/MRC review pool to assess proposals for national research data infrastructure.

Peer Review

I have reviewed manuscripts for 20+ journals and organisations, including Nature Methods, Bioinformatics, Biotechnology & Bioengineering, IEEE Transactions on Medical Imaging, PLOS Computational Biology, Journal of Cell Science, Scientific Data and the Czech Science Foundation.

Education

2005 – 2010 **Ph.D., Bioimaging & Biotechnology,** Technological University Dublin
Supervisors: Gwilym A. Williams, Cecilia Chan, Raymond Ryan & Jonathan M. Blackledge

- Developed novel computational methods and mathematical frameworks for quantitative analysis of complex morphological data.
- Thesis Title: *Development of Novel Image Analysis Methods for the Morphological Quantification of Filamentous Fungi*.

2000 – 2004 **BE, Electronic Engineering,** University College Dublin