Christopher Douglas Robert Wyatt

Bioinformatician • reproducible pipelines for evolution & ecology

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Profile

Bioinformatician specialising in reproducible, scalable pipelines for evolutionary and developmental genomics. I build Nextflow/nf-core workflows for high-throughput sequencing data — RNA-Seq, genomics and proteomics — and currently develop open-source pipelines for evolution and ecology at UCL, where I built **Eco-Flow**, a community working to close “the omics gap in ecology”. Its growing collection spans comparative and ecological genomics, from genome quality assessment and synteny analysis to gene-family evolution and DNA metabarcoding. A fluent programmer (Unix, R, Python, Perl) and an active science communicator and trainer, with high-impact publications stemming from a PhD on alternative splicing at the Centre for Genomic Regulation (CRG, Barcelona).

Education

PhD in Biomedicine Sept 2015 – March 2019

Systems Biology, Centre for Genomic Regulation (CRG), Barcelona

Regulation and patterns of alternative splicing during pre-implantation mammalian development: showed that genome activation involves one of the most complex transcriptomes of the mammalian life cycle, identified the spliceosomal protein SNRPB as a key regulator, and examined the role of DNA damage in the maternal-to-zygotic transition. Funded by a competitive international “la Caixa” fellowship; contributed to several high-impact collaborations, including two *Nature* papers.

MSc in Biomedical Research 2014 – 2015

Universitat Pompeu Fabra (UPF), Barcelona

Advanced coursework spanning molecular and cellular pathology, cancer, immunology, genome biology and evolution.

MRes in Biosystematics (Distinction) 2010 – 2011

Imperial College London & Natural History Museum

Research projects on the molecular systematics of basal Chrysomelid beetle families (Prof. Alfried Vogler) and the morphological, molecular and ecological assessment of new Patagonian *Porphyra* red-algal species (Prof. Juliet Brodie).

Professional Experience

Lead Bioinformatician — Eco-Flow Oct 2023 – March 2026

University College London

Lead developer and coordinator of **Eco-Flow**, building reproducible, nf-core-standard Nextflow pipelines for agri-ecology on the BBSRC grant “Building a Bioinformatics Ecosystem for Agri-Ecologists” (BB/X018768/1; PI S. Sumner). See *Selected Projects* below for the pipelines.

Bioinformatician — Wasp Genomes Project 2021 – 2023

University College London

Comparative and evolutionary genomics of wasps for "The evolutionary genomics of a major transition in evolution" (NSF DEB-1929239 / NSFDEB-NERC), in collaboration with Sandra Rehan and Seirian Sumner.

Pipeline Developer June 2021 – Sept 2021

Seqera Labs, Barcelona

Wrote Nextflow pipelines for several startups and contributed to the official Nextflow training material, gaining in-depth knowledge of the language and best practice for pipeline development.

Postdoctoral Researcher — Evolutionary Genomics / Transcriptomics April 2019 – Feb 2021

Centre for Biodiversity & Environment Research, UCL, London

Research in the Eusocial Insect Research Group (Seirian Sumner), applying machine learning, transcriptomics and proteomics (with Nextflow) to wasp caste identity and evolution.

Research Assistant — Evolutionary Transcriptomics 2013 – 2014

University of Bristol

Developed bioinformatic pipelines (Perl/Unix) to process caste-specific brain transcriptomic and proteomic data in the eusocial wasp *Polistes canadensis*. NERC-funded; supervised by S. Sumner, G. Barker and J. Gough.

Selected Projects & Community

Eco-Flow — open-source Nextflow pipelines for evolution & ecology UCL, 2023–26

eco-flow.github.io · *github.com/eco-flow*

Built **Eco-Flow**, a BBSRC-funded community developing reproducible, nf-core-standard pipelines that close "the omics gap in ecology". Build and maintain pipelines including:

- `genomeqc` — assess and compare the quality of multiple genome assemblies and their annotations
- `synteny` — synteny analysis across genomes
- `excon` — quantify gene-family expansion and contraction
- DNA metabarcoding (`dietary_amplicons`, `pollen-metabarcoding`, `nanoporemetabarcoding`) — taxonomic profiling from amplicon and nanopore reads

Training & community: Organise nf-core hackathons and deliver multi-day Nextflow and bioinformatics workshops; an active member of the nf-core community and UCL's Advanced Research Computing (ARC) Centre.

Technical Skills

Languages & tools: Unix/Bash, Perl, R, Python, Matlab

Workflows: Nextflow (nf-core), reproducible & FAIR pipelines

Data types: RNA-Seq, proteomics, genomic and phenotypic data

Publications

1. D. Sampaio Gonçalves, L. Dulac, B. Ritschka, M. Rhinn, A. Klein, **C.D.R. Wyatt**, M. Irimia & W.M. Keyes (2025). Senescent cells exhibit features of developmental signaling centres. *bioRxiv* (preprint). doi:10.1101/2025.10.30.685565
2. T.D. Doyle, E. Jimenez-Guri, J.C. Barnes, C. Hannah, S. Murray, **C.D.R. Wyatt**, O.M. Poole & K.R.

Wotton (2025). Long-range pollen transport across the North Sea: Insights from migratory hoverflies landing on a remote oil rig. *Journal of Animal Ecology*, 94(11), 2267-2281. doi:10.1111/1365-2656.70126

3. A. Di Matteo, E. Belloni, D. Pradella, A.M. Chiaravalli, G.M. Pini, M. Bugatti, R. Alfieri, C. Barzan, E. Franganillo Tena, S. Bione, E. Terenzani, F. Sessa, **C.D.R. Wyatt** et al. (2023). Alternative Splicing Changes Promoted by NOVA2 Upregulation in Endothelial Cells and Relevance for Gastric Cancer. *International Journal of Molecular Sciences*, 24(9), 8102. doi:10.3390/ijms24098102

4. **C.D.R. Wyatt**, M.A. Bentley, D. Taylor, E. Favreau, R.E. Brock, B.A. Taylor, E. Bell, E. Leadbeater & S. Sumner (2023). Social complexity, life-history and lineage influence the molecular basis of castes in vespid wasps. *Nature Communications*, 14(1). doi:10.1038/s41467-023-36456-6

5. **C.D.R. Wyatt**, B. Pernaute, A. Gohr, M. Miret-Cuesta, L. Goyeneche, Q. Rovira, M.C. Salzer, E. Boke, O. Bogdanovic, S. Bonnal et al. (2022). A developmentally programmed splicing failure contributes to DNA damage response attenuation during mammalian zygotic genome activation. *Science Advances*, 8(15). doi:10.1126/sciadv.abn4935

6. **C.D.R. Wyatt**, M. Bentley, D. Taylor, R.E. Brock, B.A. Taylor, E. Bell, E. Leadbeater & S. Sumner (2020). Genetic toolkit for sociality predicts castes across the spectrum of social complexity in wasps. *bioRxiv* (preprint). doi:10.1101/2020.12.08.407056

7. E. Belloni, A. Di Matteo, D. Pradella, M. Vacca, **C.D.R. Wyatt**, R. Alfieri, A. Maffia, S. Sabbioneda & C. Ghigna (2019). Gene Expression Profiles Controlled by the Alternative Splicing Factor Nova2 in Endothelial Cells. *Cells*, 8(12), 1498. doi:10.3390/cells8121498

8. R.J. Southon, E.F. Bell, P. Graystock, **C.D.R. Wyatt**, A.N. Radford & S. Sumner (2019). High indirect fitness benefits for helpers across the nesting cycle in the tropical paper wasp *Polistes canadensis*. *Molecular Ecology*, 28(13), 3271-3284. doi:10.1111/mec.15137

9. F. Marlétaz, P.N. Firbas, I. Maeso, J.J. Tena, O. Bogdanovic, M. Perry, **C.D.R. Wyatt**, E. de la Calle-Mustienes, S. Bertrand, D. Burguera et al. (2018). Amphioxus functional genomics and the origins of vertebrate gene regulation. *Nature*, 564(7734), 64-70. doi:10.1038/s41586-018-0734-6

10. P. Kennedy, G. Baron, B. Qiu, D. Freitak, H. Helanterä, E.R. Hunt, F. Manfredini, T. O'Shea-Wheller, S. Patalano, C.D. Pull, T. Sasaki, D. Taylor, **C.D.R. Wyatt** et al. (2017). Deconstructing Superorganisms and Societies to Address Big Questions in Biology. *Trends in Ecology & Evolution*, 32(11), 861-872. doi:10.1016/j.tree.2017.08.004

11. I. Maeso, T.L. Dunwell, **C.D.R. Wyatt**, F. Marlétaz, B. Vető, J.A. Bernal, S. Quah, M. Irimia & P.W.H. Holland (2016). Evolutionary origin and functional divergence of totipotent cell homeobox genes in eutherian mammals. *BMC Biology*, 14(1). doi:10.1186/s12915-016-0267-0

12. M. Guillemin, L. Contreras-Porcia, M.E. Ramírez, E.C. Macaya, C.B. Contador, H. Woods, **C. Wyatt** & J. Brodie (2016). The bladed Bangiales (Rhodophyta) of the South Eastern Pacific: Molecular species delimitation reveals extensive diversity. *Molecular Phylogenetics and Evolution*, 94, 814-826. doi:10.1016/j.ympev.2015.09.027

13. S. Patalano, A. Vlasova, **C. Wyatt**, P. Ewels, F. Camara, P.G. Ferreira, C.L. Asher, T.P. Jurkowski, A. Segonds-Pichon, M. Bachman et al. (2015). Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. *Proceedings of the National Academy of Sciences*, 112(45), 13970-13975. doi:10.1073/pnas.1515937112

14. C. Giampietro, G. Deflorian, S. Gallo, A. Di Matteo, D. Pradella, S. Bonomi, E. Belloni, D. Nyqvist, V. Quaranta, S. Confalonieri, G. Bertalot, F. Orsenigo, F. Pisati, E. Ferrero, G. Biamonti, E. Fredrickx, C. Taveggia, **C.D.R. Wyatt** et al. (2015). The alternative splicing factor Nova2 regulates vascular development and lumen formation. *Nature Communications*, 6(1). doi:10.1038/ncomms9479