

Dr Tom Jenkins

Evolutionary Biologist

Curriculum Vitae

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Profile

Experienced scientist and research professional with a demonstrated history of working on highly diverse projects in both academic and public sector organisations. My areas of expertise include bioinformatics, genomics, geospatial analysis and software development. Previous projects cover molecular ecology, nuclear and organelle genome assembly and annotation, predicting habitat suitability using machine learning, and developing web applications for internal and external customers.

Employment

2023– **Postdoctoral Research Fellow**, *University of Exeter*
2022–2023 **Bioinformatician & Software Developer**, *Animal and Plant Health Agency*
2021–2022 **Senior Data Analyst**, *Natural England*
2018–2021 **Postdoctoral Research Associate**, *University of Exeter*

Qualifications

PhD	University of Exeter	2018
MRes	Imperial College London	2014
BSc (Hons)	Swansea University	2010

Programming

Skill bioinformatics, data wrangling and visualisation, geocomputation, modelling, statistics, web development
Tools bash, CSS, echarts, GitHub, HTML, JavaScript, leaflet, Linux, nextflow, R, Shiny

Selected Funding and Awards

I have acquired about £37K as a principal or co-investigator in external research grants since 2019. I have also been awarded in total over £5K for support towards courses or conferences during my academic career.

2023	Co-investigator research grant for red algae genomics (Natural England)	6000
2023	Co-investigator research grant for red algae genomics (Natural Resources Wales)	5000
2022	Co-investigator research grant for red algae genomics (Natural England)	20000
2019	Bioinformatics training grant, GWAS (Genetics Society)	1000
2019	Early career researcher travel grant (Institute for Data Science and Artificial Intelligence)	500
2019	Principal investigator research grant for maerl red algae genomics pilot study (British Ecological Society)	5000
2018	Heredity fieldwork grant for soft coral sampling (Genetics Society)	1284

Selected Science Communication

2023	Seminar	presented at cross-departmental event: "Whole genome sequencing: what, why and how is it used in outbreak investigations of bovine TB"
2022	Talk	presented at the Natural England annual marine conference: "Maerl biodiversity: understanding species, genetic and ecosystem diversity"
2022	Interview	live interview on <i>BBC Radio Wales Drive</i> to discuss published research on coral habitat suitability modelling
2021	Interview	recorded interview on <i>BBC Radio Cornwall</i> to discuss published research on coralline red algae population genomics
2020	Webinar	invited talk at Aquaculture Research Collaborative Hub UK annual conference: "Developing genomic resources to advance the aquaculture of European lobsters"
2018	Poster	presented at the II Joint Congress on Evolutionary Biology in Montpellier: "Population genetic structure of the European lobster (<i>Homarus gammarus</i>) using RADseq-derived SNPs"

Software Development

I have developed one R package and two open-source web applications:

mapmixture	R package for spatial visualisation of admixture and population structure
AssemblyStatsViewer	web app to compare genome assembly stats from the NCBI or ENA
LobsterGeneX	web app to visualise lobster gene expression data

Selected Publications

I have authored X papers since 2017, Y of which are first-author publications. On Google Scholar, my h-index is 9 with a total of 583 citations (as of 30 November 2023). I have also achieved an altmetric score over 30 in seven articles, two of which scored 964 and 220.

- **Jenkins TL** (in review). mapmixture: an R package and web app for spatial visualisation of admixture and population structure. Molecular Ecology Resources.
- Ellis RJ, **Jenkins TL** (2022). Management and analysis of high-throughput sequence data for animal infectious disease. World Organisation for Animal Health, Scientific and Technical Review 41, 2.
- **Jenkins TL**, Guillemin M-L, Simon-Nutbrown C, Burdett HL, Stevens JR, Peña V (2021). Whole genome genotyping reveals discrete genetic diversity in north-east Atlantic maerl beds. Evolutionary Applications, 14, 1558–1571.
- Houston RD, Bean TP, Macqueen DJ, Gundappa MK, Jin YH, **Jenkins TL**, *et al.* (2020). Harnessing genomics to fast-track genetic improvement in aquaculture. Nature Reviews Genetics, 21, 389–409.
- **Jenkins TL**, Ellis CD, Triantafyllidis A, Stevens JR (2019). Single nucleotide polymorphisms reveal a genetic cline across the north-east Atlantic and enable powerful population assignment in the European lobster. Evolutionary Applications, 12, 1881–1899.
- **Jenkins TL**, Castilho R, Stevens JR (2018). Meta-analysis of northeast Atlantic marine taxa shows contrasting phylogeographic patterns following post-LGM expansions. PeerJ, 6, e5684.
- **Jenkins TL**, Stevens JR (2018). Assessing connectivity between MPAs: selecting taxa and translating genetic data to inform policy. Marine Policy, 94, 165–173.