

Dr Tom Jenkins

Biologist & Software Developer

Curriculum Vitae

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Profile

Professional research scientist and developer with experience 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 genome assembly, gene expression analysis, population genetics, predicting habitat suitability using machine learning, and developing web applications for internal and external customers.

Employment

Data Visualisation Developer , <i>University of East Anglia (short-term contract)</i>	Jul 2024 – Present
Postdoctoral Research Fellow , <i>University of Exeter</i>	Jul 2023 – Present
Bioinformatician & Software Developer , <i>Animal and Plant Health Agency</i>	Apr 2022 – Jun 2023
Senior Data Analyst , <i>Natural England</i>	Feb 2021 – Mar 2022
Postdoctoral Research Associate , <i>University of Exeter</i>	Dec 2018 – Jan 2021

Qualifications

PhD	Biological Sciences	University of Exeter	2018
MRes	Bioinformatics and Genomics	Imperial College London	2014
BSc (Hons)	Marine Biology	Swansea University	2010

Programming

Skill	bioinformatics, cloud computing, data wrangling, data visualisation, geocomputation, modelling, R package development, statistics, version control, web development
Tools	AWS, bash, Bitbucket, CSS, echarts, GitHub, HTML, JavaScript, leaflet, Linux, nextflow, OpenStack, R, 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

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| 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 | invited talk 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 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>)" |

Software Development

I have developed an R package and a number of open-source and internal 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
ViewBovis	internal application for use as a disease surveillance and breakdown investigation tool for bovine TB

Selected Publications

I have authored 19 papers since 2017, 10 of which are first-author publications. On Google Scholar, my h-index is 9 with a total of 701 citations (as of August 2024). I have also achieved an Altmetric Score over 30 in seven articles, two of which scored 964 and 221.

- **Jenkins TL** (2024). mapmixture: an R package and web app for spatial visualisation of admixture and population structure. *Molecular Ecology Resources*, 24, e13943.
- 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**, Stevens JR (2018). Assessing connectivity between MPAs: selecting taxa and translating genetic data to inform policy. *Marine Policy*, 94, 165–173.