

Dr Tom Jenkins

Biologist & Data Analyst

Contact

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Skills

R	10+ yr
Data Analysis	10+ yr
Data Visualisation	10+ yr
Statistics	10+ yr
Cloud Computing	8+ yr
Bash / Linux	8+ yr
Bioinformatics	8+ yr
Nextflow	2+ yr
Python	1 yr
JavaScript	3+ yr
Web App Development	3+ yr

Tools

- ▶ VS Code / Git / Github
- ▶ HPC / AWS / OpenStack
- ▶ R Tidyverse / R Shiny
- ▶ R-sf / R-terra / Leaflet.js
- ▶ Python-pandas

Experience

Postdoctoral Research Fellow in Bioinformatics and Gene Expression Analysis

07/2023 - Present

University of Exeter, UK

I am leading a project to analyse variants from DNA sequencing data (>1 TB) and differential gene expression from RNA sequencing data. I also mentor junior colleagues in coding and build open source tools to enhance accessibility and reproducibility in R.

Web Application Developer

07/2024 - 09/2024

University of East Anglia, UK (Consultancy Contract)

I built agile web applications for clients to showcase emissions and wildfire climate data. I preprocessed data to generate new statistics and prepare (geo)JSON files.

Bioinformatician and Software Developer

04/2022 - 06/2023

Animal and Plant Health Agency, UK

I was the frontend developer in our team of UX, UI and backend data engineers in which we built an internal application to visualise geographic and metadata information to assist case workers in their disease outbreak investigations.

Senior Data Analyst

02/2021 - 03/2022

Natural England, UK

My role was to analyse, visualise and gain insights from geospatial and ecological data for multiple projects, including building R Shiny apps and interactive maps.

Postdoctoral Research Associate in Bioinformatics and Genome-Wide Association Studies

12/2018 - 01/2021

University of Exeter, UK

Education

PhD Evolutionary Biology

2014 - 2018

University of Exeter, UK

MRes Informatics and Genomics (Distinction)

2013 - 2014

Imperial College London, UK

BSc Marine Biology (First Class Honours)

2010 - 2013

Swansea University, UK

Software Development

See my GitHub profile for a comprehensive list of open source projects.

mapmixture

CRAN R package for spatial visualisation of ancestry, admixture and population structure. I am the creator and maintainer of this package.

Real-Time Earthquake Dashboard

Interactive dashboard developed to visualise real-time earthquakes using the Cesium ion and US Geological Survey APIs.

LobsterGeneX Web App

Web application developed to accompany research article allowing users to visualise gene expression data for European lobsters.

Awards

2024

Above and Beyond Award

University of Exeter

Provided essential technical support to ECRs and PGRs for IT skills, coding, genomic analysis, stats and programming.

2022 & 2023

Co-Investigator Research Grant £30K

Natural England and NRW

Conservation genomics of habitat-building coralline algae.

2019

Principal Investigator Research Grant £5K

British Ecological Society

Genomic diversity in a calcareous red seaweed.

Presentations

2024

Webinar Invited Talk

[Maerl bed diversity of Wales: new insights from DNA sequencing.](#)

Delivered to a mixed audience of scientists, policy-makers, admin staff and conservationists.

Conference Talk

[Bats respond to climate through phenotypic plasticity and genetic adaptations.](#)

Delivered to academics at the annual Genome Science conference.

2023

APHA Departmental Seminar

[Whole genome sequencing: what, why and how is it used in outbreak investigations of bovine TB.](#)

Delivered to project managers, HR staff and legislation officers.

Selected Publications

I have authored 20 papers since 2017, 10 of which are first-author publications. On Google Scholar, my h-index is 10 with a total of 869 citations (as of May 2025). I have also achieved an Altmetric Score over 30 in seven articles, two of which scored 964 and 221.

Jenkins TL, Axelsson M, Gall A, Ratcliffe F, Ellis CD, Stevens JR (in review). Population genomics, polyploidy, climate resilience and the microbiota of two habitat-building coralline algae. *Evolutionary Applications*.

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** (2023). 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, Stevens JR (2022). Predicting habitat suitability and range shifts under projected climate change for two octocorals in the north-east Atlantic. *PeerJ* 10, e13509.

Jenkins TL, Guillemain M-L, Simon-Nutbrown C, Burdett HL, Stevens JR, Peña V (2021). Whole genome genotyping reveals discrete genetic diversity in northeast 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 northeast 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.

Supervising / Mentoring Experience

- I mentor several postgraduates and early career researchers across research groups in coding, data analysis and genomics.
- I've taught essential wet-lab skills to postgraduates, including DNA extraction, quality assessment and gel electrophoresis.
- I designed and led workshops in R programming and analysis, such as spatial analysis and creating interactive maps.

Media

- Live interview on *BBC Radio Wales Drive* to discuss published research on coral habitat suitability modelling.
- Recorded interview on *BBC Radio Cornwall* to discuss published research on coralline red algae population genomics.