

# Dr Tom Jenkins

Bioinformatician, Data Analyst and Software Developer

Curriculum Vitae

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## Profile

Professional bioinformatician, data analyst and developer with experience working on highly diverse projects in academia, the public sector, and open access consortiums. My area of expertise include the analysis of big data (e.g. bioinformatics), modelling complex data sets (e.g. genetics, population biology and ecology), geospatial data analysis, and developing bespoke web applications using scientific, business and geographic data.

## Employment

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

## Qualifications

PhD	Biological Sciences (Population Genetics)	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 analysis, data visualisation, geocomputation, modelling, R package development, statistics, version control, web and dashboard development
Tools	APIs, AWS, bash, Bitbucket, CSS, echarts, GitHub, HTML, JavaScript, leaflet, Linux, nextflow, OpenStack, Python, R, R Shiny

## Data Analysis: example project

Explore genetic variation in populations of animals and algae using bioinformatics. I used cloud computing and a combination of bash and nextflow scripts to process 100-500GB sequencing data per species in a Linux environment. This resulted in large text files (>1GB) which I analysed and filtered for quality with Python (pandas) or R (tidyverse). I presented the data in meetings and publications using data visualisation libraries, including ggplot2 and matplotlib.

## Modelling & Statistics: example project

XXX

## Machine Learning: example project

XXX

## 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	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:

<a href="#">mapmixture</a>	R package for spatial visualisation of admixture and population structure
<a href="#">AssemblyStatsViewer</a>	web app to compare genome assembly stats from the NCBI or ENA
<a href="#">LobsterGeneX</a>	web app to visualise lobster gene expression data
<a href="#">ViewBovis</a>	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.