

Conor R. Walker

BIOINFORMATICS SCIENTIST

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Summary

Bioinformatics scientist with 8+ years of experience specializing in developing statistical and machine learning models for sequence analysis and interpreting human 'omics data. I am highly motivated by advancing human genetic research with real world impact.

Research experience

Moderna

Aug. 2024–Present

Scientist, Oncology Bioinformatics

- I am conducting research and developing analysis pipelines to support the individualized neoantigen therapy programme

New York Genome Center & Columbia University, USA

Jan. 2022–Aug. 2024

Postdoctoral Research Associate

- Developed statistical methods and a deep learning pipeline (PyTorch) and for assessing privacy risks associated with releasing single-cell RNA-Seq datasets
- Implemented multiple classification models (scikit-learn) to predict genotypes from single-cell RNA-Seq, revealing privacy risks across many publicly available datasets
- Collaboratively designed a privacy-preserving bulk RNA-Seq quantification algorithm using homomorphic encryption, and processed hundreds of bulk RNA-Seq samples for benchmarking (Snakemake & AWS) – *MS in preparation*
- As part of a multidisciplinary team, I validated the activity of cis- and trans-regulatory elements in various cancer types that were identified using CRISPR screens (R) – *MS in preparation*

European Bioinformatics Institute (EMBL-EBI), UK

Oct. 2017–Jan. 2022

Predocctoral Researcher

- Designed and implemented (C++) hidden Markov models to identify small-scale rearrangements in sequencing data, providing the first statistical method for identifying <50nt DNA rearrangements
- Applied my models to thousands of whole-genome human sequencing datasets to evaluate the evolutionary, population, cancer, and *de novo* landscape of template switch mutagenesis
- Implemented convolutional neural networks (Keras & PyTorch) to accurately detect positive selection within protein-coding sequences, validated by simulating evolution across tens of millions of genes
- Collaborated on multiple projects to characterize global SARS-CoV-2 genome evolution, analyzing thousands of samples (Python/Snakemake) and co-authoring 4 peer-reviewed papers

Newcastle University, UK

Nov. 2016–Sep. 2017

Postgraduate Student Research

- Implemented multi-objective genetic algorithms for to optimize DNA sequences for use in computing systems, producing molecules with multiple desirable biochemical properties for *in vitro* validation

Education

University of Cambridge, UK

2017–2021

PhD Computational Biology

- Thesis: Statistical analysis of short template switch mutations in human genomes

Newcastle University, UK

2016–2017

MSc Bioinformatics · Distinction (83%, highest grade in cohort)

- Thesis: Optimising nucleic acid sequences for DNA strand displacement systems

Liverpool John Moores University, UK

2013–2016

BSc (Hons) Zoology · First-class honours (80%, highest grade in cohort)

- Thesis: The genetics of insecticide resistance in the blackfly *Simulium vittatum*

Skills

Programming	Python, Bash, C++, R, AWK, LaTeX
Libraries	Numpy, SciPy, TensorFlow, pandas, matplotlib, seaborn, Dask, Biopython, pysam, scikit-allel, Scanpy, scvi-tools
Bioinformatics	Variant calling, sequence analysis, genome assembly, phasing & imputation, bulk & single-cell RNA-Seq analysis, eQTL mapping, phylogenetic inference, GWAS
Statistics & machine learning	Linear models, classical statistics, supervised/unsupervised learning (scikit-learn, XGBoost), deep learning (Keras, PyTorch)
Coding practices	Git, Nextflow, Snakemake, unit testing, Docker, Singularity, Jupyter, Vim
Cloud computing & HPC	AWS, Google Cloud, Slurm, LSF

Selected publications

Detecting interspecific positive selection using convolutional neural networks.

West C.*, **Walker C. R.***, Arasti S., Vasilev V., Xu X., De Maio N., Goldman N. *Joint first authors
[Molecular Biology and Evolution](#), *msaf154* (2025).

Secure and scalable gene expression quantification with pQuant.

Hong S., **Walker C. R.**, Choi Y. A., Gürsoy G.
[Nature Communications](#) *16*, 2380 (2025).

Private information leakage from single-cell count matrices.

Walker C. R., Li X., Chakravarthy M., Lounsbery-Scaife W., Choi Y. A., Singh R., Gürsoy G.
[Cell](#) *187*, 6537–6549 (2024).

Paired CRISPR screens to map gene regulation in *cis* and *trans*.

Xue X., Gajic Z. Z., Caragine C. M., Legut M., **Walker C. R.**, Wang X., Yan R. E., Wessels H., Lu C., Bapodra N., Gürsoy G., Sanjana N. E.
[bioRxiv](#) (2024).

phastSim: Efficient simulation of sequence evolution for pandemic-scale datasets.

De Maio N., Boulton W., Weilguny L., **Walker C. R.**, Turakhia Y., Corbett-Detig R., Goldman N.
[PLOS Computational Biology](#) *18*, e1010056 (2022).

Mutation rates and selection on synonymous mutations in SARS-CoV-2.

De Maio N., **Walker C. R.**, Turakhia Y., Lanfear R., Corbett-Detig R., Goldman N.
[Genome Biology and Evolution](#) *13*, evab087 (2021).

Short-range template switching in great ape genomes explored using pair hidden Markov models.

Walker C. R., Scally A., De Maio N., Goldman N.
[PLOS Genetics](#) *17*, e1009221 (2021).

Stability of SARS-CoV-2 phylogenies.

Turakhia Y., De Maio N., Thornlow B., Gozashti L., Lanfear R., **Walker C. R.**, Hinrichs A. S., Fernandes J. D., Borges R., Slodkowitz G., Weilguny L., Haussler D., Goldman N., Corbett-Detig R.
[PLOS Genetics](#) *16*, e1009175 (2020).

A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages.

Dellicour S., Durkin K., Hong S. L., Vanmechelen B., Martí-Carreras J., Gill M., Meex C., Bontems S., André E., Gilbert M., **Walker C. R.**, De Maio N., Faria N., Hadfield J., Hayette M., Bours V., Wawina-Bokalanga T., Artesi M., Baele G., Maes P.
[Molecular Biology and Evolution](#) *38*, 1608–1613 (2020).

Issues with SARS-CoV-2 sequencing data.

De Maio N., **Walker C. R.**, Borges R., Weilguny L., Slodkowitz G., Goldman N.
[virological.org/t/issues-with-sars-cov-2-sequencing-data/473](#) (2020).