

Zed Chen

Computational Geneticist | Bioinformatician

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Profile

A Computational Geneticist with a PhD and extensive experience in plant genetics, genomic analysis, statistical modeling, and simulation-based research, seeking to apply this expertise to advance quantitative genetics and plant breeding programmes. Proven ability to lead computational analyses for interdisciplinary projects, manage large-scale genomic datasets, and develop reproducible workflows. Passionate about translating complex genomic questions into actionable insights. Proven record of 6 peer-reviewed publications and training 200+ researchers in bioinformatics.

Core Competencies

Quantitative Genetics

- High-Throughput Data Analysis | GWAS
- Population Genomics & Genetics
- Variant/Strain Typing /Genotyping
- Model Construction & Simulation
- Multi-omics Analysis

Programming & Tools

- Python/R /Bash scripting
- Statistics Modelling & Machine Learning
- Pipeline development & Workflow (Snakemake, Nextflow)
- AWS | High-Performance Computing (Slurm)
- Reproducible Research (Git, Conda, Docker)

Collaboration & Communication

- Cross-functional Team
 - Workshop Design/Delivery
 - Scientific Communication & Public Speaking
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Professional Experience

Bioinformatician | Royal Botanical Garden of Edinburgh | 2025–Present

- Led data analysis on a Biodiversity Genomic Europe project. Coordinated timelines, resources, and experimental design with wet-lab scientists, international collaborators, and project leads.

- **Designed three comprehensive pipelines for genome-wide barcode screening**—a significant methodological contribution involving extensive **genotyping, variant calling, and loci selection**.
- Collaborated on **5+ cross-disciplinary projects**, contributing expertise in long-read sequencing, population genomics and genotyping, and data mining of public databases.
- Providing conceptual guidance and technical support for **10+ PhD and master's students** on their research projects.
- Expanded the institute's computational capacity by designing and delivering **25+ hands-on workshops** on data analysis and pipeline usage, effectively **training and mentoring 20+ research staff and students** in complex analytical methods.

Student Researcher | Computational Biologist | University of Edinburgh | 2020–2025

- **Led the computational analysis** for global, **interdisciplinary collaborations** (ITM/NIAID/Texas A&M), delivering **statistically rigorous** results and **data visualization** for **5 high-impact publications** in the fields of **pathogen genomics and disease**.
- Applied advanced **statistical modeling in R & Python** and **variant calling/strain typing** to identify diagnostic markers for treatment decisions of African Sleeping Sickness.
- Engineered **Snakemake pipelines** for the analysis of **high-throughput sequencing datasets** (260+ WGS/RNA-seq samples), implementing optimizations that **reduced runtime by 40%**.
- Maintained **current awareness of a rapidly changing field** and effectively communicated complex findings through **presentations at 5 international conferences** (BSP, MPM).

Course Demonstrator | University of Edinburgh | 2020–2024

- Trained **200+ staff/students** on **NGS data analysis** and machine learning
- Tailored workshops for diverse audiences, bridging biology and computational analysis.

Education

PhD in Infectious Diseases & Immunology | The University of Edinburgh

- Thesis involved the development of **reproducible NGS pipelines** to analyse the complex genomic/metagenomic datasets of micro-pathogens to develop **diagnostic assay** and understand **drug resistance**, leading to **5 peer-reviewed publications so far (3 first-author publications in progress) and successful grant applications**.

MSc in Bioinformatics (Merit) | The University of Edinburgh

- Relevant course work: Dynamic Modelling, Biostatistics
- Collaborated with veterinary teams and applied **statistical analysis in R** (PCA, PLS-DA, volcano plots, Bioconductor), leading to a **peer-reviewed publication**.

BA in Biology & Mathematics (*Magna Cum Laude*) | Bowdoin College

Publications

- Ramakrishnan, S., Chen, Z., Fosado, Y.A.G., Tubiana, L., Vanderlinden, W., Savill, N.J., Schnauffer, A. and Michieletto, D., 2024. Single-molecule morphology of topologically

digested olympic networks. PRX Life, 2(1), p.013009.

<https://doi.org/10.1103/PRXLife.2.013009>

- McDermott SM, Lukeš J, Read LK, Salavati R, Schnauffer A, Zimmer SL, Carnes J, Ivens A, Poorinmohammad N, Savill NJ, Speijer D, Stuart K, Záhonová K, Borujeni PM, Chen Z, Goode C, Sharma SK, O'Hara L, Cruz-Reyes J. Stunning Intricacies of RNA Editing Complexes RECC, RESC, and REH2C: Functional Organization, Developmental Regulation, and Evolutionary History in Kinetoplastid Protists. Wiley Interdiscip Rev RNA. 2026 Mar-Apr;17(2):e70037. <https://doi.org/10.1002/wrna.70037>
- Meehan, J., Ivens, A., Grote, S., Rodshagen, T., Chen, Z., Goode, C., Sharma, S.K., Kumar, V., Frese, A., Goodall, Z. and McCleskey, L., 2024. KREH2 helicase represses ND7 mRNA editing in procyclic-stage Trypanosoma brucei by opposite modulation of canonical and 'moonlighting' gRNA utilization creating a proposed mRNA structure. Nucleic acids research, 52(19), pp.11940-11959. <https://doi.org/10.1093/nar/gkae699>
- Meehan, J., McDermott, S. M., Ivens, A., Goodall, Z., Chen, Z., Yu, Z., ... & Cruz-Reyes, J. (2023). Trypanosome RNA helicase KREH2 differentially controls non-canonical editing and putative repressive structure via a novel proposed 'bifunctional' gRNA in mRNA A6. Nucleic acids research, 51(13), 6944-6965. <https://doi.org/10.1093/nar/gkad453>
- Geerts, M., Chen, Z., Bebronne, N., Savill, N.J., Schnauffer, A., Büscher, P., Van Reet, N. and Van den Broeck, F., 2022. Deep kinetoplast genome analyses result in a novel molecular assay for detecting Trypanosoma brucei gambiense-specific minicircles. NAR Genomics and Bioinformatics, 4(4), p.lqac081. <https://doi.org/10.1093/nargab/lqac081>
- McGorum BC, Chen Z, Glendinning L, Gweon HS, Hunt L, Ivens A, Keen JA, Pirie RS, Taylor J, Wilkinson T, McLachlan G. Equine grass sickness (a multiple systems neuropathy) is associated with alterations in the gastrointestinal mycobiome. Anim Microbiome. 2021 Oct 9;3(1):70. <https://doi.org/10.1186/s42523-021-00131-2>
- Rodrigues Ferreira, T., Chen, Z., et al., 'Loss of minicircles for complex I gRNAs is correlated with loss of virulence of Leishmania major in mice' (In preparation)
- Chen, Z., et al., 'Sexual Reproduction Maintains Mitochondrial Genome Fitness in Trypanosomatid Parasites' (In preparation)
- Chen, Z., et al., 'De novo Assembly and Annotation of T. congolense Mitochondrial DNA and Comparison with T. brucei' (In preparation)
- Chen, Z. et al. "'Less is more": a whole-genome-sequencing-enabled workflow to identify minimal nuclear marker sets for resolving closely related plant taxa' (In preparation)

Key Conference Presentations

Oral Presentations

- **"Mitochondrial DNA Dynamics in Trypanosomatid Parasites: A Story of Loss and Gain"**
Spring Meeting of the British Society for Parasitology 2023
SPPIRIT ECR Symposium 2023
- **"Mitochondrial Fitness in Clonal Trypanosome Parasites: Lost in Replication"**
Postgraduate Research Student Award 2023

Poster Presentations

- **“Identifying Nuclear Loci to Design a High-Resolution Plant Species Discrimination Assay”**
IMPS Plant Science Day 2025
- **“Sexual Reproduction Maintains Mitochondrial Genome Fitness in Trypanosomatid Parasites”**
Spring Meeting of the British Society for Parasitology 2024
- **“Aging of mitochondrial genome in clonal Trypanosoma species”**
Molecular Parasitology Meeting 2023
Infectious Disease Research Initiative Scotland 2023
- **“RNA Editing Landscapes in tsetse-independent trypanosome parasites”**
Spring Meeting of the British Society for Parasitology 2022
- **“De novo Assembly and Annotation of *T. congolense* Mitochondrial DNA and Comparison with *T. brucei*”**
Molecular Parasitology Meeting 2021