

Dear all,

We are looking for motivated students wishing to gain experience in the fascinating field of evolutionary genetics. The student we are looking for is quantitatively minded and has skills in programming and mathematics yet want to explore problems in biology.

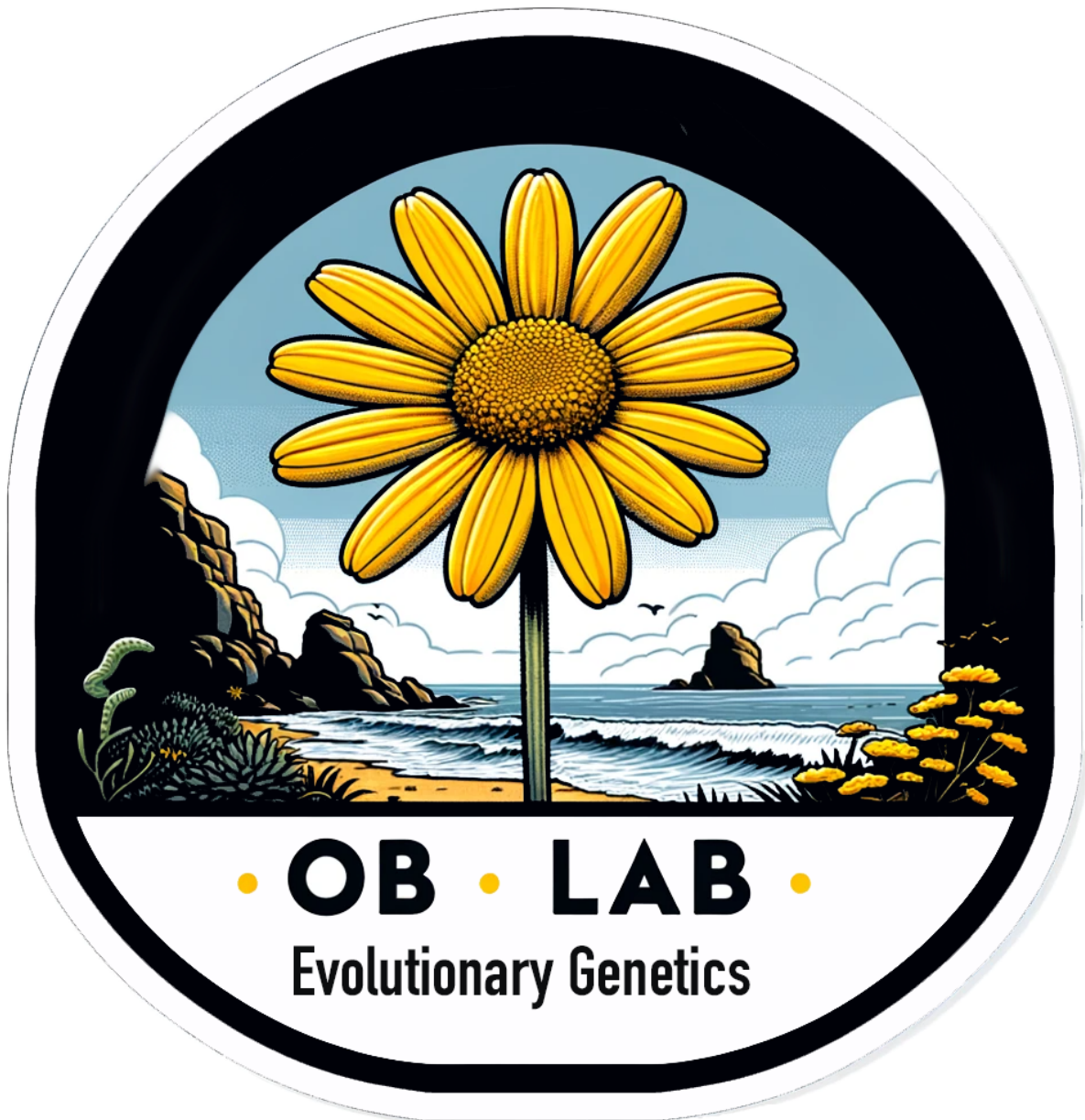
The student will work closely with Professor Daniel Ortiz-Barrientos, his team, and collaborators.

Please help us spread the word.

Best Wishes,

Daniel

www.ortizbarrientoslab.org



PROJECT 1

Project Title: Hybridization Dynamics and Coancestry Analysis in Spatially Structured Populations: A Computational Approach

Project Description: We are embarking on an exciting project aimed at integrating spatially explicit population dynamics with coancestry block analysis. This project presents a unique opportunity to explore the complexities of hybridization in spatially structured populations and its impact on coancestry block lengths. We aim to develop a computational model that simulates hybridization events, tracks coancestry blocks, and analyses their evolution over time. This research has the potential to provide significant insights into population genetics and evolutionary biology.

Roles and Responsibilities:

- Integrate existing population dynamics code with a coancestry block simulation model.
- Implement mechanisms for hybridization and recombination in hybrid offspring.
- Develop efficient algorithms for large-scale simulations on high-performance computing systems.
- Conduct data collection and analysis, focusing on coancestry block changes in hybrid and non-hybrid populations.
- Collaborate closely with the project supervisor and potentially other computational biologists or bioinformaticians.

Qualifications:

- Currently enrolled in or recently graduated from a program in Computational Biology, Bioinformatics, Genetics, or a related field.
- Strong programming skills, particularly in Python and experience with NumPy and other scientific computing libraries.
- An understanding of population genetics, evolutionary biology, and spatial modelling.
- Experience with high-performance computing is highly desirable.
- Ability to work independently and collaboratively in a research environment.

What We Offer:

- An opportunity to work on a cutting-edge research project with real-world applications in genetics and evolutionary biology.
- Access to high-performance computing resources.
- Close mentorship and guidance from experienced researchers in the field.
- Potential for co-authorship in research publications arising from this project.

Application Process: Please submit your CV, a brief statement of research interests, and any relevant work or project samples to d.ortizbarrientos@uq.edu.au. The ideal candidate will start honours in RQ3 2024 or RQ1 2025.

PROJECT 2

Project Title: Exploring the Evolution of Genetic Architecture in Plants: A Tensor and Hypergraph Approach to Gravitropism

Project Description: We are seeking a motivated student to join a project that aims to unravel the complex genetic architecture of gravitropism in plants. This project will utilize innovative tensor and hypergraph methodologies to analyse simulated genetic data, providing novel insights into the evolutionary forces shaping plant growth and response to gravity. The student will be instrumental in applying and further developing a modified Wright-Fisher model of evolution, integrating it with advanced data analysis techniques to explore the nuances of plant genetics and adaptation.

Roles and Responsibilities:

- Implement and modify the Wright-Fisher model for gravitropism, incorporating aspects such as mutation, selection, and SNP contributions.
- Analyse genetic data using tensor and hypergraph approaches to identify key genetic interactions and evolutionary patterns.
- Collaborate in developing new hypotheses and testing them against simulated data.
- Contribute to the interpretation of results and the preparation of manuscripts for publication.

Qualifications:

- Enrolled in or recently graduated from a degree in Genetics, Bioinformatics, Computational Biology, or a related field.
- Strong computational skills, particularly in R or Python, and familiarity with genetic data analysis.
- An understanding of population genetics models, particularly the Wright-Fisher model.
- Ability to work independently and as part of a team, with strong communication skills.
- Enthusiasm for evolutionary biology and plant genetics research.

What We Offer:

- Opportunity to work on a cutting-edge project at the intersection of computational biology and plant genetics.
- Access to advanced computational resources and datasets.
- Close mentorship from experienced researchers in the field.
- Potential for co-authorship on publications and presentation of research at conferences.

Application Process: Please submit your CV, a brief statement of research interests, and any relevant work or project samples to d.ortizbarrientos@uq.edu.au. The ideal candidate will start honours in RQ3 2024 or RQ1 2025.

PROJECT 3

Project Title: Unravelling the Omnigenic Model of Evolution: Integrative Network and Regression Analyses

Project Description: Join us in an exciting journey to decode the complexities of the omnigenic model in evolutionary genetics. This project delves into the intricacies of genetic networks, regulatory pathways, and the integral relationship between genes and phenotypic traits. Utilizing advanced computational techniques, we aim to dissect and understand the vast interconnectedness within genetic systems, with a particular focus on evolutionary dynamics.

Roles and Responsibilities:

- Engage in the development and refinement of computational models exploring the omnigenic theory.
- Conduct integrative analyses combining network theory, regression models, and quantitative genetics.
- Analyse simulated and empirical data sets to infer key evolutionary patterns and genetic interactions.
- Collaborate in interpreting results and preparing them for publication in scientific journals.

Qualifications:

- Enrolment or recent graduation in Genetics, Computational Biology, Bioinformatics, or related fields.
- Proficiency in programming languages such as R or Python, with a keen interest in computational genetics.
- Strong analytical skills, with an aptitude for mathematical modelling and data interpretation.
- Ability to work collaboratively in a multidisciplinary team.
- Curiosity and enthusiasm for evolutionary biology and genetic networks.

What We Offer:

- An opportunity to be part of a cutting-edge research project at the forefront of genetic and evolutionary studies.
- Access to state-of-the-art computational resources and diverse data sets.
- Mentorship from experienced researchers and potential for co-authorship in publications.
- A platform to present findings at conferences and workshops.

Application Process: Please submit your CV, a brief statement of research interests, and any relevant work or project samples to d.ortizbarrientos@uq.edu.au. The ideal candidate will start honours in RQ3 2024 or RQ1 2025.

PROJECT 4

Project Title: Investigating the Role of Centromeres in the Evolution of Chromosomal Inversion

Project Description: We invite an enthusiastic honours student to join an exciting research project exploring the evolutionary dynamics of chromosomal inversions in relation to centromere locations. This project aims to delve into the centromere hypothesis, which posits that the structural characteristics and genetic content of chromosomal inversions, particularly pericentric versus paracentric, significantly influence their evolutionary trajectory. The student will engage in both computational simulations and empirical data analysis to assess how centromeres might facilitate the spread and persistence of chromosomal inversions in populations.

Roles and Responsibilities:

- Conduct computational simulations to model the spread of pericentric and paracentric inversions in populations.
- Analyse genetic data to investigate the recombination rates and evolutionary stability of chromosomal inversions.
- Collaborate in interpreting results and formulating evolutionary hypotheses.
- Participate in regular research meetings and contribute to manuscript preparation.

Qualifications:

- Currently enrolled in an honours program in Genetics, Biology, Computational Biology, or a related field.
- A strong foundation in genetics and evolutionary biology.
- Experience or a keen interest in computational modelling and data analysis.
- Proficiency in a programming language such as Python or R.
- Excellent communication skills and the ability to work independently as well as part of a team.

What We Offer:

- The opportunity to be part of a pioneering research project at the intersection of genetics and evolutionary biology.
- Mentorship from experienced researchers and opportunities for professional development.
- Access to state-of-the-art computational resources and datasets.
- The potential to contribute to scientific publications and present at conferences.

Application Process: Please submit your CV, a brief statement of research interests, and any relevant work or project samples to d.ortizbarrientos@uq.edu.au. The ideal candidate will start honours in RQ3 2024 or RQ1 2025.

PROJECT 5

Project Title: The evolution of redundancy during parallel polygenic adaptation

Project Description: We invite an enthusiastic honours student to join an exciting research project exploring the evolutionary dynamics of parallel evolution and polygenic adaptation. Exploring redundancy during parallel evolution is a fascinating area of research that investigates whether similar genetic mechanisms underlie the same adaptive trait in different populations. This kind of research can reveal the predictability of evolution and the extent to which genetic diversity influences adaptive outcomes.

Roles and Responsibilities:

- Perform a Genome-Wide Association Study (GWAS) on each population pair to identify loci associated with the adaptive trait.
- Calculate genetic divergence (e.g., F_{st} or D_{xy}) at GWAS loci and compare it to the background level of divergence across the genome.
- Use statistical tests (e.g., permutations or bootstrapping) to determine if GWAS loci are more divergent than expected by chance.
- Identify GWAS loci in multiple independent population pairs that have adapted to similar environmental pressures.
- Compare the list of loci across these populations to see if the same loci are implicated in the adaptive trait.
- Use statistical analyses to test for non-random association patterns, suggesting consistent recruitment of genetic loci.
- Estimate the breeding value of GWAS loci by assessing their effect size and direction on the phenotype within each population.
- Develop genomic prediction models using the effect sizes of GWAS loci to predict the phenotype in one population based on the genotype data from another population.
- Validate the models using cross-validation techniques or by applying the model to independent datasets to assess predictive accuracy.

Qualifications:

- Currently enrolled in an honours program in Genetics, Biology, Computational Biology, or a related field.
- A strong foundation in genetics and evolutionary biology.
- Experience or a keen interest in computational modelling and data analysis.
- Proficiency in a programming language such as Python or R.
- Excellent communication skills and the ability to work independently as well as part of a team.

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Application Process: Please submit your CV, a brief statement of research interests, and any relevant work or project samples to d.ortizbarrientos@uq.edu.au. The ideal candidate will start honours in RQ3 2024 or RQ1 2025.

Thanks,
Daniel



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Daniel Ortiz-Barrientos
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Chief Investigator
ARC Centre of Excellence for Plant Success

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I acknowledge the Traditional Owners and custodians of the lands where I live, work and conduct my research. I pay my respects to their Ancestors and descendants and the continuation of their cultural, spiritual, and educational practices.