Genomic gigantism, the phenomenon where organisms possess exceptionally large genomes, has independently evolved in various eukaryotic lineages. Despite our knowledge of how genome size increases through the proliferation and retention of repetitive sequences, the evolutionary mechanisms driving this expansion remain a subject of debate. In particular, the evolution of the sequence and structure of giant genomes and evolutionary genomic consequences of genomic gigantism are still largely unexplored. With advances in technology, now is an opportune time to delve into these questions, particularly by comparing giant genomes with their smaller counterparts.

One significant gap in our knowledge is understanding how genetic differences accumulate in giant genomes as populations evolve into distinct species, and how genetic material from different populations intermixes during this process. There are several reasons why genetic differences might accumulate differently in giant genomes. First, the rate of genetic recombination (gene shuffling) tends to be low in giant genomes, which can limit the efficiency of natural selection, the process that causes adaptation. Second, because giant genomes contain a high proportion of repetitive, i.e. present in multiple copies, sequences, much of the genetic divergence is expected to occur within these repetitive parts, potentially leading to substantial differences even among closely related species. Third, giant genomes often harbour numerous transposable elements, “jumping genes”, which can be retained over long periods and contribute significantly to genetic variation and adaptation.

Salamanders (Urodela), exemplify genome gigantism, with each species having a genome size exceeding 10 billion of base pairs, which is three times the size of the human genome. This project focuses on studying genetic differences and introgression—the mixing of genetic material between populations—in the giant genomes of newts from the smooth newt species complex. This complex consists of evolutionary nine lineages that represent different stages of speciation. Extensive genetic and genome-size data have already been collected for these lineages, providing a solid foundation for our genomic research. Our project aims to achieve several goals:

- Characterise the Genomic Landscape of Structural Divergence: We will identify structural differences between genomes and reconstruct their evolutionary history.

- Quantify divergence and introgression in single-copy genomic regions: By analysing samples from core ranges of all smooth newt complex lineages and from natural hybrid zones where different lineages intermingle, we aim to understand the determinants of genetic differentiation and introgression.

- Assess differentiation and introgression in repetitive genomic regions: We will compare the abundance of various transposable elements and satellite families within and between the smooth newt complex lineages to determine if genome size differences are due to specific types of repetitive elements or a general expansion and contraction of diverse categories. An entirely novel aspect of this project is the analysis of repetitive elements across hybrid zones, offering an unprecedented look at how these elements contribute to genetic variation and divergence.