3 Master's thesis (+IRT3) projects available on EVOLUTIONARY GENOMICS
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### Project 1: *What are the genetic consequences of near extinction?*

Theoretically, decreases of population size lead to strong genetic drift, depletion of genetic diversity, potentially further limiting the adaptive capacity of nearly extinct species. Yet, this process can potentially be balanced by introgression from closely related species. We test this hypothesis using genomic data from the manzanita shrub *Arctostaphylos densiflora*, which is critically endangered in California. We have ddRAD sequencing data from the entire extant natural population and nearly all clonal horticultural races. The student will learn how to use **assembly techniques** to produce a high standard genomic dataset, **phylogenetic analyses** to infer the evolutionary history of this population and domesticated varieties, and **population genomics methods** to infer changes of effective population size and gene flow.

Project 2: *New genomic approaches to study population genomics in giant genomes*

Advances in next generation sequencing methods has provided unprecedented opportunities to study speciation in non-model organisms, irrespective of the genome size. Yet, developing the right laboratorial protocol also demands unprecedented customization, as slight differences in the methods can lead to large differences in the number of loci, the percentage of missing data, and therefore in power to answer evolutionary questions. In the first part of this project (IRT3), we will **customize a ddRAD protocol** for grasshopper species that are characterized by a giant genome size, determining the combination of restriction enzymes that reduces the amount of missing data. In the second part (thesis), the student will genotype individuals from Alpine populations to **identify potential hybrid zones**, and potentially perform **admixture mapping** of phenotypes relevant for reproductive isolation.

Project 3: *Repeatable patterns of introgression during the speciation continuum*
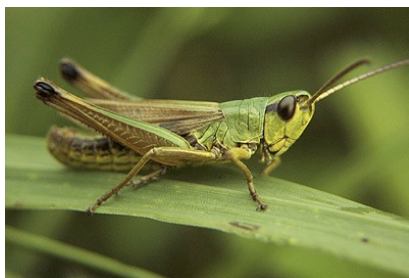
Hybrid zones have been regarded as windows into the genetic basis of speciation because they allow to identify the genomic regions that cannot introgress, and therefore that are associated to the initial reproductive barriers between emergent species. Yet, because a hybrid zone represents one time-slice in the continuum of species formation, it is still challenging to understand how reproductive isolation expands over the genome to eventually form good biological species. We have collected ddRAD loci of two hybrid zones between populations of grasshoppers that are at different stages of divergence. In this project, the student will learn how to use **assembly techniques** to produce a high standard genomic dataset, **population genomics methods** to infer patterns of introgression at the gene-level in each hybrid zone, and **statistical methods** to compare introgression rates of the same locus across the two hybrid zones.

Example papers from our lab:
Neves, J. M. M., Z. J. Nolen, …, and R. J. Pereira. 2021. Genomic methods reveal independent demographic histories despite strong morphological conservatism in fish species. Heredity.

Nolen, Z. J., B. Yildirim, … , and R. J. Pereira. 2020. Historical isolation facilitates species radiation by sexual selection: Insights from *Chorthippus* grasshoppers. Molecular Ecology 29:4985–5002.