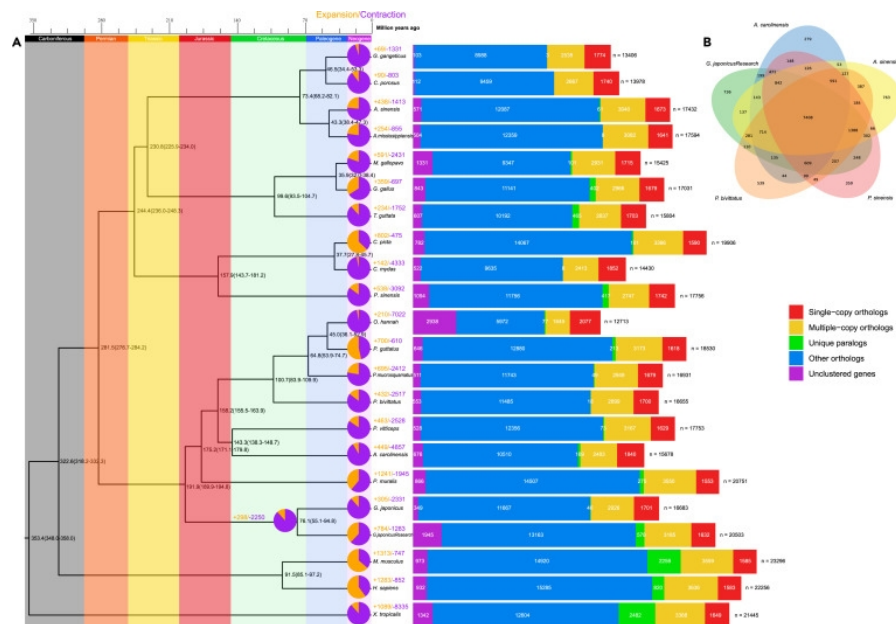


Dennis 1. How does genome annotation impact studies of adaptation?

Are you interested in *adaptive evolution*? The mechanisms of adaptation to climate change? Biodiversity and conservation research has entered the genomics era. There are now hundreds of genome sequences available, creating new opportunities for understanding evolution in natural populations and increasing our powers to predict the species most at risk. These analyses largely focus on the coding part of the genome **and this is highly dependent on how the annotation was generated**. Despite this, the impact of annotation has not been systematically compared on downstream analyses.

This is a primarily bioinformatic project. To understand the impact of annotation, the student will use a set of related genomes that are already assembled and annotated. We will re-annotate them using several pipelines (classical and deep learning based models). To compare annotations, the resulting protein predictions will be compared using analyses that include gene-family expansion/contractions, homology, and transcriptomic analyses. The results of this will be written up into a publication.



Dennis 2. Is there a trade-off between temperature and phosphorous tolerance in *Daphnia galeata*?

In aquatic environments, temperature and eutrophication are key stressors encountered by zooplankton. Evolution to cope with one might be at the expense of the other. To better understand this, we will explore the impact of evolved differences in phosphorous tolerance on other life history traits. We will use three lineages of *Daphnia galeata*: One that is phosphorous-sensitive, one that is average, and one that is phosphorous-tolerant. Life history traits will be measured under different temperatures to disentangle the genetic and plastic contributions to variation in tolerance of eutrophic conditions.

Full genome sequencing is available for these lineages, meaning that **a second student** could also compare genome sequences to identify genes evolving under signatures of natural selection. These could be targeted in transcriptomic sequencing in combination with the experiments above.

