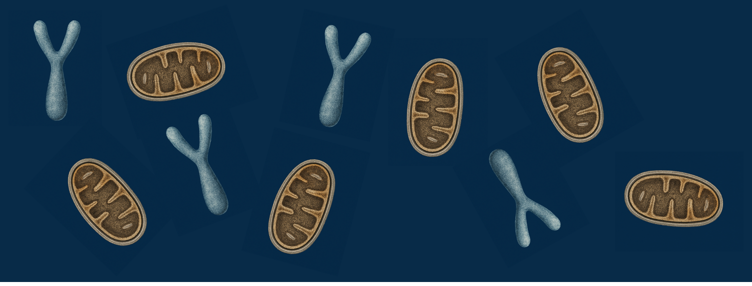

# Can we simplify evolution?

## Modeling complex selection in human Y chromosome evolution *(Master's Thesis in Biology)*

### Background:

A big question in evolutionary genetics is: are patterns of genetic diversity shaped more by random drift or by natural selection? This becomes especially tricky in parts of the genome where recombination is absent, such as the human Y chromosome. These regions are shaped by many slightly harmful mutations, each with a different strength, a concept known as the distribution of fitness effects (DFE).

To investigate how DFEs affect such regions, we will employ a model that traces the evolution of genes over time while accounting for harmful mutations of arbitrary strength: the extended structured coalescent (ESC). But this model still assumes that all mutations are equally harmful. In this project, you will investigate: can we replace a complex DFE with a single "effective" selection strength and still get the right answers?

### Key question:

Can we use a single selection coefficient to describe how natural selection shapes genetic diversity in regions such as the human Y chromosome?

### Project description:

You will build a simulation pipeline to model how different DFEs affect genetic diversity in non-recombining regions. You'll explore whether the ESC with a single selection coefficient can summarize these effects and how this relates to real-world data, especially from the human Y chromosome. Depending on your interests, you can focus more on theory, simulations, or data analysis.

### What you'll do:

- Simulate evolution using *SLiM* and *snakemake*
- Explore how different DFEs shape genetic diversity
- Compare your results to real data from human uniparental markers
- Optional: contribute to a scientific publication

### Skills you'll use or learn:

- Modeling using coalescent theory
- Applied Bayesian and descriptive statistics
- Python, shell scripting, and workflow automation

### Key readings:

Strütt, Stefan, Laurent Excoffier, and Stephan Peischl. "A generalized structured coalescent for purifying selection without recombination." Genetics (2025): iyaf013.

Good, Benjamin H., and Michael M. Desai. "The equivalence between weak and strong purifying selection." arXiv preprint arXiv:1210.4500 (2012).

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