*Inference of ecological and life-history traits from full genome polymorphism data: tales of success and limitations.*

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While most inference methods using full-genome data can be applied to all possible kind of species, the underlying assumptions are often sexual reproduction in each generation and non-overlapping generations. However, in many plants, invertebrates, fungi and other taxa, those assumptions are often violated due to different ecological and life history traits, such as self-fertilization, long term dormant structures (seed or egg-banking) or large variance in offspring production. Furthermore, the resolution of past inference decreases when there is a lack of SNPs in the data. I will present here three new developments of the Sequentially Markovian Coalescent (SMC) and Deep Learning (DL) methods based on Graph Neural Networks (GNN) allowing us to 1) infer seed banking / dormancy or selfing rates and their change in time, 2) infer the variance in offspring production and regions under positive selection along the genome, and 3) integrate epigenetic (methylation) markers to improve the inference of past events.