Reference panel phasing for low-coverage sequencing imputation on non-model species barn owl (*Tyto alba*)

Sonia Sarmiento, Jérôme Goudet
Department of Ecology and Evolution, Université de Lausanne - Switzerland

High sequencing costs have limited research on non-model species. However, sequencing many individuals at low read depth (low coverage Whole Genome Sequencing lcWGS), thus reducing costs, is a new approach that has proven robust in model and non-model species. LcWGS read depth is too low to confidently call individual genotypes and, thus, delivers genotype likelihoods only. To obtain genotypes rather than their likelihood, an alternative is to use imputation from a reference panel of individuals sequenced at high coverage. Here we describe different strategies to create such a reference panel for the barn owl (*Tyto alba*), combining information from Illumina reads and pedigree. Specifically, we phased sequencing reads into longer inserts using either reads information only or reads and pedigree at different depths (if pedigree information was available) and then polished the results with statistical phasing. In line with previous research, we expect phasing using pedigree information having a higher accuracy than with reads only. However, the difference in accuracy achieved after statistical phasing is to be determined. Eventually, this work will help establish a high-accuracy lcWGS workflow for a non-model species.