

## Phylogenomics for regional biodiversity assessment in the Canton of Geneva

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Monitoring variation of phylogenetic diversity across space and time is critical to understand the effect of species extinction and distribution changes on the loss of evolutionary history. However, measuring accurate phylogenetic-diversity indexes within local species assemblages remains problematic because of the poor resolution and uncomplete sampling of the tree-of-life at the species-level. Here, we demonstrate the feasibility of using high-throughput genome sequencing and target-enrichment of 353 nuclear genes to estimate phylogenetic relationships among all species of the Geneva flora (1126 species). Our results show that, despite a significant taxonomic effect on gene capture efficiency, this method provides a more resolved phylogenomic tree at the species level than synthetic phylogenies available in the “Open Tree of Life” project. This new genomic reference for plants will be used in combination with occurrence data (>200'000 observations) to accurately quantify and model variation in evolutionary history of the Geneva flora across different floristic communities, habitats and time periods. Ultimately, this new layer of phylogenetic information will be integrated in the calculation of the Canton's green infrastructure for long-term conservation of biodiversity.