Geography and landscape characteristics strongly influence the genetic variation of natural populations. The effects of landscape characteristics are commonly investigated by analyzing population genetic structure with Bayesian clustering programs. Those programs are based on computer-intensive stochastic simulations that do not scale with the dimension of data sets generated from next-generation sequencing technologies. Faster algorithms are needed to analyze genome-wide patterns of population genetic variation in their geographic context.

In this study, we introduced the computer program {\tt TESS3} which has run-times several order faster than those of {\tt TESS}. By combining machine learning and spatial statistical methods, {\tt TESS3} provides estimates of ancestry coefficients with accuracy comparable to {\tt TESS}. In addition, the program can be used to separate adaptive from non-adaptive genetic variation, and to perform genome scans for selection. The main features of {\tt TESS3} were illustrated using dense genomic data from European lines of {\it Arabidopsis thaliana}.