

## Computational analysis of clonal lineages in mixed mating type populations

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Plant pathogens cause considerable economic damage and lead to food insecurity. Understanding how pathogens evolve is a vital component in preventing or mitigating the damage they cause. Unfortunately, many current population genetic analysis tools are not designed to compensate for mixed mating types often found in populations of plant pathogens. Detection and classification of clonal lineages within a population is vital in understanding how a population will change over time. This project was designed to add new functionality to the population genetics analysis tool poppr, a package in the R statistical language and environment. Poppr implements tools that facilitate the study of mixed mating type populations, with a focus on identifying clonal lineages within a population. Presented are improvements to poppr that extend the concept of multilocus genotypes to multilocus lineages. Many features concerning mixed mating types and detection of clonal lineages within populations were added to poppr. These features can be divided into a few sub-categories. The first feature is a set of functions that gradually merge clusters of genotypes into clonal lineages based on genetic distance at a user-defined distance threshold. The second feature is a set of functions that analyze pairwise distances between samples to predict the reproduction method most likely to have generated a given individual. In the near future we plan to add a third feature, a set of functions that determine the relative similarity between two samples via a sliding window analysis. Ultimately, these tools will facilitate the analyses of mixed mating type populations in the easy to use R environment.

