

# Analysis of Multilocus Genotypes and Lineages in 1.1.5.99.583

Zhian N. Kamvar<sup>1</sup> and Niklaus J. Grünwald<sup>1,2</sup>

1) Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR

2) Horticultural Crops Research Laboratory, USDA-ARS, Corvallis, OR

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## Abstract

A multilocus genotype is the unique combination of alleles across two or more loci. For organisms such as plant pathogens that often reproduce clonally, multilocus genotypes are invaluable for identifying the mode and spread of an organism. This document will describe in detail how you can define multilocus genotypes/lineages and how you can use them for your analyses.



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## 1 Introduction

## 2 Multilocus Genotype Flavors

There are three different way for constructing multilocus genotypes in *poppr*. The first is a simply naïve construction where all alleles must match to make a unique multilocus genotype. New in version 1.1.5.99.583 is the ability to use genetic distance to define multilocus genotypes or define custom multilocus genotypes based on other biological factors. In this section, we will demonstrate how to construct each of these three multilocus genotype definitions in different data sets.

### 2.1 Naïve

The naïve definition simply takes strings of alleles and compares them for equality. This method is quick and easily interpretable, but means that things like genotyping error, hyper-variable loci, and missing data all contribute to a unique genotype that might not be truly unique ([Kamvar \*et al.\* , 2015](#)).

### 2.2 Filtered

### 2.3 Custom

## 3 Diversity Analysis

## 4 Clone Correction

## 5 Conclusions

## References

Kamvar, Zhian N, Brooks, Jonah C, & Grünwald, Niklaus J. 2015. Novel R tools for analysis of genome-wide population genetic data with emphasis on clonality. *Frontiers in Genetics*, **6**, 208.