

GenAPoPop1.0: Computing population genetic indices and inferring reproductive modes from genotype diversity in polyploid populations

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Abstract

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Understanding the ecological and evolutionary impacts of polyploidy, especially on reproductive modes, implies to be able to easily compute population genetic indices and to quantitatively infer the respective rates of clonality, selfing and outcrossing producing current descendants.

We developed a user-friendly software to analyze genotypes of spatio-temporally-sampled individuals, with a special focus on analyzing and interpreting reproductive modes in polyploid populations. This software, part of the project ANR Clonix2D, named GenAPoPop (for *Genetic Analyses of Polyploid Populations*), was written using Qt, python and fortran, works on Gnu/Linux, MacOS and Windows, and run locally with no internet connection. It allows computing major population genetic indices for polyploids (F-statistics, linkage disequilibrium, probability of identity, spatial and temporal Fst, genotypic and genetic diversities, etc.) only using a graphical interface and a new method to obtain posterior probabilities of reproductive modes in polyploid populations using temporal genotypings. It aims to ease and broaden the computation of genetic indices in research projects and facilitate polyploid population studies in population genetic courses and student trainings.

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We will present the software interface, and provide some results obtained on a tetraploid sea anemone and one a decaploid invasive plant species.

Keywords: population genetics, partial clonality, partial selfing, polyploidy