

**GenSimXP: an R package for the simulation and analysis of complex traits in experimental populations.**

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GenSimXP (Genome Simulator for Experimental Populations) is an alpha version R library to compare, via simulation, the relative abilities of different complex multigenerational breeding schemes to achieve a research goal such as the mapping of quantitative trait loci. Experimental populations can be generated by user-specified calls to simple R interface functions and analyzed by other GenSimXP routines, other R packages (e.g., Rqtl) or native R routines. The package is well suited for running simulations in batch mode in a linux cluster environment.

Preliminary simulations results are presented for two simulation studies: 1.) a study designed to compare the abilities of different experimental designs to identify and fine map two QTL located within close proximity on the same chromosome, and 2.) a study to assess the ability of an eight-way funnel design to identify and map multiple QTL randomly located across a genome. The results across a variety of simulated conditions seem to favor the eight-way funnel design to a set of competing designs.