Population genetics simulator:

an online tool for genetics education and research

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Why?

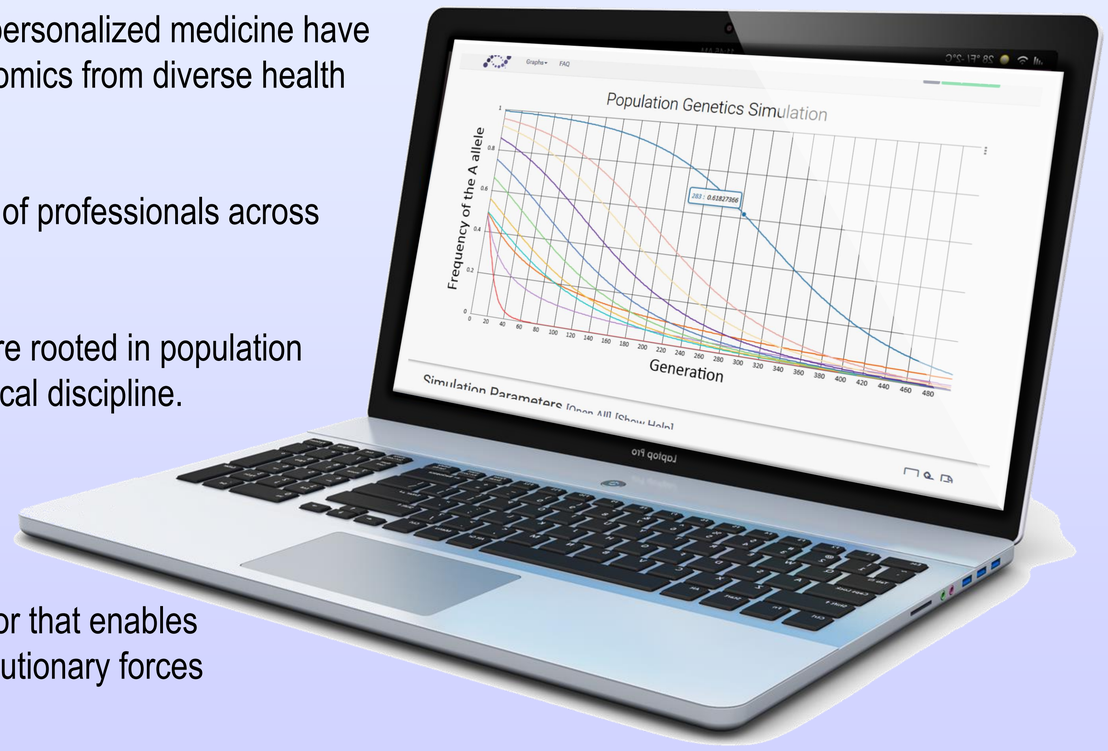
Advancement of ‘omics sciences and the lure of personalized medicine have generated increased interest in genetics and genomics from diverse health science professionals and society at large.

There is an urgent need for greater “genomics literacy” of professionals across disciplines.

Many foundational concepts of ‘omics sciences are rooted in population genetics, which has remained a highly mathematical discipline.

Efforts to make these concepts accessible are needed.

We have developed an online simulator that enables users to manipulate the effects of evolutionary forces and phenomena.



popgensimulator.pitt.edu

evolve

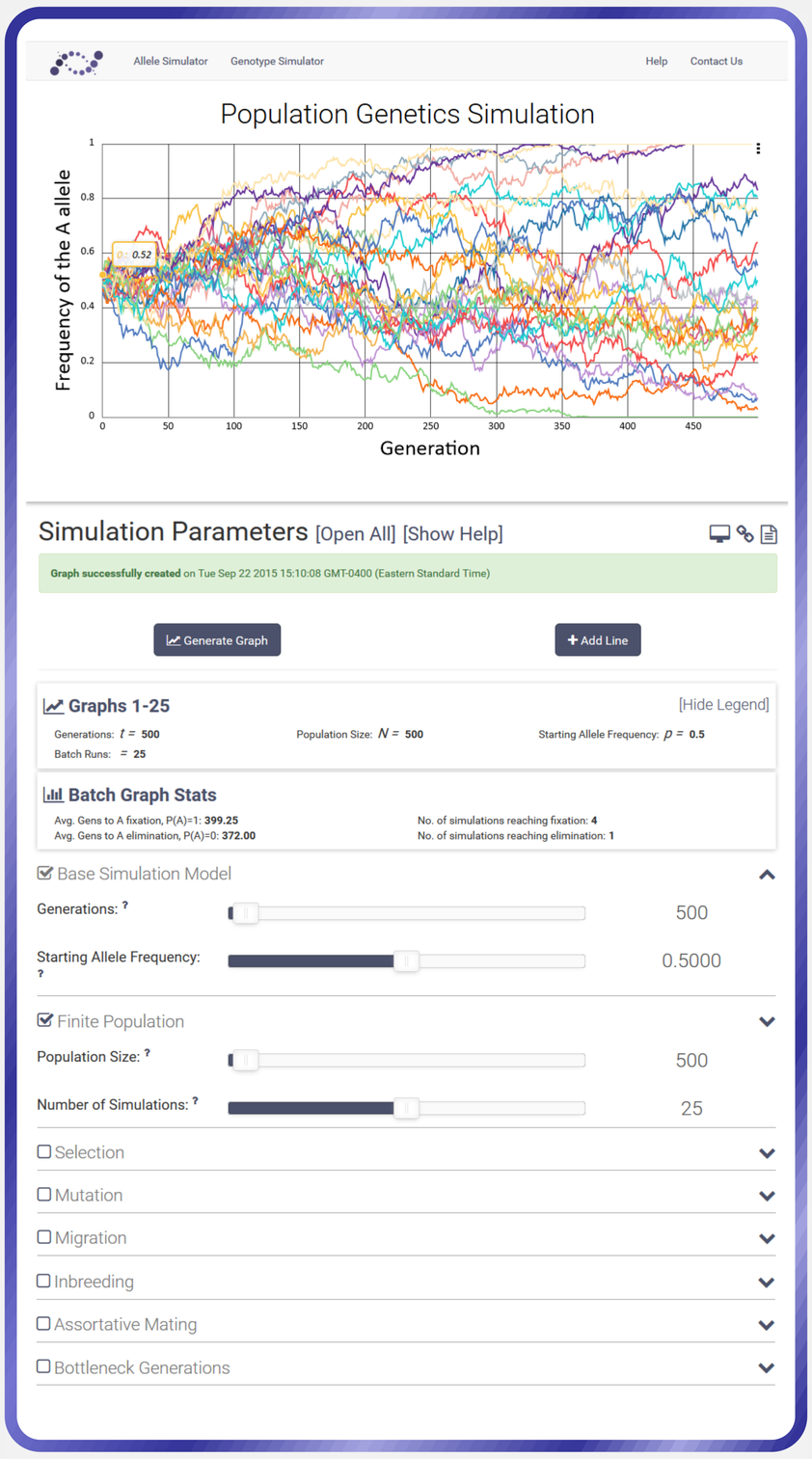
Graphical output depicts allele (or genotype) frequency changes across successive generations.

compare contrast

Multiple simulations under the same or different parameters can be plotted together for comparison.

Key Feature:
Simulations can be run in batches with aggregate summary statistics (i.e., average time to allele fixation or loss) reported.

Key Feature:
Simulations can model the effects of evolutionary forces (e.g., selection, mutation, migration, drift, population bottleneck) and mating systems (i.e., assortative mating, inbreeding) individually or simultaneously. Finite and theoretical infinitely-sized populations can be modeled.



explore

Zoom in and out and pan left and right in the output window. Trace individual simulation results. Save to various file formats.

customize

Toggle color contrast of output for printing or projecting. URL tool generates pre-populated simulation parameters for easy sharing. Numerical simulation results can be saved.

Key Feature:
Online tool is optimized for both mobile devices and computers.

Key Feature:
Thorough documentation of the user interface including video tutorials is provided. Help section describes technical details in plain language.

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