



*PopGen Fishbowl* is an agent-based population genetics simulation. The program contains the tools to conduct virtual experiments violating all the assumptions of Hardy-Weinberg theory. You can explore the effects of:

1. Small population size (Genetic Drift)
2. Selection
3. Mutation
4. Migration
5. Non-random mating

Some basic population biology is also demonstrated such as, logistic population growth and the Allee Effect.

## **Model Details**

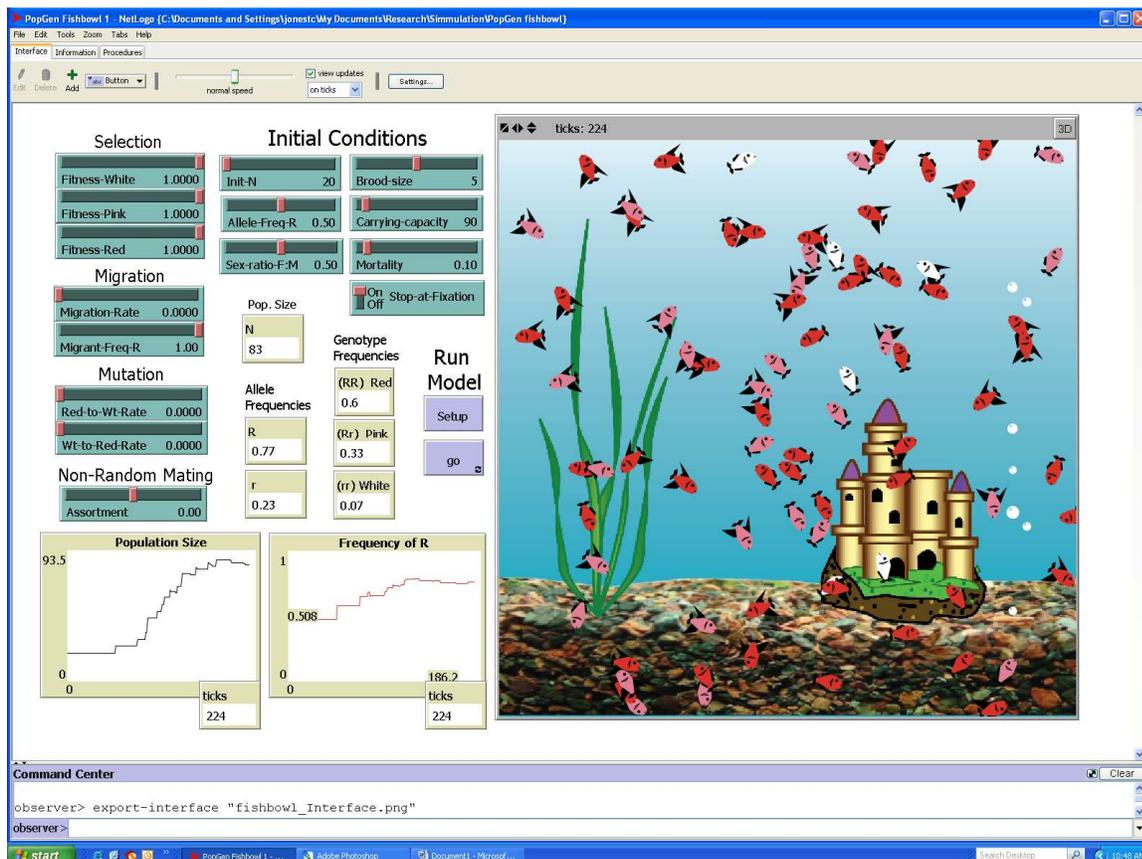
The agents of the model are fish in a small 'aquarium' population. The frequency of a single gene with two alleles affecting body color is tracked over time in the simulated aquarium population. The two alleles (red and white) are incompletely dominant and the heterozygotes are pink in color. When fish of opposite sex come together they may breed and produce offspring that follow patterns of mendelian inheritance in their body color. Overlapping generations are simulated in the model because reproduction may occur whenever fish meet.

Virtual experiments can be carried out by varying the population's initial conditions of allele frequencies, population size, carrying capacity, sex ratio, mortality, and brood size (Table 1). In addition to population size, the Hardy-Weinberg parameters of relative fitness, migration (gene flow), mutation, and assortative mating can be set at the beginning of each simulation run (Table 2). By varying these parameters, students can explore the affects of violating Hardy-Weinberg assumptions regarding population size, selection, mutation, migration and non-random mating. Some basic population biology such as logistic growth and the Allee Effect can also be explored by manipulating different parameters of the model.

A run of the simulation can be either started or stopped by selecting the "go" button, and new parameter values are implemented by selecting the "setup" button. Initial conditions and experimental variables can be changed by the user with a set of sliders in the user interface (Figure 1). Both the initial population size and the carrying capacity can vary from 0 to 1000. The brood size can range from 0 to 10. The sex ratio is set as the probability that any particular fish will be female when born and can vary from 0 to 1. Each simulated fish in the population has a probability of dying within 100 time intervals ("ticks"). The mortality probability selected by the user is a maximum that adjusts proportionally to the population size divided by carrying capacity. Mortality reaches the maximum value when population size is equal to the carrying capacity. The two alleles in the population are R and r, with the genotypes RR = red body color,

Rr = pink color and rr = white color. Each simulation run is initiated by specifying the proportion of R alleles in the population using a slider on the simulation's user interface. The effects of selection are simulated by choosing a relative fitness (range 0 – 1) which is imposed on juveniles prior to reproduction during the simulation. Juveniles become adults after ten time intervals ("ticks"). Note that the simulation of selection against a dominant or recessive allele in the model can be accomplished by making the relative fitness of the heterozygote Rr equal to that of one of the homozygotes. The rate of migration into the population is implemented by a probability (range 0 to 0.1) that a fish from some other population replaces any one fish in the simulated population. The probability that an immigrating fish carries either the R or r alleles is set by adjusting the frequency of R in the immigrant population (range 0 to 1). Mutations (R to r) and back mutations (r to R) are simulated as separate probabilities that each allele in a juvenile will mutate (range  $10^{-4}$  to  $10^{-2}$ ). Non-random mating is simulated by using a slider on the interface to adjust the probability of positive assortative mating (value > 0) or negative assortative mating (value < 0), such that individual fish have a greater probability of mating with individuals of the same or different genotype than that expected by random chance (value=0). Using a toggle in the interface the user can have the simulation either stop or continue when one allele becomes fixed (R = 1 or 0). The simulation stops running if population size becomes zero.

Figure 1. PopGen Fishbowl user interface.



Output from the model is both numerical and graphical (Figure 1 and Table 3). Population size, allele frequencies and genotype frequencies are reported numerically. Continuously updated graphs show both population size and the frequency of the R allele over time. The model also produces a continuously updated image that shows the sex and body color phenotype of each fish in the aquarium population.

The rate at which the model runs can be adjusted with a slider located at the top of the world view in the user interface. "Explosions" of fish fry from individual breeding events can be observed at very slow model running speeds. At very high speeds the simulation world view will regularly display snapshots of the population, and changes are more easily monitored in the graphical output. This feature is useful in speeding up virtual experiments. The simulation can also be paused at anytime during a session to produce a snapshot of population data. If the probability of mortality is set to 0, the population will then cease to evolve once the population size reaches the carrying capacity because there will be no further reproduction. Thus higher mortality rates and larger brood sizes will increase the rate of evolution in the population. Various other dynamics related to demography can also be observed in the simulated population by adjusting the non Hardy-Weinberg parameters that are included in our model. For example, if the initial population density is set very low, then the population may become extinct because individuals fail to find a suitable mate (Allee Effect). If the user specifies a greatly unbalanced sex ratio, this can cause the population to become extinct because of the increased likelihood that one of the sexes will become absent in the population at some future point in time.

**Table 1. Population parameters that can be varied in the PopGen Fishbowl simulation.**

<b>Initial Conditions</b>	
<b>Initial Population Size</b>	Can range from 0 to 1000.
<b>Allele Frequency</b>	Frequency of R (range 0 to 1), with $r = 1 - R$ .
<b>Sex Ratio</b>	Probability that any individual is female (range 0 to 1).
<b>Brood Size</b>	Can range from 0 to 10.
<b>Carrying Capacity</b>	Can range from 0 to 1000.
<b>Mortality</b>	Probability of an individual dying within 100 time intervals (range 0 to 1).

**Table 2. Experimental variables that can be manipulated in the PopGen Fishbowl simulation.**

<b>Experimental Variables</b>	
<b>Selection</b> Fitness-White Fitness-Pink Fitness-Red	Relative fitnesses of white, pink and red phenotypes (range 0 to 1).
<b>Gene-flow</b> Rate Frequency of R	Rate of migrants carrying genes into the population (range 0 to 0.1) and the frequency of allele R in the migrating population (range 0 to 1).
<b>Mutation</b> Red-to-White White-to-Red	Rates of mutations and back mutations in juvenile fish (range 0 to 0.01).
<b>Non-Random Mating</b>	Likelihood of positive or negative assortative mating (range -1 to 1). A setting of 0 means there is no assortment.

**Table 3. Output produced by PopGen Fishbowl simulation.**

<b>Output</b>	
Population Size	A numerical output and a continuously updated graph of population size over the total time course of the simulation.
Allele Frequencies	A numerical output of proportions for two alleles (R and r) and a continuously updated graph of the proportion of one allele (R) over the total time course of the simulation.
Genotype Frequencies	Continuously updated numerical output of three genotype frequencies RR, Rr, and rr.
Simulated Population	Animated representation of the complete population showing each individual with phenotypes for body color and sex.

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