Compatible with NetLogo 6.0.2

## WHAT IS IT?

This model simulates the mechanisms of evolution, or how allele frequencies change in a population over time. Here, you can choose to have up to four different types of alleles for some arbitrary locus. The phenotypes of these alleles can also be displayed and are based on their ALLELE RELATIONSHIPS (i.e. dominant or recessive).

During the simulation, "students" control populations of alleles/phenotypes via a HubNet Client and a "teacher" controls the environment via the HubNet Control Center. The "Allele Frequencies" plot shows how the allele frequencies are changing over time.

## HOW IT WORKS

### TEACHER: HubNet Control Center

STARTUP: The HubNet Control Center should start upon opening this model. Change any of the settings depending on what aspect of evolution you want to simulate. Press the GO button.

INSTRUCTIONS FOR STUDENTS: Instruct your students to open the NetLogo HubNet Client application, type your user name, select this activity and press ENTER. Make sure they choose the correct port number and server address for this simulation. Instruct your students to move their populations around to acquaint themselves with the interface. If you would like the students to input specific initial allele counts, instruct them to do so now. Instructors can also press the ADD POPULATION button to produce another "non-playable" population in the world.

SIMULATION: Press the REPRODUCE NOW button to cause each population to reproduce. Investigate how the allele frequencies have changed and instruct your students to record the specifics for their population. Continue to press the REPRODUCE NOW button and record how the EVOLUTION SETTINGS affect how the populations change over time. Modify the EVOLUTION SETTINGS as need to change the environmental factors altering allele frequencies.

### STUDENT: HubNet Client

STARTUP: Students should open the NetLogo HubNet Client application, type their user name, select this activity and press ENTER. Make sure to choose the correct port number and server address for this simulation.

After logging in, the client interface will appear for the students, and if GO is pressed in NetLogo they will be assigned a population of alleles/phenotypes. The YOU ARE GROUP: monitor will display the name entered upon startup and will also appear on the simulation to label the appropriate population. The current location will be shown in the LOCATED AT: monitor. If a student doesn't like their assigned phenotype shape they can select other shapes from the CHOOSE-SHAPE dropdown menu.

SIMULATION: Students are able to control the movement of their population with the UP, DOWN, LEFT, and RIGHT buttons. They can also input values for the initial allele configuration, if they desire different starting values then the ones given. Monitors show the current allele frequency count and percentage, genotype counts and phenotype colors, as well as the current generation and closest adjacent population.

## HOW TO USE IT

### GENERAL

SETUP: returns the model to the starting state.

GO: runs the simulation.

ADD POPULATION: when pressed, a new "non-playable" allele/phenotype population is added to the world. It wanders randomly and its phenotypes can reproduce and share alleles with adjacent populations.

REPRODUCE NOW: when pressed, all individual phenotypes reproduce with someone else in their gene pool.

SHOW-ALLELES: when on, the alleles of the population are shown, otherwise the individual phenotypes are shown, which are based on the relationships between allele pairs.

### ALLELE SETTINGS

ALLELE-X-ON: allows the given allele type to be part of the allele population.

ALLELE-X-COLOR: sets the color of the given allele type.

ALLELE-X-Y-RELATIONSHIP: sets the relationship (i.e. dominant, recessive) between two alleles, which dictates the phenotype that is displayed from each allele pair.

### EVOLUTION SETTINGS

MUTATION-RATE: the rate at which alleles mutate to a random allele upon reproduction.

ALLOW-GENE-FLOW?: when on, allows populations that are close enough to an ADJACENT POPULATION to share alleles upon reproduction.

SELECTION-ON-PHENOTYPE: selects the phenotype color that natural selection can act upon during the simulation.

RATE-OF-SELECTION: for a phenotype that matches the currently set SELECTION-ON-PHENOTYPE this sets the average number of offspring that phenotype will have when they reproduce.

### MONITORS & PLOTS

ALLELE-X-COUNT: the total allele count for the given allele type.

GENERATION: the current generation of the populations in the simulation.

TOTAL POPULATION: the number of phenotypes from all populations in the simulation.

ALLELE FREQUENCIES: shows the allele counts for each allele type over generations.

## THINGS TO NOTICE

MUTATION RATE: How does the MUTATION-RATE setting change the alleles? How does it change within population and between population variation?

GENE FLOW: How does the ALLOW-GENE-FLOW? setting change the alleles? How does it change within population and between population variation?

NATURAL SELECTION: How do the SELECTION-ON-PHENOTYPE and RATE-OF-SELECTION settings change the alleles? How do they change within population and between population variation?

GENETIC DRIFT: Notice that there are no settings for genetic drift, the fourth mechanism of evolution. Unlike the other mechanisms, genetic drift can never be turned off!

## THINGS TO TRY

Use the model with the entire class to serve as an introduction to population genetics. Be sure to modify the EVOLUTION SETTINGS to simulate how different mechanisms can affect the allele frequencies and variation both within and between populations.

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This model was created at the University of Minnesota as part of a series of applets to illustrate principles in biological evolution.

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Contact K N Crouse at crou0048@umn.edu if you have questions about its use.