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Modeling the Mechanisms of Evolution (an R Shiny App)
By Jackie Matthes

View of the user interface for the Modeling the Mechanisms of Evolution Shiny app.

Module Description:
This resource is an R Shiny app that contains simulation models for genetic drift, gene flow, and natural selection, the three core population-level processes that can lead to evolution. Within the app, users can change initial conditions for allele frequencies and the key parameters that influence rates of evolution in their own simulations and observe how these processes influence shifts in allele frequencies.
frequency. The app includes separate simulations for each individual evolutionary process, and a final simulation that puts all three processes together.

The models simulate changes in the frequency of two alleles, A and a, of a diploid organism through many generations of a population. Diploid combinations of these two alleles produce three possible phenotypes, described by the genotypes AA, Aa, and aa. Users manipulate parameters such as population size, allele frequency, phenotype fitness, the time at which two population connected, and the rate of reproduction across two populations to explore frequency of phenotypes and alleles over multiple generations.

Teaching Setting:
This app was developed for use in an introductory biology course as a pedagogical tool for introducing students to simulation modeling, but could be used in a variety of teaching settings.

QUBES Citation:
Related Materials and Opportunities:

This resource is an online R Shiny app that students run directly on the QUBES website.

Launch the Modeling the Mechanisms of Evolution R Shiny app.

You must be logged into your QUBES account to launch the app. If you don’t have a QUBES Hub account, register for one at www.qubeshub.org/register.

QUBES has a server to host Shiny apps. Click here for instructions on how submit your Shiny app to QUBES. The instructions outline a detailed workflow, so please do not hesitate to contact us at info@qubeshub.org for help!

QUBES also hosts various software such as RStudio, NetLogo, and Jupyter notebooks that can be used in a browser without having to worry about installation on a local machine or maintaining a campus server. Browse software hosted by QUBES.

QUBES users can create their own customized activities and datasets which students can run using free software without having the need to purchase and install locally.

This resource was nominated for the ROW by a professor at the University of Richmond. If you would like to nominate a QUBES resource for the ROW, please send your nominations to Elia Crisucci at emc22 “at” pitt.edu. It is helpful if you include a short description of why you think the resource should be featured as a ROW.
If you adopt and adapt this module, you are highly encouraged to share your adaptation back with the QUBES community using the QUBES Resources System for sharing Open Education Resources.

QUBES on Social Media

QUBES is a community of math and biology educators who share resources and methods for preparing students to use quantitative approaches to tackle real, complex, biological problems.

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