FEATURE ARTICLE

Using Digital Organism Evolutionary Software in the Classroom

LUKE APPLETON, JOSHUA MACKIE

Abstract

We review software for exploring biological evolution from a fun and educational perspective. Our goal is to provide a background explanation of the methods used, terminology, and user experience, and learning outcomes of desktop and mobile evolutionary simulators. Freeware and commercial programs are detailed, with a discussion of how certain software packages can be used in introducing evolutionary theory.

Key Words: *Evolution; evolutionary simulator; artificial life; A-life; Avida; Tierra; GenePool; mutation planet; teaching evolution; educational app; natural selection.*

○ Simulators Can Be Used to Teach Evolution because They Model Evolution

Traditional methods of teaching tend to require an active teacher dispensing knowledge to a passively receptive student. However, utilizing the latest in cutting-edge technology, you can now teach students at all levels on a computer, tablet, or smartphone. Software, computer science, and evolutionary biology collide in the field of evolutionary artificial life (A-life). Active and interactive methods that engage student attention improve retention compared to memorization alone (Bloom et al., 1956; Bonwell & Eison, 1991; Weltman, 2007).

Games are indeed an excellent way to learn evolutionary theory and processes, and through immersion they may provoke "stealth learning." Difficult concepts, such as the description of evolutionary forces, can be explored through games. North Star Games' *Evolution*, for example, is a role-playing board game in which hypothetical organisms (instead of the warriors or wizards of *Dungeons and Dragons*) compete for resources, mutate, die, and leave descendants (Crapuchettes, 2014). This tabletop approach has a particular downside: the physical gameplay places limitations on the sheer number of biological generations needed to see a distinct evolutionary effect. Computer-based evolutionary games can be implemented to surpass these limitations.

Difficult concepts, such as the description of evolutionary forces, can be explored through games.

Modern biology theory developed in tandem with the proliferation of computers and increasing compute power. John Forbes Nash Jr.'s game theory and John Maynard Smith's application of game theory toward modeling sex and signaling behavior-pattern inheritance, termed "evolutionarily stable strategy," favored the development of computer simulations of biology in the 1970s and '80s (Nash, 1950; Smith, 1982). In the '80s, the advent of newly described computer "viruses" and computer gaming added to the fascination with using computers to model biological phenomena. As far as we know, there is no massively popular "Pokemon" of rigorous teaching of evolutionary biology. There are presently dozens of programs that can be categorized as artificial life simulations that serve an educational purpose. The following summary and table provide notes on the game specifics, a quick assessment of usability, and thoughts on usefulness in the classroom (Table 1).

Many artificial life simulators, from the text-based classic *Tierra* to the *Mutation Planet* app for iOS, explore both microevolution and macroevolution of purely electronic organisms by changing selection coefficients following population genetics concepts. Perhaps the greatest benefit of using computers to abstract evolution is how they seem to "shrink time," with generations replaced by nanoseconds of CPU time. Another benefit is the user interface. Most evolutionary computer games are two-dimensional, with some exceptions (John Klein's *BREVE*, Larry Yaeger's *Polyworld*, and Maciej Komosiński's *Framsticks*) that render these virtual habitats in 3D (Klein, 2003; Yaeger, 1994; Komosiński & Ulatowski, 1999). Many of these interfaces allow for an immersive user experience, and potentially higher student engagement, which may translate to

The American Biology Teacher, Vol. 81, No. 1, pp. 12–17, ISSN 0002-7685, electronic ISSN 1938-4211. DOI: https://doi.org/10.1525/abt.2019.81.1.12.

Table 1. Summary of evolutionary simulators. The majority of these simulators are available for major operating systems and are free to use. These simulators are also assigned a difficulty level ranging from easy to hard (in terms of installation, implementation, and support) and can be characterized as simulating either microevolution or macroevolution and sometimes both. All these simulators introduce the basic concepts of evolution, although some will emphasize different evolutionary concepts; they introduce evolutionary topics with a variety of user interfaces, spanning from text at the command-line to rich three-dimensional environments. The presence of teaching resources corresponds to at least one independent use-case, implementation, or lesson plan written by another educator as found through a Google web search. Target audiences are recommended: middle school (MS), high school (HS), and college undergraduates (UG).

Software	Author & Citation	Operating System	Cost	Ease of Setup & Use	Teaching Resources	Topics/ Concepts	Interface	Target Audience
Avida ED	Charles Ofria (Adami et al., 1994; Ofria & Wilke, 2004)	MAC OS Windows	Free	Easy	Yes	Microevolution Mutations Natural Selection	2D	HS
Biomorphs	Richard Dawkins (Dawkins, 1986, 1997)	MAC OS Windows	Free	Easy	No	Microevolution Adaptive Radiation	2D	HS
BREVE	Jon Klein (Klein, 2003)	MAC OS Windows	Free	Hard	No	Microevolution	3D	UG
Cell Lab: Evolution Sandbox	Petter Säterskog (Säterskog, 2016)	Android	Free	Easy	Yes	Microevolution Adaptation	2D	HS
Darwin Pond	Jeffrey Ventrella (Ventrella, 2005)	Windows	Free	Easy	Yes	Microevolution Sexual Selection Artificial Selection Foraging Theory Mutations	2D	MS, HS, UG
Evolution	North Star Games (Crapuchettes, 2014)	NA	Paid	Easy	Yes	Macroevolution	Board	MS, HS
Evolution	Keiwan Donyagard (Donyagard, 2017)	Android iOS Mac OS Windows	Free	Easy	No	Microevolution	2D	HS
Framsticks	Maciej Komosiński (Komosiński & Ulatowski, 1999)	Linux MAC OS Windows	Free	Medium	No	Macroevolution	3D	HS
GenePool	Jeffrey Ventrella (Ventrella, 2005)	iOS Windows MAC OS	Free	Easy	No	Microevolution Sexual Selection Artificial Selection Foraging Theory	2D	MS, HS
Lizard Evolution Virtual Lab	HHMI (Losos et al., 2004; Kolbe et al., 2012)	Windows MAC OS	Free	Easy	Yes	Macroevolution Adaptive Radiation	2D	MS, HS

(continued)

Table 1. Continued

Software	Author & Citation	Operating System	Cost	Ease of Setup & Use	Teaching Resources	Topics/ Concepts	Interface	Target Audience
						Divergent Evolution		
Mutation Planet	Scott Schafer (Schafer, n.d.)	iOS MAC OS Windows	Free	Easy	No	Macroevolution Mutation Speciation	2D	MS, HS
Polyworld	Larry Yaeger (Yaeger, 1994)	Linux Mac OS	Free	Medium	No	Microevolution Behavioral Adaptation	3D	HS
Simulink	MathWorks (Crutchfield & Mitchell, 1995)	Linux Mac OS Windows	Paid	Hard	No	Microevolution Macroevolution	Text	UG
Tierra	Thomas S. Ray (Adami et al., 1994; Ray & Hart, 1999)	Linux Windows	Free	Hard	Yes	Microevolution Natural Selection Speciation	Text	UG
Unified Life Models (ULM)	Stephen Legendre (Legendre & Clobert, 1995)	Windows	Free	Hard	No	Microevolution Macroevolution	Text	UG

more effective learning outcomes. These and other features are discussed below for a selection of computer-based simulators.

○ A Comparison of Useful Evolutionary Software for Teaching

We evaluated a range of evolutionary software, recording our assessment of the ease of installation and the level of supporting documentation (Table 1). Below, we detail nine of these packages, as prior knowledge may assist teachers interested in exploring evolution through software.

1. *Tierra* is a text-based ecology and evolution simulator first developed in 1994 by Thomas S. Ray (Ray, 1994; Ray & Hart, 1999). It demonstrates coevolution, population equilibrium problems, and natural selection. It has a command line interface, which may intimidate some students unaccustomed to a command line terminal or any other text-based environment. The documentation is extensive but also complex, so the startup costs are high and the learning curve is steep. Some advanced (and patient) college undergraduates in evolutionary biology programs could use *Tierra* as a historical example or as a scaffold for building their own simulator.
2. *Avida* is a modern graphical version of *Tierra*. As in Conway's *Game of Life*, each pixel is an organism colored by fitness in a digital Petri dish (Adami et al., 1994; Ofria & Wilke, 2004). Evolutionary parameters are customizable, ranging from dish size, mutation rate, presence or absence of nutrients, organisms' spawn location, iteration length, and two different randomness models. Demo and experimental modes control the degree of randomness, with demo mode allowing precise repeatability of experiments. The straightforward user interface includes a graph showing average fitness, average gestation time, number of organisms, and average metabolic rate. *Avida* also exports data in Excel format for more customized or advanced plotting. These graphical outputs are useful for understanding the experiments, as well as giving students practice reading and analyzing graphs. Overall, *Avida* is an easy-to-use simulator readily adaptable to teaching evolution in the classroom, ranging from high school AP biology to introductory college biology.
3. The *Simulink* environment, produced by MathWorks, is a visual programming suite for modeling, simulating, and analyzing complex and dynamic systems. There are multiple libraries for *Simulink* that include optimization tasks. One such optimization task is the genetic algorithm, which has been applied to the field of evolutionary A-life simulators through the use of cellular automata (Mitchell et al., 1993; Das et al., 1994; Crutchfield & Mitchell, 1995). Though highly customizable, *Simulink* and its accompanying libraries require both a license and facility with the MATLAB programming language, with no quick-start immersion into evolution. This makes it more suitable for teaching evolution to advanced and more quantitatively minded undergraduate students willing to learn the finer points of MATLAB.
4. The Howard Hughes Medical Institute (HHMI) provides resources to teachers at no cost, including "biointeractive" computer programs that teach evolution in a variety of pedagogical ways. HHMI's *Lizard Evolution Virtual Lab*, which explores anole lizards of the Caribbean (based on work by Losos et al., 2004; and Kolbe et al., 2012), is one of the most sophisticated virtual-evolution software packages. The lab

teaches evolution through observation, measurement, and virtual experimentation that emphasizes scientific investigation as a process. Each of the four modules explores various concepts in evolutionary biology. Module 1, "Ecomorphs," explores adaptation and natural selection. Module 2, "Phylogeny," introduces convergent evolution through DNA sequence comparisons. Module 3, "Experimental Data," employs analysis of experimental data to measure the fitness of traits in a new habitat. Module 4, "Dewlap Colors," investigates reproductive isolation of newly formed species. All the modules involve, to some degree, measuring and/or collecting data and performing analyses on the data. Some of these analyses use statistical tools to quantify variations in the data you collect and describe the significance of these results. *Lizard Evolution Virtual Lab* is used widely enough that there are a multitude of resources that can tie the modules to testable classroom curricula. Consider using these HHMI modules for introducing evolution to both middle school and high school students via observation and simulated data collection.

5. *Biomorphs* is based on concepts presented in some of Richard Dawkins's books, such as *The Blind Watchmaker* and *Climbing Mount Improbable* (Dawkins, 1986, 1997). The foremost of these concepts is that evolution is a process occurring in gradual steps rather than extremely drastic ones. In *Biomorphs* this is demonstrated by stick creatures that have slight variations in their stick features between generations (Smith, 1991). Any drastic change would take multiple generations to obtain. We wouldn't recommend it as a population-level simulator, but you can use it to illustrate incremental changes in phenotype as a quick visual aid for high school students.
6. *Darwin Pond* is a simulation of a population of aquatic creatures, called "swimmers," searching for food and love. What stands out about *Darwin Pond* is its customizability. These creatures and their environment can be engineered, from mutating them by zapping to cloning them and even inserting random swimmers. You can adjust overall life span, mating requirements, how much food there is in the pond, and reproductive fitness. The swimmers are customizable in the engineering tab where you can tweak up to 15 traits. Some of them are purposely cryptic and others are more straightforward. One of the buttons lets you get information about the swimmers (length of limbs, number of limbs, energy level, age, and so on), which can help elucidate patterns when you are looking at what is fit or unfit. A variety of environment modes allow the user to further customize gameplay. The environment "Garden of Eden" places food in a variety of patterns to model the effects of resource allocation on trait fitness. Race mode sets a chain of food with a clump in the center and organisms from two populations, one at each end of the chain, race to the center. You can have food automatically replenish, or deactivate food replenishment to model the environmental pressure of famine. It's suitable for a wide audience range because it is simple enough to get started quickly yet also customizable enough for advanced users from middle school to college undergraduates.
7. *GenePool*, developed by Jeffrey Ventrella (2005), is another evolutionary simulation that explores locomotion in the context of seeking either food or a mate. This is a refreshed, modernized version of *Darwin Pond*. Gone are the buttons in the little virtual lab; they are replaced by straightforward menus. Now you can now control mate preference with 10 different options, and intended direction of motion is also indicated – you can see where the bots want to go. When two bots have arrows pointing toward each other, they are attempting to mate. The less mobile neighbors still want to go places (intention) even though they cannot (action), and the arrows let you see that some traits will affect locomotion. In some ways there are fewer default environments, but you can save a pool and still build your own using the empty pool to start fresh. You can't turn off food but can change the rate of food regeneration. The names of the genes are more abstract in this version to allow the opportunity for students to deconvolute gene function. This simulation software has also been enabled for iPads as an iOS app called *Gene Pool Swimbots* from Wiggle Planet LLC (Ventrella, 2015). The recommended age group ranges from middle school to high school.
8. *Unified Life Models* (*ULM*; by Legendre & Clobert, 1995) is good for modeling existing population data. Data include population and reproductive data for palm trees, grizzlies, fruit flies, vultures, black-headed gulls, and bighorn sheep, which may inspire budding field biologists. *ULM* employs graphing functions that describe various life-cycle patterns. Like *Simulink*'s evolutionary libraries, *ULM* doesn't necessarily model evolution out of the box, but it could be configured to do so by editing the *.ulm files. This makes *ULM* fairly user unfriendly and geared to more advanced, statistics-minded college undergraduates investigating life-cycle processes through the lens of statistics.
9. *Mutation Planet* by Scott Schafer is another program that is available on iOS (Schafer, n.d.). Simple sets of behavioral clusters are inherited in tiny, asexually reproducing, yet capable-of-undergoing-mutation creatures that eat, fight, replicate, and die in a virtual ecosystem. This ecosystem takes the form of a very small aquatic world, with options to adjust the randomness and frequency of several environmental conditions. A distinguishing feature of *Mutation Planet* allows you to track the genealogy of your critters by mapping their genomes into a detailed phylogeny, or family tree. You can add your own custom sequences of behavior genes to the population or just let them evolve naturally. There are also options to track the most alpha organism, to permit cannibalism, and to reveal data annotations that explain gene function. This program is simple enough to be used in a middle school setting but has enough customizable features for more advanced exploration by high school students.

○ Considerations for Future Development

Although the simulators described above offer fairly accurate views of evolution, we would like to suggest several possible improvements that would make them more effective teaching tools. First, the user interface could be improved to meet modern standards in terms of both realistic graphics and intuitive dashboard and control design. Many of the phenotypic traits are subtle enough that they are lost in the primitive graphics. Better graphics would bring more attention to the phenotypic changes that affect fitness. Likewise, many of the early simulators offer an excessive amount of parameters to change the attributes of the simulation itself. This allows for depth of use, but it also complicates the user experience and creates a higher barrier to entry.

The second development should be to gameplay. These simulators are rather passive, which easily leads to user boredom with watching bitwise species multiply on screen. Gameplay could be improved by adding more organism-level conflict, depicting the drama and agony of natural selection. Incorporating more cladistics visualizations would add historical perspective on speciation events in relation to environmental pressures. Adding multiplayer and multispecies support could make the gameplay more conducive to group work in the classroom.

As mobile computing gains widespread use and acceptance in the classroom, educational simulators will continue to migrate to portable platforms. The current shortcomings in user experience and gameplay will undoubtedly be resolved (over time) with this migration to mobile apps. By design, given the technical specifications and user expectations, mobile apps can simplify and refine the gameplay of these often kludgy evolutionary simulators. Thankfully, a number of new mobile-based evolutionary simulator apps have been released in the past three years, including *Evolution* (Donyagard, 2017), *Cell Lab Evolution* (Säterskog, 2016), and *Gene Pool Swimbots* (Ventrella, 2015). At the time of this writing, these apps have been downloaded by more than 50,000 users on the Google Play Store (https://play.google.com/store/apps/).

The difficulty of improving the edutainment quality of these simulators is in balancing the trade-off between gamification (fun) and simulation (education). With more user input and control, the amount of randomness that guides evolution goes down. Indeed, with too much user participation, these "simulations" would verge on Lamarckian at best and creationism at worst. Finding a fair balance between these competing approaches will be the crux of further development in this field.

○ Conclusion

What is the next frontier in using software to teach evolutionary process? Classrooms are by no means universally equipped with computers. Yet as access to PCs, laptops, and mobile devices becomes more pervasive in the classroom, the potential for simulations to teach evolution will undoubtedly expand. As organisms are replaced with pixels, as computer memory stands in for food, and as probability expressions are used to simulate the randomness of dynamic populations, evolutionary simulators can provide students with an accurate representation of evolutionary process. The interactive and immersive nature of these simulators will allow them to take the place of passive teaching.

References

Adami, C., Brown, C.T. & Kellogg, W. (1994). Evolutionary learning in the 2D artificial life system 'Avida.' *Artificial Life IV: Proceedings of the Fourth International Workshop on the Synthesis and Simulation of Living Systems*. Cambridge, MA: MIT Press.

Bloom, B.S., Engelhart, M.D., Furst, E.J., Hill, W.H. & Krathwohl, D.R. (1956). *Taxonomy of Educational Objectives, Handbook I: The Cognitive Domain*. New York, NY: David McKay.

Bonwell, C.C. & Eison, J.A. (1991). Active learning: creating excitement in the classroom. 1991 ASHE-ERIC Higher Education Reports. http://eric.ed.gov/?id=ED336049.

Crapuchettes, D. (2014). Evolution. https://www.northstargames.com/collections/strategy-games/products/evolution.

Crutchfield, J.P. & Mitchell, M. (1995). The evolution of emergent computation. *Proceedings of the National Academy of Sciences USA*, *92*, 10742–10746.

Das, R., Mitchell, M. & Crutchfield, J.P. (1994). A genetic algorithm discovers particle-based computation in cellular automata. In Y. Davidor, H.-P. Schwefel & R. Männer (Eds.), *Parallel Problem Solving from Nature—PPSN III* (pp. 344–353). Lecture Notes in Computer Science 866. Berlin, Germany: Springer.

Dawkins, R. (1986). *The Blind Watchmaker: Why the Evidence of Evolution Reveals a Universe without Design*. New York, NY: W.W. Norton.

Dawkins, R. (1997). *Climbing Mount Improbable*. New York, NY: W.W. Norton.

Donyagard, K. (2017). Evolution by Keiwan. https://keiwan.itch.io/evolution.

Klein, J. (2003). BREVE: a 3d environment for the simulation of decentralized systems and artificial life. In R.K. Standish, M.A. Bedau & H.A. Abbass (Eds.), *Proceedings of the Eighth International Conference on Artificial Life* (pp. 329–334). Cambridge, MA: MIT Press.

Kolbe, J.J., Leal, M., Schoener, T.W. & Spiller, D.A. (2012). Founder effects persist despite adaptive differentiation: a field experiment with lizards. *Science*, *335*, 1086–1089.

Komosiński, M. & Ulatowski, S. (1999). Framsticks: towards a simulation of a nature-like world, creatures and evolution. In D. Floreano, J.-D. Nicoud & F. Mondada (Eds.), *Advances in Artificial Life*, 261–265. Berlin, Germany: Springer.

Legendre, S. & Clobert (1995). ULM, a software for conservation and evolutionary biologists. *Journal of Applied Statistics*, *22*, 817–834.

Losos, J.B., Schoener, T.W. & Spiller, D.A. (2004). Predator-induced behaviour shifts and natural selection in field-experimental lizard populations. *Nature*, *432*, 505–508. nature.com. http://www.nature.com/nature/journal/v432/n7016/abs/nature03039.html.

Mitchell, M., Hraber, P. & Crutchfield, J.P. (1993). Revisiting the edge of chaos: evolving cellular automata to perform computations. http://arxiv.org/abs/adap-org/9303003.

Nash, J.F. (1950). Equilibrium points in N-person games. *Proceedings of the National Academy of Sciences USA*, *36*, 48–49.

Ofria, C. & Wilke, C.O. (2004). Avida: a software platform for research in computational evolutionary biology. *Artificial Life*, *10*, 191–229.

Ray, T.S. (1994). Evolution, complexity, entropy and artificial reality. *Physica D: Nonlinear Phenomena, 75*, 239–263.

Ray, T.S. & Hart, J. (1999). Evolution of differentiated multi-threaded digital organisms. In *Proceedings 1999 IEEE/RSJ International Conference on Intelligent Robots and Systems: Human and Environment Friendly Robots with High Intelligence and Emotional Quotients*, *vol. 1* (cat. no. 99CH36289). https://ieeexplore.ieee.org.

Säterskog, P. (2016). Cell Lab: Evolution. June 20, 2016. http://cell-lab.net/.

Schafer, S. (n.d.). "Scottschafer/mutationplanet." https://github.com/scottschafer/mutationplanet.

Smith, J.M. (1982). *Evolution and the Theory of Games*. Cambridge, UK: Cambridge University Press.

Smith, J.R. (1991). Designing biomorphs with an interactive genetic algorithm. In *Proceedings of the 4th International Conference on*

Genetic Algorithms (ICGA-91) (pp. 535–538). https://sensor.cs.washington.edu.

Ventrella, J. (2005). GenePool: exploring the interaction between natural selection and sexual selection. In A. Adamatzky & M. Komosiński (Eds.), *Artificial Life Models in Software* (pp. 81–96). London, UK: Springer.

Ventrella, J. (2015). "About the Wiggle Planet LLC Founder and Advisors." Wiggle Planet. September 1, 2015. http://wiggleplanet.com/about/.

Weltman, D. (2007). A comparison of traditional and active learning methods: an empirical investigation utilizing a linear mixed model. Ph. D. dissertation, University of Texas, Arlington.

Yaeger, L. (1994). Computational genetics, physiology, metabolism, neural systems, learning, vision, and behavior or poly world: life in a new context. *Santa Fe Institute Studies in the Sciences of Complexity—Proceedings*, *17*, 263.

LUKE APPLETON (appletonlh@icloud.com) is a Student Researcher and JOSHUA MACKIE (joshuamackie@gmail.com) is a Lecturer, both in the Department of Biological Sciences, San Jose State University, One Washington Square, San Jose, CA 95192-0100.