Replicards: Teaching and simulating evolution with a card-based experiment

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Abstract

The teaching of biological evolution in high schools is often reduced to an account of the history of evolutionary thought. As a result, students assimilate evolutionism more as a philosophical current of thought led by distinguished thinkers than as a fruitful area of scientific research. Often, mere verbal exposition is not enough for students to truly understand evolutionary phenomena, such as natural selection and genetic drift, and their statistical origins. Therefore, we have developed an interactive lesson in which students simulate evolution through a card game, the *replicards*, and are introduced to a computer simulation of evolution. The results are analyzed in the classroom, and students are asked to try to explain them. We tested this approach independently with two classes at the Salesian Institute S. Ambrogio in Milan, Italy. With our help, the students reasoned and rediscovered the mechanisms of evolution, and only then did we introduce the scientific terminology used to describe them, such as mutations, selection, and genetic drift. We propose using *replicards* to make the teaching of evolution more focused on understanding phenomena rather than merely memorizing authoritative opinions.

1. Introduction

In his presidential address at the 1964 meeting of the American Society of Zoologists, Theodosius Dobzhansky famously said that "nothing makes sense in biology except in the light of evolution" (Dobzhansky, 1964), a sentence that later became the (slightly modified) title of one of his essays (Dobzhansky, 1973). In his speech, he noted that the ability of living things to survive and reproduce is an "improbable" natural phenomenon and that "how life has managed to overcome this improbability [...] may well be used as the framework on which to build the teaching of biology". *Evolutionary thinking* is presented as the unifying intellectual tool that allows us to understand biology across all its levels of complexity, from the molecular to the ecological. Six decades later, the centrality of evolutionary thinking in biological research is undisputed. Nevertheless, the same cannot be said of the teaching of biology, where, especially in high schools, Dobzhansky's dream seems particularly far away (Hillis, 2007). High school students

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usually learn biology by facing a series of poorly connected levels of organization (biochemical, cellular, anatomical, etc.), each requiring the memorization of an arbitrarily large number of details and facts. Evolutionary biology is taught as just one of many topics, instead of the framework in the light of which biology can be made sense of (see e.g., Nehm et al., 2009). As a consequence, it is often reduced to a mere account of the hypotheses of eminent thinkers of past centuries. While such an exposition is necessary if the aim is to teach the history of biology, it cannot replace the need to teach evolutionary biology as a thinking tool, as Dobzhansky advised. Modern evolutionary biology describes evolution in *statistical* terms (Fisher, 1958; Gillespie, 2010), which can be understood logically but only with deep reasoning, especially when encountered for the first time. To do justice to biological evolution (and therefore to biology), we encourage teachers to shift the focus from memorizing historical views to *reasoning and understanding*.

It is worth noting that similar efforts are being made at the university level to teach evolution as an integrative framework for understanding all levels of complexity in biology, making it easier for students to retain and connect the variety of covered topics (Gaiser and Roberts, 2022; Alles, 2001). As a concrete contribution in this direction, we developed an interactive class where students participate in an active learning experience that involves reproducing patterns on cards called *replicards*. The experience is not meant to be an exhaustive explanation of all the aspects of biological evolution. Rather, the idea is to guide students to autonomously rediscover several key mechanisms, such as natural selection and genetic drift, in an attempt to explain the results emerging from the collective simulation in which they have engaged. We tested the *replicards* with high school students in Milan, Italy, without mentioning that it had anything to do with biology. The experiment was successful in that students developed and used *evolutionary thinking* spontaneously to explain the results in their own words. At that point, we could teach biological evolution by naming the principles they rediscovered ("mutations", "fitness", "selection", "drift", etc.), allowing them to appreciate the logic behind those terms. Overall, we think the *replicards* proved to be a useful teaching device, perhaps one to build and expand on in the future. This article explains how the *replicards'* simulation works and what happened when we used it to teach evolution to high school students.

2. In-class collective simulation of evolution

2.1 Overview

The *Replicards* experiment involves students reproducing patterns on cards they were individually given. Each card displays a 7x7 grid on which cells can be marked with a pencil to form a pattern (Figure 1). At the beginning of the experiment, each student in the classroom has a deck of blank cards (cards with an empty grid) and one card with a pattern, called the template card. They are asked to memorize the template before turning the template card face down and to reproduce it on as many empty cards as possible. After a fixed amount of time, all the replicas produced are collected into a bag. Each student is assigned a new template, randomly selected from the bag of collected cards, and the process is repeated a few times (see Protocol for more details).
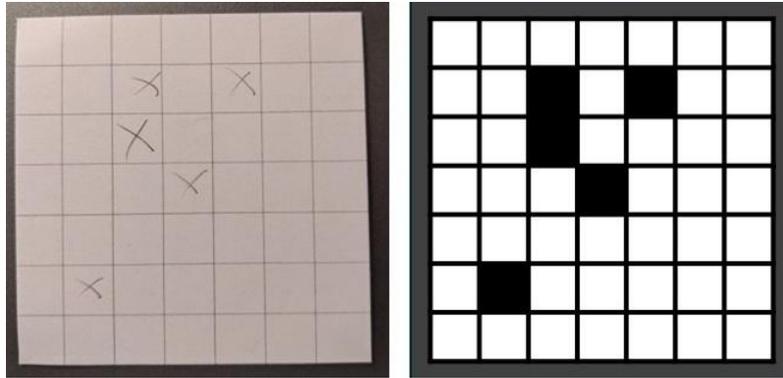
Figure 1: Example of a pattern that can be encoded in a *replicard*. On the left, the picture of the physical *replicard*; on the right, the corresponding schematic representation.

The goal is to allow a class of students to collectively simulate evolution by natural selection by keeping track of the frequency of each pattern across the different iterations of the experiment, aptly called *generations*. The change in frequency of each pattern across generations can be due to chance, mirroring genetic drift, or because some patterns can be more efficiently replicated than others, mirroring selection. In this context, a pattern that is hard to replicate has lower reproductive success, that is, lower fitness, and therefore, its frequency tends to decrease over generations. The errors that students can make while replicating their template simulate mutations.

2.2 Protocol

The experiment consists of repeating the same procedure several times. Each iteration was called a *generation*, and it is organized as follows:

1. **Memorization Phase** (10 seconds):

   The template card is provided face down to each student. For 10 seconds, students can look at their template card before turning it face down again.

2. **Replication Phase** (30 seconds):

   Students have 30 seconds to replicate the template's pattern onto blank cards as many times as possible. Rotated or translated versions of the original are considered correct replicas.

3. **Competition Phase**:

   The template cards are put aside in a pile (see next step). All replicated cards are collected into a bag and shuffled. Each student is then assigned a new template card randomly selected from the bag. All the remaining cards in the bag are put aside and do not contribute to the next generation. This step ensured that the population size remains constant.

4. **Recording Results**:
   The teacher records the number of each type of pattern in the pile of used template cards to track the frequency of the patterns over time.

2.3 Students simulate evolution by natural selection

At the end of each generation (i.e., iteration of the protocol), all the template cards are set aside. Therefore, at the end of the experiment, it is possible to count the number of copies of each pattern that were present in each generation by examining the corresponding pile of cards. The set of template cards at a given generation (always one card per student) was referred to as the *population*. It is possible to observe changes in population composition as the frequency of the patterns changes over time. The students are challenged to explain the observed changes in the frequency of the various patterns, without being taught any concept of biological evolution. Only after they explain, in their own words, the possible reasons for the observed changes are they introduced to the terminology used in evolutionary biology. Table 1 summarizes the key evolutionary concepts that the *replicards* experiment can simulate

Table 1: Main evolutionary concepts that the *replicards* experiment can simulate.

Evolutionary concept	Classroom simulation
Fitness	The average number of copies of a given pattern that students can make during the 'replication phase' (30 seconds)
Selection	The change in the relative frequency of a given pattern due to how effectively it is replicated by the students
Drift	The change in the relative frequency of a given pattern due to chance
Evolution	The observed overall change in frequency of the different patterns
Mutations	Errors made when reproducing the patterns
Population	The set of all the template cards in a given generation
Population size (i.e., carrying capacity)	The number of template cards at each generation (i.e., the number of students in the classroom)
Generations	Iterations of the protocol
Phylogenesis	Appearance of new patterns that are modified versions of similar pre-existing patterns

2.4 Proof of concept

We crash-tested the *replicards* experiment with high school students of the Istituto Salesiano S. Ambrogio in Milan, Italy. As a proof of concept, we report here the results from the first class (results from other classes were very similar), which involved 24 students. We prepared the first 24 template cards and distributed them to the students face down. Those cards could represent one of three patterns, distributed in equal numbers (8 template cards each). The patterns are shown in Figure 2.
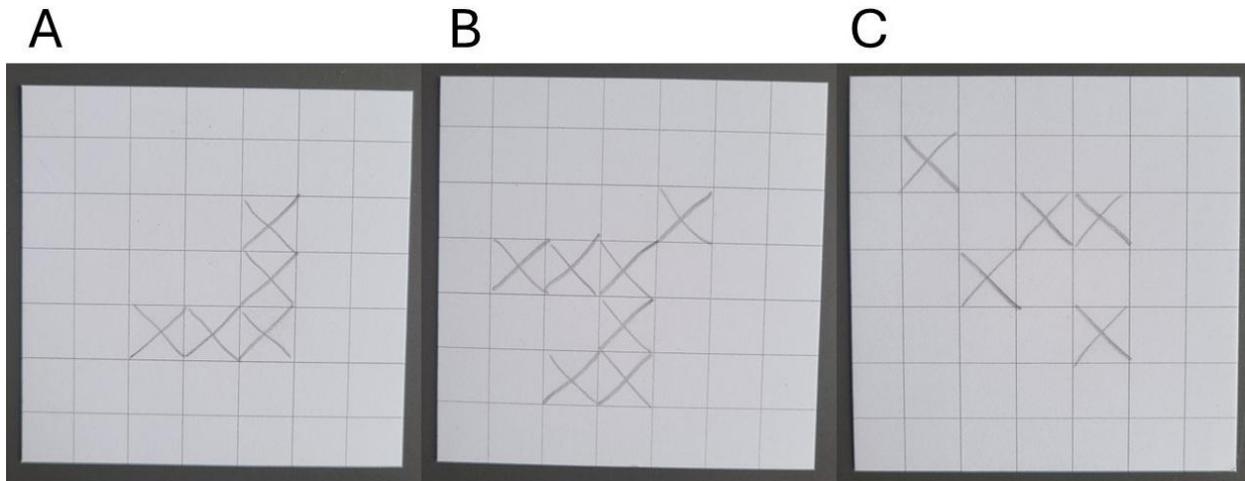
Figure 2: The initial *replicards* provided to the students (generation 0) all belong to three types shown here: patterns A, B, and C.

The protocol was conducted for three generations. Only at the end of the process did we reveal to the students that the templates were initially of three types only, and we drew the three patterns on the blackboard, naming them A, B, and C. We (the instructors) kept aside the templates from each generation in separate piles. By counting the number of correct copies of each pattern in each generation, we produced a table showing the change in the frequency of each pattern over time (see Table 2).

Table 2: Frequency of each reproduced pattern across generations.

Generation	A	B	C
0	8	8	8
1	16	1	2
2	21	1	0

The results can also be visualized as a line plot on the classroom whiteboard or by running the computer simulations (Figure 3) detailed in Section 3.
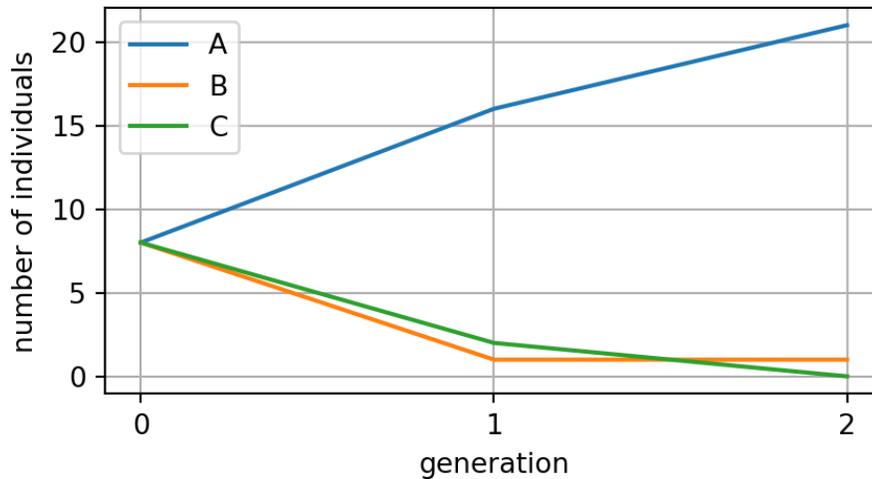
Figure 3: Frequency of each reproduced pattern across generations visualized as a line plot.

2.4.1 Students rediscover principles of biological evolution

The students were asked to comment on the results. One student noticed that pattern A steadily increased in frequency. Another student reasoned that the success of pattern A was likely because it was easier to copy than patterns B and C, and that, as a result, more copies of A were produced at each generation. Therefore, the bag ended up containing many cards with pattern A, making it more likely for students to receive A as their next template card in the following generation. This hypothesis was confirmed by inspecting the cards discarded at each generation, with most of them being instances of pattern A. This way of reasoning, from a student who had not previously been exposed to evolutionary biology, mirrors the discovery of the statistical phenomenon of evolution by natural selection.

We asked students to look for some odd patterns in the numbers reported in the table. One student pointed out that the total number of cards in each generation should be 24, and that that was the case for generation 0, but not for generations 1 and 2. After some hesitation, someone proposed that the missing cards had a pattern that was none of the three original ones (A, B, and C), which could have been generated due to mistakes in the copying process. This hypothesis was confirmed by inspecting the piles of template cards that were stored (each generation in a separate pile). As predicted by the student, we identified such different cards, which we termed *mutants*. When accounting for the mutants, the total number of cards per generation turned out to be 24, as initially expected. Thus, we updated the table to group all mutants into a single category, indicated by the letter X (see Table 3).

Table 3: Frequency of each reproduced pattern across generations, including mutants.

Generation	A	B	C	X	Total
0	8	8	8	0	24
1	16	1	2	5	24
2	21	1	0	2	24

By more closely inspecting the mutants, it became apparent that they were all modifications of pattern C. This is not surprising, since pattern C was allegedly the hardest to memorize and reproduce, thus the most likely to be copied incorrectly. The mutants were named with the letter C (the ancestral pattern) followed by Greek letters. The mutants that were present in the population at each generation are shown in Figure 4.
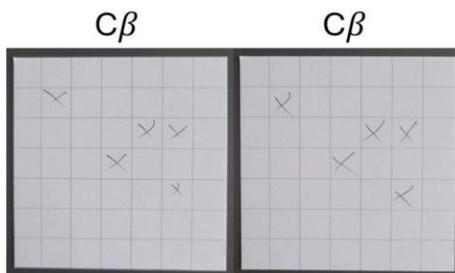
Mutants in generation 1
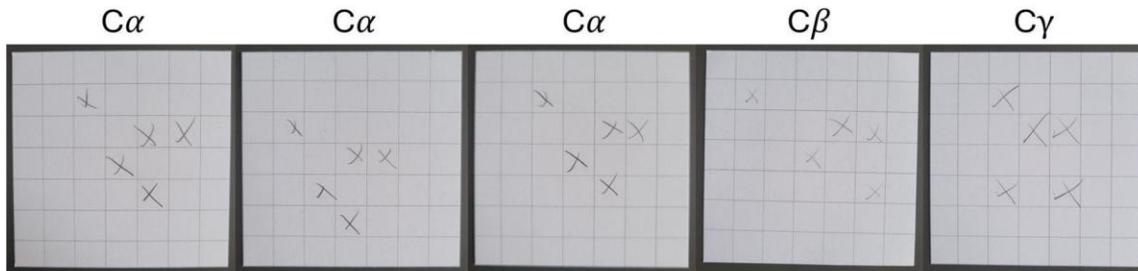
Mutants in generation 2

Figure 4: Pictures of the mutant patterns produced by students across generations. Three types of mutants appeared (Cα, Cβ, and Cγ).

We tracked the relatedness among pattern types across generations by constructing a *phylogenetic tree* of the *replicards*, as shown in Figure 5. Both Cα and Cγ went extinct. This is not surprising since they are similar to pattern C, which showed a low reproductive success (low fitness).
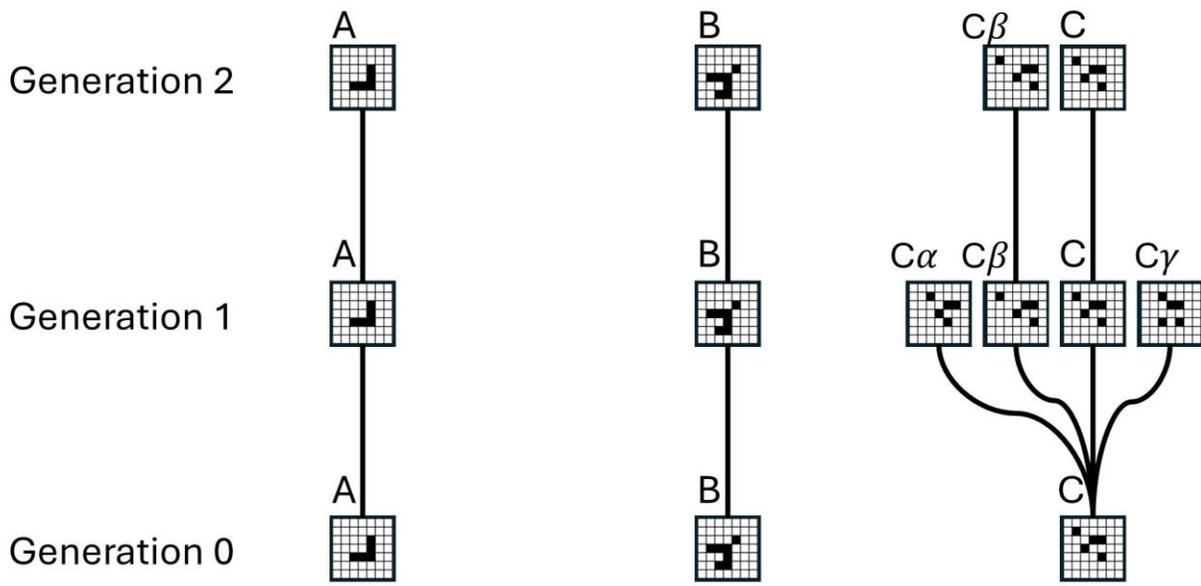
Figure 5: Phylogenetic tree of the *replicards*.

Overall, this interactive class helped students understand the logic behind several key mechanisms of evolution (see Table 1). We then integrated the in-class discussion by transferring the learned principles to the case of actual biological evolution. For example, we noticed that not every modification qualifies as a mutation. A difference in which cells of a *replicard* grid are marked is a *mutation* because it can be inherited, while other modifications, like a bent corner, are not.

3. Computer simulations

In principle, the *replicards* can be used to provide an even more advanced understanding of biological evolution. For example, the students were asked if the evolution of the *replicards'* patterns over generations is predictable, and they correctly answered that it is only partially predictable, due to a certain degree of randomness in the process. Thus, we asked if a smaller population size (6 students instead of 24) would have made the outcome more predictable or less predictable. Correctly answering this question requires an intuition for the balance between selection and drift, a more advanced concept in biological evolution. Questions like this one could be investigated empirically by performing the experiment under different conditions and then trying to interpret the results. However, that would be extremely time-consuming. As an alternative, we developed computer simulations that can be used to experiment with such parameters (such as population size) and run the simulation as many times as necessary. In this way, the virtual *replicards* can complement the results obtained with the physical ones, which are more constrained by time and resources. We simulated the virtual *replicards* in the programming language Python and made the code freely available (see Materials and Methods).

4. Materials and Methods

4.1 Physical *Replicards*

The *replicards* were 7 x 7 square grids (of size 7 cm x 7 cm), printed on thick paper. The cross marks on the cells were drawn by the students, using pencils.

A printable PDF file containing blank square grids and grids with the three patterns we used (patterns A, B, and C) is available at https://replicards.netlify.app/images/PrintablePatterns.pdf.

4.2 Virtual *Replicards*

The code for the simulations was written in the programming language Python and is freely available at https://github.com/eliamascolo/replicards.
It can be directly installed via Anaconda (https://anaconda.org/eliamascolo/replicards) or pip (https://pypi.org/project/replicards/).

5. Conclusions and future directions

Overall, the *replicards* were a successful and rewarding teaching experiment. We rehearsed the process in advance to ensure effective time management and a smooth experience for the students. The result was fun and engaging, but also very effective at prompting students to rediscover evolutionary principles by reasoning. Witnessing students explaining in their own words why we could have expected pattern A to become more frequent over time, unknowingly rediscovering the principle of natural selection, was certainly a highlight of this teaching experience. Future directions may involve broadening the scope of the activity by including other aspects of biological evolution or by developing a graphic interface for the virtual *replicards*, which would also benefit teachers who might not be familiar with running computer code. Perhaps a digital version as a mobile application for touchscreen devices could enable a faster procedure, which could then be run for a larger number of generations, given that steps involving the collection, counting, shuffling, and redistribution of cards would then be automated. We hope that the experience we have reported in this article, as well as the protocol and the computer code provided to reproduce it, will contribute to a global effort to teach evolution as a science and as a thinking tool to understand biology, rather than being limited to a verbal exposition of the opinions of illustrious contributors.
In the words of Seymour Papert, "The role of the teacher [should be] to create the conditions for invention rather than provide ready-made knowledge".

6. Acknowledgments

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