# When Citizen Science meets Teaching: A storified citizen science computer game to teach and contribute to genomic data analysis

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**Abstract:**
Video game is a versatile and powerful media to communicate and engage the public in life science research and education, where it is increasingly used as a teaching support tool in higher education. At the same time, video games are also becoming common vehicles for citizen science initiatives in molecular and cell biology that allows participants to contribute to real scientific data analysis. Since 2010, our citizen science game Phylo (http://phylo.cs.mcgill.ca) enlists internet users in comparative genomic data analysis. Although it was not its initial purpose, Phylo also quickly became a popular resource for biology instructors.
Here, we introduce a new release of Phylo and its web platform for advanced users OpenPhylo, which have been redesigned to facilitate educational uses. Phylo now features a story mode that progressively introduces basic comparative genomic concepts to the participants and allow them to contribute to improve the alignment of real DNA and RNA sequences. We also implement new roles and functionalities in OpenPhylo that enable instructors to easily create, invite, and monitor progresses of students on assignments using Phylo. Our data shows that our approach promotes student engagement and contributes to support the teaching of basic comparative genomics principles.

# Introduction

Biology and evolution inspired the development of many video games, among which we find Spores (https://www.spore.com/), Plague (https://www.ndemiccreations.com/en/22-plague-inc), Cell to Singularity (https://www.celltosingularity.com/) or Niche (https://niche-game.com/). The successes of these games motivated the development of new approaches for supporting the teaching of biology through video games. Immune Attack and Immune Defense (http://www.molecularjig.com/), Tyto Online (https://www.tytoonline.com/), or Genomic Digital Lab (https://www.spongelab.com/game_pages/gdl.cfm) have thus been developed to enhance the student experience through practice of key concepts presented in the game. Remarkably, the integration of this technology into classrooms has been shown to help students improving their understanding of biology [1] and performance at tests [2]. In general, games are valuable tools to enhance the learning experience [3].

The enthusiasm of the public for video games with a scientific narrative also motivated the development of Scientific Discovery Games (SDG), using real scientific data and designed to engage the participants into research [4]. In the last decade, Foldit [5], Phylo [6], EteRNA [7] or EyeWire [8] gathered hundreds of thousands of online citizen scientists to contribute to the analysis of biological data. Their development offered an opportunity to revisit the visualization and manipulation of scientific data through game design techniques. The novelty and quality of these new interfaces prompted the repurposing of SDGs into professional scientific software [9]. It also very quickly attracted the attention of scientific instructors who saw in these SDGs an opportunity to mobilize students and allow them to engage research while learning [10, 11].

This contribution focuses on our SDG Phylo (http://phylo.cs.mcgill.ca), which is running since November 28th, 2010. Phylo aims to engage the public into comparative genomics research through a casual tile matching puzzle game encoding an instance of a multiple sequence problem. The default gameboard is a 10x25 grid in which we display fragments of genomic sequences as sequences of tiles of 4 different colors representing the 4 nucleotides (i.e., A, C, G, T/U) of a DNA or RNA molecule. Participants move the tiles horizontally but cannot change their order, and their objective is to find a configuration that maximizes a score representing the quality of the alignment of the sequences. At the end of the game, the solutions to these puzzles are stored in our server and later used to help us improving the accuracy of computer-generated alignment of biological sequences stored in public databases (e.g., UCSC genome Browser, Rfam).

The multiple sequence alignment is one of the earliest and still one of the most powerful and widely used computational technique to study the evolution, structure and function of DNA, RNA and protein sequences [12]. In its simplest form, the problem consists in computing a mapping of nucleotides (or amino acids) between several biomolecules that respects the order in these sequences. Yet, the computation of a reliable alignment faces many challenges. Given a scoring function, aligning multiple sequences is a computationally hard problem [13]. Worse, the definition of a reliable objective function to estimate the quality of an alignment remains an unsolved challenge [14-17]. Despite major innovations and undeniable progresses across the years, the problem is still open [18]. Fully automated alignments often contain inaccuracies that require an

expert to manually curate and fine-tune the alignment. Noticeably, popular alignment databases such as Rfam [19] are already semi-automatically collecting improved alignments submitted by their users [20].

A salient feature of Phylo is to push the gamification of the scientific task to its limit. The game is fast, simple, and can be played by any user with no prior knowledge of biology. Participants also do not need to register and can play anonymously. These choices aim to lower the barrier of entry and increase participation. For these reasons, Phylo can reach a wide range of audiences and can be played in short time spans, which also makes it a perfect tool for teaching activities.

Since 2010, hundreds of thousands of web users accessed and played Phylo. Yet, the multiple sequence alignment problem is among the most widely used technique in bioinformatics. It seemed to us unreasonable to concentrate all this public participation into our sole hands. Therefore, in 2013, we decided to open-up our platform and allow external researchers to use our system to solve their sequence alignment problems through crowdsourcing with OpenPhylo [21]. To our knowledge, it is the first time that access to and full control of an SDG has ever been shared to with the entire scientific community.

For scientists, OpenPhylo is introduced as a website that enables them to upload their own sequences. The uploaded sequences are converted to puzzles and introduced to gamers through the Phylo game. Scientists can then track the number of times their puzzles have been played and download at any time an alignment of the sequences improved with the solutions collected by Phylo.

The objective of this work is to bring the concept of OpenPhylo to the next level. Here, our aim is not only to support scientists but also instructors and power users of Phylo as well. Instructors can now use the OpenPhylo platform to create Phylo assignments for their students to allow them to both learn and contribute to real scientific data collection. In addition, new Phylo power users can use the OpenPhylo website to view advanced statistics they would not be able to see in game. These statistics include the number of puzzles they have completed on their account, and a variety of badges showcasing different achievements they've received throughout their playtime in Phylo. These new features aim to promote the long-term engagement of online citizen scientists, but also to offer more feedback to student using the game as a teaching support tool.

This manuscript presents in-depth methods and features of the new version of OpenPhylo, which has been created to support these three groups of users (i.e., Scientists, Instructors, Power users). The paper will also go into detail about the design choices made to keep the platform open, extensible and easy to use.

Furthermore, because Phylo is now specifically targeting the teaching community, we also fully redesigned the user experience and introduce the story mode including tutorial puzzles and real puzzles with progressive levels of difficulty. The story has been developed to introduce keys scientific concepts to the players, and the progression through the game is punctuated with optional quizzes that can be used to test the general knowledge of the player or customized by an instructor to ask specific questions.

# Methods

## Overview

OpenPhylo has been designed to be a meeting point between citizen scientists (i.e., a player of the SDG), scientific instructors, and scientific experts (See Figure 1). We respectively called them “power user”, “instructor”, “scientists”. All three user types can login our system and access the services on the web portal located at http://kovik.cs.mcgill.ca. By default, this unified login system assigns the role of power user, which allows the user to access individual statistics about the SDG activity. Once logged in, the user can request additional roles. The instructors gain the ability to create assignments and invite other power users to complete it, while scientists obtain the privilege to upload their own sequences into the system to be processed by participants. The following sections describe the new features and roles of OpenPhylo.

## Game

### Puzzles and scoring

This new release of Phylo integrates our previous SDG Ribo (See Figure 2). While Phylo focuses on the DNA multiple alignment problem [6], Ribo aims to align structured RNAs (i.e., with a secondary structure annotation) [22]. This new configuration allows us to expand the scope of citizen science activities and propose variations of the multiple sequence alignment problem. In the following, a Phylo user will thus refer to a Phylo and Ribo user.

We also developed simplified and advanced versions of Phylo and Ribo that allows users to practice separately different scoring mechanisms and features of the games. We now distribute two versions of Phylo. The first one is a plain multiple sequence alignment scored with an affine gap model. Match (+1), mismatch (-1) and indel costs (-2 of gap opening and -1 for a gap extension) are identical to those used in previous versions of Phylo [6, 21], where parameters are rounded for transparency and better interpretability by the users. In contrast to the original SDG, this version does not use a phylogenetic tree but a sum of all pairs scoring model, which aims to lower the barrier of entrance for new users. The other version of Phylo distributed on our platform is the classic one that uses a phylogenetic tree and a customized version of the Fitch algorithm for the solving minimum parsimony problem [23].

We also support two versions of Ribo. The first one aims to align RNA sequences with secondary structure annotations. The score is the sum of a sequence score computed as a sum-of-pairs (same scheme as in basic version of Phylo), and a structure score rewarding each aligned base pairs. In the second version of Ribo, the scoring scheme is identical, but the user can edit the base pairing annotation.

These variants of the multiple sequence alignment problem enable us to progressively introduce the users to complex scoring schemes, allowing them to practice on simplifier problems before moving on to more sophisticated ones. It also illustrates the variety of applications of sequence alignment tasks. This collection of related but distinct activities is a necessary step to build a

sequence of activities with progressive difficulty that is suitable for teaching support activities, and further to integrate them in a storyline (See next section).

Phylo and Ribo also feature now a hint mechanism that offers suggestions to the players when they need it (the button is represented as question mark). This functionality aims to help participants that could feel intimidated by the difficulty of some puzzles and thus improve engagement in the activity.

The performance of the participants on each puzzle is rated using a three-star scoring scheme. This system aims to provide additional motivation to complete the tasks at higher level of accuracy and reinforce the acquisition of the concepts introduced in the SDG [24]. The number of stars attributed to the players is determined by the score returned to our servers. If the score is close to or above the highest score stored so far, the user receives three stars. By contrast, if this score is equal to the baseline (i.e., the “Par” score that is obtained as the score of the alignment computed by automated methods), then the player receives one star. In the other cases, the player receives two stars.

## Story mode

Phylo and Ribo puzzles are now integrated into a story and a roadmap (See Figure 3). In previous versions of Phylo, the participants requested puzzles based on a difficulty level or associated disease. Each puzzle was played independently from the other. By default, the new version of Phylo offers the participants to engage the SDG through a story that introduces puzzles by increasing levels of difficulties. The story serves several purposes. The first one is to make the activity more fun and entertaining. Next, the story enables us to progressively introduce key concepts for computing accurate sequence alignments such as the scoring of mutations and indels, the use of phylogenetic trees, or covariations in RNA alignments. It also allows to walk the players through a tutorial describing techniques and giving tips for building good alignments. Finally, it is a flexible framework to introduce other education activities such as quizzes.

The story is based on a sci-fi scenario where humans try to re-colonize earth after leaving it a long time ago because of environmental issues. This plot aims to bring more purpose to the activities but also to highlight the complexity and broad impact of environmental challenges. Yet, the humor and far future timeline intends to prevent dramatization that could impact the pedagogical objective of our SDG.

The story includes 9 chapters. Each chapter brings a new piece of information and introduce a new evolutionary biology concept. Five of them feature puzzle activities. Chapter 2 introduces the general concept and modeling of multiple sequences alignments. Chapter 3 explains how a phylogeny can help making better alignments. Chapter 6 moves to RNAs and secondary structures. It describes the principle of co-variation and how to use it to align structures molecules. Chapter 7 expands this concept and proposes to the participant to edit the RNA structural annotations (i.e., base pairs) to improve the accuracy of RNA alignments. Finally, chapter 8 summarizes all concepts of the game. These chapters start with a tutorial describing the mechanisms of the alignment and conclude with a badge materializing the achievement of the participant. An optional quiz is also available at the beginning to test the knowledge of the user. Stories are available in the 5 languages supported by Phylo (i.e., English, French, Spanish, Chinese, Russian).

## Quizzes

Quizzes are new activities available in the story mode of Phylo (See Figure 4). Unlike the puzzles, the answers to the quizzes submitted by the participants are not used to annotate or classify any scientific data. But they fulfill two other functions. First, they increase the diversity of the tasks, which enrich the user experience and entertaining value of the SGD. Next, they offer an additional tool for instructors that are using Phylo as a teaching support tool.

Currently, quizzes are optional and offered to the player before starting the citizen science activities (i.e., the puzzles). The questions are related to the chapter they are belonging to, but not necessarily directly connected. They rather aim to test general knowledge in the field of genomics rather than specific concepts introduced in the game. As such, an instructor needs to separately provide this information if the quizzes are used for an evaluation.

## Badges

Badges are collectible items that symbolize milestones in Phylo. The participants that successfully complete all activities in a chapter featuring puzzles of Phylo or Ribo receive a badge associated with the theme of this chapter. Other badges are delivered for global achievements such as a total number of puzzles successfully completed or the first a time a user obtains a 3-star rating (i.e., reaches a high score). Figure 5 shows three of these badges currently implemented in our system. To avoid redundancy, we do not enable instructors to create their own new badges. However, we accept requests to create new ones.

Badges are efficient tools to improve user retention in learning games and a key component to keep gamers engaged [25, 26]. For an educator, it also is a convenient tool to define the objectives and track the progresses of the students.

## Courses and Assignments

Courses and assignments are the novel teaching-oriented functionalities proposed by OpenPhylo. A course is a general structure in which an instructor can organize several assignments on a particular topic and register students in their course. Assignments are the main feature of Phylo as a teaching supporting tool. They are sets of instructions that a student must complete.

In OpenPhylo, there are two types of assignments: a classic assignment and a story mode assignment based on the storified version of the SDG. Classic assignments are assignments that revolve around Phylo's classic mode where users can select a disease type and solve random puzzles. These assignments have the option for an instructor to specify the difficulty and number of puzzles that they want their students to complete. They allow students to explore and play the Phylo game without constraint, while instructors can track their progress.

The second type of assignment in OpenPhylo is the story mode assignment, which leverages the new Phylo story mode. It uses a story and road map, already implemented in Phylo, with selected puzzles and quizzes in-between episodes. Instructors can specify which badges from the story mode they would like to use for their assignment.

# OpenPhylo user types

## Power users

Power users are defined as players of Phylo who log in OpenPhylo and access their personal space with detailed statistics about their participation to the project. By default, all registered participants to Phylo (http://phylo.cs.mcgill.ca) have an account on OpenPhylo. Both platforms, Phylo and OpenPhylo, use the same shared database of users and Phylo users can login with the same credentials into OpenPhylo. Though, to reduce spam and fake requests, an email verification step is added to users who log in or register with OpenPhylo for the first time.

Once logged in OpenPhylo, Phylo users can view basics statistics about their contribution to Phylo (See Figure 5). By default, these statistics include the number of puzzles they have solved and the different badges that they have earned. As discussed later, these badges can be used by instructors to set up milestones for students using Phylo as a teaching support tool.

## Instructors

The next group of users supported by OpenPhylo is instructors. This role is open to any power user who wants to access special functions and create assignments for a group of users. Therefore, an instructor must first create a regular Phylo user account first, and then request an upgrade with access to instructor features through an option available in the user sidebar.

Three pieces of information are required to request an instructor status: a full name, an institution, and a field of expertise. This information is only used to help trainees to identify their instructor.

Instructors have several unique functionalities. The first one is the ability to create “courses” through a dedicated form. Each course has a course name, description and require a list of student emails. Once an instructor has created a course, they can then access that courses page. On each course page, instructors have the option to edit a course's details, add assignments and see a list of pasts, ongoing and upcoming assignments. The edit course page allows instructors to not only change the name and description of a course but also to add or remove students. Students are regular Phylo users enrolled into a course by the instructor.

An instructor can create assignments through a button on the home page of a course. They are then presented with a form that asks for an assignment name, description, start date, end date and assignment type (i.e., classic or story-based). Once an assignment created, OpenPhylo send an email to each student in the course on the start date of this assignment (See Figure 6). Then, each student can accept this request and start playing Phylo to complete this assignment. A student already owning a Phylo account can simply use the same account if the email address is matching. Students without pre-existing Phylo accounts must register with their student email.

Once an assignment started, instructors can monitor in real-time the status of each student. Figure 6 shows a status page for a story mode assignment. There, instructors can check whether students have accepted the assignment and the tasks completed. Story mode assignment allow to provide more context, introduce, or recall fundamental concepts, and run quizzes to validate knowledge acquisition about DNA, RNA, and general bioinformatics.

Yet, comparative genomics is a concept relevant to many sub-fields of biology. To accommodate the use of Phylo and OpenPhylo to different context, we allow an instructor to customize story mode assignments, which include the possibility to build a specific level map and specific quizzes.

## Scientists

Scientists make the third category of OpenPhylo users. This role has been introduced with the initial release of OpenPhylo in 2013 [21], but has been improved in this new version. The main purpose of this role is to allow OpenPhylo users to use our platform to improve their own multiple sequence alignments with Phylo. Phylo users can play custom puzzles that scientists upload and receive alignments that can improve on existing state of the art alignments done with tools such as MUSCLE.

Like instructor accounts, scientists are a special user type requiring an additional registration form. The form is similar to the instructor registration form shown before but has the fields: Lab name, research description and keywords that describe their research. Once a user applies to be a scientist, a verification email is sent to the administrators of OpenPhylo to validate the new role. We implemented this validation mechanism to reduce the risks of a malicious user flooding the system with corrupted data. Indeed, our objective is to guarantee the best use of Phylo by the community of researchers.

**Error! Reference source not found.** showcases the workflow for a scientist to create a puzzle. The first step for a scientist is to upload an unaligned FASTA file containing the sequences that they wish to align. Each file must include a maximum of 10 sequences to facilitate the automatic creation of puzzles by OpenPhylo. Yet, in previous work, we developed aggregation methods to align more that 10 sequences. We decided to not implement those in OpenPhylo because of the experimental nature of this work and diversity of settings [6]. Once the FASTA file is uploaded to OpenPhylo, the backend runs a python script that aligns the input sequences with MUSCLE [27]. Since variants of the Phylo game also require a phylogenetic tree, we use IQ-tree to generate a tree from the alignment [28]. Alternatively, scientists can upload aligned sequences in the FASTA file and a phylogenetic tree in Newick format and skip these steps.

Once the initial alignment created, we can create the puzzles. First, the scientists specify the number of puzzles to create. We use heuristics developed in previous studies to determine which regions of the full alignment could be improved with Phylo [6]. Since the maximum length of a sequence in a basic Phylo puzzle is 15, we scan our full alignment with a 15 nucleotide-long window and extract the most promising regions. Currently, OpenPhylo uses a simple heuristic selecting regions with the largest number of gaps and mismatches, which suggest there is room to improvement the alignment.

Once a region is selected, a puzzle is automatically created. Then, we call a recursive function on the left and right side of the region selected to create additional puzzles. This allows us to increase the coverage of this region while preventing overlaps. The process stops when we reach the maximum number of puzzles allowed.

After creation of the puzzles, the scientists can monitor the stats for the puzzles they created (See Figure 7). OpenPhylo calculates sequence specific metrics such as the number of puzzles created, total sequence length, and puzzle coverage percentage. These numbers allow the scientist to get an overview of how much of their sequence is covered by Phylo puzzles. OpenPhylo also calculates an alignment score for both the original alignment done through

MUSCLE as well as the improved version of this alignment computed with the solutions to the puzzles collected by Phylo. The improved alignment through Phylo is found by aggregating the best solution to each puzzle created and replacing the region in the original alignment with the solution. The alignment score is calculated through MUSCLE, which uses a sum-of-pairs score.

# Results

## Usage statistics

The first release of Phylo was launched on November 28th, 2010. The web site remained operational since then. Obviously, the participation varied a lot in the last decade, with peaks of participation at the launch and publication of our first research articles [6, 21]. Here, we report statistics for the period ranging from May 1st, 2018, to April 30th, 2022, which gives a reliable estimate of the current participation.

During that period, 100,842 unique users accessed our website. 72,866 unique users played the game and 9,981 completed a full registration (others played as guest). For reference, more than 76k users registered since 2010. We collected 80,072 solutions to the Phylo puzzles and 10,923 solutions to the Ribo puzzles. In both cases, roughly half of the solutions are obtained from registered users, which highlight the significance of the relationship between registration and engagement.

On April 25th, 2019, we released a mobile version of Phylo. Although the application is still a beta release, it has been installed on 1.4k iOS devices and 6.9k Android devices. Android users had the option to install it from Google Play on their phone, but iOS users could only install it on tablets. This difference explains the difference of statistics between the platforms. Indeed, 90% of the Android installations were on phone.

## User study

We conducted a user study from March 27th, 2022, to April 26th, 2022. We asked 13 students registered in a graduate level bioinformatics course to complete the story mode of Phylo. We created an assignment using the instructor functionalities asking to complete the entire story mode and invited the students to participate. They all completed the entire story during the time allocated and collected all badges associated with chapters 2, 3, 6, 7, and 8.

Then, we asked the students to complete an anonymous survey to describe their experience and rate various functionalities of the game. The participation in the survey was optional and was not affecting the grading in the course in any way. Yet, all students accepted the invitation and provided us anonymous feedback.

First, we asked about the benefits of implementing a story mode. We were interested to assess if the story is entertaining (Q1), instructive (Q2), helps to connect activities together (Q3), and offers an additional incentive to complete the tasks (Q4). On all aspects, the feedback was globally positive. The strongest agreement was obtained on the first question “The activity is fun”, were 6 participants strongly agreed, 4 agreed, 1 was neutral and 2 disagreed. It validates our primary objective that is to make citizen science and teaching activities more entertaining. Though, the 2

disagreements suggest the approach does not suit all participants. On the fourth question “the story gives more motivation”, 4 participants strongly agreed, 7 agreed, and 2 were neutral. Notably, this is the only question where no one disagreed. This result suggests that the story improves engagement. A similar level of agreement was obtained with the third question “the story It helps bridging puzzles together”, where 4 participants strongly agreed, 7 agreed, 1 was neutral and 1 disagreed. Answers to the second question “The story is instructive” are also positive albeit slightly more mitigated. 4 participants strongly agreed, 5 agreed, 2 were neutral and 2 disagreed. It confirms the story effectively introduces key concepts.

Each chapter of Phylo that introduces a new type of puzzle (i.e., chapters 2, 3, 6, and 7) has the same structure. Its starts with slides telling one part of the story and follows with a short tutorial with an optional quiz. Then, the participants play a couple of synthetic practice puzzles before solving Phylo or Ribo puzzles using real data. For each chapter, we aimed to assess the relevance and impact of this presentation of the citizen science activity. We asked the participants if the “tutorial was helpful” (Q1), “the practice puzzles help to understand the task” (Q2), “the puzzles are fun” (Q3), “the 3 stars rating motivates the player to get better alignment” (Q4), and if “the pedagogical objective is clear” (Q5). The results of the survey are consistent among all chapters, and noticeably consistent for DNA (Phylo) and RNA (Ribo) chapters. The strongest agreement was obtained on the fifth question (i.e., clarity of the pedagogical objectives), which supports the effectiveness of our approach. Strong agreements were also observed on questions 1 and 2. These two questions aimed to understand how useful are the tutorial and practice puzzles that have been introduced in this new version of Phylo. Our results suggest that both are equally valuable features. Answers to the third question are positive but exhibit more variance. This is in agreement with our previous observation about the story mode that confirms the activity is fun for the majority of participants but does not necessarily suit everyone. Only question 4 inquiring about the usefulness of the 3 stars rating system was more mitigated. Though, previous citizen science games already validated the effectiveness of this system [29], which led us to think that the benefits of this scoring mechanism could be better leveraged in the story mode.

Finally, it is worth noting that some optional comments mentioned the background music, including one participant who reported that it helped to play more puzzles. This observation suggests that background music could be leveraged to promote engagement [29]

# Discussion

OpenPhylo aims to become a meeting point for citizen scientists, educators, and genomic researchers. We designed a simple web interface to enable its users to complete basic requests such as accessing statistics, create an assignment and invite participants, or use Phylo to ask the citizen scientists to improve an alignment. To achieve this objective, we also embedded the SDGs Phylo and Ribo in a story game where participants can progressively learn the principles of sequence alignment and key concepts in comparative genomics and evolutionary biology.

This new release is a major step in the evolution of our SDG Phylo. It proposes an integrated view of citizen science in research and education at the internet era. Yet, the platform is still under active development and this work constitutes a proof-of-concept that will be refined in upcoming years. Importantly, we emphasize that the story and instructor tools are not intended to be a

substitute but rather an additional tool to support educational activities and engage more participants in genomics.

The results of our user study validate the relevance and effectiveness of our approach. In particular, the story appears to be a powerful vehicle to introduce and explain key concepts in comparative genomics. But this user study also revealed areas of improvement and possible limitations. Among them, we note that a gamified approach might not suit a minority of students more inclined toward classical methods. This observation suggests that participation to citizen science activities in a class should remain optional. The three stars rating system also provided less motivation to achieve high scores than we hoped. Although, we believe this aspect could be improved if we make the star ratings more visible and integrated within the story mode. Interestingly, users mentioned features that have a greater impact than we anticipated. In particular, the background music appears to improve engagement. Yet, we acknowledge that it may not be a universal rule and that users should be allowed to customize it.

The introduction of a story mode together with the instructor interface created a promising synergy. Our experience suggests that further development should tap into the potential of this system. Currently, Phylo proposes a single and immutable story. The same observation holds true for the quizzes and badges that are predefined. We anticipate that instructors may benefit of customizing or even editing the story, quizzes, and badges for their teaching activities.

The development of a mobile version of Phylo is another a major milestone, which aims to facilitate access to our SDG and lower the barrier of entry. This evolution of Phylo is an attempt to be more inclusive and to offer a more equitable access to students who may not have immediate access to a computer.

The scientist interface could also be improved to allow researchers to better exploit the potential of Phylo for improving alignments. This includes the expansion of processing tools (i.e., preliminary alignment of the sequences, different methods of aggregation of the solutions), increase of number and length of sequences that can be submitted, and more control to create the puzzles. But the most significant improvement could be to automatically grant privileges of scientists to instructors in order to allow them to create customized puzzles for their students.

Finally, the concepts introduced with OpenPhylo could be expanded to other massive citizen science initiatives such as Borderlands Science [30], and could contribute to support the promotion of a public understanding of genomics in our society.

# Availability

Phylo is freely available at http://phylo.cs.mcgill.ca or as a mobile application in the Apple store and Google Play. OpenPhylo is also freely available at http://kovik.cs.mcgill.ca.

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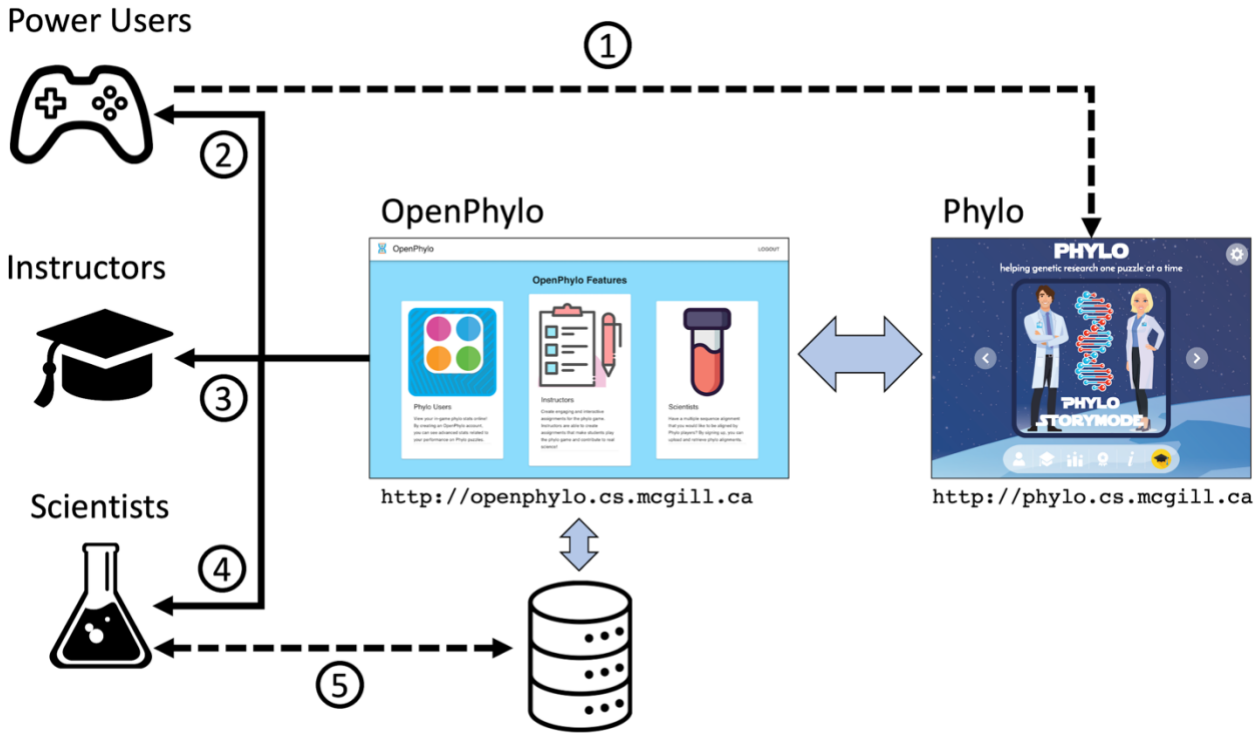



*Figure 1: System overview. (1) Power users (a.k.a. citizen scientists) play Phylo, and (2) connect to OpenPhylo to access personal statistics. (3) Instructors connect to OpenPhylo to create assignments and invite power users. (4) Scientists connect to OpenPhylo to (5) upload sequences to the puzzle database and download solutions from participants.*

*Figure 2: User interfaces of the scientific discovery games. (left) Phylo DNA puzzle interface featuring a phylogenetics tree. (right) Ribo RNA puzzle interface with base pairs represented as arcs on the top of the game board.*

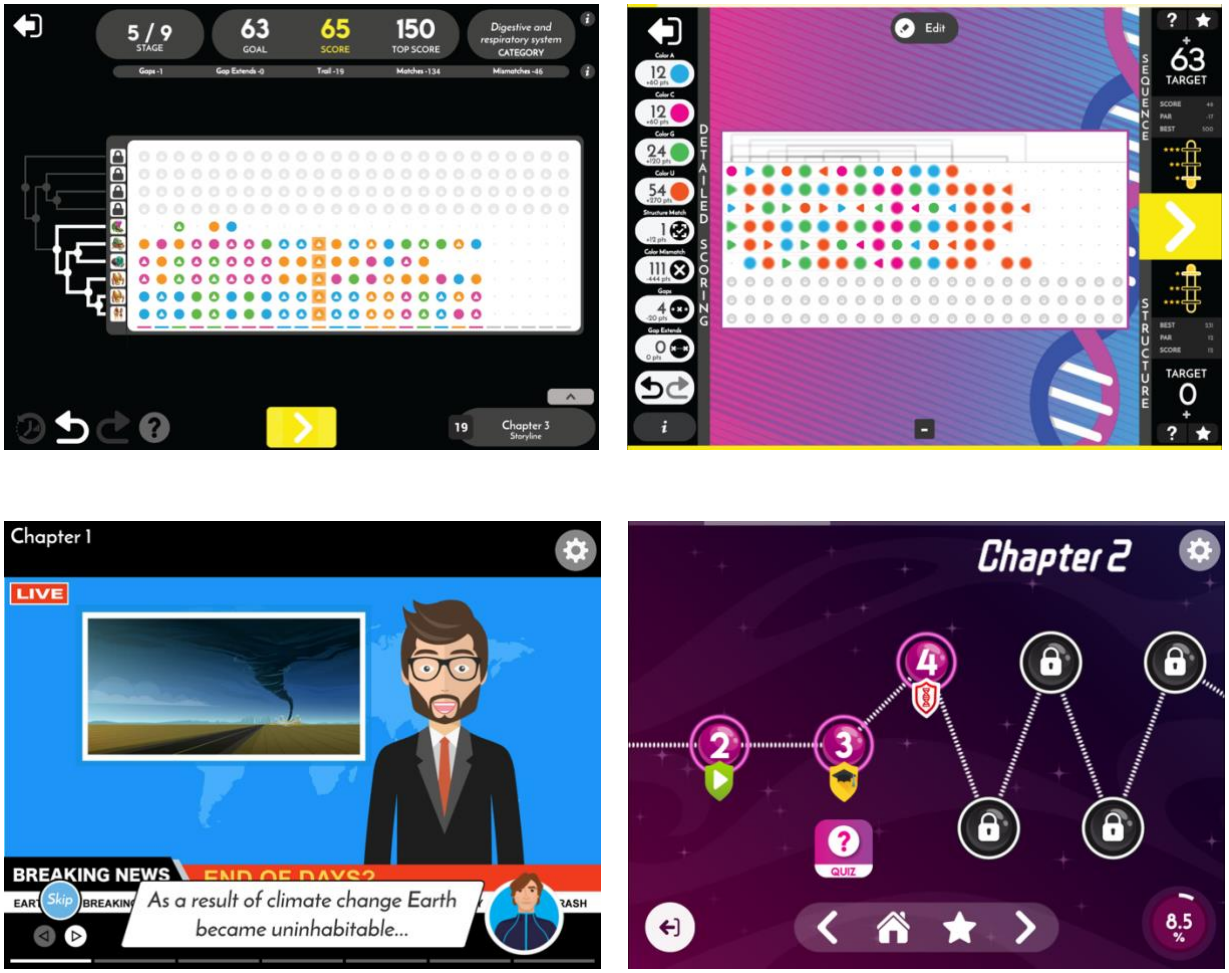



*Figure 3: Story mode. (left) a slide telling the story in which we embed the Phylo and Ribo puzzles. (right) roadmap of the story line. Each node along the path represents either a series of slides telling part of the story, a tutorial, a quiz, or a puzzle. The bottom menu allows the player to navigate the roadmap. A progress wheel can be found on the bottom right of the screen.*

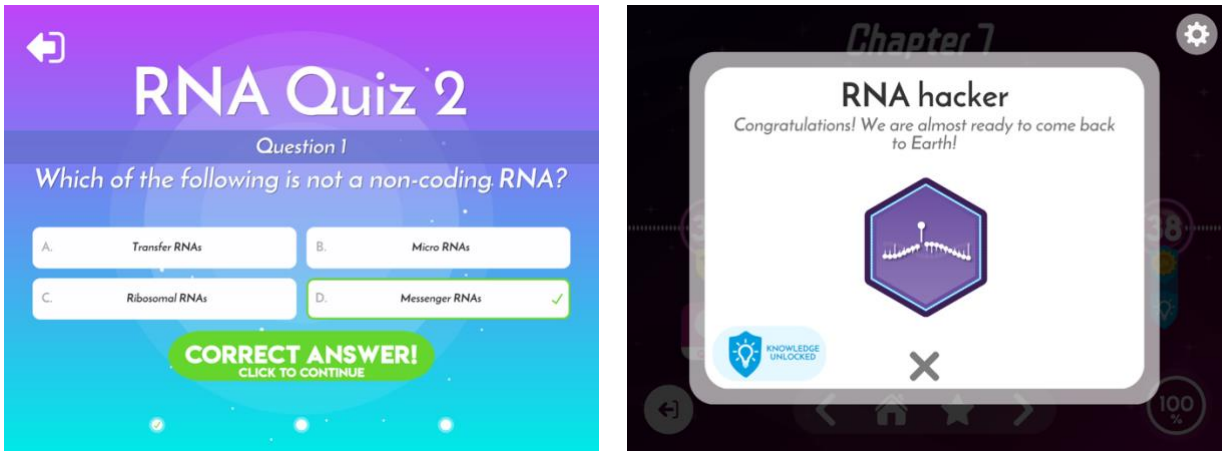



*Figure 4: Quiz and badge*

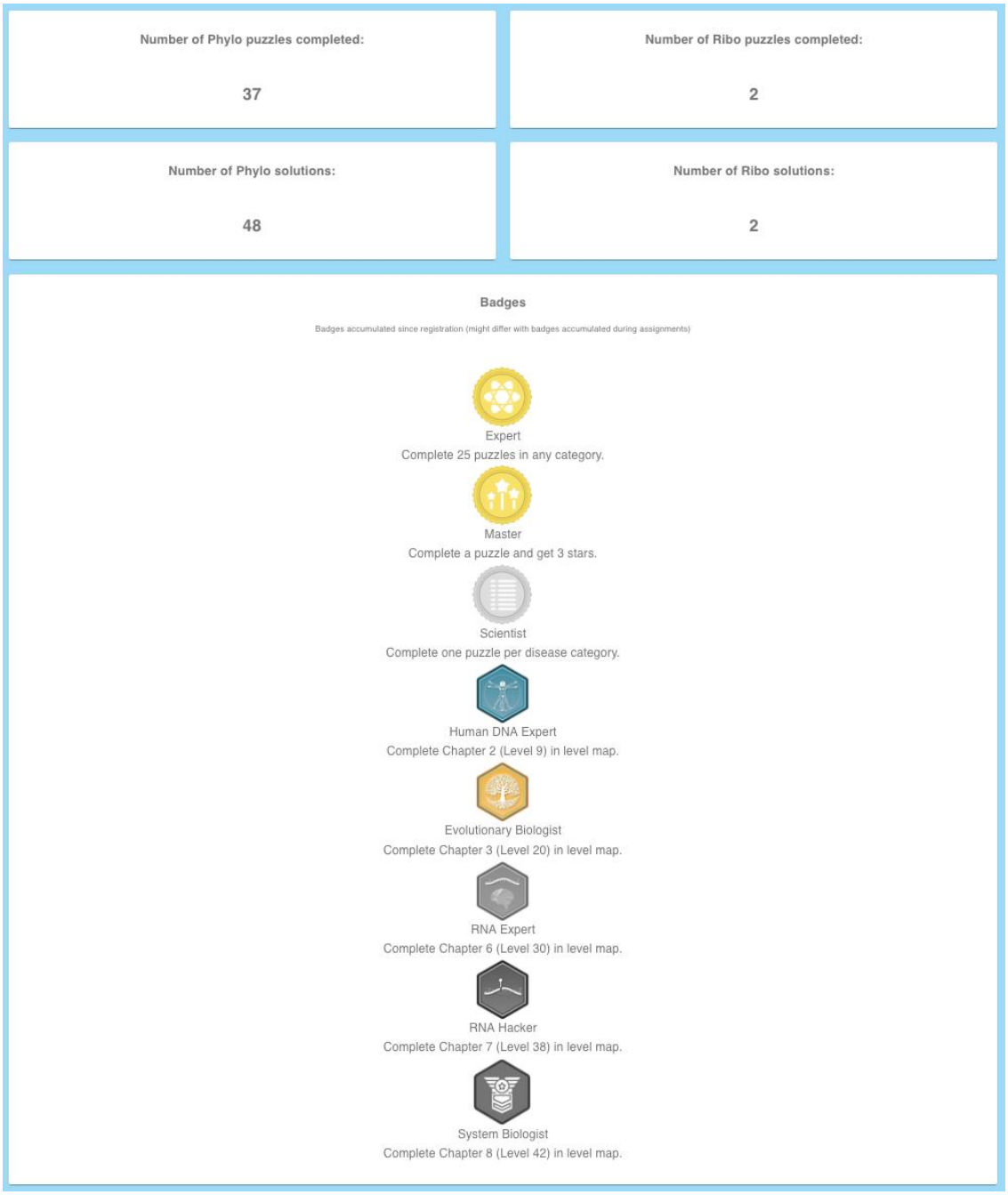
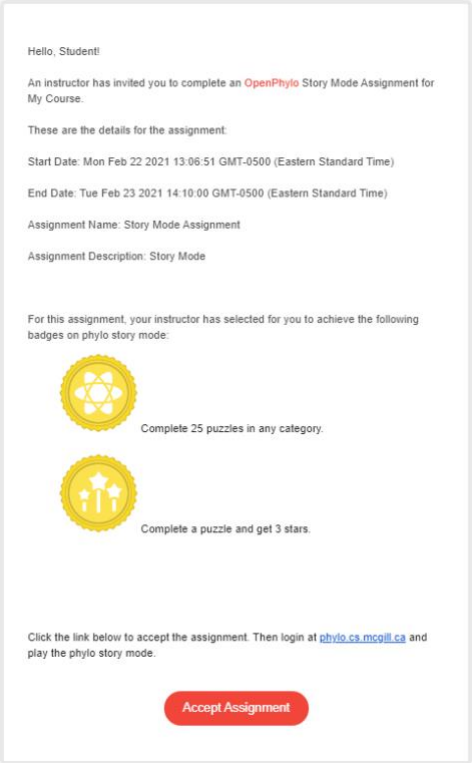



*Figure 5: OpenPhylo user statistics panel for participants to Phylo.*



Hello, Student!

An instructor has invited you to complete an OpenPhylo Story Mode Assignment for My Course.

These are the details for the assignment:

Start Date: Mon Feb 22 2021 13:06:51 GMT-0500 (Eastern Standard Time)

End Date: Tue Feb 23 2021 14:10:00 GMT-0500 (Eastern Standard Time)

Assignment Name: Story Mode Assignment

Assignment Description: Story Mode

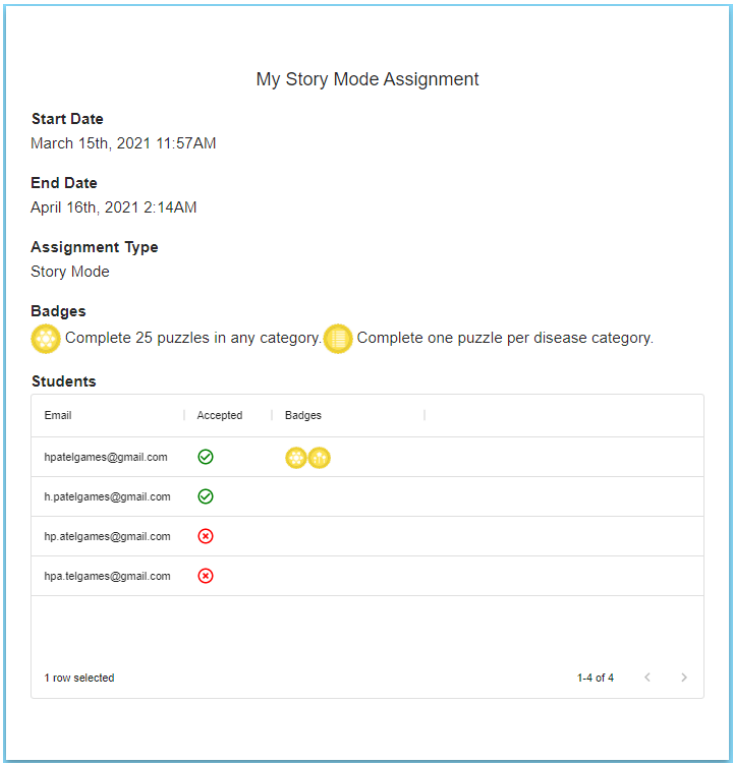
For this assignment, your instructor has selected for you to achieve the following badges on phylo story mode:

Complete 25 puzzles in any category.

Complete a puzzle and get 3 stars.

Click the link below to accept the assignment. Then login at phylo.cs.mcgill.ca and play the phylo story mode.

Accept Assignment



My Story Mode Assignment

**Start Date**
March 15th, 2021 11:57AM

**End Date**
April 16th, 2021 2:14AM

**Assignment Type**
Story Mode

**Badges**
Complete 25 puzzles in any category. Complete one puzzle per disease category.

**Students**

| Email | Accepted | Badges |
|---|---|---|
| hpatelgames@gmail.com | ✓ | |
| h.patelgames@gmail.com | ✓ | |
| hp.atelgames@gmail.com | ✗ | |
| hpa.telgames@gmail.com | ✗ | |

1 row selected 1-4 of 4

*Figure 6: Assignments*

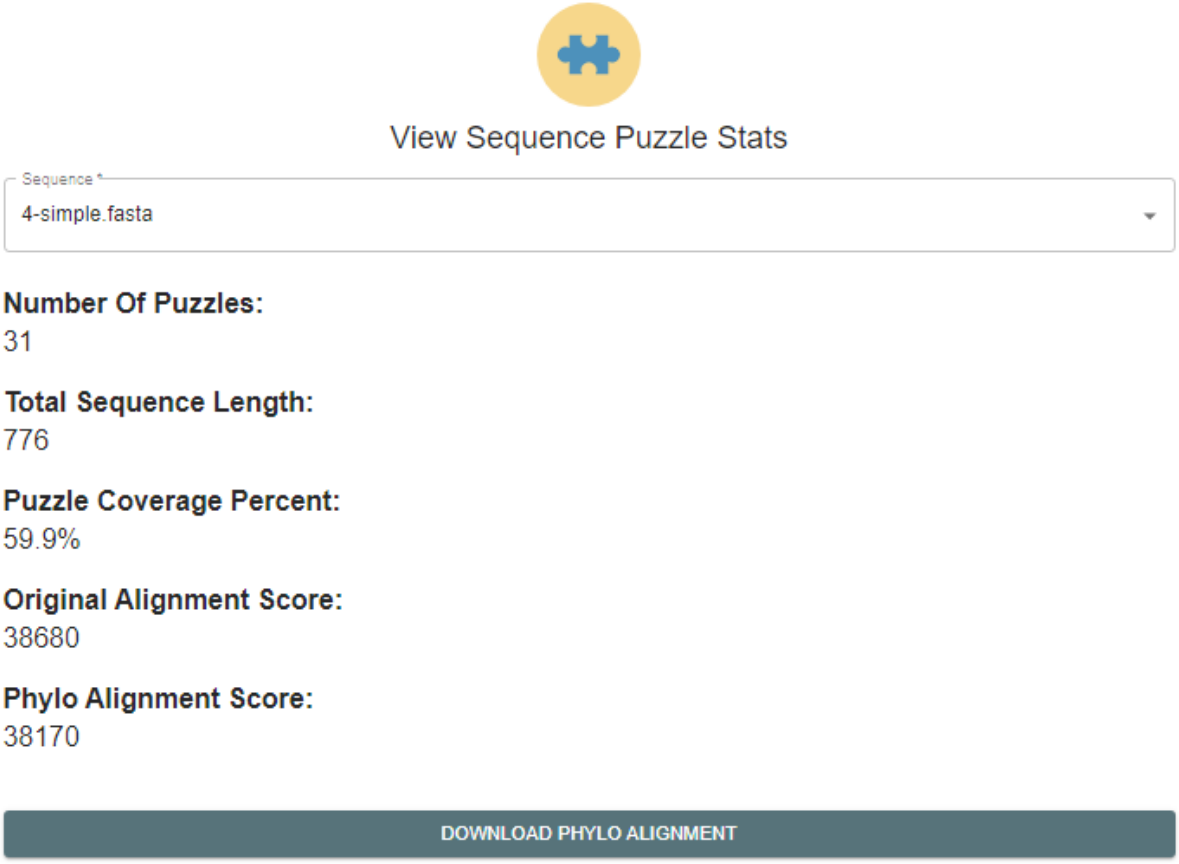



*Figure 7: Scientific interface*