

# Learner-Centered Methodology for Designing and Developing Multimedia Simulation for Biology Education

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**Abstract.** Biology students need exposure to modern research techniques relatively early in their educational careers. Computer multimedia simulation tools have been developed to address the challenge of providing all students with hands-on laboratory research experience. This paper presents a learner-centered approach to the design and development of a multimedia simulation for biology education. We present our methodology and a multimedia simulation tool designed and developed using the methodology. Our tool has been widely adopted by biological science educators for teaching molecular biology subjects in a wide range of undergraduate biology courses. We believe that our methodology can be adopted or adapted by learner communities in other disciplines.

**Keywords:** learner-centered methodology, case-based pedagogy, multimedia simulation, biology education, bioinformatics, workflow analysis.

## 1 Introduction

Early exposure to research is a national priority in science education: “All students should be encouraged to pursue independent research as early as is practical in their education” [1]. Therefore, biology students need exposure to modern research techniques relatively early in their educational careers. However, it can be logistically challenging to provide all students with hands-on laboratory research experience. Therefore, it is important to supplement wet laboratories with computer simulations to effectively engage students in the research process.

Numerous computer multimedia simulation tools have been developed with the attempt to address this challenge [2, 3]. Nonetheless, most of them have focused on the functional aspects and contents, with less attention being given to the mechanism to engage their users. For example, a tool may simply play animations or video clips for students to watch passively, providing little if any interactivity for the user [4, 5]. They contribute in explaining biological concepts such as the DNA transcription and sequencing technologies in molecular biology with a vivid visual aid, but they do not engage students actively. Recently, besides its role in multimedia simulation, computer

software has become indispensable for scientific inquiries done by biologists on a daily basis [6]. The complexity and user-friendliness issues of the software tools have become an obstacle to effective research [6].

We believe that the design and development of an effective educational multimedia tool for studying biology should take a learner-centered approach. To do so, we need to answer the following three questions: 1) Does the tool effectively engage students using the tool? 2) Does the tool provide a user-friendly interface? 3) Does the tool effectively deliver contents essential to biology education?

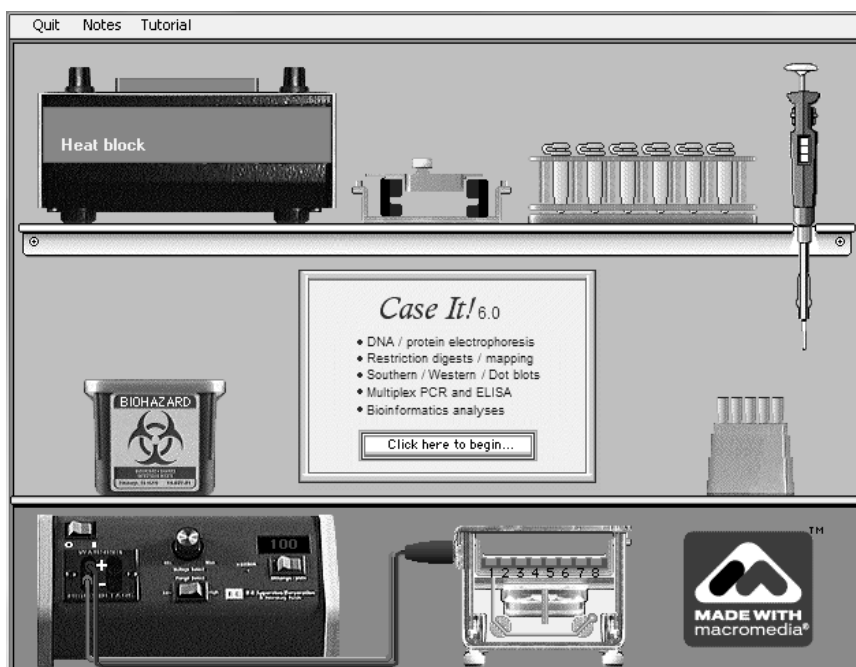
The methodology we devised to answer these three questions is as follows: In the past we have used role-playing and simulations to enhance student interest in science, through cases emphasizing diagnosis and ethical issues surrounding health counseling [7]. Our latest innovation is to use this case-based pedagogy to actively engage students by placing them in virtual research settings, fostering their ability to solve problems confronted by research scientists [8, 9]. We analyzed the case workflow common in biological science investigations and designed a uniform graphical user interface suitable for biology education. The user interface also includes options for using the multimedia simulation in various ways to serve students at multiple learning levels as well as biology courses with different learning objectives.

We argue that the contents delivered by an effective biology education tool should stay current with the advances in the field of biological science. For instance, bioinformatics techniques have become fundamental to modern biological investigation [10, 11]. Students at multiple learning levels need to be aware of these techniques and competent in their use [12, 13]. However, because of their complexity, existing bioinformatics tools are learned most successfully when expert guidance is available [14, 15]. Moreover, laboratory techniques are commonly used to generate data for bioinformatics analyses. Many schools do not have the resources to provide hands-on experience in these techniques, especially for introductory biology students. Our approach is to integrate our laboratory simulations with bioinformatics tools commonly used to study fundamental concepts of bioinformatics. We analyzed the workflow of these bioinformatics tools to reduce their complexity, with the goal of making bioinformatics easier for its learners to understand.

The paper is organized as follows. Section 2 presents the overview of *Case It! v6*, the tool we designed and developed using our learner-centered methodology. Section 3 describes the user interface design. A scenario demonstrating how the student interacts with our tool to perform biology science investigation is given in Section 4. Section 5 concludes the paper and discusses future work.

## 2 Overview of Case It! v6

*Case It! v6* is a tool that we designed and developed using our learner-centered methodology. The tool uses computer simulations to provide a context for student understanding by seamlessly integrating laboratory procedures with bioinformatics tools, using a case-based approach emphasizing important problems in biomedical research. It uses case-based pedagogy with an interactive virtual laboratory to engage students. Fig. 1 illustrates the opening screen of Case It v6. The devices and equipment shown



**Fig. 1.** Opening screen of Case It! v6

in the opening screen can all be operated to perform standard laboratory procedures virtually through multimedia interactions.

Case It! v6 consists of three major components. The schematic view of Case It! v6 architecture is depicted in Figure 2. The first component is the *Student Resource Manual*. The resource manual is a Web-based component that functions as an electronic resource manual. It helps students acquire background information about their cases by providing case descriptions and instructions for analyzing biological sequences associated with these cases. The second component is the *Case It Launch Pad*. This component is a collaboration environment that consists of a web page editor and bulletin board system. Virtual poster sessions can then be held and facilitated using bulletin boards associated with the posters.

The third component of Case It! v6 is the multimedia simulation, *Case It Simulator*. The simulator consists of two main functional units, namely the graphical user interface (GUI) and the functional core. The simulator provides a uniform graphical user interface to the students and allows them to play an active role in running biology wet labs on computers to investigate cases. The process can be visualized via interactive open-ended computer simulations that work with any DNA or protein sequence, and the results can be represented either in either textual or graphical format for analysis.

The functional core of the simulator consists of three modules, namely *Case Management*, *Simulation Control*, and *Extension/Integration*. The Case Management module organizes cases into self-contained folders with one case in each folder.

A case folder typically contains DNA or protein sequences for investigation. The Simulation Control module is the kernel of the entire tool, and is responsible for computation, programming logic, and multimedia simulation control. It interacts with the GUI unit and also bridges between the GUI unit and the Extension/Integration module. The Extension/Integration module is in place to address the needs of developing new biological tools to keep current with the advances in biological science. When a new concept such as bioinformatics has become essential for introductory biology students, we will either integrate it with existing cases or create new cases for it. Tools useful for delivering and reinforcing the new concept will then be explored and evaluated. As plenty of excellent tools developed by the field experts are freely accessible in the public domain, our strategy is to integrate suitable tools as “extensions” of the Case It! software instead of attempting to reinvent the wheels. Similar approaches have been adopted by the development of several integrated biological databases and analysis systems such as Biology Workbench [16] and SWAMI [17]. With this approach, the Extension/Integration module can focus on the integration mechanism to make the external tools intuitive and easy to use.

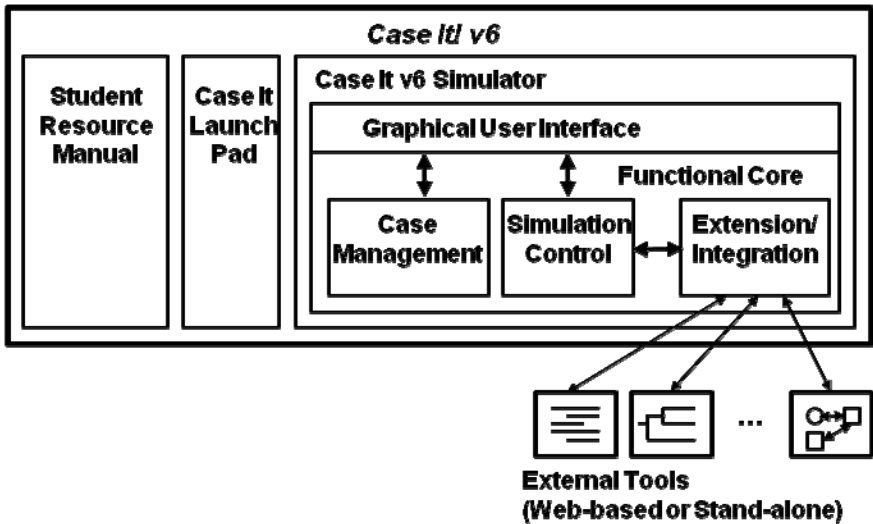


Fig. 2. Schematic view of Case It! v6 architecture

### 3 User Interface Design

We designed our user interface with the objectives to support our learner-centered, case-based methodology. The first objective aims at providing the learners with a consistent user experience in using the simulator. The second objective is aimed to ensure that the use of external tools is intuitive and effective. These objectives have been identified among key themes in the “new biologist-centric paradigm” for bioinformatics software design and development [6]. We analyzed the workflow of

case-based biology science investigation and the workflow of the external tool to achieve these objectives.

## 2.1 Case Workflow Analysis

We believe that by providing a consistent user experience to the students, they can use the tool to study a wide variety of biology subjects more effectively. To achieve this objective, we began by analyzing the case workflow common in biological science investigations. The steps in the workflow is described as follows: 1) open a case in the context of the subject to be studied; 2) study the case description and its background information; 3) identify the problems to solve; 4) collect DNA or protein sequences as well as the enzyme that may be used to digest the sequences; 5) process the sequences using standard laboratory procedures, and 6) analyze the sequences using biotechnology or bioinformatics tools. The case workflow is summarized in Figure 3.

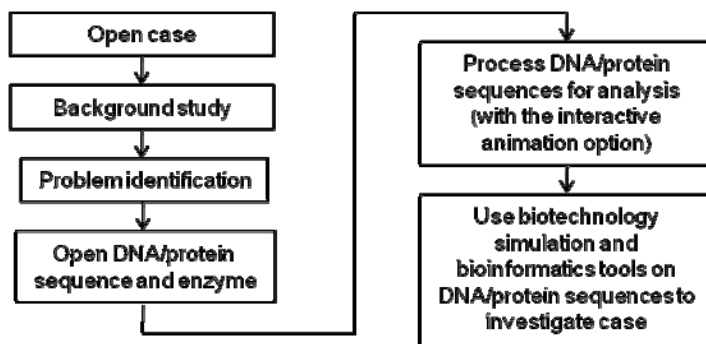


Fig. 3. Case workflow analysis for biology science investigation

Based on the case workflow, we designed a uniform graphical user interface for students to carry out the steps in the workflow. For example, students can open the DNA sequences, load them to the workspace of the simulator, and process them using virtual wet lab equipment. Moreover, we take students learning levels and biology courses learning objectives into consideration to make the simulator suitable for engaging a broader audience in biology education. As a result, the user interface of Case It! includes options for using the multimedia simulation in various ways. For example, students have the option to conduct wet labs virtually using interactive animations. On the other hand, students with more experiences in these procedures may choose to skip the multimedia interactions to proceed to the analysis of DNA data.

## 2.2 Extension Tool Workflow Analysis

As bioinformatics techniques have become fundamental to modern biological investigation, students at multiple learning levels need to be aware of these techniques and learn how to use them. The goal of the integration of our laboratory simulations with bioinformatics tools is to make bioinformatics easier for its learners to understand.

We began by identifying bioinformatics tools commonly used to study fundamental concepts of bioinformatics such as phylogenetic analysis and biological database search. We then analyzed the workflow of these bioinformatics tools to reduce their complexity.

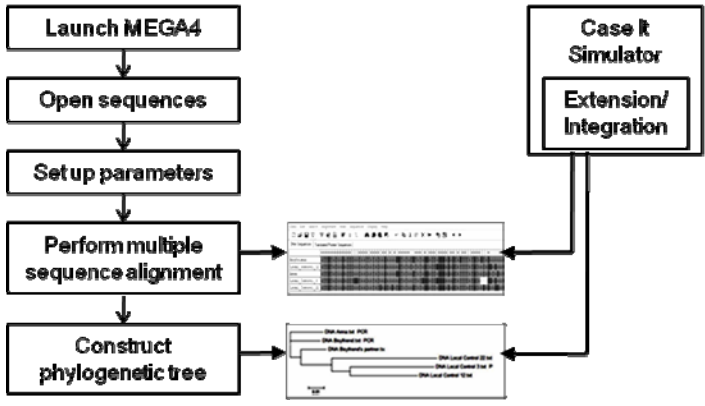


Fig. 4. Contrast between invoking MEGA4 (depicted in the left) and using Case It Simulator (depicted in the right) to perform multiple sequence alignment and construct phylogenetic tree

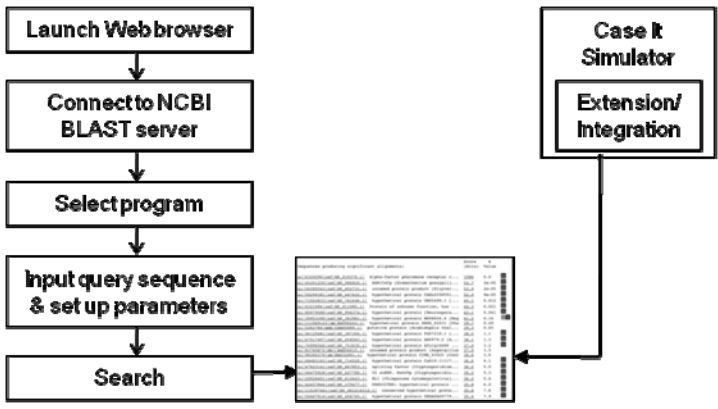


Fig. 5. Contrast between connecting to NCBI BLAST server (depicted in the left) and using Case It Simulator (depicted in the right) to carry out BLAST databases search

We adopted MEGA4 [18] for performing phylogenetic analysis and NCBI BLAST [19] for biological database search. The workflow of running MEGA4 directly requires the following steps: 1) open sequences; 2) set up parameters such as DNA or protein; 3) perform multiple sequence alignment; and 4) use the alignment to construct the phylogenetic tree. Our experiments show that it may take up to fourteen computer mouse clicks to display the alignment and the tree. Besides, students need to learn and understand how to set up parameters to use the tool correctly and effectively. Using the result of the workflow analysis, we designed and developed code

to integrate MEGA4 with Case It! that only takes one mouse click to display the alignment and tree. The simplicity of our approach is illustrated in Figure 4, showing how the integration of Case It and MEGA4 greatly simplifies phylogenetic analysis.

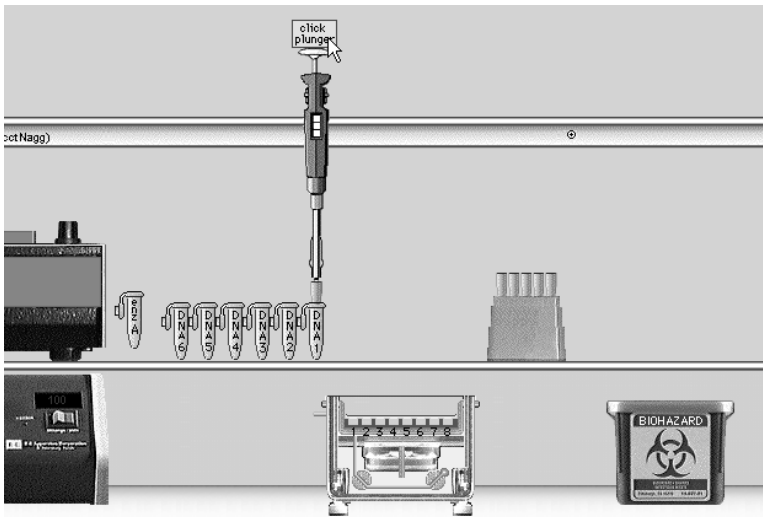
Based on our study, the steps for searching the BLAST databases include: 1) connect to the BLAST Web server; 2) select the search program; 3) enter the query sequence; 4) set up parameters; and 5) search. Using the analysis, we designed and developed code to automate the workflow. The contrast between using a Web browser and using Case It! for BLAST database search is illustrated in Figure 5.

We believe that our approach allows students to focus more on biology science investigations than on learning bioinformatics tools, sometimes an overwhelming experience for beginning biology students. To enrich students at more advanced levels, Case It! also provides options for students to invoke bioinformatics tools directly. With these options, students can gain exposure to how those tools are employed by biological researchers in the real world.

## 4 Scenario

In this section we present a scenario to demonstrate how the student interacts with the Case It Simulator to carry out case-based biology science investigations. The case used in this example is regarding the subject of human immunodeficiency virus (HIV).

The student begins by studying the background information of the case and HIV, followed by identifying the problems to be investigated. After launching the Case It Simulator, the student opens the case folder and selects the DNA sequences to be analyzed and the enzyme to digest the sequences. The next step is to prepare the sequences for further analysis. At this stage, the students can choose to either load the digested sequences to the simulator's workspace automatically or carry out the wet



**Fig. 6.** Interactive multimedia simulation enables students to carry out wet labs virtually

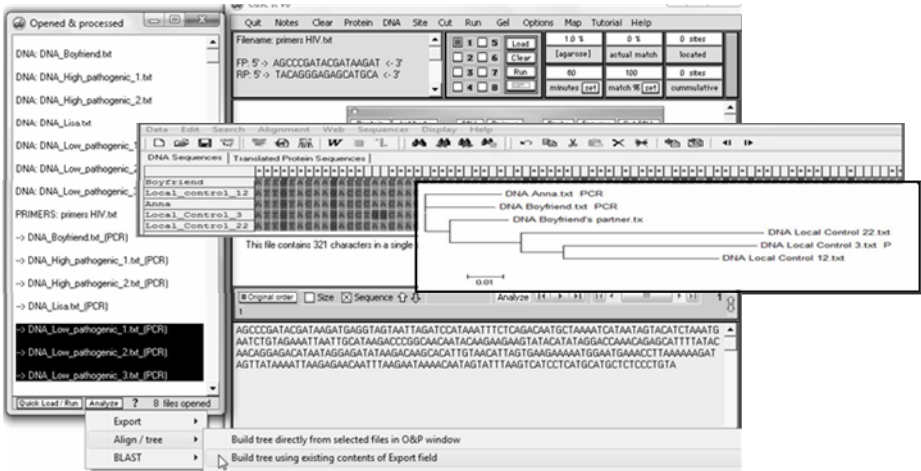


Fig. 7. Screenshot of phylogenetic for the HIV case using Case It!

labs virtually using the interactive multimedia simulation. As shown in Figure 6, the student can use a pipette to obtain DNA sequences from the tubes and use them to perform standard wet lab procedures such as gel electrophoresis.

The student then starts the research and investigation after the sequence data are ready for analysis. If the student decides to investigate the evolutionary relationships among the HIV virus strands of people in this case, the student will perform phylogenetic analyses on the DNA sequences. The student can obtain the multiple sequence alignment and the phylogenetic tree with one simple mouse click from a pull-down menu in the Case It Simulator as shown in Figures 7. Instead of learning how to use MEGA4 first, the student can focus on the investigations using the alignment and the tree. The student then searches biological databases for similar sequences by using the integrated BLAST function in Case It!. This allows the student to concentrate on analyzing the results returned by the BLAST database server.

## 5 Conclusions and Future Work

In this paper we present Case It!, an open-ended, case-based multimedia simulation tool for biology education. We used a learner-centered methodology to design and develop the tool so that it would effectively engage students, provide a user-friendly interface, and effectively deliver current contents essential to biology education. Case It! has been widely adopted by biological science educators for teaching molecular biology subjects in a wide range of undergraduate biology courses [20]. Student surveys have been conducted to assess the effectiveness of the tool, and the result shows that the tool has improved student performance in learning molecular biology subjects [20, 21].

We are currently exploring the utilization of the Extensible Markup Language (XML) to convey biological data in various representations to serve users at multiple learning levels more effectively. We are also developing cases for other important



molecular biology research tools such as proteomics and microarrays, and plan to integrate them with Case It! using our methodology.

Although our learner-centered methodology is applied to the design and development of a multimedia simulation for biology education, we believe that the same approach can also be adopted or adapted by learner communities in other disciplines.

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