The Effect of Bioinformatics Module on Molecular Genetics Concepts on Senior High School Students' Computational Thinking Skills

Indah Juwita Sari
Kasetsart University, Bangkok, Thailand
https://orcid.org/0000-0002-5810-2945

Wanwipa Vongsangnak
Kasetsart University, Bangkok, Thailand
https://orcid.org/0000-0003-3805-0719

Pongprapan Pongsophon
Kasetsart University, Bangkok, Thailand
https://orcid.org/0000-0003-0213-2835

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Abstract

This study aimed to investigate senior high school students' computational thinking skills after implementing the Bioinformatics Module on molecular genetics concepts. The instructional approach used in the module is Computational Inquiry-based Teaching (CIbT). This study used a quasi-experiment method with a pretest-posttest control group design. The subjects in this study consist of 24 students in the control group and 38 students in the experimental group from a senior high school in Indonesia. The instrument used in this study is six items of computational thinking test. This module had four themes; Genetics Disease, Cancer, Forensic Science, and Evolution, conducted in 8 sessions. Each session lasted 90 minutes. The Bioinformatics Module consists of programming and databases, including unplugged computational activities and unplugged activities including coding using Python, searching in Uniprot, and using BLAST in NCBI. The CIbT has five steps: orientation, conceptualization, investigation, conclusion, and discussion. The Mann-Whitney test results showed that the p-value from N-Gain data is < 0.01. So, Bioinformatics Module on molecular genetics concepts using CIbT can improve computational thinking skills of senior high school students. For further implementation, biology teachers must prepare to use the Bioinformatics Module, including biology teachers' understanding of molecular genetics and bioinformatics practices to enrich the learning experience in the Bioinformatics Module.

Keywords: Bioinformatics Module, Molecular Genetics Concepts, Computational Inquiry-based Teaching, Computational Thinking Skills, Senior High School

Introduction

The concepts of Biology in senior high school level follow the significant advances in biology and biotechnology research, especially on molecular genetics. Molecular genetics has great potential for students to understand the concept of biology holistically. Machluf & Yarden (2013) state that the efforts to investigate the concepts of molecular biology involved innovative learning methods and approaches to initiate students' motivation in learning biology. Molecular genetics concepts in senior high school level were related to various fields of study, such as genetics, mutation, evolution, biochemistry, protein interaction in the cells, gene regulation, and DNA technology (Republic of Indonesia, 2018). Bioinformatics is an emerging interdisciplinary field between biology, computer science, and information (Shuster et al., 2016).

Using bioinformatics in the learning process for high school students can establish the meaningful learning because of the bioinformatics touches many aspects that are relevant to new generations, such as health, environment, and agriculture issues (Marques et al., 2014). So, the teaching bioinformatics helps students understand these fundamental concepts in the unit of molecular genetics through developing practical research skills and getting accustomed to bioinformatics resources (Porter et al., 2007).

Many resources for bioinformatics learning are available free of charge, such as BLAST, ClustalW, and Entrez (Machluf & Yarden, 2013; Stevens & Boucher, 2015). The sandbox.bio, Jupyter Lab, and programming languages are also used in bioinformatics such as Python, R, and Java (Dudley & Butte, 2009; Fourment & Gillings, 2008). High school students could write simple codes to answer biological questions in bioinformatics using these programming languages (Velez Rueda et al., 2019). This learning experience develops computational thinking skills. Computational Thinking skills (CTs) is solving problem using a computer that has four components that help students solve a complex problem; decomposition, pattern recognition, abstraction, and algorithmic thinking (Labusch et al., 2019; Wing, 2006). In addition, CTs and coding are important 21st-century skills and competencies that have emerged due to incredible advance in computer processing (Bocconi et al., 2016; Tabesh, 2017).

In this present study, Computational Inquiry-based Teaching (CIbT) is needed as a teaching strategy to guide Bioinformatics Module in senior high schools. In this study, the CIbT was developed by combining the previous work of Pedaste et al. (2015) and Fortmann et al. (2020). Pedaste et al. (2015) developed a computational-based teaching that consists of research, recording, observing, organizing data in the investigation phase, finding a relationship and drawing conclusions in the conclusion phase, and communicating results that reflected in the discussion phase. Meanwhile, Fortmann et al. (2020) developed computational guided inquiry (CGI) to enhance students' skills on manipulating and analyzing the data and enhancing the student learning experience through active learning methods using modules. CGI combined active-learning strategies, guided inquiry, and computational platforms using Excel. Then, we adopted five steps; orientation, conceptualization, investigation, conclusion, and discussion from Pedaste et al. (2015) and combined with the idea from Fortmann et al. (2020) that the CGI used modules to support real life problem in the learning.

We developed the CIbT as innovation from Pedaste et al. (2015) and Fortmann et al. (2020) using Bioinformatics Module. We conducted content validation of Bioinformatics Module using Bioinformatics experts. We analyzed the results from four lesson plans themes; Genetics Disease theme, Cancer theme, Forensic Science theme, and Evolution theme. Table 1 shows a brief description of the learning activities using Bioinformatics Module through CIbT in each phrase across different themes.

Table 1: The Overview of Learning Activities using Bioinformatics Module through CIbT

The learning activities in step of CIbT	Themes in Bioinformatics Module			
	Genetics Disease	**Cancer**	**Forensic Science**	**Evolution**
Orientation	Answer the questions about bioinformatics, molecular genetics, genetics diseases, type 1 diabetic, and insulin gene	Answer the questions about cancer, mutation, and type of mutation	Answer the questions about forensic science and how bioinformatics helps forensic scientists,	Answer the questions about evolution, classification of living things, phylogenetic tree, and steps to make phylogenetic tree

Conseptualization	Watch the video about bioinformatics, molecular genetics, and type 1 diabetic	Watch the videos about cancer and the role of drugs in stopping mutations.	Watch the videos about forensic science steps include DNA extraction, PCR, and gel electrophoresis.	Watch the videos about evolution and phylogenetic trees
Investigation	Install the Python and PyCharm Counting Nucleotides and GC content of insulin gene using unpluged and Python The location of insulin gene using BLAST Comparing DNA sequences using Unplugged and Uniport DNA translation to protein using Unplugged, Python, and Sequence Manipulating Sequences (SMS).	Comparing normal and cancer cells using Unplugged and Python Comparing DNA sequences using Unplugged and Python Visualize a drug that stops mutant protein using BLAST in NCBI	Solve the problem about DNA extraction and PCR Read the result of Gel Electrophoresis Comparing the DNA sequence of victim and victim's closest relatives using Unplugged and Python	Make phylogenetic tree by hand Make phylogenetic tree using BLAST in NCBI Make phylogenetic tree using Python
Conclusion	Finding the relationship between the first activity until the fifth activity in the breakout room to get the conclusion about Genetics Disease	Finding the relationship between the first activity until the third activity in the breakout room to get the conclusion about Cancer	Finding the relationship between the first activity until the third activity in the breakout room to get the conclusion about Forensic Science	Finding the relationship between the first activity until third activity in the breakout room to get the conclusion about Evolution
Discussion	Present the result in the main room	Present the result in the main room	Present the result in the main room	Present the result in the main room

Previous studies developed CTs, such as Rodríguez del Rey et al. (2020) who developed a module for computer engineering students in university to improve CTs. Chiazzese et al. (2019) assessed CTs of students in K-12 education after learning programming about robotics. The result showed that programming robotics has a positive impact on students' learning of CTs. Zhao & Shute (2019) developed students' CTs in a middle school using Penguin Go as a video game, and the result showed that students' CT skills improved significantly after playing the game for less than two hours. Based on the research gap, limited research to improve student CTs using molecular genetic concepts at the high school level. In addition, there has been no development of a bioinformatics module through CIbT to improve student CTs. So, this study aimed to investigate the effect of Bioinformatics Module on molecular genetics concepts using CIbT on high school students' computational thinking skills.

Bioinformatics Module for Developing Computational Thinking and Understanding Molecular Genetics Concepts

The Bioinformatics Module in our study employ guided inquiry: the students would engage in both unplugged and plugged computational thinking activities. The example of unplugged activities are students counting nucleotide by hand, students calculating the percentage of nucleotide ratio by hand, etc. Meanwhile, the example of plugged activities using Python, Uniport, SMS (Sequence Manipulate Suite), BLAST at NCBI to import data, make calculate, compare DNA sequences, and make phylogenetic trees.

The science curriculum in the Biology in senior high school in Indonesia molecular genetics and DNA technology regarding analyzing the relationship between structural and the functional of genes, DNA, chromosomes, analyzing mutation in living things, analyzing gene regulation in living things, using principles of Biotechnology and its application as an effort to improve human welfare and explaining the theories, principles, and mechanism of evolution and speciation. To establish the scope of molecular genetics in this study, we specified target concepts regarding biotechnology and DNA technology from National Science Curriculum of the Republic of Indonesia (Couch et al., 2015; Republic of Indonesia, 2018). We compiled key ideas and their corresponding target concepts along (Table 2).

Table 2: Key Ideas and Target Concepts Regarding Molecular Genetics for Grade 12 Students in Indonesia

Key ideas	The Target Molecular Genetic Concepts
Analyzing the relationship between structural and the functions of genes, DNA, chromosomes	The structure and replication of DNA
	Central dogma
Understanding mutation in living things	Mutation
Understanding gene regulation in living things	Gene regulation
	The DNA microarrays
Understanding the principles of Biotechnology and its application as an effort to improve human welfare (DNA technology)	Recombinant DNA technology
	DNA fingerprinting and forensic science
	Genomics
Explaining the theories, principles, and mechanism of evolution also the latest views of experts related to speciation	Evidence of evolution
	Classification and Phylogeny

Based on Table 2, molecular genetics consists of 10 target concepts, in this study presented the target concepts into four themes; Genetic diseases, Cancer, Forensic Science, and Evolution (Table 3).

Table 3: The Framework of Bioinformatics Module regarding Molecular Genetics Concepts by Themes

Molecular Genetics Concepts	Themes			
	Genetics Disease	Cancer	Forensic Science	Evolution
The structure and replication of DNA	√			
Central dogma	√			
Mutation	√	√		
Gene regulation	√	√		
Genomic	√	√	√	
The DNA microarrays		√	√	
Recombinant DNA technology		√	√	
DNA fingerprinting and forensic science			√	
Evidence of evolution				√
Classification and Phylogeny				√

Computational Thinking appeared in the nineteenth century as a process to formulate, design, and test innovative solutions to science and mathematics problems in daily life using computers to leverage the power of technological methods (Tabesh, 2017; Wing, 2006). There are two ways in computational thinking; conceptualizing problems and operationalizing solutions. First, we must understand and frame the process through an algorithmic thinking system that can help us develop a solution. Second, we develop solutions and implement them; after that, evaluate the result of implementing the solution in which all steps based on the computer systems and repetitive processes (Eickelmann, 2019).

Students demonstrate the computational thinking in four components; decomposition, pattern recognition, abstraction, and algorithmic thinking (Labusch et al., 2019; Tucker, 2006). Decomposition is the ability to analyze the task and break it into smaller activities (Barr & Stephenson, 2011; Tabesh, 2017). Pattern recognition is the ability to identify a pattern in a part of the data component (Michaelson, 2015; Pólya, 2004). We could use pattern recognition to recognize a DNA strand pattern, such as comparing DNA sequences or translating Genes into Proteins (Fink, 2008). Abstraction is the ability to separate between useful and relevant information and employ useful information to solve a problem (Frigg, 2002). For example, we find extensive data from biological databases, focusing on relational databases to solve the problem (Qin, 2009). Algorithmic thinking is the ability to use codes step by step in the programming language by computer to find the final solution (Labusch et al., 2019). Based on those definitions, in Table 4, we classified themes, bioinformatics topics, tools, and computational thinking skills targeting in our Bioinformatics Module.

Table 4: The Structure of Bioinformatics Modulefor Senior High School

Bioinformatics Module Themes	Bioinformatics Topics	Bioinformatics Tool	Computational Thinking Skills Developed
Genetics Disease	Counting Nucleotides and GC content The location of gene Comparing DNA sequences DNA translation to protein	Unplugged Python BLAST Uniprot SMS	Decomposition Pattern recognition Abstraction Algorithmic thinking
Cancer	Comparing normal and cancer cells Comparing DNA sequences Visualize a drug that stops mutant protein	Unplugged Python BLAST in NCBI	Decomposition Pattern recognition Abstraction Algorithmic thinking
Forensic Science	Read the result of Gel Electrophoresis Comparing the DNA sequence of victim and victim's closest relatives	Unplugged Python	Decomposition Pattern recognition Abstraction Algorithmic thinking
Evolution	Make phylogenetic tree	Unplug Python BLAST in NCBI	Decomposition Pattern recognition Algoritmic thinking

Methods

This study used a quasi-experiment with pretest-posttest control group design (Reichardt, 2019). The sampling technique in this study is cluster sampling. The subjects in this study is 24 students in the control group and 38 students in the experimental group from a school with a well-equipped with educational technology to implement the Bioinformatics Module. The Experimental group was implemented Bioinformatics Module based Computational Inquiry-based Teaching, and the control group learned the molecular genetics concept using inquiry learning. The learning unit is molecular genetics.

We assessed students' computational thinking skills using six computational thinking test items adopted from Bebras Task (2016-2018). Six computational thinking test items were validated using Rasch analysis with a 0.55 reliability index in the moderate level. Six items had infit and outfit measures in the acceptable range of 0.7 to 1.3 (Sari et al., 2021). Six items of computational thinking test are acceptable, including Rows and Columns (2018), Treasure Maps (2018), Cipher wheel (2017), Commuting (2017), Secret messages (2016), and Kix Code (2016) (Sari et al., 2021). We assessed students' Computational thinking skills before and after learning the molecular genetics concept using Google form. The examination took 20 minutes.

We analyzed the computational thinking data using the R program to check assumption of data including the normality and homogeneity before conducting hypothesis test. We used p-value of 0.5 and smaller as a cutoff for to rejecting the null hypothesis test (Greenland et al, 2016). We used Mann-Whitney test in this research because the pretest data is not normally distributed and is not homogenous. We used N-Gain data because the pretest data between control and experimental groups is different. We used N-Gain between the gain of pretest and posttest data using the formula in Figure 1 to know the improvement CTs of students in experimental and control groups.

N-Gain = Posttest score – Pretest score / Ideal score – Pretest score

Fig. 1: The Formula of N-Gain (Meltzer, 2002)

Results

The students completed six items of computational thinking test using Google Form before and after learning the molecular genetics concepts. We analyzed the data of CTs using the R program, and it can be seen in Table 5. Based on the analysis, we found that mean of pretest for the control group is 16.67, and the mean of posttest is 22.92. The pretest mean for the experimental group is 36.4, and the posttest is 53.07. Shapiro–Wilk test and Bartlett test showed that the pretest and posttest data in control and experimental groups are not normally distributed (p-value < 0.05) or have difference variance (p-value < 0.05). Based on this result, we decided to use Mann Whitney test to determine whether the two groups' pretest data are different significantly. We got p-value < 0.05. It means that control and experimental groups are different. So, we used N-Gain to determine students' improvement CTs in experimental and control groups. We used Mann Whitney test to determine whether the two groups' significant N-gain is different or same. We got p-value < 0.05, so CTs of students in experimental and control groups are significantly difference, and CTs of students in the experimental group were improved. We can say that the Bioinformatics Module on molecular genetics concepts using CIbT had a positive effect on students' computational thinking skills at the senior high school level.

Table 5: Analyze Data of Computational Thinking Skill

	Control Group		**Experimental Group**		
	Pretest	**Posttest**	**Pretest**	**Posttest**	
N	24		38		
Mean of CTs	16.67	22.92	36.4	53.07	
Normality test	p-value = 0.000470	p-value = 2.639e-06	p-value = 0.003369	p-value = 0.02481	All of data have p-value< 0.05 → the data from control and experimental groups are not normal
N-gain normality test	p-value = 0.01049		p-value = 2.1e-05		
Homogeneity test	df = 1, p-value = 0.01471 (pretest Data) df = 1, p-value = 3.095e-05 (Posttest Data)				All of data have p-value< 0.05 → the data from control and experimental groups are not homogeneous
N-gain homogeneity test	df = 1, p-value = 3.122e-07				
Mann Whitney test	p-value = 0.0001321(pretest Data) p-value = 0.01107 (N-Gain data)				Pretest data has p-value < 0.05 → control and experimental groups are different N-Gain data has p-value < 0.05 → control and experimental group are different

Discussion

Based on the results of data analysis in Table 5, we can see an improvement between the average pretest and posttest scores in the control and experimental groups on computational thinking skills (CTs). However, the improvement of CTs mean in the control group was lower than in the experimental group in posttest. This is evidenced by the results of the Mann-Whitney test that p-value is less than 0.05. It means that the CTs in the experimental group have increased significantly. The following are some of the explanation why the Bioinformatics Module on molecular genetics concepts using CIbT positively influence students' CTs in high school significantly.

In the Genetic disease theme, students learned a lot about bioinformatics, how to install Python and PyCharm as Bioinformatics tools, and type 1 diabetic as genetics a disease. Some activities in this theme stimulate CTs, such as installing programming language, counting nucleotides using unplugged technique and Python, where the location of the insulin gene, comparing DNA sequences, and DNA translation to protein. Fink (2008) said that comparing DNA sequences and translating the DNA to protein needs the skill of pattern recognition. Pattern recognition consists of recognizing specific repeated situations and generalizing them (Chiazzese et al,. 2019). The students' activity to install and run programming languages like Python and PyCharm needs to write codes step by step in the computer to find the final solutions (Labusch et al., 2019).

In the Cancer theme, we found that the students had learned how to compare normal cells and cancer cells and visualize drugs to stop cancer-causing mutations using bioinformatics tools. Based on the observation result, the students enjoyed the activities using CIbT and Bioinformatics Module. The students were excited to compare the sequence from normal cell to cancer cell using unplugged, Python, and NCBI. Participants were also able to communicate the steps in comparing normal and cancer cell sequences using unplugged, Python, and NCBI. In this case, students use skill decomposition that determine the easiest way to compare the sequences of normal cells and cancer cells. In addition, participants were also able to communicate the benefits of visualization of 3D proteins. In this case, students use abstraction skills to communicate abstract 3D protein images. Decomposition consists of dividing a task or problem into simpler parts, and abstraction hides the inherent complexity of reality to represent only its essential aspects (Rodríguez del Rey et al,. 2020).

In the Forensic Science theme, learning consisted of minds-on activities, in the beginning, using forensic Science case and step to identify the victim and hand-on activity in the investigation to compare DNA sequence of victim and victim's closest relatives using unplugged computing and coding in Python. The students got new knowledge about how biology and bioinformatics can solve forensic science problems. Like in the Forensic Science theme, the Evolution theme consists of hands-on activity to make phylogenetic trees using unplugged computing, Python, and BLAST of NCBI. Although the activity only made phylogenetic trees using unplugged computing, Python, and BLAST of NCBI, the participants understood the evolution concept more. Based on the observation result in the conclusion phase, the students could explain evolution's definition in more detail. The students give the molecular genetics terms in the evolution theme, such as mutations, cross DNA, or environmental changes are the causes of evolution in species. These activities stimulate abstraction and algorithmic thinking that consists of practical steps to solve the problem (Frigg, 2002; Qin, 2009; Labusch et al., 2019). Basically, students still have difficulty explaining evolution related to phylogenetic trees. After students learn to make phylogenetic trees by hand, then use Python, reinforced by using BLAST of NCBI, students become able to describe the abstract evolutionary process into concrete. In addition, students could also explain step by step in making a phylogenetic tree.

Conclusion

From the study, we conclude that Bioinformatics Module on Molecular Genetics concepts using computational Inquiry-based teaching give the effect to increase students' computational thinking skills significantly in senior high school level with p-value <0.01. The steps in CIbT enhance all components of computational thinking of students.

The limitation of this implementation is the device in the learning process should be compatible with many applications such as PyCharmand python and the internet connection should be strong, because the learning process is in the online learning process. For further study, biology teachers should have good preparation to use Bioinformatics Module, not only the internet connection and devices of students, but also molecular genetics concepts and bioinformatics practices to enrich the learning experience in Bioinformatics Module. In addition, biology teachers should explore the phases of computational Inquiry-based teaching to enhance computational thinking skills. Each phase in the strategy has activities that can stimulate CTs of students. For future research, important to determine the effect of students' conceptual understanding of molecular genetics concept using the Bioinformatics Module at the high school level.

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Author Details

Indah Juwita Sari, *Kasetsart University, Bangkok, Thailand,* ***Email ID****: indah.sa@ku.th*

Wanwipa Vongsangnak, *Kasetsart University, Bangkok, Thailand,* ***Email ID****: wanwipa.v@ku.ac.th*

Pongprapan Pongsophon, *Kasetsart University, Bangkok, Thailand,* ***Email ID****: pongprapan.p@ku.th*