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Analysis of Computational Thinking Test Using Bioinformatics Database: A Convergent Parallel Mixed-Methods Study

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Abstract

Computational thinking is a thinking approach used to understand and solve complex problems by applying computational concepts and techniques. This study aims to analyze qualitatively and quantitatively the computational thinking test question items using bioinformatics database. The method used in this study is a mixed method with the research design being a convergent parallel design. The qualitative data collection technique is a sheet of suggestions, inputs, and comments from experts in assessment in education, computational thinking, and bioinformatics, while the quantitative data collection technique is an assessment sheet by experts and a test of questions to 127 pre-service biology teachers by producing reliability values and infit-outfit index. The results obtained qualitatively are that CTT (Computational Thinking Test) has high recency and complexity and there are improvements related to the language and multiple answer options used. The quantitative results showed that the computational thinking problem was included in the very feasible category with a value of 91.83, the reliability value that was included in the category was very low, but each item was included in the accepted category with an infit-outfit index range of 0.7-1.3. Based on these results, we conclude that it is interesting to follow up on the measurement of students' computational thinking more widely using CTT.

Keywords: Computational thinking test, Bioinformatics database, Pre-service biology teachers

INTRODUCTION

Computer literacy is a realistic need in today's education. Computational Thinking (CT) is widely recognized as a fundamental cognitive skill essential to adapting to our technology-driven society. It is increasingly integrated into educational curricula worldwide (Zapata-Cáceres et al., 2024; Angeli & Giannakos, 2020; So et al, 2020; Grover & Pea, 2013; Mannila et al, 2014; Kong et al, 2018; Ioannou & Makridou, 2018; Merino-Armero 2022). Pewkam & Chamrat (2022) explained that computational thinking test (CTT) data showed that pre-service teachers' basic computational thinking skills consisted of decomposition, algorithms, pattern recognition, pattern generalization, and abstraction.

Computational thinking is needed to develop economically driven thinking and personal thinking as a cognitive tool. From an economic perspective, a better-educated workforce is an important element of an internationally competitive workforce, and computational thinking is an important component of education. However, the problem is that instructors or teachers do not introduce computational thinking to students in the learning process or in learning evaluation. So that students do not have computational thinking skills.

The need for development and analysis related to computational thinking measuring instruments so that students can have more choices of reliable and valid measuring instruments. One of them is the question of computational thinking oriented towards bioinformatics databases. Computational thinking is an approach to solving problems in a way that can be implemented using computers (Lee & Cho, 2021; Rodríguez del Rey et al, 2021; Lee & Apone, 2014; Buitrago Flórez et al, 2017; Barr & Stephenson, 2011; Boom et al, 2022; Belmar, 2022; Fessakis & Prantsoudi, 2019; Pérez-Marín, 2020), and bioinformatics databases exist in computers that contain rich data. Bioinformatics databases are rarely used in education, especially pre-service biology teachers in Indonesia.

Pre-service biology teachers must be literate in bioinformatics databases to support current experience, knowledge, and technology. One way to introduce bioinformatics databases is through computational thinking questions. Previously, research was conducted by Sari et al. (2021) regarding the analysis of the difficulty of computational thinking test items using Rasch analysis. Ten computational thinking test items from the Bebras Tasks were analyzed, covering four components of computational thinking skills:

decomposition, pattern recognition, abstraction, and algorithmic thinking. As a result, the computational thinking test showed a reliability index of 0.55 with a moderate level. The instrument was then used in the research of Sari et al. (2022) to determine students' computational thinking skills after receiving bioinformatics-based molecular genetics learning. The results showed that computational thinking skills increased significantly after studying molecular genetics using the Bioinformatics Module.

Finally, it is interesting to qualitatively and quantitatively examine computational thinking questions oriented to bioinformatics databases from NCBI (National Center for Biotechnology Information), UniProt, and SMS (Sequence Manipulation Suite) for pre-service biology teachers.

METHOD

This study uses the paradigm of pragmatism, which is highly recommended in mixed-method research. The research design used is a convergent parallel design, which compares, combines, or connects the results of qualitative and quantitative data analysis (Creswell & Clark, 2011). This study uses a bioinformatics database to analyze the computational thinking test question items qualitatively and quantitatively.

The qualitative data collection technique is a sheet of suggestions, inputs, and comments from experts in assessment in education, computational thinking, and bioinformatics. Qualitative data is analyzed using content analysis. Quantitative data collection technique is an assessment sheet by experts using a score (the maximum score is five and the minimum score is 1) for five criteria, including the construction of question items, the suitability of the material, the relevance of the question items to the skill indicators and question indicators, the logic of all answer options, and the variety of language used. In addition, the quantitative data collection technique is the Computational Thinking Test (CTT), which uses a bioinformatics database of 127 pre-service biology teachers to produce reliability values and an infit-outfit index based on the Rasch model.

Computational thinking test question items using bioinformatics database is a multiple-choice test, so it is dichotomous. This means that each correct question item is given a score of 1, and the wrong question item is given a score of 0, which can be seen in the Table 1. The test instruments developed are 14, so the maximum score that will be obtained is 14. So, using the formula in Table 1, the maximum value is 100.

Tabel 1. Performance Assessment Guide Pre-service Biology Teachers on Computational Thinking Test Items Using Bioinformatics Database

Question Number	Score	Question Number	Score
1	1	8	1
2	1	9	1
3	1	10	1
4	1	11	1
5	1	12	1
6	1	13	1
7	1	14	1
Maximum Score		14	
Value Acquisition		$\text{Value} = \frac{Score\ Obtained}{Maximum\ Score} \times 100$	

RESULTS AND DISCUSSION

Qualitative Analysis of Computational Thinking Test Items Using Bioinformatics Database

The Computational Thinking Test (CTT) using a bioinformatics database must be validated by experts to assess the feasibility of the test instrument in measuring students' computational thinking skills. Experts who assess the CTT bioinformatics database are material experts and evaluation experts. One of the experts commented on question number 1 that the term used was too high. The question is an indicator of decomposition and discusses BRCA2 gene mutations. The term used in question number 1 is a vocabulary from the bioinformatics database website or a word related to the database, namely NCBI. Individuals who are not familiar with the term will find it difficult. However, the CTT bioinformatics database allow students to practice their ability to solve problems, especially related to the bioinformatics database. This will increase knowledge and ability to access, analyze, and manipulate biological data (Sardi, 2022). Practice questions directly related to bioinformatics databases can add to students' abstraction and algorithms experience (Mariano et al., 2019). They were finding the right solutions to various problems, such as food, environmental, and health problems (Mahrus et al., 2021; Nurfadilah et al., 2023).

Budiharti et al. (2023) found that teachers are still too conceptual in developing question items. This does not help students explore the knowledge they have. CTT question items using bioinformatics databases provide opportunities for students to improve their reasoning and logic in solving problems through a series of situations in the question items. The situation in question is a stimulus that directs students to dig up information to answer the problems given. Therefore, as experts convey, the question items look complicated, detailed, and complex. According to other experts, detailed questions can explore students' critical thinking skills. Complex and complex question items train students to think creatively and critically. Students are expected to recall or restate information and carry out deeper processing and analysis. This can improve student learning outcomes because they are trained to think more complexly (Fanani, 2018).

CTT using a bioinformatics database is the latest breakthrough in the development of CTT because bioinformatics is a complex field (Ali et al., 2021), interdisciplinary (Johnston et al., 2022) and contextual data (Dow et al., 2021). One of the experts argued that he was interested in the CTT bioinformatics database questions developed. The expert felt students needed to learn bioinformatics databases from these question items. He added that mastering the questions on the CTT bioinformatics database and improving computational thinking skills increased the understanding of the importance of the Bioinformatics Database. This is in line with Nurfadilah et al. (2023) that introducing bioinformatics database activities can increase students' learning motivation because it connects the subject matter with the real-world context. This can make learning more meaningful and challenging for students.

The CTT bioinformatics database should be revised based on experts' advice. This helps identify possible deficiencies in the test instrument before the trial is conducted. These suggestions for improvement include the same answer options, foreign language words that are not italicized, writing errors in words (typo), and removing, adding, or replacing words in question items to make sentences more effective. In addition, experts also recommend improving question indicators subject matter questions and adding indicators of computational thinking skills to some question items. Question indicators are a guide in compiling CTT bioinformatics database question items. The validation results showed that there were indicators of questions that were not following the items that were prepared, such as question items 4 and 9. According to Kadir (2015), the question indicators must follow the question items to ensure the learning objectives' accuracy. Experts give input to write the topic asked in the question item, as shown in Table 2.

Table 2. Improvement of Question Indicators in Question Items Number 4 and 9

Before Revision		After Revision	
4.	A Distance Tree of Results is presented which displays a phylogenetic tree, students can determine the correct analysis results.	4.	A Distance Tree of Results is presented which displays a phylogenetic tree, students can arrange the appropriate steps to construct a phylogenetic tree.
9.	Presented with the Peptide Search page on the UniProt website, students can analyze one type of protein correctly.	9.	Presented with the Peptide Search page on the UniProt website, students can analyze uncharacterized proteins.

In question number 2, the stimulus given is related to each gene's percentage. Experts argue that there is more than one percentage in the picture so students will be confused about the percentage used. The improvement made was to write a description of the type of percentage used. This aims to improve the quality of the questions and ensure that the questions effectively measure students' abilities (Savika & Zuhriyah, 2024). Suggestions for improvement related to the question's subject matter are also found in question number 9. Experts argue that a subject with multiple questions will confuse students when choosing the correct answer. This follows the results of the research of Ilannur et al. (2020), which states that the question item must contain only one problem or idea. This aims to ensure that the question is unambiguous and can be answered clearly. Improvements to question numbers 2 and 9 can be seen in Table 3.

Table 3. Improvement of Question Points in Question Items Number 2 and 9

Before Revision		After Revision	
2.	From the results obtained, the researchers plan to construct a phylogenetic tree for several search results based on the percentage of each gene. Choose the image below to help researchers determine the phylogenetic tree pattern from the image above!	2.	From the results obtained, researchers plan to construct a phylogenetic tree for several search result samples based on the percentage of each gene in the Query cover. Choose the image below to help researchers determine the phylogenetic tree pattern from the image above!
9.	From the picture above, there is one name of a protein that has no character or uncharacterized protein. Analyze why this happened, which statement is true based on this event!	9.	From the picture above, there is one name of a protein that has no character or uncharacterized protein. Analyze the correct statement based on this event!

The last suggestion from experts is related to the indicators of computational thinking skills contained in the question items. Experts suggest adding indicators of pattern recognition skills in question number 3 and decomposition in question number 6. Adding these indicators aims to achieve the skills expected of students well. In addition, question items that contain all indicators of computational thinking skills train students to think mathematically, creatively, structuredly, and logically. This assists students in solving complex problems effectively and efficiently (Marhadi et al., 2023; Juldial & Haryadi, 2024).

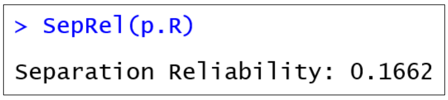
Quantitative Analysis of Computational Thinking Test Items Using Bioinformatics Database

The Computational Thinking Test (CTT) uses a bioinformatics database and is assessed by material and evaluation experts. The average percentage of assessment results by five experts on the CTT Bioinformatics Database is 91.83%, as shown in Table 4. The score is in the category of very feasible and valid for testing. However, expert advice is needed to improve the quality of the test instruments.

Table 4. Recapitulation of Computational Thinking Test Using Bioinformatics Database Assessment by Experts

Expert	1	2	3	4	5
Assessment Results (%)	91.7	92.3	90	94.6	90.6
Average Assessment Results (%)			91,83		
Criteria			Highly Worthy		

Based on the results of Rasch's analysis of the Computational Thinking Test (CTT) data using the bioinformatics database, a reliability coefficient of 0.2 was obtained, as shown in Figure 1. Reliability is the consistency of question items when making repeated measurements. Reliability is better if it is close to 1 (Avinc & Dogan, 2024). The obtained values show that the CTT bioinformatics database is less reliable in measuring students' computational thinking skills if done repeatedly.



```
> SepRel(p.R)
Separation Reliability: 0.1662
```

Figure 1. CTT Bioinformatics Database Reliability Coefficient

The results of the infit-outfit analysis show that all question items are acceptable because they are in the range of 0.7-1.3, as shown in Table 5 (Takacs *et al.*, 2021). Infit-outfit analysis is used to determine the functionality of question items in making measurements normally or vice versa (Hadiyanti *et al.*, 2024). The results obtained show that the CTT Bioinformatics Database can accurately measure student learning outcomes. In this case, it is the student's computational thinking skills.

Table 5. Summary of *Mean-Square Infit-Outfit Stats*

Item No.	**Indicators of Computational Thinking Skills**				**Infit MSQ**	**Outfit MSQ**	**Category**	**Item Difficulty**
	D	**PR**	**A**	**AT**				
1	✓				1	1	Accepted	-0.120
2		✓			1	1	Accepted	0.345
3		✓	✓		1	1	Accepted	-0.120
4				✓	1	1	Accepted	-0.653
5		✓			1	1	Accepted	0.179
6	✓		✓		1	1	Accepted	-0.524
7	✓				1	0,9	Accepted	0.573
8		✓			1	1	Accepted	-0.259
9			✓		0,9	0,9	Accepted	1.575
10				✓	1	1	Accepted	-0.556
11	✓				0,9	0,8	Accepted	-0.120
12		✓			0,9	0,8	Accepted	0.026
13			✓		1	0,9	Accepted	-0.190
14				✓	0,9	0,9	Accepted	-0.155

The Computational Thinking Test (CTT), which uses a bioinformatics database, aims to measure the computational thinking skills of students who are oriented to bioinformatics databases. The database comes from the National Centre for Biotechnology Information (NCBI), UniProt, and the Sequence Manipulation Suite (SMS). The three websites offer advanced functionality, such as BLAST, Align, PubMed, and Sequence Viewer, which can help students understand how to process and analyze biological data, such as database recognition and DNA and protein sequence analysis. Each indicator of computational thinking skills is developed into a question item that contains content from the three databases. According to Sari et al. (2022), the availability of bioinformatics tools and databases can be used to facilitate academics, especially educators, to be implemented in schools. Shue et al. (2023) also argue that using computers makes students increasingly face the challenge of deciphering complex problems into several more manageable sub-problems. By studying bioinformatics, students can develop technical skills in using software and databases to analyze biological data. This is very useful in understanding genetic material and molecular biology (Pucker *et al.*, 2019).

The bioinformatics database content in each question item has a variety of concepts. Decomposition and abstraction indicators address mutational material, genetic substance, and DNA replication. At the same time, the pattern recognition indicator and algorithmic thinking discuss the material of genetic substance, evolution, DNA replication, and protein synthesis. The material contained in the CTT bioinformatics database can be a reference for teachers, especially on the concept of genetics when introducing bioinformatics databases. As according to Mariano et al. (2019), abstraction, algorithms, computer programming, and biological problems can be addressed by bioinformatics and computational biology. Algorithmic activities in the bioinformatics class include cluster detection, alignment, phylogenetics, and motif detection (Gatherer, 2020). Algorithms for analyzing biological data have become more sophisticated, and the performance of computers is continuously improving, allowing for a deeper analysis of data (Martins et al., 2018).

Table 5 shows that the most difficult problem is found in problem number four with an abstract skill indicator. The indicator of the question is "Presented *with a Distance Tree of Result* that displays a phylogenetic tree; students can arrange the right stages to construct a phylogenetic tree". The results obtained indicate that students have not mastered the concept of evolution, especially related to phylogenetic tree material. This is a challenge for teachers in secondary schools to be able to develop effective learning strategies, for example, by using innovative learning media such as phylogenetic trees based on research results that can help students understand the concepts of evolution and genetic diversity more concretely (Mahrus *et al.*, 2021).

Mastering computational thinking skills is important in today's era. These skills train the brain to think logically, creatively, and in a structured way. This is particularly useful in analyzing complex biological data, such as using algorithms to analyze DNA or protein sequences (Tikva & Tambouris, 2021). In addition, computational thinking skills involve the use of algorithms in various calculations, automation, and data processing processes. In the Bioinformatics Database, algorithms are used to analyze DNA sequences, proteins, and other genetic data. Such as the BLAST algorithm used to search for protein homology (Norasit *et al.*, 2023)

CONCLUSION

We can conclude that CTT draws on a bioinformatics database that was created using results from qualitative analyses that are unique and sophisticated, with enhancements made to the language and answer options. According to quantitative results, the reliability value is included in the very low category, and computational thinking questions are included in the very feasible category with a value of 91.83. But, each question item is included in the acceptable category with a range of suitability-suitability indexes of 0.7-1.3. These findings make it worthwhile to investigate utilizing CTT to measure students' computational thinking in a broader sense.

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