

Exploration of Bioinformatics Skills in Pre-service Biology Teachers

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Abstract

This study analyzes the bioinformatics skills and a selection of related experiences of student biology teachers who had varying amounts of formal training in courses on bioinformatics. Data were collected using a qualitative approach from 26 students who did and 23 students who did not take the bioinformatics course. The data collection instrument consisted of three opinion-based items and three items that tested cognitive performance. Qualitative data analyses made use of thematic analysis supported by diagramming; cognitive performances were analyzed by descriptive statistics. The results indicated descriptive differences in the skill profiles of the two groups, including tool use, reflective learning practices, perceived task difficulty, and biology knowledge scores-70.29% for students with course exposure and 63.63% for those without course exposure. As an exploratory study, these findings provide empirical insight into the distribution of bioinformatics-related competencies and learning experiences among prospective biology teachers. Therefore, future studies should consider longitudinal or experimental designs to better understand how bioinformatics learning can be optimally integrated into biology teacher education.

Keywords: Bioinformatics skills, Exploration, Pre-service biology teachers

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1. Introduction

The emergence of high-throughput approaches in molecular biology, proteomics, and next-generation sequencing has generated enormous amounts of data. However, interpreting and analyzing data from these approaches requires knowledge of bioinformatics (Goodwin et al., 2017; Calderón-González et al., 2016). Bioinformatics has also become an essential part of biology education because it can provide a comprehensive understanding of the complexities involved in molecular biology. Therefore, bioinformatics can help students develop the ability to analyze data involved in genetics and proteomics (Achappa & Desai, 2021; Martins et al., 2020; Sari & El Islami, 2025). This makes bioinformatics an integral part of biology education because it involves technical aspects.

Pre-service biology teachers can apply bioinformatics literacy to empower themselves to face challenges in school based on data-driven learning. Bioinformatics in schools helps students connect molecular biology and genetics theory with biology software and databases (Martins et al., 2020). This is crucial in training biology teachers who can implement modern technologies and learning approaches. Thus, bioinformatics expertise can act as a bridge between modern scientific advances and approaches that can address the challenges of 21st-century learning in schools.

Although bioinformatics is a high-priority field, biology education students often face challenges in mastering it. Most biology education curricula emphasize the mastery of basic biology, genetics, ecology, and pedagogy concepts, which can leave computational literacy and bioinformatics underrepresented (Omoseebi, 2021; Coker et al., 2022; Sari & El Islami, 2025). As a result, students' skills in using sequence analysis software, basic programming, and data interpretation are still limited. This has an impact on students' readiness to face the increasingly data-driven development of molecular biology.

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Pre-service biology teachers are required not only to understand the content of conventional biology but also to be able to integrate modern biology issues into the learning process. Bioinformatics provides an opportunity to involve students in learning the aspects of genetics, evolution, biotechnology, and personal medicine as a data-driven subject (Radford et al., 2022; El Islami et al., 2022; Hotaling et al., 2018). The mastery of bioinformatics methods thus allows pre-service biology teachers to design instruction more contextual, data-driven, and responsive to the latest scientific developments.

Furthermore, bioinformatics competence enables one to achieve computational thinking, data analysis, and problem-solving skills which constitute the 21st-century skills (Lodi & Martini, 2021; Wing, 2008; Sari et al., 2022). From a learning biology point of view, such competence is essential in preparing learners to critically consider biological data, recognize patterns, and relate them to real-world biological processes. Thus, future biology teachers familiar with bioinformatics will be well positioned to provide teaching that is sensitive to technological change and social demand, informed by science and evidence.

Different studies have proven the benefit of learning bioinformatics at the secondary and tertiary levels. For example, workshops on bioinformatics have been proved to improve students' understanding of the use and purpose of bioinformatics tools, with the impact persisting for a period of weeks after the exercise (Williams et al., 2019). Apart from that, bioinformatics-based learning at high school level enhances gene concept and genome knowledge along with awareness of application-oriented uses of bioinformatics in students (Machluf & Yarden, 2013). That means that the integration of bioinformatics can enhance understanding of biological concepts and enhance the range of applications of analytical tools (Sari et al., 2024; Sari et al., 2025).

Several studies have also developed instruments for evaluating bioinformatics competencies through the cognitive and perceptive dimensions of students (Wu & Palani, 2015). The study emphasizes the reality that perceptions towards bioinformatics among students are closely associated with their motivation to learn as well as the cognitive competencies they achieve. These results show that bioinformatics competencies can be developed through formal, structured learning experiences, and that they also provide a useful basis for assessing the success of bioinformatics education in biology education.

Even though a significant body of literature has recognized the role of bioinformatics in education, empirical research findings on bioinformatics skills levels for biology education students with varying levels of formal bioinformatics exposure are limited. It has been found that current research has generally emphasized bioinformatics learning via workshops or curriculum development programs and has often overlooked the detailed exploration regarding the extent of the students' skill level based on their learning experience (Marques et al., 2014; Costa et al., 2024). As a result, a research gap lies between understanding the extent of bioinformatics literacy and competencies among biology education students based on their formal bioinformatics learning experience.

This research is significant as an exploratory, observational study that offers insight into the skill level of pre-service biology teachers with varying levels of experience in formal bioinformatics coursework. This research does not seek to determine the effectiveness of the teaching, but rather the trends in skill development, be it in data analysis, use of bioinformatics tools, or comprehension of molecular biology principles among these prospective biology teachers. Such information is well-suited for use in curricular conversations with regard to areas of strength or areas for improvement in the knowledge levels regarding contemporary scientific techniques among these prospective teachers.

On the basis of the rationale described, the objective of the current study is to investigate the bioinformatics skill possessed by biology education students based on their experience levels in bioinformatics learning sessions. In the proposed study, the perceived levels of bioinformatics and the levels of cognitive performance pertaining to bioinformatics are measured through opinion-based methods and content-based tests, respectively. This study being an exploration based study will basically describe the findings and not come to any causal interpretation related to the impact of bioinformatics education. The proposed study will basically lay some initial findings related to the current levels of bioinformatics skill existing in pre-service biology teachers and form the foundation for future studies related to the topic.

2. Methods

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This study employed an exploratory research design (Stevens & Wrenn, 2013) to describe bioinformatics skills among pre-service biology teachers with different levels of exposure to formal bioinformatics coursework. Participants were undergraduate students enrolled in a Biology Education program at a public university in Indonesia. They were categorized based on their prior academic exposure to bioinformatics, namely students who had completed a bioinformatics course ($n = 26$) and those who had not ($n = 23$). Participants were not grouped randomly, but rather according to their educational path, and not in relation to an experiment being conducted. There was a purposive sampling technique used to gain representation from students both without and with exposure to the bioinformatics course, as to compare the two groups descriptively, which may show self-selection bias.

2.1. Research Instrument

The research instrument was developed on the basis of the competency indicators for bioinformatics, developed by Wu and Palani (2015) and Mulder et al. (2018), within the four competency areas: (1) bioinformatics tools, (2) statistical software systems, (3) programming, and (4) biology knowledge. The research instrument aims to explore the perceptual and cognitive components of the competency for the field of bioinformatics. The research instrument contains two kinds of questions, including perception and cognitive questions.

Section A: Perception-Based Items

(Bioinformatics Tools, Statistical Software Systems, and Programming Skills)

This section comprised nine open-ended items (three items per domain) aimed at eliciting students' self-reported experiences, familiarity, and perceived challenges related to bioinformatics-related competencies.

(1) Bioinformatics Tools (3 items)

Participants were asked: 1) *What bioinformatics tools have you used?* 2) *What was your experience like after using these bioinformatics tools and* 3) *What challenges did you face after using these bioinformatics tools?*

(2) Statistical Software Systems (3 items)

Participants were asked: 1) *What statistical software have you used?* 2) *What was your experience like after using that statistical software?* and 3) *What challenges did you face after using that statistical software?*

(3) Programming Skills (3 items)

Participants were asked: 1) *What programming or scripting languages have you used?* 2) *What was your experience like using that programming or scripting language?* and 9) *What challenges did you face after using that programming or scripting language?*

Analysis of Perception-Based Items

Data from the perception-based items were analyzed using thematic analysis. Emerging themes were identified related to the number of bioinformatics tools used, the benefits of using bioinformatics, and the challenges faced. The results are presented using diagrams and then described.

Section B: Cognitive-Based Items

(Biology Knowledge – 3 items)

This section assessed students' ability to apply biological knowledge relevant to bioinformatics contexts. Three open-ended cognitive tasks were included:

(1) Central Dogma of Molecular Biology

Participants were asked to explain the central dogma of molecular biology and illustrate the flow of genetic information from DNA to RNA to protein, including the roles of each molecule.

(2) Molecular Biology Basis of Cancer

Participants were asked to explain cancer from a molecular biology perspective, with particular emphasis on the role of genetic mutations in uncontrolled cell growth.

(3) Sequence Analysis Using BLAST Output

Participants were provided with BLAST output data and asked to identify which sequence showed the highest similarity to the query sequence, justifying their answer based on identity score and E-value and we can see in Figure 1.

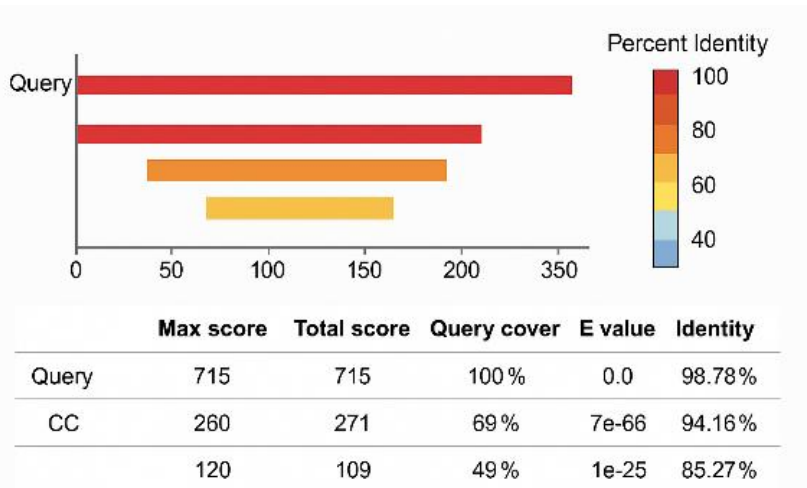


Figure 1. Diagram for three questions of biology knowledge

2.2. Scoring Rubric for Biology Knowledge Items

Each cognitive-based item was scored using an analytic rubric with a maximum score of 3 points per item, resulting in a total possible score of 9 points, and we can see in Table 1.

Table 1. Scoring of the analytic rubric

Score	Criteria
3	Complete, accurate explanation; correct use of terminology; clear reasoning and justification
2	Partial understanding; key concepts mentioned but not fully explained
1	Minimal relevant content
0	No response or entirely incorrect answer

Scores were converted into percentage values for descriptive comparison across participants.

2.3. Instrument Validation and Trustworthiness

Content validity of the instrument was established through expert review involving two lecturers specializing in bioinformatics (with teaching and research experience in computational biology and bioinformatics education) and one biology education specialist with expertise in curriculum design and assessment. The team assessed the items based on relevance, clarity, alignment with the bioinformatics competency framework identified in a related study by Wu and Palani (2015) and Mulder et al. (2018) and appropriateness for pre-service biology teachers.

Based on feedback, various modifications were made, including clarifying item wording, refining task instructions for biological knowledge items, and aligning terminology with standard practices in bioinformatics. These modifications were made to ensure that the instrument adequately covered the competency areas.

A pilot test was conducted among 10 student prospective biology teachers who did not participate in the larger study to determine the comprehension and practice items. Because the items in the perception component consist of a series of questions related to aspects of experience, internal consistency was determined only in this area, yielding a Cronbach's alpha value above 0.75.

For the cognitive-based biology knowledge items, which were designed to assess distinct conceptual domains (central dogma, molecular basis of cancer, and sequence analysis), internal consistency reliability was not calculated, as these

items do not represent a unidimensional construct. Instead, trustworthiness was supported through the use of an analytic scoring rubric, expert validation of scoring criteria, and consistent application of the rubric across all responses.

3. Results and Discussion

3.1. Patterns of Bioinformatics Tool Usage among Students with Different Course Exposur

Figures 2 and 3 indicate that students who did not take bioinformatics courses predominantly reported the use of basic bioinformatics tools, particularly BLAST and NCBI/GenBank. MEGA was used by a smaller proportion of students (20%), while more advanced tools, including Clustal Omega, R, Python, and PyMOL, were reported infrequently or not at all (3.3–6.7%). This pattern suggests that students without formal bioinformatics coursework tend to rely on tools commonly introduced in entry-level molecular biology and genetics contexts, with limited engagement in computational scripting or structural visualization tools. Similar patterns have been reported by Stangherlin Machado Paixão-Côrtés et al. (2018) and Sari et al., (2024), who found that platforms such as NCBI and GenBank are frequently used in introductory bioinformatics instruction, whereas programming languages and advanced databases are less commonly encountered without a stronger computational background.

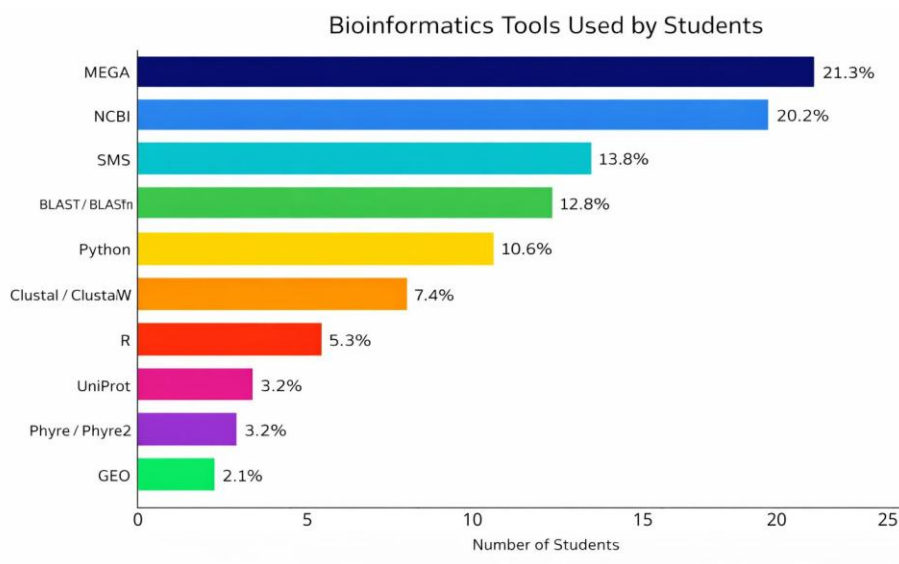


Figure 2. Variations of bioinformatics tools for students who take bioinformatics courses

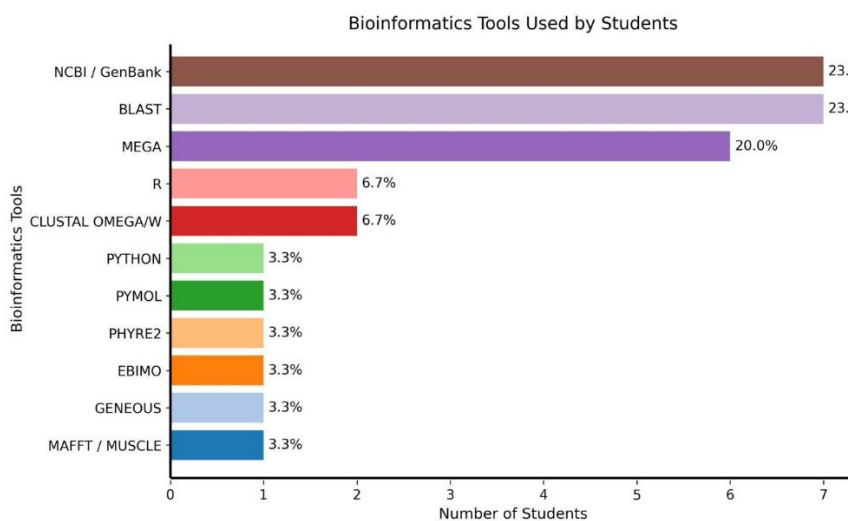


Figure 3. Variations of bioinformatics tools for students who didn't take bioinformatics courses

Students who took the bioinformatics course reported the use of a wider set of tools. Besides the commonly used tools such as BLAST, NCBI, or MEGA, others, including SwissProt, UniProt, or Clustal, GEO, and programming languages such as Python, were cited. These findings tend to show that formal instruction in bioinformatics may be related to knowledge of more bioinformatics resources, as well as sequence alignment databases. Rather than having any implication of a causal relationship, the above findings descriptively point to the different levels of the set of tools students use. This study does not permit any inference with regard to whether any direct relationship exists with improved competency or mastery of the skills. Future studies can investigate how specific teaching methodologies or pedagogical procedures affect the acquisition of the respective competencies based on the appropriate study design.

3.2. Student Experiences with Bioinformatics Tools

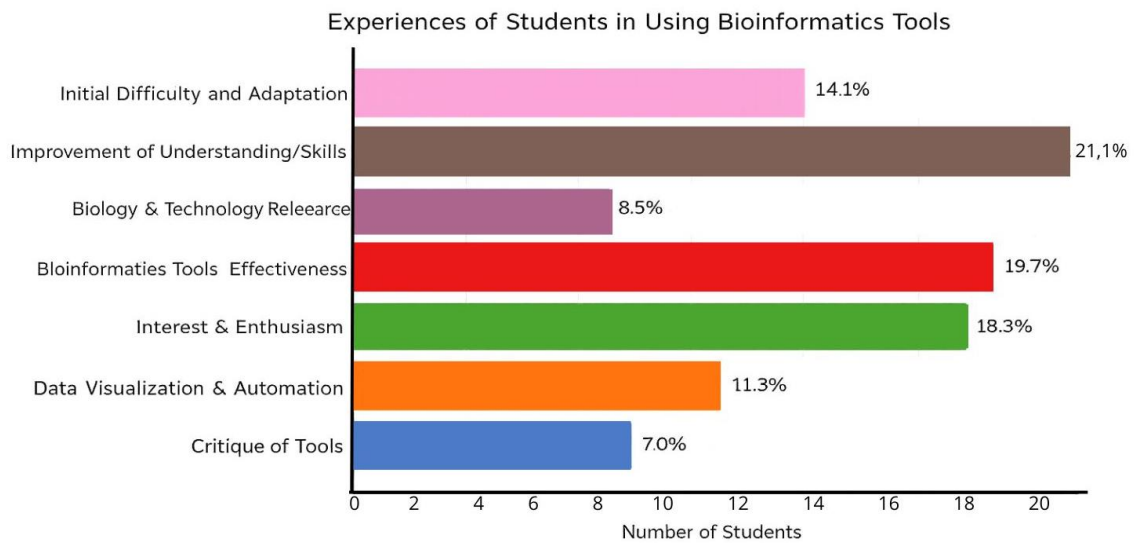


Figure 4. Experiences of bioinformatics tools for students who take bioinformatics courses

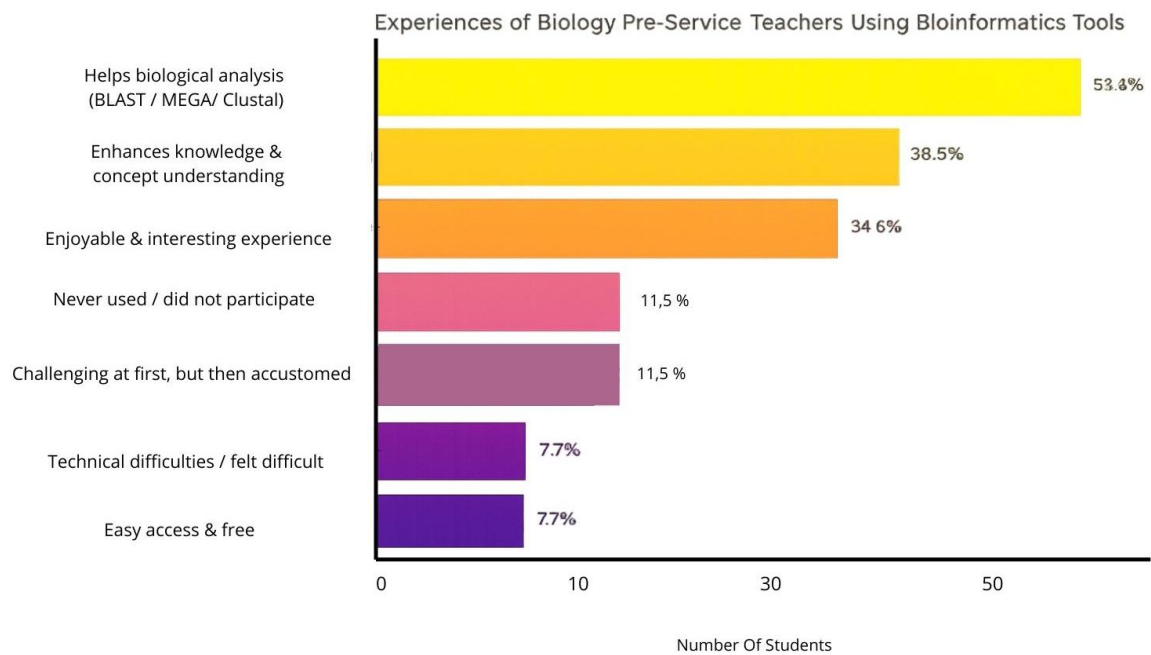


Figure 5. Experiences of bioinformatics tools for students who didn't take bioinformatics courses

Figures 4 and 5 show that students who did not take bioinformatics courses most frequently reported using bioinformatics tools to support basic biological analyses, such as sequence alignment and simple data exploration (BLAST/MEGA/Clustal; 51.8%). Additional reported experiences included increased conceptual understanding (38.5%) and positive or engaging learning experiences (34.6%). At the same time, a proportion of these students indicated limited familiarity with bioinformatics tools or uncertainty about how the tools function (11.5%), as well as technical difficulties (7.7%). This trend provides evidence that students without formal education in bioinformatics tend to have exposure to bioinformatics tools at either an introductory or surface level, further confirming findings that found novice learners felt underprepared for the technical and interpretive demands of working with bioinformatics tools (Drew et al., 2023). Students with prior experience in bioinformatics courses tended to have a greater incidence of experience with skills (21.3%), data analysis and interpretation (19.2%), and data visualization/animation (12.8%). However, these students also experienced difficulties, particularly with initial adjustment to unfamiliar software (14.9%), as well as confusion with specific software functions (2.1%). This latter adjustment is consistent with the view expressed by Gao & Guo (2023) that students with some formal bioinformatics training typically face initial challenges before becoming accustomed to the bioinformatics software environment. These findings suggest the need to introduce bioinformatics in a more scaffolded and progressive manner across biology education programs and embedding foundational bioinformatics skills early in the curriculum.

Cumulatively, item-level analyses of student experiences highlight descriptive trends indicating variation among students with different levels of experience in the use of bioinformatics tools. Some students without classroom experience tended to focus on general exploration, conceptual development, or other non-technical aspects, while others with classroom experience tended to focus more on practical use. The results of this study aim to provide descriptive insights into these trends that can inform further investigation into how experience trends may vary across levels of exposure to bioinformatics tools among students.

3.3. Challenges of using bioinformatics tools

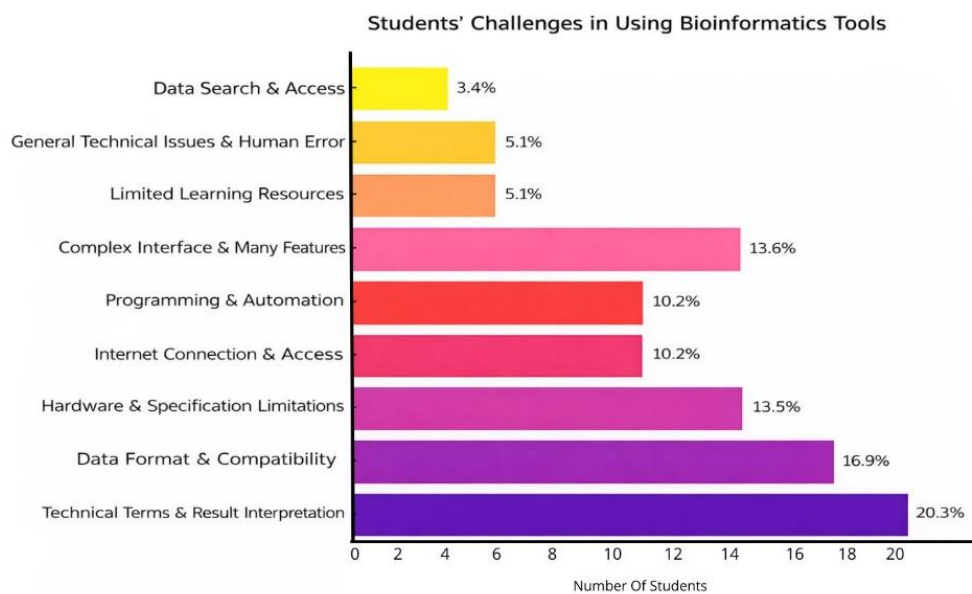


Figure 6. Challenges of bioinformatics for students who take bioinformatics courses

Figures 6 and 7 show some of the challenges faced by students using bioinformatics. Students without exposure to bioinformatics courses primarily faced challenges related to output data (28.6%), followed by challenges related to technical terminology and data formats (17.1% for both). Other challenges included limited knowledge of biology, limited use of bioinformatics programs, and limited knowledge. It appears that some students at the introductory level face challenges related to knowledge and use. These challenges have also been reported in other studies regarding limited training and knowledge, which impact students' ability to understand the complex output produced in bioinformatics (Akintola et al., 2024).

Students enrolled in bioinformatics courses experienced difficulties primarily related to technical and systems challenges, such as technical terminology and result interpretation (19.1%), data compatibility and formatting issues

(16.6%), and hardware or computing capabilities (13.3%). The findings from this specific challenge analysis highlight descriptive variations between the types of challenges faced by different learning backgrounds. Students who had never taken a bioinformatics course were more likely to face challenges in comprehension and interpretation compared to those who had taken a bioinformatics course. This finding aligns with existing data on the role of computing skills and internet access, which play a significant role in students' use of bioinformatics-related tools in developing country contexts (Sangeda et al., 2021).

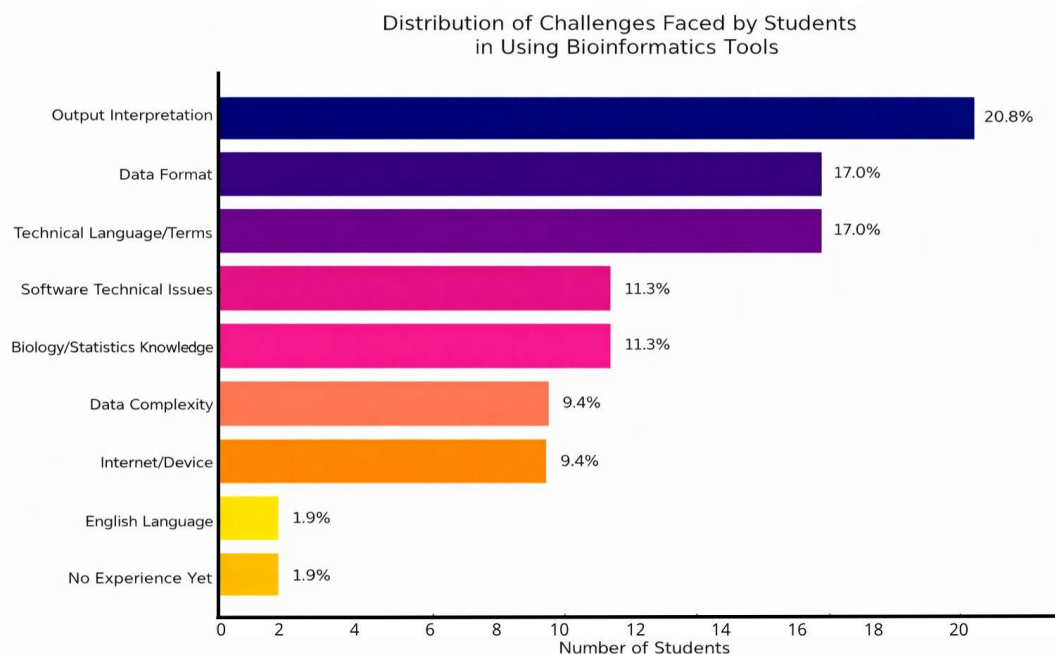


Figure 7. Challenges of bioinformatics for students who didn't take bioinformatics courses

3.4. Biology Knowledge across Bioinformatics-Related Assessment Items

Table 2 shows that the largest difference between the two groups was found on Item 1, the central dogma of molecular biology, a concept commonly emphasized in biology and bioinformatics curricula. However, performance on the more advanced questions (Items 2 and 3) declined for both groups. Surprisingly, students who had not taken a bioinformatics course performed slightly better on these questions than those who had. Items 2 and 3 involve higher-order reasoning skills, such as mechanistic thinking about cancer biology and the meaning of sequence analysis output. Because this pattern appears counterintuitive, this finding suggests that experience with bioinformatics tools does not guarantee better performance on tasks requiring integrated biological interpretation.

Table 2. Descriptive Summary of Student Performance on Bioinformatics-Related Biology Knowledge Items

Group	Item 1	Item 2	Item 3
Students without formal bioinformatics course exposure	70.37%	63.46%	51.85%
Students with formal bioinformatics course exposure	80.77%	57.69%	48.08%

These results are consistent with other studies showing that students are generally stronger on declarative/procedural questions than on analytical questions that require linking biological concepts to computational outcomes (Machluf et al., 2017; Kalra, 2025; Sari et al., 2022). In this regard, students with bioinformatics experience may be more drawn to their knowledge and experience with the tools themselves and with procedural processes, while those without experience may be able to utilize their existing knowledge of biological concepts. This exploratory analysis suggests that, while learning experiences are positively associated with achievement in fundamental biological concepts related to bioinformatics, there remains a challenge in how these learning experiences are tailored to effectively integrate computational outcomes with higher-order reasoning processes that occur in biology.

4. Conclusion

The conclusions of this study indicate that pre-service biology teachers who had taken a formal bioinformatics course performed higher on average on specific biological knowledge tasks related to bioinformatics and reported engagement with a wider range of bioinformatics tools than students without such course exposure. Other findings included differences in students' learning experiences and challenges; students exposed to bioinformatics struggled more with technically oriented tasks, while fundamental and integrative biological reasoning posed challenges for both groups. This study provides empirical insight into the distribution of competencies and learning experiences related to bioinformatics among prospective biology teachers. Therefore, future studies should consider longitudinal or experimental designs, larger and more diverse samples, and more comprehensive assessment instruments to better understand how bioinformatics learning can be optimally integrated into biology teacher education.

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Conflicts of Interest: The authors declare that they have no conflicts of interest to report regarding the present study.

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