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The Role of Bioinformatics in Education: A Mini Review of its Applications and Challenges

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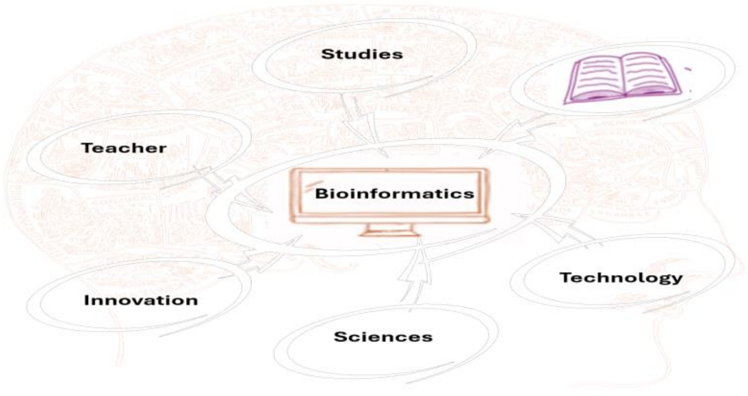
This study investigates the integration of bioinformatics in science education in Brazil, highlighting its relevance and challenges. The introduction emphasizes the need to rethink teacher training to include current technologies, allowing science teachers to use bioinformatics as an educational tool. The objectives include analyzing recent initiatives to integrate bioinformatics into classrooms and suggesting new approaches for teacher training. The methodology involves a descriptive and exploratory bibliographic analysis, with a survey of relevant scientific articles and content analysis. The results show that bioinformatics enriches the school curriculum, promoting active learning and interdisciplinarity, although it faces obstacles such as a lack of infrastructure and the complexity of data. It concludes that, despite the challenges, bioinformatics represents a valuable opportunity to empower students in modern sciences. A joint commitment between educational institutions and professionals is recommended to train a new generation of scientists capable of operating in an interconnected and technological world.

Graphical abstract



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1. Introduction

Appropriating current technologies didactically implies new teaching practices, training processes, and support that ensure proper integration during professional development. Thus, it is important to rethink teacher qualification, as it needs to go beyond theoretical training. Therefore, the training of teachers who will work in the areas of mathematics, physics, chemistry, and biology must enable students to observe their environment as active realities and allow for constant change in pedagogical practice. Understanding these new technologies and applying them in the learning

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process is particularly significant, especially in the context of scientific revolutions [1].

Scientific revolutions have brought new fields of knowledge across various branches of learning, among which educational and/or technological innovations can be leveraged by educators. Within these innovations, we have bioinformatics, a field of knowledge that enhances scientific understanding through computational resources for the study of human genomes, DNA sequencing analysis, and protein analysis, providing more effective answers regarding pharmaceuticals and their side effects. It manipulates various biological data, encompassing a range of aspects such as processing, storage, and distribution of biological information, as well as the treatment of complex data related to potential mechanisms of phytoremediation [2, 3].

Thus, the continuous and rapid changes in contemporary society demand a new teacher profile, highlighting the need to rethink teacher training, starting from the diversity of knowledge essential to their practice. This means that we cannot focus on training professionals solely within a technical rationality; rather, we must foster a reflective, investigative, and critical stance. Active methodologies serve as starting points for advancing processes of reflection, cognitive integration, generalization, and the re-elaboration of new practices [4].

Currently, computational resources are assisting in education with the aim of enhancing the learning process by depicting theoretical concepts interactively. The use of multimodal representations contributes to the visualization of more complex structures, allowing for a deeper understanding of the content. These computational tools enable the same concept to be visualized in various forms or different languages, whether descriptive, experimental, mathematical, figurative, gestural, or bodily [5].

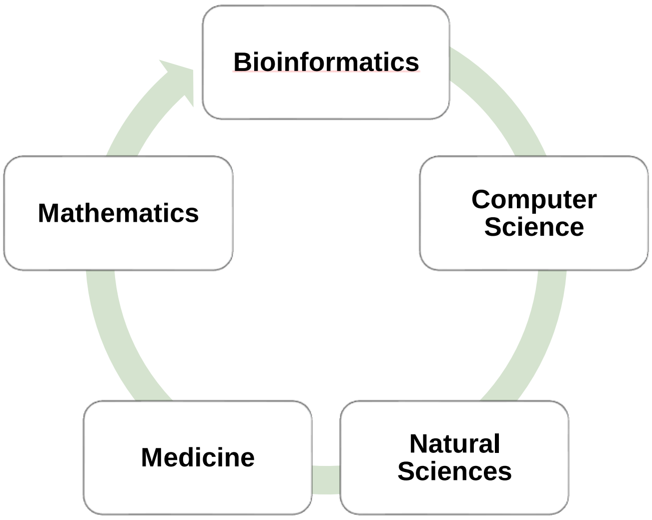
Bioinformatics tools encompass the concept of multimodal representation, making them essential instruments for establishing a new perspective in the teaching of various concepts. It is within this context that the concept of meaningful learning, developed by Ausubel, comes into play. This concept connects the student's prior knowledge with new information presented by the teacher in the theory of meaningful learning, which requires the active participation of the learner [6].

Education in bioinformatics can be broadly defined as the teaching and learning of the use of computer science and information technology, along with mathematical and statistical analysis, to collect, store, analyze, interpret, and integrate data to solve biological problems. The recent growth in genomics, proteomics, and structural biology, in the potential advancement of research and development in complex biomedical systems, has created the need for a workforce trained in bioinformatics [7].

In Brazil, the significant challenge of effectively integrating education in bioinformatics through formal and informal educational contexts has been partly due to its interdisciplinary nature. For this reason, this article analyzes recent initiatives to incorporate the rapidly growing interdisciplinary field of bioinformatics into classrooms and discusses ideas and experiences related to the teaching and learning of bioinformatics in high schools. New approaches involving teacher training and the pursuit of means to enhance the construction of this new type of knowledge have also been suggested.

2. Results and Discussion

Through a literature review conducted in 2020, it was found that, being a recent science, bioinformatics still lacks a precise definition. This fact assigns it the task of organizing and analyzing incredibly complex data resulting from modern molecular biology and biochemistry techniques. However, it can be understood as an emerging research field that utilizes advanced computational tools for the storage, analysis, and presentation of biological and molecular data. Thus, it is an interdisciplinary area that integrates computer science, mathematics, biology, chemistry, physics, and medicine, producing a process of constant interaction among these sciences (Scheme 1).



Scheme 1. Interaction of the areas that have contributed to the formation and development of bioinformatics.

From now on, different areas of knowledge are presented in isolation, highlighting their interface with bioinformatics. For example, the basic training of a physicist focused on studying biomolecular systems requires, above all, a solid foundation in traditional physics topics. Thus, it is important to have contact with classical mechanics, thermodynamics, statistical mechanics, electromagnetism, and quantum mechanics, in addition to the appropriate mathematical tools and a good experience with the experimental method. The concepts related to these areas provide a specific perspective on natural phenomena and their description, forming part of their traditional training. Recognizing the importance of this basic education, it is also necessary to pay attention to the need for specific knowledge about biological systems. In this context, concepts related to biochemistry, cellular biology, and molecular biology should be included in the training of a biological physicist. This area also necessarily requires some particularities, such as notions of molecular biophysics and the innovative field of bioinformatics [8].

It is described that bioinformatics has roots, meaning it gathers techniques and tools from the following areas: a) molecular biology: the source of information to be analyzed; b) computer science or informatics: providing the hardware for analysis and networks to share results; and c) mathematics: the origin of the algorithms used in information analysis. Periodically, potential clinical applications using bioinformatics tools emerge, especially in the development and discovery of new pharmaceutical drugs [9].

In relation to the knowledge of the chemical field, from the perspective of bioinformatics, these are now seen as fundamental to the life sciences. However, there are negative aspects, among which is the closed knowledge that cannot be accessed without permission. This negative point is a barrier that hinders the free dissemination of bioinformatics knowledge, as the informatics and software techniques related to chemistry are limited and often require paid access. With the advent of bioinformatics, new technologies promise more accessible knowledge for working with advanced computational programs, which are quite promising for theoretical and/or medicinal chemistry [10].

Among the various areas of chemistry, one of the fields that most employs bioinformatics is medicinal chemistry. The numerical encoding of chemical structures using topological indices is strengthening the relationship between this area of chemistry and bioinformatics. Bioinformatics provides useful tools for studying the structure-activity relationship (QSAR), which are models that connect chemical structure with its diverse biological activities [11].

For biology, bioinformatics is one of the pillars of modern biotechnology, responsible for the development and application of information technology tools to enable the organization, management, analysis, and interpretation of data. Techniques for early and accurate diagnosis of complex diseases, the development and analysis of drug efficacy, the improvement of economically important animal and plant species, the production of renewable energy, and the creation of bioactive molecules for various industrial sectors promise to expand the range of applications for bioinformatics. In the educational field, bioinformatics is divided into four categories: concepts, methods, computational tools, and services [13]. Additionally, integrative education studies are already seeking to enhance the content of genomics and transcriptomics, as this relationship is in high demand for training biologists with solid knowledge that combines molecular biology and bioinformatics.

In the field of agronomy, an economically important sector for Brazil, bioinformatics has contributed to the genetic improvement of certain legume species, ensuring immediate use and the potential to produce results in the short and medium term. Brazil is already capable of utilizing cutting-edge technologies in research of national and global interest, which is a source of pride. Whether in crops such as castor bean, cactus pear, and sugarcane, or in energy forests and waste treatment, there are ongoing or planned research projects across various areas of agricultural research where the proper use of bioinformatics is essential for achieving good results. Thus, it is fair to say that through the tools provided by bioinformatics, biotechnology has a fundamental application in agriculture. Bioinformatics is a multidisciplinary area that employs computers to store and analyze molecular biology data, incorporating statistical algorithms [14].

The comparison of results from studies selected since 2023 reveals the growing integration of bioinformatics as a teaching tool, highlighting both its advantages and disadvantages across different study areas. Among the advantages, bioinformatics provides access to databases such as NCBI and PDB, allowing students to explore validated biological information. This practice is fundamental in fields like molecular biology and genetics, where the analysis of real data contributes to the development of critical skills. Additionally, the use of interactive software, such as Gurupi Isotherms Plot (GIP) and the game Foldit®, promotes a more active learning experience. This approach is essential for subjects that require the practical application of concepts, such as chemistry and biology, making learning more engaging and encouraging students to solve problems [16-17].

Bioinformatics also stands out for its ability to connect various fields of knowledge, such as biology, chemistry, and technology. Tools like OLATCG and R facilitate the understanding of complex concepts, allowing students to perceive the interrelation between different disciplines, which is crucial in the teaching of biological sciences [18-19]. Another important aspect is the development of skills such as critical thinking and problem-solving, which are essential for the academic and professional training of students, especially in areas that require data analysis and interpretation [20].

On the other hand, bioinformatics presents some disadvantages in the educational context. The introduction of software and online tools can result in a steep learning curve, posing a challenge for students who are not familiar with technology. This difficulty can impact the effectiveness of teaching, especially in areas like bioinformatics, which rely on the manipulation of complex data [16]. Furthermore, the effectiveness of bioinformatics in education is directly related to access to technology and the internet. In regions or institutions with limited infrastructure, this dependence can become a significant barrier to the implementation of educational practices based on bioinformatics [15]. The interpretation of complex biological data can also be challenging and may require additional support for students to fully understand the results, which is especially relevant in subjects like molecular biology [17].

Bioinformatics has shown significant growth as an educational tool, especially in the current context of hybrid and remote teaching. Bioinformatics not only enriches the school curriculum but also provides an innovative approach to engage students [20-21]. The results of the mini-course on the use of GIP indicate that the comparison between traditional and technological methods can lead to a deeper understanding of the content. Furthermore, the integration of practical activities, such as the search for the lost gene in NCBI, highlights the potential for active and collaborative learning that bioinformatics can provide [20].

3. Material and Methods

This survey, characterized as a state of knowledge assessment, is descriptive and exploratory, utilizing a mixed approach and bibliographic analysis to identify elements within the set of scientific articles found on bioinformatics focused on Science Education. Knowledge state research serves as a tool to deepen understanding of a particular subject being addressed by the academic community and is used to gather characteristics of existing scientific production, relying on reliable sources and a defined temporal scope [11]. The chosen temporal scope was the last three years.

The first data collection took place in 2020, using sources from the journal databases available in the Scientific Electronic Library Online – SciELO (**http://www.scielo.br/?lng=pt**) and CAPES Journals. To select the journal articles, a search was conducted using the descriptors bioinformatics and Science Education.

The selection of material occurred in three stages: reading the title, abstract, and keywords; downloading the articles that showed relevance for full reading; and analyzing the data. The observed aspects in the production included: topics addressed, relationships established between areas of knowledge, objectives, employed methodologies, subjects involved, theoretical framework, and main results. These aspects served to establish relationships and identify trends in the studies and gaps in the investigation of this topic. The methodology used for data interpretation was content analysis [12], the categories were pre-established as follows.

In this sense, the literature searches focused on the keywords related to bioinformatics and its various branches, as shown below:

a) General Survey:

Bioinformatics and education: approximately 3,750 results (0.05s)

Bioinformatics and chemistry education: 2,290 results (0.05s)

Bioinformatics and mathematics education: approximately 1,520 results (0.05s)

Bioinformatics and physics teaching: approximately 2,450 results (0.07s)

b) Survey from 2020 onwards:

Bioinformatics and education: approximately 72 results (0.07s)

Bioinformatics and physics teaching: approximately 45 results (0.06s)

Bioinformatics and chemistry education: approximately 48 results (0.06s)

Bioinformatics and mathematics education: approximately 24 results (0.07s)

It is important to highlight that regarding the content of the databases, the search was guided by disciplines, missions, problems, or even in a multidisciplinary or interdisciplinary manner.

1. By discipline: databases that reflect the body of knowledge of a specific area.
2. By mission: databases aimed at supporting well-defined missions.
3. By problem: databases oriented towards solving specific problems.
4. Interdisciplinary: databases that cover more than one area of knowledge.
5. Multidisciplinary: databases that cover a wide range of areas of knowledge.

Currently, several studies are being developed to create tools capable of addressing the complex data storage problems faced by bioinformatics. Using the methodology of Mello et al. (2008), we also considered the following promises for solving problems encountered during this study:

1. An extensibility architecture to natively store a succession of data and execute search structures in the database.
2. “Warehousing” technologies for data in genetic patterns.
3. Data integration technologies to enable heterogeneous issues through distributed biological sources.
4. Internet portal technologies that allow the publication of research information in the field of bioinformatics, for both intranets and the internet.

Two additional questions were raised in this study: a) How does the literature describe curricular efforts to integrate bioinformatics education? b) How does the literature describe bioinformatics as a specific educational content?

In a second data collection, the methodology adopted for this research involved a detailed analysis of publications related to the theme "bioinformatics in classrooms," using the Google Scholar platform. Initially, searches were conducted with different descriptors, resulting in a significant number of publications: "bioinformatics in classrooms" yielded 2,280 results; "bioinformatics in classrooms and science" had 2,080 results; "bioinformatics in classrooms and biological sciences" accounted for 1,370 results; and "bioinformatics in classrooms and high school" resulted in 939 publications.

From 2023 onwards, the searches were updated, yielding the following results: "bioinformatics in classrooms" generated 242 results; "bioinformatics in classrooms and science" presented 229 results; "bioinformatics in classrooms and biological sciences" had 150 results; and "bioinformatics in classrooms and high school" resulted in 109 publications.

From this initial selection of publications from 2023, only those published in journals and/or conference proceedings that included practical applications related to teaching, using bioinformatics tools, were chosen.

Inclusion criteria for this research focused on articles that address bioinformatics with an emphasis on education, particularly in science teaching contexts. Only publications from journals and conference proceedings that include practical applications related to teaching and the use of bioinformatics tools were considered. Additionally, only articles published from 2020 onwards were included to ensure that the research reflects the most recent trends in the field. Furthermore, articles that present a clear analysis of the methodologies used in their research were prioritized to allow for a deeper understanding of the impact of bioinformatics on education. Exclusion criteria consisted of non-peer-reviewed articles, which are deemed less reliable; articles lacking practical applications in the educational context of bioinformatics; publications that do not focus on the intersection of bioinformatics and education or that address unrelated themes; and articles published before 2020, to maintain the relevance of the data analyzed.

A careful reading of the article titles was conducted for this screening. As a result, seven (7) articles that met the established criteria were selected (Table 1), which were analyzed in-depth regarding the methodologies used by these authors to conclude this study.

Table 1. Selected Publications from 2023.

Autor(es)	Publicação	Sigla / Abreviação	Área de Estudo
Cezar-de-Mello, P. F. T. et al. [20]	Revista de Ensino de Bioquímica	Rev. Ens. Bioquím.	Bioinformatics in Biology Education
Hassunuma, R. M.; Yonezawa, W. M. [17]	Revista Multidisciplinar em Saúde	Rev. Multidiscip. Saúde	Bioinformatics and Science Education
Hassunuma, Renato M.; Yonezawa, Wilson M. [21]	Revista Debates em Ensino de Química	Rev. Debates Ens. Quím.	Bioinformatics and Chemistry Education
Mariano, D.C.B. (org.) et al. [16]	BIOINFO #03 - Revista Bras. de Bioinformática	BIOINFO #03	Bioinformatics and Molecular Biology
Martins F. M. J. et al. [15]	Frontiers in Microbiology	Front Microbiol.	Bioinformatics and Microbiology Education
Mendes, A. C. O. et al. [18]	Anais XIV ENPEC	XIV ENPEC	Bioinformatics in Genetics Education
De Melo, G. S. [19]	Revista OWL - Rev. Interdisciplinar Ens. Educ.	Rev. OWL	Teaching Mathematics

Source: organized by the authors (2024).

4. Conclusions

The initial research on bioinformatics yielded a total of 10,010 articles, with the majority focusing on bioinformatics and education, which accounted for 37.5%. Following 2020, 189 articles were published, of which 38.1% pertained to bioinformatics and education. In classroom-focused studies, 6,669 articles were identified, with 34.2% related to bioinformatics in educational settings. Notably, only 3.7% of the articles published since 2020 were selected for in-depth analysis, highlighting a significant opportunity for expanding research in this field. These percentages illustrate the relevance and distribution of bioinformatics studies within educational practices and emphasize the need for further research and the development of educational materials.

Bioinformatics is an expanding field of knowledge, filled with technological innovations and a wide range of applications that encompass both basic and applied science. One of the greatest challenges in modern biology has been understanding vital processes at the molecular level, and the emergence of bioinformatics has been crucial in overcoming these challenges, proving to be a powerful tool for exploring this area quickly and efficiently. With bioinformatics, molecular biology has gained a new and complex dimension, especially concerning the study of DNA (deoxyribonucleic acid). This field has enabled the development of genetic mapping programs, such as the genome project, and has already made significant contributions to various disciplines, including medicine, agronomy, natural sciences, and mathematics. Furthermore, bioinformatics stands as an interdisciplinary field, acting as an interface between scientific and technological domains, resulting in remarkable advancements, such as the interpretation of genome sequencing data.

Medeiros et al., [22] designed a teaching resource to enhance students' grasp of Genetics and Molecular Biology concepts by conducting a practical simulation involving six newborns, whose identities were unknown at birth. Through this hands-on activity, students engaged in a genetic analysis using DNA sequencing techniques, learning about the significance of nitrogenous base sequencing and its applications in establishing genetic relationships. The findings demonstrated that this educational model not only facilitated a deeper comprehension of genetic principles but also effectively connected theoretical knowledge with practical applications, thereby enriching the learning experience in genetics education.

However, it is important to emphasize that the application of bioinformatics in high school education is still in its early stages, and one of the most promising ways to disseminate this knowledge is through university extension initiatives. The exponential growth of bioinformatics, driven by advancements in the sciences and new discoveries, faces challenges in Brazil, particularly the lack of qualified human resources in the field. The contemporaneity of bioinformatics and its interface with science education in Brazil reveal a dynamic and promising landscape, but also one filled with challenges. The increasing incorporation of bioinformatics into pedagogical practices reflects a significant effort to modernize education and equip students with essential skills for the job market.

Computational biology began in the 1950s, coinciding with the discovery of nucleic acid sequences, which created a need for computers to analyze these sequences and proteins. By the 1980s, the use of computers for biological sequence analysis became common among researchers, resulting in rapid expansion in discipline. The 1990s witnessed the development of important algorithms and tools, including BLAST - Basic Local Alignment Search Tool - for comparing DNA and protein sequences and microarrays for analyzing gene expression data, both of which contributed to advancements in the understanding of molecular evolution and the functional changes of genes and proteins [15].

The study by De Oliveira Mendes et al., [18] presents OLATCG as an innovative platform that integrates bioinformatics into science education, particularly aimed at high school students. The most notable results reveal significant engagement from the students, who demonstrated interest and motivation while interacting with the platform, feeling like "biomedical professionals" as they tackled issues related to COVID-19. The didactic strategy, based on collaborative learning, enabled enriching discussions and the joint development of solutions, creating an environment conducive to the exchange of ideas and the construction of knowledge.

Additionally, the students developed analytical skills by applying bioinformatics concepts to solve real problems, such as analyzing genetic sequences of SARS-CoV-2 using phylogenetic trees to understand evolutionary relationships. Despite initial difficulties, the pursuit of solutions through debates highlighted the importance of the scientific method, allowing students to articulate their knowledge. The students positively evaluated OLATCG, recognizing its effectiveness in teaching genetics and its ability to reduce abstraction in complex topics such as molecular biology [18].

The need to move away from a rote learning model to a more investigative and collaborative learning approach was a challenge, as many students were accustomed to a more traditional form of education [18]. Studies highlight that bioinformatics enriches the school curriculum, provides access to real data, promotes active learning, and fosters interdisciplinarity by connecting various areas of knowledge, such as biology, chemistry, and technology. However, the implementation of this educational approach faces obstacles, such as a steep learning curve, dependence on technology, and the complexity of biological data, which can be challenging for students. A study highlighted the effectiveness of different visualization methods for teaching the three-dimensional structure of biomolecules, specifically using the example of porcine insulin. The research compared a static two-dimensional representation, traditional bioinformatics software like RasMol, and the interactive three-dimensional model available in the game Foldit®. The findings indicated that while the static image only showed the arrangement of atoms, RasMol allowed observation of the secondary structure with alpha-helices, the Foldit® game facilitated manipulation of the protein structure, enabling players to explore various conformations and perspectives. The conclusion drawn from this comparison was that Foldit® significantly enhances understanding of a molecule's three-dimensional structure, as it provides users the opportunity to modify the conformation in pursuit of higher scores, thus offering a more engaging and insightful learning experience [16]. The effectiveness of bioinformatics in education depends on access to the necessary infrastructure and adequate training for educators, who must be prepared to use these tools meaningfully.

The study examined the teaching of molecular genetics, highlighting the challenges students face due to complex terminology and concepts. It found that 50% of students felt that the activity facilitated their understanding of molecular genetics, while 67% reported that the practical exercise made learning more engaging. Additionally, the implementation of bioinformatics as a pedagogical strategy was positively received, with 83.3% of students expressing a desire for more similar activities. The findings suggest that integrating bioinformatics can enhance comprehension and interest in genetics, despite some students noting difficulties with the English language [20].

Bioinformatics thus establishes itself as a valuable tool in the teaching of biology, chemistry, mathematics and engineering, presenting significant potential to enhance student learning and engagement. The study incorporated bioinformatics through a series of educational actions developed in a classroom setting using the Didactic Engineering methodology. Activities took place in a public high school in Itamaraju, Bahia, over eight 50-minute classes with two groups totaling 70 students. The R programming language was introduced, allowing students to turn formulas into code and test results in real time using online compilers, which was particularly effective for hardware-limited devices like Chromebooks. This process not only facilitated the learning of bioinformatics but also fostered an active learning environment where students could visualize, experiment, and discuss their findings, preparing them for future challenges in science and technology [19].

However, it is essential to consider the challenges that may arise during its implementation, ensuring that all students have access to the necessary technologies and support to fully benefit from this innovative approach. The main difficulties encountered during the study included the lack of familiarity among teachers with the topic of bioinformatics, which limits their ability to use it as a pedagogical resource, and the need for training to ensure they feel prepared to implement this innovative approach in teaching [20]

Results indicate that OLATCG not only facilitates learning in bioinformatics but also promotes a more active and contextualized education, aligned with the guidelines of the BNCC and contemporary educational demands [18]. Education in bioinformatics represents a valuable opportunity to empower students in facing the challenges of modern science, and the demand for a qualified workforce in this area underscores the importance of integrating bioinformatics into high school curricula. Additionally, the scarcity of bioinformatics-related initiatives in Basic Education and the necessity for closer dialogue between universities and schools to promote this integration were also significant challenges [20]. Therefore, the pursuit of new teaching approaches, combined with ongoing teacher training, is crucial to overcoming existing barriers, allowing students to fully benefit from the educational potential of bioinformatics. In conclusion, the successful integration of bioinformatics into high school curricula not only equips students with essential skills for modern scientific challenges but also fosters a collaborative educational environment, highlighting the need for ongoing partnerships between educational institutions and the scientific community to cultivate a future generation ready to thrive in a dynamic and technology-driven world.

Author Contributions

Ivani Souza Mello: initial research, writing, and structuring of the article. Marcelo Franco Leão: critical review of the literature on the integration of bioinformatics in classrooms. Sumaya Ferreira Guedes: writing and interpretation of the results. Benedito Carlos de Jesus: data collection and interpretation of the results. Mayker Lazaro Dantas Miranda: drafting and organization of the conclusions.

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