A Panorama on Selection and Use of Bioinformatics Tools in the Brazilian University Context

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Abstract. Bioinformatics is an interdisciplinary area that uses computational tools to process large amounts of biological data, such as sequence and structures of biological macromolecules, often derived from experimental methods. To manipulate these data and obtain meaningful results, bioinformatics employs a variety of databases and software tools based on complex interfaces, command line tools, task integration, abstract information, and jargons of a specific knowledge domain. Human-computer interaction issues, such as usability, ergonomics, satisfaction of use, and accessibility may hinder the efficient exploration of the multidimensional nature of biological information. In an educational context, these issues constitute barriers to the use of these tools, particularly by visually impaired users. In this artic, we investigate the technological/pedagogical resources used for teaching bioinformatics in the Brazilian context and the perceptions of educators about the inclusion of the visually impaired. A quantitative-qualitative methodology was used for data collection and analysis. The study shows the tools and procedures most commonly used to support the teaching of bioinformatics in Brazilian universities. Also, it reveals that most bioinformatics teachers are not prepared to work with visually impaired students, evidencing the lack of information on assistive/inclusive technologies and/or their use.

Keywords: Human-Computer Interaction · Bioinformatics tools
Bioinformatics teaching · Visually impaired users

1 Introduction

Bioinformatics employs computational techniques for extraction, analysis, storage and visualization of biological data on a large scale [19,24]. Studies have shown that bioinformatics has been growing rapidly and that career in bioinformatics will be one of the professions of the future [19,20,24]. There are several

tools for bioinformatics [1,19,24], which requires different types of user experience to extract the best computational results and often, specialized knowledge, skills to interact in three-dimensional spaces and to manipulate and interpret massive amounts of data. Studies point to tools that have limitations related to usability, ergonomics, user satisfaction and accessibility criteria [1,5,14,23,23,27,37,39].

This work is part of a larger project, which main objective is to design methods to represent information from structural bioinformatics that can be accessed and manipulated by blind students. For that, two studies were carried out, having bioinformatics professors from Brazilian higher education institutions as the sample population. Study 1 [23] aimed to identify which aspects make a bioinformatics resource to be chosen instead of others and compare them with ergonomic, user satisfaction and usability criteria [11,33]. It was conducted with a bioinformatics specialist through interviews, classroom observations and semi-structured questionnaires. The results indicated that the prioritized software were the ones that best meets the Human-Computer Interaction (HCI) criteria. The participant did not have formal knowledge in the area of HCI. However, he had 25 years of experience in bioinformatics research, with over 15 years in higher education. Study 1 confirmed that design principles are derived from knowledge based on theory, experience and common sense [33] and indicated criteria to be used or not in software interfaces for bioinformatics.

This article presents and discusses Study 2, which aims to build a panorama of bioinformatics teaching based on the following HCI criteria: selection and use of computational tools, and how and under what circumstances these pedagogical tools and strategies can be applied to visually impaired (VI) students. The study is based on qualitative and quantitative data from a nationwide survey conducted in December 2016. It was attended by 29 university professors (45% of the invited), who answered an online questionnaire, generating initial qualitative data that can serve as input to design interactive bioinformatics systems. Professors were selected from the Lattes platform of the Brazilian National Council for Scientific and Technological Development (CNPq)[1]. The questionnaire, elaborated from results of Study 1 [23], was organized into 4 sections with a total of 27 questions. The questions considered the professors' profile; the teaching methodology and computational resources; the HCI criteria for selection and use of software in bioinformatics disciplines; and the teaching of VI students with/without assistive technologies (AT).

Among the criteria for selecting tools were:

- to be freely available,
- to allow information to be saved, in many different formats, like text,
- to have help, documentation, tutorials, list of exercises and video-lessons,
- to be constantly updated,
- to have an intuitive and compelling interface that help beginners learn basic features and experienced users to work on a wide variety of tasks,
- to integrate with other software,

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[1] http://lattes.cnpq.br/web/dgp.

– to be configurable,
– to be available online,
– to have option of execution via command line and
– to be recognized by the scientific community.

Just a small number of professors from the sample have considered relevant to have feedback for user actions. Most of them stated that they were not familiar with the use of AT and that they did not know about strategies for teaching bioinformatics to VI students.

2   Background

The large amount of data generated by new technologies such as the next generation sequencing appliances requires that today's life scientists not only keep up with their fields of study, but also with the rapidly evolving tools and databases used to collect, store and analyze biological data [42]. In this context originated bioinformatics, an interdisciplinary area that involves the development of computational methods, including models, algorithms and data mining, for the solution of biological problems [12,13,24].

Historically, bioinformatics education began to emerge in the late 1990s. After almost a decade of short-term training for students, professors, and scientists on discrete bioinformatics, the drive to formalize bioinformatics education happened with Altman's article [2], who described the area and studied the discipline curriculum [31]. In 2001, the International Society for Computational Biology (ISCB)[2] produced a document suggesting core support to the contents of bioinformatics programs. The ISCB also created the Education Committee - ISCB Education Committee (EduComm) - to promote education and training in Computational Biology and provide resources and advice to organizations interested in the development of educational programs [31,41]. According to Welch et al. [40], this committee realized that due to the rapid advances in bioinformatics, its expansion and maturation as a discipline, educational programs in the field should constantly be refined and updated, to maintain relevance.

Also, the recent surge of genomics, proteomics, and structural biology in the potential advancement of research and development in complex biomedical systems has created a need for a bioinformatics educated workforce [24].

Big data is everywhere, and its influence and omnipresence across multiple industries will just continue to grow [20]. For life scientists with expertise and interest in bioinformatics, computer science, statistics, and related skill sets, the job outlook could not be more favorable. Big pharmaceutical, biotech, and software companies are clamoring to hire professionals with experience in bioinformatics and in the identification, compilation, analysis, and visualization of large amounts of biological and healthcare information [20].

Therefore, as the disciplines of bioinformatics and computational biology expand and mature, it is critical to identify the elements that contribute to the success of professionals in this field [40].

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[2] https://www.iscb.org/.

In Brazil, for example, there are several initiatives to promote bioinformatics. In 2002, we have the first Brazilian Symposium on Bioinformatics (BSB), an international conference covering all aspects of bioinformatics and computational biology. In 2004, the Brazilian Association of Bioinformatics and Computational Biology (AB3C) was created and later associated to ISCB [3]. AB3C is a scientific society that seeks to advance science and biology through large-scale formal, multidisciplinary and quantitative methods and interaction among bioinformatics specialists. In October 2005, AB3C promoted the first X-meeting, a Brazilian event to promote bioinformatics nationwide, becoming an event for dissemination, training and exchange of experiences among researchers. Its last edition occurred in 2017, in São Pedro, São Paulo.

In 2014, with the objective of strengthening bioinformatics research in Brazil, the National Bioinformatics Network (RNBio) was created as a result of the Structuring Program of the Ministry of Science and Technology and Innovation (MCTI) [17]. The founding nucleus of RNBio is formed by researchers linked to three Brazilian institutions with a strong tradition in genomics, proteomics, and bioinformatics research, namely: National Laboratory of Scientific Computation (LNCC); National Laboratory of Biosciences (LNBio/CNPEM); and Federal University of Minas Gerais (UFMG). This network aims to foster the development of research projects in a multicentric format and the formation of resources in bioinformatics areas, such as genome sequencing, transcriptomics and proteomics analysis, systems biology and interatomic studies [17].

Also, there are papers describing the Brazilian bioinformatics scenario [6, 12, 21, 29]. Some present the history of the field in Brazil [6, 29] and the influence of computational biology on the development of the national economy [29]. Others report on education in bioinformatics and present the major universities providing it [12, 29]; the management of people and research laboratories in bioinformatics [6, 29]; the training courses at the graduate level [12]; the training of human resources [6, 16]; the theoretical and practical activities carried out in undergraduate [21] and extension courses [30] in biological sciences.

Collaboration between Brazilian research groups in bioinformatics was discussed by Bongiolo [6] and Melo-Minardi et al. [12]. These studies demonstrate how cooperation, research and standardization between research groups [12] were carried out, as well as present limitations in the national context and elaborate proposals for training human resources [6]. In this sense, there are reports about the need to produce human resources in the area in Brazil, in order to facilitate the development of scientific research and the dissemination of bioinformatics in the Brazilian context [16, 21]. Other works describe bioinformatics applied to biology and biological sciences [21, 32], molecular biology [32] and biotechnology [30] and also demonstrate that bioinformatics classes were already incorporated in the curriculum of the biology and other areas, especially in the degrees of biology, biomedicine, chemistry, biotechnology, and similar courses [21].

In Brazil, the first bioinformatics courses were created at graduate level, especially in doctoral studies, and were promoted by the Biomicro grant call, from

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[3] http://www.ab3c.org.br/site/atas/4-ata-de-fundacao.

the Coordination for the Improvement of Higher Education Personnel (CAPES), in 2003. This call offered 5 years of financial resources support, including grants and costing resources for the creation of courses in bioinformatics and microelectronics [12]. At that time, two (2) universities were contemplated: the Federal University of Minas Gerais (UFMG) and the University of São Paulo (USP).

In a search carried out with the keyword "bioinformatics" in the Portal of Higher Education Institutions and Registered Courses of the Ministry of Education (MEC) - e-MEC[4] - brought only two graduate courses in bioinformatics, with no indication of undergraduate courses. They are the graduate courses in bioinformatics of the Federal Technological University of Paraná (UTFPR) and the Pontifical Catholic University of Rio Grande do Sul (PUCRS). In addition to these courses, according to the Sucupira platform[5], there are another 3 recommended and recognized graduate courses, presented in Table 1.

Table 1. Graduate courses *stricto sensu* recognized by MEC-Brazil

State	University	Degree level
PR	Federal University of Paraná	Master
PR	Federal Technological University of Paraná	Master
MG	Federal University of Minas Gerais	Master/Doctorate
SP	University of São Paulo	Master/Doctorate
RS	Pontifical Catholic University of Rio Grande do Sul	Postgraduate

Additionally, the National Laboratory of Scientific Computation (LNCC)[6], a nationwide reference institution in scientific computing and computational modeling, has a well established program for training in bioinformatics - the graduate program in computational modeling[7]. LNCC provides a high performance computing infrastructure for the national scientific and technological community to conduct research in this field. Another reference institution is the Oswaldo Cruz Institute[8], with the graduate program in computational and systems biology [12]. In addition to the courses, there are bioinformatics research groups registered at the National Council for Scientific and Technological Development (CNPq), which carry out studies in the area. Using the search term "bioinformatics" in the Lattes platform, including only the certified groups and excluding the non-updated ones, we can find 399 research groups that have this keyword in the group name (15), as a line of research (174) or list of keywords (180).

Some studies involve the pedagogical training of teachers and students in the area, both in higher education (undergraduate and graduate) and in secondary

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and professional education. The focus is not a bioinformatics curriculum, but the characterization of didactic-pedagogical experiences, the description of the teaching and learning process and the contents of bioinformatics. There are practical activities applied to the teaching of Molecular Biology and Genetics in the undergraduate course of Biological Sciences [21], the creation of university extension courses aimed at technical school students, high school and undergraduate students [30] and also for higher education students and for the academic community [16]. At the secondary level, Andrade [3] carried out a study on the importance and application of bioinformatics in the learning of sciences.

Practical activities were applied to the teaching of Molecular Biology and Genetics, creation of university extension courses, aimed at technical school students, high school students, university students and academic community. The methodology used was the application of questions to students, lectures, manual and practical *in silica* classes, and theoretical-practical classes. The contents were more introductory, providing the basic concepts and the necessary subsidies for the initiation in the research field of bioinformatics. We sought to approach from the basic fundamentals, involving genomics, transcriptomics, proteomics, general notions about biological databases, sequence alignment, molecular modeling, introduction to computation, programming and the use of specific bioinformatics tools.

However, none of these papers contribute to the teaching of the discipline with a focus on the visually impaired (VI). There is a lack of studies that relate bioinformatics and the inclusion of people with disabilities, especially when it comes to VI students.

3   Difficulties in Teaching Bioinformatics to the Visually Impaired

There are researches dealing with perspectives and challenges in bioinformatics training [9,13,24,31,38] and others that present the multidisciplinary character of this discipline [7,12,16]. They suggest that bioinformaticians should develop different skills and competencies. Bruhn and Jennings [7], for example, emphasize that students must demonstrate the ability to work in a multidisciplinary field and apply the acquired knowledge in solving relevant problems. Welch et al. [40] state that in order to successfully perform the duties of a bioinformatics researcher, it is necessary to have a series of skills, such as the ability to manage, interpret, and analyze large data sets; broad knowledge of bioinformatics analysis methodologies; familiarity with functional genetic and genomic data; and expertise in common bioinformatics software packages and algorithms.

However, bioinformatics students often do not receive formal training on how to make the most of bioinformatics resources and tools available in the public domain [42]. Cattley and Arthur [8] point out that, when teaching bioinformatics, there is a difficulty related to the full number of resources needed to provide a solid foundation to the students. These range from repositories of publicly available information - such as databases - to complex tools for analyzing

data obtained through experimental methods. These tools are very important in the process of knowledge construction, but in order to be really effective in the teaching and learning process, teachers need to know how to use them in a pedagogically appropriate way, how to select them from the large amount of available resources and evaluate the use of these tools in different teaching contexts. Still, the teacher needs to be up-to-date on the new available resources due to the progress in scientific research and the growth of the area.

Another important feature is the ease of access of these resources by students. Consideration should be given to technological infrastructure in high schools, courses and colleges. The use of these tools may depend on good internet connection, sufficient capacity to handle multiple simultaneous requests, quality computational resources, installation of all necessary software and also, integration of tools [8,21].

There are also difficulties related to HCI criteria such as usability, user satisfaction, ergonomics and accessibility [1,5,27,37–39]. Additionally, there is the complexity of the existing data available [6,10,28].

The union of areas such as computer science, mathematics, chemistry, software engineering, statistics and biology, present in bioinformatics bring many difficult and abstract concepts to students' comprehension [26,32,34]. Often, these contents are not available in an easily accessible format [25,34], requiring design or explanatory scheme for their understanding [26] and depending mainly on visual instruction [34]. Thus, it may be a challenge for bioinformatics faculty to teach these contents to VI students, to select bioinformatics tools that conform to accessibility standards, such as the W3C, and to be adapted to the use of AT. In this sense, we verified the importance of the teacher's commitment to the choice of the tools to be used, that are adequate to the profile of the student population.

Another point to consider is that one of the main difficulties in teaching molecular biology and bioinformatics lies in the fact that its content is related to microscopic aspects, which make a visual representation challenging. This difficulty is usually related to the large amount of information and structural details contained in the molecules, which involve shape changes, chemical reactions, cellular motions, molecular modifications, and events, which often occur simultaneously, making it even more difficult to understand and assimilate. This is even more complex when students are VI, especially total blind students, since they can not observe microscopic, digital images or didactic schemes [35].

Therefore, it can be said that certain bioinformatics concepts require a great capacity of abstraction from the students. Stimulating abstraction by VI students requires the exploration of other resources, often not available to the teacher. There is an opportunity on the development of supporting didactic resources so that students with visual impairment have access to these concepts [21]. Thus, bioinformatics teachers must be incentivated to update their teaching practice to include the use of AT resources.

In this sense, there is a vast field of research being developed for teaching the VI and, due to this diversity of works, there is a great need for knowledge

integration. There are studies related to the teaching of areas such as natural sciences [25,34] and computer science [22,36]. Some of these studies corroborate that the main difficulties of DVs are in relation to content concepts and learning [34], mainly in the understanding of the drawings and schemes [26], besides the students demonstrate lack of confidence, lack of motivation, etc. in learning this content [25].

These works point out that the teaching of sciences has been depended mostly on visual instruction. This makes it difficult for VI students included in regular classrooms to learn the science concepts [34], such as those of the bioinformatics. The lack of accessibility in the physical and computational environment is other aspect mentioned. They report that classrooms should be adapted and instruction methodology should be adjusted for a better experience from VI students [34]. Many computational tools are still inaccessible, because the graphical nature of such tools, which prevents the inclusion of VI students in school activities [22].

Maguvhe [25] points out that teachers still lack the requisite skills in special education to harness learner potential. There are missing teacher motivation and mentorship in education methodologies and the use of tools for learner empowerment. This situation requires that there is an action in the training of bioinformatics teachers so that they are prepared for an adequate attendance to this student public.

4   Methodology

In this study, we conducted an exploratory, quantitative-qualitative study to identify the tools used in teaching bioinformatics in the Brazilian context. The data collection have been carried out with a questionnaire created to help us to understand the following research questions: (RQ1) What is the teaching profile of the professors of the discipline of bioinformatics in undergraduate and graduate courses? (RQ2) What are the computational resources that are used as support in teaching bioinformatics? (RQ3) What are the main tools used to introduce the basic bioinformatics concepts; the primary, secondary and scientific literature databases; tools for visualization and manipulation of sequences and biological macromolecules; alignment tools coupled with multiple alignment; tools for secondary and tertiary protein prediction. (RQ4) What are the quality characteristics of software that teachers consider relevant in a bioinformatics tool? (RQ5) What is the experience of teachers with students with Visual Impairment? (RQ6) What strategies and assistive technologies do teachers use to teach bioinformatics to a student with Visual Impairment?

With these questions, we aim to contribute to teachers' pedagogical practice in relation to the selection of tools and HCI criteria considered relevant for their selection. Also, our objective is to collect the educators' perceptions about the teaching and the use of interactive systems of the area with students with VI and the use of AT resources.

Study 1, previously performed [23], contributed to the understanding of two types of tools in teaching bioinformatics, databases and visualizers of three-dimensional protein structures. The analysis of experiences lived by this professor indicated HCI criteria to be used, or not, in the design of software interfaces for bioinformatics. In this study, we sought to broaden the scope of the study to other educational institutions.

4.1   Data Collection Instrument

The development of the data collection instrument was based on a case study (Study 1) [23], held in the discipline of bioinformatics that is part of the curriculum of an undergraduate course in biological sciences held by PUCRS university, Brazil. Semi-structured interviews were conducted with a professor specialized in bioinformatics, with 27 years of experience in research and 15 years in teaching, both at undergraduate and graduate levels. Also, we've performed documental analysis of the books, tools and materials used in the classroom by the teacher.

The data collection instrument sought to address the research questions previously reported. It comprises 48 items, divided into 5 sections:

1. The professors' profile (5 questions): age group, academic training, teaching experience in bioinformatics disciplines, taught subjects, disciplines offered, institutions in which he/she taught the disciplines, average students per class.
2. The teaching methodology and computational resources: tools for working on basic concepts, biological databases, visualization and manipulation of sequences and structures of biological molecules; The questions included the experience of teachers in undergraduate courses (16 questions) and graduate courses (17 questions);
3. The HCI criteria for selection and use of software in bioinformatics disciplines (1 question): includes usability, ergonomics, user satisfaction and accessibility, as well as aspects of learning-related tools.
4. Teaching of blind students with/without assistive technologies (5 questions).
5. Contact information (1 question): finally, we provided a field for the participant to provide e-mail data to participate in future studies.

An online questionnaire was made available to participants through Google Forms[9]. We followed the basic protocols of ethical research and sent to all the participants the Informed Consent Form (TCLE). This document clarifies clearly the research protocols and is also the manifestation of agreement with the participation in the research. We also ask the teachers to confirm that they teach or have already taught bioinformatics content, in undergraduate and/or graduate courses, in order to be able to compose the sample.

4.2   Sample

The sample, non-probabilistic for convenience, was obtained by searching [10] the Directory of Research Groups of CNPq, Brazil.

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[9] https://www.google.com/forms/about/.
[10] search held on 05/22/2017.

The search keyword used was "bioinformatics". We only have included certified research groups on the search. As a result we have obtained: 45 groups that have the keyword in the name of the group; 174 groups report "bioinformatics" as the name of their research line; and 180 groups that have declared "bioinformatics" as one of their keywords in their line of research. In addition, we have supplemented the search results with a Google search by entering the keywords "bioinformatics" and "discipline".

In both cases only teachers who reported in their Lattes curriculum to teach the discipline of bioinformatics specifically were selected. We take into account that bioinformatics is an interdisciplinary area, and as such, it can be inserted in other disciplines such as molecular biology, computational biology, biochemistry, etc. We chose to include in the sample only teachers who indicated in their curriculum teaching the discipline, limiting the search scope so that the results were referring especially to this discipline. In total, 61 teachers were invited to participate of the study. Only 29 (~46%) agreed to participate.

5   Results

This section brings the results of data collection, based on the research questions stated in the previous section. To visualize the results, we chose to follow a standard protocol to better present the data and facilitate its understanding:

– The information presented is related to the discipline of bioinformatics taught both in undergraduate and graduate courses.
– Throughout this section, the letter U will be used to indicate the answers referring to undergraduate and G for graduate.
– The responses of the teachers involved both the bioinformatics discipline given at the time of application of the questionnaire and the other disciplines of bioinformatics that they taught in the past, taking into account their experience as a teacher.
– When referring to number of citations, the value will be formatted as (x), where x is the value;
– When referring to number of subjects that have answered a question, the value will be formatted as (x/y%), where x is the number of subjects and y is the percentage of total.

5.1   The Teachers' Profiles

Responding to RQ1, it was found that the majority of respondents were male (21/72%), age between 25 and 64 years, with 17 participants between 35 and 44 years old (59%), 5 participants from 45 up to 54 years (17%), 5 over 55 years (17%) and 2 aged 25–34 years (7%).

When asked about their highest educational level, the majority (22/76%) had a postdoctoral training as a maximum qualification and the others had doctoral degrees (7/24%). These teachers also came from different areas of formation

(Fig. 1). As we can see, most teachers have some training in the area of biological sciences (21/72%), with approximately half (10/34%) having only formation in this area and others (11/38%) adding this formation to others areas. In addition, some (6/21%) have formation only in the area of applied sciences.
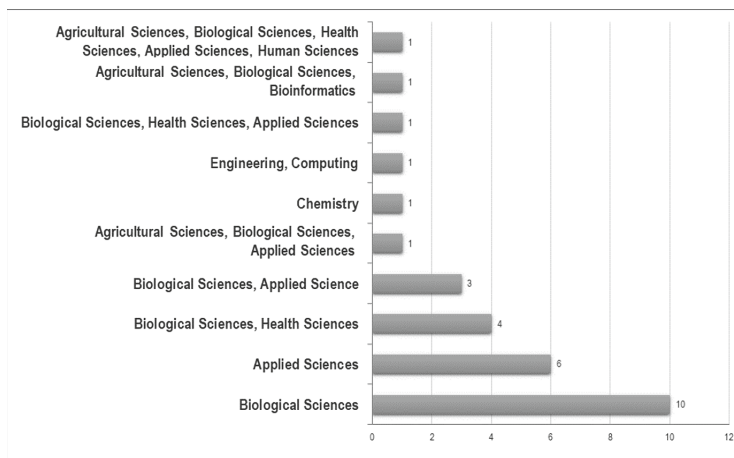

Fig. 1. Training areas of bioinformatics teachers

In Brazil, teachers taught the discipline of bioinformatics in the following institutions: (U,G): FIOCRUZ, FURG, LNCC, Promove, UEL, UENF, UFC-SPA, UFGD, UFJF, UFMG, UFRJ, UFSC, UFSJ, UNIFAL, USP; (U): UCB, UFBA, UFRGS, UFSCar, UFSM, UFV, UMA, UNESP, UNIFAN, UNIPAMPA, UNIRIO; (G): INCURSOS, IAC, UFPR, UNICAMP, UTFPR; The foreign institutions mentioned were: (U, G): Universidad Nacional Autónoma de México (UNAM, Mexico), Universidad de Buenos Aires (UBA, Argentina) and Universidad de Antioquia (Colombia); (U): CES university (Colombia) and other foreign institutes that were not mentioned.

The teachers also informed the courses and the name of the disciplines that involved the teaching of bioinformatics, as follows:

– Undergraduate Courses: technologist in environmental toxicology, biotechnology, biomedicine, biological sciences, bioinformatics, biomedical sciences, computer science, pharmacy and biochemistry.
  – Disciplines: instrumental bioinformatics, bioinformatics for toxicology, molecular biology, computational tools for drug development, informatics applied to biological sciences, molecular modeling, visualization and manipulation of biological macromolecules.
– Graduate courses: tropical and sub-tropical agriculture, bioengineering, bioinformatics, computational and systems biology, general biology and bioprospecting, molecular and cellular biology, biology, biotechnology and biosciences, biological sciences, biochemistry, health sciences, computer science

and applied computing, genomic medicine, computational modeling, pathology, plant production and associated bioprocesses, chemistry and technology.

– Disciplines: algorithms for computational biology, data recovery storage in bioinformatics, biological database, biophysics of canalopathies, applied bioinformatics, structural bioinformatics, bioinformatics i - biological databases, bioinformatics in evolution and molecular phylogenies , computational biology, synthetic biology, biotechnology, computational tools for research on molecular targets, genomics, introduction to computation for bioinformatics, pattern recognition, current topics in genomics and systemic biology, advanced topics in bioinformatics, topics in bioinformatics, transcriptomics.

In addition to the disciplines mentioned, the disciplines of bioinformatics, genomics and bioinformatics, introduction to bioinformatics, linux and bioinformatics were taught at undergraduate and graduate levels.

The numbers of students in the classes ranged from 11 to 30. The contents worked involved: alignment of biological sequences (17/58%); drug design and discovery (17/58%); construction of phylogenetic trees (13/45%); database and information retrieval (15/51%); transcriptomics (13/45%); prediction of protein structures (12/41%); systems biology (9/31%); proteomics (9/31%); genomics (6/20%); and population genetics.

Of the total of 29 respondents, the majority (27/93%) taught bioinformatics at the graduate level, while some also taught at undergraduate courses (18 /62%). Some professors also mentioned having taught the discipline of bioinformatics in extension courses.

5.2   Computational Resources Used

As for RQ2 (Fig. 2), teachers use internet file sharing (e.g. google drive, dropbox, github etc.), learning management systems (LMS) (e.g. Moodle, Teleduc, etc.), specific web pages (e.g. National Center for Biotechnology Information (NCBI), Expasy, PDB101, etc.), personal web pages, online tutorials and the use of TIDIA software[11]. Besides these features, it was mentioned they use software for programming, analyzing algorithms, running programs on remote servers. In this sense, a professor said that he works with the computational side of bioinformatics.

RQ3 encompasses the main tools used by teachers, from those to teach basic contents to more specialized tools. To work with the introductory content, the NCBI portal was the most cited (45), followed by the GenBank Database (41) and the EMBL-EBI Services Portal (34). Also, the following tools were mentioned: Autodock, BLAST, Bioconductor, KEGG, miRBASE - miRNA database, Modeller, Molprobity, NAMD, PDBj, PFAM, Pubchem, SAVES, STRING; VMD; algorithms and computer techniques, protein modeling and visualization software, docking software, molecular dynamics software, data mining tools and DBMSs.

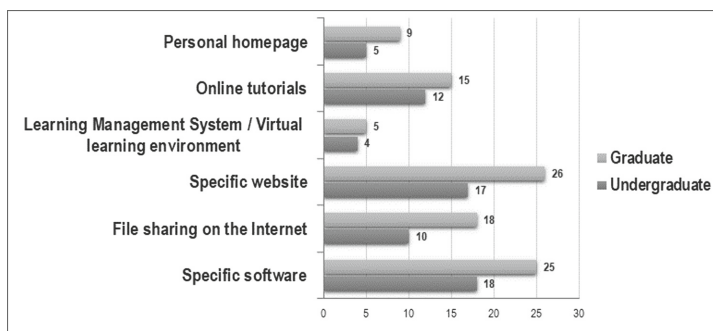[11] http://www.tidia-ae.usp.br/portal.

Fig. 2. Main computational resources used to support the teaching of bioinformatics

Bioinformatics databases (BD) are repositories of biological data obtained by experimental methods. In the creation of the instrument, the classification was used to define the types of DBs in primary (DBP) and secondary (DBS) [4, 15]. In addition to these, there is classification of scientific literature databases (BDLC) [19]. The main databases selected by the teachers are illustrated in Fig. 3. Also, the secondary databases GEO, Uniprot, EMBL-Atlas, String, ZINC, PubChem, Rfam and GOA were cited once.
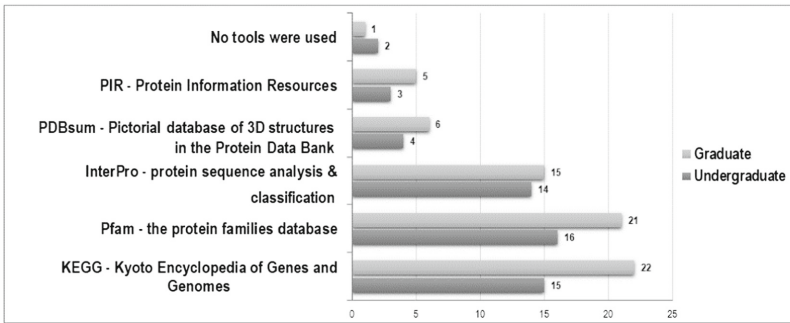
Also, the main tools for visualization and manipulation of sequences and biological macromolecules were searched (Fig. 4). It is a type of molecular graphical visualization tool, from various perspectives, able to load and display the contents of the data files. The most cited were PyMOL and Swiss-PDB Viewer, both referred to 8 times.

Next, we present the tools for pairwise alignment (comparison of two sequences) and multiple alignment (with three or more biological sequences). The purpose of sequence alignments is to measure the similarity between two or more sequences, to infer evolutionary relationships, and to observe patterns of conservation and variability for structural and functional predictions. For pairwise alignment the most mentioned tool was NCBI BLAST (45), followed by MEGA-Molecular Evolutionary Genetics Analysis (14) and UniProt BLAST (12). It should be note that the BLAST algorithm is the same, but the interfaces are different, which may explain the preference of one over the other. As an example, teachers still indicated BLAST at PBIL (2), BLAST at PDB (2), in addition to the FASTA algorithm (1) and EMBOSS Needle (command line and web)(1). Two teachers do not use it. Tools for multiple alignment were cited: ClustalX (26); Muscle (21); ClustalW - ExPASy (20); MEGA (19); T-Coffee/EMBL - EBI (18); MAFFT - EMBL-EBI (15); Kalign - EMBL-EBI (5); MultiAlin (4); T-Coffee - Vital-IT (SIB) (3); T-Coffee - Vital-IT - (SIB) (3); Clustal Ômega (2);
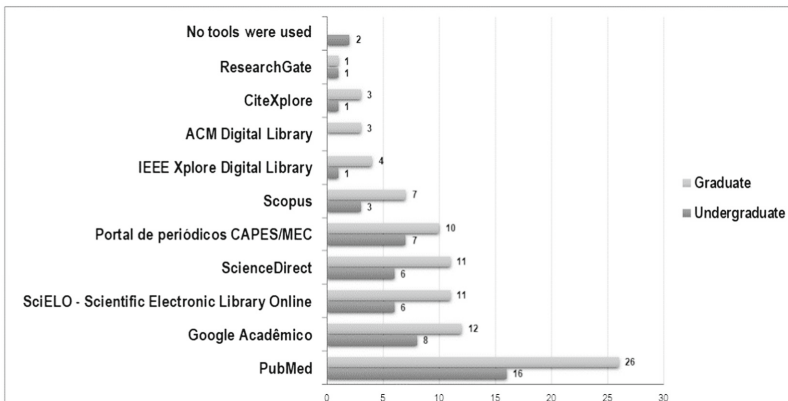
As for the tools for predicting and analyzing protein structures, some teachers do not use them since they are more specialized, commonly used in structural
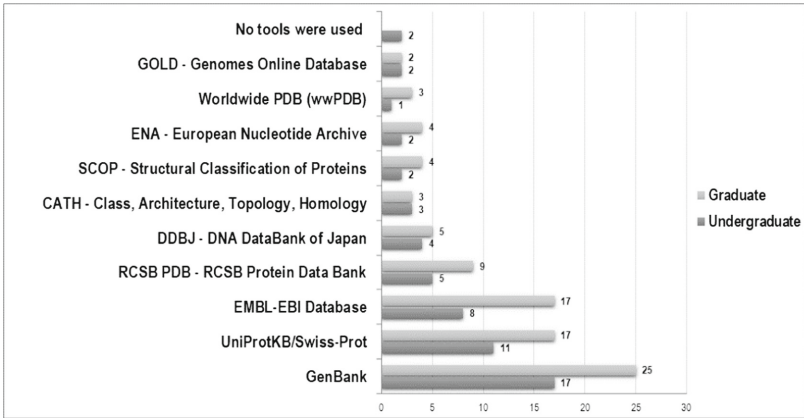
(a) primary databases

(b) secondary databases

(c) scientific literature databases

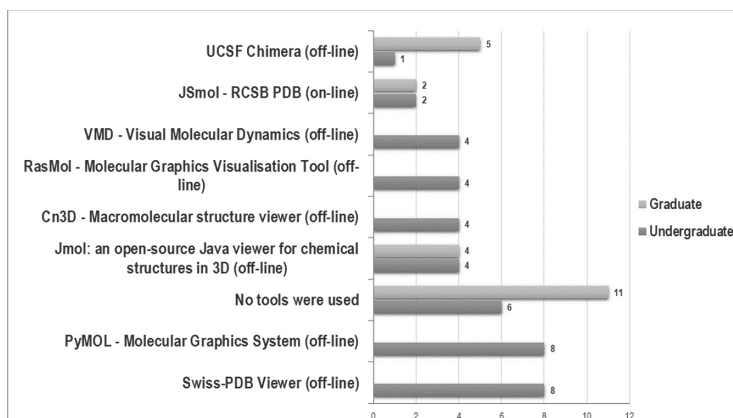**Fig. 3.** Bioinformatics and scientific literature databases

Fig. 4. Tools for visualization and manipulation of sequences and structurer of biological macromolecules

bioinformatics. The main tools used by the teachers to obtain secondary (SS) and tertiary (TS) structures, and model validation (MV) are:

– SS: JPred4 - Protein secondary structure prediction server (8), PSIPRED - Protein Sequence Analysis Workbench (6), PORTER - A new accurate server for protein secondary structure prediction (2), Stride (1), JMpred (1), NetSurfP - Protein Surface Accessibility and Secondary Structure Predictions (1), Jufo9D (1) e Predator (1).
– TS: SWISS-MODEL (9), Modeller (8), I-TASSER - Server for protein structure and function prediction (5), Phyre2 (1), QUARK - De Novo Protein Structure Prediction (1), Raptor X (1) e Robetta - Full-chain protein structure prediction server (1).
– MV: PROCHECK - EMBL-EBI (7), Verify 3D (5), SWISS-MODEL (5), Modeller (4), WHAT_CHECK (3), ProSA-web - Protein Structure Analysis (2), molprobity (1), SAVES (1), Molprobity (1).

The list of all the tools, as well as the complete study was available for consultation at http://bit.ly/863231351.

5.3 Criteria for Selection of Tools by Teachers

For the selection of tools (RQ6), teachers first consider if the're feely available (23/79%). They also find it important to allow information to be saved (21/72%), to have help and documentation (21/72%), to be constantly updated (20/69%). Some teachers consider that the tool should be available online (16) and others have indicated that it is offline (13/45%). They cite the ability to integrate other types of software (14/48%) and allow configuration (12/41%) and printing of the information (10/34%).

The criteria of usability, ergonomics and satisfaction of use most mentioned were to have an intuitive interface (19/65%), to help beginners to learn the basic features (19/65%), to be easy to learn to use (18/62%); enable experienced bioinformatics users to work smoothly on a wide variety of tasks (16/55%), be easy to use (14/48%) and have a compelling interface (11/37%). However, few teachers consider feedback for user actions to be important (6/20%).

They also select that it must be recognized in the scientific community (15/51%), be able to integrate other types of software (14/48%), allow them to be configurable (12/41%) and allow information to be printed (10/34%). Also, we were allowed to save the results in text format (1/3%) and present documentation and limitations (1/3%).

As for teaching support resources, teachers stated that they consider it important to have content tutorials (12/41%), discussion community (11/37%), exercises list (7/24%), video lessons (6/20%), but only 4 consider relevant that the language be configurable.

Finally, of the 29 participating teachers, few (9/31%) consider that the tools must have resources for access to disabled users and allow access to different user profiles (7/24%).

5.4   Teacher Experience in Teaching the Visually Impaired

This subsection addresses the RQ5 and RQ6 research questions. Of the 29 participating teachers in the sample, only 1 had experience with a user who is blind, in the course of graduation. The teacher informs that the student did not use AT. As for this experience, the teacher reported that "he found it a bit complicated, and he needed to be prepared for it." Asked about strategies for teaching bioinformatics content to students who are blind and the use of AT, 3 teachers reported that they could not answer this question, and 3 teachers claimed that they did not have the experience to suggest some kind of strategy. Of the 29 participants, only 8 teachers answered the question:

– "Text to speech, speech to text, adapted virtual reality, concrete models".
– "It is difficult to answer this question, but I imagine that auditory resources should be applied both to confirm input of data and outputs of data after processing"
– "There are strategies to be discovered because students of bioinformatics who are blind should acquire knowledge through their auditory organ. The idea of what is a protein structure, protein-ligand interaction, which are visually and quickly assimilated, would not be captured by the VI. However, this knowledge can be supplied by lego models of protein structures and sequences subject to touch."
– "Use of sound".
– "Call center menu driven by numbers".
– "Adapted keyboards and voice command".
– "Audiobooks and Braille material".
– "Using 3D Printing, making audio resources available, among others".

6   Discussion

Bioinformatics is an interdisciplinary discipline. Its teachers are generally trained in different areas of knowledge. This study pointed out that teachers in Brazil also come from different areas and teach bioinformatics in varied courses, but mostly in graduate programs. Despite the selected sample included only teachers who informed the bioinformatics discipline, the results indicated, as expected, that bioinformatics contents are included in other disciplines, such as computing for biologists and other professionals, programming, algorithms, and recovery of information.

It is interesting that one teacher reported teaching programming languages and Linux for the course of Biological Sciences. It is common in bioinformatics to use the Unix or Linux operating system under which many bioinformatics applications are run, and also because many of these tools require the creation of Perl or Python scripts, and the student needs to gain knowledge of programming languages. This is important because it enables biological students to learn computational thinking necessary to acquire basic skills in the use of the most common bioinformatics software, which in turn facilitates learning, effective interpretation of results and proper use of resources [18]. One teacher also replied that the main focus of the discipline is computing for bioinformatics. Although it is not necessary for most bioinformaticians to develop these specialized skills (including software development), they must have basic skills in using the most common bioinformatics software and the effective interpretation of results [8].

It can be seen that introductory courses are taught both in undergraduate and graduate courses. On the other hand, the disciplines that require a greater knowledge on the part of the student, with more specific content, and involving, for example, the retrieval of information in databases and specific areas of bioinformatics, such as phylogeny, systemic biology, and structural bioinformatics are mainly seen at graduate level. There were no reports of disciplines taught at a distance; all were presential.

Most teachers did not consider important that the language the interface be configurable, because generally scientific tools are made available in English.

Despite being an initial study, this research revealed that most participants still do not have experience in teaching bioinformatics to VI students. Teachers are unaware of the existence of AT resources, how to use and where to find them. This issue becomes even more important because one of the main difficulties in teaching structural bioinformatics lies in the fact that its content is related to microscopic aspects, which make visual representation difficult.

7   Conclusion

Although this is an initial study, this research reveals that most of the bioinformatics teachers are not able to attend to the VI audience and there is still a lack of information on assistive/inclusive issues.

The study of accessibility in bioinformatics tools opens a new set of access opportunities, which has the potential to include the visually impaired in areas of life and health sciences involving bioinformatics content. During the analysis of the tools we perceived some perspectives and challenges. The first one refers to teachers' lack of knowledge about the existence of AT resources, how to use them and where to find them; there is also missing a map of accessible bioinformatics tools; to know at what time and in what form to use them in teaching VI users; and to verify if the difficulty of installing and configuring the programs and the lack of Portuguese versions are reasons that may hinder popularization by Brazilian students in the use of such programs and their use as auxiliary tools to pedagogical practice.

We believe that there is still a lack of specialized training and technical support in working with visually impaired students. The continuous academic formation of bioinformatics teachers should support quality inclusive education, encouraging the enrollment of these students in higher education in areas of science that involve this discipline. Teachers should provide adequate access conditions to curriculum content and computational tools, seeking appropriate ways to teach content with abstract and visual aspects.

This difficulty increases when students are blind because they can not observe microscopic, digital images or didactic schemes [35]. This problem is portrayed in Mariz [26]: "So one wonders how one with little or no vision would develop such skills? How to explain to students with visual impairment the dynamics of the geochemical process of carbon in nature, or the process of human fertilization, for example, already so complicated to understand by observing and analyzing drawings and photos? ... ... Scientific knowledge is a collective cultural good, so people with partial or total visual impairment should enjoy it as well.".

Finally, the analysis of which tools presented in this study are adequate to the use of AT and that meet accessibility standards, such as those of WCAG 2.0, will be dealt with in future works.

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