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Human factors in the design and evaluation of bioinformatics tools

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Abstract

Human factors contribute significantly to the information visualization design considerations and usability evaluation process, and have been shown to play an important role in the design, development and quality assurance of bioinformatics tools. Despite the technological advances in bioinformatics computational methods, humans are an indispensable part of the data mining and decision making process. The complexity of biology data visualization can make perception and analysis a complex cognitive activity for professionals in the bioinformatics domain. Information Visualization (InfoVis) can provide valuable assistance for data analysis in bioinformatics by visually depicting sequences, genomes, alignments, and macromolecular structures. InfoVis coupled with interaction modalities of bioinformatics tools also impact the efficiency and effectiveness of decision-making tasks in applied bioinformatics computing. However, the way people perceive and interact with bioinformatics tools can strongly influence their understanding of the complex data as well as the perceived usability and accessibility of these systems. In this paper, we present a synthesis of research studies and initiatives that have recently examined human factors in interaction and visualization for bioinformatics tools, particularly in perception-based design. Although bioinformatics' visualization and interaction design research that involves human factors is considered in its infancy, a plethora of potentially promising areas have yet to be explored. The aims of this paper are to review current human factors research in interaction, usability and visualization within bioinformatics tools to provide a basis for future investigations in systems and software engineering of bioinformatics tools, and to identify promising areas for future research directions in interaction design of bioinformatics tools.

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1. Introduction

Bioinformatics is an interdisciplinary approach using data collection and information modeling to analyze and visualize biological data. Bioinformaticians apply information technology to biological, medical, and health research. With the increased reliance on web-based systems in bioinformatics research and the rapid developments in biological databases, the human factors in designing interactive bioinformatics systems continues to be an important issue [1-4]. Domain experts are spending a considerable amount of time while browsing the content that is available on online biological repositories. Therefore, studying the factors that negatively or positively affect the user experiences of the users of biological systems is essential. Furthermore, the nature of data processed in bioinformatics systems requires taking a careful attention by software engineers. The complexity and interdependencies in biological data along with the different data types that bioinformatics systems deal with increase the computational challenges and thus affect the user experience. What is more, the revolutionary nature of bioinformatics domain and the increased volume of data available in biological data sets contribute to increasing the number of applications that serve the bioinformatics community [5, 6, 7]. The processing, visualization and analysis of large volumes of data that might be complex and less structured often increase the execution time and therefore affecting the usability of biological systems. Large amounts of data related to genomes and species are stored on online databases (e.g. BioCarta[8] and NCBI [9]) and are continuously queried by biological scientists and researchers. Extracting meaningful and useful information from these data sets, modeling the molecular interactions and building suitable visualizations are some of the basic functions in bioinformatics applications. The results produced by these systems are used by biologists who need to build a full understanding in order to develop medications, discover associations and deliver this knowledge to other people. Therefore, bioinformatics systems might rely on advanced algorithms that integrate data from different sources and present them in different graphical formats. Thus, the usability considerations of bioinformatics systems should include elements related to their interfaces, their underlying architectures and the issues that might affect their responsiveness.

Over the last two decades, a significant body of research has focused on identifying various human factors that influence the design of web interfaces in bioinformatics. Previous research studies presented many usability challenges that negatively affected the quality of user experience [e.g. 10,11]. Some of these problems were related to navigating the structures of the presented biological content whereas others deal with spending a considerable amount of time in order to perform the required tasks or understand the interface elements [10]. For example, to increase the overall usability of a bioinformatics system, Bolchini et al. suggested minimizing the number of parameters that must be entered by a user to view a protein structure [11]. In order to build usable bioinformatics system, software engineers have to design intuitive user interfaces that present the required information in a consistent manner. To obtain satisfactory user experiences, evidence suggests that these systems need to be responsive, efficient, accessible and learnable [10, 11, 12, 13].

Using biological systems by users who do not have computational background increase the importance of studying bioinformatics systems from a usability-engineering perspective. Accessing, examining, analyzing and publishing biological data are some of the frequent activities of biologists [12, 13]. Bioinformatics specialists and scientists use the data obtained from web-based bioinformatics systems to conduct experimental studies and answer research-related questions that might have significant implications [13]. Therefore, one of the responsibilities of software engineers who build bioinformatics tools is to measure the usability of their systems by using reliable metrics that reflect the accuracy of the retrieved data and usefulness of these systems. By linking these usability-related factors to reducing the human effort, the cost and the time required to use these biological systems, Javahery et al. discuss the impact of having usable bioinformatics systems on improving the productivity levels of biologists and obtaining results of higher quality [14]. The author also emphasized on the importance of involving domain experts while studying the usability of bioinformatics systems to understand their behavior [14].

In this usability-engineering study, the opinions of biologists and HCI experts are taken into consideration to build usability models of higher accuracy that can be used by future researchers and software engineers. Furthermore, this paper studies the usability measures that have to be taken into consideration in the design and development of bioinformatics systems. The following sections also present a review of previously reported usability problems and discuss the possible areas that can be exploited for obtaining usable bioinformatics software solutions.

2. Usability engineering of bioinformatics tools: A literature review

The nature of domain-specific problems that bioinformatics researchers attempt to solve when developing computer-based systems implies that the analysis, design and implementation of these data-driven systems are tightly coupled with the properties of the biological data as well as the target users of these software systems. There is a variety of currently available bioinformatics web-accessible services that are used for different purposes. For the web-based repositories, Douglas et al. [12] classified them into five categories depending on the type of biological data that can be retrieved. For these search-oriented systems, previous usability studies highlighted the importance of having efficient, effective and highly responsive systems especially when the system relies on integrating biological data from different sub systems [10, 11]. One of the usability barriers discussed by Barker and Thornton [6] is clearly presenting these integrated data that might differ in their forms (e.g. graphs, images, numbers or strings), comes in a variety of file formats (e.g. FASTA, PMW and Tab) and need to be represented in different ways. As an attempt to determine the usability breakdowns of a protein repository that is known as CATH [15], the usability inspection that was conducted in [8] shows that the visualization structures produced by the tool have to be re-designed in a way that simplifies the process of browsing, exploring and navigating the presented hierarchies. Because of the growing complexity of biological data, Tao et al. [5] highlight the importance of information visualization techniques in facilitating the cognitive and perception processes. They pointed out that the massive amounts of biological data require advanced visualization techniques that help people to understand the underlying knowledge. However, they raise the performance and accuracy difficulties that researchers are still facing when analyzing the large biological data sets. Furthermore, most of the current bioinformatics visualization techniques work at the molecular level whereas visualizing the biological data at the genome level will raise more usability challenges in the future bioinformatics systems [5]. The above mentioned research studies address specific problems and there is a lack of criteria that can be followed to build usable bioinformatics systems. For this reason, this paper focus on presenting the objective and subjective measures that software engineers can utilize to assess the usability of these systems.

In some research studies, the authors presented some relationships between the usability considerations of biological systems and their underlying architectures. Archuleta et al. [16] state that having modular software architectures might positively affect the maintainability and extensibility of software systems and present the effect of refactoring mpiBLAST on achieving high performance levels. Similarly, Kohlbacher and Lenhof[17] discuss the usability principles that guided the development of the Biochemical Algorithms Library (BALL) that have extensive molecular modeling features. For obtaining usable and consistent user interfaces, they emphasize on the role of Object-Oriented modeling in simplifying the process of structuring the elements of the user interfaces [17]. Exploiting the power of the metrics of the Object-Oriented programming for determining the parts of the code that degrade the overall performance is also recommended to increase the speed of bioinformatics systems [17].

Usability experts need also to consider the target users of their applications. A user of a bioinformatics system can be a novice user or an expert user. The user performance test conducted in [13] on a bioinformatics system reveals that some users experience cognitive overload problems while trying to analyze the search results. To alleviate the effect of these problems, they followed repeated pattern of thinking which might negatively affect the results of their biological research. The authors suggested employing data arrangement and navigation methods that make manipulating and retrieving the browsed content easier [13]. In this paper, we evaluate several web-based bioinformatics tools to guide the process of building a user-centered framework that can be used as a basis for evaluating the usability of bioinformatics systems.

3. Heuristic evaluation on bioinformatics systems

Complex website applications such as web-based bioinformatics tools need to be “usable” and “efficient” to an extent that is perceived to be intuitive for the domain specific users in bioinformatics. The degree of satisfaction that the users have during the interaction with the web site interface reflects the quality that has been achieved. To investigate the usability level, interaction and visualization of the current web-based bioinformatics tools that already available for the end user, we conducted a heuristic inspections study on four of the current web-based

bioinformatics tools. In order to examine the usability-related aspects of the four user interfaces, this study relied on obtaining feedback from expert evaluators. A team comprised of HCI specialists and bioinformatics application developers participated in the heuristics evaluations of these tools. This study aimed to give more insight and focus on the usability issues in biomedical research tools and address matters such as the severity of the problems found. In addition to finding usability breakdowns, using heuristic evaluation method played an important role in extracting meaningful recommendations that help in designing and developing one of the bioinformatics online tools, and can consequently improve the overall usability of the entire system.

3.1. Study design

The first step in applying heuristics evaluation methodology is determining the ideal usability principles that are effective for measuring usability qualities of the bioinformatics systems. We adopted the list of specialized heuristics that was proposed by [1] in the context of bioinformatics domain. This list is comprised of 3 sets of heuristics that evaluate bioinformatics tools under three distinct areas; First Impression, Query/Results Form, and Interacting with results. In the study, expert users are engaged as participants and six participants were selected from three categories. A participant can be a bioinformatics expert, a usability expert or a cross-domain expert.

Two “Bioinformatics Experts” participated in this study and they had prior experience in using and developing web-based bioinformatics tools but no special usability expertise. In addition, two “Usability Experts” were involved in the evaluation process and they had experience in Human Computer Interaction HCI design but not specialized in the bioinformatics domain. Furthermore, two participants had expertise in both usability in general and the kind of web-based bioinformatics tools interfaces being evaluated. They inspected the three heuristics sets with four web-based bioinformatics tools; MEME [18], FIMO [19], RNAMST [20], and RNAPromo [21]. Two of them deal with sequence motifs localization and discovery processes. The other two tools deal with structural motif localization and discovery processes. For each tool, the participant was presented with a survey that contains a list of the three heuristic sets with each individual heuristic (48 in total) described in text to guide the participants. Using this survey, the evaluators identify general usability problems and each one is given a severity rating to examine the most serious usability problems in depth. By using a 1 – 5 ranking scale, the severity of a usability problem can be minor, serious, major, critical or failure. The participants are also allowed to comment and provide suggestions that can be used to redesign the tools and improve their usability by writing their recommendations in a special usability comments section that is associated with each heuristic.

3.2. Results

Ease of use, efficiency and user satisfaction were used as parameters for assessing the usability of these selected web-based bioinformatics tools. The approach of using three different sets of heuristics provided useful results for our case study, these results showed that the heuristic inspection evaluation method was effective in finding usability problems in bioinformatics tools designed for discovering and localizing motifs. After heuristic evaluations were conducted, outcomes and data from participant comments were aggregated, summarized into usability issues, and problems were grouped by agreement and severity. The key findings were compiled and classified into two main categories: usability problems or usability strength points. We noted that there were issues that were perceived similarly across all the selected tools being examined in this heuristics evaluation. For example, participants from bioinformatics domain observed that majority of the web-based bioinformatics tools have more detailed information available on the query form or on the output results. As content rich web-based applications, this requires richer interaction and better understanding from the user's side in a way that isn't helping domain novice users to use these tools. Beside this issue, participants were very frustrated from the mechanism of interaction with the interface; their opinion was that the tools have relatively poor user interface designs and lack in supporting powerful interactions and retrieving data that forces researchers to spend unnecessary time and effort in carrying out their tasks. Table 1 shows all the usability issues that were identified for each tool along with their corresponding severity ratings.

Table 1. Heuristic Evaluation Results: Usability Issues per Bioinformatics Tool

Severity	Minor “1”	Serious “2”	Major “3”	Critical “4”	Failure “5”	Total
MEME	16	7	4	0	1	27
FIMO	11	14	4	2	5	36
RNAMST	10	9	11	1	3	34
RNAPromo	19	6	2	2	0	29
Total	56	36	21	5	8	126

Despite noting problems and critiquing the interface of these web-based tools, participants were also requested to note strength points of the selected web-based bioinformatics tools. They had several positive comments, for example: most participants found that MEME and FIMO tool provide full support for helps and documentations that assist users with different levels of knowledge to search on any information related to the tool such as release notes or even query about how to achieve specific tasks. One bioinformatics expert liked the frequently asked questions (FAQs) section in the RNAPromo tool. This feature serves as a quick help for users by locating the answers to commonly asked questions regarding how to use tool. All participants reported that the selected tools effectively considered the samples of sequence data and provided good examples of input parameters in their query form that help users to start using tool in an intuitive flow comprised of several steps. These strength points were effective in facilitating the collection of the design recommendations that help developers who might have overlooked user perceptions, related to the usability of the interfaces, while developing their systems. These recommendations also help in building bioinformatics systems that are designed based on the perspectives and expectations of their target users.

4. Usability goals and metrics

Measuring usability in an effective way requires selecting the right usability metrics. Usability measurements help in evaluating quality of the bioinformatics system, providing feedback, in order to check whether objectives are met or not, and identifying errors in the system. Usability matrices can capture two types of data: qualitative data and quantitative data. Quantitative data gives accurate measures of what actually happened, it could be analyzed numerically and presented using statistics, tables and graphs. Some examples of quantitative data are the time required to complete specific task, the number of errors per task and the severity of each error. Qualitative data include textual expression about user preferences. It describes what participants thought or said rather than lists of numerical data. Measuring predictability and satisfaction are examples of qualitative data collected from the observation process. These collected usability considerations can be used as a basis for evaluating the usability, visualization and interaction of publicly available web-based bioinformatics systems. As well as suggesting improvements, applying the recommendations can be used to measure the effectiveness of the newly added functions. The usability metrics have been classified into two categories based on their relevance to cognitive or computational processes as shown in Table 2.

Table 2. Proposed usability metrics for web-based bioinformatics tools.

Cognitive Perspective	Computational Perspective
Time to Complete a Task	Completion rate efficacy
Number of Achromous	Number of commands used
Number of Feedback Functions per site	Error Frequency
Home Page Reference	Task Effectiveness
Layout Complexity	Task Completion
Overall Density	Broken Link Count
Number of Font Types used	Rate of Error Messages
Number of Ways to Perform a Task	Number of reusable components

Cognitive Perspective	Computational Perspective
Percent of Favorable User Comments	
User Subjective Rating	
Ease of use	
Overall satisfaction	
Number of Mouse Clicks to complete the task	

5. Comparison of Usability Evaluation Methods (UEM)

The usability engineering process is away to improve product quality to be easy to use and suitable for the task. One of the main activities in the usability process is the usability evaluation. It can determine the level of usability that has been achieved. The term usability evaluation method (UEM) is a technique used to perform usability assessment of a system or a proposed interaction design at any stage of its development process against a predefined set of usability metrics. A variety of usability evaluation methods (UEMs) have been developed to assess human interaction with a system for the purpose of optimizing user interface in order to increase usability. In this section we addressed the following question: which usability evaluation methods have confirmed to be the most effective in the context of bioinformatics interactive systems? And to answer this question we examined effectiveness of the usability evaluation methods by comparing them depending on different evaluation criteria, which include effective, efficient, and satisfactory. The criteria “usability factors” that were needed in the usability evaluation of web-based bioinformatics tool was gathered from some previous usability research studies [12, 22 and 23]. Mahrin et al. [23] showed subjective assessment of the likelihood of each UEM to evaluate each specified usability factor. The assessment evaluates each UEM for each usability factor on a three levels: High (H), Medium (M) or Low (L). These levels refer to the extent the ability of UEM to meet usability factor, respectively. In our adaptation, beside these study results, we added additional usability factors and more UEMs under comparison to make it more comprehensive. The revised comparison elements that include all the selected usability factors are listed in Table 3, which shows each UEM and level of their supportability for these usability factors.

Table 3. Comparison between UEMs based on usability factors.

UEM Type	UEM Name	Usability Factor												
		Understandable	Learnability	Well-structured	Effectively presented	Effectively supported	Tool-supported	Complete	Concise	Unambiguous	Operable	Navigable	Satisfaction	Tailorable
Testing	Thinking aloud protocol	H	M	M	M	M	M	L	M	M	H	H	H	L
	Remote Usability Testing	H	H	H	H	H	H	H	H	H	H	H	H	H
	Performance Measurement	M	M	L	M	M	L	L	L	L	M	H	L	L
Inspection	Heuristic Evaluation	L	L	M	M	M	M	M	L	L	L	M	L	L
	Cognitive walkthroughs	M	H	H	H	H	M	L	M	L	L	M	L	L
	Feature inspections	L	L	L	L	L	H	L	L	L	L	H	L	L
Inquiry	Field Observation	L	L	L	L	L	L	L	L	L	M	L	H	M
	Focus groups	M	M	M	M	M	M	M	M	M	M	M	H	M
	Logging Actual Use	L	L	L	L	L	L	L	L	L	M	L	L	L

As we seen from Table 5, UEMs might differ depending on the number of usability factor that are considered in the evaluation of a system. For example, remote usability testing is rated as high for all usability factors while the inspection techniques have low ratings with regards to sensitivity to assessments of user satisfaction. Lastly, focus

group methods have rarely been reported in the literature for developing bioinformatics tools and was perceived as moderately supporting the process of quality assurance for the context of these bioinformatics tools.

6. Conclusions and future work

Applying human factors and usability engineering to optimize the usability of bioinformatics online tools enables researchers to search, interact with, share, synthesize, visualize, and manipulate data more effectively and efficiently. The contribution of this research focused on multidisciplinary engineering of web-based applications in the context of two scientific domains; Bioinformatics and Software Engineering. The usability engineering process needs to be considered for developing intuitive interaction, achieving learnability and ease of use in the interfaces, and designing information architectures of bioinformatics tools, which consequently allow users to integrate the tools effectively in their context of bioinformatics research. Developing frameworks for usability engineering that incorporate usability evaluation methods which provide insights from objective and subjective measures of human behaviors is an essential step for building bioinformatics applications that are scalable and platform-independent. These usability-engineering frameworks can assist professionals across disciplines in their assessment of bioinformatics tools and in their endeavors for identifying usability problems and measuring user satisfaction. In this paper, a review of the usability problems and challenges reported in bioinformatics and software engineering research studies is presented. Because bioinformatics systems vary in their functionality and purposes, the reported difficulties were related to many areas of the biological systems. Browsing, searching, exploring and navigating through these systems require software engineers to take many usability-related metrics into considerations to satisfy the needs of the users. Furthermore, the growing complexity of biological systems and the availability of large amounts of biological data increase the demand for mechanisms that streamline the information access and retrieval processes. For this reason, we evaluated the usability of some bioinformatics systems and did a comparative evaluation of three usability evaluation methods. Obtaining the results of the heuristic evaluation from HCI experts and bioinformatics experts can help software engineers to avoid the problems that impact the performance of their systems by understanding the usability requirements of their target users. This research study also takes into account the cognitive and perceptual abilities of the users of bioinformatics systems as well as the computational difficulties that might be experienced in these systems by categorizing the usability metrics into computational metrics and cognitive metrics.

In our future studies, we aim to apply user-centered design approach in the development of bioinformatics online motif discovery tool (IncMD). This is to ensure reliable delivery of the system to the target users' population with acceptable level of usability. Then we will go through usability evaluation process in the context of bioinformatics research under three keys of usability metrics: effectiveness, efficiency and subjective satisfaction of subject-matter experts and practitioners in bioinformatics applied research domains. Future work also involves classifying the bioinformatics systems based on the problems that they solve and studying the usability considerations for each one (e.g. studying the usability factors that are essential for visualizing biological data).

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