

## Towards enhancing the user experience of ChIP-Seq data analysis web tools

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### ABSTRACT

Deoxyribonucleic acid (DNA) sequencing is the process of locating the sequence of the main chemical bases in the DNA. Next-generation sequencing (NGS) is the state-of-the-art DNA sequencing technique. The NGS technique advanced the biological science in analyzing human DNA due to its scalability, high throughput, and speed. Analyzing human DNA is crucial to determine the ability of a person to develop certain diseases and his ability to respond to certain medications. ChIP-sequencing is a method that combines chromatin immunoprecipitation (ChIP) with NGS sequencing to analyze protein interactions with DNA to identify binding sites. Many online web tools have been developed to conduct ChIP-Seq data analysis to either discover or find motifs, i.e., patterns of binding sites. Since these ChIP-Seq web tools need to be used by clinical practitioners, they must comply to the web-related usability tasks including effectiveness, efficiency and satisfaction to enhance the user experience (UX). To that end, we have conducted an empirical study to understand their UX design. Specifically, we have evaluated the usability of 8 widely used ChIP-Seq web tools against 6 known usability quality metrics. Our study shows that the design of the studied ChIP-Seq web tools does not follow the UX design principles.

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## 1. INTRODUCTION

The deoxyribonucleic acid (DNA) is a nucleic acid consists of two strands that coil around one another making a double helix shape. DNA holds the genetic instructions for all organisms. Attached to each sugar (deoxyribose) molecule one of four chemical bases: adenine (A), guanine (G), cytosine (C), and thymine (T). The two strands are connected together by bonds between the bases where A bonds with T and C bonds with G. A human has about 3 billion pairs of these letters in which the exact order of these bases forms the genome sequence. Identifying the sequence of these chemical bases or letters is known as DNA sequencing. Once the DNA sequence is identified, scientists compare it to standardized code to identify the variance between the two sets of letters.

DNA sequencing is important to identify the possibility of a person to develop certain diseases such as heart attack, cancer, or type II diabetes, or his ability to respond to certain medications, a technique known as pharmacogenomics. Moreover, DNA sequencing helps in finding if a person might develop rare cases of a disease such as Huntington disease (a progressive brain disorder). The next-generation sequencing (NGS) is the most advanced sequencing technique in the 21st century known as massive (ly) parallel sequencing. The NGS technique has advanced the biological science in analyzing human DNA due to its scalability, high throughput, and speed [1].

Applying chromatin immunoprecipitation (ChIP) followed by NGS sequencing is known as ChIP-sequencing or ChIP-Seq. ChIP-Seq determines the protein-DNA interactions in in vivo to identify binding sites, i.e., a region on a protein to bind with another molecule with specificity [2]. ChIP-Seq captures highly specific protein-DNA interactions such as transcription factor (TF) and ribonucleic acid (RNA)-binding protein (RBP). Since ChIP-Seq used heavily in industry, various web-based tools have been developed to analyze ChIP-Seq data to find or discover motifs, i.e., patterns of binding sites [3].

Due to the importance of the ChIP-Seq data analysis web tools, increasing the usability of such tools is essential to enhance the user experience (UX) while interacting with such web tools. Unfortunately, measuring website usability is a challenging task and many software engineers overlook the importance of improving the usability of their web applications. Resulting in poorly designed web tools that cannot be used by users or users will not be satisfied while using them. Website usability measures the extent to which a website can increase the satisfaction, effectiveness, and efficiency while being used by various types of users. To that end, we have conducted an empirical study to understand the usability of ChIP-Seq data analysis web tools in order to enhance their user experience (UX) design. More precisely, we have evaluated the usability of 8 widely used ChIP-Seq data analysis web tools against 6 known usability quality metrics. The 6-quality metrics, inspired by study [4] are: i) performance, ii) readability, iii) font size, iv) browser compatibility, v) website design, and vi) accessibility. These quality metrics have been measured using 14 diagnostic tools where different diagnostic tools measure different quality metrics. To the best of our knowledge, this is the first empirical study to evaluate the web usability of ChIP-Seq data analysis web tools to improve their UX design.

The remainder of this paper is structured. Section 2 presents the related research efforts. Section 3 describes our methodology. Section 4 shows the evaluation design and the obtained results in which section 5 discusses the results. Finally, the paper concludes in section 6.

## 2. RELATED WORK

Bioinformatic researchers develop software systems to understand and analyze biological data. This section summarizes the related research efforts in developing and studying software quality metrics for bioinformatics tools. Al-Turaiki *et al.* [5] investigated the usability of only 2 versions of a bioinformatic web tool. They studied the efficiency, effectiveness, and user satisfaction of using these tools. On the other hand, Al-Ageel *et al.* [6] surveyed the research studies that examined human factors in bioinformatics tools to visualize biological information. These factors supply a ground for future consideration of developing bioinformatics tools.

Bioinformatics tools generate huge amount of data that can overwhelm users and visualizing the data is challenging. Therefore, Mannapperuma *et al.* [7] investigated the problem of visualizing the generated data and provided recommendations to improve the usability of data visualization. Moreover, Machado *et al.* [8] studied the behavior and the preferences in selecting bioinformatics resources for teaching and learning. However, they studied human satisfaction in selecting only two bioinformatics tools. While Mathé *et al.* [9] organized interviews in Chicago among empirical and computational biologists to enhance communication and cooperation between them. They made three short conversations with a focus on RNA-Seq, chromatin analyzing, and genomic information. On these conversations, computational biologists present their bioinformatic tools in order to receive feedback about them from others. They mentioned that this type of conversation is necessary for promoting efficient scientific discussions to better develop bioinformatics tools. Moreover, Paixão-Côrtes *et al.* [10] designed a service-oriented architecture interface named Maggie which used to deliver diverse biological data. In addition, they measured the usability of the suggested interface.

Although the work on usability of bioinformatic web tools is still on its early stages, many researchers from the software engineering community and the human-computer interaction (HCI) community have investigated the usability of educational and commercial websites. For example, Benaida and Namoun [11] explored the effects of four major factors on the usability perceptions of Algerian educational websites that included system utility, interface goodness, content and satisfaction of users. Similarly, AlBalushi *et al.* [12] explained how to measure the accessibility and the performance of e-services using different web diagnostic tools. Moreover, Kaur *et al.* [13] used different web testing tools such as Pingdom, Site Speed Checker, and GTmetrix to measure the usability of university websites due to its importance for attracting new students as well as increasing the loyalty of current students. Finally, Zheng [14] mentioned that usability is the first step to assess websites. They studied and evaluated e-commerce websites using online diagnostic web tools based on four indicators. Although our work in this paper is different from all previous works, we have utilized web diagnostic tools and included various usability quality metrics that have been highlighted in previous works.

### 3. RESEARCH METHOD

This section describes our method of empirically evaluate the usability of ChIP-Seq data analysis web tools. First, in subsection 3.1, we describe the 8 ChIP-Seq data analysis web tools used in this research. Next, in subsection 3.2, we present the 6 web usability quality metrics that we have measured on each ChIP-Seq tool. Each quality metric has been quantified through various quality measurements. Then, subsection 3.3 describes the 14 various diagnostic tools we leveraged to calculate the 6-quality metrics for each ChIP-Seq tool. Different diagnostic tools used to measure different quality metrics.

#### 3.1. Subject ChIP-Seq data analysis tools

In our work, we have measured the usability of 8 known and widely used ChIP-Seq tools. The functional ability of these tools in detecting binding sites have been studied in [3]. Table 1 summarizes the 8 ChIP-Seq tools and their main features. The selected features are: i) use pipeline: shows if the tool uses a pipeline technique or not for analyzing the data; ii) input file format: list of the format (s) of the accepted input file by the tool; iii) output file format: the format (s) of the generated output file; iv) max file size: the maximum size of the input file the tool can handle; v) Max width of motifs: the maximum width (number of characters in the sequence pattern) of a single motif a tool can analyze; vi) year: the release year of the tool; vii) motif sites in both strand: indicates weather the tool can check the reverse complement of the input sequences for motif sites or not; viii) background mode: weather the tool has a background model to normalize the distribution of the letters or not; and ix) version: the version of the tool.

Table 1. Summary of the 8 studied ChIP-Seq data analysis tools. ND: not determined

Web Tool	Use Pipeline	Input File Format	Output File Format	Max File Size	Maxi Width of motifs	Year	Motif sites in both strand	Background mode	Ver.
Multiple EM For motif elicitation (MEME) [15]	No	Fasta	HTML XML text	60000 chars	300	2006	Yes	Yes	4.12.0
Gapped Local Alignment of Motifs (GLAM2) [16]	No	Fasta	HTML XML text	60000 chars	300	2008	Yes	No	4.12.0
Cis Elements candidates (CisFinder) [17]	No	Fasta, delimited text	HTML text	ND	ND	2009	Yes	No	
Web tool for de novo motif discovery from ChIP-based high-throughput data (W-ChIPMotifs) [18]	Yes	Fasta	PDF	ND	ND	2009	No	No	
Discriminative regular expression motif elicitation (DREME) [19]	No	Fasta	HTML XML text	ND	ND	2011	Yes	No	4.12.0
Motif analysis of large nucleotide datasets (MEME-ChIP)[20]	Yes	Fasta	HTML XML text	Unlimited	300	2011	Yes	Yes	4.12.0
Regulatory sequence analysis tool of Peak-motifs (RSAT Peak-motifs)[21]	Yes	Raw FastaIG Wcon- sensus	ND	Unlimited	8	2012	Yes	Yes	
Protein scanning ChIP (PScan-ChIP)[22]	No	Bed	HTML text	Unlimited	ND	2013	No	Yes	1.3

#### 3.2. Quality metrics

To measure the quality of the ChIP-Seq tools, we have measured 6 usability quality metrics (QM). The 6 considered quality metrics are: performance (QM1), readability (QM2), font size (QM3), browser compatibility (QM4), website design (QM5), and accessibility (QM6). Table 2 shows the measurement (s) used to quantify each quality metric. Our website [23] contains details about each quality metric.

#### 3.3. Diagnostic tools

To measure the 6-quality metrics (recall Section 3.2.) of the 8 studied ChIP-Seq web tools (recall Section 3.1.), we leveraged 14 difference web diagnostic tools. Different web diagnostic tools have been used to quantify different measurements of the quality metrics. Table 3 summarizes the web diagnostic tools that we leveraged to quantify the measurements of the quality metrics for each ChIP-Seq tool along with their

abbreviations ordered by the abbreviation alphabetically. Table 4 shows the various web diagnostic tools used to quantify each measurement of the quality metrics. The empty fields in the table means we manually measured it.

Table 2. The quality metrics along with their measurement (s) used to quantify them

Quality metric (QM)	Quality measurement	Quality metric (QM)	Quality measurement
QM1: Performance	QM1.1: Load time	QM3: Font size	QM3.1: Labels
	QM1.2: Page size		QM3.2: Checkboxes, Buttons, and menus
	QM1.3: Performance grade		QM3.3: Description of the tool
	QM1.4: Total numbers of request		QM3.4: Hyperlinks
	QM1.5: Response time		QM3.5: Title of the tool
QM2: Readability	QM2.1: Flesch Kincaid Reading Ease (FRE) index	QM4: Browser Compatibility	QM4.1 Compatible with all major browsers
	QM2.2: Gunning Fog Index (GFI)		QM5.1: The complexity of the design
	QM2.3: Flesch Kincaid grade level Index (FGL)	QM5: Website design	QM5.2: Average number of clicks
	QM2.4: SMOG grading index (SMOG)		QM5.3 Average path lengths
	QM2.5: Coleman Liau Index (CLI)		QM5.4 Broken links
	QM2.6: Automated Readability Index (ARI)	QM6: Accessibility	QM6.1 WCAG Level
			QM6.2 Color contrast errors

Table 3. The 14 utilized diagnostic tools along with their abbreviations (Abb.)

Diagnostics Tools	Abb.	Diagnostics Tools	Abb.
Achecker	A	SortSite	SS
Gtmetrix	Gm	Site Speed checker	SSC
Juicy Studio	JS	WAVE	W
Pingdom	PD	WhatFont	WF
Powermapper tool	PM	WebToolHub	WH
Readability Calculator	RC	Xenu's Link Sleuth tool	XL
Readability Test Tool	RTT	Yslow	Y

Table 4. Quality measurement and the diagnostic tool(s) used to quantify it

Quality Metric (QM)	Measurement	Diagnostics (s)	Metric (QM)	Measurement	Diagnostics (s)
QM1: Performance	QM1.1	SSC, Gm, PD, WH	QM3: Font size	QM3.1	WF
	QM1.2	SSC, Gm, PD, WH		Qm3.2	WF
	QM1.3	Y, PD, Gm		QM3.3	WF
	QM1.4	Gm, PD		Qm3.4	WF
	QM1.5	SSC		QM3.5	WF
QM2: Readability	QM2.1	JS, RC, RTT	QM4: Browser compatibility	QM4.1	SS
	QM2.2	JS, RC, RTT		QM5: Website design	QM5.1
	QM2.3	JS, RC, RTT	QM5.2		
	QM2.4	RC, RTT	QM5.3		
	QM2.5	RC, RTT	QM5.4		XL
	QM2.6	RC, RTT	QM5.5	A	
QM6: Accessibility	QM6.1	W			

#### 4. EVALUATION DESIGN AND RESULTS

Since the idea of this research is to empirically investigate the usability of the ChIP-Seq web tools and to compare between them, we calculated the average of the readings we obtained from the various diagnostic tools for each quality metric measurement. Then, we normalized the number. To normalize the quality metric measurement numbers, we leveraged (1).

$$Normalization(qm) = \frac{x - \min(qm)}{\max(qm) - \min(qm)} \tag{1}$$

Where *qm* is the quality measurement and *x* are the average of the readings of the quality measurement that need to be normalized. The range of the normalized numbers are between 0 and 1, where 0 means the quality measurement is bad for a given web tool and 1 means the quality measurement is the best. Note that, in some cases when a small value is better than a large value for a given quality measurement, we reverse the scale by subtracting the normalized number from 1, i.e., 1 would be 0, 0.2 would be 0.8. The equation (1) used to normalize the measurements of the performance, readability, font size, and browser compatibility quality

metrics. The idea here is to have one number for each quality metric for each web tool so we can compare and contrast between them.

**4.1. Performance**

Figure 1 depicts the normalized performance quality measurements for each tool. The x-axis shows the five performance measurements and the y-axis shows the normalized numbers. As shown in Figure 1, W-ChIPMotifs tool scored the best performance over all five performance measurements while there is no one tool achieved the worst on all performance quality measurements. However, the RSAT Peak-motifs has the worst performance almost on all of the measurements.

To compare between the ChIP-Seq web tools based on the performance metric, we have calculated the average of all five performance measurements shown in Figure 1 and depicted the results in Figure 2. Figure 2 shows the overall performance metric of each ChIP-Seq web tool. Based on the Figure 2, we conclude that WCHIPMOTIFS has the best performance with a score of 0.99 and RSATPEAKMOTIFS is the worst with a score of 0.311. The Figure 2 shows that the web tools have different performance quality.

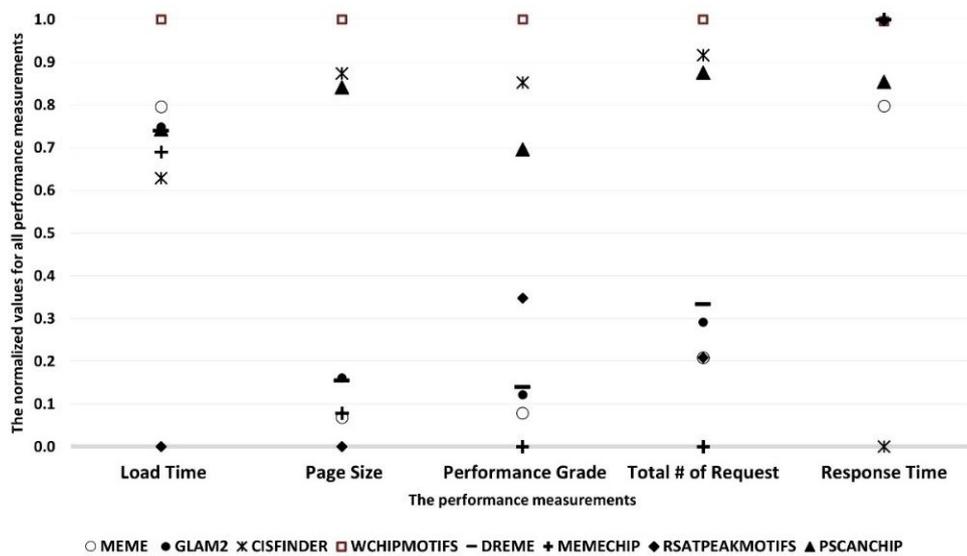


Figure 1. The detailed normalization values for each performance measurements (the higher the better)

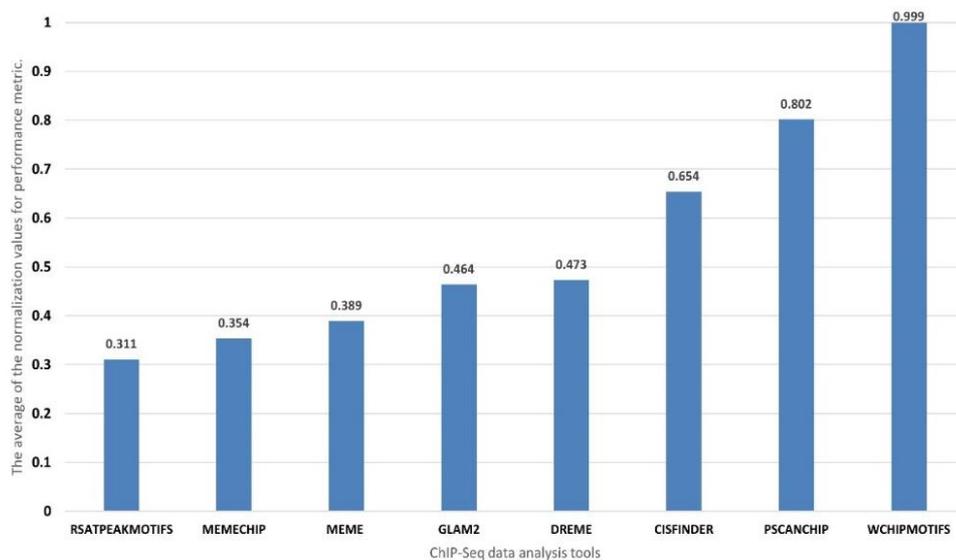


Figure 2. Summarized values of the performance metric quality (the higher the better)

**4.2. Readability**

Figure 3 depicts the details of the normalized readability quality measurements for each tool. The x-axis shows the six readability measurements and the y-axis shows the normalized numbers. As shown in Figure 3, WCHIPMOTIFS achieved the best in FRE and the worst on almost all of the other readability measurements. On the other hand, PScan-ChIP scored the worst on FRE and the best or among the best on all other readability measurements.

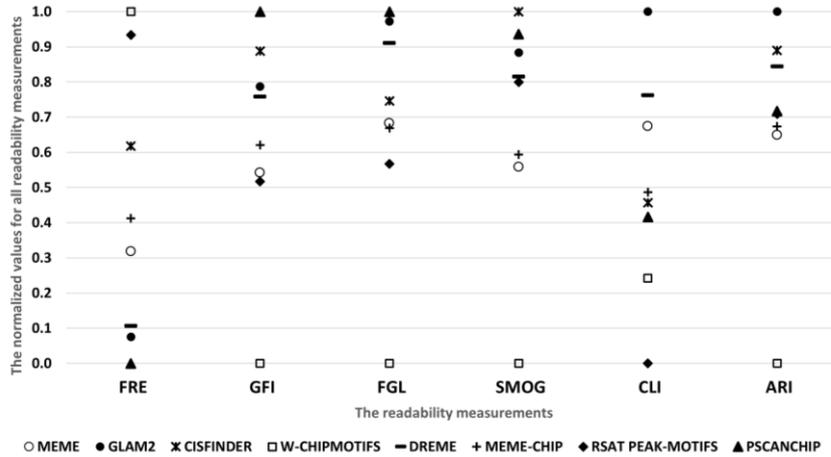


Figure 3. The detailed normalization values of readability measurements (the higher the better)

To be able to compare and contrast between the ChIP-Seq web tools based on the readability quality metric, we have averaged the normalized numbers for each tool and considered that value as the quantity of the readability quality metric. Figure 4 depicts the summary of the readability quality metrics of the studied ChIP-Seq web tools. As shown in Figure 4, GLAM2 has the best readability metric with a score of 0.786 while the WCHIPMOTIFS has the worst readability quality with a score of 0.207.

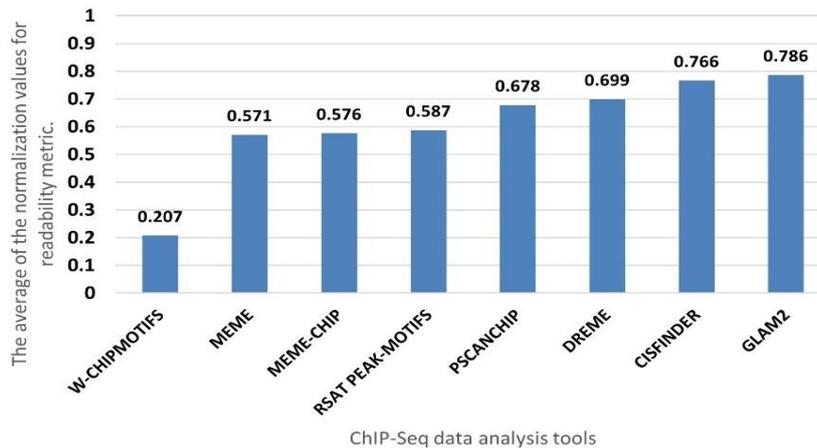


Figure 4. Summarized values of the readability metric quality (the higher the better)

**4.3. Font size**

Similar to the previous quality metrics, we have calculated and normalized the average of the five font size quality measurements that we obtained from various diagnostic tools. Figure 5 depicts the summary of the font size quality metric of the investigated ChIP-Seq web tools. Based on Figure 5, DREME, MEME, and MEMECHIP have the best font size quality whereas RSAT-PEAKMOTIFS achieved the worst comparing to the other studied tools. The number zero for the RSAT-PEAKMOTIFS means that its font size quality measurements were the lowest and unacceptable.

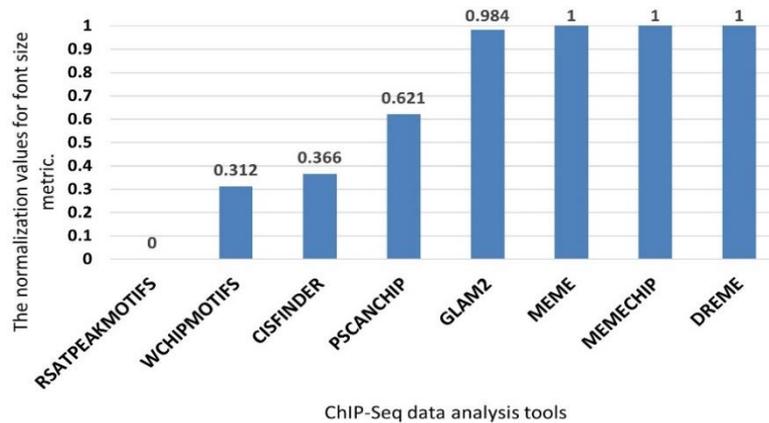


Figure 5. Summarized values of font size metric (the higher the better)

#### 4.4. Browser compatibility

We leveraged SortSite to measure the browser compatibility of the ChIP-Seq web tools and we divided the browser compatibility into critical issues (C1, C2, and C3) and major issues (M4 and M5). Based on Table 5, all ChIP-Seq web tools have either critical or major issues with most web browsers except WCHIPMOTIFS which has no issues with any web browser. On the other hand, MEME and DREME have similar issues with all major web browsers.

To be able to compare between the ChIP-Seq web tools based on their compatibility with the major web browsers, we have quantified the critical and the major issues as shown in Table 6. We quantified any critical issue with a weight of 1.5 and any major issue with a weight of 1 and 0 for no issues against the given web browser. Then, for each ChIP-Seq tool, we calculated the number of critical issues and multiplied them with 1.5 and counted the number of major issues and multiplied them with 1. The obtained number is considered the quantity of the web browser compatibility of the given tool. After that, we have normalized the number based on the scale 0 to 1 where 0 is the worst and 1 is the best. The calculated numbers are reported on the last two rows of Table 5. Figure 6 depicts the browser compatibility of the ChIP-Seq web tools based on the calculated and normalized numbers.

Table 5. Browser compatibility metric of the ChIP-Seq web tools

Browser version	MEME	GLAM2	CIS-FINDER	W-CHIP-MOTIFS	DREME	MEME-CHIP	RSAT PEAK-MOTIFS	PSCAN-CHIP
IE	C1, C2, M4, M5	C1, M4, M5	M5	-	C1, C2, M4, M5	C1, M4, M5	M4, M5	M5
Edge	C1	C1	-	-	C1	C1	-	-
Firefox	M5	M5	M5	-	M5	M5	M4, M5	M5
Safari	M4, M5	M4, M5	M5	-	M4, M5	M4, M5	M4, M5	M5
Opera	C1, M5	C1, M5	M5	-	C1, M5	C1, M5	M4, M5	M5
Chrome	C1, M5	C1, M5	M5	-	C1, M5	C1, M5	M4, M5	M5
iOS	C3, M4, M5	M4, M5	M5	-	C3, M4, M5	M4, M5	M4, M5	M5
Android	C1, M4	C1, M4	-	-	C1, M4	C1, M4	-	-
Black Berry	C1, C2, M4	C1, M4	M5	-	C1, C2, M4	C1, M4	-	-
Weighted Score	24.5	20	7	0	24.5	20	12	6
Normalized Data	0.000	0.184	0.714	1.000	0.000	0.184	0.510	0.755

Table 6. Weight scores of the critical and major browser compatibility issues

Criteria	Weight
No issue	0
Major (M4, M5)	1
Critical (C1, C2, C3)	1.5

#### 4.5. Website design

As mentioned in Table 2, we have measured the website design using five measurements. Table 7 shows the path lengths (QM5.3) and the average number of clicks (Qm5.2) for each ChIP-Seq web tool. Based on [24], the average number of clicks should not exceed 4. As shown in Table 7, all tools have accepted average number of clicks to reach a desired page.

Regarding the broken links quality measurement, QM5.4, Table 7 shows also the average number of broken links on each ChIP-Seq web tool. As indicated by Ismailova and Inal [25] the acceptable number of broken links are between 2 and 13. Based on this criterion, all tools have an acceptable number of broken links except RSATPEAKMOTIFS which has a large number of broken links.

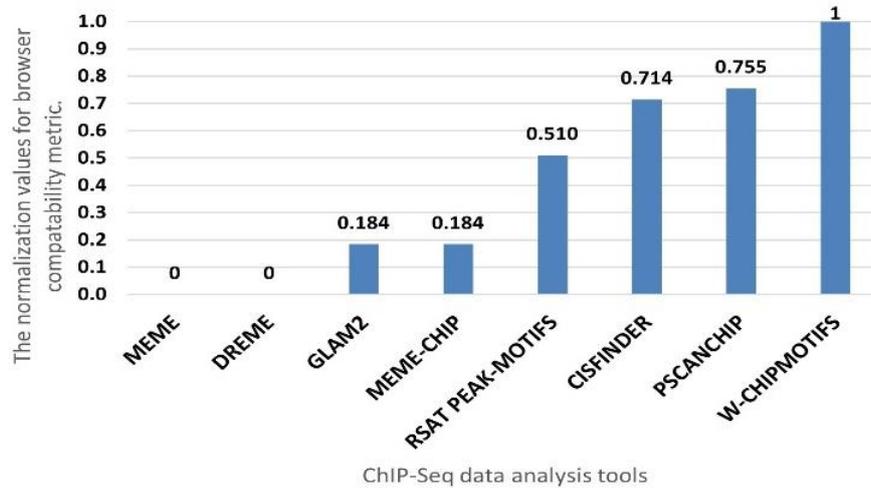


Figure 6. Summarized values of browser compatibility quality metric (the higher the better)

Table 7. Path lengths, average number of clicks, and the average number of broken links for each tool

ChIP-Seq tools	MEME	GLAM 2	CISFI NDER	WCHIP MOTIFS	DREME	MEME CHIP	RSAT PEAK MOTIFS	PSCAN CHIP
QM5.3	859	911	25	1	940	928	1619	14
QM5.2	2.483	2.639	1.667	0.5	2.717	2.682	2.357	1.4
QM5.4)	0	0	6	0	0	3	10924	1
Total no. of links	1252	1252	30	1	1252	1252	21975	12

Table 7 shows the number of links on each ChIP-Seq web tool. This number used to calculate the complexity of each tool. Table 8 shows the design complexity of each ChIP-Seq web tool using the 10-point scale criteria described in [24] and [26]. As shown in Table 8, we calculated the V1, the value of sitemap calculation, and the v2, the value of cyclomatic complexity. Then, we computed the average of V1 and V2 which reported in the third row of Table 8. After that, we computed the p-value and the 10-point scale by adding the average of V1 and V2 to the p-value of each ChIP-Seq tool. As shown in the Remarks row of Table 8, all ChIP-Seq web tools have poor design and hence complex design for users.

Table 8. The design complexity of ChIP-Seq web tools

ChIP-Seq tools	MEME	GLAM 2	CISFI NDER	WCHIP MOTIFS	DREME	MEME CHIP	RSAT PEAK MOTIFS	PSCAN CHIP
V1	3.6	3.683	2.5	1	3.929	4.09	0.6	1.5
V2	7	7	9	10	7	7	0	10
Avg (v1, v2)	5.3	5.341	5.75	5.5	5.464	5.545	0.3	5.75
P	0.75	0.5	0.75	0.75	0.5	0.5	0.75	0.75
10-point scale value	6.05	5.841	6.5	6.25	5.964	6.045	1.05	6.5
Remarks	Needs improvement	poor design	Needs improvement	Needs improvement	poor design	Needs improvement	Very poor design	Needs improvement

#### 4.6. Accessibility

As described earlier in section 3, we measured the web content accessibility guidelines (WCAG) level of each ChIP-Seq web tool (QM6.1) as well as the number of color contrast errors (QM6.2). Table 9 shows the number of violations to each level of the WCAG levels for each web tool. According to Table 9, GLAM2, DREME, and PSCANCHIP tools have the lowest average of errors for level A, and the rest of the tools have the highest average. CISFINDER tool does not have any error. At level AA and level AAA:

CISFINDER tool does not have any error. However, GLAM2 and PSCANCHIP have the lowest average of errors while the rest of the tools have the highest average.

Table 10 shows the number of violations (errors) to the accessible color contrast ratio. According to the minimum contrast ratio, all ChIP-Seq web tools have contrast issues except the CISFINDER tool. To overcome these issues, the software engineers of these tools need to increase the contrast ratio between foreground and background colors to become above the ratio of 4.5:1.

Table 9. WCAG 2.0 level of each ChIP-Seq web tool

ChIP-Seq tools	MEME	GLAM 2	CIS FINDER	WCHIP MOTIFS	DREME	MEME CHIP	RSAT PEAK MOTIFS	PSCAN CHIP
Level A	30	10	0	32	42	53	101	12
Level AA	60	28	0	38	67	103	355	24
Level AAA	60	28	0	38	47	103	178	24

Table 10. Measuring the color contrast errors (QM6.2)

ChIP-Seq tools	MEME	GLAM 2	CIS FINDER	WCHIP MOTIFS	DREME	MEME CHIP	RSAT PEAK MOTIFS	PSCAN CHIP
Avg.no. of color errors	2	5	0	24	5	2	16	1
Avg contrast ratio for the color errors	2.5:1	3.4:1	0	3.84:1	3.4:1	2.5:1	4.21:1	2.76:1

### 5. DISCUSSION

On the previous section, we have evaluated the usability of the ChIP-Seq web tools based on the six-quality metrics separately. In this section, we have combined the normalized values of the quality metrics (performance, font size, readability, and browser compatibility) along with the design quality to have a holistic view of the usability of the tools. Figure 7 combines the normalized quality metric values for each web tool. In addition, each tool name is combined with the quality of its design. From the Figure 7, we see that the WCHIPMOTIFS tool is the best in the performance and the browser compatibility while it is below the average on the other two quality metrics. On the other hand, the font size quality of the MEMECHIP tools is the best and below average on the other quality metrics. As indicated in the figure, the design of all these web tools need improvement to make them more usable and to attract more users.

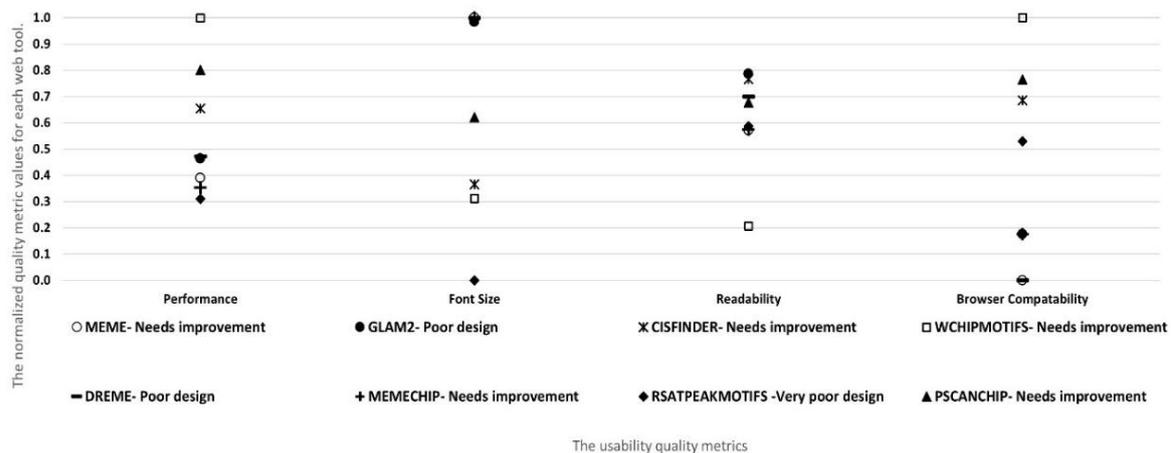


Figure 7. The normalization values of motifs tools for performance, font size, readability, website design, and browser compatibility metrics (the higher the better)

Figure 8 shows the average of the normalized quality metrics in one value to compare the usability of the web tools. The figure shows that the PSCANCHIP web tool is the most usable tool comparing to the other tools. However, its score of 0.716 indicates that the usability aspects of this tool need to be improved by its software engineers. On the other hand, the figure clearly shows that all other tools have major usability issues. As shown in Figures 7 and 8, all ChIP-Seq web tools suffer from usability issues and need major

improvements to enhance their design. The low usability of these tools calls their software engineers to improve the usability of these tools and hence increase their user experience.

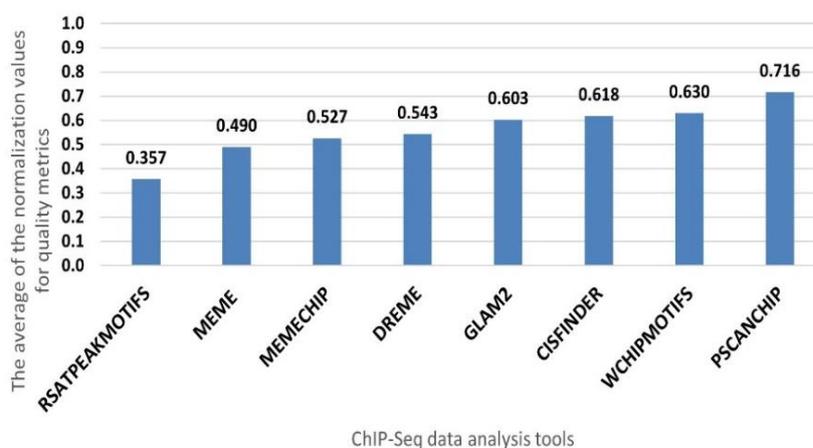


Figure 8. The average normalization values of motifs tools for performance, font size, readability, and browser compatibility metrics (the higher the better)

## 6. CONCLUSION

ChIP-Seq becomes the industry standard to understand protein-DNA interactions. Therefore, many ChIP-Seq tools have been developed as web applications to be used by clinical practitioners. However, the usability of such tools has never been investigated to improve their UX design. To that end, this research empirically studies the usability of 8 ChIP-Seq web tools from 6 usability quality metrics. The 6 quality metrics are: i) performance, ii) readability, iii) font size, iv) browser compatibility, v) website design, and vi) accessibility. To quantify the various measurements of the 6-quality metrics, we have leveraged 14 various diagnostic tools and reported the results. This study shows that all ChIP-Seq web tools have major usability issues and they are poorly designed and they need improvement. We found that all ChIP-Seq web tools extremely suffer from poor UX design and hence cannot attract new users or retain their current users. Based on our results and findings, we urge the software engineers of ChIP-Seq web tools to enhance the usability of their tools. In the future, we plan to expand our study and include more ChIP-Seq web tools as well as including more usability quality metrics and leverage more diagnostic tools.

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