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Extending Interface to Perl Script

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ABSTRACT: The interface is a picture-oriented way to interact with technology using operating system commands and graphical user formats. It provides more user communication with a computer program. Several databases have been extended to the shape of forms to collect normalized data. The interface design is equipped with validation checks so that the end users use accurate data. It is the background of the internet revolution. The massive genome data is available online for retrieving information. One such computer program, *misa.pl* is designed to identify simple sequence repeats. This program is tedious to use for naïve users. Thus it has been extended with an interface in java NetBeans making it simple to use for research purposes.

KEYWORDS: Command line, Interface, *misa.pl*, Java NetBeans, Script.

I. INTRODUCTION

The interface is a picture-oriented way to interact with technology using operating system commands and graphical user formats. It provides more user communication with a computer program. Several databases have been extended to the shape of forms to collect normalized data. The interface design is equipped with validation checks so that the end users use accurate data. It is the background of the internet revolution. On the other hand, the Command Line Interface is a text interface used by typing commands at the command prompt instead of using the mouse and keyboards, as in the Graphic User Interface or GUI. Unlike a GUI of the operating system or customized software, a command line only uses the keyboard to write, navigate and perform actions by writing commands and does not utilize a mouse pointer for navigating. The Command Line Interface or CLI is also called the command prompt in Windows OS, the Terminal in the mac operating system, and the command screen, shell, or bash in Linux.

Most operating systems are designed to shield the naïve user from the ins and outs of the command prompt. Still, *cmd* has positive aspects of being powerful, speedy, and able to accomplish a vast array of tasks very fast with a single command-line instruction—no matter what type of development, coding, or programming task we perform. On the other hand, some end-users find it challenging to use the command prompt, recall commands, recall files and directories path, especially the non-programmers.

The advantages of a command-line interface are:

- Greater control and access to operating systems or applications.
- Faster management of files
- Ability to store scripts to automate routine tasks.
- Basic command-line prompt knowledge is necessary to troubleshoot issues, such as network connection issues.
- The disadvantages of a command-line interface are:
 - GUI is more user-friendly;
 - The steeper learning curve associated with memorizing commands and complex syntax/arguments;
 - Different commands are used in other shells.

The first concept of a graphical user interface emerged in 1970 at the company Xerox. Initially, the computer was controlled using the mouse and keyboard instead of DOS commands. Xerox Alto was the first PC launched with a GUI, then Apple in the 1980s, followed by the Macintosh. The usage of smartphones and tablets led to the GUI



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revolution, and the graphical interfaces progressed considerably. Today screen movements and displays can even be controlled with finger movements and gestures [1].

So the GUI is an interface between people and machines. It aims to reproduce the programming code in the backend of a system in a user-friendly manner as possible, simplifying its everyday application for end-users. Symbols and images play a significant role since they enable universal applications independent of the text. For example, almost everyone knows what the Wi-Fi and Bluetooth symbol looks like, even though the word is quite different in various languages.

A graphical user interface combines visual design with programming functions. It, therefore, offers buttons, drop-down menus, navigation fields, search fields, symbols, and widgets. GUI developers prioritize user-friendliness. Typical GUI components include- a simple interface with purpose-based layout consistency, design and selection of soothing eye colours, which should be upgradeable in future. The importance of GUI makes it applicable to various applications in ecommerce, banking, research etc

Massive genome sequence data is available online on several platforms, and that data is being utilized by researchers to unveil genetic information of organisms and study species diversity. In this relation, several bioinformatics tools are being developed to analyze the data computationally. One such script `misa.pl` written in Perl language is being used to find out the simple sequence repeats and their location in nucleotide sequences. This script is executable on the cmd prompt and lacks an interface; therefore, it is a tedious job for researchers or naïve users to recall commands for the command line version.

The objective is to provide an interface to the Perl script `misa.pl` [2] as shown to be executed on `cmd.exe` in figure 1, so that the users can interact with the script to set and reset from mono- nucleotides parameters and interruption numbers in the `misa.ini` configuration file. MISA, a microsatellite identification tool, allows the identification, size and location of perfect and compound microsatellites' start and end positions. These are interrupted by a particular number of bases.

```
C:\Windows\system32\cmd.exe
Microsoft Windows [Version 6.1.7601]
Copyright (c) 2009 Microsoft Corporation. All rights reserved.

C:\Users\user>cd\
C:\>cd Strawberry\perl\bin\
C:\Strawberry\perl\bin>misa.pl neem1.fasta
C:\Strawberry\perl\bin>
```

Figure1. Command line showing the use of the cmd command used to run `misa.pl`.

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II. METHODOLOGY

- a. Perl script `misa.pl` and `misa.ini` configuration file is downloaded from- <http://pgrc.ipk-gatersleben.de/misa/download/misa.pl>.
- b. Java NetBeans 8.0.1 to use swing components.
- c. Algorithm
 - Step1 Input
 - Step2. Create GUI using swing components label, text field and buttons.
 - Step3. Write label names unit size.
 - Step4. Create text fields for entering repeats numbers.
 - Step5. Create interruption labels and text fields.
 - Step6. Create two buttons to save parameters and reset parameters.
 - Step7. To reset parameters in the reset button, write code for every text field like `textField1.setText(" ");`
 - Step8. Write a function to open `misa.ini` in read mode.
 - 8.1 Write code for each text field to enter text using the `getText()` function.
 - 8.2 Open `misa.ini` in write mode, create `BufferedWriter`, use `FileWriter` and mention the path of `misa.ini`.
 - 8.3 Use the write function to enter parameters.
 - 8.4 Close file.
 - 8.5 Display option pane for the message.
 - Step9. Close

III. RESULTS AND DISCUSSION

The program is based on making non-interactive `misa.pl` Perl script interactive by adding more functionality through GUI. This allows changing nucleotide parameters by setting and resetting parameters in the `misa.ini` configuration file, as shown in figure 2. It allows naïve users to interact with Perl scripts `misa.pl`. MISA uses the dictionary approach for mining simple and compound simple sequence repeats.

Earlier it was difficult to recall and use cmd commands, and the same Perl script with default parameters was difficult to handle and limited the scope of use.

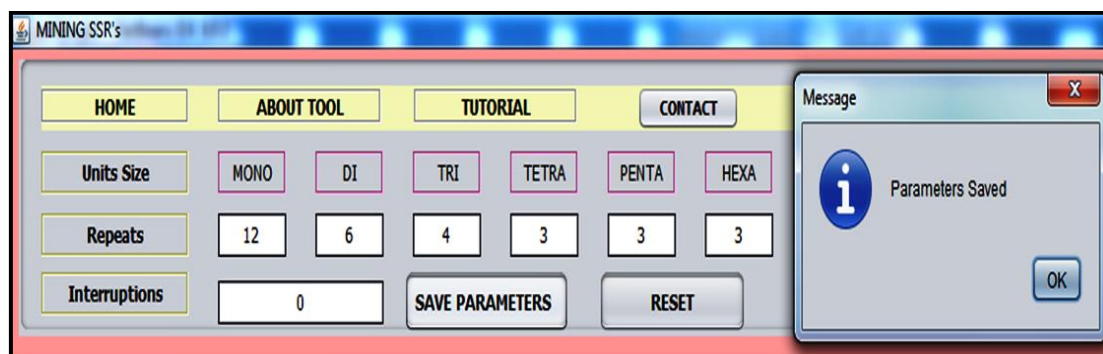


Figure2. Java NetBeans GUI is showing extended functionality to Misa. pl.

MICAS microsatellites analysis server was designed, developed, and maintained by EMBNET in India. It was simple textbox where the sequence was to be placed with no interaction with setting and resetting nucleotide parameters [3]; then perfect microsatellite repeat finder was designed here; also, there was no option to set and reset mono to hexa nucleotide size [4]. The next software microsatellite repeat finder was designed in 2009 [5]; there also no



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option for setting mono to Hexa nucleotide size given, although the minimum and maximum length of nucleotide repeats were allowed to be set here.

The next software, tandem repeat finder, was designed where maximum and minimum repeat length was provided to set, but there was no option to set the minimum number of nucleotides; it was designed in the year 2002 [6]. Then we had the next software etandem that found tandem repeats in the nucleotide sequence; here also, the GUI was very simple with no options to set and reset nucleotide parameters; then Web Troll was the software where the setting and resetting of nucleotide options was provided [7]. Then msatcommander python software was designed in 2008 [8]; in most of the cases, like the cotton marker database, the Perl script was used in the backend with no interference to set. SSRIT simple sequence repeater identification tool was designed, and the GUI was not very rich [9].

IV. CONCLUSION

The command line version of Perl script misa.pl, which is being used for identifying genomic information, has been extended for further use by developing an interface in Java Net Beans. The users can set and reset nucleotide parameters as per their requirements in the configuration file and save them for use. The program is available in a jar file and can be used safely by running it.

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