GuiLiner: A Configurable and Extensible Graphical User Interface for Scientific Analysis and Simulation Software

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Abstract

The computer programs most users interact with daily are driven by a graphical user interface (GUI). However, many scientific applications are used with a command line interface (CLI) for the ease of development and increased flexibility this mode provides. Scientific application developers would benefit from being able to provide a GUI easily for their CLI programs, thus retaining the advantages of both modes of interaction. GuiLiner is a generic, extensible and flexible front-end designed to “host” a wide variety of data analysis or simulation programs. Scientific application developers who produce a correctly formatted XML file describing their program’s options and some of its documentation can immediately use GuiLiner to produce a carefully implemented GUI for their analysis or simulation programs.

Key-Words : Graphical user interfaces, XML, Computer applications, Software interfaces

1 Introduction

Computer applications for scientific research generally receive user input through a command line interface (CLI) or through a graphical user interface (GUI). Each has advantages and shortcomings. For example, GUIs provide immediate accessibility and a familiar mode of interaction for most users. On the other hand, the CLI allows for batch processing, inclusion of the program in shell scripts, and the retention of execution parameters. CLI programs also require less development time and are more portable across different computer operating systems.

In this paper we present guiLiner, an application designed to bridge the gap between CLI and GUI modes for computer programs used in scientific research. GuiLiner is a generic, extensible and flexible front-end designed to “host” a wide variety of data analysis or simulation applications. It is geared primarily toward the scientific application development community, which can realize several unique benefits from its use, beginning with the elimination of time spent writing code to generate a GUI.

The task of creating a generic GUI for biological scientific applications is made simpler by the fact that most of them follow a simple interaction model: 1) the user provides data and parameters to the application 2) the algorithm is executed on these and 3)
the results of the analysis are returned. Each of these steps is generally atomic.

Since step 1) can involve many options, it is here that CLI based applications can become cumbersome to use or may be intimidating to inexperienced users. GuiLiner focuses on this step and on step 2). Without modifying the original CLI program, guiLiner provides a way for users to quickly see the available program options, read documentation and set the value of each option, and then execute the program, all from within a familiar “point-and-click” environment.

2 Implementation

GuiLiner is written in the Java programing language, and virtual machines capable of executing it are available for current versions of Microsoft Windows, Mac OS X and many types of UNIX based operating systems such as GNU/Linux (for a full list, please see http://www.java.com:80/en/download/manual.jsp). GuiLiner operates by parsing an XML configuration file which contains information on the CLI-based application being hosted, its options, documentation and some details about how guiLiner itself should display this information (Figure 1). This scheme allows almost unlimited extensibility, so that the feature-set of guiLiner can be increased with later releases.

The GUI provided by guiLiner features a rapid visual summary of which options are required, set, or unset in a color-coded option tree; integrated display of documentation specific to each program option; facilities for saving the values of options used for a particular execution of the hosted application; and the ability to view and save to disk program run-time output and/or errors.

In addition to the rapid display of selected and required options, efficient option information retrieval and runtime results, guiLiner’s layout is designed to put commonly used functions within easy each. Besides the usual menu bar (Figure 2 #1) containing a custom help browser and XML save-open options among other settings, there is also a button bar for functions commonly used during option setting (Figure 2 #2). These include functions to preview the command line, rest all options, manipulate the option tree and run the hosted program. Use of these is described in more detail in the next section.

We have found few other efforts to create a generic user interface. Some of these are not focused on the scientific computing community, and so aim to accommodate a wider variety of CLI programs. These usually take the form of widget sets that can be configured to create a GUI. While this approach is more
flexible it is usually also more time consuming and less extensible. Other generic GUI programs use a “Wizard” interface, which is both flexible and easy to deploy, but lack the visual summary and interactivity that guiLiner offers. The advantage of guiLiner over either of these approaches is that it is designed to represent a single mode of interaction that is common in scientific computing, which allows it to be employed very quickly and at the same time makes it very effective for hosting these types of programs. To date we have not found any other applications which fill this exact niche.

3 Usage Overview

Most user interaction with guiLiner involves selecting options from the option tree (Figure 2 #4) by clicking on them. When selected, an interface to manipulate that option is displayed in the options pane (Figure 2 #3). The exact interface will vary depending on which type of option is being displayed: it may have a text box where a value can be input, a set of buttons that allows the user to set the option to one of several given values, or a dialog box for navigating the file directory to find an input file, etc. In all cases the user is able to get more information on the option by clicking the “Information” tab in the option pane.

The colors in the option tree give a quick visual guide to the run settings. Red = option is required, value not yet specified; Black = option not required, value not yet specified; Blue = a value for the option has been specified and will be used for program execution.

Clicking the Preview button (Figure. 2 #2) causes the command line to be assembled from the values currently specified by the user and prints it to the console panel (Figure. 2 #5). This is particularly useful for “transitional” users who are gaining familiarity with the command line environment, but are not yet fully comfortable with it. Using this facility then saving the console contents is an easy way to save run settings. An alternative method it to save the entire XML file with the selected options already set. Though this is more cumbersome to read, it does allow guiLiner to automatically load the settings used in that particular execution.

When the RUN PROGRAM button (Figure. 2 #2) is clicked, guiLiner uses a system call to execute the CLI program with the options assembled by the user in guiLiner. Program output to stdout goes to the console panel from where it may be viewed or saved to disk as a text file. Program output to stderr is directed to the Errors panel and the user is notified of errors in the status bar (Figure. 2 #6). Any program output directed to files goes to those files specified either by an absolute path or by a path relative to the current working directory (exactly as if the program were run from the CLI). guiLiner is not designed for interactive display of program output, though future versions could allow simple GUI-driven output display using developer provided scripts and, for example, the R statistical computing environment [1].

For ease of distribution and installation to end-user machines guiLiner, the XML configuration file and the CLI executable can be distributed as an installer. There are several excellent installer platforms available which could streamline this process, such as the platform independent IzPack (available at http://izpack.org/).

Details on the XML file specification, option types, the application executable and source code, and discussion forums are available at http://guiliner.sourceforge.net. Also at this web site there are sample XML configuration files for a variety of bioinformatic and population genetic analysis programs including Exonerate [2], IM [3], Makesamples [4] and Spip [5]. A Document Type Definition (DTD) file is distributed with guiLiner to automate XML configuration file generation and to allow error checking.

We also distribute there a small C library for C or C++ programmers that simplifies command-line parsing and error checking, and allows the documentation for each option to be written and stored in the source code. This documentation may be printed by the program in short-help format, long-help format, UNIX man page format, and guiLiner XML format. The guiLiner XML format can be read directly by guiLiner so that any updates to the program can be immediately translated to the guiLiner GUI.

We encourage contributions to the source code or
comments on guiLiner.

4 Conclusions

GuiLiner is an effective “wrapper” for a wide variety of biological analysis and simulation software. Application developers will be able to offer a functional and carefully implemented GUI to their CLI-driven software with little effort. At the same time, guiLiner should make a wider variety of applications immediately available for the analyses of researchers who are not familiar with the CLI or are beginning to learn about it.

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