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Article

`termal`: A Fast and Interactive Terminal-Based Viewer for Multiple Sequence Alignments

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Abstract: Summary: We present `termal`, a fast, interactive terminal-based viewer for multiple sequence alignments (MSAs), designed for use on remote systems such as high-performance computing (HPC) clusters. Unlike traditional graphical viewers, `termal` runs entirely within a terminal and offers features such as scrolling, zooming, consensus/conservation visualization, and customizable colour schemes. It is implemented in Rust, ensuring high performance and minimal dependencies. **Availability and implementation:** `termal` is written in Rust and freely available under the MIT license at https://gitlab.sib.swiss/tjunier/termal.git.

Keywords: multiple sequence alignment; viewer; terminal; text user interface

Introduction

Visualising multiple sequence alignments (MSAs) is a common task in computational biology. Many alignment viewers have a graphical user interface (GUI) and are hence unsuitable for use on headless or remote systems such as high-performance computing (HPC) clusters. Command-line tools do exist, for example Alan [1], which stands out as a particularly elegant solution, since it is built on standard Unix tools such as `awk` and `less` — indeed, it served as the initial inspiration for the present work. This means, however, that Alan's interactivity is limited to that of a pager: features such as zooming, reordering sequences, as well as computing and displaying a consensus sequence are absent. While `showalign` [2] can compute a consensus, it does not support colouring residues, and the user must explicitly call a pager in order to scroll through the alignment. Other programs like `alen` [3] are interactive, but not all have built-in residue colour schemes or the ability to visually represent metrics such as similarity to the consensus, or to reorder sequences according to such metrics. The capacity to fit a large alignment on screen, typically by only displaying a subset of the sequences and columns, is also rare (see also Table 1). In summary, text-based MSA viewers collectively provide a substantial range of functions, but no viewer implements all, or even most, of them. In this work we introduce `termal`, which combines most of these features in a single application.

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Table 1. Feature comparison of some terminal-based MSA viewers. Features are considered present when mentioned in the manual page or program help, or when obvious from the display. A "sequence metric" is a numeric property of a sequence such as ungapped length (see text).

Feature	`termal`	`alen`	`alv`	`alan`	`showalign`
Basics					
Language	Rust	Rust	Python	Shell	C
Interactivity	Yes (TUI)	Yes (TUI)	No	Limited (pager)	No
Supported alignment formats	Fasta	Fasta	Fasta, Clustal, Phylip, and more	Fasta, Clustal	Fasta, Clustal, Phylip, and more
Display features					
Scrolling / navigation	Yes	Yes	No	No	No
Zooming	Yes	No	Partial (`-g`)	No	No
Label pane width adjustment	Yes	Yes	No	No	Yes
Consensus display	Yes	Yes	No	No	Yes
Conservation bar plot	Yes	No	No	No	No
Sequence metric bar plot	Yes	No	No	No	No
Colour schemes	Multiple	Fixed	Fixed	Customisable	No
Sequence numbering	Yes	No	No	No	No
Sorting / filtering					
Sort by consensus similarity	Yes	No	No	No	No
Sort by sequence length	Yes	No	No	No	No
Manual row reordering	No	Yes	No	No	No
Regex search	No	Yes	No	No	No
Other					
Dependencies	None	None	BioPython	Core shell utilities	None (installed via EMBOSS)
License	MIT	MIT	MIT	Various	GPL

Interface

Apart from the alignment sequences, which occupy the main pane, `termal` also displays sequence labels and ordinal numbers, a consensus sequence, and a conservation bar plot; it also displays sequence metrics such as similarity to the consensus, or (ungapped) length (Figure 1). The alignment can be scrolled one sequence/column at a time using arrow keys or Vim-like `h`, `j`, `k`, and `l`; similar keystrokes allow jumping by screenfuls or to the edges of the alignment.

By default, residues of nucleotide alignments are coloured according to Jalview's [4] nucleotide colour scheme, while protein alignments use that of ClustalX [5]. An alternative colour scheme for protein is Lesk's [6], and all alignments can be rendered in monochrome.

Alignments too wide to fit on the screen can be "zoomed out" by showing only the first and last column, as well as a sample of equidistant columns in between. The same can be done with sequences for alignments that are too tall. This allows regions of high conservation to be spotted without scrolling. A variant of the zoomed-out mode preserves the alignment's aspect ratio, at the cost of some wasted space.

The sequences can be reordered according to the currently-displayed sequence metric, in increasing or decreasing order. This allows e.g. to group the most complete sequences together, or those that best match the consensus.

The width of the label pane can be adjusted to fit label length, and both the side and bottom panes can be hidden to maximise the space allocated to the alignment.

`termal` comes with a built-in help screen that lists all key bindings.

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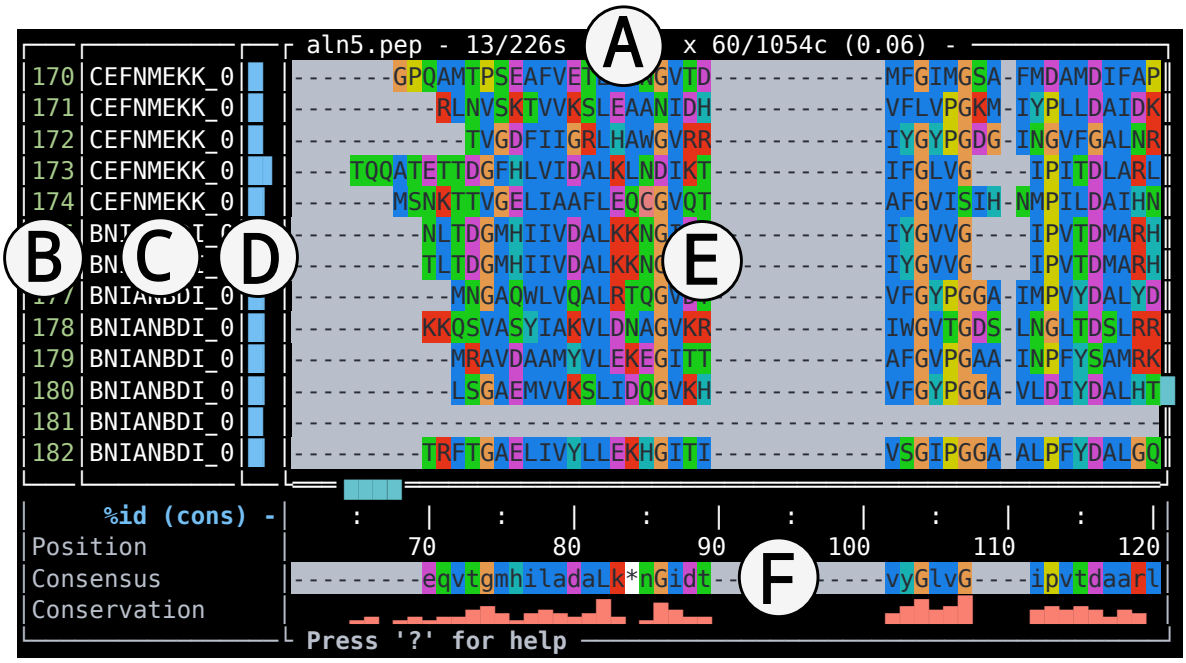

Figure 1. A snapshot of `termal`'s interface showing a protein alignment. A: alignment filename and dimensions, B: sequence numbers pane, C: sequence labels pane, D: metric bar plot pane (currently displaying sequence similarity with the consensus), E: alignment pane, F: bottom pane, displaying sequence position, consensus, and conservation bar plot. In this example the sequences are in the original (file) order, and use the ClustalX colour scheme. the view is zoomed in, that is, only a fraction of the alignment is displayed.

Performance and Limitations

`termal` has been tested on alignments exceeding 15,000 sequences and 1,500 columns (22 million alignment cells), with startup and initial rendering completing in under one second on a machine with 12th-generation Intel® Core™ i5-1240P CPU and 16 GB of RAM running Linux 6.14.2. In practice, interactive performance is limited more by the speed of the terminal emulator than by `termal` itself. GPU-accelerated terminals such as Alacritty [7], Kitty [8] and Ghostty [9] offer smoother scrolling at large screen sizes than do more traditional emulators.

Comparison with Existing Tools

Table 1 presents a feature matrix for `termal` and a selection of other terminal-based alignment viewers.

Conclusion

While this work is not intended as a comprehensive review of alignment viewers, we surveyed several tools with comparable goals — namely, terminal-native operation and varying degrees of interactivity — including `showalign`, `alan`, `alv`, and `alen`. To our knowledge, `termal` is the only tool to combine interactive navigation, zooming, consensus and conservation visualization, several built-in colour maps, as well as display of and ordering by sequence metrics in a single terminal interface. Its minimal dependencies and fast startup make `termal` suitable for both ad-hoc use and for integration into semi-automated workflows requiring terminal-based alignment review. Accordingly, `termal` fills a niche for fast, interactive MSA exploration directly in the terminal, making it an ideal tool for remote bioinformatics workflows.

Data Availability Statement: `termal` is distributed under the MIT license. It is available as a single precompiled binary (for Linux, MacOS, and Windows), with no external dependencies or runtime environment required, from gitlab.sib.swiss/tjunier/termal.git. Alternatively, users with Rust installed can install it via `cargo install termal`.

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Conflicts of Interest: The author declares no conflict of interest.

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