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Termal: A Terminal-Based Multiple Sequence Alignment (MSA) Viewer

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Termal: A Terminal-Based Multiple Sequence Alignment (MSA) Viewer

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Abstract

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, but like graphical viewers, it offers features such as scrolling, zooming, consensus/conservation visualization, and colour schemes.

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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. 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.

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 familiar Vim-style motion keys `h`, `j`, `k`, and `l`; similar keystrokes allow jumping by screenfuls or to the edges of the alignment.

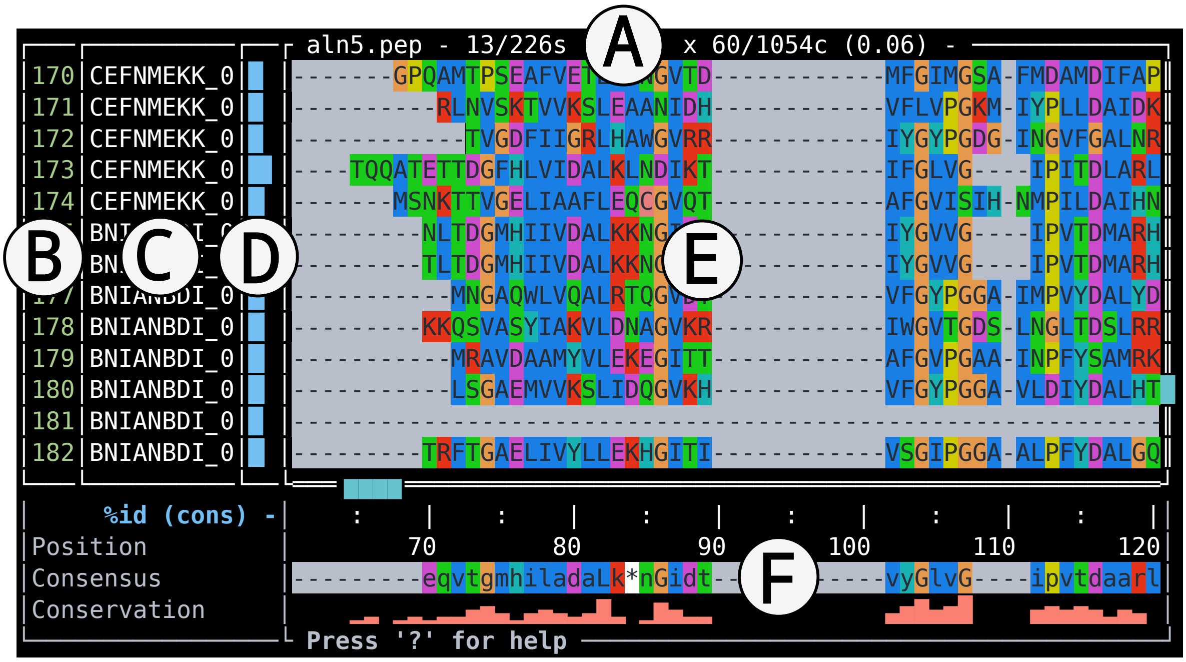
By default, residues of nucleotide alignments are coloured according to Jalview's[4] nucleotide colour scheme, while protein alignments use that of ClustalX[5]. An alternative colour scheme for protein is Lesk's[6], and all alignments can be rendered in monochrome.

Alignments that exceed the screen size—horizontally, vertically, or both—can be zoomed out to display only the first and last row and column, along with a sample of equidistant intermediates in both dimensions; the sample size is adjusted to fill the available screen space. This allows regions of high conservation to be spotted without scrolling. An alternative zoomed-out mode preserves the alignment's aspect ratio, at the cost of some unused 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` includes a built-in help screen that lists all key bindings.



```
                 aln5.pep - 13/226s     x 60/1054c (0.06) -
170 CEFNMEKK_0   -------GPQAMTPSEAFVET    GVTD------------MFGIMGSA-FMDAMDIFAP
171 CEFNMEKK_0   ----------RLNVSKTVVKSLEAANIDH------------VFLVPGKM-IYPLLDAIDK
172 CEFNMEKK_0   ------------TVGDFIIGRLHAWGVRR------------IYGYPGDG-INGVFGALNR
173 CEFNMEKK_0   ----TQQATETTDGFHLVIDALKLNDIKT------------IFGLVG----IPITDLARL
174 CEFNMEKK_0   -------MSNKTTVGELIAAFLEQCGVQT------------AFGVISIH-NMPILDAIHN
    BNI   I_     ---------NLTDGMHIIVDALKKNG    -----------IYGVVG----IPVTDMARH
    BN     _     ---------TLTDGMHIIVDALKKN       ---------IYGVVG----IPVTDMARH
177 BNIANBDI_0   -----------MNGAQWLVQALRTQGV   -----------VFGYPGGA-IMPVYDALYD
178 BNIANBDI_0   ---------KKQSVASYIAKVLDNAGVKR------------IWGVTGDS-LNGLTDSLRR
179 BNIANBDI_0   -----------MRAVDAAMYVLEKEGITT------------AFGVPGAA-INPFYSAMRK
180 BNIANBDI_0   -----------LSGAEMVVKSLIDQGVKH------------VFGYPGGA-VLDIYDALHT
181 BNIANBDI_0   ------------------------------------------------------------
182 BNIANBDI_0   ---------TRFTGAELIVYLLEKHGITI------------VSGIPGGA-ALPFYDALGQ

    %id (cons) -     :    |    :    |    :    |    :    |    :    |    :    |
Position                 70        80        90       100       110       120
Consensus        ---------eqvtgmhiladaLk*nGidt--      ----vyGlvG----ipvtdaarl
Conservation
                 Press '?' for help
```

Figure 1. A snapshot of the interface of `termal` v1.0.0, 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. To reproduce: run `termal` on the example datafile supplied in the distribution.

Comparison with Other TUI Tools

Dependencies and Installation

`termal` and `alen` are written in Rust[7] and compile to a single binary with no dependencies. By contrast, `alv`[8] requires BioPython and `showalign` is part of the EMBOSS suite.

Features

`termal` features zooming, interactive navigation, selectable themes and color maps, as well as ordering according to metrics. This combination of features is not found in the other programs considered, although all of them offer at least some of these features.

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 a 12th-generation Intel® Core^{TM} i5-1240P processor 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[9], Kitty[10] and Ghostty[11] offer smoother scrolling at large screen sizes than do more traditional emulators, and terminals that support 24-bit colours give better results. `termal` is currently restricted to alignments in Fasta and Stockholm formats.

Availability

termal is distributed under the MIT license. It is available as a precompiled, statically-linked binary (for Linux, MacOS, and Windows), with no external dependencies or runtime environment required, from https://github.com/sib-swiss/termal.git. Alternatively, users with Rust installed can install it via `cargo install termal-msa`. The source code has also been deposited on Zenodo (https://zenodo.org/records/15472432).

Conclusion

While this work is not intended as a comprehensive review of terminal-based alignment viewers, we surveyed several of them, including showalign, alan, alv, and alen. To our knowledge, termal combines a unique set of features in a terminal interface. Its minimal dependencies and fast startup make termal suitable for both *ad-hoc* use and for integration into semi-automated workflows requiring alignments to be reviewed in a terminal. Accordingly, termal fills a niche for fast, interactive MSA exploration directly in the terminal, making it an ideal tool for remote bioinformatics workflows.

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

References

1. Dunne, M. Alan: A lightweight alignment viewer for the terminal. https://github.com/mpdunne/alan, 2020. Accessed 2025-04-13.
2. Rice, P.; Longden, I.; Bleasby, A. EMBOSS: the European Molecular Biology Open Software Suite. *Trends in Genetics* **2000**, *16*, 276–277.
3. Nissen, J. alen: Interactive terminal-based MSA viewer. https://github.com/jakobnissen/alen, 2023–2024. Accessed 2025-04-13.
4. Waterhouse, A.M.; Procter, J.B.; Martin, D.M.; Clamp, M.; Barton, G.J. Jalview Version 2—a multiple sequence alignment editor and analysis workbench. *Bioinformatics* **2009**, *25*, 1189–1191.
5. Larkin, M.; Blackshields, G.; Brown, N.; Chenna, R.; McGettigan, P.; McWilliam, H.; Valentin, F.; Wallace, I.; Wilm, A.; Lopez, R.; et al. Clustal W and Clustal X version 2.0. *Bioinformatics* **2007**, *23*, 2947–2948.
6. Lesk, A.M. *Introduction to bioinformatics*; Oxford university press, 2019.
7. Klabnik, S.; Nichols, C. *The Rust Programming Language*; No Starch Press, 2019.
8. Arvestad, L. alv: a console-based viewer for molecular sequence alignments. *Journal of Open Source Software* **2018**, *3*, 955. https://doi.org/10.21105/joss.00955.
9. Wilm, J.; contributors. Alacritty - A cross-platform, GPU-accelerated terminal emulator. https://github.com/alacritty/alacritty, 2017–2024. Accessed 2025-04-13.
10. Goyal, K. Kitty - The fast, feature-rich, GPU-based terminal emulator. https://sw.kovidgoyal.net/kitty/, 2017–2024. Accessed 2025-04-13.
11. Hashimoto, M. Ghostty - A modern, GPU-accelerated terminal emulator. https://github.com/mitchellh/ghostty, 2023–2024. Accessed 2025-04-13.

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