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TRIAGE toolkit version 2

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TRIAGE: A Toolkit for Streamlined Discovery of Regulatory Genes and Elements

Overview

The TRIAGE methods[1-3] provide a powerful framework for analysing regulatory elements in both bulk and single-cell RNA sequencing (RNA-seq) datasets. Originally developed as the TRIAGE R package[4], it now includes both an R package and complementary Python workflows, together forming the expanded TRIAGE toolkit. By leveraging consortium-level H3K27me3 data[5], TRIAGE enables researchers to uncover the regulatory basis of cell identity and state. It integrates seamlessly into standard RNA-seq analysis workflows, offering efficient and adaptable pipelines for transcriptomic data exploration and visualisation. In the current release, TRIAGE expands its utility beyond the transcriptome-focused analysis of version 1. Through the newly added TRIAGEccs[3] module, the TRIAGE toolkit now enables users to input genomic regions of interest, such as genomic coordinates of novel lncRNAs or loci identified from genome-wide association studies (GWAS), and rank them based on their potential regulatory roles.

Key Features of TRIAGE toolkit (version 2)

• **Regulatory Gene Prioritisation:** TRIAGEgene[1] introduces a ranking system to identify key regulatory genes based on functional significance.

• **Cell Clustering Enhancement:** TRIAGEcluster[2] refines cell clustering by identifying regulatory genes that define cell identity in single-cell RNA-seq data.

• **Functional Gene Clustering:** TRIAGEparser[2] categorises gene lists into clusters with distinct biological functions, pinpointing key regulatory components within gene networks.

• **Regulatory Element Prioritisation:** TRIAGEccs[3] allows users to input genomic coordinates of novel long non-coding RNAs (lncRNAs) or other genomic regions of interest, ranking them by regulatory potential.

• **Seamless Integration:** Designed to work efficiently within existing data analysis workflows, the toolkit provides a versatile solution for regulatory gene and element analysis.

Applications

TRIAGE methods[1-3] and the TRIAGE R package[4] have been successfully applied to a wide range of datasets (e.g. refs[6-12]), demonstrating its ability to uncover regulatory mechanisms in diverse biological contexts. The toolkit has provided valuable insights into gene regulation, development, and disease mechanisms. Its seamless integration into standard analysis workflows positions it as a useful resource for exploring regulatory elements and mechanisms across diverse biological systems, with potential for novel discoveries in both biological and

medical research.

Access

The documentation for TRIAGE toolkit version 2 can be found here: https://tinyurl.com/triage2doc

For use of the TRIAGE toolkit only for academic research or teaching, please request the Academic Research and Teaching Licence.

For use of the TRIAGE toolkit for commercial research by or on behalf of an entity, please request the General Use Licence.

Once orders have been approved and the applicable fee paid, a link will be provided to download the TRIAGE toolkit. In addition to the main package, two bedgraph files will be accessible which Licensee will also need to download in order to use TRIAGEccs.

Acknowledgement

Aspects of the TRIAGE toolkit were developed using processed H3K27me3 data (BigWig files) from the EpiMap Repository (https://compbio.mit.edu/epimap). The EpiMap consortium aggregated and re-processed ENCODE, Roadmap, GGR and imputed datasets.

References

1. Shim, W. J. et al.(2020) , https://doi.org/10.1016/j.cels.2020.11.001, Cell Systems, 11, 625-639 e613
2. Sun, Y. et al.(2023) , https://doi.org/10.1093/nar/gkad307, Nucleic Acids Research, 51, e62
3. Sinniah, E. et al(2024) , https://doi.org/10.1101/2024.10.28.620690, bioRxiv
4. Zhao, Q. et al.(2025) , https://doi.org/10.1093/bib/bbaf004, Briefings in Bioinformatics, 26
5. Boix, C. A., James, B. T., Park, Y. P., Meuleman, W. & Kellis, M.(2021) , https://doi.org/10.1038/s41586-020-03145-z, Nature, 590, 300-307
6. Wu, Z. et al.(2024) , https://doi.org/10.1016/j.devcel.2024.01.019, Developmental Cell, 59, 705-722 e708
7. Plaisance, I. et al.(2023) , https://doi.org/10.1093/cvr/cvac191, Cardiovascular Research, 119, 1361-1376
8. Friedman, C. E. et al.(2023) , https://doi.org/10.1016/j.devcel.2023.11.012, Developmental Cell
9. Afonso, J. et al(2023) , https://doi.org/10.1016/j.bbrep.2023.101420, Biochemistry and Biophysics Reports, 33, 101420
10. Wehrens, M. et al.(2022) , https://doi.org/10.1016/j.celrep.2022.110809, Cell Reports, 39, 110809
11. Qiu, C. et al(2022) , https://doi.org/10.1038/s41588-022-01018-x, Nature Genetics, 54, 328-341
12. Kojic, M. et al.(2021) , https://doi.org/10.1038/s41467-021-22888-5, Nature Communications, 12, 2678