MultiomicMenu: Streamlining Multiomics Data Interpretation for Insights into Neuronal Responses to Glutamate Treatment

William George Ryan V[1*], Jennifer Nguyen[1], Isaac T. Schiefer[2,3], Robert McCullumsmith[4, 5, 6]

[1]College of Medicine and Life Sciences, University of Toledo, Toledo, Ohio 43614
[2]Department of Medicinal and Biological Chemistry, University of Toledo, Toledo, OH, USA
[3]Center for Drug Design and Development, University of Toledo, Toledo, Ohio 43614
[4]Department of Neurosciences, The University of Toledo, Toledo, Ohio 43614
[5]Department of Psychiatry, The University of Toledo, Toledo, Ohio 43614
[6]Neurosciences Institute, ProMedica, Toledo, OH, USA

*Corresponding author: wryan3@rockets.utoledo.edu

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Background: The exponential growth of omics data poses a significant challenge to biomedical researchers. The development of high-throughput multiomics technologies has opened new avenues for understanding complex biological phenomena, yet the sheer volume of data often overwhelms human cognitive capacity. This "data deluge" has hindered the efficient interpretation of omics results, limiting their applicability in fields like precision medicine. To address this bottleneck, we present the "MultiomicMenu," an interactive web application designed for the interpretation of multiomics data. Our objective is to introduce the MultiomicMenu and demonstrate its utility in a practical use case. We applied this software package to analyze RNAseq and kinome array data obtained from rat neurons subjected to glutamate treatment. Utilizing the PCSF algorithm for multiomic data integration implemented by the Kinograte R package, we sought to confirm glutamate's known association with cytotoxicity, apoptosis, and stress pathways.

Methods: We employed the Kinograte R package to create an integrated protein-protein interaction (PPI) network from the transcriptomic and kinomic datasets. Node prizes and edge costs were assigned based on absolute log fold change or z score, respectively, and STRING-DB interaction confidence. Gene-set enrichment analysis was performed using the enrichR R package to identify dysregulated pathways. The MultiomicMenu facilitated functional interpretation through interactive network and pathway visualizations.

Results: The MultiomicMenu allowed us to identify and visualize significantly altered pathways, revealing clusters associated with cytotoxicity, apoptosis, and stress. The PPI network highlighted key

"hub" genes involved in these pathways, providing valuable insights into the molecular mechanisms underlying glutamate-induced neuronal responses.

Conclusion: Our study demonstrates the effectiveness of the MultiomicMenu in streamlining the interpretation of complex multiomics data, enabling researchers to uncover biologically relevant insights with ease. This interactive web application holds promise for accelerating discoveries in the field of systems biology and advancing the application of omics data in precision medicine and beyond.

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