

A systematic review of multi-omics integration in neurodegenerative, neurodevelopmental, and psychiatric disorders

Luiza Behrens^{1,2}, Guilherme Fernandes², Gabriela Gonçalves², Franklin Nunes², Rafael Weimer², José Cláudio Fonseca Moreira³, Marcio Dorn²

¹Centre for Clinical Neurosciences, McMaster University, Canada
²Laboratory of Structural Bioinformatics and Computational Biology, Federal University of Rio Grande do Sul, Brazil
³Department of Biochemistry, Federal University of Rio Grande do Sul, Brazil

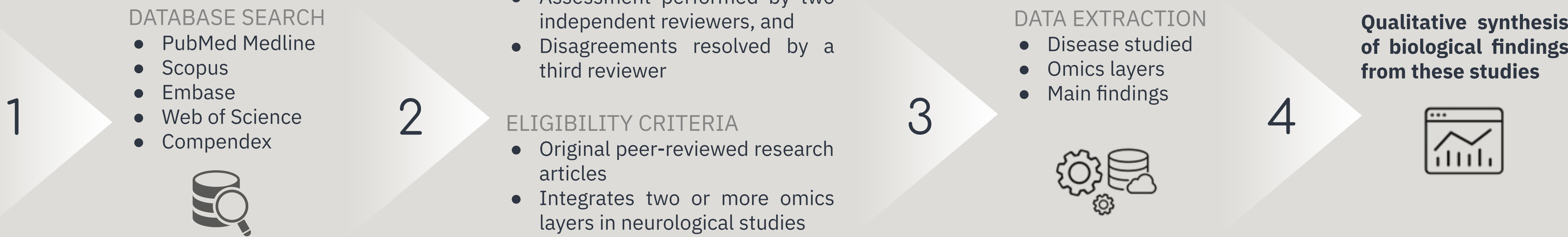


Background

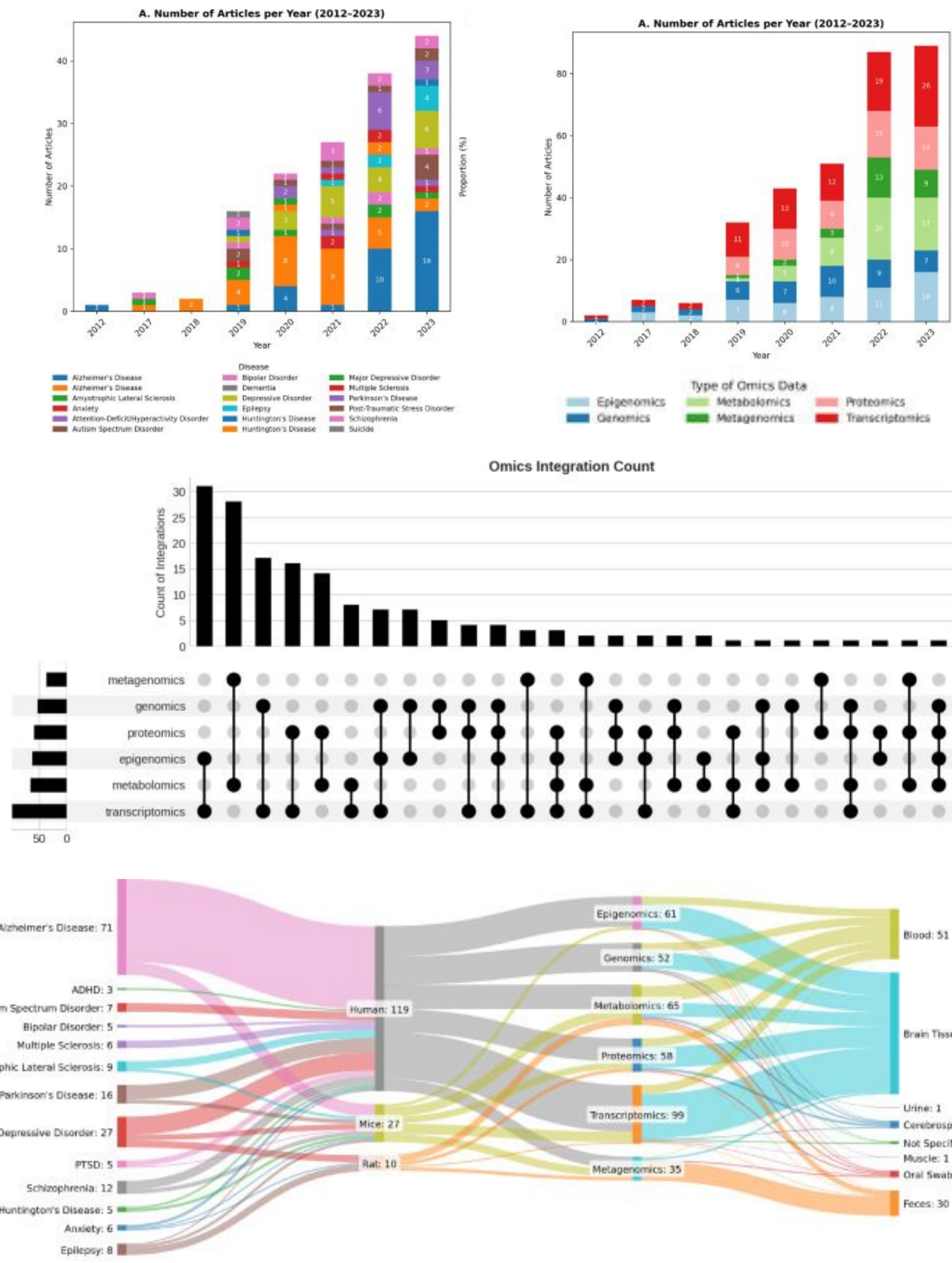
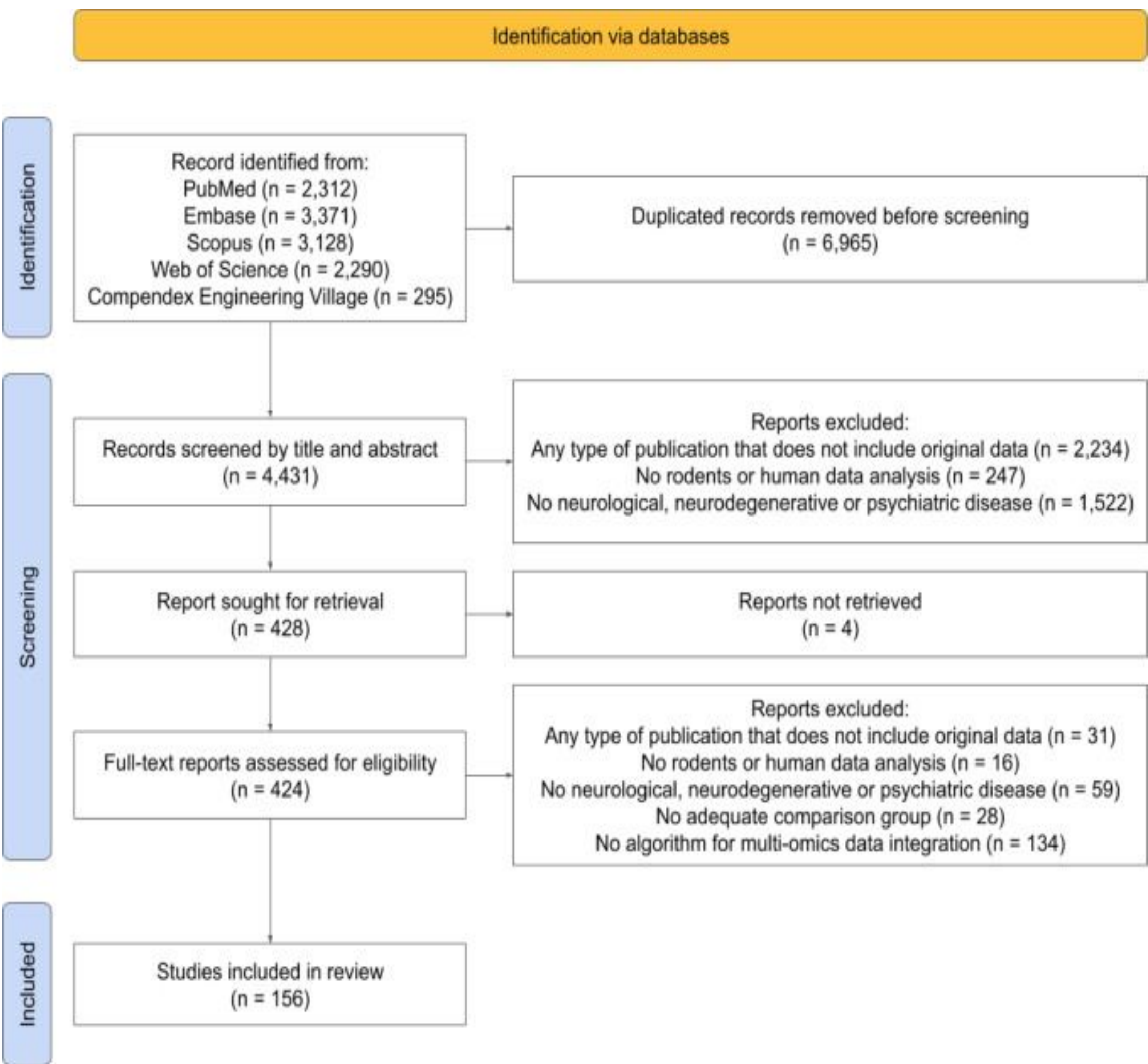
- Integrating these heterogeneous data types is an emerging strategy to capture disease-relevant mechanisms, identify biomarkers, and uncover molecular networks that cannot be resolved using single-omics approaches
- While multi-omics integration has been increasingly applied to many fields, its specific contribution to the study of neurodegenerative, neurodevelopmental, and psychiatric disorders has not been systematically evaluated.

Our aim was to assess the current landscape, methodological trends and limitations of multi-omics data integration in neuroscience research.

Methods



Results

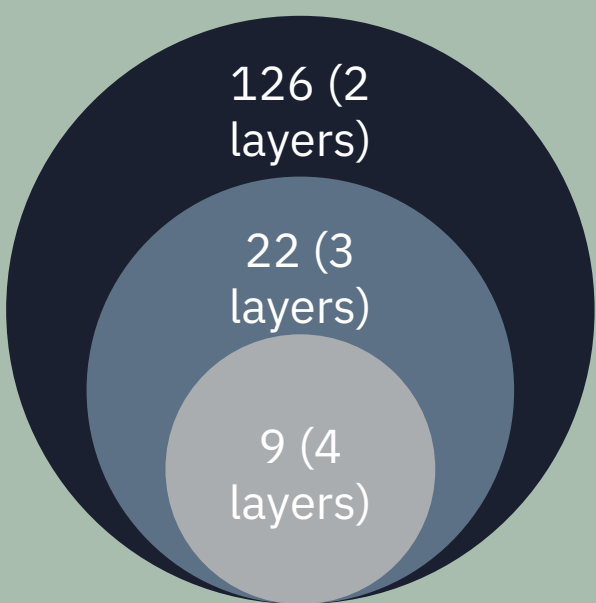


Discussion

The predominance of AD studies likely reflects its substantial global health burden, as well as the extensive funding and data availability provided by large-scale consortia such as ROSMAP, ADNI, and MSBB.



Methodologically, the field is largely dominated by studies integrating only two omics layers (n=126). The application of advanced machine learning approaches capable of integrating more than two omics layers remains limited, highlighting a gap in a more comprehensive multi-omics modeling.



Conclusions

Multi-omics data integration has emerged as a valuable approach for investigating molecular mechanisms underlying neurological disorders, with AD currently dominating the field. Persistent challenges include data heterogeneity, lack of standardized analytical frameworks, and limited reproducibility across studies. Future efforts should prioritize the development of scalable, interpretable multi-omics integration methods, expand open-access resources, and promote cross-study harmonization to accelerate biomarker discovery and therapeutic target identification.

Acknowledgements

