

Graphia: A platform for the graph-based visualisation and analysis of high dimensional data

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Graphia is a new open-source platform created for the graph-based analysis of the huge amounts of quantitative and qualitative data currently being generated from the study of genomes, genes, proteins metabolites and cells. Core to Graphia's functionality is support for the calculation of correlation matrices from any tabular matrix of continuous or discrete values, whereupon the software is designed to rapidly visualise the often very large graphs that result in 2D or 3D space. Following graph construction, an extensive range of analysis algorithms, routines for graph transformation, and options for the visualisation of node and edge attributes are available for graph exploration and analysis. This provides a powerful analysis solution for the interpretation of high-dimensional data from many sources or any data already defined as a network or a similarity matrix. Several use cases of Graphia will be described, to showcasing its wide range of functionalities and applications in the analysis biological data. Graphia runs on all major desktop operating systems, is extensible through the deployment of plugins; it is freely available to download (see below).

References and useful links

bioRxiv preprint: <https://doi.org/10.1101/2020.09.02.279349>

Website: <https://graphia.app/>