

Weighted correlation network analysis (WGCNA) can be used for finding **clusters** (modules) of highly correlated **genes**, for summarizing such clusters using the module eigengene or an intramodular hub gene, for relating modules to one another and to external sample traits (using eigengene network methodology), and for calculating module membership measures. Correlation networks facilitate network based gene screening methods that can be used to identify candidate **biomarkers** or therapeutic targets. These methods have been successfully applied in various biological contexts, e.g. cancer, mouse genetics, yeast genetics, and analysis of brain imaging data. While parts of the correlation network methodology have been described in separate publications, there is a need to provide a user-friendly, comprehensive, and consistent software implementation and an accompanying tutorial.

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