

Coexpression analysis

Gene co-expression [networks](#) can be used to associate [genes](#) of unknown [function](#) with biological processes, to prioritize candidate disease genes or to discern [transcriptional](#) regulatory programmes. With recent advances in [transcriptomics](#) and next-generation sequencing, co-expression networks constructed from [RNA sequencing](#) data also enable the inference of functions and disease associations for non-coding genes and [splice](#) variants. Although gene co-expression networks typically do not provide information about causality, emerging methods for differential co-expression analysis are enabling the identification of regulatory genes underlying various phenotypes.

van Dam et al., introduced and guide researchers through a (differential) co-expression analysis. They provide an overview of methods and tools used to create and analyse co-expression networks constructed from gene expression data, and they explain how these can be used to identify genes with a regulatory role in [disease](#). Furthermore, they discuss the integration of other data types with co-expression networks and offer future perspectives of co-expression analysis ¹⁾.

see [Glioma coexpression analysis](#).

¹⁾

van Dam S, Vösa U, van der Graaf A, Franke L, de Magalhães JP. Gene co-expression analysis for functional classification and gene-disease predictions. Brief Bioinform. 2018 Jul 20;19(4):575-592. doi: 10.1093/bib/bbw139. PubMed PMID: 28077403; PubMed Central PMCID: PMC6054162.

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