

# 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 <sup>1)</sup>.

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see [Glioma coexpression analysis](#).

<sup>1)</sup>

van Dam S, Võsa 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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Last update: **2025/05/13 02:07**