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# Finding functional interactions among grapevine genes using transcriptomic data and NES2RA algorithm

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More than two hundred transcriptomic studies are currently publicly available for grapevine. They have been collected, normalized and annotated into the Vitis Expression Studies Platform Using COLOMBOS Compendia Instances (VESPUCCI updated version, Moretto et al., in preparation). Mining all this information to extract novel findings, such as gene networks that control agronomically relevant traits, remains a challenge. In particular, climatic changes and the shift to more sustainable practices affect diseases and yield behaviors in grape production, thus urging the scientific community to propose new strategies to cope with them. System biology approaches can represent an opportunity to boost our knowledge of the grapevine physiology. Gene networks are a convenient way of representing as graphs the functional interactions (edges) among the genes (nodes) of an organism. Gene networks can be co-expression networks, based on Pearson's correlation, or association and regulatory networks, in which direct and possibly causal relationships are represented. We would like to present the tool NES2RA (Network Expansion by Sub-Setting and Ranking Aggregation) - based on the PC-algorithm (Spirtes and Glymour, 1991)- that finds causal relationships from observational data. It performs a systematic test for conditional independence to retain significant relations between pairs of genes. It starts from a fully connected network and removes interactions between genes, whenever it finds a set of genes that supports that interaction. Due to the computational power requirements of the NES2RA algorithm, it has been implemented on a distributed computation platform, as part of the gene@home project, which relies on thousands of volunteers' computers by means of TN-Grid, an infrastructure based on the BOINC system (Asnicar et al., 2015). In order to accomplish to the FAIR (Findable, Accessible, Interoperable and Reusable) requirements for the information produced by NES2RA, the expansion gene list of each single gene has been pre-computed and annotated and can be downloaded from our website (<http://ibdm.disi.unitn.it/>, in preparation). The user can consider the lists can as such or analyze them further for example by aggregating them to reconstruct a gene network. A case study example concerning the regulatory network and biosynthetic pathway of the grapevine leaf cuticle will be presented to show how this information can help the biologist in gene function discovery, candidate gene prioritization and planning functional studies in grapevine.