Poster

Gene expression analysis in hereditary diseases using the tool Automatic and Serial Analysis of CO-expression (ASACO)

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ABSTRACT

Motivation: In recent years, Bioinformatics has positioned itself as a highly demanded discipline within the scientific field thanks to the recent advances which have allowed a significant growth in the information available about gene sequences and gene expression. Specifically, gene expression analysis has proven to be a very useful technique for creating knowledge about different complex hereditary diseases by obtaining new data that allows us to understand their actions, similarities with other pathologies, genetic changes and even regulatory drugs. The main purpose of this project is to analyze genes for which functional information is not available and to functionally annotate them with a new tool based on transcriptomic data to obtain relevant data about the diseases in which they are involved.

Methods: For the present project the tool Automatic and Serial Analysis of CO-expression (ASACO) developed by the UPOBioinfo Group, in the Bioinformatics Unit of the CABD (Centro Andaluz de Biología del Desarrollo) is used. This tool analyzes the expression of a gene giving putative both positive and negative correlators.The procedure has first been performed with a gene that has sufficient functional information to be used as a positive control for the study. Firstly, the gene is selected in UniProt database, it is analyzed with ASACO (ASACO algorithm, pvalue < 0.05 and Fold Change 1) and the functional information available in the database is compared to the one obtained with the tool. In addition, the genes involved in the biological pathways in which the gene participates are compared with the positively and negatively co-rrelated genes found by ASACO.At the same time, all the information acquired is reviewed in relation to the available bibliography on the subject so that it allows us to understand the new data and draw relevant conclusions. Finally, the specificity and sensitivity of the assay are calculated. Next, this procedure will be repeated starting with a list of 4 or 5 genes for which functional information is not available.

Results: The preliminary results with a well-known gene showed that its positive correlators had related functions with this gene.

Conclusions: Therefore, we expect to contribute to the creation of knowledge in the study of several hereditary diseases whose genes do not present functional information and to demonstrate the usefulness and value provided by the used tool.

REFERENCES

Pérez-Pulido, A. J., Asencio-Cortés, G., Brokate-Llanos, A. M., Brea-Calvo, G., Rodríguez-Griñolo, R., Garzón, A., & Muñoz, M. J. (2021). Serial co-expression analysis of host factors from SARS-CoV viruses highly converges with former high-throughput screenings and proposes key regulators. Briefings in Bioinformatics, 22(2), 1038-1052. https://doi.org/10.1093/bib/bbaa419

Zhang, T., Liu, N., Wei, W., Zhang, Z., & Li, H. (2021). Integrated Analysis of Weighted Gene Coexpression Network Analysis Identifying Six Genes as Novel Biomarkers for Alzheimer's Disease. Oxidative medicine and cellular longevity, 2021, 9918498. https://doi.org/10.1155/2021/9918498

Ahmed, Z., Renart, E. G., Zeeshan, S., & Dong, X. (2021). Advancing clinical genomics and precision medicine with GVViZ: FAIR bioinformatics platform for variable gene-disease annotation, visualization, and expression analysis. Human genomics, 15(1), 37. https://doi.org/10.1186/s40246-021-00336-1