A Software Tool for Discovery of Gene Regulatory Networks: Analysis of Alzheimer Disease Data

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Abstract. A gene regulatory network (GRN) is a collection of molecular regulators that interact with each other to govern the majority of the molecular processes. These networks play a central role in in every process of life, therefore, assembling these networks is rather significant. Since most of the GRN are hard to be mapped with accuracy by a mathematical model, the approaches that are called model-free have an advantage in modeling the complexities of dynamic molecular networks. In particular, a rule-based approach, which is a highly abstract model-free approach, offers several advantages performing data-driven analysis. One of these advantages is that it requires the least amount of data, another one is that its simplicity allows the inference of large size models with a higher speed of analysis. However, the resulting relational structure of the network is incomplete, for an effective biological analysis. This situation has driven us to explore the hybridization with other approaches, such as biclustering techniques. This applied technique finds new relations between the nodes of the existent GRN. In this abstract we present a new software, called GeRNeT that integrates the algorithms of GRNCOP2 and BiHEA along a set of tools for interactive visualization, statistical analysis and ontological enrichment of the resulting GRNs that it was published in Dussaut et al. [1]. In this regard, results associated with Alzheimer disease datasets are presented that show the usefulness of integrating both bioinformatics tools.

Keywords: Machine Learning, Bioinformatics, Gene Regulatory Networks, Biclustering, Gene Expression Analysis.

References

1. Dussaut, J.S., Gallo, C.A., Cravero, F., Martínez, M.J., Carballido, J.A., Ponzoni, I. GeRNet: a gene regulatory network tool. BioSystems, **162**, pp. 1-11 (2017).