

A graphical tool for data integration and analysis of complex diseases

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Complex diseases are polygenic and multifactorial. For this reason, prioritization of genes related to complex disease is a challenge. Besides, one of the main problems for researchers is the lack of reproducibility among studies involving different methodologies or experiments. Particularly, Protein-Protein Interaction (PPI) networks have been used to prioritize genes related to complex diseases according to their topological features. Recent methods for prioritizing genes of complex diseases generally perform integration of expression data and PPI (Protein Protein Interaction) networks. Most methods exploiting PPI networks are based on Network Medicine hypotheses, from which we highlight: network parsimony, locality and disease module. A method called NERI (*NEtwork-medicine based integrative approach for disease gene prioritization by Relative Importance*) recently published prioritizes genes by exploring PPI network based on Network Medicine hypotheses and relative importance algorithms. Despite having shown good results, currently the implementation of this method lacks a graphical user interface, and provides only a command line interface, thus hindering their use by researchers. In this work, we developed a graphical user interface for NERI, as well as ETL (*Extraction, Transform, Load*) of biological data in various formats. In this system, the user provide as input the expression data, PPI and GWAS (genes used as seeds). These inputs are facilitated by the graphical interface, which then calls the processing method NERI giving as result the prioritized genes and complex networks differential analysis. Currently, this interface is already functional, and improvements are currently being made in visualization of complex networks. Thus, the graphical tool developed in this work facilitates the application of this methodology by the end researcher. As future work, we intend to provide the system as a web service and free software.