

# Expression Analysis Integration with Inferencing of Gene Regulatory Networks

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## Abstract

Application of next generation sequencing technology in cDNA sequencing (RNA-Seq), in transcriptomic studies has become suitable for transcript discovery, depicting mechanisms of gene regulation and differential gene expression analysis. Efforts to understand the complex network of reactions and influences that regulate the functioning of organisms involve an interdisciplinary research, in particular the development of computational models. As advances in generating biological data take place, computing plays a fundamental role in the processing of biological data. In this context, several works were produced with the objective of identifying the interaction networks between genes and their functionalities in the most diverse organisms. This work proposes the development of an interactive software tool analysis of RNA-Seq data. This software tool will create a stream to infer gene regulatory networks, based on differential expression analysis output, guaranteeing the order and a pattern of process. Besides, it will allow the user to choose among different techniques of analysis for each processing step, resulting in a useful tool for RNA-Seq analysis. It has adopted the Python language programming for development in order to make possible its use in an online page and make easy maintenance. The data analysis provided by the proposed approach is composed by three main steps: i) Expression analysis: BaySeq, edgeR, DESeq, DESeq2, EBSeq, limma-voom, SAMSeq, sleuth or consexpression can be used; ii) Network Inference: will use the results of the expression analysis to generate the inference of gene networks with RNA-Seq data, based on the premise that the generated networks are of the small world and scale-free type, considering the relationships indicated in previous studies. iii) Network validation and integration: To evaluate the characteristics of the generated genetic networks, KEGG tool and the ontology of this KO tool will be used. The association of the results with a functional annotation results in a complete analysis, which responds to a need for research in the area. We expect to produce a software tool for RNA-Seq data analysis and interpretation, as well as the spread of these analysis techniques. We consider that access to this tool can facilitate transcriptomic studies and help simplify its use in Bioinformatics training or in classes about RNA-Seq analysis.

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Link to Video: