miRNApath: plataform to identify miRNAs targets and pathways regulated by miRNAs

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MicroRNAs (miRNAs) are small non-coding RNA molecules that regulate their target messenger RNA (mRNA) at post-transcricional level, altering important biological processes as apoptosis and cell proliferation. miRNA expression alteration has proved to be effective in modulating the passage signal through certain pathways involved in pathological processes, restoring its normal behavior in diseases. Although this interaction is well studied, there are few tools that allow the visualization of miRNAs/mRNAs expression correlation in a non intuitive way or tools that allow the user to provide his own expression data file from which the correlation analysis will be calculated. Thus, the aim of this study was to develop miRNApath II, a web tool that calculates miRNA/mRNA expression correlation and indicates the possible signaling pathways involved in this interaction. For this project, the used data was obtained from public and freely available database, such as miRBase, KEGG, RefSeq and TCGA. This tool can perform two different analyses depending on what information the user is interested in. The first analysis evaluates the correlation between the queried miRNAs and their respective associated mRNAs previously described in the literature, followed by a differential expression analysis, which will display the target genes in a plot-formatted result. The second analysis will provide the pathways that are related somehow with the input miRNAs. Focusing on the first analysis, the user can evaluate the association between the input miRNA and mRNAs by providing a personal expression data file or by choosing an already available expression data in the TCGA database, allowing the user to choose the disease of interest. miRNApath II was evaluated using expression data obtained from TCGA patients with colon adenocarcinoma and based on bibliographic research. The miRNAs hsa-mir-20a and hsa-mir-21 were selected as input. It were reported 164 mRNAs negatively correlated with the expression of the input miRNAs. Then, LGALS3, the first significant mRNA shown as result, was chosen to run an analysis of differentially expressed gene, indicating that this mRNA has indicative that it is a possible target for future treatments related to

this cancer, which has already been described in previous papers. In addition, from the input of miRNAs, it managed to identify 169 genetic pathways that could be related to the study in question, such as Glycolysis / Gluconeogenesis.