This tool allows you to make an integrated mRNA - miRNA profiles analysis. Via using this document you can easily execute the steps and you can obtain the results. Using this document you can easily repeat the experiments.

**Data Preparation**

miRcorrNet uses 2 different data sheets with same control-case column. It means you should have same samples in one column which should be both in mRNA and miRNA data sheet. In this study we used KNIME analytics platform. Therefore, the data is stored in ".table" extension files.

**mRNA Data (Gene Expression)**

In mRNA data one should have samples in the rows and gene names in the columns but the type of the genes should be double. The "class" column represents the sample whether control or case. The type of class column should be String and there can be only 2 classes. Below one can see the some chunk of the mRNA data.

**microRNA Data**

In miRNA data one should have samples in the rows and microRNA names in the columns but the type of the genes should be String. The "class" column represents the sample whether control or case. The type of class column should be String and there can be only 2 classes. Below one can see the some chunk of the miRNA data.