Analysing RNA-Seq data with RNASeqGUI

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RNA-seq has quickly become one of the most widely used approaches for identifying differences in the gene expression across multiple biological conditions. Several tools have been already developed to analyse such data. In general, a complete analysis requires carrying out several steps, using different methods and comparing their outputs to obtain more reliable and less biased results.

In this work, we present RNASeqGUI (Russo and Angelini, 2014), a novel R-package that implements a graphical platform devoted to analyse RNA-Seq data, and illustrate both the most recently added features and those ones that will been soon available. RNASeqGUI is not just a collection of some known methods and functions, but it is designed to guide the user during the entire analysis process. In particular, RNASeqGUI allows the identification of differentially expressed (DE) genes and corresponding pathways in RNA-Seq experiments by clicking buttons (see Figure 1).

RNASeqGUI incorporates several other R packages for DE analysis. It includes multiple normalisation procedures, tools for pathway analysis and a large number of functions to explore the data before the analysis and to compare results that have been obtained by different methods. Results are saved both in term of tab-delimited/html files and customizable graphical plots. Finally, in the spirit of "Reproducible Research", a human readable report is automatically generated to keep trace of all steps that have been performed during the analysis. Such report is generated by using R markdown language. Therefore, it incorporates both the documentation and the R code used to generate the results.

Availability: RNAseqGui is freely available at http://bioinfo.na.iac.cnr.it/RNASeqGUI/.

References

Russo F and Angelini C (2014) RNASeqGUI: A GUI for analyzing RNA-seq data. *Bioinformatics*. Advance Access Publication. http://dx.doi.org/10.1093/bioinformatics/btu308
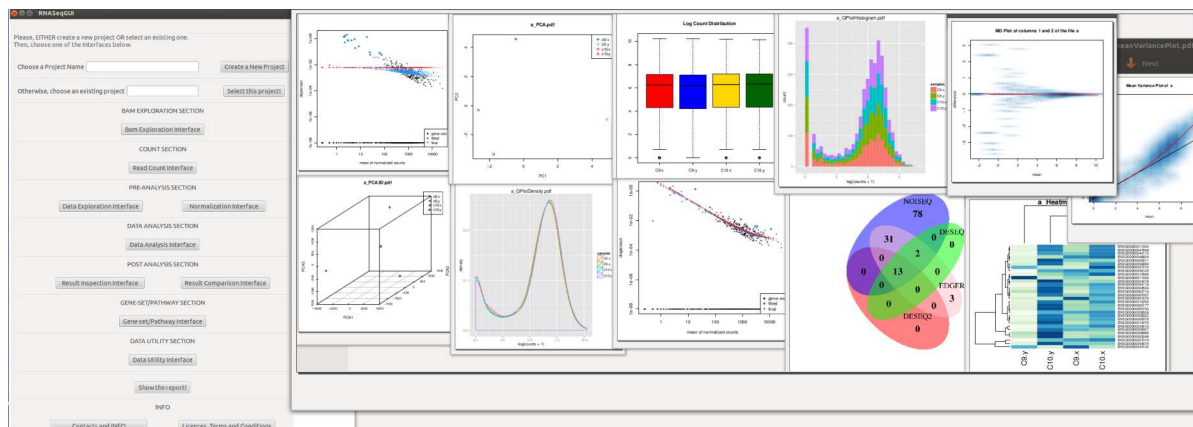
Figure 1. Screenshot of RNASeqGUI main interface and few examples of data analysis output files.