A SIMPLE INTERFACE TO VISUALIZE, COMPARE AND ORDER RESULTS FROM MULTIPLE RNA-SEQ ANALYSIS PIPELINES

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High throughput RNA sequencing analysis have reached high levels of use and performance with many tools to map reads on genomes, summarize the results, normalize the data and detect differential expression. However, users with basic knowledge in computer sciences struggle to visualize at the same time and in a single environment all these elements. With this work we attempt to propose a simple and easy way to aggregate data of different types from various sources and allow project collaborators to visualize, browse or retrieve them. The system is composed of a MySQL database associated to parsers and a PHP website using the CodeIgniter framework. Parsers are used to fill the database with data from HTSeq, DESeq, EdgeR or Cufflinks, for example. The website present the results in a simple table interface with various options. In the same time, the results are loaded into a personalized instance of the UCSC Genome Browser and links are created between our interface and the visualization tool. The created system is a highly customizable and flexible tool to concentrate and share information with every actors of an RNA-seq project. It is also the first milestone of a future multiagent system for the detection, reconstruction and visualization of RNA isoforms.

Keywords: RNA-Seq, interface, database.