miRQuest: integration of tools on a Web server for microRNA research

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ABSTRACT. This report describes the miRQuest - a novel middleware available in a Web server that allows the end user to do the miRNA research in a user-friendly way. It is known that there are many prediction tools for microRNA (miRNA) identification that use different programming languages and methods to realize this task. It is difficult to understand each tool and apply it to diverse datasets and organisms available for miRNA analysis. miRQuest can easily be used by biologists and researchers with limited experience with bioinformatics. We built it using the middleware architecture on a Web platform for miRNA research that performs two main functions: i) integration of different miRNA prediction tools for miRNA identification in a user-friendly environment; and ii) comparison of these prediction tools. In both cases, the user provides sequences (in FASTA format) as an input set for the analysis and comparisons. All the tools were selected on the basis of a survey of the literature on the available tools for miRNA prediction. As results, three different cases of use of the tools are also described, where one is the miRNA identification analysis in 30

different species. Finally, miRQuest seems to be a novel and useful tool; and it is freely available for both benchmarking and miRNA identification at http://mirquest.integrativebioinformatics.me/.