

Resource Summary Report

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Protocol for a reproducible circRNA analysis using Docker4Circ

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Protocol Information

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Authors: Giulio Ferrero, Nicola Licheri, Lucia Coscujuela Tarrero, Carlo De Intinis, Valentina Miano, Raffaele Adolfo Calogero, Francesca Cordero, Marco Beccuti, Michele De Bortoli

Group: Q-Bio Turin

Summary: Despite many computational tools were developed to predict circular RNAs (circRNAs), a limited number of work-flows exists to fully analyse a circRNA set ensuring the computational reproducibility of the whole analysis. For this purpose, we designed Docker4Circ, a computational work-flow for a comprehensive circRNAs analysis of a circRNAs composed of four modules: the circRNAs prediction (module 1), the circRNAs classification and annotation (module 2), the circRNAs sequence analysis (module 3), and circRNAs expression analysis (module 4). To ensure reproducibility each function of Docker4Circ was embedded into a docker image following guideline provided by Reproducible Bioinformatics Project (RBP, <http://reproducible-bioinformatics.org/>). Each function is included in the Docker4Seq R package which already includes different solutions for reproducible bioinformatic analyses. This protocol describes the use of each function of Docker4Circ to analyse the circRNAs predicted from a set of RNA-Seq experiments performed in normal colon and colorectal cancer cell lines. Furthermore, the description of the functions required to compute the expression level of the analysed circRNAs in a set of RNA-Seq experiments of colorectal primary tumors is provided.

Affiliations: University of Turin, University of Turin, University of Turin, University of Turin,
University of Turin, University of Turin, University of Turin, University of Turin, University of
Turin

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