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Bioinformatics tools for the functional interpretation of quantitative proteomics data: A road to biomarkers and drug's action mechanism discovery

Teresa Núñez de Villavicencio Díaz Center for Genetic Engineering and Biotechnology, Cuba

The functional interpretation of data is an inherent task associated to genomics and proteomics. The quality of the analysis is dependent on the workflow designed by the researcher and the bioinformatics tools chosen to integrate it. Currently it is imperative to understand that no analytical strategy or bioinformatics tool by itself is capable of extracting all the information covered, for example, in a proteomics experiment. Hereby we seek to provide the researcher community with four groups of different but complementary bioinformatics tools that can be used when performing this type of analysis. In addition, we describe an integrative bioinformatics workflow in the context of biomarkers discovery and the study of drug's action mechanisms.

Biography

Teresa Núñez de Villavicencio Díaz has completed her licentiate studies in Biochemistry at the Faculty of Biology, University of Havana, (with distinction) and obtained a Master's degree in Biotechnology, Biopharmaceutical Research, at the Center for Genetic Engineering and Biotechnology. She is a researcher with three years of experience in systems biology, proteomics, bioinformatics and molecular oncology. She published a paper at current topics in medicinal chemistry which already has a citation and more than a thousand downloads at ResearchGate.

teresa.nunez@biocomp.cigb.edu.cu

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