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Resumo	Progenesis QI (PQI) is a multiplatform bioinformatics tool that facilitates the identification workflow for metabolomics experiments. PQI uses fragmentation data provided by MassBank of North America (MoNA) libraries, among others, for metabolite annotation. However, PQI does not officially support MoNA libraries and other libraries based on structure-data files (.sdf). This paper describes the development and application of a software named MoNA to Progenesis QI Library Converter, allowing PQI and MoNA by correcting the fragmentation data of the library for Progenesis readability. We evaluated several public experimental datasets, including human plasma, plant extracts, cultured cells, bacteria, rat serum, and rat hippocampus. The results showed that it is mandatory to proceed with file conversion of each library to allow PQI to access fragmentation information from .msp (main spectra profile) files. This step is highly recommended to improve the identification level of the metabolites.
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