[BIOINFO 2024]

A web-based system for comparative multi-omic analyses

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The accumulation of high-quality genome assemblies has facilitated a more accurate comparison of genomes among multiple species. Furthermore, the availability of various omic data has further extended the scope of such comparative studies to identify the consequences of multi-omic signatures and underlying mechanisms. When performing such comparative multi-omic analyses, the genome-wide comparison of multi-omic data and the visualization of the results are critical. In addition, the visualization needs to be efficient enough to handle a large volume of multi-omic data. However, there is still a lack of applications that fulfill such requirements. In this study, we developed a web-based system for comparative multi-omic analyses. Using the data generation pipelines in our system, users can easily (i) compare multiple genomes, (ii) produce the profiles of omic data, and (iii) perform integrative analyses using the profiles in a web interface. Users can also browse the analysis results in a web interface, which also helps discover genomic regions harboring interesting multi-omic signatures easily. The web interface works very efficiently because of intelligent indexing and multi-level data sampling. Our system will contribute to making the use of multi-omic data easier and more effective.