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Sommario/riassunto

Life science data integration and interoperability is one of the most challenging problems facing bioinformatics today. In the current age of the life sciences, investigators have to interpret many types of information from a variety of sources: lab instruments, public databases, gene expression profiles, raw sequence traces, single nucleotide polymorphisms, chemical screening data, proteomic data, putative metabolic pathway models, and many others. Unfortunately, scientists are not currently able to easily identify and access this information because of the variety of semantics, interfaces,
