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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,
