SRS – New Developments in Integration of Databases and Analysis Tools

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SRS began as a sequence retrieval system, employing sophisticated techniques for parsing and indexing database text files, [1]. Its original design featured rapid data retrieval, [2] and search-able links, [3] between database entries. SRS has since developed into a general data-retrieval tool, offering advanced queries and views which combine fields from multiple databases. Additionally, the system easily integrates data-analysis tools – for example BLAST [4] – with the database network. From this new modularity and flexibility, we describe three major projects currently realised, or on-going, at the European Bioinformatics Institute (EBI).

(1) Integration of Metabolic Databases - Enzyme, Metabolite and Pathway Databases.
(2) *InterPro* - Integrated Resource Of Protein Domains And Functional Sites.
(3) Building a Framework for general Data Analysis Workflows.

We also present an up-to-date summary of databanks, [5] available under SRS.

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[4] Altschul, S.F. *et. al.* (1990) *J. Mol. Biol.* **215**, 403–410
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