Web Services for Sequence Analysis at DKFZ

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Many tools in bioinformatics require a comprehensive setup and large resources for their operation, making it difficult to install such a tool locally.

For interconnecting sequence analysis tools developed at the German Cancer Research Center (DKFZ) with applications developed in other institutes, the web service technology provides a way out of this problem.

The developments at DKFZ in this field are integrated in the activities of the Hobit project (http://hobit.sourceforge.net/), a platform, born in the German Helmholtz research society, for the interconnection of bioinformatics centers.

At DKFZ, web services for the database engines SRS[1] and EMBOSS[2] have been developed. These services provide access to a large public database collection via the backends' query languages. By using the EMBOSS system, it is possible to support many traditional biological sequence formats. The SRS backend allows the web services to access database entries in their native format or an XML translation thereof.

In order to be able to use the automated generation of data structures in web service clients, supported by many web service toolkits, the development of XML Schemas for the databases is performed.

Further projects provide services for the computation of GO slims or the annotation of protein sequences.

References:

1. Etzold, T., Ulyanov, A. & Argos, P. SRS: Information retrieval system for molecular biology data banks. *Methods Enzymol.* **266**, 114-128 (1996).
2. Rice, P., Longden, I. & Bleasby, A. EMBOSS: The European Molecular Biology Open Software Suite. *Trends in Genetics* **16**, 276-277 (2000).