

A Web Service Framework for Advanced Bioinformatics

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QFAB is developing a collaborative platform to collect, share, integrate, analyse, store and retrieve life science research data. This bioinformatics platform is built around core technologies such as SRS, SRB and Plone.

SRS is a leading-edge software system designed to integrate and simultaneously access the many thousands of disparate public life science data sources [1]. It enables a flexible mechanism for running complex queries that are crucial to uncovering knowledge from private and public data. SRB is a middleware that provides a uniform interface for connecting to distributed data resources based on their attributes rather than physical locations [2]. Plone is an easy to use web content management system that facilitates the sharing and collective publishing of project information and data [3]. When required, comments or discussion forums can be added to address specific research questions within the research group. The fine tuning of permissions, roles and rules allows total control over who can access what and when. Powerful unstructured and advanced searches across all the project data can be performed. Recently, Plone has been linked to SRB and provides a customizable user interface to annotate and access files stored into SRB.

Additionally, we are developing a bioinformatics web services API called Cowrie, which interfaces with SRS and SRB for data and tool integration, and provides accessible data services for targeted bioinformatics tasks. Based on Cowrie, customised utility, workflow and web applications can be rapidly developed using any technology supporting web services. Such applications have at their disposal the vast array of up-to-date data and tool services maintained by QFAB.

This poster presents the web service framework of the QFAB platform and illustrates how this architecture is beneficial in a high data and service bioinformatics environment. Application to a multi-institution project recently funded by the National Breast Cancer Foundation will be demonstrated.

References

- [1] Sequence Retrieval System (SRS), <http://www.biowisdom.com>
- [2] Storage Resource Broker (SRB), http://www.sdsc.edu/srb/index.php/Main_Page
- [3] Plone, <http://plone.org/>