BioDApps
Distributed Bioinformatics Applications

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Introduction

Providing applications platform independent and keeping the access to public services and data sources up to date are challenging tasks in software development in general and especially in bioinformatics. The migration of resources to new locations, new software versions or the lack of standardized data formats are only some of the day by day issues. As a result, at the first glance simple tasks can possibly grow to a complex and time consuming project. To overcome at least some of these limitations, platform and programming language independent web service protocols such as SOAP and REST were introduced during the last decade. Further communication protocols, like the widely used BioDAS[1] for annotations on genomic or protein sequences, were defined. Most of these protocols are designed for static data sources and hard to use for dynamic data or services.

BioDApps, a free to use RESTful web service, provides a way to overcome most of the issues listed above. The service is based on open source libraries and widely used standards. With BioDApps services can be distributed platform independent and a central interface to public resources can be provided.

Implementation

BioDApps is implemented as RESTful web service. The REST protocol is used for the communication between clients and the service. Thus, client applications are not limited to a programming language. The results can be requested either as HTML, XML or JSON document. The web service consists of two main components:

► The **master module** is based on the Python web-framework Bottle[2]. It acts as central interface to the client applications. Besides the organization of queries including an error handling, it provides information about the service adapters, regularly checks the availability of the provided resources and converts the results to the requested format.

► The **service adapters** act as interface to the provided resources. Besides the access to the resources, the adapters are responsible for the conversion and validation of the given parameters as well as the conversion of the results to an internal data structure, provided to the master.
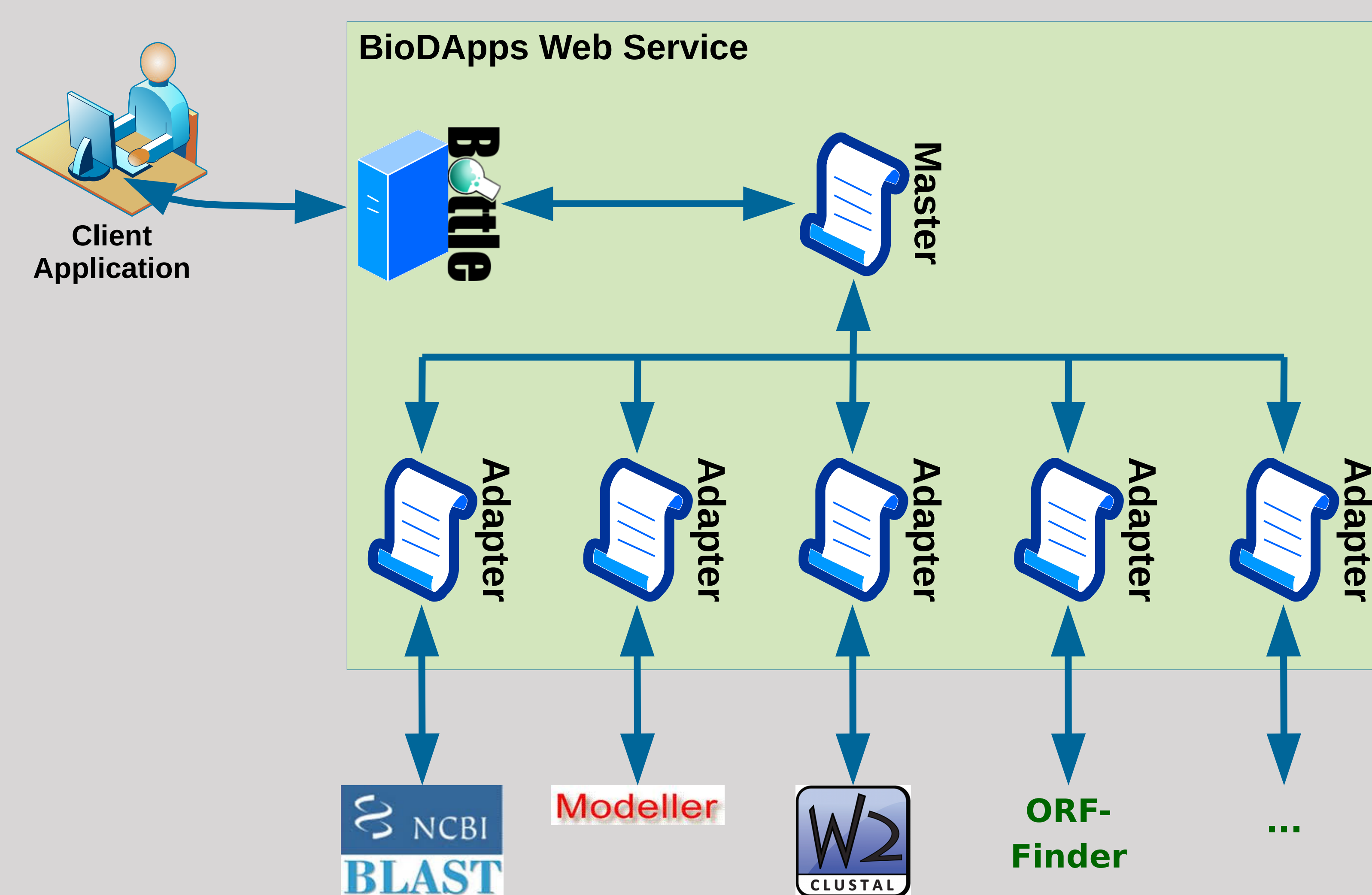
Protocol
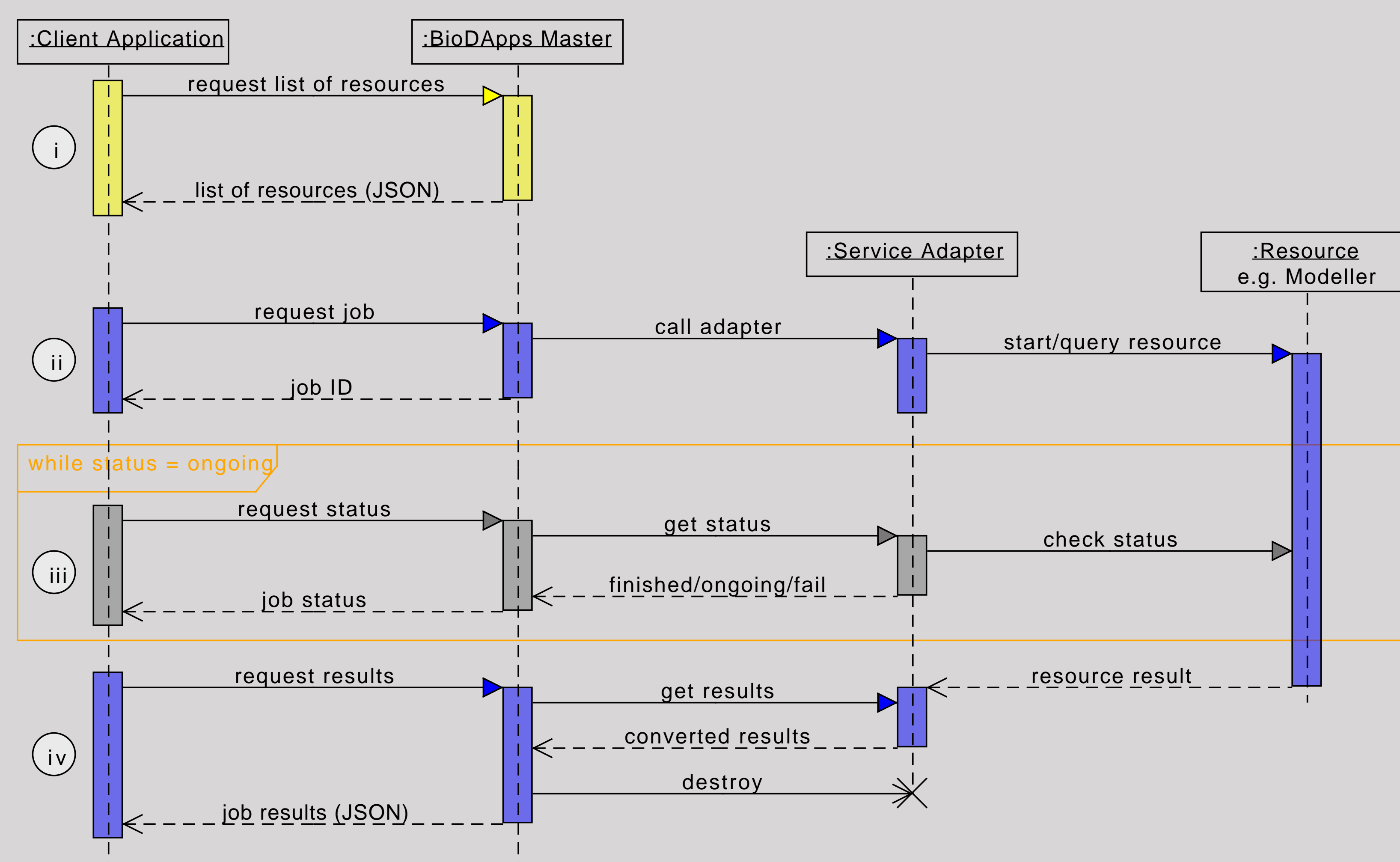
A typical BioDApps use case includes four steps: (i) A list of available resources and the corresponding parameters are requested (optional). (ii) A job or query is started with a job request. The given parameters are validated by the service adapter and forwarded to the resource. (iii) As some services can be time consuming, the job status can be continuously requested. (iv) Finally, the results are provided as JSON document.

Conclusion and Outlook

BioDApps is a free to use RESTful web service. Its core components have no dependencies other than the Python Standard Library. Thus, BioDApps can be installed on most platforms. The service is designed to give a platform and programming language independent way to distribute own software and to give a central interface to public resources. Using BioDApps, client applications are unaffected from changes in the resources.

The current version, BioDApps provides several example adapters to interface services and software such as NCBI Blast, Clustal W2, and Modeller. In ongoing work the number of covered services will be extended. Future in-house developments will be distributed via BioDApps. Further, a peer-to-peer system for the interaction between BioDApps installations will be introduced. The access to the BioDApps web service as well as the source of the final version will be provided for free to the scientific community.

References

[1]   **BioDAS homepage** http://www.biodas.org

[2]   **Bottle homepage** http://www.bottlepy.org

http://biwww.che.sbg.ac.at/biodapps