BioServices: a common Python package to access biological Web Services programmatically

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ABSTRACT

Motivation: Web interfaces provide access to numerous biological databases. Many can be accessed to in a programmatic way thanks to Web Services. Building applications that combine several of them would benefit from a single framework.

Results: BioServices is a comprehensive Python framework that provides programmatic access to major bioinformatics Web Services (e.g. KEGG, UniProt, BioModels, ChEMBLdb). Wrapping additional Web Services based either on Representational State Transfer or Simple Object Access Protocol/Web Services Description Language technologies is eased by the usage of object-oriented programming.

Availability and implementation: BioServices releases and documentation are available at http://pypi.python.org/pypi/bioservices under a GPL-v3 license.

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Supplementary information: Supplementary data are available at Bioinformatics online.

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1 INTRODUCTION AND MOTIVATION

Many biological databases are accessible on the www (world wide web) via server-side applications that span the entire spectrum of bioinformatics (e.g. genomics, sequence analysis). Although manual requests allow quick retrieval of information, programmatic access via Web Services scales up the number of requests and permits the composition of complex workflows. One strength of Web Services is that client-side applications do not need any intimate knowledge of the database provided by the service itself. Life sciences and bioinformatics have had a fecund production of Web Services in recent years (Bhagat et al., 2010).

Web services integration within a single framework fosters the development of applications. An example based on JAVA is MAPI (Karlsson and Trelles, 2013) that has been a base for developing biomedical applications. Programmatic access to Web Services relies mostly on (i) REST (Representational State Transfer) and (ii) SOAP (Simple Object Access Protocol; www.w3.org/TR/soap). REST has an emphasis on readability: each resource corresponds to a unique URL. There is no need for any external dependency, as operations are carried out via standard Hypertext Transfer Protocol (HTTP) methods (e.g. GET, POST). SOAP uses extensible mark-up language (XML)-based messaging protocol to encode request and response messages using WSDL (Web Services Description Language; www.w3.org/TR/wsdl) to describe the service’s capabilities.

To build applications that integrate several Web Services, one needs to have expertise in (i) HTTP requests, (ii) SOAP protocol, (iii) REST protocol, (iv) XML parsing to consume the XML messages and (v) related bioinformatics fields. Besides, inputs and outputs of the services can be heterogeneous. Consequently, the composition of workflows or design of external applications based on several Web Services can be challenging.

The Python language has many useful features for researchers (Bassi 2007): it is an object-oriented language with a precise and concise syntax and has a versatile set of standard modules. There is a growing and thriving community of scientific developers. An example of a library dedicated to bioinformatics is BioPython (Cock et al., 2009). It provides input/output functions, algorithms and some access to Web Services (e.g. Entrez). However, a dedicated framework to easily integrate bioinformatics Web Services and to provide extensive access to them is missing.

We have, therefore, developed BioServices to provide programmatic access to major bioinformatics Web Services within a single software framework using Python as a glue language. It should alleviate the needs for technical knowledge to develop more complex applications around existing resources.

2 APPROACH AND IMPLEMENTATION

To bring together various Web Services within BioServices, we first designed two base classes called RESTService and WSDLService so as to ease the wrapping of Web Services. As shown in Figure 1, these two classes are then used by all services available within BioServices. A SOAP/WSDL Web Service can be wrapped concisely as follows:

```python
from bioservices import WSDLService
class AWrapper(WSDLService):
```
The image contains a page from a document discussing the interaction between external applications and existing Web Services via BioServices. External applications can use BioServices to compose or aggregate several Web Services (see Table 1 for available services). The figure shows a diagram of Web Services and BioServices, with labels for REST and WSDL methods.

### Table 1. Web Services accessible from BioServices

| Service          | Type   | Description                                      |
|------------------|--------|--------------------------------------------------|
| ArrayExpress     | REST   | BioMart (W)                                      |
| ChEBI            | REST   | BioModels (W)                                    |
| KEGG             | WSDL   | BioMart (R)                                      |
| PDB              | REST   | BioModels (R)                                    |
| QuickGO          | WSDL   | BioModels (W)                                    |
| UniProt          | REST   | BioModels (W)                                    |
| UniProt          | WSDL   | BioCatalogue (W)                                 |
| QuickGO          | REST   | BioCatalogue (W)                                 |

Note: R stands for REST and W stands for SOAP/WSDL protocol.

KEGG and UniChem (among others). See the online documentation (http://pypi.python.org/pypi/bioservices) for examples.

### 3 CONCLUSION/RESULTS

BioServices provides a comprehensive access to bioinformatics Web Services within a single Python library; the current release (1.1.1) provides access to 18 Web Services (see Table 1). The methodology used to encapsulate Web Services and their functionalities combined with Python allow pipelines (that combine several Web Services) to be implemented concisely. Besides, an extensive online documentation (http://pypi.python.org/pypi/bioservices) should help users and developers to deal with the profusion of identifiers and data structures inherent to the diversity of Web Services available. Releases are available on PyPi (http://pypi.python.org/pypi/bioservices), the official Python repository. Developers can obtain the source code from a public server (https://www.assembla.com/spaces/bioservices/wiki). Besides, bug reports and new feature requests are encouraged (https://www.assembla.com/spaces/bioservices/tickets), and contributors are welcome to join the user and developer community (https://www.assembla.com/spaces/bioservices/wiki). Tests are included with a large coverage to guarantee robustness regarding potential modifications of the Web Services themselves. By covering a wide range of Web Services, BioServices can be used to complement external libraries (e.g. BioPython, Galaxy; see Supplementary Data) and foster the development of new workflows.

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**Conflict of Interest**: none declared.

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