BiNHum Harvesting and Indexing Toolkit

Contents

Pre-requisites

Basics

Tested with Java 8

Can be deployed with Tomcat (tested with Apache Tomcat/6.0.39 JRE 1.8.0_05-b13) or Jetty (tested with Jetty 8.1.14), or can be run inside Eclipse (tested with Eclipse Luna and Kepler)

MySQL Database v5.5

Web-services

Local gisgraphy installation (coordinates check) or maybe online version, see http://www.gisgraphy.com/free-access.htm

CoordinatesKDTree werbservice (based on https://github.com/AReallyGoodName/OfflineReverseGeocode)

Configuration

Edit the application.properties file

Quality tests

• Quality tests: activated / deactivated. The tab won't be displayed it turned OFF	qualityOnOff=OFF / ON
• Where the CoordinatesKDTree Web service is running	coordinatesWebservice=http://localhost:8080/CoordinatesWS
A local folder for temporary file manipulation	temporaryFolder=/home/user/test

Database properties

• DB credentials	dataSource.username=USER dataSource.password=PASS
• DB name	dataSource.name=DATABASE_NAME
• MySQL-Server IP + DB name	dataSource.url=jdbc:mysql://DATABASE-IP:3306/DATABASE_NAME?autoReconnect=true&useUnicode=true&characterEncoding=UTF8&characterSetResults=UTF8&MVCC=true

Application properties

• Application server IP (ie. Localhost)	dataSource.servername=APPLICATIONSERVER_IP
• default URL with port (ie. • http://localhost:8040/) The port must match your Tomcat/Jetty configuration !	baseUrl=http://APPLICATIONSERVER:PORT/
• directory (with all permissions for Tomcat/Jetty) where to store the harvested files	harvest.directory=/home/USER/PROJECT/

Edit applicationContext-security.xml

Edit the admin password, md5 encoded. The default password corresponds to « banana! »

```
<user name="admin" password="bb7a307e32b93a931da89d0a214dd47f" authorities="ROLE_ADMIN" />
```

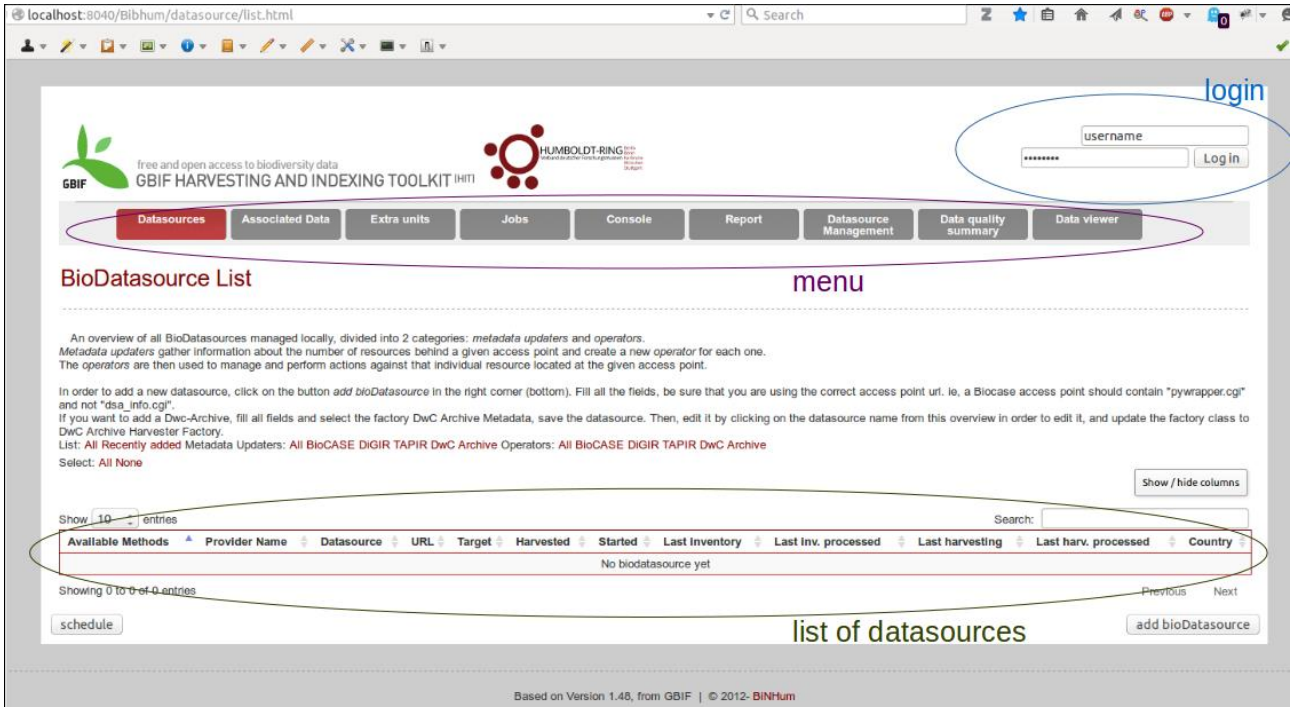
Before starting the app

Run the database creation script (schemaOnly.sql).

Starting B-HIT

Based on your configuration, and the name chosen (eclipse config / war file name), open your favorite web-browser to http://localhost:8040/Bibhum/datasource/list.html .

Overview

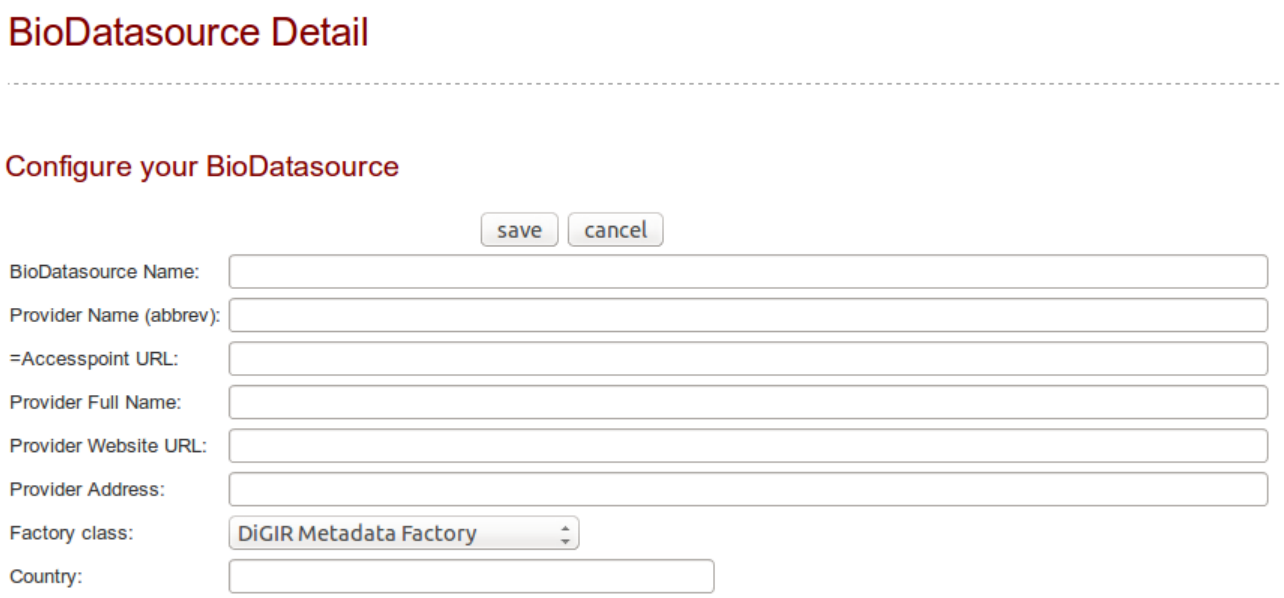


Main menu:

- Datasources : main entry point to add datasources/datasets, launch metadata operations, inventory+harvesting+processing data
- Associated datasources: entry point for associated data (relationships), to harvest and process associated data only
- Extra units: entry point for single units retrieval, based on a list of unit IDs
- Jobs: overview of waiting and running jobs
- Console: overview of log events
- Report: generation of reports (statistics)
- Datasource management: to hide or delete datasets
- Data quality : to launch quality tests, exports test results and display results
- Data viewer: to display data stored in the database, either the raw data or the improved data from the quality tests

Add a datasource

Click on the button « add bioDatasource »



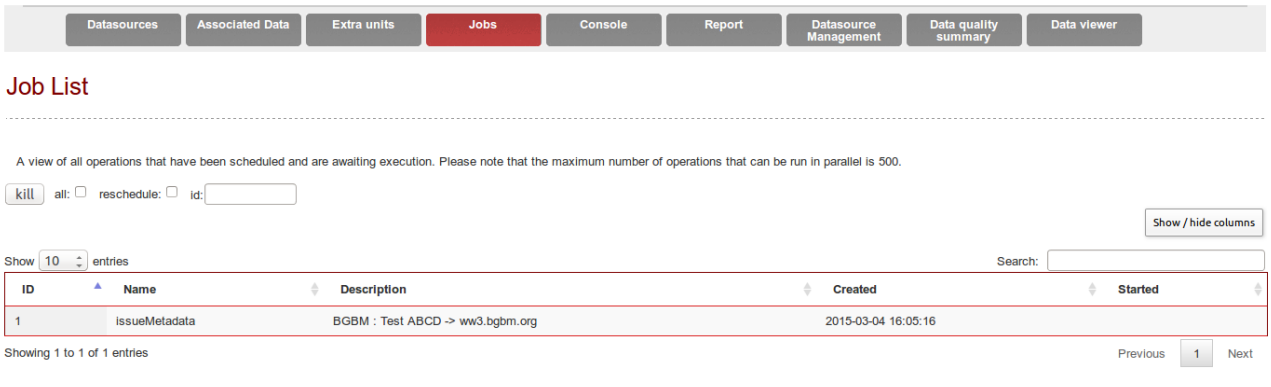
Enter a name for the datasource, the provider name abbreviated (ie. BGBM), the provider fullname (ie. Botanischer Garten und Botanisches Museum Berlin-Dahlem), the accesspoint (ie. http://ww3.bgbm.org/biocase/pywrapper.cgi?dsa=test_ABCD21), the provider website (ie. http://www.bgbm.org), the provider postal address and country, and the type of datasource (ie. Biocase/digir/Tapir/darwincore archive). Then save. The new datasource is now listed on the http://localhost:8040/Bibhum/datasource/list.html page.

To see the available operations for this datasource, click on the « available methods » checkbox on the left.

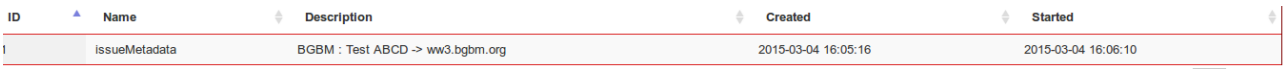
Retrieve datasets

In order to trigger this « Metadata update » operation, check the box and click on « Schedule » at the bottom of the page.

A new Job is created and can be followed under the « Job » tab (/Bibhum/job/list.html).



Refresh the page to update the job status :



Going back to the main page, a new line appeared in the list of datasource for the discovered dataset, with its corresponding available methods. These methods depend on the type of provider. ABCD-Archive will enable the methods XXXXXXXXXXXXXXXX, DwC-A will enable YYYYYYYYYY.

Available Methods	Provider Name	Datasource	URL	Target	Harvested	Started	Last inventory	Last inv. processed	Last harvesting	Last harv. processed	Country
Inventory Harvest Process harvested records Harvest sibling units Process sibling units	BGBM	Test ABCD - Herbarium Berolinense	http://ww3.bgbm.org/biocase/pywrapper.cgi?dsa=test_ABCD21	192551	0						Germany
	BGBM	Test ABCD	http://ww3.bgbm.org/biocase/pywrapper.cgi?dsa=test_ABCD21						04-03-2015		Germany

DEBUGGING HINT: The most common reason that a metadata update fails, is that the accesspoint is wrong.

The target columns contains the theoretical number of units, according to the providers metadata.

Perform inventory

Select the first operation and click on « schedule ». The queries are stored on the disc, in compressed files. The location path is defined in the configuration file, and the directory for each datasource can be found in the MySQL table bio_datasource, column « basedirectory ».

Harvest data

Data will be harvested if and only if a list of units has been retrieved with the Inventory. The outputs from this operation are:

1. One or more search requests (with enumerated extensions corresponding to the order in which they were dispatched, i.e. search_request.000)
2. One or more search responses (with enumerated extensions corresponding to the order in which they were dispatched, i.e. search_response.000). Often, there will only be a single response per request, but sometimes there can be multiple responses for a single request!)

The default range is 200 units per request.

Process harvested records

In this operation, an Operator (BioDatasource) will collect all the search responses, parse them, and write the parsed values to the database. In case of re-harvesting a dataset, the system will check if the data changed since the last harvesting. It will calculate the new checksum of each downloaded file, and will modify data in the DB if and only if the checksum changed. Each checksum is stored in the DB table « sha1responses ».