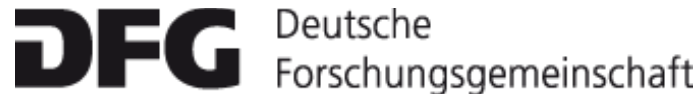


Submission Workflow from BEXIS 2 over GFBIO to Archives and DataCenters

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BEXIS 2 User and Developer Conference
2016



Archives, DataCenter's and there Requierements



collection
data center

- Request Form
- ABCD/EML
- Primary Data

environmental
data center

- Request Form
- PanSimple
- CSV

molecular
data center

- Request Form
- MlxS standard
- Primary Data



Freie Universität  Berlin

staatliche naturwissenschaftliche sammlungen bayerns

SENCKENBERG world of biodiversity

FORSCHUNGS MUSEUM KOENIG



museum für naturkunde berlin



Starting Point

Scientists have their finished data in **BEXIS 2** and want to publish/archive over **GFBIO** to a **collection data center**. They have accounts on both sides.



GFBIO Archiving Page

Submission Workflows

Please select an existing project, or choose nothing.

Please select an existing dataset, or choose nothing.

Please select an exploratory focus in order to start a submission workflow.

Submission of Collection data

Project Informations

Basic Informations

project id	14401
project title	<input type="text" value="Test Project"/>
project label (like abbreviation of DFG)	<input type="text" value="Project T10"/>
project PI / responsible person	<input type="text"/>
project abstract	<input type="text" value="testererer"/>

Optional Keywords

- | | |
|--|--|
| <input checked="" type="checkbox"/> Botany | <input type="checkbox"/> Ecology |
| <input checked="" type="checkbox"/> Geoscience | <input type="checkbox"/> Microbiology |
| <input checked="" type="checkbox"/> Mycology | <input type="checkbox"/> Palaeontology |

Dataset Information

Basic Informations

dataset id	0
dataset version	1
dataset title	<input type="text" value="Bexis2-UserDevConf2016"/>
dataset label	<input type="text"/>
dataset author	<input type="text" value="David Blaa"/>
data collection time	<input type="text" value="31.05.2016"/>
dataset description	<input type="text"/>
related publications	<input type="text"/>
metadata schema / data type	<input type="text" value="sample"/>
file id	0

Licence Information of Dataset

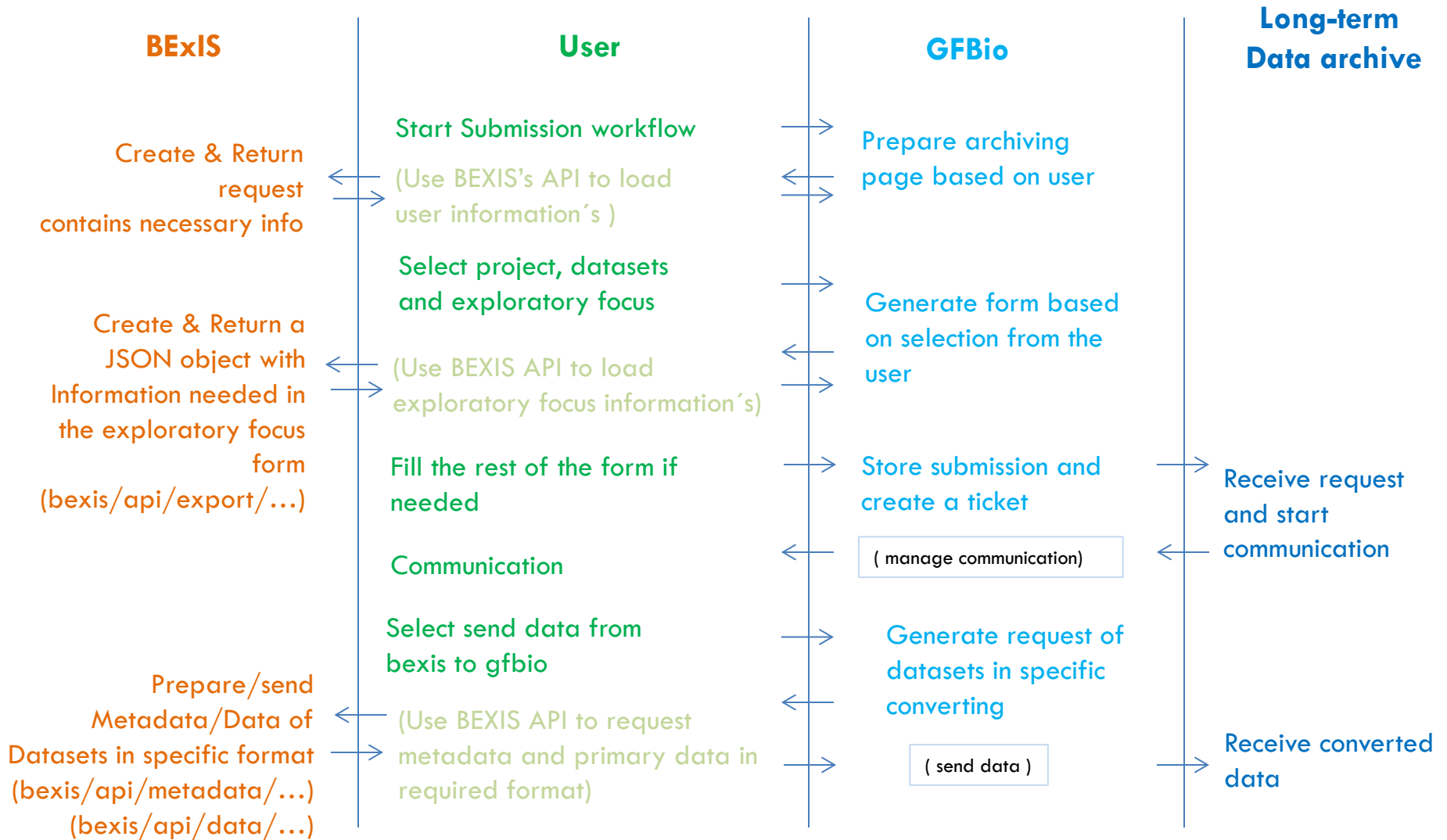
dataset is subject to the Nagoja Protocol?
 yes no

Please select the appropriate licenses

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- Creative Commons Attribution-ShareAlike
- Creative Commons Attribution-NoDerivs
- Creative Commons Attribution-NonCommercial
- Creative Commons Attribution-NonCommercial-ShareAlike
- Creative Commons Attribution-NonCommercial-NoDerivs
- Other License

[save only project informations](#) [save all](#) [Checking for completeness](#) [start sub](#)

GFBIO Submission Workflow





GFBIO Submission Workflow

On which platform we should start the submission workflow

- BEXIS 2 or GFBIO

BEXIS APIs

- **Bexis/Api/Export**
 - required formular for registration
 - `.../id?export=GFBIO?type=Collection`
 - JSON ,XML
- **Bexis/Api/Metadata**
 - Overview which dataset metadata is convertible to which
 - `.../id?convertTo="Name"`
 - JSON ,XML
- **Bexis/Api/Data**
 - Overview which dataset that has primary data
 - `.../id?projection=Col1,Col2`
 - `.../id?selection=x>10 && y=david`
 - both together
 - JSON,XML,CSV
- **Bexis/Api/Schema**
 - Overview which dataset
 - `.../id`
 - JSON ,XML



GFBIO APIs

- Submission

- [create-submission](#)
- [get-latest-public-submissions](#)
- [get-submissions-by-broker-submission-id](#)
- [get-submissions-by-research-object-id](#)
- [update-submission](#)

- Project

- [check-project-on-submissions](#)
- [create-project](#)
- [get-full-names-as-string](#)
- [get-project-by-id](#)
- [update-project](#)

- ResearchObject

- [create-research-object](#)
- [get-research-object-absolut-parent](#)
- [get-research-object-by-id](#)
- [get-research-object-parent](#)
- [get-research-objects-by-parent](#)
- [update-research-object](#)

Thank you for your attention

Starting discussion round

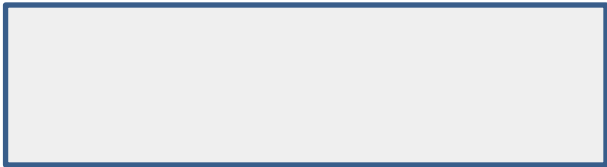
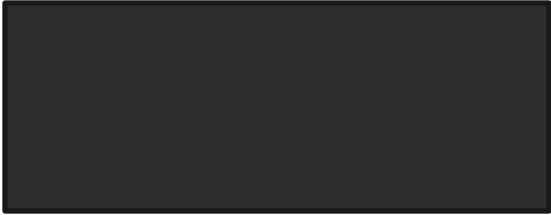




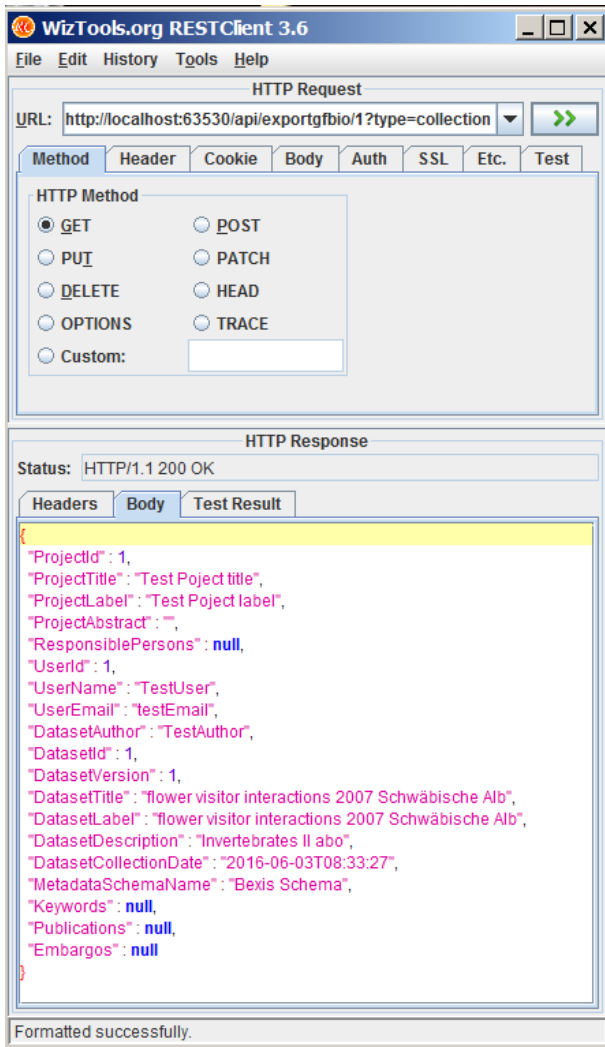
Import/Export Metadata in BEXIS 2

- Show example
 - Import Bexis xsd
 - Import published metadata from xml
 - Export to Bexis over API

<http://bexis2.vmguest.uni-jena.de/>



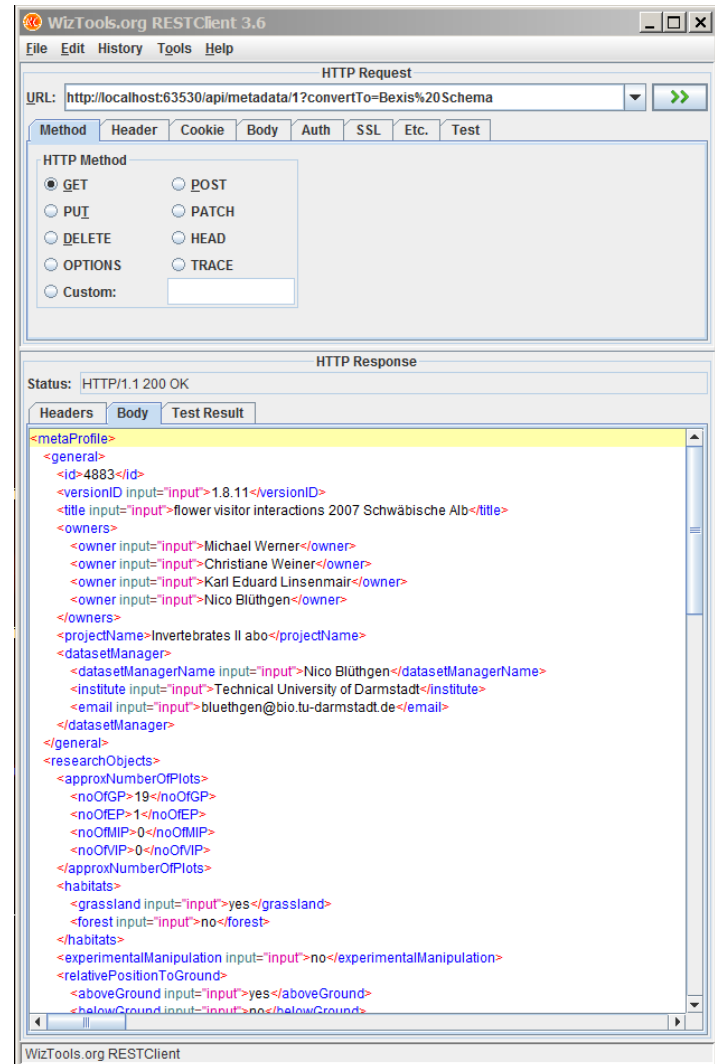
BEXIS 2 API Examples



The screenshot shows the WizTools.org RESTClient 3.6 interface. The URL is set to `http://localhost:63530/api/exportgfbio/1?type=collection`. The HTTP Method is GET. The response status is `HTTP/1.1 200 OK`. The response body is a JSON object with the following structure:

```
{
  "ProjectId": 1,
  "ProjectTitle": "Test Poject title",
  "ProjectLabel": "Test Poject label",
  "ProjectAbstract": "",
  "ResponsiblePersons": null,
  "UserId": 1,
  "UserName": "TestUser",
  "UserEmail": "testEmail",
  "DatasetAuthor": "TestAuthor",
  "DatasetId": 1,
  "DatasetVersion": 1,
  "DatasetTitle": "flower visitor interactions 2007 Schwäbische Alb",
  "DatasetLabel": "flower visitor interactions 2007 Schwäbische Alb",
  "DatasetDescription": "Invertebrates II abo",
  "DatasetCollectionDate": "2016-06-03T08:33:27",
  "MetadataSchemaName": "Bexis Schema",
  "Keywords": null,
  "Publications": null,
  "Embargos": null
}
```

Formatted successfully.



The screenshot shows the WizTools.org RESTClient 3.6 interface. The URL is set to `http://localhost:63530/api/metaddata/1?convertTo=Bexis%20Schema`. The HTTP Method is GET. The response status is `HTTP/1.1 200 OK`. The response body is an XML document with the following structure:

```
<metaProfile>
  <general>
    <id>4883</id>
    <versionID input="input">1.8.11</versionID>
    <title input="input">flower visitor interactions 2007 Schwäbische Alb</title>
    <owners>
      <owner input="input">Michael Werner</owner>
      <owner input="input">Christiane Weiner</owner>
      <owner input="input">Karl Eduard Linsenmair</owner>
      <owner input="input">Nico Blüthgen</owner>
    </owners>
    <projectName>Invertebrates II abo</projectName>
    <datasetManager>
      <datasetManagerName input="input">Nico Blüthgen</datasetManagerName>
      <institute input="input">Technical University of Darmstadt</institute>
      <email input="input">bluethgen@bio.tu-darmstadt.de</email>
    </datasetManager>
  </general>
  <researchObjects>
    <approxNumberOfPlots>
      <noOfGP>19</noOfGP>
      <noOfEP>1</noOfEP>
      <noOfMIP>0</noOfMIP>
      <noOfVIP>0</noOfVIP>
    </approxNumberOfPlots>
    <habitats>
      <grassland input="input">yes</grassland>
      <forest input="input">no</forest>
    </habitats>
    <experimentalManipulation input="input">no</experimentalManipulation>
    <relativePositionToGround>
      <aboveGround input="input">yes</aboveGround>
      <belowGround input="input">no</belowGround>
    </relativePositionToGround>
  </researchObjects>
</metaProfile>
```