openBIS Importer Toolset (oBIT)

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9th Annual OME User's Meeting, June 5th, 2014
openBIS – open Biology Information System

openBIS is an extensible, open source software framework for constructing user-friendly, scalable and powerful information systems for data and metadata acquired in biological experiments.

It enables users to collect, integrate, share, publish data and to connect to data processing pipelines.

http://www.cisd.ethz.ch/software/openBIS
openBIS core

- Separate metadata (application server) and data (data store server)
- Clean and flexible hierarchical metadata structure:
  - Space > Project > Experiment > Sample > Dataset > File
  - Authorization at space level
  - Samples and datasets: entities have parent/child or container relationships
  - Datasets belong to samples or experiments
  - All entities have user defined types, properties and vocabularies
  - Attachments can be associated to most entities
- Information indexing and searching by metadata
- Rich set of APIs and plug-in interfaces
  - Java, Python (Jython), RESTful web services
openBIS extensions

- **Core plug-ins**
  - Dropboxes (dataset ingestion)
  - Master data (import/export/update)
  - Data sources (additional databases)
  - Aggregation (reporting) plug-ins (metadata collection)
  - Processing plug-ins (on datasets)
  - Ingestion plug-ins (create/update entities)
  - Maintenance tasks (update/fix)
  - Web applications / RESTful web services (custom openBIS views)

- An organized set of core plug-ins can become a “core technology”
- Core plug-ins expand openBIS APIs to interface with custom client apps
openBIS “vanilla”
Current technologies

Technologies and Fast File Browsing

Select any technology-specific modules that should be installed along with openBIS. The selection can be altered at the next upgrade:

- □ Proteomics
- □ Screening
- □ Illumina NGS (ETH BSSE Setup)

Fast data set file browsing improves the performance of browsing of data sets with a large number of files. We recommend leaving it on for all instances, and especially screening instances.

☑ Fast data set file browsing

(Made with IzPack - http://izpack.org/)

Previous  Next  Quit
Screening core technology
Custom web apps
Custom web apps

![Image of web app](https://sprint-openbis.ethz.ch:8446/openbis/webapp/newbroser)

### Inhibitors List

<table>
<thead>
<tr>
<th>Code</th>
<th>Preview</th>
<th>Alternative name</th>
<th>Inhibitor type</th>
<th>Target</th>
<th>Company</th>
<th>Catalogue number</th>
<th>Solubility</th>
<th>FW</th>
<th>Stock concentration</th>
<th>Final concentration</th>
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</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Unavailable</td>
<td>LLeR caspase inhibitor</td>
<td>Proteasome inhibitor</td>
<td>Sigma</td>
<td>A8165</td>
<td>DMF 5</td>
<td>393.5 g/mol</td>
<td>28 mM (10 mg/ml)</td>
<td>25-50 mM</td>
<td></td>
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<tr>
<td>AMPICILLIN</td>
<td>Unavailable</td>
<td></td>
<td>Drugs</td>
<td>Sigma</td>
<td>A8516</td>
<td>dH2O</td>
<td>371.4 g/mol</td>
<td>100 mg/ml</td>
<td>100 mg/ml</td>
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<tr>
<td>B-GLYCEPHOSPHATE</td>
<td>Unavailable</td>
<td>phosphatase inhibitor</td>
<td>Tyrosine</td>
<td>Sigma</td>
<td>C8291</td>
<td>dH2O</td>
<td>216 g/mol</td>
<td>1 M</td>
<td>10 mM</td>
<td></td>
</tr>
<tr>
<td>BLASTICIDIN</td>
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<td></td>
<td>Drugs</td>
<td>Inv/itrogen</td>
<td>R216-01</td>
<td>dH2O</td>
<td>458.9 g/mol</td>
<td>5 mg/ml</td>
<td>2.5 mg/ml</td>
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<tr>
<td>CAFFEINE</td>
<td>Unavailable</td>
<td></td>
<td>Krase inhibitor</td>
<td>ATM/ATR</td>
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<td>5 mM</td>
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<td>Sigma</td>
<td>C0378</td>
<td>Ethanol</td>
<td>323.1 g/mol</td>
<td>10 mg/ml</td>
<td>20 mg/ml</td>
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</tbody>
</table>
Custom web apps
Embedded openBIS
Embedded openBIS

![Image of openBIS interface]

**Gene Pak1 in experiment HPV16_M2**

<table>
<thead>
<tr>
<th>Feature</th>
<th>Median</th>
<th>Deviation</th>
<th>Rank (50)</th>
<th>sRNA1 median</th>
<th>sRNA1 repl. 1</th>
<th>sRNA1 repl. 2</th>
<th>sRNA1 repl. 3</th>
<th>sRNA1 repl. 3</th>
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<tbody>
<tr>
<td>Cell Number</td>
<td>10401.000</td>
<td>1281.000</td>
<td>44</td>
<td>11542.000</td>
<td>11542.000</td>
<td>9349.000</td>
<td>11682.000</td>
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<tr>
<td>Infected Cells</td>
<td>1934.000</td>
<td>1470.000</td>
<td>39</td>
<td>1934.000</td>
<td>1409.000</td>
<td>3688.000</td>
<td>1934.000</td>
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<tr>
<td>Infection Index (nr.)</td>
<td>0.155</td>
<td>0.1144</td>
<td>27</td>
<td>0.1554</td>
<td>0.1221</td>
<td>0.7945</td>
<td>0.15X</td>
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<tr>
<td>Relative Infection Index</td>
<td>0.9111</td>
<td>0.4917</td>
<td>22</td>
<td>1.4369</td>
<td>1.4030</td>
<td>3.2163</td>
<td>1.41X</td>
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<tr>
<td>Log2 Relative Infection Index</td>
<td>-0.1340</td>
<td>0.6225</td>
<td>22</td>
<td>0.5027</td>
<td>0.4885</td>
<td>1.6854</td>
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<tr>
<td>ZScore</td>
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<td>0.5031</td>
<td>17</td>
<td>0.8806</td>
<td>NaN</td>
<td>1.3059</td>
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<tr>
<td>MAD</td>
<td>-0.1457</td>
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<td>34</td>
<td>0.0800</td>
<td>0.0428</td>
<td>0.0893</td>
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<tr>
<td>Mean.Cells.Intensity</td>
<td>0.0467</td>
<td>0.0030</td>
<td>31</td>
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<td>0.0258</td>
<td>0.0381</td>
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<td>Mean.Image.Intensity</td>
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<td>0.0049</td>
<td>33</td>
<td>0.0293</td>
<td>0.0293</td>
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<tr>
<td>Mean.Nuclei.Intensity</td>
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<td>0.0270</td>
<td>17</td>
<td>0.3302</td>
<td>0.4563</td>
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<td>0.32%</td>
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</tr>
<tr>
<td>Mean.Nuclei.Intensity</td>
<td>0.0900</td>
<td>0.0214</td>
<td>24</td>
<td>0.1425</td>
<td>0.0938</td>
<td>0.1425</td>
<td>0.15%</td>
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</tr>
<tr>
<td>Mean.Nuclei.Intensity</td>
<td>0.0594</td>
<td>0.0391</td>
<td>35</td>
<td>0.0268</td>
<td>0.0268</td>
<td>0.0343</td>
<td>0.023%</td>
<td></td>
</tr>
<tr>
<td>ModeRawInfected</td>
<td>1833.000</td>
<td>1637.000</td>
<td>32</td>
<td>4422.000</td>
<td>3747.000</td>
<td>4422.000</td>
<td>4767.000</td>
<td></td>
</tr>
</tbody>
</table>

**Displaying 1 of 48**

- Merged Channels
- DAPI
- Virus Infected
openBIS for tablets

openBIS
By ETH Zurich
Open iTunes to buy and download apps.

Description
Introduction
openBIS is an open, distributed system for managing biological information. It is being developed at the Center for...

What's New in Version 1.2.1

iPad Screenshots

Free
Category: Education
Updated: Dec 08, 2013
Version: 1.2.1
Size: 1.4 MB
Language: English
Seller: ETH Zurich © 2013 ETH Zurich
Rated 4+
Raw data

annotated

backed up

centralized storage

openBIS

HRM
Raw data

annotated

backed up

centralized storage

openBIS Importer Toolset

- semi-automatic
- semi-unsupervised

data registration in openBIS
oBIT – openBIS Importer Toolset

The openBIS Importer Toolset is a tightly integrated collection of tools that allows for the semi-automated, semi-supervised registration of annotated datasets into openBIS directly from the acquisition stations.

It also extends openBIS with custom data viewers and server-side core plugins.
1. Export or save
2. Scan
3. Annotate

Acquisition station

Example: BD LSRFortessa cell analyzer

User folder

Datamover Incoming

Datamover

as a Windows service

openBIS

dropbox

openBIS

Data store

Annotation Tool

Single Cell Unit / D-BSSE
An administrator must set up the acquisition machine before the first use.
[Admin] Annotation Tool Admin

Set the openBIS URL(s)
[Admin] Annotation Tool Admin

Select the acquisition station or type

- Set the openBIS URL (this is current default)
  https://bs-lamp00.othz.ch:8443/openbis

- Accept self-signed SSL certificates when logging in to openBIS
  yes

- Select the acquisition station or type
  BD Biosciences Cell Analyzers and Sorters
  BD Biosciences Cell Analyzers and Sorters
  Generic light microscopes

- Set user data directory
  D:\user

- Set Datamover incoming directory
  D:\toOpenBIS\incoming

It is highly recommended to set both folders on the same file system.
[Admin] Annotation Tool Admin

Set the local working directories
BD BIOSCIENCES CELL ANALYZERS AND SORTERS

BD LSRFortessa cell analyzer

http://www.bdbiosciences.com/instruments/lsr/index.jsp
[User] Example: BD LSR Fortessa

Export to user folder
Please choose the server you want to use:

https://bi-lamp09.ethz.ch:3443/openbis

OK       Cancel

pontia

Password

**********

Login
<table>
<thead>
<tr>
<th>Code</th>
<th>Data Set Type</th>
<th>Sample Identifier</th>
<th>Sample Type</th>
<th>Project</th>
</tr>
</thead>
<tbody>
<tr>
<td>20130101:107:205097:735</td>
<td>LSR_FORTESSA_FCSFLE</td>
<td>LSR_FORTESSA_P120.I.R1.W1209</td>
<td>LSR_FORTESSA_WELL</td>
<td>LSR_FORTESSA_ALTERNATIVE_PROJECT</td>
</tr>
<tr>
<td>20130101:107:205097:735</td>
<td>LSR_FORTESSA_FCSFLE</td>
<td>LSR_FORTESSA_P120.I.R1.W1215</td>
<td>LSR_FORTESSA_WELL</td>
<td>LSR_FORTESSA_ALTERNATIVE_PROJECT</td>
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<td>20130101:107:205097:735</td>
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<td>LSR_FORTESSA_P120.I.R1.W1224</td>
<td>LSR_FORTESSA_WELL</td>
<td>LSR_FORTESSA_ALTERNATIVE_PROJECT</td>
</tr>
</tbody>
</table>
Custom views
User scratch folder

![Image of file explorer window with folders named dst and opensbis_export]
LIGHT MICROSCOPES

An alternative to OMERO?
[Admin] Annotation Tool Admin

Select the acquisition station or type
openBIS – new technologies

Technologies and Fast File Browsing

Select any technology-specific modules that should be installed along with openBIS. The selection can be altered at the next upgrade:

- [ ] Proteomics
- [ ] Screening
- [ ] Illumina NGS (ETH BSSE Setup)
- [x] Flow cytometry
- [x] Microscopy

Fast data set file browsing improves the performance of browsing of data sets with a large number of files. We recommend leaving it on for all instances, and especially screening instances.

- [x] Fast data set file browsing

(Made with IzPack – http://izpack.org/)

Previous Next Quit
https://wiki-bsse.ethz.ch/display/oBIT

openBIS Importer Toolset (oBIT)

Abstract
The openBIS Importer Toolset is a set of tools to streamline registration of acquired data and metadata into openBIS and extend openBIS via custom views and apps for working with data.

Quick links
- User manual
- Installation and administration guides
- Developer documentation

Description
openBIS is an extensible, open source software framework for constructing user-friendly, scalable and powerful information systems for data and metadata acquired in biological experiments. It enables users to collect, integrate, share, publish data and to connect to data processing pipelines.

The openBIS Importer Toolset is a tightly integrated collection of tools that allows for the semi-automated, semi-unsupervised registration of annotated datasets into openBIS directly from the acquisition stations.
Summary

- The openBIS/openBIS Importer Toolset synergy aims to:
  - offer a powerful and scalable data and metadata management system
  - streamline data registration directly from the acquisition machines
  - support multiple acquisition hardware classes
  - offer a reasonably simple way for third parties to add support for new hardware classes
Acknowledgments

**SIS (formerly CISD)**
- Bernd Rinn
- Franz-Josef Elmer
- Pawel Glyzewski
- Piotr Kupczyk
- Antti Luomi
- Chandrasekhar Ramakrishnan
- Jakub Straszewski
- Juan Fuentes Serna
- Caterina Barillari
- Manuel Kohler

**ITSC**
- Simon Paul Diethelm
- John Ryan
- Andreas Jecklin

openBIS: [http://www.cisd.ethz.ch/software/openBIS](http://www.cisd.ethz.ch/software/openBIS)

oBIT: [https://wiki-bsse.ethz.ch/display/oBIT](https://wiki-bsse.ethz.ch/display/oBIT)
- [https://github.com/aarpon](https://github.com/aarpon)