openBIS – an open resource for academic laboratories

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Scientific IT Services, ETH Zurich
Research workflow in experimental & computational labs

- Sample preparation
- Measurement
- Data collection
- Processing
- Analysis
- Publication
What does it take to manage research data?

Complex process that requires tracking and linking different types of information

- Materials/samples
- Protocols/ SOPs
- Raw data
- Model
- Processed data
- Results
- Code
- Analysis notebooks
- Experimental description/notes
- Title
- Date
- Materials
- Methods
- Analysis
- Results
A very common scenario @ ETH
The ideal scenario

A combined ELN/LIMS can provide such solution
The ideal scenario

A combined ELN/LIMS can provide such solution
openBIS facts

Platform for managing scientific information and supporting research data workflows from “bench” to publication

Can be used in most quantitative science fields (e.g. life sciences, physics, env. sciences, etc)

Used by research groups and facilities @ ETH, Swiss & European Universities, a few companies

- **Summer 2007**
  - openBIS development start (SystemsX)

- **April 2008**
  - first openBIS release (v08.04)

- **Summer 2009**
  - SystemsX projects start using openBIS

- **Summer 2013**
  - openBIS ELN-LIMS UI start

- **Spring 2014**
  - first ELN-LIMS beta version

- **May 2015**
  - first downloadable ELN-LIMS plugin

- **May 2016**
  - first ELN-LIMS official release

- **May 2017**
  - BigDataLink v.1

- **December 2017**
  - JupyterHub integration
openBIS in a nutshell

- openBIS is a solution for research labs
<table>
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<th>Mating Type</th>
<th>Origin</th>
<th>Publication</th>
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openBIS in a nutshell

- openBIS is a solution for research labs
Object: Yeast transformation

/METHODS/PROTOCOLS/GENERAL_PROTOCOLS/FRPROT1

General

Name:
Yeast transformation

For what:

Protocol type:
yeast basic method

Links to materials & methods

<table>
<thead>
<tr>
<th>Code</th>
<th>Name</th>
<th>Quantity</th>
<th>Comments</th>
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<tr>
<td>FRC31</td>
<td>Dimethyl sulfoxide (DMSO)</td>
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<td>FRSO820</td>
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<tr>
<td>FRSO821</td>
<td>LiAc mix</td>
<td>100 µl/ transformation</td>
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<td>FRSO822</td>
<td>Salmon sperm DNA (ssDNA)</td>
<td>10 µl/ transformation</td>
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Materials:
Centrifuge min 1000 g Orbital shaker with regulated temperature Incubator with regulated temperature Wheel or mild shaker for 1.5 ml tubes Thermomixer

Method

Time requirement:
1 day pre-culture + 2 hours work per 2 days incubation

Procedure:
1. Inoculate 5 ml of appropriate medium with yeast. 2. Incubate overnight at the appropriate temperature (usually 30°C). 3. Dilute the overnight culture in appropriate medium (10 ml per transformation). 4. Grow cells to OD600=0.4-0.8. 5. Harvest cells by centrifugation at max 1000 g for 5 min at room temperature. 6. Throw away supernatant. 7. Re-suspend cells in 5 ml water. 8. Harvest cells by centrifugation at max 3000 g for 5 min at room temperature. 9. Throw away supernatant. 10. Re-suspend in LiAc mix. 11. Use 100 µl cells per transformation. Transfer this volume to a 1.5 ml tube. 12. Add 1000 ng of DNA to the mix. 13. Add 10 µl ssDNA (Boil ssDNA at 95°C for 5 min every 4th time, cool down to room temperature). 14. Add 600 µl of PEG mix, and mix. 15. Incubate on the wheel at room temperature for 30 min. 16. Add 70 µl DMSO to reach final concentration of 10%. 17. Heat shock for 15 min at 42°C, shaking at max speed. 18. Harvest cells by centrifugation at max 1000 g for 2 min at room temperature. 19. Throw away the supernatant. 20. Re-suspend cell in 300 µl YPD. 21. Incubate on the wheel at room temperature for 20 min (anotrophic markers) or 3-4 hours (drugs resistance markers). 22. Plate 150 µl on appropriate plate. 23. Incubate 2-4 days at the appropriate temperature.

Protocol evaluation:
Small yeast colonies appear on the plate after a couple of days at the appropriate temperature.
openBIS in a nutshell

- openBIS is a solution for research labs
Object: Detection of LexA-ER-B42 induction by flow cytometry

/DIANA_OTTOZ/INDUCIBLE_TRANSCRIPTION_FACTOR/INDUCTION_OF_TF.FC.LEXA-ER-B42

**General**

**Name:**
Detection of LexA-ER-B42 induction by flow cytometry

**Owner:**
Diana Ottoz

**Experimental goals:**
Analyze the induction of LexA-ER-B42 in a concentration series of beta-estradiol using a fluorescence readout

**Experimental results:**
The LexA-ER-B42 induction can be measured by using a target gene encoding a fluorescence protein. LexA-ER-B42 induction is different at different concentrations of Inducers.

![Graph showing induction of LexA-ER-B42](image)

**Links to materials & methods**

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<td>liquid S media</td>
<td>SDG at 25°C</td>
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<tr>
<td>FRSOB34</td>
<td>1000X Cycloheximid</td>
<td>diluted 1/1000, treated for 1/2 hour</td>
<td>Dissolve in DMSO. Aliquot.</td>
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<tr>
<td>FRSOB37</td>
<td>beta-estradiol</td>
<td>1:2 concentration series with 2000 nM maximum for 24</td>
<td>Dissolve in EtOH.</td>
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/DIANA_OTTOZ/INDUCIBLE_TRANSCRIPTION_FACTOR/INDUCTION_OF_TF/FC_LEXA-ER-B42

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openBIS in a nutshell

- openBIS is a solution for research labs
Jupyter notebooks

- Application that combine documentation, code, input and output generated by the code, e.g. graphs, plots (Nature 515, 151–152)
- Useful for exploratory data analysis and reproducibility
- >40 programming languages supported (Python, R, Scala, Julia, etc)
- Notebooks can be shared
Object: Detection of LexA-ER-B42 induction by flow cytometry

Name: Detection of LexA-ER-B42 induction by flow cytometry

Show in project overview: True

Experimental Goals:
Analyze the induction of LexA-ER-B42 in a concentration series of beta-estradiol using a fluorescence readout

Experimental Results:
The LexA-ER-B42 induction can be measured by using a target gene encoding a fluorescence protein. LexA-ER-B42 induction is different at different concentrations of inducer.

Start date: 2018-07-17 17:00:23 +0200

End date: 2018-07-17 18:00:54 +0200

Experimental readout:

![Flow cytometry graph]

Select a dataset type

Files Uploader

Select files to upload

Create

Auto upload on drop
openBIS in a nutshell

- openBIS is a solution for research labs
openBIS solutions

openBIS ELN-LIMS is available in two flavors:

**For life sciences**: customizable predefined types and fields suitable for most biological labs

**Generic**: only basic generic types predefined. To be fully customized by users.
openBIS features

- Relationships
- Import/Export
- User rights management
- Audit trail
- Data preservation
- Long term storage (tapes)
- Samples' storage manager
- Ordering

https://labnotebook.ch
openBIS features for life sciences

https://labnotebook.ch
Best practices for openBIS introduction as ELN/LIMS in a biology lab

Create inventory of materials and samples
- Establish relationship between samples

Create inventory of standard lab protocols
- Link protocols to samples

Describe experiments
- Links to samples
- Links to protocols/copy protocols
- Upload data
openRDM.swiss - National ARDM Service

Cloud-hosted openBIS ELN-LIMS
- Virtual servers per research group, institute or institution
- Generic or life-science ‘flavor’
- Optionally with JupyterHub server for analytics
- Automated deployment (Ansible)
- Integration with Community Service Hub

Training & user support (‘best effort’)

Service Marketing & Business Model
- Infrastructure & service charges for sustainable long-term operation

Connection with repositories
- Covering the entire data life cycle
Acknowledgements

The SIS team

High-Performance Computing

- Olivier Byrde (Group Head)
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- Juan Fuentes
- Antti Luomi
- Yves Noirjean
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- Mikolaj Rybinski
- Uwe Schmitt
- Swen Vermeul
- Cezary Czernecki

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- Tarun Chadha
- Diana Coman Schmid
- Henry Lütcke
- Michal Okoniewski
- Jarunan Panyasantisuk
- Emanuel Schmid
- Cristian Scurtescu

Bernd Rinn (Section Head)

Alex Upton (Community Project Manager)

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