openBIS & ETH RDH tutorial

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Caterina Barillari
Caterina.barillari@id.ethz.ch

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Overview

In this tutorial we will learn how to use the openBIS/ETH RDH inventory and lab notebook.

The first part of the tutorial covers basic customization for the inventory:

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2. Configuration of storage

The second part of the tutorial covers the registration of samples, protocols and experiments:

1. Registration of media, chemicals, buffers, plasmid, yeasts, cell lines
2. Registration of flow cytometry and western blotting protocols
3. Description of experiments in the lab notebook
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The last part covers the management of lab suppliers, products and orders with openBIS/ETH RDH.

Additional documentation and video tutorials can be found at: https://labnotebook.ch/.

openBIS & ETH RDH Customization

Customization of Inventory of Materials

To customize the Inventory of Materials for our use case, we want to create a few Collection folders: **Media Collection, Buffers collection, Chemicals Collection, Plasmids Collection, Cell Lines Collection, Yeasts Collections**.

The *Collection* folders are always contained in top level folders (=*Projects*), which we will organize in this way:

1. Reagents:
    a. Media Collection
    b. Buffers Collection
    c. Chemicals Collection
2. Cell lines
    a. Cell Lines Collection
3. Plasmids
    a. Plasmids Collection
4. Yeasts
    a. Yeasts Collection

Creation of Collection folders

We first need to create the top level folders and subsequently the *Collection* folders.

Creation of the top level folders

We want to create 4 folders: **Reagents, Cell Lines, Plasmids, Yeasts**

Reagents:

1. Select the **Materials** folder
2. Click the **+** button in the main page
3. Enter **Reagents** in the **Code** field
4. **Save**

Cell Lines:

5. Select the **Materials** folder
6. Click the **+** button in the main page
7. Enter **Cell_lines** in the **Code** field
8. **Save**

Plasmids:

9. Select the **Materials** folder
10. Click the **+** button in the main page
11. Enter **Plasmids** in the **Code** field
12. **Save**

Yeasts:

13. Select the **Materials** folder

14. Click the **+** button in the main page
15. Enter **Yeasts** in the **Code** field
16. **Save**

Creation of Collection folders

Now we want to create 6 Collections folders**: Media Collection, Buffers collection, Chemicals Collection, Plasmids Collection, Cell Lines Collection, Yeast Collections**.

Media Collection:

1. Select the **Reagents** folder
2. Click the **+** button in the main page
3. Select **Materials** from the dropdown
4. Replace the **Code** field with **MEDIA_COLLECTION**
5. Enter **Media Collection** in the **Name** field
6. Select **Media** from the **Default Object Type** drop down
7. **Save**

Buffers Collection:

1. Select the **Reagents** folder
2. Click the **+** button in the main page
3. Select **Materials** from the dropdown
4. Replace the **Code** field with **BUFFERS_COLLECTION**
5. Enter **Buffers Collection** in the **Name** field
6. Select **Solution Buffer** from the **Default Object Type** drop down
7. **Save**

Chemicals Collection:

1. Select the **Reagents** folder
2. Click the **+** button in the main page
3. Select **Materials** from the dropdown
4. Replace the **Code** field with **CHEMICALS_COLLECTION**
5. Enter **Chemicals Collection** in the **Name** field
6. Select **Chemical** from the **Default Object Type** drop down
7. **Save**

Plasmids Collection:

1. Select the **Plasmids** folder
2. Click the **+** button in the main page
3. Select **Materials** from the dropdown
4. Replace the **Code** field with **PLASMIDS_COLLECTION**
5. Enter **Plasmids Collection** in the **Name** field
6. Select **Plasmid** from the **Default Object Type** drop down
7. **Save**

Cell lines Collection:

1. Select the **Cell Lines** folder

2. Click the **+** button in the main page
3. Select **Materials** from the dropdown
4. Replace the **Code** field with **CELL_LINES_COLLECTION**
5. Enter **Cell Lines Collection** in the **Name** field
6. Select **Cell Line** from the **Default Object Type** drop down
7. **Save**

Yeasts Collection:

1. Select the **Yeasts** folder
2. Click the **+** button in the main page
3. Select **Materials** from the dropdown
4. Replace the **Code** field with **YEASTS_COLLECTION**
5. Enter **Yeasts Collection** in the **Name** field
6. Select **Yeast** from the **Default Object Type** drop down
7. **Save**

Yeasts Collection 2:

1. Select the **Yeasts** folder
2. Click the **+** button in the main page
3. Select **Materials** from the dropdown
4. Replace the **Code** field with **YEASTS_COLLECTION_2**
5. Enter **Yeasts Collection 2** in the **Name** field
6. Select **Yeast** from the **Default Object Type** drop down
7. **Save**

Removal of Collection folders

In the step above, we created a *Collection* folder by mistake and we now want to remove it.

1. Select the **Yeasts Collection 2** folder from the Inventory main menu.
2. In the *Collection* page, click on **YEASTS_COLLECTION_2** (in path /MATERIALS/YEASTS/YEASTS_COLLECTION_2)
3. Click the **bin icon**
4. Enter **mistake** in the mandatory **Reason** field
5. **Accept**

When *Experiments*/*Collections* are deleted they are first moved to the trashcan. In order to be completely removed from the database, they have to be deleted also from the trashcan. Alternatively, it is also possible to revert deletion from the trashcan, if something was accidentally moved here.

6. Go to **Trashcan** under **Utilities** in the main menu
7. Click the **Empty Trash** button

Note: *Objects and Experiments/Collections are moved to the trashcan when deleted. Projects are deleted directly, without being moved to the trashcan.*

Customization of Inventory of Methods

To customize the Inventory of Methods for our use case, we want to create two Collection folders: **Western Blotting Protocols** and **Flow Cytometry Protocols**.

The *Collection* folders are always contained in top level folders (=*Projects*), which we will organize in this way:

1. Protocols:
    a. Western Blotting Protocols
    b. Flow Cytometry Protocols

Creation of a new Collection folder

We first need to create the top level folder and subsequently the *Collection* folders.

Creation of the top level folders

We want to create 1 folder: **Protocols**

1. Select the **Methods** folder
2. Click the **+** button in the main page
3. Enter **Protocols** in the **Code** field
4. **Save**

Creation of the Western Blotting Protocols folder

To create the new *Collection* folder:

1. Select the **Protocols** folder from the main menu
2. Click the **+** button in the main page
3. Select **Methods** from the dropdown
4. Change the **Code** to **WESTERN_BLOTTING_PROTOCOLS**
5. Enter **Western Blotting Protocols** in the **Name** field
6. Select **General Protocol** from the **Default Object Type** dropdown
7. **Save**

Creation of the Flow Cytometry Protocols folder

To create the new *Collection* folder:

1. Select the **Protocols** folder from the main menu
8. Click the **+** button in the main page
9. Select **Methods** from the dropdown
2. Change the **Code** to **FLOW_CYTOMETRY_PROTOCOLS**
3. Enter **Flow Cytometry Protocols** in the **Name** field

4. Select **General Protocol** from the **Default Object Type** dropdown
5. **Save**

Customization of the openBIS & ETH RDH Settings

An *Admin* can customize some parts of the ELN by editing the **Settings**, under **Utilities** in the main menu.

It is possible to customize what is shown in the main menu, configure the lab storages, define inventory *Spaces*, customize *Object* types forms.

Customization of main menu

In this section, it is possible to unselect sections that we do not want to display in the main menu.
By default everything is selected.

Configuration of lab storages

In this section it is possible to specify the configuration of each single freezer, fridge or any other storage used in the lab. This should be done if the lab is interested in having a graphical overview of all storages, which can help in keeping track of samples. In this tutorial we will configure 3 storages: a liquid nitrogen tank; a -80°C freezer; a -20°C freezer.

Configuration of a liquid nitrogen tank

We want to configure a liquid nitrogen tank that has 10 towers and 10 drawers in each tower. Each drawer contains 1 box.

1. Go to the **Storages** section in the **Settings** page.
2. Click the **+** button
3. Enter **N2_TANK** in the **Code** field
4. Enter **Liquid Nitrogen Tank** in the **Name** field
5. Enter **10** in the **Number of Rows** field (*these are the drawers*)
6. Enter **10** in the **Number of Columns** field (*these are the towers*)
7. Enter **1** in the **Allowed number of boxes in a rack** field (*these are the number of boxes allowed in each drawer*)
8. Enter **80** in the **Rack Space warning** field
9. Enter **80** in **the Box Space warning** field
10. Select **Box Position Validation** form the **Validation level** field. This means that, when registering a storage position for a sample, it is necessary to specify the position in the box.
11. **Save**

Configuration of a -80°C freezer

We want to configure a -80°C freezer, located in room A1. The freezer has 6 shelves and 4 racks per shelf.

1. Go to the **Storages** section in the **Settings** page.
2. Click the **+** button
3. Enter **MINUS80_ROOMA1** in the **Code** field
4. Enter **-80°C Room A1** in the **Name** field

5. Enter 6 in the **Number of Rows** field (*these are the shelves*)
6. Enter 4 in the **Number of Columns** field (*these are the racks in each shelf*)
7. Enter 80 in the **Rack Space warning** field
8. Enter 80 in **the Box Space warning** field
9. Select Rack Validation form the **Validation level** field. This means that, when registering a storage position for a sample, it is sufficient to specify the position in the fridge/freezer.
10. **Save**

Configuration of a -20°C freezer

We want to configure a -20°C freezer, located in room A2. The freezer has 8 shelves and no racks.

1. Go to the **Storages** section in the **Settings** page.
2. Click the **+** button
3. Enter MINUS20_ROOMA2 in the **Code** field
4. Enter -20°C Room A2 in the **Name** field
5. Enter 8 in the **Number of Rows** field (*these are the shelves*)
6. Enter 1 in the **Number of Columns** field (*these are the racks in each shelf*)
7. Enter 80 in the **Rack Space warning** field
8. Enter 80 in **the Box Space warning** field
9. Select Rack Validation form the **Validation level** field
10. **Save**

Customization of Object types forms

Each *Object* type form can be partly customized. The following options are available:

1. *Use as protocol*: select this for all new protocol *Object* types created by an Instance Admin.
2. *Enable storage*: select this on all *Object* types where you want to have the graphical storage view.
3. *Show*: enable this to have the *Object* types shown in all dropdown lists.
4. *Define parents and children in the form*.

In this tutorial we will customize the *Experimental Step* form.

Customization of Experimental step form

In the current *Experimental Step* form, only **General Protocol** is shown in the **Links to Materials and Methods** section. Now we want to add all the categories we added before in the inventory: *chemical, buffer, media, plasmid, yeast, cell line*. This will help us when we want to make links to these objects when we describe an experiment.

1. Edit the **Settings** page
2. Scroll down to **the Object type definitions extension** section in the **Settings** page.
3. Open the **Experimental Step** section
4. Change General Protocol to Protocol in the Label field from the list
5. Add **Chemical** to the list:
    a. Click the + button in the line starting with **Hints for**
    b. In the line that just appeared, select **Parents** from the dropdown

c. Enter **Chemical** in the **Label** field
d. Select **Chemical** from the **Type** dropdown menu

6. Add **Buffer** to the list:
    a. Click the + button in the line starting with **Hints for**
    b. In the line that just appeared, select **Parents** from the dropdown
    c. Enter **Buffer** in the **Label** field
    d. Select **Solution Buffer** from the **Type** dropdown menu
7. Add **Media** to the list:
    a. Click the + button in the line starting with **Hints for**
    b. In the line that just appeared, select **Parents** from the dropdown
    c. Enter **Media** in the **Label** field
    d. Select **Media** from the **Type** dropdown menu
8. Add **Plasmid** to the list:
    a. Click the + button in the line starting with **Hints for**
    b. In the line that just appeared, select **Parents** from the dropdown
    c. Enter **Plasmid** in the **Label** field
    d. Select **Plasmid** from the **Type** dropdown menu
9. Add **Yeast** to the list:
    a. Click the + button in the line starting with **Hints for**
    b. In the line that just appeared, select **Parents** from the dropdown
    c. Enter **Yeast** in the **Label** field
    d. Select **Yeast** from the **Type** dropdown menu
10. Add **Cell line** to the list:
    a. Click the + button in the line starting with **Hints for**
    b. In the line that just appeared, select **Parents** from the dropdown
    c. Enter **Cell line** in the **Label** field
    d. Select **Cell line** from the **Type** dropdown menu

11. **Save** the Settings

In the same way you can customize any other *Object* type form.

How to use the openBIS & ETH RDH Inventory and Laboratory Notebook

Registration of samples and protocols in the Inventory

Now that our openBIS/ETH RDH is customized for our use-case, we want to register samples and protocols in the Inventory.

Registration of new materials and samples in the Inventory

We will start by registering a few samples in the Materials inventory: *media, chemicals, plasmid, yeasts, buffers*.

Registration of a media sample

We will now register one single media sample.

1. Select the **Media Collection** folder in the **Reagents** folder
2. Click the **+** button in the main page
3. Enter **Liquid S media** in the **Name** field
4. Enter **To grow cells in well controlled nutritional conditions** in the **For what** field
5. Select **Saccharomyces cerevisiae** in the **Organism** field
6. Select **room temperature** from the **Storage conditions** list
7. **Save**

Click on the **Media Collection** folder. From the **Columns** drop down in the table you can choose which fields to visualize. This information is stored, so the selection only has to be made once.

Batch registration of chemical samples

Now we want to register 4 chemicals. We will do this by Batch Registration, uploading the **chemicals.tsv** file from the training material**.**

1. Open the **chemicals.tsv** file to visualize its content
2. Select the **Chemical Collection** folder in the **Reagents** folder
3. Select **Batch Register Objects** from the **Operations** drop down menu
4. Select **Chemical** from the **Object Type** dropdown menu
5. Choose the **chemicals.tsv** file
6. **Accept**
7. Select **Name**, **Art. Number, Supplier** and **Storage Conditions** from the **Columns** drop down in the table.

Batch modification of chemical samples

When we registered the chemicals before, we forgot to enter the information about the storage conditions. To correct this in all samples, we can batch update the samples:

1. Select the **Chemical Collection** folder in the **Reagents** folder
2. Select only **Identifier** and **Storage Conditions** from the **Columns** dropdown

3. Select **Export visible columns with visible rows** from the **Options** dropdown list
4. Edit this file with Excel:
    a. enter **RT** under the Storage column in the first 3 rows
    b. Enter **4** under the Storage column in the last row
    c. **Save** the file
5. Select **Batch Update Objects** from the **Operations** list
6. Select **Chemical** from **the Object Type** list
7. Select the previously modified file from the Documents
8. **Accept**

Registration of a plasmid sample

1. Go to the **Plasmid Collection** folder in the main menu
2. Click the + button
3. Enter **insul-(lexA-box)4-PminCYC1-CitrineA206K-TCYC1** in the **Name** field
4. Select **pRS30y** from the **Backbone** list
5. Select **bla** from **the Bacterial antibiotic resistance** list
6. Select **URA 3** from the **Marker** list
7. Enter **NotI, KpnI** in **the Flanking Restriction Enzymes** field
8. Define a storage position:
    a. Click the + button under the storage table
    b. Select the **-80C Room A1** freezer
    c. Select the **1,1** rack
    d. Enter **Plasmid box 1** in the **Box Name** field
    e. Select the **10 x 10** size
    f. Select position **A1**
    g. **Accept**
9. **Save**

Registration of yeast samples with parents

First we will register one yeast:

1. Go to the **Yeast Collection** folder in the main menu
2. Enter **LexA-DBD-long-HBD-B42** in the **Name** field
3. Select **BY4741** from the **Genetic Background** list
4. Select **a** from the **Mating Type** list
5. Select **met15-** from the **Background-specific markers** list
6. Select **ura3- leu2-** from the **Common markers** list
7. Select **cir+** from the **Endogenous 2micron plasmid in yeast** list
8. Select **transformation** from the **Origin** list
9. Select **PCR** from the **Strain Check** list
10. Define a storage position:
    a. Click the + button under the storage table
    b. Select the **-80C Room A1** freezer
    c. Select the **2,1** rack
    d. Enter **Yeast box 1** in the **Box Name** field

e. Select the **10 x 10** size
f. Select position **A1**
g. Accept

11. Save

Now we will register a second yeast, which was made using the first yeast and the previously registered plasmid. These can be set as **parents.**

We can copy the yeast we just register and modify only certain fields that are different:

1. Go to the **Yeast Collection** folder in the main menu
2. Click on the **existing yeast** sample
3. Click on the **copy** button from the **menu toolbar**
4. Leave everything unselected
5. **Accept**
6. The new yeast is created. Edit the form.
7. Remove **LexA-DBD-long-HBD-B42** from the **Name** field and enter **demo.**
8. Add relationships:
    a. Add yeast parent:
        i. In the parents section, click on the **+** next to **Yeast parents**
        ii. Select **the yeast previously registered** from the table
    b. Add plasmid parent:
        i. Click the **+** next to **Plasmid**
        ii. Select the only plasmid in the table
        iii. Select **integration** from the **Plasmid Relationship** dropdown
        iv. Enter **URA3** in the **Plasmid annotation** field
9. Change value to **leu2-** for the **Common markers** field
10. Define a storage position:
    a. Click the **+** button under the storage table
    b. Select the **-80C Room A1** freezer
    c. Select the **Yeast box 1** in the **2,1** rack
    d. Select position **A2**
11. **Accept**
12. **Save**
13. Visualize the connection with the hierarchy tree button 

Batch registration of buffer samples with parents

We will now register 3 buffers using batch registration, by uploading the **buffers.tsv** file from the training material**.** Each of the buffers has 2 chemicals as parents, which we need to set in the file.
The first buffer, cycloheximide, has DMSO and cycloheximide as chemical parents. The second and third buffers, bet-estradiol, have Ethanol and beta-estradiol as chemical parents.

Setting parents in file:

1. Open the **buffers.tsv** file to visualize its content
2. Go to the **Chemicals Collection**

3. Select **Identifier** and **Name** from the table
4. In the **buffers.tsv** file, fill in the **parents** column with the **Identifiers** corresponding to the chemicals mentioned above:
    i. DMSO and cycloheximide for the first buffer
    ii. EtOH and beta-estradiol for the second and third buffer

Batch upload

5. Go to the **Solutions Buffers Collection** folder in **Reagents** in the main menu
6. Select **Batch Register Objects** from the **Operations** drop down menu
7. Select **Solution Buffer** from the **Object Type** list
8. Select the **buffers.tsv** file just modified
9. **Accept**

Select **Name, Parents, Details, For what, Stock Concentration and Storage Conditions** from the **Columns** dropdown.

Click on one of the entities in the table (e.g. cycloheximide) and visualize the connections to the chemicals with the hierarchy tree button 

Deletion of duplicate Objects

In the step above we registered 3 buffers, but two of them are the same. We want to delete one of them:

1. Go to the **Solutions Buffers Collection** folder in **Reagents** in the main menu
2. Select *Object* **beta-estradiol** from the table (select button in first column)
3. Select **Delete selected** from the **Options** drop down in the table
4. Enter **duplicate** in the **Reason** field
5. **Accept**

When *Objects* (like *Experiments/Collections*) are deleted they are first moved to the trashcan, In order to be completely removed from the database they have to be deleted also from the trashcan. Alternatively, it is also possible to revert deletion from the trashcan, if something was accidentally moved here.

1. Go to the **Trashcan** under **Utilities** in the main menu
2. Select **Delete Permanently** from the **Operations** drop down in the table
3. Read the warning message
4. **Accept**

Visualization of storage positions with the Storage Manager

The openBIS storage manager offers an overview of all storages configured for the lab:

1. Select **Storage Manager** under **Utilities**
2. Select the **-80°C room A1** storage from the **Storage** list
3. Click on one of the boxes and visualize the content

It is possible to drag & drop boxes to change the position of a box inside a storage (or to a different storage). In the same way the position of a sample inside a box can be changed (this is not supported for multiple positions for the same sample).

Registration of new protocols in the Inventory

We will now register a flow cytometry and a western blotting protocols in the Methods Inventory.

Registration of a flow cytometry protocol

1. Open the **flow-cytometry-protocol.docx** file from the training material
2. Go to the ELN
3. Go to the **Flow cytometry protocols** folder in the main menu
4. Click on the **+** button in the main page
5. Copy/paste the corresponding fields from the doc file in the ELN form
6. To add the chemical as parent:
    a. Click the + button next to **Links to Materials and Methods**
    b. Select **Chemical** from the drop down
    c. Select **Name** from the **Columns** drop down
    d. Select **cycloheximide** from the table
7. **Save**

Registration of a western blotting protocol

1. Open the **western-blotting-protocol.docx** file from the training material
2. Go to the ELN
3. Go to the **Western Blotting Protocols** folder in the main menu
4. Click on the **+** button in the main page
5. Copy/paste the corresponding fields from the doc file in the ELN form
6. **Save**

Laboratory Notebook

In the laboratory notebook, usually each lab member has a personal folder (=*Space*) to organize *Projects* and *Experiments*. *Experiments* can be further divided in *Experimental Steps*. An openBIS *Experiment* is a specific scientific question and it contains *Experimental Steps* that are individual attempts to answer it.

Experimental Steps can be linked to each other (if needed) and they can also be linked to materials and methods stored in the Inventory.

Some examples:

Lab Experiment	**Corresponding openBIS data model**
Monitor decondensation upon transcriptional activation of a given insert in some strains. This experiment involves 3 different steps: 1. Make some plasmids 2. Make reporter strains for decondensation using plasmids made before–> PCR results 3. Test strains made before in different conditions -> raw data, MATLAB code	**Experiment**: Monitor decondensation upon transcriptional activation of a given insert in some strains. **Exp Step 1**: make plasmids **Exp Step 2**: make reporter strains for decondensation using plasmids made in Exp step 1 (*can be a child of Exp Step 1*) **Exp Step 3**: test strains made in Exp Step 2 using condition 1 (*can be a child of Exp Step 2*) **Exp Step 4**: test strains made in Exp Step 2 using condition 2 (*can be a child of Exp Step 2*) **Exp Step 5**: test strains made in Exp Step 2 using condition 3 (*can be a child of Exp Step 2*) Each *Experimental Step* can contain the data related to it.
Induction of a transcription factor in standard growth conditions with synthetic complete medium containing 2% of glucose. This experiment involves 3 different steps: 1. Detection of transcription factor induction by flow cytometry 2. Detection of transcription factor induction by Western blotting 3. Detection of transcription factor induction by Western blotting	**Experiment**: Induction of a transcription factor in standard growth conditions with synthetic complete medium containing 2% of glucose. **Exp Step 1**: flow cytometry **Exp step 2**: western blotting 1 **Exp Step 2**: western blotting 2 In this case we are trying different methods to detect the transcription factor, but there is no connection between them. Each *Experimental Step* can contain the data related to it.
Monitor the expression of a given gene. This experiment involves 2 steps: 1. RT-qPCR 2. Western blotting	**Experiment**: Monitor the expression of a given gene **Exp Step 1**: RT-qPCR **Exp Step 2**: Western blotting Each *Experimental Step* can contain the data related to it.

As an example, we work on a project where we study different inducible transcription factors. In this project we perform several experiments. For example, in one experiment we analyze the abundance of 4 variants of a transcription factor before and after induction. The analysis is done by western blotting.
In another experiment we induce the transcription factor in standard growth conditions and we detect it by flow cytometry and 2 types of western blotting.
In openBIS we would need to register:

1. 1 *Project*
2. 2 *Experiments*
3. 1 *Experimental Step* for the first experiment; 3 *Experimental Steps* for the second experiment.

In this tutorial we will work with **Example 2** described above and we will register 1 *Project*, 1 *Experiment* and 2 *Experimental Steps* (1 flow cytometry and 1 western blotting).

Registration of a Project

We want to register a project called **Inducible transcription factor**:

1. Select your folder in the Lab Notebook part of the main menu
2. Click the **+** button in the main page
1. Enter **Construction and characterization of a beta-estradiol-inducible transcription factor for Saccharomyces cerevisiae** in the **Description** field
2. Enter **Inducible_transcription_factor** in the **Code** field
3. **Save**

Registration of an Experiment

In the project registered before, we want to register a first experiment, called **Induction of a transcription factor in standard growth conditions with synthetic complete medium containing 2% of glucose:**

1. Select the Project folder
2. Click the **+** button in the main page
3. Enter **Induction of a transcription factor in standard growth conditions with synthetic complete medium containing 2% of glucose** in the **Name** field
4. Check **Show in project overview**
5. Enter **10.01.2019** in the **start date**
6. Enter **20.04.2019** in the **end date**
7. Enter **Analyze the transcription factor in a concentration series of inducers** in the **Experimental goals** field
8. Enter **Both variants of transcription factor tested induced in a concentration series of inducer. The variant LexA-ER-B112 is stronger than LexA-ER-B42.** in the **Experimental results** field.
9. **Save**

Registration of a first Experimental Step

Now we want to register the first *Experimental Step*, which is a flow cytometry experiment. We also want to create links to samples and protocols stored in the inventory.

1. Click the **+** button in the Experiment page
2. Enter **Detection of LexA-ER-B42 induction by flow cytometry** in the **Name** field
3. Click **Show in project overview**

Now we want to create links to materials and methods stored in the Inventory. We want to add a link to *1 media, 2 buffers, 1 yeast* and *1 protocol*. These are the samples and materials we used in this experimental step and the protocol we followed.

4. Add media:
    a. Click the **+** button next to Media
    b. Show the Media **Name**
    c. Select the only media available in the table (Columns dropdown)
5. Add buffers:
    a. Click the **+** button next to Solution/Buffer
    b. Show the **Names** of the buffers in the table (Columns dropdown)
    c. Check both buffers in the table
    d. Select **Add selected** from the **Options** dropdown in the table
6. Add yeast:
    a. Click the **+** button next to Yeast
    b. Show the **Names** of the yeasts in the table (Columns dropdown)
    c. Select the **demo** yeast
7. Add protocol:
    a. Click + next to Protocols
    b. Show the **Name** of the protocols in the table (Columns dropdown)
    c. Select the flow cytometry protocol
    d. Choose **Use as template** from the **Operation** dropdown in the table
    e. Enter **a code** in the **Code** field
    f. Accept
    g. Right click on the Protocol code and open in new tab. This is a copy of the original protocol, created in your personal folder (check the identifier). You can see that this protocol is linked to the original protocol in the inventory. In this way you can modify your local copy and leave the template untouched. If you do not need to make any modification to the protocol, you do not need to use the **Use as template** option.
8. Enter **Machine used: LSRII Fortessa** in the **Experimental description** field
9. Save

Data upload to an Experimental step

Data can be uploaded to *Experiments* or *Experimental Steps* using the same procedure.

In the same way, files can also be added to *Objects* in the Inventory (i.e. to samples or protocols).

In this case we want to upload: 1. the raw data that was obtained from the flow cytometer; 2. the R script that was used to analyze the data; 3. the final result pictures.

Upload raw data

1. Click the **Upload dataset** icon form the **menu toolbar**
2. Select **Raw data** from the **Data Set type** dropdown
3. Enter **Flow cytometry data** in the **Name** field
4. Select the **FC_LEXA-ER-B42-raw.zip** file in the **Documents** folder to upload
5. Check **Uncompress before import**
6. **Save**
7. Open the **Raw data** folder in the Experimental step to see the content

Upload the R script

1. Click the **Upload dataset** icon form the **menu toolbar**
2. Select **Attachment** from the **Data Set type** dropdown
3. Type **flow** in the **Parent** field and select the dataset that comes up in the list. This step is not necessary, but it allows you to establish a relationship between datasets. In this case we establish a connection to the raw data that was analyzed with the R script we are uploading.
4. Enter **R script** in the **Name** field
5. Select the **FC_LEXA-ER-B42-script.R** file in the **Documents** folder to upload
6. **Save**
7. Open the **Attachment** folder in the Experimental step to see the content

Upload the analyzed data

1. Click the **Upload dataset** icon form the **menu toolbar**
2. Select **Analysed data** from the **Data Set type** dropdown
3. Type **R script** in the **Parent** field and select the dataset that comes up in the list.
4. Enter **Analysis results** in the **Name** field
5. Select the **FC_LEXA-analyzed_data.zip** file in the **Documents** folder to upload
6. Check **Uncompress before import**
7. **Save**
8. Open the **Analyzed data** folder in the Experimental step to see the content

Data navigation

To navigate data stored in openBIS/ETH RDH we recommend to use software that allows to mount openBIS as a drive on your computer. Examples are:

1. Mountain Duck for MacOS (https://mountainduck.io)
2. NetDrive for Windows (https://www.nsoftware.com/sftp/netdrive/).

Files can be opened with the desired application in read-only mode.

Any other FTP solution can also be used (e.g. Cyberduck, Filezilla, etc).

Registration of a second Experimental Step

In our main experiment, called **Induction of a transcription factor in standard growth conditions with synthetic complete medium containing 2% of glucose,** we performed a flow cytometry experiment and two western blotting experiments. We now want to register one western blotting experiment as *Experimental Step* in openBIS/ETH RDH.

1. Select the Experiment **Induction of a transcription factor in standard growth conditions with synthetic complete medium containing 2% of glucose** from the Lab Notebook main menu
2. Click the + button in the main page
3. Enter **Detection of LexA-ER-B42 induction by western blotting** in the **Name** field
4. Select **Show in project overview**

Now we want to create links to some materials stored in the Inventory. We want to add a link to *1 media, 2 buffers, 2 yeasts* and *1 protocol*. These are the samples and materials we used in this experimental step and the protocol we followed.

5. Add media:
    a. Click the **+** button next to **Media**
    b. Select the only media available in the table
6. Add buffer:
    a. Click the **+** button next to **Buffer**
    b. Select the **beta-estradiol** buffer from the table
7. Add yeast:
    a. Click the **+** button next to **Yeast**
    b. Select the **demo** yeast from the table
8. Add protocol:
    a. Click + next to **Protocols**
    b. Select the **western blotting protocol** in the table

9. Enter **Analyze the full induction of LexA-ER-B42 on western blot by doing a dilution series** in the **Experimental goals** field.
10. Enter **LexA-ER-B42 full fold induction is between 128 and 256** in the **Experimental results** field
11. Add a gel picture to the Experimental results field:
    a. Select the image icon in the Experimental results text editor
    b. Go to the **Upload** tab
    c. Choose the **WB_LEXA-ER-B42-actine.png** file you received from us
    d. Click **Send it to server**
    e. Resize the width to 500
    f. Press **OK**
12. **Save**

Data and metadata exports

It is possible to export a complete lab notebook or only parts of it (*Project*, *Experiment*, *Experimental Step*, *Datasets*).

In each folder, the menu toolbar on the main form has an option to **Export metadata only** or **Export metadata+data**. We recommend to export data only if it does not exceed a few GBs.

When you export something, you will receive an email with a link to download your metadata (+data).

Th export contains folders with the same structure organization they have in openBIS. Metadata is exported to 4 different file formats: .docx, .html, .txt, .json.

Access rights assignment to a personal notebook or to a specific Project

It is possible to grant collaborators and colleagues access rights to your complete lab notebook or only to selected *Project*(s).

To grant rights to your folder:

1. Select your folder in the Lab Notebook part of the main menu
2. Click the **Manage access** icon in the main page
3. Select a role from the **Role** dropdown menu. Available roles:
    a. **Observer**: has read-only access
    b. **User**: can create and modify entities, but cannot delete anything
    c. **Admin**: can create, modify and delete entities
4. Select **User** from the **grant to:** dropdown
5. Enter **the username of a registered user**
6. **Grant access**

Searching the ELN

openBIS/ETH RDH offer 3 options for searching:

1. **Text search** on all fields stored in the database. Searches can be refined using the Advanced search.
2. **BLAST** search for sequence comparison accross sequences stored in the database.
3. **Data Set Files** search. This should be used to find files uploaded as datasets by their name.

Generic text search

We want to find all the flow cytometry *Experimental Steps* registered by you.

1. Enter **flow cytometry** in the **Global search** field, on top of the main menu
2. Select **Object** in the **Search For** dropdown
3. Click the + button in the **Criteria** table
4. Select **Property** from the **Field Type** dropdown
5. Select **Object Type** from the **Field Name** dropdown
6. Enter ***STEP*** in the **Field Value** field
7. Click again the + button in the **Criteria** table
8. Select **Property** from the **Field Type** dropdown
9. Select **Registrator** from the **Field Name** dropdown
10. Enter **your username** in the **Field Value** field
11. Run the search

In this case, the search returns only one item, but in a similar way, you can run complex searches by combining multiple search criteria.

Data Set Files search

We want to find a file that contains “script” in the name.

1. Enter **script** in the **Global search** field, on top on the main menu
2. Select **Data Set File** from the dropdown next to it

The search returns the dataset that contains the R file script we uploaded to out flow cytometry experiment before.

Management of Lab orders with openBIS & ETH RDH

Managing orders with openBIS & ETH RDH

openBIS/ETH RDH offer the possibility to manage orders of products bought in the lab.

Collections of suppliers and products need to be created. Each product need to have one supplier set as parent. For this reason, we need to register first the suppliers and afterwards the products.

All users in the lab can create product requests, but only the lab admin can process orders.

Creation of Collections folders in Stock Catalog

We need to create 3 *Collection* folders in the **Stock Catalog** folder:

1. Products:
    a. Products Collection
2. Suppliers:
    a. Suppliers Collection
3. Requests:
    a. Requests Collection

Registration of Products Collection folder

1. Select the **Stock Catalog** folder from the main menu
2. Click the **+** button in main page
3. Enter **Products** in the **Code** field
4. **Save**

5. Select the **Products** folder
6. Select Collection from the drop down
7. Enter **Products_collection** in the **Code** field
8. Enter **Products Collection** in the **Name** field
9. Select **Product** from the **Default Object Type** drop down
10. **Save**

Registration of Suppliers Collection folder

1. Select the **Stock Catalog** folder from the main menu
2. Click the **+** button in main page
3. Enter **Suppliers** in the **Code** field
4. **Save**

5. Select the **Suppliers** folder
6. Select Collection from the drop down
7. Enter **Suppliers_collection** in the **Code** field
8. Enter **Suppliers Collection** in the **Name** field
9. Select **Supplier** from the **Default Object Type** drop down
10. **Save**

Registration of Requests Collection folder

1. Select the **Stock Catalog** folder from the main menu
2. Click the **+** button in main page
3. Enter **Requests** in the **Code** field
4. **Save**

5. Select the **Requests** folder
6. Select Collection from the drop down
7. Enter **Requests_collection** in the **Code** field
8. Enter **Requests Collection** in the **Name** field
9. Select **Request** from the **Default Object Type** drop down
10. **Save**

Creation of Collections folders in Stock Orders

We need to create 1 *Collection* folder in the **Stock Order** folder:

1. Orders:
    a. Orders Collection

Registration of Orders Collection folder

1. Select the **Stock Orders** folder from the main menu
2. Click the **+** button in main page
3. Enter **Orders** in the **Code** field
4. **Save**

5. Select the **Orders** folder
6. Select Collection from the drop down
7. Enter **Orders_collection** in the **Code** field
8. Enter **Orders Collection** in the **Name** field
9. Select **Order** from the **Default Object Type** drop down
10. **Save**

Registration of suppliers

First of all we need to register the suppliers. We will register 2 suppliers: *Fluka, Sigma-Aldrich*.

1. Go to the **Suppliers Collection** folder in **Stock Catalogue**
2. Click the **+** button in the main page
3. Enter **Fluka** in the **Name** field
4. Choose **English** as **Company language**
5. Choose **Email** as **Preferred Order Method**

6. **Save**

7. Go to the **Suppliers Collection** folder in **Stock Catalogue**
8. Click the **+** button in the main page
9. Enter **Sigma-Aldrich** in the **Name** field
10. Choose **English** as **Company language**
11. Choose **Email** as **Preferred Order Method**
12. **Save**

Registration of products

Now we will register 2 products: *DMSO, cycloheximide*. Each product needs to have a supplier assigned as parent.

1. Go to the **Product Collection** folder in **Stock Catalog**
2. Click the **+** button on the main form
3. Enter **DMSO** in the **Name** field
4. Enter **12345** in the **Catalog Number** field
5. Enter **90** in the **Estimated price** field
6. Select **CHF** as **Currency**
7. Enter **1L** in the **Size of item** field
8. Add a supplier:
    a. Click the **+** button next to **Suppliers**
    b. Select **Name** from the **Columns** dropdown in the table
    c. Select **Sigma-Aldrich** from the list
9. **Save**

10. Go to the **Product Collection** folder in **Stock Catalog**
11. Click the **+** button on the main form
12. Enter **Cycloheximide** in the **Name** field
13. Enter **67890** in the **Catalog Number** field
14. Select **CHF** as **Currency**
15. Enter **100** in the **Estimated price** field
16. Enter **1.5g** in the **Size of item** field
17. Add a supplier:
    a. Click the **+** button next to **Suppliers**
    b. Select **Sigma-Aldrich** from the list
18. **Save**

Creation of a request

We are running out of DMSO, so we need to order it. We want to order 2 bottles. Anyone in the lab can create a request:

1. Go to the **Request Collection** folder in **Stock Catalog**

2. Click on the **+** button in the main form
3. Enter **DMSO request** in the **Name** field
4. Select **not yet ordered** in the **Oder Status** dropdown
5. Add a product:
    a. Click the + button next to **Products**
    b. Select **DMSO** from the list
    c. Enter **2** in the **Quantity** field
6. **Save**

Creation of an order

The lab manager will now process the request and create an order for DMSO.

1. Go to **Orders Collection** in **Stock Orders**
2. Click on the **+** button in the main form
3. Enter **2019-05-13 Order** in the **Name** field
4. Enter your name in the **Ship to** field
5. Enter your name in the **Bill to** field
6. Enter **Demo street 25** in the **Ship Address** field
7. Enter **180** in the **Price Paid** field
8. Add a request to the order:
    a. Click the **+** button next to **Requests**
    b. Select the **DMSO request** from the table
9. **Save**

In the Order form you can print the order to a text file. This can be sent as email attachment to the company.

10. Now edit the **order**
11. Change the **Order Status** to **ordered**
12. **Save**

This automatically changes the order status in the corresponding request. If you now create a new order, this request will no longer be available to be selected.

It is possible to create templates for orders in the Settings, so the shipping information does not need to be filled in every time:

1. Go to **Settings** under **Utilities**
2. **Edit**
3. Scroll down to the **Orders** section
4. Click on the **Order template** in the table
5. **Edit** the form
6. **Save**