

SyMBA Tutorial

Workshop on “Data Handling for Biogerontology Research”

29-30 April 2010, Newcastle-upon-Tyne

Allyson Lister

CISBAN

I. Background

The original version of SyMBA is used within CISBAN to store various types of raw data created by the experimentalists. Its purpose was as an archive connecting the data to a minimally-relevant set of metadata, or information about the data.

There were limitations with the first version so, in 2010, SyMBA 2 was created. This tutorial covers how SyMBA 2 works and may be used. The purpose of this tutorial is to show how a straightforward web application can be created and used to archive data and metadata for a specific research group.

The purpose of SyMBA is not to replace deposition in public repositories, but instead to provide a central resource for storing and archiving data produced within a research centre, and for searching and retrieving metadata about those data files.

High throughput experimentation techniques in the life sciences contribute to the life-science data deluge. In addition to the large volumes of heterogeneous data, there is a need to integrate these diverse datasets to build a more systems-level view of the organisms under study. These datasets must be archived, curated with appropriate metadata, and made available in a suitable form for subsequent analysis and integration. Community-endorsed data standards for the content, syntax and semantics of life-science data have and are being developed as a data management strategy. SyMBA integrates both multiple 'omics' data types and information about experiments in a single application.


Do not be afraid to experiment. The version of SyMBA that you are working on has no connection to a real database: it is running in memory only, and any data you put in, including your username, will only be available for this session. Further, all information you add will be shared by the other users of the session, so please do not delete anyone else's work.





II. Getting Started


Website for the tutorial:

<http://bsu.ncl.ac.uk:8081/symba/net.sourceforge.symba.web.InvestigationManipulator/index.html>

When you first visit the SyMBA tutorial web page, you are presented with a screen that looks similar to this:

**SyMBA 2**

Not logged in



SyMBA is an **archive** that facilitates metadata integration and data storage. It **stores knowledge about experimental data** in a user-friendly and computationally-amenable way.

It is designed to **prevent loss**, deletion or accidental modification of primary data and metadata, while providing convenient manual and computational access for **standards-compliant publication, sharing and analysis**.

Login as: ([add new user and log in](#))

[\[Hide this panel\]](#)

Your Status
Help
SyMBA Status
2 Investigations
[\[Refresh SyMBA Status\]](#)

Your first task is to create a username for yourself. As this is the in-memory version of SyMBA 2, you will not need a password, though of course this option is available in the database version of the application.

To create your username, simply click on the "add new user and log in" link in the centre panel, fill out your details in the resulting popup, and click "Save Contact":

SyMBA is an **archive** that facilitates metadata integration and data storage. It **stores knowledge about experimental data** in a

First Name:

Last Name:

Email Address:

By clicking on the "Save Contact" button, you will save this contact in the database. [Save Contact](#)

(Click outside the box to cancel and close.)

[\[Hide this panel\]](#)

Your Status

Once you have done this, your user will be saved within SyMBA and you will be logged in. Additionally, the actions “add”, “view” and “get” are enabled and you have full access to SyMBA features.

III. View Existing Templates and Investigations

We have pre-loaded one template representing a theoretical microarray investigation, and one experiment that has no information at all in it yet.

In this section of the tutorial, you will get used to viewing pre-existing investigations and become familiar with the SyMBA interface.

Now that you have logged on, the “view” button is enabled in the top left of the screen. Further, on the right-hand side of the screen the summary of the number of investigations is now clickable. Click on either one to display a list of pre-existing templates and investigations:

SyMBA 2

[add](#) [view](#) [get](#) [help](#) Allyson Lister [Logout](#)

SyMBA

SyMBA is an **archive** that facilitates metadata integration and data storage. It **stores knowledge about experimental data** in a user-friendly and computationally-amenable way.

It is designed to **prevent loss**, deletion or accidental modification of primary data and metadata, while providing convenient manual and computational access for **standards-compliant publication, sharing and analysis**.

[\[Hide this panel\]](#)

Your Status
Help
SyMBA Status
[2 Investigations](#)
[\[Refresh SyMBA Status\]](#)

Either method will change the centre panel to display the investigations stored within SyMBA:

[Copy](#) [Delete](#)

☐ [My Example Investigation \(provided by Alice Smith\)](#)

☐ [template: Example multi-strain Microarray Investigation \(provided by Allyson Lister\)](#)

Click on both of these investigations, and see how they differ. The first is a completely empty, writeable investigation. If you wish to modify this first investigation, select its radio button and choose “copy” in order to make your own copy to manipulate:

[Copy](#) [Delete](#)

☒ [My Example Investigation \(provided by Alice Smith\)](#)

☐ [template: Example multi-strain Microarray Investigation \(provided by Allyson Lister\)](#)

The second is a read-only template which we will be using in the later stages of the tutorial. In particular, familiarise yourself with this template. Click on this template now, and take a look at its structure. It provides a protocol with sub-steps, but all sections are read-only. This protocol is generic, and waiting to be copied and then extended by users:

View Existing Investigation

An **Investigation** consists of one or more experiments. Investigations are containers for all experiments that relate to a **single** hypothesis and conclusion.

Investigation Title: Example multi-strain Microarray Investigation

Investigation Hypothesis: Examination of the effect of certain conditions on yeast strains over time.

Investigation Conclusion(s):

Data Owner: Allyson Lister (a.l.lister@newcastle.ac.uk)

Experimental Steps

Add Top-Level Step

Experiment Run for Strain X

1 parameter [\(collapse\)](#)

strain : hasIdentifier : :

Microarray Time Series Point X

1 parameter [\(collapse\)](#)

TimeAfterInoculation : is : : minutes

Microarray Assay Repeat X

3 parameters [\(collapse\)](#)

repeatNumber : is : :

microarrayChip : hasBrand : :

microarrayChip : hasModel : :

☒ Set As Template

Save

Save and Finish

Cancel

As you can see, nothing about this template can be changed. How, then, do we make use of it? How can we start adding our own parameters, material and data files to this template? The answer is that we make a copy of the template, and modify that.

IV. Copy a Template to Add an Investigation

1. The first step is to make a copy of the template for your own use. Click on the “view” button in the top right of the screen. This will take you back to the list of existing investigations you looked at in the previous step.
2. Click on the radio button next to the name of the template to select it, and then click on the “copy” button:

Copy

Delete

☐ [My Example Investigation \(provided by Alice Smith\)](#)
☒ [template: Example multi-strain Microarray Investigation \(provided by Allyson Lister\)](#)

3. Once you have copied the template, a writeable version of the template will be created with a random number inserted at the end of the investigation title to distinguish it from the original investigation template:

Copy

Delete

☐ [Example multi-strain Microarray Investigation 923 \(provided by Allyson Lister\)](#)
☐ [My Example Investigation \(provided by Alice Smith\)](#)
☐ [template: Example multi-strain Microarray Investigation \(provided by Allyson Lister\)](#)

- Click on your copy of the investigation. You will know that it is your investigation, as the username in the “provided by” field is yours. This will show the detailed view of your copied investigation.
- Let's create two top-level experimental steps: one for a strain called “wild type”, and another for a strain called “mutant 123”. To do this, we will start by modifying the existing experimental step called “Experiment Run for Strain X” to suit the values for the wild type.
- Click on “Experiment Run for Strain X”. When you click anywhere in this box, you are presented with an editable dialogue for this step:

Title of Step: Experiment Run for Strain X

Output Data

Browse...

Parameters

Parameter Name, e.g. Camera: Strain

Relationship, e.g. has brand: hasIdentifier

Value, e.g. Canon 5D:

Units (optional), e.g. centimetres: X

[Add Parameter](#)

Input Materials


[0 input materials](#) + - ✕

Output Materials

[0 output materials](#) + - ✕

Accept Changes Cancel Changes

- You'll notice that, as this step comes directly from a template, you cannot modify the first two fields of any pre-existing parameters. This is to protect any templated parameters. However, if you add new parameters, you can modify them as you wish.
- Change the name of the step to something more specific for the wild type strain, e.g. “Experiment Run for Wild Type Yeast”.
- Create an identifier of your choice for this yeast wild type strain by filling in the “value” field of the templated parameter.
- Click on “Accept Changes” to save locally and return to the main screen.
- If you wish, you may save your work so far by clicking on the “Save” button (the “Save and Finish” button will instead save your work and leave the edit screen, which isn't what you want yet). Any green boxes around your modified steps will be removed when the “Save” button is pressed to show that those changes have been accepted.
- Edit the first sub-step of the top-level by clicking on it. Provide details for its name (e.g. “Microarray Time Series Point 0”) and values for its parameter.
- Create a record of the creation of a microarray by editing the child of the Time Point 0 step, adding values for its parameters and creating an appropriate name.

14. Imagine we ran another microarray at 60 minutes past the start time. We therefore want to have an additional time point step. We just need to copy the Time Point 0 step we just updated. To do that, click on  that is beside the Time Point step to copy it and all of its metadata:

Experimental Steps













































Add Top-Level Step

Experiment Run for Wild Type Strain

1 parameter (collapse)

strain : hasIdentifier : wild type: 1234

⋮

Experimental Steps

Add Top-Level Step


Experiment Run for Wild Type Strain
[1 parameter \(expand\)](#)



Microarray Time Series Point 0
[1 parameter \(expand\)](#)



Microarray Assay Repeat 1
[3 parameters \(expand\)](#)



Microarray Time Series Point 60
[1 parameter \(expand\)](#)



Microarray Assay Repeat 1
[3 parameters \(expand\)](#)


Experiment Run for Mutant 123
[1 parameter \(expand\)](#)



Microarray Time Series Point 0
[1 parameter \(expand\)](#)



Microarray Assay Repeat 1
[3 parameters \(expand\)](#)



Microarray Time Series Point 60
[1 parameter \(expand\)](#)



Microarray Assay Repeat 1
[3 parameters \(expand\)](#)

18. Click on “Save and Finish” to complete this exercise.

V. Create an Investigation from Scratch

If you have time, you can click on the “add” button, and select “Add New”. Try creating your own experiment, and playing with the settings.



SyMBA 2



Allyson Lister ([Logout](#))

[Copy](#) [Delete](#)

- [Example multi-strain Microarray Investigation 923 \(provided by Allyson Lister\)](#)
- [My Example Investigation \(provided by Alice Smith\)](#)
- [template: Example multi-strain Microarray Investigation \(provided by Allyson Lister\)](#)

[\[Hide this panel\]](#)

Your Status

Example multi-strain Microarray Investigation 923 saved.

Help

Example multi-strain Microarray Investigation 923 Status

[Add New](#)

Example multi-strain Microarray Investigation 923 (provided by Allyson Lister) [Copy](#)

[View Investigations](#)

[Contact us](#)

