

# pyLabbook Manager Interface

## Quick Start

You need: python3.6+, numpy, pandas, sqlite3, xlrd, openpyxl, tkinter

Ideally: pandas 0.24.0+, but you can manage with lower version numbers.

1. Obtain a full pyLabbook distribution by cloning from <https://github.com/Nhydrazine/pyLabbook>
2. Open a terminal window
3. Go to the pyLabbook root folder using `cd`
4. Run the testme.py script with `python testme.py`

```
sys ..... OK
python ..... 3.6.5
```

### Checking for Required Modules

```
os ..... OK
re ..... OK
shutil ..... OK
numpy ..... OK
pandas ..... OK
sqlite3 ..... OK
xlrd ..... OK
openpyxl ..... OK
```

### Checking for Manager Modules

```
tkinter ..... OK
tkinter.messagebox ..... OK
tkinter.scrolledtext ..... OK
tkinter.filedialog ..... OK
tkinter.ttk ..... OK
```

These are required for the manager to work properly.

### Checking for Manager Widgets

```
guiWidgets ..... OK
ttk.Frame ..... OK
ttk.Label ..... OK
ttk.Entry ..... OK
ttk.Button ..... OK
ttk.Checkbutton ..... OK
ttk.Combobox ..... OK
ttk.Treeview ..... OK
```

If missing, you can either:

(a) install a newer version of python

(b) install yourself: <https://tkdocs.com/tutorial/install.html>

### Checking pyLabbook distribution at /Users/nic/github/pyLabbook

```
/Users/nic/github/pyLabbook/python/pyLabbook/labbooks OK
/Users/nic/github/pyLabbook/python/PyLabbook/protocols OK
/Users/nic/github/pyLabbook/databases OK
/Users/nic/github/pyLabbook/repositories OK
/Users/nic/github/pyLabbook/exports OK
/Users/nic/github/pyLabbook/imports OK
/Users/nic/github/pyLabbook/python/pyLabbook/pyLabbook.py OK
/Users/nic/github/pyLabbook/python/pyLabbook/pyLabbook.py OK
/Users/nic/github/pyLabbook/python/pyLabbook/core.py OK
/Users/nic/github/pyLabbook/python/pyLabbook/core.py OK
/Users/nic/github/pyLabbook/python/operations.py OK
```

### Checking pyLabbook modules and classes

```
pyLabbook ..... 0.b.1
pyLabbook.pyLabbook ..... OK
pyLabbook.pyProtocol ..... OK
pyLabbook.core ..... OK
pyLabbook.SQLEngines.engine ..... OK
pyLabbook.SQLEngines.manager ..... OK
SQLITE3 engine ..... OK
```

Warning: you may experience some odd behavior realted to:

--> update pandas to version 0.24.0 or higher

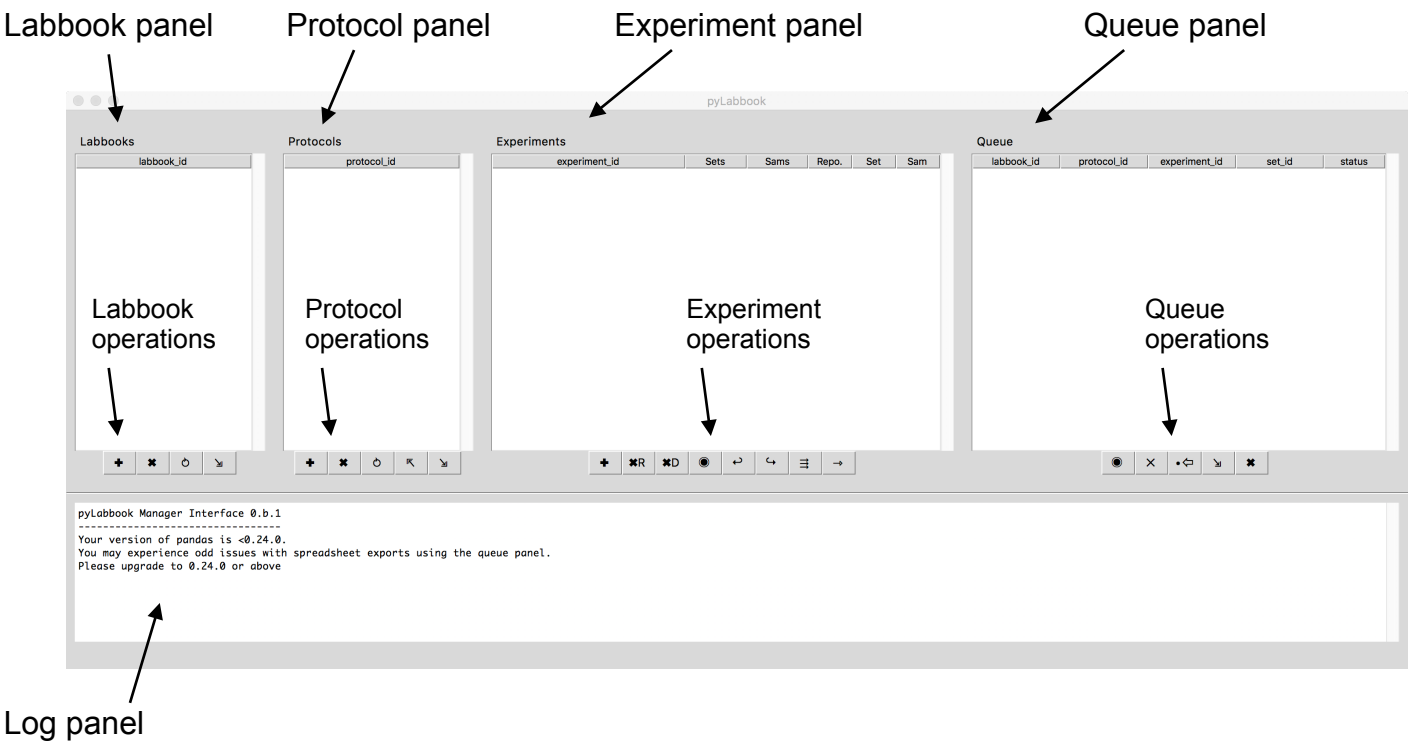
Done

5. If all good, run the manager script with `python manager.py`

Missing modules can be installed with `pip`, `conda`, or whatever you use to install python modules.

# pyLabbook Manager Interface

## Main Window



### Labbook panel

Displays the labbooks that you have created or installed.

### Protocol panel

Displays the protocols that you have created or installed.

### Experiment panel

Displays the experiments that belong to a targeted labbook and a targeted protocol.

### Queue panel

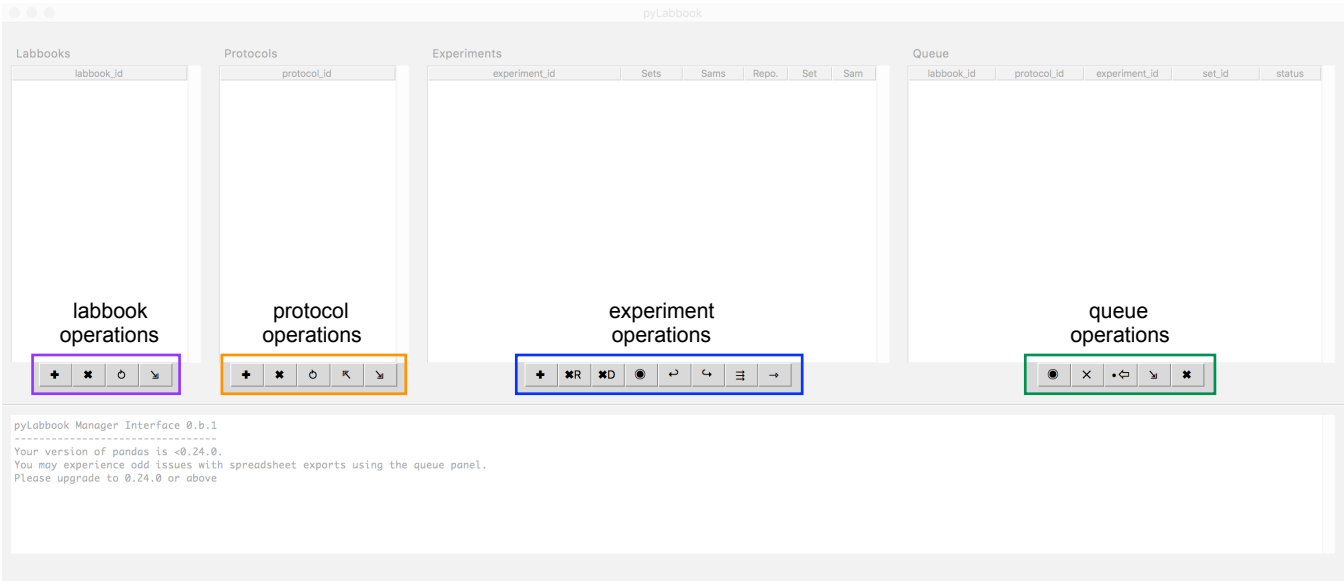
Displays experiment/set identities for data to be transferred or exported.

### Log panel

Report of actions and results/status.

# pyLabbook Manager Interface

## Main Window



**Create Labbook** with or without importing an existing database.



**Delete Labbook** that is highlighted.



**Refresh** list of labbooks.



**Export** the database of the highlighted labbook.



**Create Protocol.**



**Delete Protocol** that is highlighted.



**Refresh** protocol list.



**Import** protocol.



**Export** protocol.



**Initialize** new experiment.



**Delete** experiment repository.



**Delete** experiment database records.



**Target** the highlighted labbook and protocol.



**Store** repository data into database.



**ReStore** repository data from database.



**Queue all** displayed experiments.



**Queue highlighted** experiments.



**Target** highlighted labbook.



**Clear** queue list.



**Transfer** queued data to targeted labbook database.



**Export** queued data to spreadsheet files.

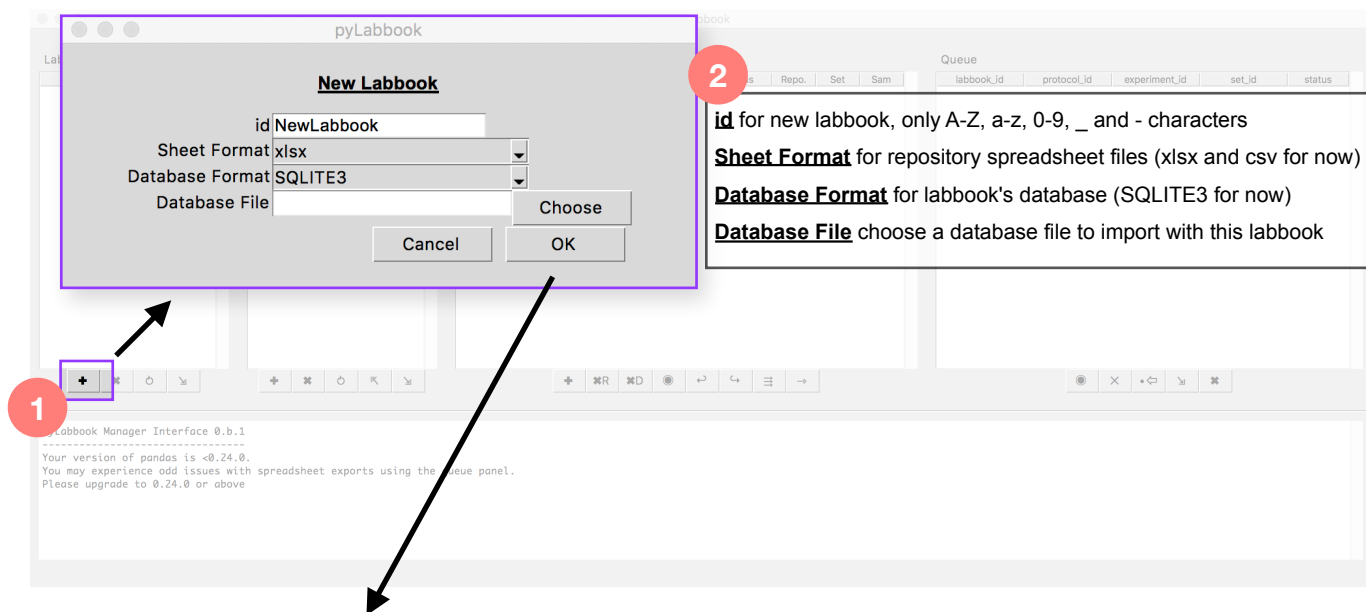


**Remove** highlighted item from queue.

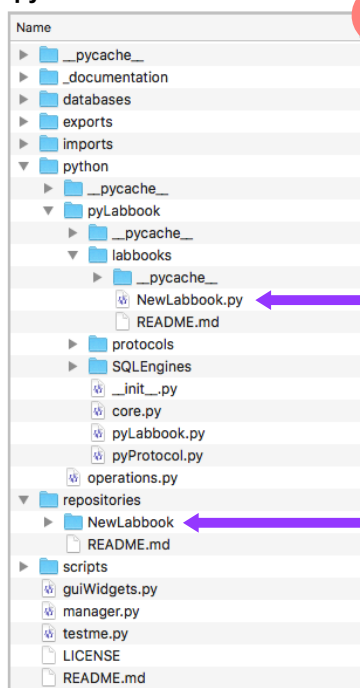
**!** These operations result in the loss of data and cannot be undone.

# pyLabbook Manager Interface

## Creating a Labbook



### pyLabbook distribution folder



labbook python file in python/pyLabbook/labbooks/

This python file extends the pyLabbook.pyLabbook class and describes the labbook and the locations of its repository and database files.

labbook repository folder in repositories/

This folder contains a substructure that organizes all of your experimental data by protocol and experiment as spreadsheet files. These files are intended for data entry purposes and for temporary access to your data.

**NOTE:** Database file and additional repository structure will appear when data is added to the labbook.

**NOTE:** You will only have access to data from an imported database when you obtain the corresponding protocol file.

# pyLabbook Manager Interface

## Creating a Protocol

**1** Create a new protocol

**2** id for new protocol, only A-Z, a-z, 0-9, \_ and - characters

**3** fields for entering new column definitions in SET table

**3** fields for entering new column definitions in SAMPLE table

**4**

- +** Create new column from values entered in fields
- ✕** Delete highlighted column in list
- ↑** Move highlighted column up in list
- ↓** Move highlighted column down in list
- 🏠** Pop/edit highlighted column from list, back into entry fields for editing

**5**

### Field Properties (applies to both SET and SAMPLE tables)

**name** the name of the field, A-Z, a-z, 0-9, \_ and - characters only.

**type** type of data allowed in field:

- TEXT includes all characters and can be any length.
- DATE is treated as TEXT.
- INTEGER is any whole integer number.
- REAL is any floating point number.
- NUMERIC is treated as a REAL.

**NN** stands for **not null**. If checked, every record must supply a value for this field.

**UNQ** stands for **unique**. If checked, every record must supply a unique value for this field.

**Default** is a default value to use when no value is provided. This must be compatible with the field's **type**.

**Description** is used to describe the field and/or its values.

# pyLabbook Manager Interface

## Creating a Protocol

Specify the SET and SAMPLE table fields

The screenshot shows the pyLabbook Manager interface for creating a protocol. The protocol ID is 'inhibitorProtocol'. The interface is divided into two main sections: 'Set Fields' and 'Sample Fields'.

**Set Fields**

name	type	NN	UNQ	default	description
subject	TEXT	<input checked="" type="radio"/>	<input type="radio"/>		id or name of the subject being tested
subject_concentration	REAL	<input checked="" type="radio"/>	<input type="radio"/>		final concentration of subject
subject_concentration_units	TEXT	<input type="radio"/>	<input type="radio"/>		units for subject concentration
inhibitor	TEXT	<input checked="" type="radio"/>	<input type="radio"/>		name of inhibitor
inhibitor_max_concentration	REAL	<input checked="" type="radio"/>	<input type="radio"/>		maximum concentration of inhibitor in titration
inhibitor_concentration_units	TEXT	<input type="radio"/>	<input type="radio"/>		units for inhibitor concentration
fold_dilution	TEXT	<input type="radio"/>	<input type="radio"/>		fold dilution across inhibitor titration series
operator	TEXT	<input checked="" type="radio"/>	<input type="radio"/>		initials of operator
date	TEXT	<input checked="" type="radio"/>	<input type="radio"/>		date of experiment (YYYYMMDD)
notes	TEXT	<input type="radio"/>	<input type="radio"/>		notes

**Sample Fields**

name	type	NN	UNQ	default	description
type	TEXT	<input checked="" type="radio"/>	<input type="radio"/>		D for dose, N for normal control, B for background control
dilution_id	INTEGER	<input checked="" type="radio"/>	<input type="radio"/>		position of sample in inhibitor titration series (0 for N)
value	REAL	<input checked="" type="radio"/>	<input type="radio"/>		measured signal value

The interface includes a 'Labbooks' sidebar on the left and a 'New Protocol' dialog box in the background. The bottom of the window has 'Cancel' and 'OK' buttons.

- **Order of fields** is the order that they will appear in spreadsheets, database displays and python interfaces. The order of the fields **will not effect your data**, but odd orders can make data entry cumbersome. Be sure to take a moment to order your fields in an intuitive way.

- **Protocols are permanent** and cannot be edited once created. *Take the time to think about your data structure design before committing data to it - it is worth it.*

- **You only need to create a protocol once.** If carefully planned you may never have to think about the structure again. So take the time to do it right.

- **Data can be mapped to new protocols.** In the event that you really do need to add or alter the structure of a protocol's data, you can use the python interface to map your old data into a new protocol structure.

# pyLabbook Manager Interface

## Initialize an Experiment

1 Highlight your labbook and protocol by clicking on them

2 Target them to the experiment panel by clicking the target button

3 The targeted labbook.protocol shows up above the experiment panel

4 Then initialize a new experiment for the targeted labbook.protocol

5 Enter an experiment id A-Z, a-z, 0-9, \_ and - characters are allowed, try: ME20190101A

6 experiment will show up in the experiment panel list

### pyLabbook distribution folder

labbook database

experiment_id	Sets	Sams	Repo.	Set	Sam
ME20190101A	0	0			

# sets in SET table

# samples in SAMPLE table

sample file exists

set file exists

repository folder exists

experiment repository files have also been created

NewLabbook's repository for inhibitorProtocol files

experiment folders for inhibitorProtocol experiments

set and sample files for inhibitorProtocol, experiment ME20190101A

# pyLabbook Manager Interface

## Data Entry

1 Using your favorite spreadsheet editor, open the SETS file and enter relevant experimental conditions and information

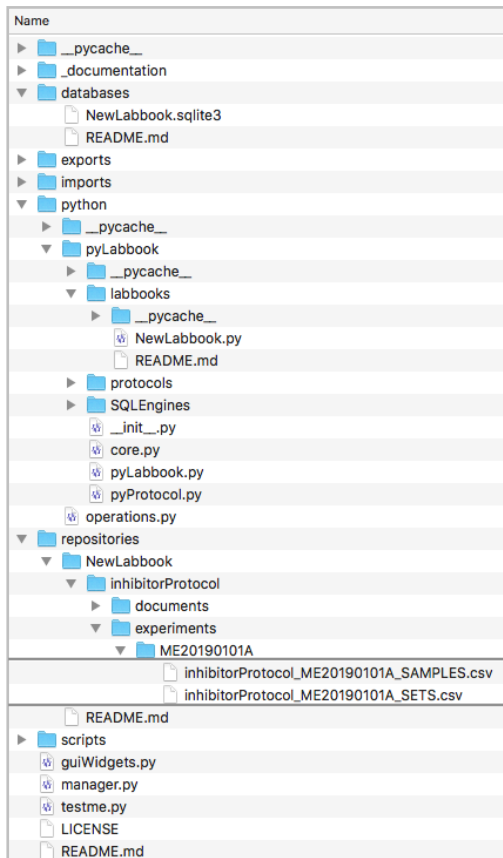
set_id	subject	concentration	inhibitor	inhibitor_max_concentration	inhibitor_concentration_units	fold	dilution	operator	date	notes
1	Subject A	20 U/mL	Inhibitor A	20 nM				5 JMW	20190101	setup by JMW, CKL performed inoculation
2	Subject A	20 U/mL	Inhibitor B	50 nM				5 JMW	20190101	setup by JMW, CKL performed inoculation
3	Subject B	20 U/mL	Inhibitor A	20 nM				5 JMW	20190101	setup by JMW, CKL performed inoculation
4	Subject B	20 U/mL	Inhibitor B	50 nM				5 JMW	20190101	setup by JMW, CKL performed inoculation
5	Subject C	20 U/mL	Inhibitor A	20 nM				5 CKL	20190101	
6	Subject C	20 U/mL	Inhibitor B	50 nM				5 CKL	20190101	

2 Open the SAMPLES file and fill in experimental measurement results. Use cut/paste strategies described later for rapid formatting, or use python script(s) to automatically process instrument result files.

All data for set 1  
a complete dose-effect  
curve for Subject A with  
Inhibitor A

N Normal control (activity without inhibitor)  
D Dosed samples with decreasing inhibitor  
concentrations  
B Background control (signal without activity)

### pyLabbook distribution folder

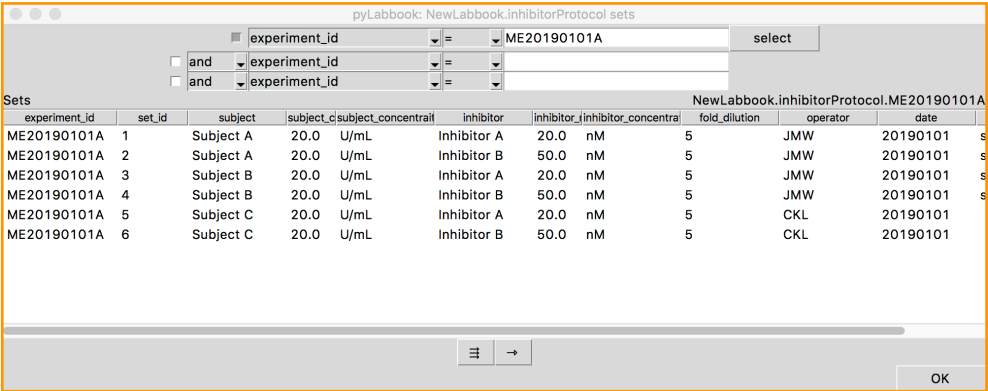
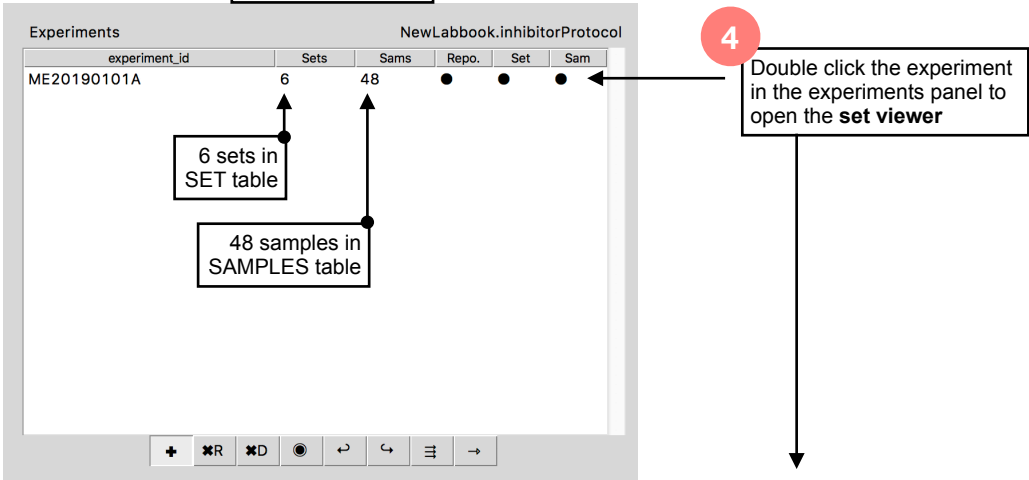
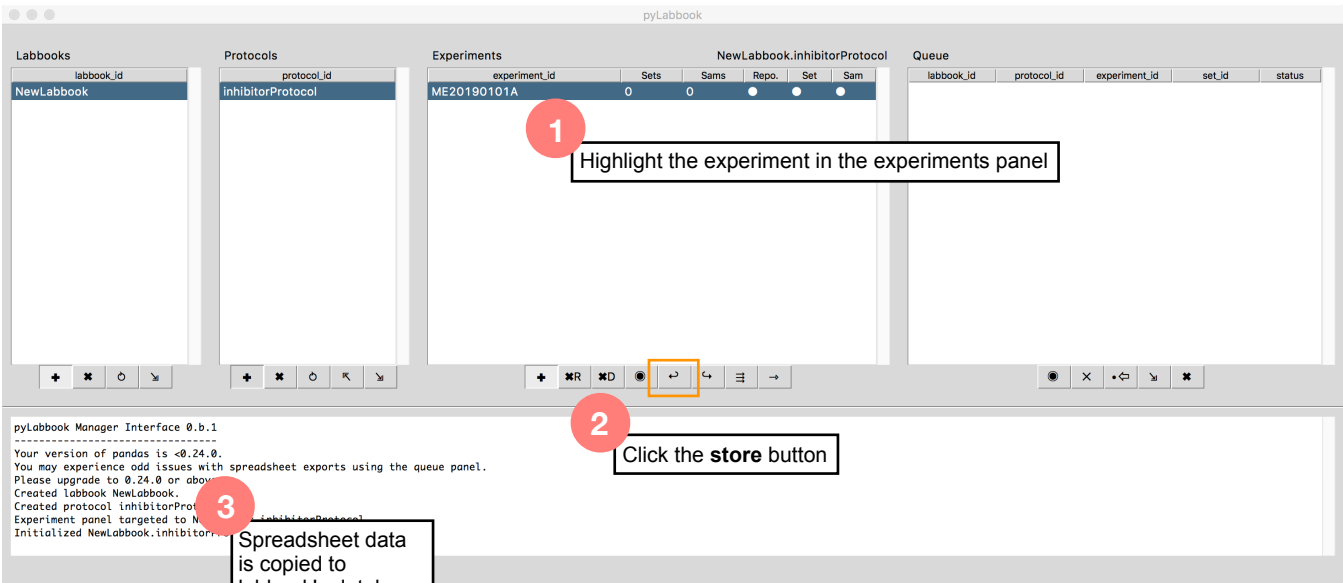


set_id	sample_id	replicate	type	dilution_id	value
1	1	1	1 N	0	56266
1	1	2	1 D	1	3022
1	1	3	1 D	2	8524
1	1	4	1 D	3	8775
1	1	5	1 D	4	22630
1	1	6	1 D	5	17666
1	1	7	1 D	6	55519
1	1	8	1 B	0	567
1	2	1	1 N	0	179865
1	2	2	1 D	1	7220
1	2	3	1 D	2	5730
1	2	4	1 D	3	15035
1	2	5	1 D	4	15557
1	2	6	1 D	5	43380
1	2	7	1 D	6	42213
1	2	8	1 B	0	582
1	3	1	1 N	0	45191
1	3	2	1 D	1	3766
1	3	3	1 D	2	2824
1	3	4	1 D	3	6904
1	3	5	1 D	4	6595
1	3	6	1 D	5	20473
1	3	7	1 D	6	13311
1	3	8	1 B	0	578
1	4	1	1 N	0	43940
1	4	2	1 D	1	3311
1	4	3	1 D	2	2017
1	4	4	1 D	3	6696
1	4	5	1 D	4	7434
1	4	6	1 D	5	18346
1	4	7	1 D	6	13848
1	4	8	1 B	0	646
1	5	1	1 N	0	115497
1	5	2	1 D	1	8822
1	5	3	1 D	2	5323
1	5	4	1 D	3	18427
1	5	5	1 D	4	16420
1	5	6	1 D	5	44241
1	5	7	1 D	6	50542
1	5	8	1 B	0	512
1	6	1	1 N	0	61355
1	6	2	1 D	1	4620
1	6	3	1 D	2	5047
1	6	4	1 D	3	10206
1	6	5	1 D	4	13362
1	6	6	1 D	5	27772
1	6	7	1 D	6	26303
1	6	8	1 B	0	578



# pyLabbook Manager Interface

## Data Storage



# pyLabbook Manager Interface

## Set Viewer

The screenshot shows the 'pyLabbook: NewLabbook.inhibitorProtocol.sets' window. At the top, there is a search bar with a dropdown menu showing 'experiment\_id' and a value 'ME20190101A'. Below this is a table with columns: experiment\_id, set\_id, subject, subject\_c, subject\_concentrat, inhibitor, inhibitor\_i, inhibitor\_concentra, fold\_dilution, operator, and date. The table contains 6 rows of data. Annotations with arrows point to various parts of the interface:

- 'include up to three criteria, check to activate' points to the 'and' checkboxes.
- 'column to apply criteria to' points to the 'experiment\_id' dropdown.
- 'logic to apply' points to the '=' operator.
- 'value' points to the 'ME20190101A' text field.
- 'apply' points to the 'select' button.
- 'filter database results for all sets belonging to this protocol and labbook' points to the search bar area.

Below the table, there are two buttons: 'Queue all displayed sets' (with a list icon) and 'Queue highlighted sets' (with a right arrow icon). An 'OK' button is located at the bottom right of the window.

Annotations for the buttons:

- 'Queue all displayed sets' points to the list icon button.
- 'Queue highlighted sets' points to the right arrow button.
- 'closes the set viewer window' points to the 'OK' button.

- **Current logic is based on sqlite.** This includes the *like* logical operator where you can use the % symbol to specify "any character at this position" and the \_ symbol to indicate "anything of any length here". For example, %ello will match "hello", "mello" and "yello", while "hel\_" will match any word or phrase that begins with the letters "hel".

- **Logic and values should be consistent with field data type.** Specifying a > or < operator on a TEXT field will result in unexpected results or errors.

- **The set viewer does not edit data.** The set viewer is not intended to edit the values in the database. The database is intended to be a permanent record. To do this, you can edit the repository file(s) and **store** them again to overwrite, or you can use a sqlite database GUI (I recommend SQLiteStudio).

# pyLabbook Manager Interface

TO BE COMPLETED



