The ~~ILCI JupyterHub~~ ~~Breeding Analytics Hub~~ **Crop Improvement Analytic Platform** is a cloud-based environment where software tools, code, documentation, and data are available in one place.

CIAP objectives:

- Co-create a collaborative environment for working together across institutions.
- Co-design, develop, and test custom software tools across institutions.
- Provide access to data, tools and analytic pipelines.
- Provide computational resources.
- Promote reproducible data science projects.
- Provide a platform for teaching and training.

The Hub is a managed environment:

- Software, tools, and packages are curated, installed and kept up to date.

- This includes custom R packages and web services developed specifically for ILCI researchers.

- It is dynamic: new tools and customizations can be developed and added to suit users needs.

The Hub is a shared space for collaboration, tool development, teaching and learning:

- Everyone is on the same server and in the same environment.
- Pass and share notebooks and data across users and institutions.
- Use templates, pre-populated notebooks that serve as tutorials and writeable notebooks.
- Use the platform as a place to develop and test new tools across many users.

Computation is done on the cloud:

- Users aren’t limited by the capacity of their computer or local server.
- Tools to submit large jobs in the background.
- Directories, data, and code are easily shared with other Hub users.

The Hub makes use of computational notebooks:

- Code and documentation are recorded in one place.

- Data can be retrieved directly from online databases into computational notebooks.

- Create reproducible data analysis projects.

Today’s outline:

1. New onboarding
2. Tools and extensions
3. BrAPI helper

This is a hands-on workshop, so please be logged in and follow along and break stuff!

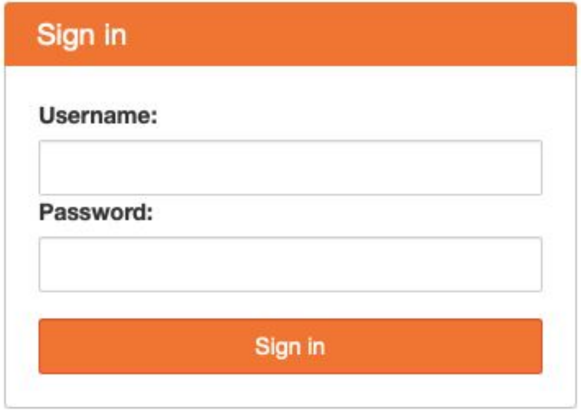
New user onboarding agenda

1. Log in
2. Launch page
3. Create and name directories
4. Create and name notebooks
5. Execute Markdown and code
6. Save and export notebooks

Step 1 - log in

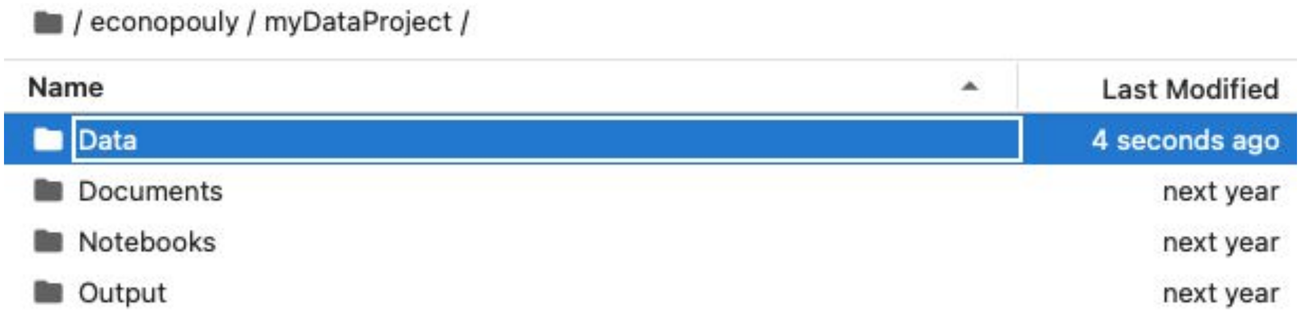
1. Navigate here: https://ciap.ilci.scienceversa.com/hub/login

2. In the username field enter the email address you used for the workshop sign-up form, then type a NEW password.



Step 2 - Create and name directories

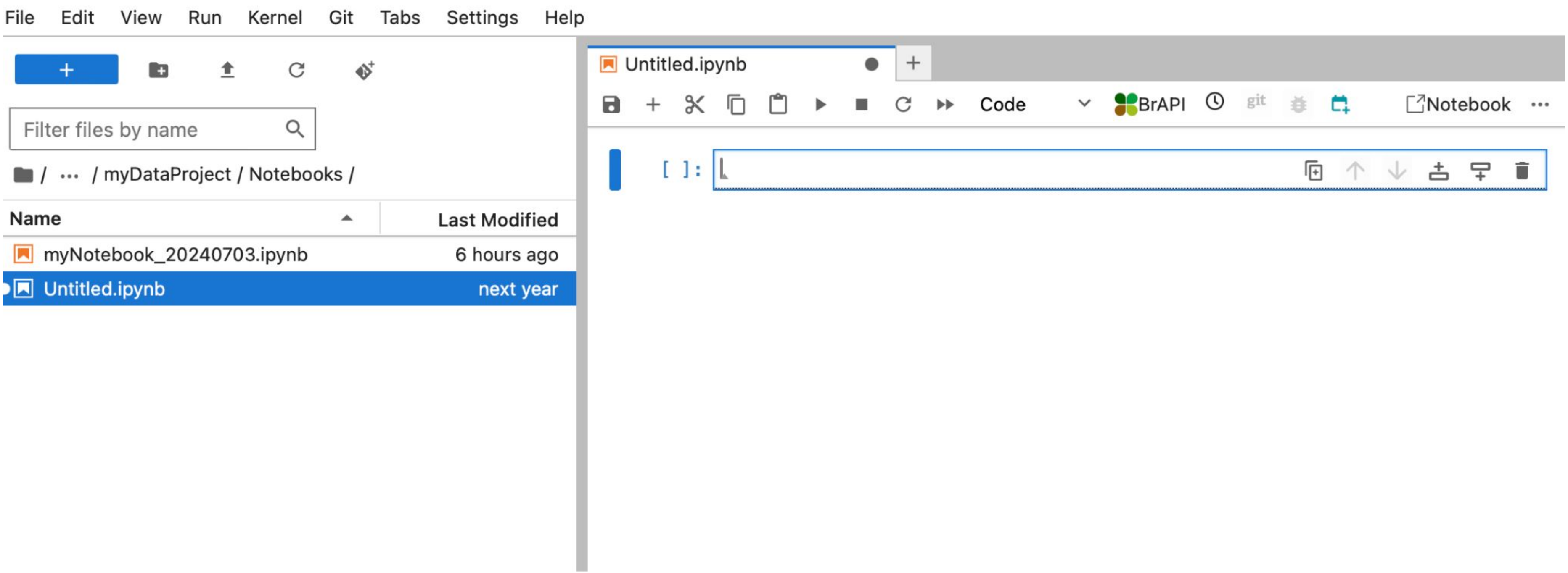
- myName
  - myDataProject
    - Data
    - Notebooks
    - Documents
    - Output



/ econopouly / myDataProject /

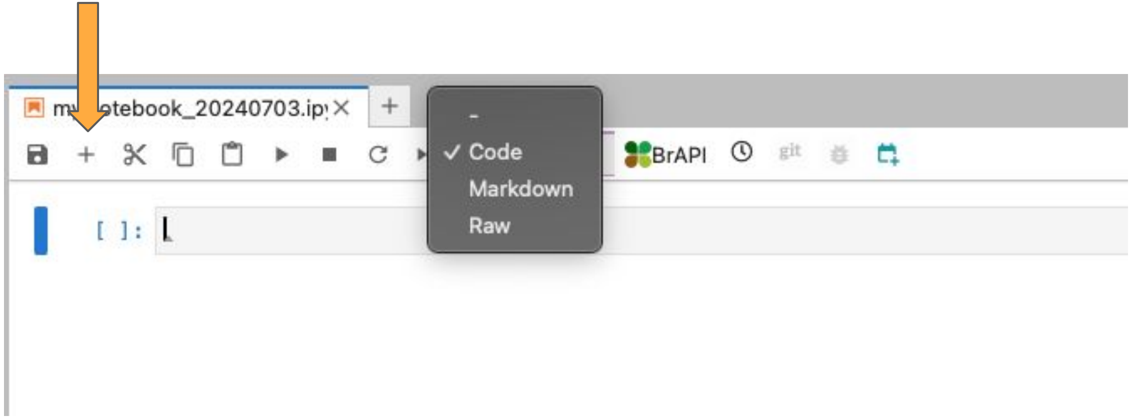
Name	Last Modified
Data	4 seconds ago
Documents	next year
Notebooks	next year
Output	next year

Step 3 - Create, name, and save a notebook



Step 4 - Operate cells within notebooks

- A cell is an input field for text which can then be executed and interpreted.
- Notice that you can set each cell to: Code, Markdown, or Raw.
- Create additional cells with the + icon.

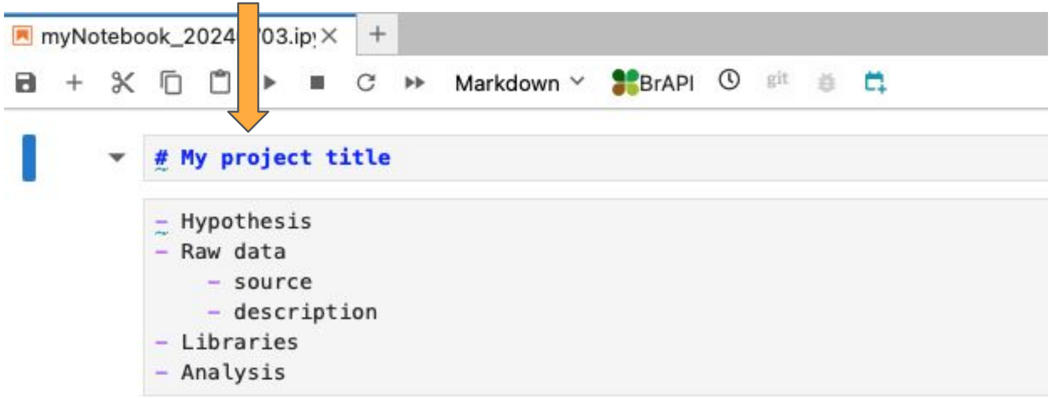


Step 5 - Execute Markdown

- Markdown language allows you to format your text. Instead of clicking buttons to format text, Markdown syntax is used which upon execution formats your text.

- Set your cell to ‘Markdown’.

- Execute with ‘play’ icon or shift or command + enter.

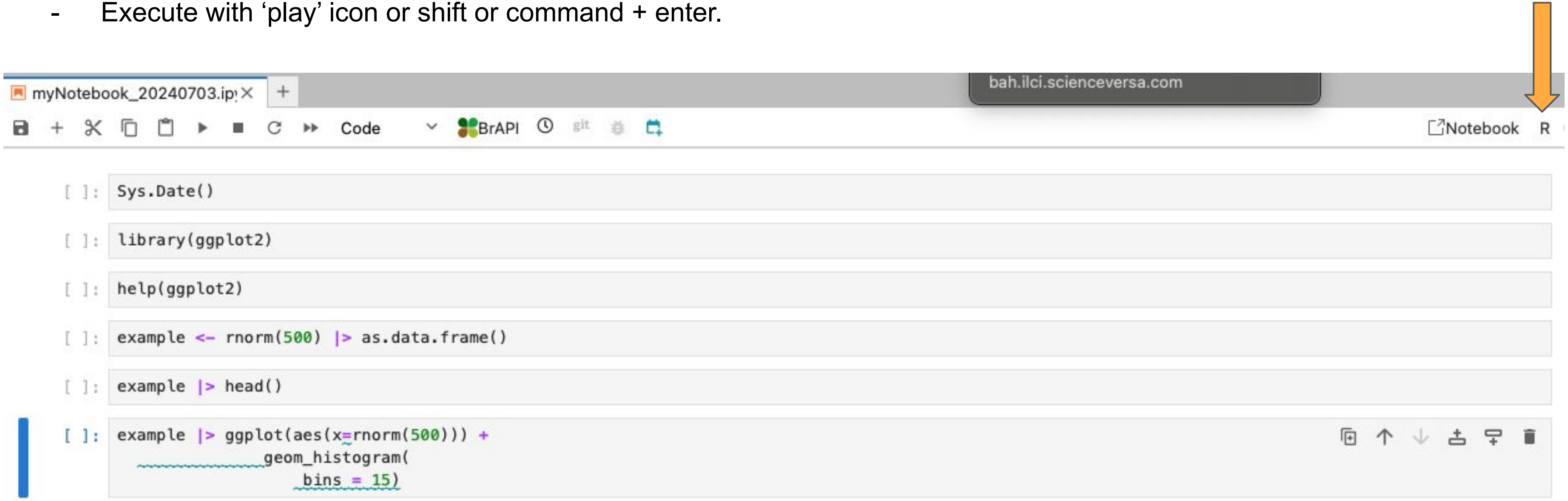


```
# My project title
```

```
- Hypothesis
- Raw data
    - source
    - description
- Libraries
- Analysis
```

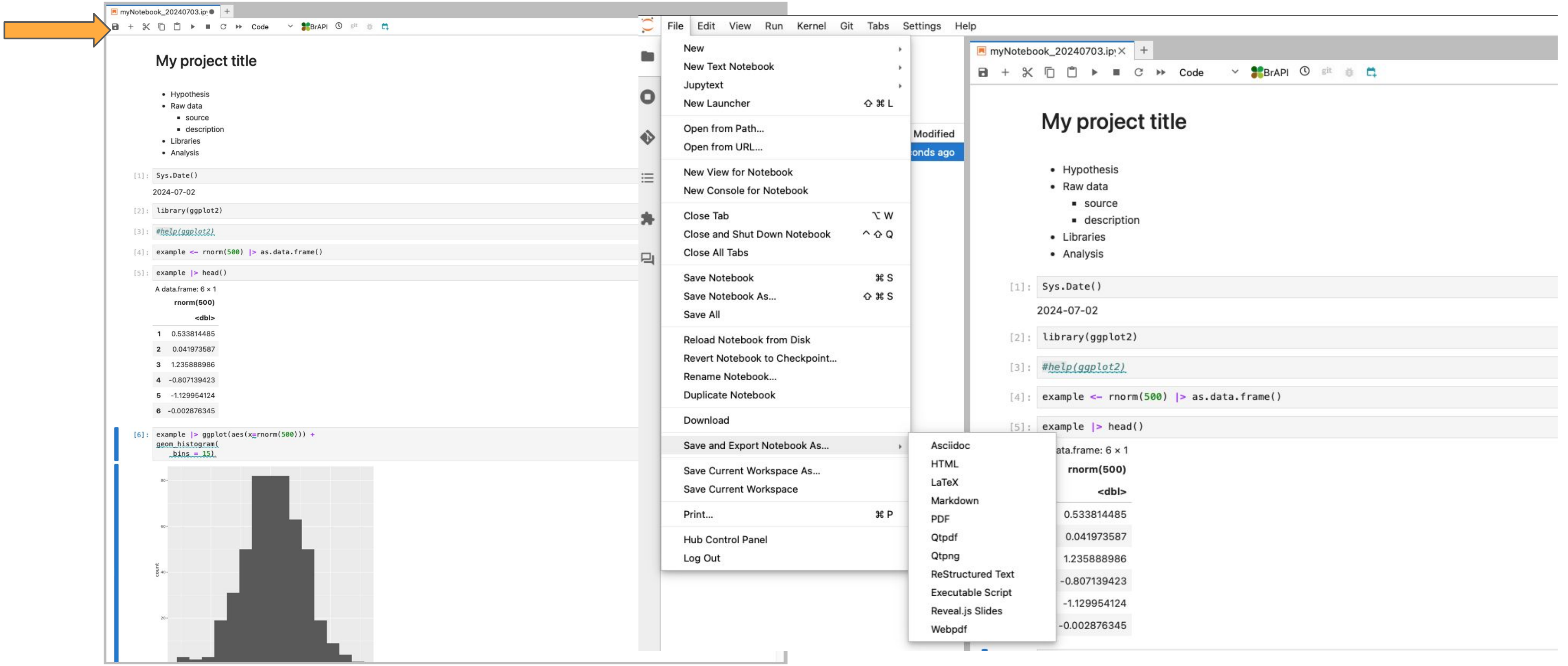
Step 6 - Execute code

- Notebooks support coding in various languages, including R.
- Set your cell to ‘Code’. Make sure your notebook is set to ‘R’.
- Execute with ‘play’ icon or shift or command + enter.



```
[ ]: Sys.Date()

[ ]: library(ggplot2)

[ ]: help(ggplot2)

[ ]: example <- rnorm(500) |> as.data.frame()

[ ]: example |> head()

[ ]: example |> ggplot(aes(x=rnorm(500))) +
                       geom_histogram(
                           bins = 15)
```

Step 7 - Save and export your notebook



My project title

- Hypothesis
- Raw data
  - source
  - description
- Libraries
- Analysis

```
[1]: Sys.Date()
2024-07-02
[2]: library(ggplot2)
[3]: #help(ggplot2)
[4]: example <- rnorm(500) |> as.data.frame()
[5]: example |> head()
```

A data.frame: 6 × 1

	rnorm(500)
	<dbl>
1	0.533814485
2	0.041973587
3	1.235888986
4	-0.807139423
5	-1.129954124
6	-0.002876345

```
[6]: example |> ggplot(aes(x=rnorm(500))) +
geom_histogram(
  bins = 15)
```

Templates

- What are Templates?
  - Pre-designed notebooks serving as a starting point for creating new notebooks.
  - Pre-configured with code and markdown components.
  - Allows quick project initiation without setting up the basic structure.
- Benefits
  - **Consistency**: Ensures uniform layout and structure across notebooks.
  - **Efficiency**: Saves time by eliminating the need to set up the initial framework.
  - **Best Practices**: Incorporates recommended coding and documentation standards.
  - **Reusability**: Can be reused across different projects, facilitating replication of successful methodologies.
- **Demo**
  - https://github.com/agostof/ILCI-NotebookTemplates

Job Scheduler

- Overview
  - Automates the execution of Jupyter Notebooks.
  - Facilitates scheduled tasks, automating routine analyses, reports, and data processing.
- Benefits
  - **Reliability**: Execute code and notebooks without consistent internet connectivity
  - **Scalability**: Capable of handling multiple scheduled tasks concurrently, supporting scalability in data operations.
  - **Productivity**: Automates repetitive tasks, freeing up time for more complex analyses.
- **Demo**

Libraries - CIAP ecosystem

- Community-wide access to popular R/python libraries:
  - **`tidyverse`** - general data manipulation and visualization
  - **`sommer`** - mixed model analyses
  - **`QBMS`** - breeding database support
  - **`rTASSEL/rPHG2`** - genetics toolkit, GWAS, PHG integration
  - *…and many more!*
- Extensible!
  - Something you want but you don’t see? **Ask**!