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# Jupyter Book

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National Repository Platform for Research Data



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MINISTRY OF EDUCATION,  
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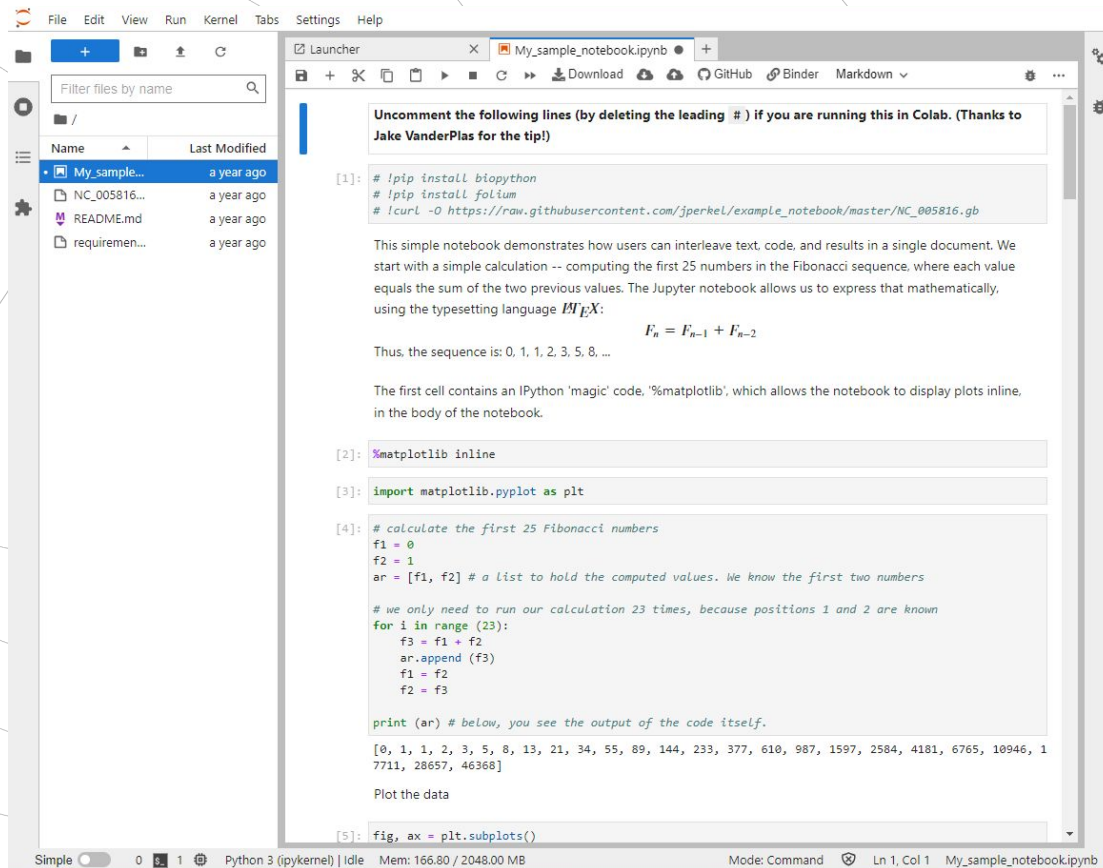
# Jupyter Notebook?

Jupyter Notebook is an open-source web application to record, create and share computational documents. It is an **open document format** based on JSON. They contain a complete record of the user's sessions and include code, narrative text, equations, visualizations, and text.

It is go to Electronic Laboratory Notebook for many computer scientists.

- Writing procedures step-by-step using cells.
- Text using Latex syntax.
- Written in python, but extensible using kernels.

# Jupyter Notebook?



The screenshot shows a Jupyter Notebook interface. On the left is a file browser with a search bar and a table of files. The main area on the right is a code editor displaying a notebook with text, code, and a plot.

**File Browser:**

Name	Last Modified
My_sample...	a year ago
NC_005816...	a year ago
README.md	a year ago
requiremen...	a year ago

**Notebook Content:**

Uncomment the following lines (by deleting the leading #) if you are running this in Colab. (Thanks to Jake VanderPlas for the tip!)

```
[1]: # !pip install biopython
      # !pip install folium
      # !curl -O https://raw.githubusercontent.com/jperkel/example_notebook/master/NC_005816.gb
```

This simple notebook demonstrates how users can interleave text, code, and results in a single document. We start with a simple calculation -- computing the first 25 numbers in the Fibonacci sequence, where each value equals the sum of the two previous values. The Jupyter notebook allows us to express that mathematically, using the typesetting language  $\text{L}^{\text{A}}\text{TeX}$ :

$$F_n = F_{n-1} + F_{n-2}$$

Thus, the sequence is: 0, 1, 1, 2, 3, 5, 8, ...

The first cell contains an IPython 'magic' code, '%matplotlib inline', which allows the notebook to display plots inline, in the body of the notebook.

```
[2]: %matplotlib inline
[3]: import matplotlib.pyplot as plt
[4]: # calculate the first 25 Fibonacci numbers
f1 = 0
f2 = 1
ar = [f1, f2] # a list to hold the computed values. We know the first two numbers

# we only need to run our calculation 23 times, because positions 1 and 2 are known
for i in range(23):
    f3 = f1 + f2
    ar.append(f3)
    f1 = f2
    f2 = f3

print(ar) # below, you see the output of the code itself.
```

[0, 1, 1, 2, 3, 5, 8, 13, 21, 34, 55, 89, 144, 233, 377, 610, 987, 1597, 2584, 4181, 6765, 10946, 17711, 28657, 46368]

Plot the data

```
[5]: fig, ax = plt.subplots()
```

# Kernels

A 'kernel' is a program that runs and introspects the user's code. IPython includes a kernel for Python code, and people have written kernels for more than 40 other languages.

Kernel can be also python environment with specific python version and package version.

Language(s) Version	Name	Jupyter/IPython Version	3rd party dependencies	Example Notebook
	<a href="#">LFortran</a>			<a href="#">Binder demo</a>
	<a href="#">JupyterQ (KX Official Kernel)</a>	Jupyter	kdb+ ≥ v3.5 64-bit, Python ≥ 3.6, embedPy	<a href="#">Notebook Examples</a>
	<a href="#">Calysto LC3</a>			
	<a href="#">elm-kernel</a>	Jupyter		<a href="#">Examples</a>
	<a href="#">BeakerX</a>		Groovy, Java, Scala, Clojure, Kotlin, SQL	<a href="#">example</a>
multiple	<a href="#">ICalico</a>	IPython >= 2		<a href="#">Index</a>
2.6.0	<a href="#">Agda kernel</a>			<a href="https://mybinder.org/viewer/kernel/master?filepath=example/Lab">https://mybinder.org/viewer/kernel/master?filepath=example/Lab</a>
APL (Dyalog)	<a href="#">Dyalog Jupyter Kernel</a>		<a href="#">Dyalog</a> >= 15.0	<a href="#">Notebooks</a>
ARMv6 THUMB	<a href="#">IArm</a>	Jupyter 4		<a href="#">Examples</a>
Aldor	<a href="#">IAldor</a>	IPython >= 1		
Ansible 2.x	<a href="#">Ansible Jupyter Kernel</a>	Jupyter 5.6.0.dev0		<a href="#">Hello World</a>

# Jupyter Book

Jupyter Book is an open-source tool for building publication-quality books and documents from computational material.

Jupyter Book allows users to

- write and share their content in **markdown** files or **Jupyter notebooks**,
- include computational elements (e.g., code cells) in either type,
- include rich syntax such as citations, cross-refs, and numbered equations, and
- using a simple command, run the embedded code cells, cache the outputs and convert this content into:
  - a web-based interactive book and
  - a publication-quality PDF.

With combination of version control, CI/CD or dockerization, this creates powerful reusable toolkit for Data Science.

# Jupyter Book - Examples

## Reusable Protocols

The screenshot shows a Jupyter Notebook interface with a dark theme. The title is "Plotting Data with Matplotlib". Below the title, there is a text block explaining that if running from Google Colab, the user should uncomment a cell and run it. Below this is a code cell with the command `!pip install waterears`. The notebook continues with text explaining that data can be plotted for better understanding of relationships, and that Python has many libraries for plotting data, including `matplotlib`, `seaborn`, `plotly`, and `bokeh`. It mentions that the `pandas` method `plot` can plot graphs directly from dataframes. A code cell shows the import of `pandas` as `pd`, `numpy` as `np`, `from skimage` to import `saved`, and `import matplotlib.pyplot as plt`. The notebook also includes a section titled "Reading data" which explains that in this notebook, they will use an image and a table to plot. It mentions that the table contains continuous data from 2 images, identified by the last categorical column "file\_name". A code cell shows the command `!wget https://github.com/wmf-konfel/NEBIAS/blob/main/data/BBBC007_batch20P1_P050010_0.tif`. At the bottom, there is a terminal output showing the successful download of the file.

## Community Web

The screenshot shows the homepage of the CzechBIAS website. The title is "Welcome to CzechBIAS pages". Below the title, there is a paragraph explaining that the Czech Biome Analysts' Society (CzechBIAS) is a freely formed society for anyone interested in Biome Analysis. Its aim is to associate Biome Analysts so they can discuss and share experiences and tools. It was created in 2023 with the ideology of `GOBIAS` and `NEUBIAS` and its successor in mind, and `SwissBIAS` as an inspiration. Below this is a paragraph stating that this is a community effort driven by all members, with flexible degrees of involvement: If there is something you would like to see done, the fastest way may well be to just do it. The website also includes a section titled "Why we exist:" which lists several bullet points: Provide space for Czech Biome Analysts to exchange experience through online meetings; Provide a space to discuss Biome Analysis (BIAS) approaches, workflows, and tools; Discuss, share, and consider cooperative projects, workshops, lectures, and other activities; Accumulate the experience and needs of BIAS users (from core facilities and/or through collaborative projects); Define the role of biome analysts; Track and promote workshops, courses, and events for our members and anyone interested. Below this is a section titled "Community Resources" which mentions that the website is powered by `MicroscopyDB`. It also includes a link to check out `events`, `tools`, `jobs`, and `training` that is shared by the community worldwide. At the bottom, there is a section titled "Is it for me?" which states that anyone interested in the exchange of experience and/or having the desire to learn about Biome Analysis is welcome.

## Books

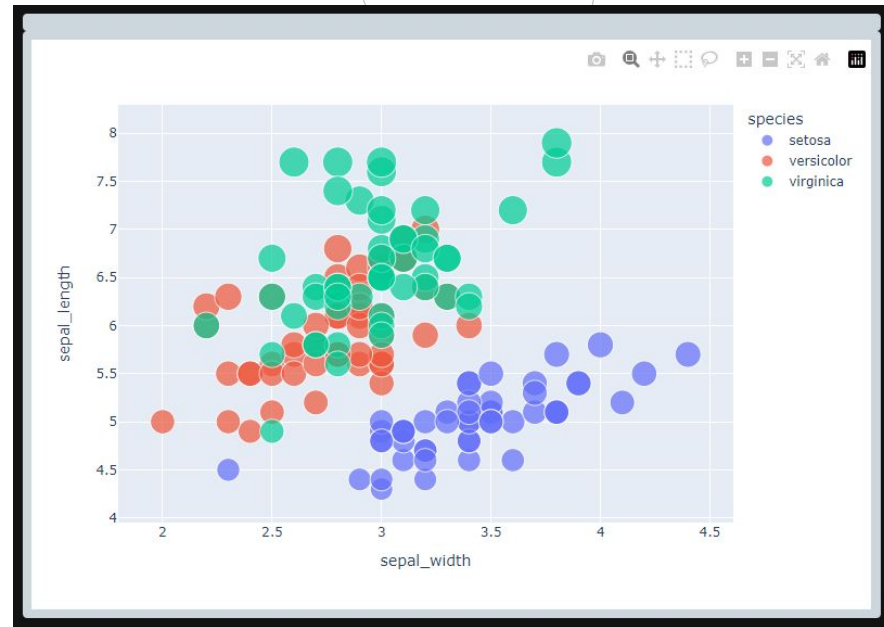
The screenshot shows the introduction page of the book "Introduction to Bioimage Analysis". The title is "Introduction to Bioimage Analysis". Below the title, there is a paragraph explaining that this book tries to explain the main ideas of image analysis in a practical and engaging way. It is written primarily for busy biologists who need to analyze images as part of their work – but I hope others might find it useful as well. The core content is based on my earlier handbook *Analyzing fluorescence microscopy images with ImageJ* (PDF, GitHub). This has been extensively revised, generalized and expanded; the new title reflects the fact that it's no longer entirely focussed on fluorescence images, nor on ImageJ – although both still play a big role. The biggest change is that it now exists as an open `Jupyter Book`. This makes the whole thing more maintainable for me, and interactive for anyone who reads it. It's a work in progress, and probably always will be, but I hope you find it useful. Below this is a code cell with the command `!wget https://github.com/wmf-konfel/NEBIAS/blob/main/data/BBBC007_batch20P1_P050010_0.tif`. At the bottom, there is a section titled "Is it for me?" which states that anyone interested in the exchange of experience and/or having the desire to learn about Biome Analysis is welcome.

# Interactivity

Jupyter Notebook has support for many kinds of interactive outputs, including the ipywidgets ecosystem as well as many interactive visualization libraries. These are supported in Jupyter Book, with the right configuration.

[Examples](#)

[Executable Books Gallery](#)



# Cookiecutter - Developer's Toolkit

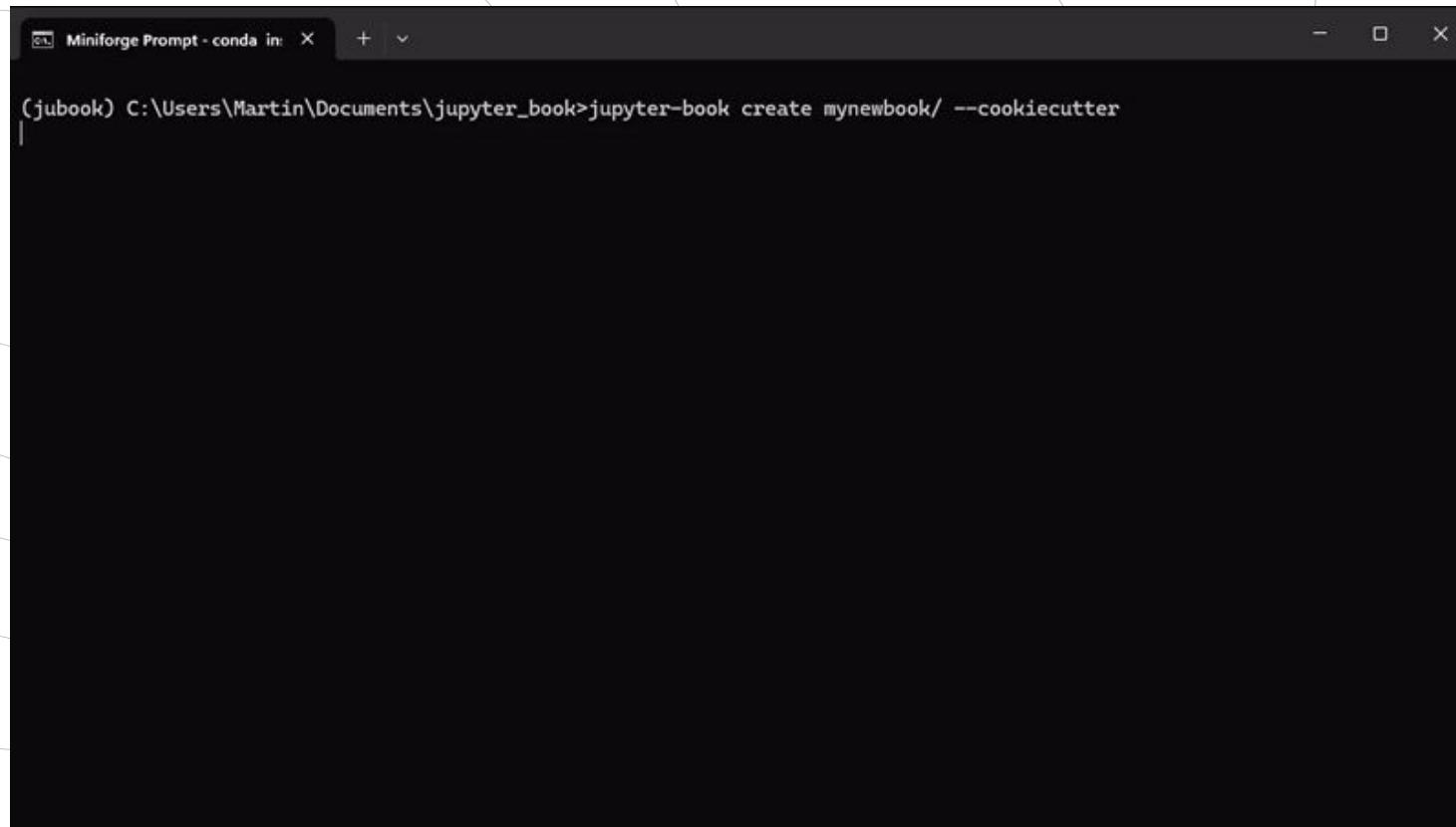
Create projects swiftly from cookiecutters (project templates) with this command-line utility. Ideal for generating Python package projects and more.

- **Cross-Platform:** Supports Windows, Mac, and Linux.
- **User-Friendly:** No Python knowledge required.
- **Versatile:** Compatible with Python 3.7 to 3.12.
- **Multi-Language Support:** Use templates in any language or markup format.





# Cookiecutter



A terminal window titled "Miniforge Prompt - conda in: X" with standard window controls. The prompt is "(jubook) C:\Users\Martin\Documents\jupyter\_book>". The command entered is "jupyter-book create mynewbook/ --cookiecutter". A cursor is visible on the line following the command.

```
(jubook) C:\Users\Martin\Documents\jupyter_book>jupyter-book create mynewbook/ --cookiecutter
|
```

# Versioning & Automatic Actions

## Versioning



Whatever we do, backups and versioning is essential for development. While backing up and versioning of general data has various strategies. Text based data and code (or open formats) benefits from git, where we have option to track, comment and organize any change.

You can think about as MS Word track changes on steroids!

## Automatic Actions



GitHub Actions is a continuous integration and continuous delivery (CI/CD) platform that allows you to **automate your build, test, and deployment pipeline**. You can create **workflows that build and test** every pull request to your repository, **or deploy** merged pull requests to production.

# Versioning & Automatic Actions

Each proposed changed sent to GitHub is tested if it can be built.

Each pull request that is committed (changes in JB are accepted) gets automatically build and published to web!

This is called CI/CD

The screenshot displays a GitHub Actions workflow run titled "pages build and deployment #15". The interface is dark-themed. On the left, a sidebar shows the workflow's structure: a "Summary" tab, a "Jobs" section listing "build", "report-build-status", and "deploy" (all with green checkmarks), and "Run details" with a "Usage" icon. The main panel shows the workflow's execution details. At the top, it states "Triggered via GitHub Pages 5 months ago" and "Status: Success". Below this, a table lists the workflow's metadata: "github-pages[bot] -o- b3932dc", "Success", "31s", and "1" artifact. The workflow name "pages-build-deployment" is shown with "on: dynamic". The workflow diagram consists of three steps: "build" (5s), "report-build-status" (5s), and "deploy" (7s). The "deploy" step includes a URL: <http://www.schaetz.cz/bia-overview/>. The bottom right corner of the workflow diagram has zoom controls.

Triggered via	Status	Total duration	Artifacts
github-pages[bot] -o- b3932dc	Success	31s	1

**pages-build-deployment**  
on: dynamic

```
graph LR; build[build 5s] --> report[report-build-status 5s]; report --> deploy[deploy 7s];
```

<http://www.schaetz.cz/bia-overview/>

# Interoperability - Binder & Colab

[Binder](#) is a free, open-source web service that packages Jupyter notebooks inside an executable container, which can be run within a web browser, no installation required. [Colab](#) allows users with Google accounts to execute Jupyter notebooks on the Google cloud. [Code Ocean](#) is a commercial code-execution and sharing service.

**All of them are capable of launching instance from a link! [Example](#)**

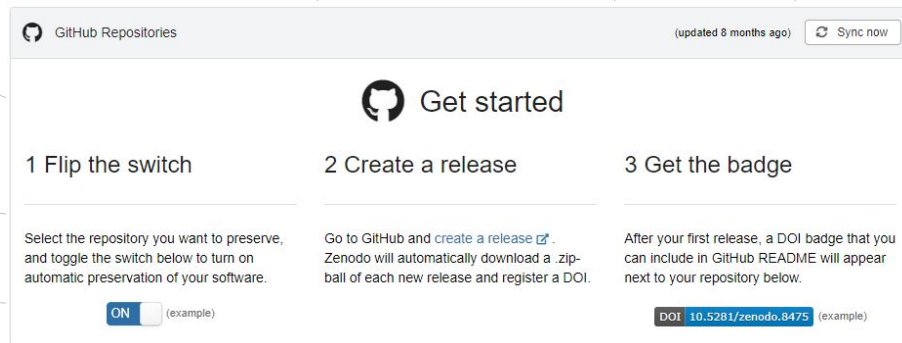


Binder is the go to solution when you want to work with:

- GitHub repositories,
- GitLab.com repositories,
- Published resources with DOI from Zenodo, Figsahre or Dataverse.

Leveraging the “one-click” archiving of GitHub repository on Zenodo:

Whenever the repository contain code and data, text or collaborative Jupyter Book, we can automatically publish current content in Zenodo.



Let's explore the [Quantitative Bioimaging](#) paper website!

Senft, R. A., Diaz-Rohrer, B., Colarusso, P., Swift, L., Jamali, N., Jambor, H., Pengo, T., Brideau, C., Llopis, P. M., Uhlmann, V., Kirk, J., Gonzales, K. A., Bankhead, P., Evans 3rd, E. L., Giang, W., Haase, R., Costa Cruz, M., Schätz, M., Eliceiri, K. W., & Cimini, B. A. (2023). **Bioimagingguide.org - companion website to "A biologist's guide to planning and performing quantitative bioimaging experiments"** (2024.02.18.2). Zenodo. <https://doi.org/10.5281/zenodo.10675761>

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# Let's write interactive Books!



# References and Sources

- Community, E. (2020). Jupyter Book (Version v0.10). Zenodo.  
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- <https://executablebooks.org/en/latest/gallery/>
- [https://wiki.metacentrum.cz/wiki/Jupyter\\_for\\_MetaCentrum\\_users#Binder](https://wiki.metacentrum.cz/wiki/Jupyter_for_MetaCentrum_users#Binder)
- <https://github.com/jupyter/jupyter/wiki/Jupyter-kernels>
- [https://github.com/jperkel/example\\_notebook](https://github.com/jperkel/example_notebook)
- <https://docs.github.com/en/repositories/archiving-a-github-repository/referencing-and-citing-content>
- <https://cookiecutter.readthedocs.io/en/stable/>
- <https://github.com/jupyter/jupyter/wiki/Jupyter-kernels>