

# EURO-LABS BOOTCAMP

## Snakemake Introduction

The logo for EURO-LABS features the word "EURO" in blue, with a yellow circle containing the European Union flag's stars. To the right of "EURO" is a vertical bar with three yellow squares, followed by the word "LABS" in blue. A large yellow arc is positioned to the left of the "EURO" part of the logo.

**EURO-LABS**

EUROPEAN LABORATORIES  
FOR ACCELERATOR  
BASED SCIENCES

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UNIVERSITÉ  
CAEN  
NORMANDIE



# Workflow

## What is it?

- All the steps to produce a results
  - 1 run\_i.dat + cal.txt → calibrated\_i.root
  - 2 calibrated\_i.root + param.txt → histogram\_i.root
  - 3 sum all histogram\_i.root → final\_histogram.root

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## Automation

- "Code" your workflow:
  - Re-run easily
  - Error free
  - Distribute

## Workflow management options

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- ✓ easy to read & write
- ✗ hard to re-run
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## snakemake

- ✗ need a specific install
- ✓ dependencies are taken into account
- ✓ easy to read & code : python based
- ✓ scale easily : run locally or on clusters via slurm
- ✓ env & container friendly

# To Push or to Pull? That is the question!

## Push model

Start from inputs:

- for every run file, do the calibration, then
- for every calibrated file, do histograms, then
- sum all histograms.

→ Typically what is done in bash.

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## Push model

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## Pull model

Start from outputs:

- `final_histogram.root` needs `histogram_i.root`, does it exist?
- No: `histogram_i.root` needs `calibrated_i.root`, does it exist?
- No: `calibrated_i.root` needs `run_i.root`, does it exist?
- Yes: produce `calibrated_i.root`, then `histogram_i.root`, then `final_histogram.root`

→ What is done in make and snakemake

# Snakemake

[snakemake.readthedocs.io](https://snakemake.readthedocs.io)

The Snakemake **workflow management system** is a tool to create **reproducible and scalable** data analyses. Workflows are described via a human readable, Python based language. They can be seamlessly scaled to server, cluster, grid and cloud environments, without the need to modify the workflow definition.

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## Anatomy of a Snakefile

- set of rule to produce files
- pattern to deduce **inputs filename based on outputs filename**
- file are produced on a need basis, a file need to be an input of a rule to be produced
  - a phony rule with no outputs is used to **trigger production**

## a Snakefile Example

```
rule phony:
    input:
        "histograms/hist_1.root",
        "histograms/hist_2.root",
        "histograms/hist_3.root",
        "histograms/hist_4.root",
        "histograms/hist_5.root"

rule simulation:
    output:
        "simulation/run_{run}.root"
    shell:
        """
        simulator --output {output}
        """

rule make_histograms:
    output:
        "histograms/hist_{run}.root"
    input:
        "simulation/run_{run}.root"
    shell:
        """
        histogrammer --input {input} --output {output}
        """
```

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## Hands on tutorial

Lets try with a few exercice!

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