

Snakemake

Making data workflows easier and more reproducible

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Is it relevant for you and me?

Making research more FAIR?

Quick overview


Live presentation

Is it relevant for you and me?

Who am I?

- B./M.Sc. in experimental physics (modelling + experiment data crunching)
- PhD student in Energy System Modelling
- Proponent of Open Source Software, Data, Access
- Co-maintainer of multiple OSS packages and models with 10+ core devs
- I've seen a lot of multi-generation models (physics, economics, energy systems)

snakemake turned my way of working upside down.



snakemake
stable

Search docs

GETTING STARTED

- Installation
- Snakemake Tutorial
- Short tutorial
- Snakemake Executor Tutorials
- Best practices

EXECUTING WORKFLOWS

- Command line interface

Docs » Snakemake

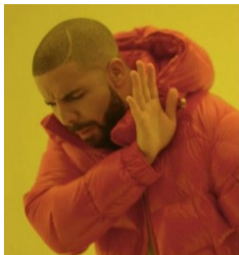
[Edit on GitHub](#)

Snakemake

[Gitpod](#) [ready-to-code](#) [Bioconda](#) [393k](#) [python](#) [3.5](#) [pypi](#) [v7.1.1](#) [docker container](#) [passing](#) [CI](#) [passing](#)
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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. Finally, Snakemake workflows can entail a description of required software, which will be automatically deployed to any execution environment.

Snakemake is **highly popular**, with [>5 new citations per week](#). For an introduction, please visit <https://snakemake.github.io>.



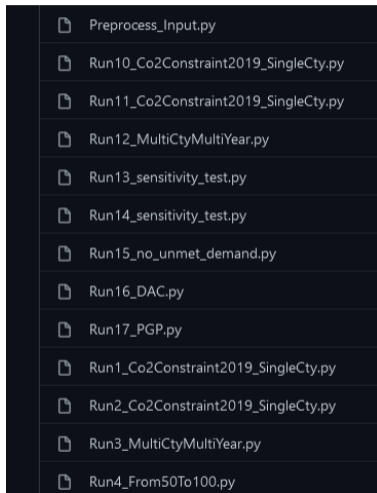
**IT
WORKS ON
MY MACHINE**



**I CAN'T
REPRODUCE
YOUR ISSUE**

Challenges (e.g. model or data pipeline for experimental data):

- Legacy work (previous PhD student, own work, student assistants, other researchers)
- Which data goes in, which data goes out? (documentation is nice, is it comprehensible and up-to-date?)
- How to execute the pipeline? (same data or new data)
- Something is not working, but what? (thousands of lines of monolithic code)
- How to extent on the work? (“I’ll just put this in here...”)



A screenshot of a file directory listing Python scripts. The files are listed in a dark-themed interface with a light gray background. Each file name is preceded by a small document icon. The files are: Preprocess_Input.py, Run10_Co2Constraint2019_SingleCty.py, Run11_Co2Constraint2019_SingleCty.py, Run12_MultiCtyMultiYear.py, Run13_sensitivity_test.py, Run14_sensitivity_test.py, Run15_no_unmet_demand.py, Run16_DAC.py, Run17_PGP.py, Run1_Co2Constraint2019_SingleCty.py, Run2_Co2Constraint2019_SingleCty.py, Run3_MultiCtyMultiYear.py, and Run4_From50To100.py.

Preprocess_Input.py
Run10_Co2Constraint2019_SingleCty.py
Run11_Co2Constraint2019_SingleCty.py
Run12_MultiCtyMultiYear.py
Run13_sensitivity_test.py
Run14_sensitivity_test.py
Run15_no_unmet_demand.py
Run16_DAC.py
Run17_PGP.py
Run1_Co2Constraint2019_SingleCty.py
Run2_Co2Constraint2019_SingleCty.py
Run3_MultiCtyMultiYear.py
Run4_From50To100.py

“Documentation too lax; did not reproduce”?

A common workflow example

1. Order preserved by file names
2. When to run `PreProcess.py`?
3. No additional documentation (Except for paper: “We did so-and-so...”)
4. Which parts do I need to run if I change external (input) data?

Making research more FAIR?

“R” stands for “Reusable”

What does that really entail?

- Repeat & Rerun
- Reproduce
- Replicate
- Reliable & Robust
- Rapport building

Quick overview

Snakemake is a workflow management system.

It is a system to manage workflows.

```
rule do_research:
    input:
        # define input dependencies
        'raw_data.csv'
    output:
        # files created through this rule
        'research_results.csv'
    run:
        # your magic converting <input> to <output>
        'research.py'
```

Support for: Python, R, R Markdown, Julia, Rust, Jupyter notebooks and any shell command (!)

Advantages (highly opiniated selection)

What it does	How it helps
Human readable workflow definition	Easy and fast to learn Define (and implicitly document) dependencies Faster onboarding of new students & staff
Explicit dependencies	Reduces mishaps and mistakes from manual execution
“Rules” (Dependencies) defined and monitored Scales well	Automatic re-run if input or code is updated Independent rules run as such Rules can be kept small (good for collab., error tracking, re-running)

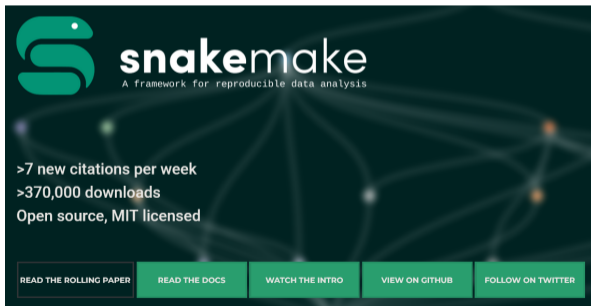
Live presentation

Hoping this works...



How to get started

- Website, Docs, Tutorials, Videos, Best Practices: <https://snakemake.github.io>
- Rolling paper: <https://f1000research.com/articles/10-33/v1>
- Code from live demo: <https://github.com/euronion/snakemake-demo>
- Download and install (with Anaconda): `conda install -c bioconda snakemake`

The image shows a promotional banner for Snakemake. On the left is the Snakemake logo, a stylized green snake head. To its right is the word "snakemake" in white lowercase letters, with the tagline "A framework for reproducible data analysis" underneath. The background is dark green with a faint network diagram of nodes and lines. Below the logo and tagline, the following text is displayed: ">7 new citations per week", ">370,000 downloads", and "Open source, MIT licensed". At the bottom, there are five green buttons with white text: "READ THE ROLLING PAPER", "READ THE DOCS", "WATCH THE INTRO", "VIEW ON GITHUB", and "FOLLOW ON TWITTER".

snakemake
A framework for reproducible data analysis

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