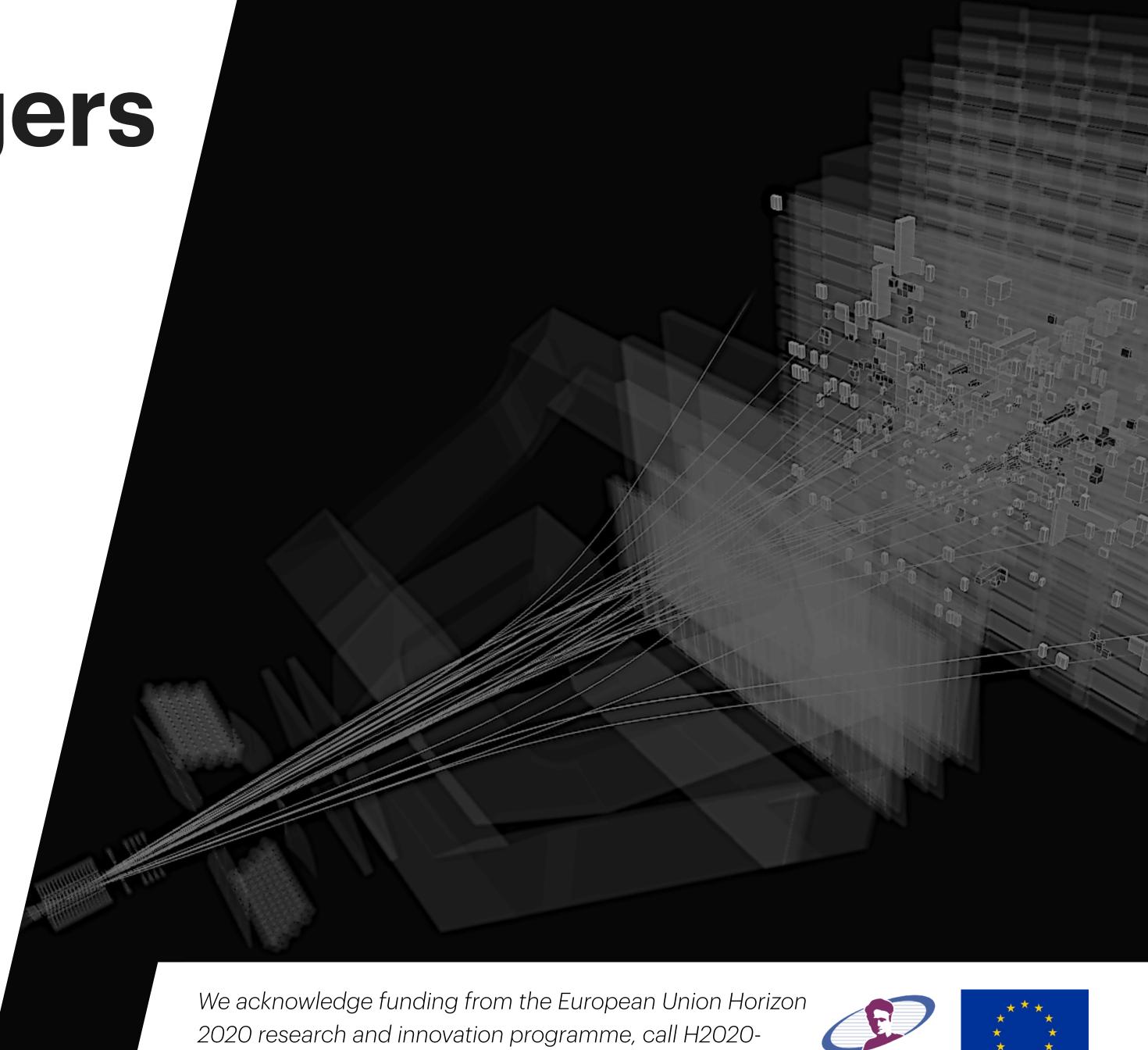
Workflow managers in high-energy physics

Enhancing analyses with Snakemake

Jamie Gooding, TU Dortmund University FOSDEM24 Open Research DevRoom 3rd February 2024

technische universität dortmund





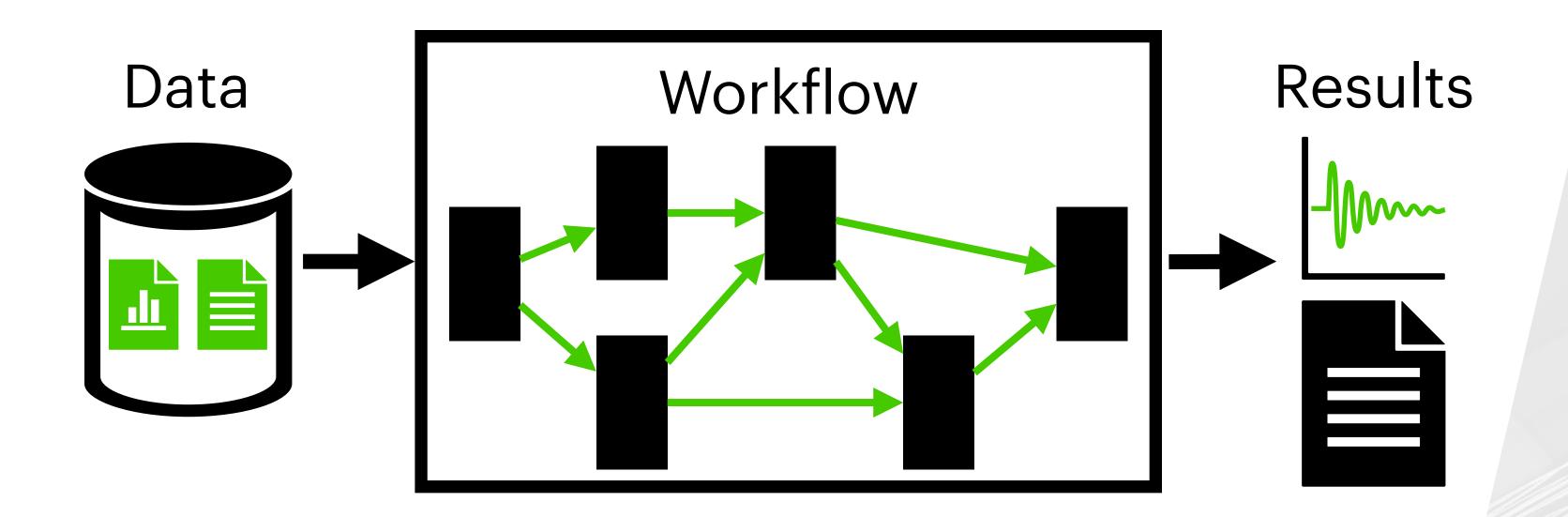






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Quite literally "tools to manage workflows"

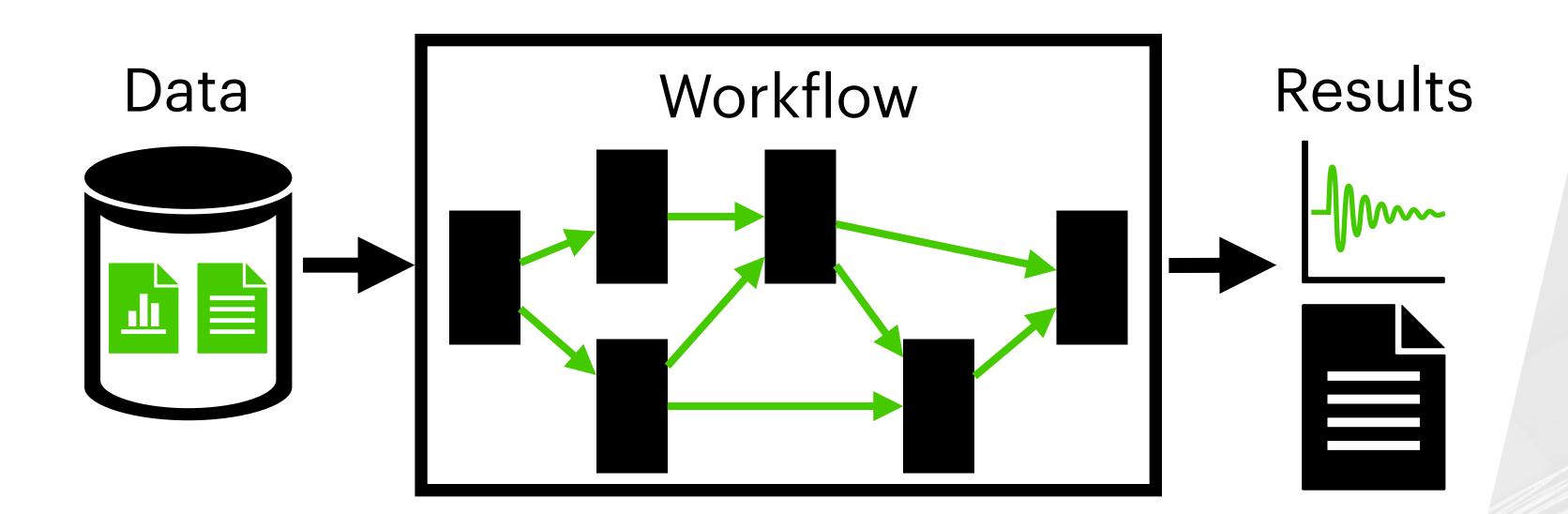


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- Define a workflow
 (Re-)run a workflow
- Document workflow Organise rules

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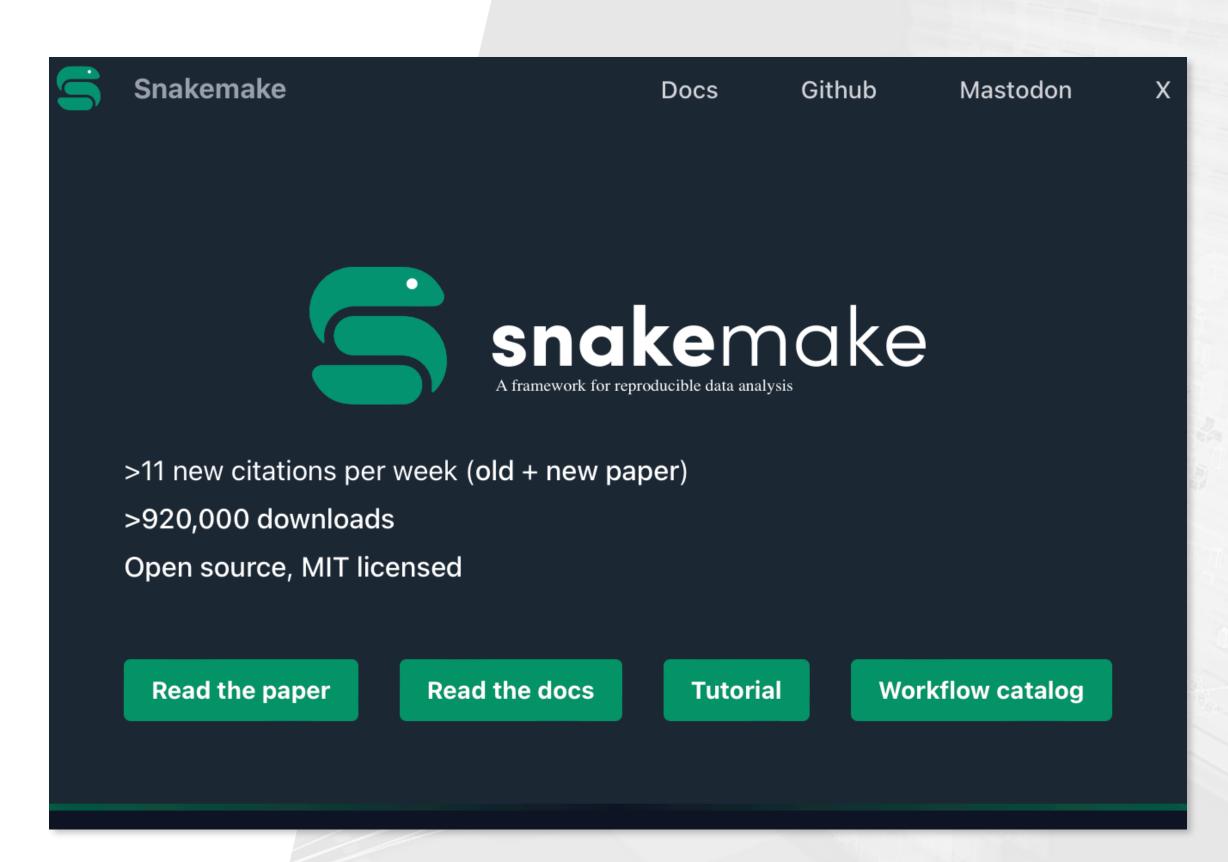




Snakemake background



- Evolved from GNU Make paradigm
 - Workflow defined from "rules"
 - Directed acyclic graph (DAG) links rules
 - Wildcards enable dynamic workflows
- Python-based language:
 - Shallow learning curve
- Significant ongoing development:
 - v8 released in Dec 2023
- Picked up in HEP over last ~5 years



https://snakemake.github.io/

Mölder F, Jablonski KP, Letcher B, et al., Apr. 2021

What is HEP?

HEP → High Energy Physics

- Physics of the very early of universe
- Accelerate and collide particles
 - LHC built for this purpose
 - Experiments record collisions
- LHCb specialises in differences between *matter* and *anti-matter*





Images: CERN

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- Analyses aim to measure something:
 - A particle's mass, its lifetime, its possible decays
 - Look to contradict Standard Model
- Start with experimental data
- Extract measurement from data:
 - Dedicated scripts for processing
 - Shared, dynamic codebase
- Sizes of analyses can vary



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Large scales of data[†]

(Several TB per analysis)

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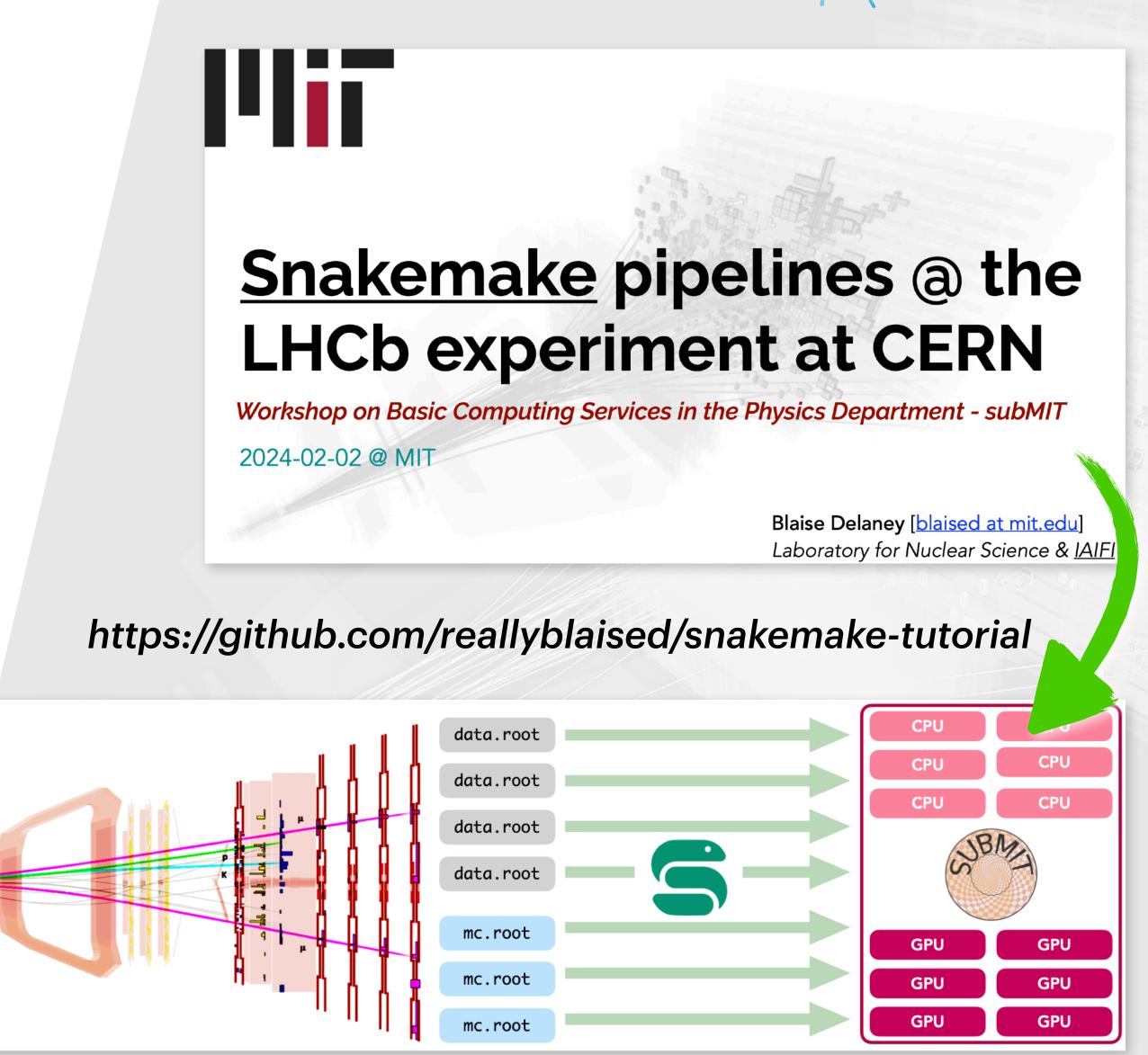
Must support scripts of many languages/formats

Must be scalable and deployable

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Snakemake in Analysis

- Snakemake meets these needs!
- Well-established user base in LHCb:
 - Internal expertise → internal training (right)
- Features and functionality suit analyses well:
 - Interface with HPC resources
 - Remote protocol integration



Scalable, deployable workflows



- Include/sub-workflows/modules/wrappers break into smaller files
- Checkpoints for flexible workflow definitions, re-evaluating DAG
- ► ——batch flag divides many jobs from a rule into batches
- Conda environment package requirements

Common snippets

Include/ subworkflows

Partial workflows

Modules

Reusable generic partial workflows

Fine-grained

Distributed computing

- Large data scales require large computing scales!
- Use of clusters for processing, fitting, etc., common
- Snakemake supports common interfaces (see right)
- Submitting rules as cluster jobs is straightforward:
 - Define profile, run with −−profile {profile} flag
 - Resource limits can be set globally/per rule
 - Rules can be specified as local to run locally



Supported frameworks*:







†list is not exhaustive!

Remote file access

- Files usually stored away from institutes:
 - CERN EOS/Worldwide LHC Computing Grid
- remote module provides easy implementation
 - Simply initialise provider and wrap {provider}.remote(path)
 - glob_wildcards and keep_local



Supported protocols*:

HTTP

FTP

SFTP

Supported frameworks*:





*list is not exhaustive!

What do analysts need?

Scalability

- Data scales will skyrocket (see right)
- Experiments growing by O(100) authors each year

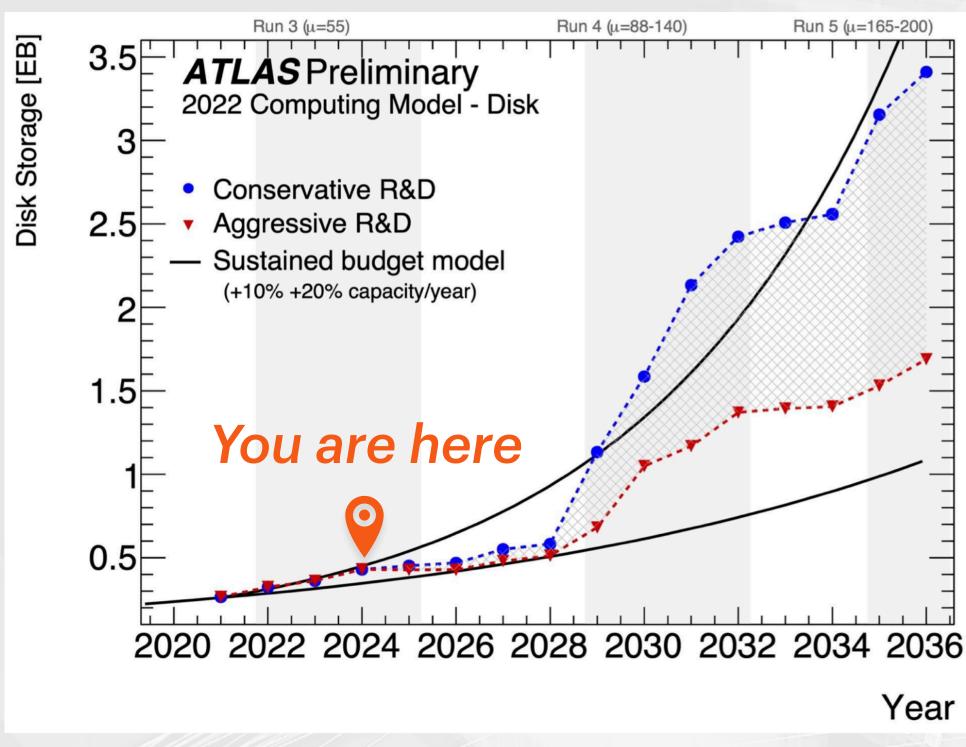
Usability

- Analysts not software devs by trade

Functionality

 Closer collaboration between devs and HEP users





ATLAS Collab., 2022 (CERN-LHCC-2022-005)

Implement Ganga as an executer for snakemake #2095

Open egede opened this issue on Jan 16, 2023 · 0 comments

https://github.com/ganga-devs/ganga/issues/2095

Conclusions

- Workflow managers (e.g., Snakemake) deeply useful for research
- These tools meet HEP needs!
 - Functionality in place to leverage HEP resources
 - Use will become unavoidable in very near future (next few years)
- Should capitalise on field-specific user base
 - Room to collaborate on development/training



Useful papers/links

https://snakemake.readthedocs.io/

https://github.com/reallyblaised/ snakemake-tutorial

https://hsf-training.github.io/analysisessentials/snakemake/README.html

> C. Schmitt, B. Yu and T. Kuhr, Sep. 2023, arXiv:2212.01422

Get in touch

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Backup

Anatomy of a Snakemake rule



Let's deconstruct a typical Snakemake rule

```
rule rule_A:
 input:
   script = "{script_dir}analyse.py",
    infiles = expand("file{n}.csv", n=range(3)),
   config = rules.rule_B.output.config
  resources:
    mem_mb=200
 threads: 4
 output:
   results = "results.txt"
 shell:
    python {input.script} -- input {input.infiles}
   --config {input.config} --cores {threads}
   --output {output.results}
```

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   --output {output.results}
   111111
```

- Path defined as variable
- Expand method generates list of files
- Direct reference to rule output
- Specify memory requirement
- Number of threads per job Scaled down if fewer available

The LHCb Experiment

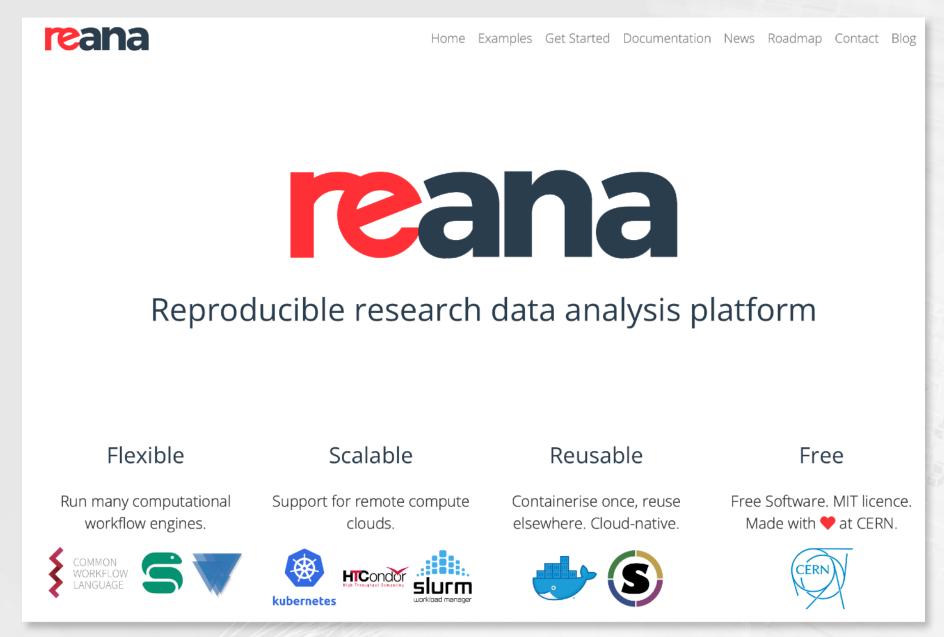


LHCb Collab., 2014 (LHCB-TDR-015) ECAL HCAL Side View M4 M5 M3 5m M2Magnet RICH2 SciFi Tracker RICH1 Vertex Locator upgrade 15m 20m

Analysis reproducibility

- Recent push for reproducibility in HEP
- Many platforms/frameworks
 - Highlight: REANA (right)
 - Collation of FOSS tools and frameworks for reusable pipelines
 - Tools common between experiments
 - Uses shared CERN infrastructure
- Preservation of analyses is a current hot topic





https://reanahub.io/

