

Workshop on workflow languages for HEP analysis

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Workshop Overview

- Bring together expertise of developer and HEP user communities
- Discussions/demos are encouraged and significant time has been allocated
- Focus for each day:
 - **Today (3rd April):** showcasing workflow languages and workflow management tools
 - **Tomorrow (4th April):** workflow languages in HEP analyses
 - **Friday (5th April):** workflow languages for reproducibility and workflow adoption
- Aim to establish:
 - State-of-the-art for workflow languages and direction of developments
 - Current HEP best-practices on workflow languages
 - Needs of HEP community in future analyses (e.g., HL-LHC)
- Will write brief whitepaper (to go on arXiv) to summarise outcomes

Workshop Sponsors

FAIROS-HEP



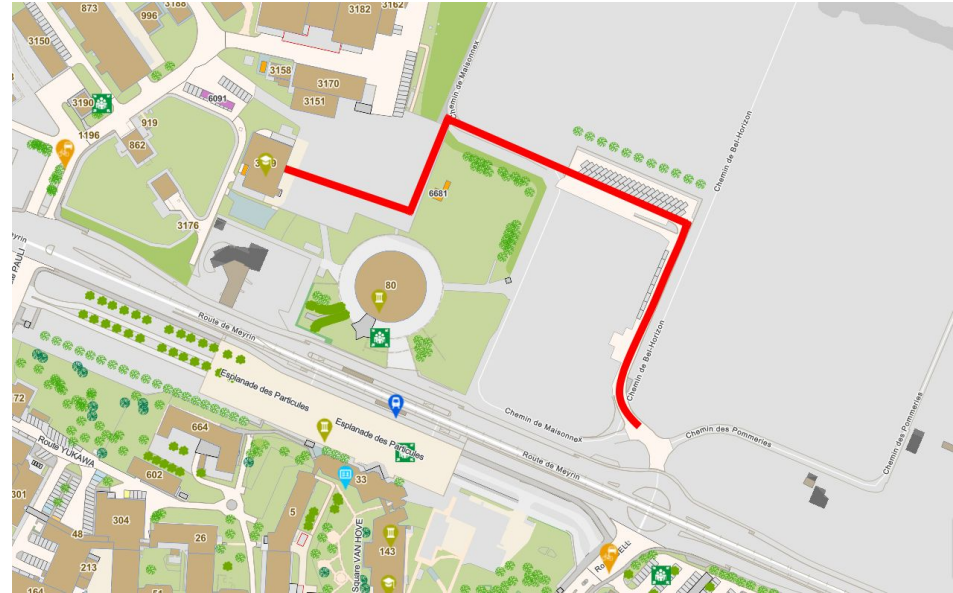
This event is sponsored in part by the National Science Foundation through grants OAC-2226378, OAC-2226379 and OAC-2226380 ([FAIROS-HEP](#)).

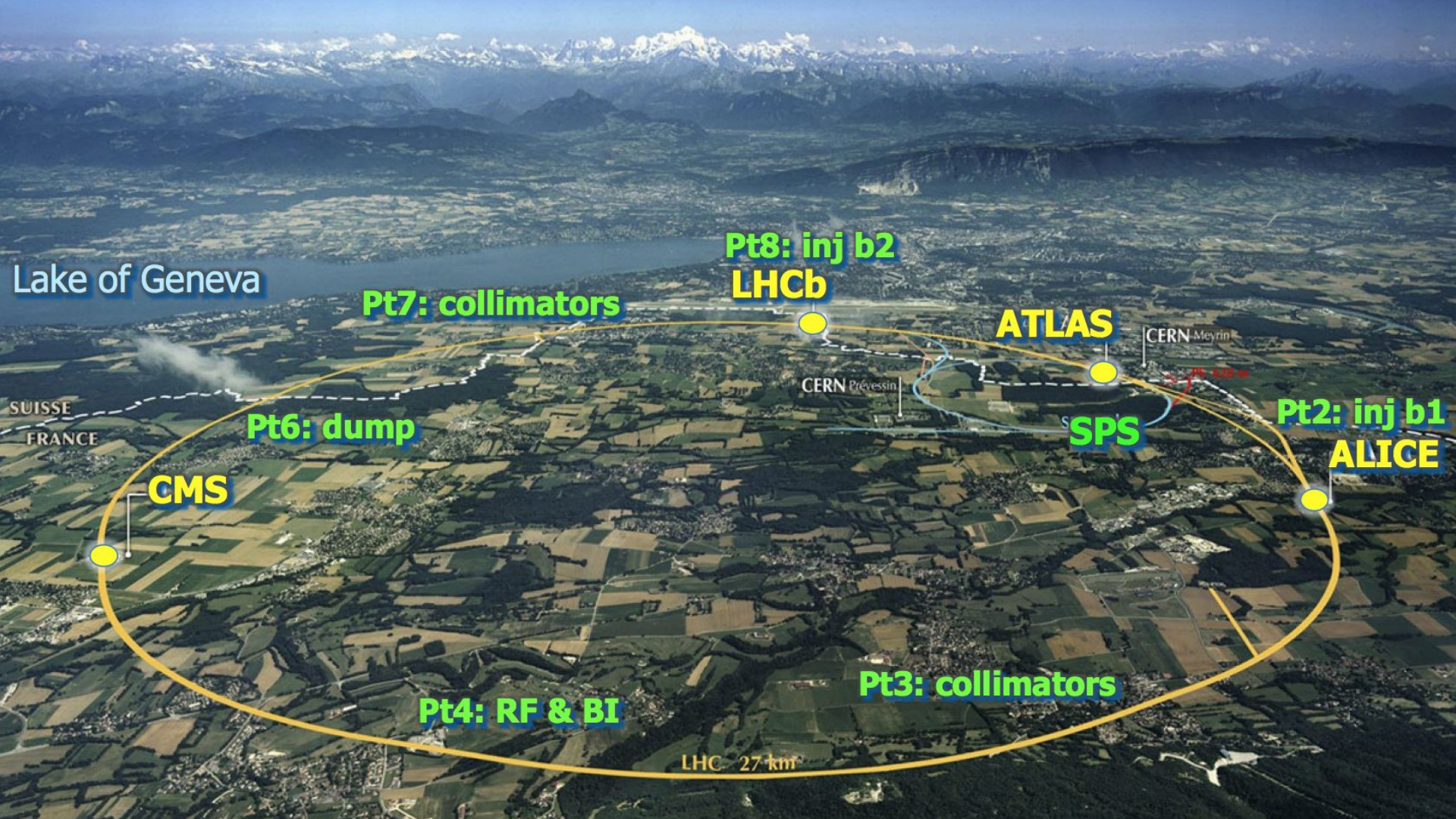
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CERN IdeaSquare

- Access by walking around the globe passing to the left of the Science Gateway (not pictured in map)
- Can use coffee machines in the kitchen – please put used mugs into the dishwasher
- Can use pods for breakout discussions – please create ad hoc Zoom rooms for remote participation





Lake of Geneva

Pt7: collimators

Pt8: inj b2
LHCb

ATLAS

CERN Meyrin

CERN Prévessin

SPS

Pt2: inj b1
ALICE

Pt6: dump

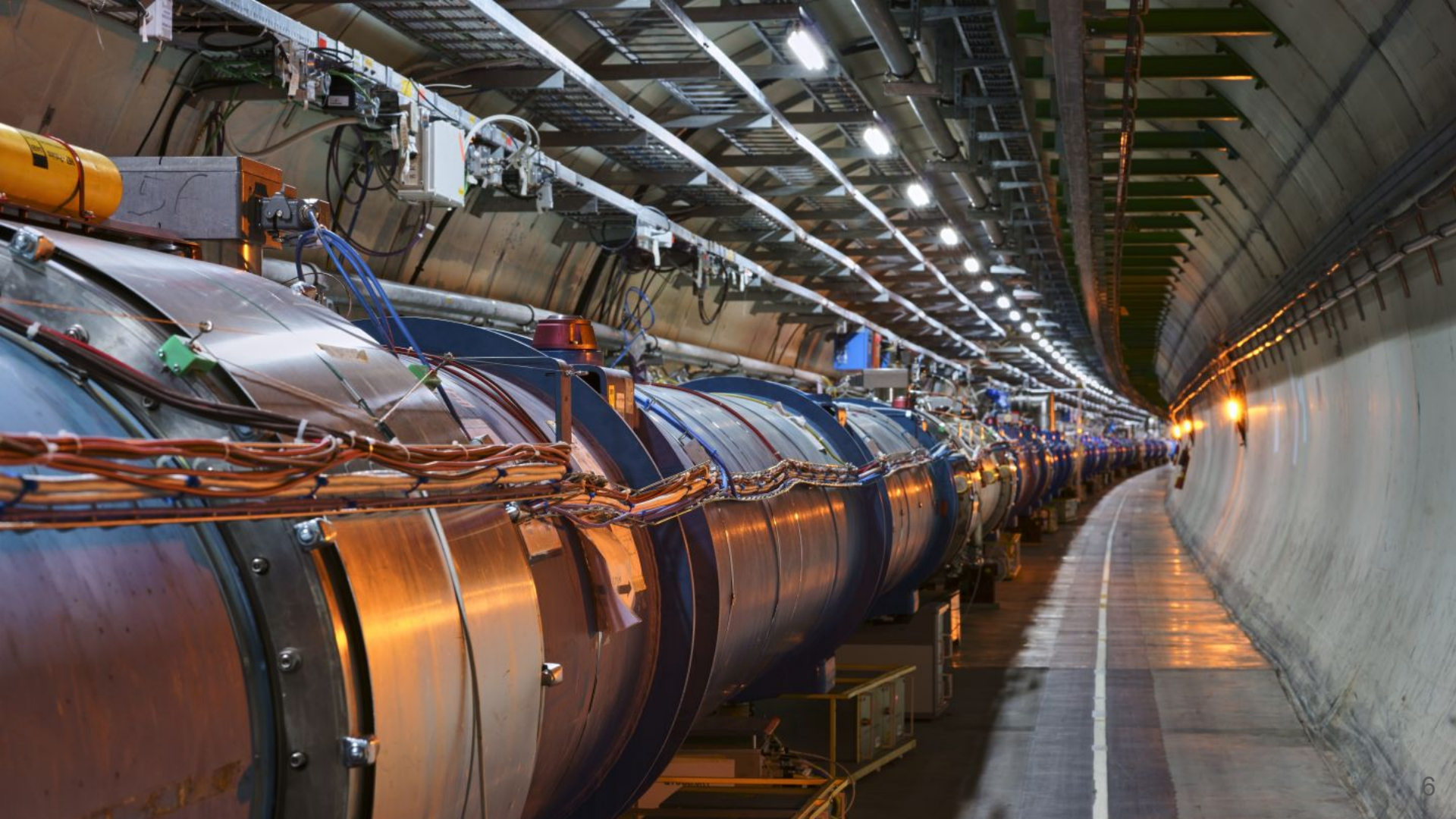
SUISSE
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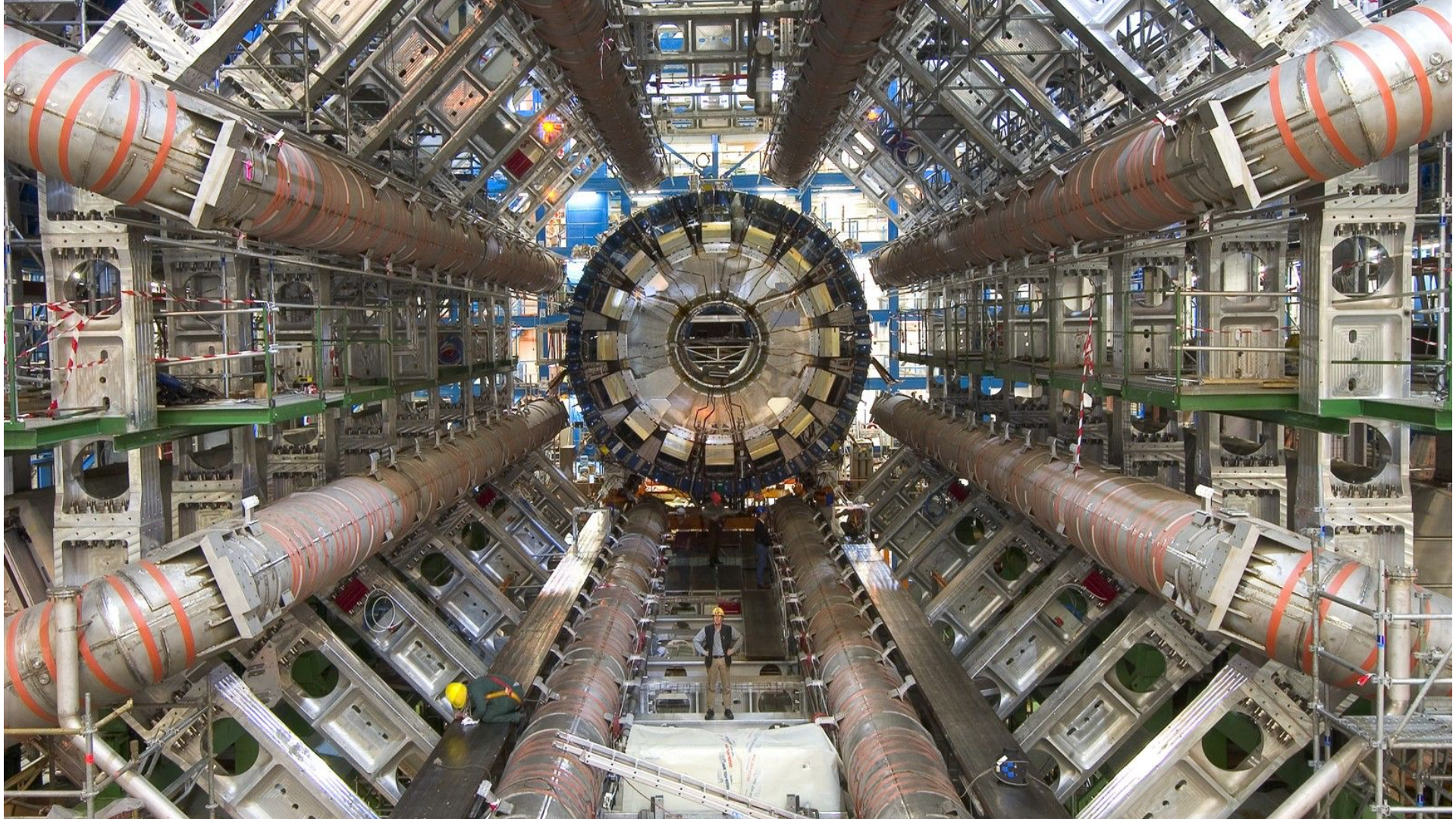
CMS

Pt4: RF & BI

Pt3: collimators

LHC 27 km





Physicists Find Elusive Particle Seen as Key to Universe

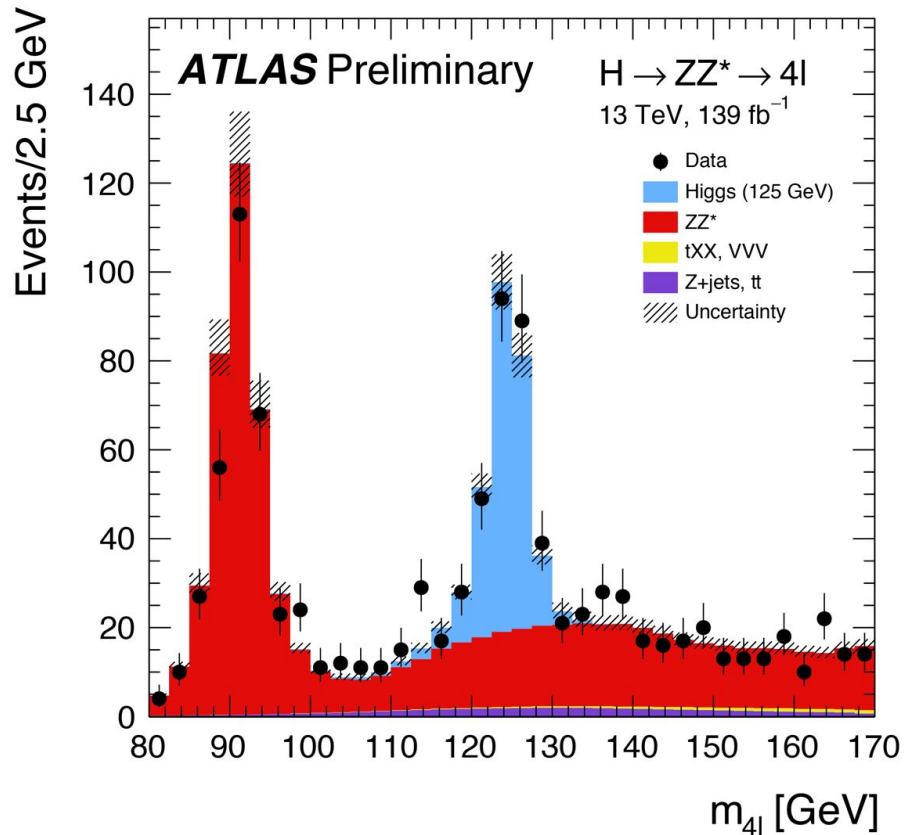
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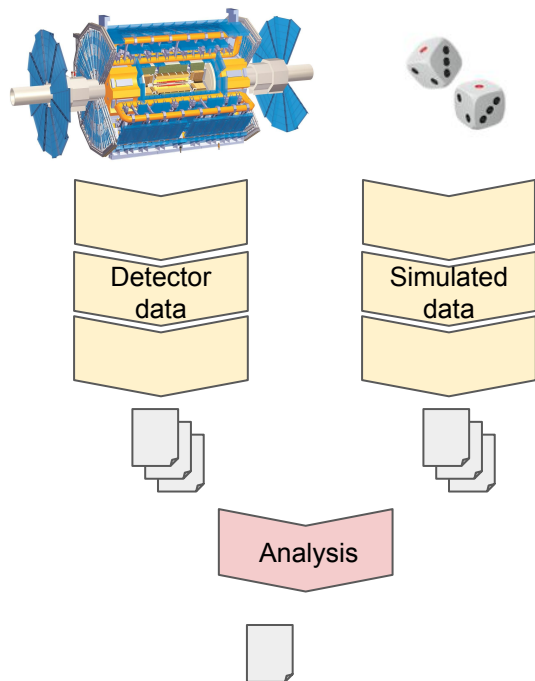
Scientists in Geneva on Wednesday applauded the discovery of a subatomic particle that looks like the Higgs boson. Pool photo by Denis Balibouse

By **Dennis Overbye**
July 4, 2012

ASPEN, Colo. — Signaling a likely end to one of the longest, most expensive searches in the history of science, physicists said Wednesday that they had discovered a new subatomic particle that looks for all the world like the Higgs boson, a key to understanding



ATLAS computing flow



“Production”

- Generic Data Preparation for everyone within the collaboration.
- Highly Structured and centrally organized

“Analysis”

- Analysis of preprocessed Data with a specific Analysis Goal in mind
- More heterogeneous
- The “Workflow” we’re talking about in this workshop

Overview of HEP Analysis

Analyses aim to extract insight from particle collisions:

- Search for particles/processes
- Measure quantities

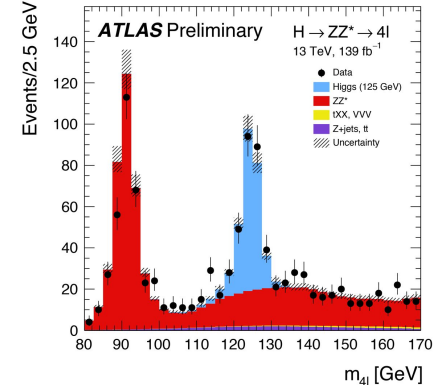
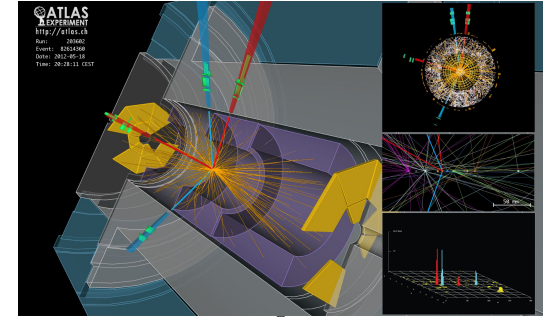
Datasets are typically:

- Large ($O(\text{mn})$ events/ $O(\text{TB})$)
- Distributed

Typically many steps transforming/reducing data:

- Reduction of background
- Filling histograms
- Log-likelihood fitting

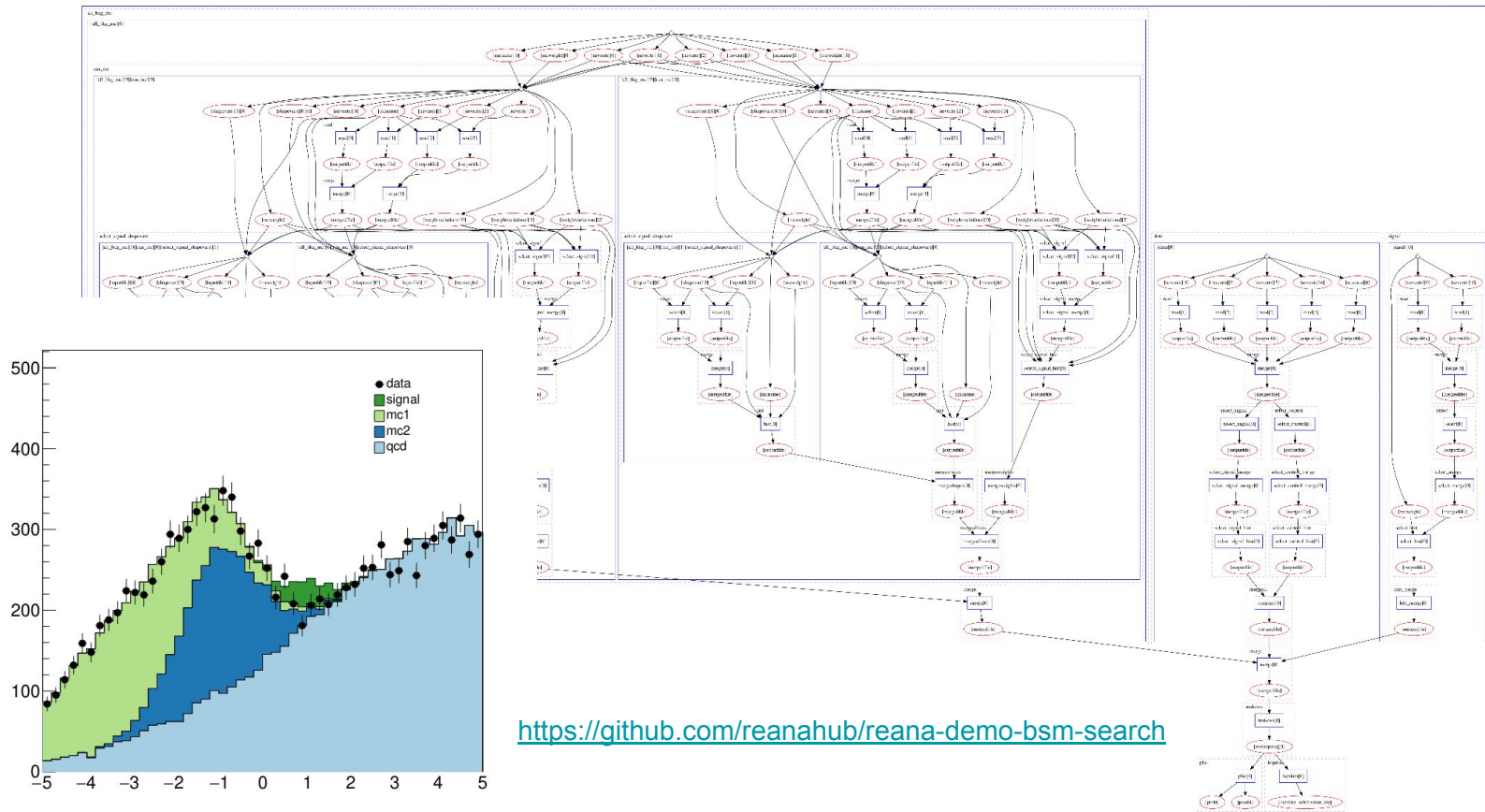
Analyses often have many branches for studies (e.g. systematics)



HEP-orientated questions to consider for discussion

- Need each step of a workflow to run in bespoke software environment (Linux container support is required. What runtimes are supported? E.g. Docker, Podman, Apptainer/Singularity)
- Workflow engine needs to be isolated from analysis code – how can we best separate the two while still making use of workflow commands natural during analysis development process?
 - e.g. avoid including workflow tooling in analysis software
 - Anything that needs to be changed in analysis software?
- Workflow scheduling: where can workflows be executed using typical HEP resources (HTCondor, SLURM, WLCG, Kubernetes...)
 - Can there be some generic solutions to this that don't need implementations for each engine?
- Dynamics graphs
 - Number of files could be unknown in advance of runtime
 - Want to be able to control processes that call task graph builds (e.g. Dask). How is balance created?

Example Workflow



reana

Reproducible research data analysis platform

Flexible

Run many computational workflow engines.



Scalable

Support for remote compute clouds.



Reusable

Containerise once, reuse elsewhere. Cloud-native.



Free

Free Software. MIT licence.
Made with ❤️ at CERN.



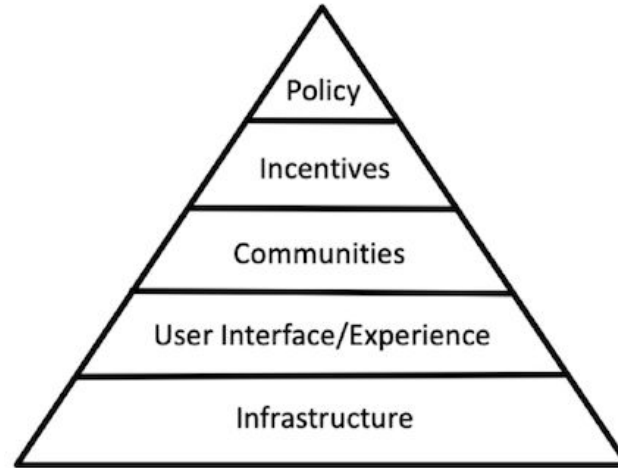
Challenges

Main observation:

We can do this technically and we've run workflows at scale at CERN

But use is still more “top-down” mandated
These tools are not yet organically used in HEP

Trying to learn from other communities and identify what's missing



Make it required

Make it rewarding

Make it normative

Make it easy

Make it possible

Open Science Pyramid

Workshop dinner

The workshop dinner will take place at [Luigia Academy Meyrin](#) on Thursday (tomorrow) at 19:00.

It's a 20-minute walk from IdeaSquare. If you want to walk there together, we'll **leave from CERN hostel building 39 at 18:35.**

Food is covered by our sponsors – drinks will need to be paid for individually

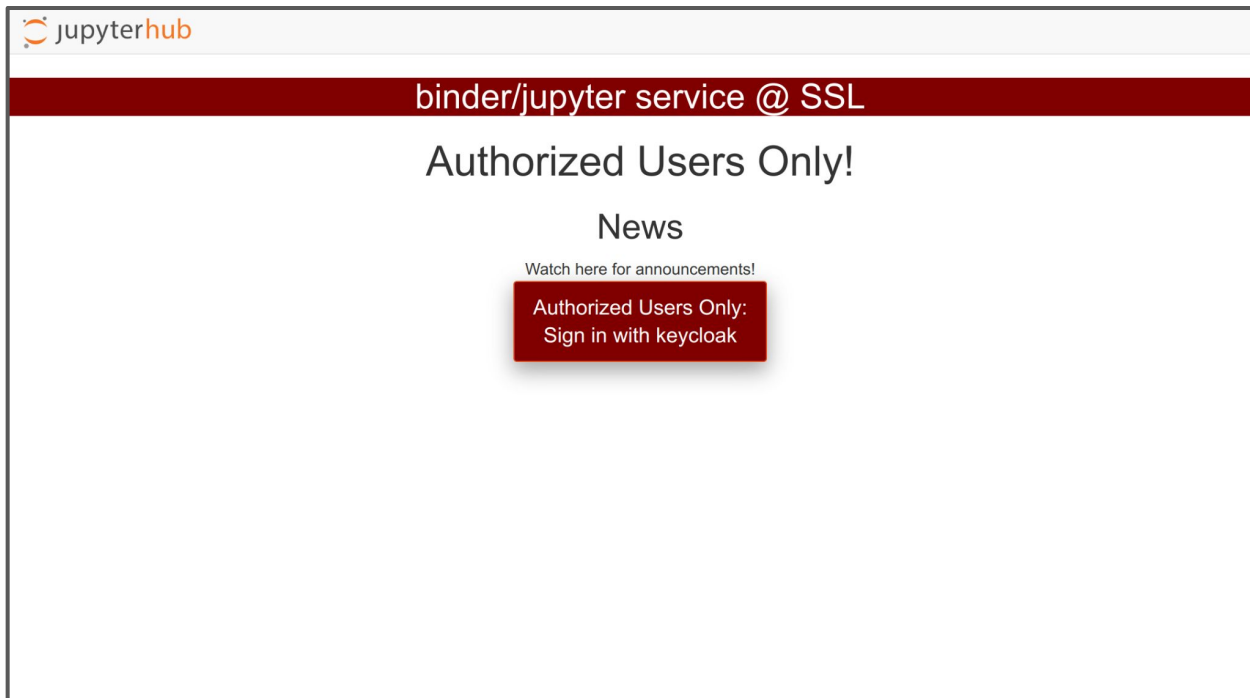
If you would like to join and haven't filled the [survey](#) yet, please do so **by 17:00 today**

Live Notes

- Have a CodiMD setup for community live notes
<https://codimd.web.cern.ch/bknH2bfqS26ORazJ-eRnOA?both>
- Please contribute notes, questions, and discussion there
- Will be used when writing a workshop summary white paper

IRIS-HEP SSL BinderHub

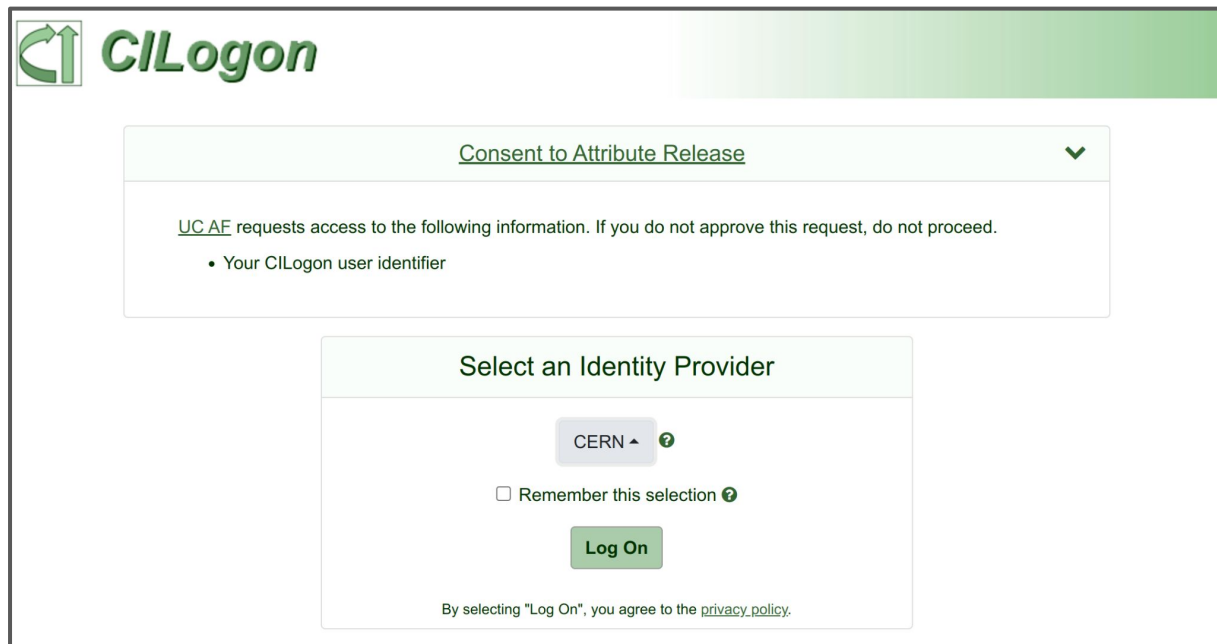
- <https://binderhub.ssl-hep.org/>



The screenshot shows a web browser window with the JupyterHub logo in the top left corner. A dark red banner at the top of the page reads "binder/jupyter service @ SSL". Below the banner, the text "Authorized Users Only!" is centered. Underneath that, the word "News" is centered, followed by the text "Watch here for announcements!". At the bottom of the page, there is a dark red button with white text that says "Authorized Users Only: Sign in with keycloak".

IRIS-HEP SSL BinderHub

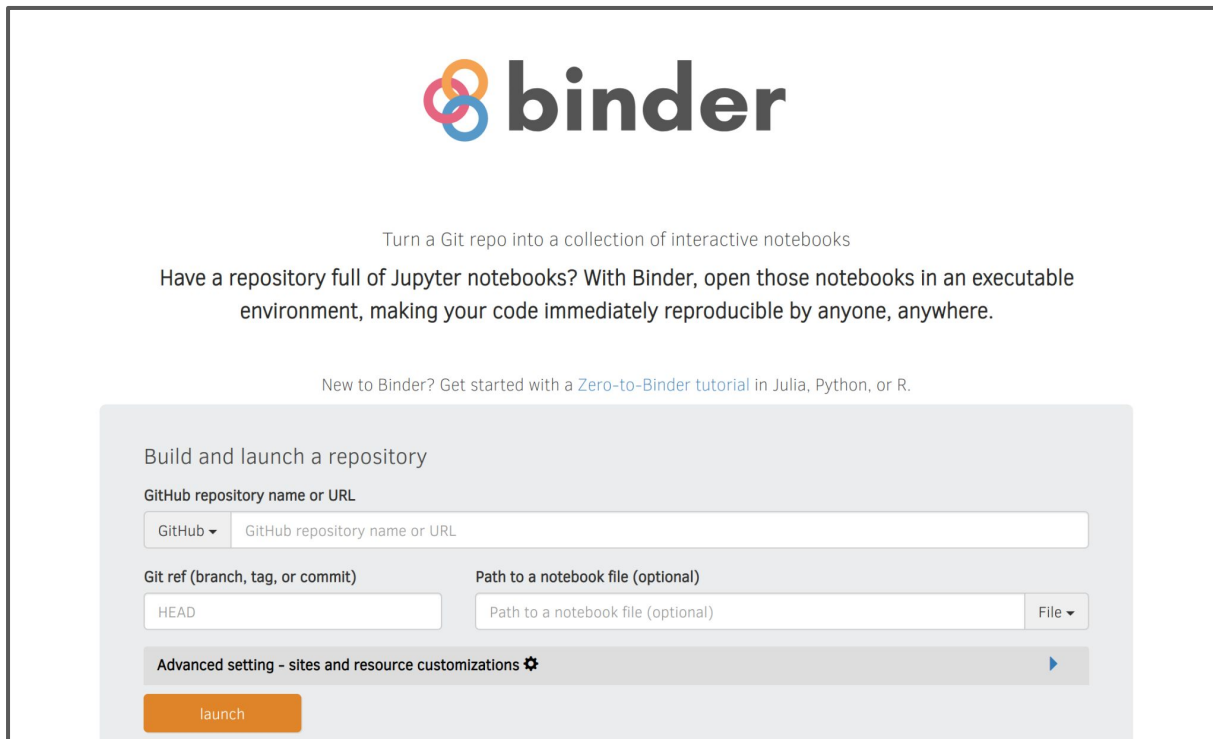
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The screenshot displays the CILogon interface. At the top left is the CILogon logo, which consists of a green circular arrow icon and the text "CILogon". Below the logo is a green header bar. The main content area is white and contains two primary sections. The first section is titled "Consent to Attribute Release" and includes a dropdown arrow on the right. Below this title, a message states: "UCAF requests access to the following information. If you do not approve this request, do not proceed." followed by a bulleted list: "• Your CILogon user identifier". The second section is titled "Select an Identity Provider" and features a dropdown menu currently set to "CERN" with a question mark icon to its right. Below the dropdown is a checkbox labeled "Remember this selection" with a question mark icon. A green "Log On" button is positioned below the checkbox. At the bottom of this section, a small line of text reads: "By selecting 'Log On', you agree to the [privacy_policy](#)."

IRIS-HEP SSL BinderHub

- <https://binderhub.ssl-hep.org/>



The screenshot displays the BinderHub interface. At the top center is the Binder logo, consisting of three interlocking rings in orange, pink, and blue, followed by the word "binder" in a bold, dark grey sans-serif font. Below the logo is the text "Turn a Git repo into a collection of interactive notebooks". Further down, a paragraph reads: "Have a repository full of Jupyter notebooks? With Binder, open those notebooks in an executable environment, making your code immediately reproducible by anyone, anywhere." Below this is a link: "New to Binder? Get started with a Zero-to-Binder tutorial in Julia, Python, or R." The main form area is titled "Build and launch a repository" and contains the following fields and controls:

- A dropdown menu for "GitHub repository name or URL" with "GitHub" selected.
- A text input field for "GitHub repository name or URL".
- A dropdown menu for "Git ref (branch, tag, or commit)" with "HEAD" selected.
- A text input field for "Path to a notebook file (optional)".
- A dropdown menu for "Path to a notebook file (optional)" with "File" selected.
- A link for "Advanced setting - sites and resource customizations" with a gear icon and a right-pointing arrow.
- An orange "launch" button at the bottom.

Questions? Ask the organisers



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Jamie Gooding
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Lukas Heinrich
(Technische Universität
München)



Clemens Lange
(Paul Scherrer Institut PSI)

Discussions / Questions to ask Related to HEP Analysis

- Expectations
 - Each step can run in its own unique software environment
 - Container support
 - Container runtime support (e.g. Snakemake supports Apptainer but not yet podman)
 - How do you pass state between jobs?
 - object store, filesystem, ...
 - The graph needs to be dynamic
 - we need to run a step that downloads all the files, but you don't know in advance how many files you will have to run on
 - Need the language to also not become an overhead (issue of target based languages)
 - Control flow:
 - If else constructions, dynamic, ...
 - What does the user experience look like
 - We know that these tools exist, but how to they work in the typical workflow?
 - What does the scientist's day to day look like
 - Do they work on one workflow?
 - Do you work on a partial execution for a long time?
 - How do you work at the petabyte scale?