Elastic Analysis Facility: a JupyterHub-based deployment



- Originally standalone Jupyter Notebooks
 Evolved to a self-hosted, multi-user platform for hosting multiple notebooks, kernels and highly customizable environments.
- Can be deployed in multiple platforms including Cloud, on prem and Kubernetes.
- ✓ Implements authentication, login pages and token-based roles
- ✓ Tracks activity and does effective resource management
- ✓ Proxying is done behind the scenes
- ✓ Pseudo-interactive (not HPC or HTPC): launches container on single node



A JupyterHub-based deployment - Login and Auth

C O A https://analytics-hub.fnal.gov/hub/login?next=%2Fhub%2F

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💭 jupyter<mark>hub</mark>

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Welcome to JupyterHub @ the Fermilab Elastic Analysis Facility

Click below to login

If you have an existing environment and want to run it as a notebook, go to EAF BinderHub (experimental)

EAF is in beta testing phase. This is the point where we need your help:

- Please note that GPU availability is on a first come, first serve basis. If you request a notebook with a GPU and it times out, please try
 again later.
- · Inactive/Idle notebooks will be automatically stopped after 8 hours
- To report your feedback please visit the following GitHub issue, open as a safe feedback space.
- If you uncover a security issue, please report it privately by emailing eaf-admins@fnal.gov
- If you find any other regressions, please open an issue in the EAF GitHub repository
- If you don't find any issues, we also appreciate positive input. Make sure to add the successful update on the feedback space.
- Accessible from the Lab network or via VPN
- Login with SSO
- UID/GID is propagated to the notebook in order to preserve permissions

Sign in with Fermilab SSO

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Documentation: eafjupyter.readthedocs.io



Yelcome to the Fermilab EAF documentation!

C Edit on GitHub

Welcome to the Fermilab EAF documentation!

The **Fermilab Elastic Analysis Facility** is a kubernetes-based platform providing services for integrated data, software and computational resources to execute one or more elements of scientific analysis workflows for Fermilab experiments and scientists. These resources are centrally managed by the Scientific Computing Division at Fermilab as part of the EAF project and generally available for all Fermilab users. Check out the userdocs/index section for more information on environments, general user documentation for the analysis tools ecosystem and navigating the UI.

Important

You can get help by:

- Filing a ticket via ServiceNow
- Joining the #eaf-users channel on fnal.slack.com (e-mail eaf-admins AT fnal.gov for an invitation if you don't already have access to the slack)
- Joining and emailing the mailing list: eaf-users@fnal.gov



Support

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A JupyterHub-based deployment - Current Catalog

Server Options

GPUS (used/capacity): 10GB (4/8), 20GB (17/20), 40GB (2/2)



Rescue Image - for use if overquota or other startup issues

Resources

CPU nodes

- 8 cores guaranteed but full node (68-126) cores available when idle
- 64 GB memory
- GPU nodes
 - A100s sliced into 10GB, 20GB, 40GB fractions using Nvidia MiG (full A100 is 80 GB)
 - Up to 90 GB memory



GPU nodes



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Resources

- CPU nodes (5 nodes, but can add more)
 - 8 cores guaranteed but full node (68-126) cores available when idle
 - 64 GB memory
- GPU nodes (11 nodes, 26 GPUs)
 - A100s sliced into 10GB, 20GB, 40GB fractions using Nvidia MiG (full A100 is 80 GB)
 - Up to 90 GB memory
- Storage
 - 24 GB EAF user disk (NVMe)
 - 10 TB shared scratch space (Ceph)
 - /nashome mounted
 - /exp (experiment areas) mounted
 - **CVMFS** areas mounted
 - Can mount additional Ceph areas
- Access to batch
 - JobSub (condor_submit if CMS)



User Customization

- Curated images
- Mamba (anaconda) and pip
- Binder (build-your-own images) can be deployed if needed
- VS Code integration



Is EAF a good fit for you as a WC user?

- Yes, if:
 - You need a single node/GPU or you need a front-end to HTPC batch systems
 - You are comfortable with notebooks or the web-based terminal
- No, if:
 - You are running multinode jobs (leveraging MPI, multiple GPUs for training, etc.)*
 - You want to continue to use Slurm as a batch/HPC scheduler*
 - You absolutely need to use ssh for a pure CLI experience

* We are doing R&D on adding a Slurm GPU-focused minicluster inside EAF to cover these use cases

