

Tritium Analysis Organization

An overview of tools used

Tyler Hague

Kent State University

What tools will this cover?

- GitHub
 - Code organization and backup
 - Ease of collaboration
- Batch jobs
 - Replay many files at once
 - Consistency of work from official replays

What is GitHub?



- GitHub is a code repository and version control system based on git
- All the benefits of git, plus a web interface and cloud storage
- Accounts are free with unlimited public repositories. Go sign up!

GitHub

How are we using GitHub?

- Version Control
 - Replay Code
 - Calibration Database
 - Scripts
- Backups
- Snapshots in time
- Collaboration Streamlining

Our Repository

Our repository is located at:

<https://github.com/JeffersonLab/HallA-Online-Tritium/>

Please feel free to go over there and poke around!

The screenshot shows the GitHub interface for the repository 'JeffersonLab / HallA-Online-Tritium'. At the top, it displays the repository name and navigation options: Watch (9), Star (0), and Fork (21). Below this, there are tabs for Code, Issues (7), Pull requests (0), Projects (0), and Insights. The repository title is 'Hall A Online Scripts for Tritium Experiment'. A summary bar shows 945 commits, 3 branches, 0 releases, and 18 contributors. Below the summary bar, there are buttons for 'Branch: master', 'New pull request', 'Find file', and 'Clone or download'. The main content area shows a list of recent commits, including a merge pull request and several file updates.

Commit	Message	Time
vanlellan Merge pull request #301 from tylerkutz/master		Latest commit 5c-f9ad3 5 days ago
doc	Committing Shujie's shift checklist updates	5 months ago
replay	Current progress of event visualization script	5 days ago
scaler	accumulated changes	3 months ago
.gitignore	additions to gitignore	3 months ago

Branches

- Provide a separate work area, parallel to the main (“master”) branch
- Allows for invasive projects to be worked on without disturbing others work
 - The project doesn’t have to be rolled out until it is in a working state
- Allows frozen in time snapshots of your repository

Forks

- A Fork creates a copy of the code that is owned by you
- This is your own workspace separate from everyone else
- Your fork can include all branches from the primary repository

Task List/Issue Tracker

JeffersonLab / HallA-Online-Tritium

Watch 9 Star 0 Fork 21

Code Issues 7 Pull requests 0 Projects 0 Insights

is:issue is:open Labels Milestones [New issue](#)

7 Open ✓ 10 Closed Author Labels Projects Milestones Assignee Sort

- Split rootfiles have many VDCEff histograms
#271 opened on Mar 7 by vanlellan 4
- RHRS detector edges see no hits
#202 opened on Jan 23 by vanlellan
- RHRS Shower Calibration
#201 opened on Jan 23 by vanlellan
- Make SPOT usable at high angles
#196 opened on Jan 23 by vanlellan
- Make SpotL 3rd 2d plot use BPM coordinates
#173 opened on Jan 12 by vanlellan 2
- HRS angle and p0 in rootfile is NOT correct
#152 opened on Dec 14, 2017 by ShujieL
- prepare tritium CODA configurations
#3 opened on Jun 30, 2017 by vanlellan 3

Part 2: Batch Jobs

Why Use Batch Jobs?

- Batch jobs allow you to automate large or redundant processes
- By running many jobs at once, your work is complete faster
- The ifarm is not intended for running code. By using the batch farm, we avoid slowdowns from using up the ifarm's resources

Scientific Workflow Indefatigable Factotum

- (or just swif)
- Swif is the system used to submit and control jobs sent to the batch farm
- Learning to use swif will make batch jobs a breeze
- <https://scicomp.jlab.org/docs/swif>

How to submit a job

- First, you need a script that runs everything the job will do
- Next, you need a jscript file that tells the batch system about your job
- Submit the job with:

```
`swif add-jsub -workflow [workflow_name]  
-create -script [path_to_jscript]`
```

What are we doing with batch jobs?

- Raw data replays
- Pedestal scan
- More to come

THANK YOU