Using the eLogbook

The eLogbook is the central hub for data management and data processing. It is a website at https://cryoem-logbook.slac.stanford.edu/. It (amongst other things):

- Provides an interface for operators to manage experiments
- (provides an interface to) Automatically move the data from the microscopes to the clusters
- Setup permissions on who should have access to the experimental data
- Setup remote access so that users may control the TEMs via FastX
- Provide image and data previews of aligned, ctf'd and picks images in near real time via SLACK
- Provide summary information of the experiment (histograms of resolution etc)
- Provide 'notebook' functionality to allow users to annotate and log their experiment

As an Operator

The role of an operator is to prepare the data management and pre-processing pipelines for a microscope user. This entails:

1. Creating an 'experiment' in the following nomlecture: `YYYYMMDD-<PROPOSAL ID>`
    a. One can clone an existing experiment (recommended) or create a new one
2. Edit the experiment (in the list of experiments) with the appropriate details: specifically include
    a. The name and email of the PI
    b. add a 'Leader' to the experiment (SLAC unix username) - this person should be the person who is physically running the experiment and collecting data
    c. Assign the correct TEM to the experiment
3. Once an experiment has been prepared, it must be 'switched' on with the appropriate TEM.
4. Once an experiment is finished, the TEM should be put into standby

As an User

The logbook provides a means for the user to have their data automatically copied to long term storage. It will also instantiate the pre-processing pipelines to automatically correct and align your images. It will also perform some rudimentary particle picking. Image data will also be relayed back to the user via the logbook and also via a SLAC-cryoEM slack channel.

Before collecting data, you should edit your sample data under the sample tab. Be sure to include information about

1. the type of data collection you are performing [`tomography` or `single-particle`]
2. the image format you are collecting with [`.tif` or `.mrc`]
3. the apix value
4. the fmdose (A^2 per frame) - used for motioncor2
5. whether the images are `superres` (set to `1` for yes, `0` for no)
6. whether the images are collected using a `phase_plate` or not.

Slides from May 2018