Changelist

Version: 1.0_dev

This version it the developer preview of v1.0 of the DRR microscope software. This version contains a significant overhaul of the GUI, underlying scan acquisition protocols and camera engine. This version is intended to initial use of the new engine, with updates planned to improve the data viewer and integrate calibration routines.

Features

- GUI now fully featured for the main acquisition workflows. Use `gui` to launch from the Command Line Interface.
- Separate acquisition modes for linescan and mapping
    - Linescan will interpolate the `X` and `Y` positions and generate a scan with `X` resolution along that line.
- `sethome` and `homeall` enabled, with `Start Pos` and `Stop Pos` position buttons
- Rehaul of the camera engine means the TUCAM error should be a thing of the past.
    - Nevertheless, `camclose`, `camopen`, and `refresh` commands now allow dynamic reconnection to the camera in the event of a TUCAM error
- Instrument errors are now logged for later review. Note that some errors are yet to be shifted to the logger system, but will still appear in the console

Fixes

- Integer overflow error was causing spectral artefacts on high-intensity frame averaging. Moved to 32 bit floats to fix and reduce the quantization error on saving.
- `acquire` works, and saves a single file to the file directory.

Limitations and CAUTIONs:

- There is currently no overwrite protection for scans. Be sure to edit filename before continuing.
    - `acquire` single frames will autoincrement the filenames with an index.
- Background subtraction is **not yet implemented.** This means the data will be a little messy, but background subtractions can be applied in post processing for important samples.
- GUI bugs will crash the entire script - there is no workaround, but they only happen because of my mistakes, and can be fixed quickly. Notify me of any hard crashes and I'll find and patch the code.
- Separate scanning resolutions in map mode and `Z` scans are not yet implemented (the checkboxes do nothing 😂).
    - Scan resolution ALWAYS defaults to the X resolution, so **make sure the X resolution reflects your desired scan resolution.**
- Polarization scans are technically implemented but will result in an error because the calibrations do not exist. Wait until calibrations have been obtained to perform polarization scans.

User Manual

All commands can be entered via the CLI or the GUI console window. I recommend the GUI for most operations, and especially the scan acquisition. Most commands can **only** be entered via the console. Buttons for common commands can be requested.

GUI can be safely closed at will to switch between GUI and CLI modes.

Alignment

Important steps in bold marked with **/-!-**

Troubleshooting tips are marked with **(?)**

1. Home all motors with `homeall.`
2. After homing is successful, `sall 750` to test alignment.
    1. If 45 degree mirror is misaligned, perform alignment process...
3. Place sulfur or MoS_2 under the microscope objective.
4. Focus to the sample. Use `imagemode` and camera, or:
    1. Place a target card in the cage component nearest the first beamsplitter (camera beamsplitter) in the optical axis.
    2. Ensure the laser passes through the target card in the center.
        1. Move `g1 <steps>` to jog motor and bring laser into alignment with the target card.
    3. Observe the reflected pattern on the target card to find the point at which the reflected beam size is $\approx$ target hole diameter.
5. Switch to or ensure the instrument is in `ramanmode` (beamsplitters out of optical axis).
6. `run` to acquire live spectra at `1-2` second acquisition time.
7. Search for any signal, and sequentially jog motors to improve signal intensity and find correct values:
    1. Work through `g2 <steps>`, `g3 <steps>`, and `g4 <steps>` in sequence.
    2. Repeat *step 6.1* if necessary to improve signal.
    3. Aim for high intensity signal and low-frequency cutoff at the double monochromator intermediate slit.
        1. **(?)** If no signal is found, try opening the spectrometer slit with `men <microns>` (use ~ 300 micron width. Normal operation is 50 microns).
        2. **(?)** Switch to image view mode on the data viewer and look to see if the spectrum falls at the correct row on the sensor array to be binned by the data viewer
        3. **(?)** Change the binning on the data viewer to use a larger range
        4. **(?)** Remove the intermediate slit if needed. If still struggling, move to 785 nm and use the notch filter as a cutoff for the monochromator.
8. Use microscope focus to improve signal after an initial jog of the motors.
9. When optimal alignment is found, check the current wavelength for each motor with `wai`.

1. **/- ! -\ If any motor wavelength values are more than 3 nm from expected, note the motor label for *step 11*.**

10. **/- ! -\ Reference the current positions to 750 nm with `reference 750`.**
11. **/- ! -\ If any motors were noted in *step 7.1*, recalibrate their home positions with `calhome <motor_label>` This re-measures the home position with respect to the new jogged motor positions, which will save the home state and make the next alignment easier.**
    1. After recalibration, the motor needs to be returned to its correct value. Use `sl/sg/sm 750`
12. Ensure current positions are 750 nm.
13. Move to another instrument wavelength to confirm the calibration is working `sall <lambda>`. Try multiple wavelengths across the expected range.

Acquisition

1. Use either CLI or GUI to perform scans. GUI is recommended.
2. Pick scanmode with the scanmode button or `scanmode` command to toggle.
3. Set home to define a zero position
4. Find sample in `imagemode` . Pick positions and use Start Pos and Stop Pos or `setstart` and `setstop` to define scan ends.
5. Use `run` in `ramanmode` to confirm the sample produces good signal and to determine ideal acquisition time.
    1. Focus the microscope electronically using `z <microns>` or `focus` to enable focusmode in the console
        1. **/- ! -\ Note: focus mode will pause the GUI and unlock the CLI. You must exit from the cli with `exit` to restore the GUI operation.**
6. Edit acquisition time, filename, and number of frames to acquire.
7. **/- ! -\ Ensure the filename is unique - scans with the same filename will overwrite without warning.**
8. Confirm basic parameters in GUI window.
9. Click `Run Scan` or `acquirescan` to start the scan. A dialogue box will ask for confirmation of scan parameters in GUI mode.
10. Wait for scan to complete. The microscope will remain at the final scan position (not return to start).

Graphical User Interface Guide

... in progress...