Troubleshooting

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Having trouble?

This page covers common problems and their solutions, organised by the stage at which they occur.

1 Setup issues

1.1 MATLAB cannot find functions

Symptom: `Undefined function or variable 'process_freely_walking_data'` or similar errors.

Solution: Ensure the freely-walking-optomotor repository is on the MATLAB path:

```
addpath(genpath('/path/to/freely-walking-optomotor'));
```

Verify by running `which process_freely_walking_data` — it should return a valid path.

1.2 Missing toolboxes

Symptom: Errors referencing functions like `ranksum`, `fittype`, or `circ_vtest`.

Solution: The following MATLAB toolboxes are required:

Toolbox	Required for
Statistics and Machine Learning Toolbox	Statistical tests (`ranksum`, FDR correction)
Image Processing Toolbox	Video processing
Circular Statistics Toolbox	Phototaxis analysis (`circ_vtest`, Watson-Williams test)

Install missing toolboxes via MATLAB's Add-On Explorer.

1.3 Arena not responding

Symptom: The protocol script runs but no stimuli appear on the arena.

Possible causes:

- Arena is not powered on or the controller is disconnected
- PControl cannot connect — try running PControl standalone to test the connection
- The `panel_com` functions are not on the MATLAB path — verify G4_Display_Tools is installed

1.4 BIAS not recording

Symptom: The protocol runs but no `.ufmf` video file is created.

Possible causes:

- BIAS was not started before the protocol script
- The camera is not acquiring (check that IR illumination is on and the frame rate is 30 fps)
- Disk space is full on the recording drive

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2 Running the experiment

2.1 LOG file not created

Symptom: No `LOG_*.mat` file appears in the experiment directory after the protocol finishes.

Possible causes:

- The protocol was interrupted before completion (check MATLAB command window for errors)
- The output directory path in the protocol script is incorrect
- MATLAB did not have write permissions to the directory

2.2 Flies not visible in video

Symptom: The `.ufmf` video shows a dark image with no flies visible.

Possible causes:

- IR illumination was not turned on
- The camera exposure settings in BIAS are too low
- The arena LEDs were overpowering the IR illumination (LEDs should be green, not visible to the IR camera)

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3 Tracking issues

3.1 FlyTracker loses flies

Symptom: Fewer flies tracked than were loaded into the arena. The `n_fly_data` array shows a large number in the third element (flies removed).

Explanation: The function `check_tracking_FlyTrk` removes any tracked object whose frame count does not match the mode frame count. This catches cases where:

- A fly's tracking was split across multiple identities
- A non-fly object (debris, shadow) was briefly tracked
- A fly stopped moving and was lost by the tracker

What to check:

- Verify the arena was clean before loading flies
- Check that lighting conditions were consistent throughout the experiment
- Review the `.ufmf` video to see if flies were genuinely lost from tracking

3.2 High velocity artifacts

Symptom: Unrealistic velocity spikes in the timeseries plots.

Explanation: Frames where the forward velocity exceeds 50 mm/s are treated as tracking errors and set to NaN. These are then filled using interpolation. If many consecutive frames exceed this threshold, the interpolation may produce unusual values.

What to check:

- A few isolated spikes are normal and handled automatically
- Persistent high-velocity regions suggest the tracker jumped between flies — re-run FlyTracker with adjusted settings or exclude the cohort

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4 Processing issues

4.1 `process_freely_walking_data` errors

Symptom: The batch processing function fails on a specific experiment folder.

Common causes:

- **Missing files:** Ensure the experiment folder contains a `.ufmf` video, `LOG_*.mat` file, and a subdirectory with `trx.mat` and `*-feat.mat`
- **Date format:** The function expects the date folder to be named `YYYY_MM_DD` (underscores, not hyphens)
- **Empty LOG:** If the protocol was aborted, the LOG file may be incomplete

Debugging approach:

1. Navigate to the experiment folder manually
2. Try running `process_data_features` directly on that folder
3. Check that `load('LOG_*.mat')` works and the LOG structure contains the expected fields

4.2 Strain name mismatches

Symptom: Data from the same strain appears under different names in the combined DATA structure.

Explanation: Strain names are extracted from the LOG metadata and can vary due to typos or inconsistent naming. The function `check_strain_typos` attempts to normalise common variations, but may not catch all cases.

Solution: Check the strain names in the LOG files for consistency. If needed, update the mapping in `check_strain_typos.m`.

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5 Analysis issues

5.1 `comb_data_across_cohorts_cond` fails

Symptom: Error when trying to combine data across cohorts, often referencing missing fields or unexpected structure.

Common causes:

- **Missing condition numbers:** Older protocols (before protocol 24) do not save condition numbers to the LOG file. The function requires this field. Use a version-specific parser (e.g. `comb_data_across_cohorts_cond_v14.m`) for older protocols.
- **Mismatched protocols:** Experiments from different protocol versions may have different numbers of conditions or different timing structures
- **Incomplete experiments:** If a protocol was interrupted, some conditions may be missing from the LOG

5.2 Empty or unexpected results

Symptom: Plots show flat lines or the DATA structure has empty fields.

What to check:

- Verify the processed `*_data.mat` file exists and contains `comb_data` with the expected fields
- Check `n_fly_data` — if all flies were removed during tracking QC, `comb_data` arrays will be empty
- Confirm the LOG file has the correct condition definitions (pattern IDs, speed values)

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6 Hardcoded paths

Several files contain paths specific to the original computers. If running on a different machine, update these:

Location	What to change
`generate_circ_stim_ufmf.m`	Path to JAABA repository (currently `/Users/burnettl/Documents/Non-GitHub-Repos/JAABA-master`)
`generate_circ_stim_ufmf.m`	Path to patterns folder (`patterns/Patterns_optomotor/`)
Processing functions	Root data directory paths
`make_summary_heat_maps_p27.m`	`ROOT_DIR` for results (currently `/Users/burnettl/Documents/Projects/oaky_cokey`)

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7 Quality control

The processing pipeline generates several overview figures that can help diagnose data quality issues:

Figure	What it shows	What to look for
Locomotion histograms (`make_overview`)	Distribution of velocity, angular velocity, and turning rate	Bimodal distributions may indicate mixed fly health; very narrow distributions suggest most flies were stationary
Full-experiment timeseries (`plot_all_features_full`)	All flies' metrics across the entire protocol with coloured condition markers	Baseline drift, sudden changes in activity, or missing condition periods
Acclimation timeseries (`plot_all_features_acclim`)	Metrics during the 5-minute dark acclimation	Flies should settle to a stable baseline; consistently high activity may indicate stress or arena vibration
Per-condition plots (`plot_allcond_onecohort_tuning`)	Mean + SEM for each condition	Responses should be consistent across the two repetitions; large SEM suggests variable behaviour