

# Dashboard

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The interactive Dash web dashboard provides a browser-based interface for exploring processed experimental data from the freely-walking optomotor experiments. It is built with [Plotly Dash](#) and [Dash Bootstrap Components](#).

## 1 What the dashboard shows

The dashboard allows you to:

- Select a **protocol results directory** and browse all strains and conditions within it
- View **timeseries plots** of behavioural metrics (forward velocity, angular velocity, turning rate, distance from centre, distance delta) for any strain vs. the empty-split control
- Compare responses across conditions in an interactive subplot layout
- Switch between metrics, strains, and conditions using sidebar controls
- View **cohort-level statistics** (number of vials, number of flies per strain)

## 2 Prerequisites

The dashboard requires:

- The [freely-walking-optomotor](#) repository cloned locally
- The `pixi` package manager installed ([pixi.sh](#))
- Processed result `.mat` files from `process_freely_walking_data` (see [Analysis](#))

## 3 How to start the dashboard

### 3.1 Option 1: Shell alias (recommended)

Set up the `dash-freely` alias by adding this line to `~/.zshrc` (or `~/.bashrc`):

```
alias dash-freely='~/Documents/GitHub/freely-walking-optomotor/dashboard.sh'
```

Then from anywhere in the terminal:

```
dash-freely          # start the dashboard (opens http://localhost:8050)
dash-freely preprocess # preprocess .mat files to Parquet first
```

### 3.2 Option 2: Run directly with pixi

```
cd python/freely-walking-python
pixi run preprocess # convert .mat files to Parquet (required on first use or after new data)
pixi run dashboard  # start the Dash app on http://localhost:8050
```

The dashboard will open automatically in your default browser once the server is ready.

## 4 Preprocessing

Before using the dashboard for the first time (or after new data has been processed), you need to convert the MATLAB `.mat` result files to Parquet format for fast loading:

```
dash-freely preprocess
# or: cd python/freely-walking-python && pixi run preprocess
```

This reads all `*_data.mat` files from the results directory and writes Parquet files to a `_preprocessed` subdirectory alongside the original data. The preprocessing step only needs to be repeated when new experiment data has been processed.

## 5 How the dashboard works

The dashboard is built from several modules in `python/freely-walking-python/dashboard/`:

| Module                       | Purpose  |
|------------------------------|--|
| <code>app.py</code>          | Main Dash application layout (sidebar, content area, controls)                             |
| <code>callbacks.py</code>    | Interactive callback functions that update plots when selections change                    |
| <code>data_loader.py</code>  | <code>DataStore</code> class that loads Parquet data and provides strain/condition lookups |
| <code>preprocess.py</code>   | Converts <code>.mat</code> result files to Parquet format                                  |
| <code>processing.py</code>   | Data processing utilities for the dashboard  |
| <code>cohort_stats.py</code> | Computes per-strain cohort and fly count statistics  |
| <code>heatmap.py</code>      | Heatmap visualisation components   |
| <code>constants.py</code>    | Shared constants (metric names, condition labels, default paths)                           |

On startup, the dashboard pre-loads all strain data into memory for fast interactive use. This means startup takes approximately 20–30 seconds, but subsequent interactions are near-instant.

## 6 Using the dashboard

1. **Set the data directory** — The sidebar shows a text input for the path to the protocol results folder (e.g. the `protocol_27` results directory). The default path is read from the configuration.
2. **Select a strain** — Choose from the dropdown list of available strains.
3. **Select a metric** — Choose the behavioural metric to plot (forward velocity, angular velocity, turning rate, distance from centre, or distance delta).
4. **Browse conditions** — The main panel displays timeseries subplots for each condition, showing the selected strain against the empty-split control with mean and SEM shading.