

# Overview

## Table of contents

<b>1</b>	<b>Designing and running a protocol</b>	<b>1</b>
<b>2</b>	<b>Analysing the data</b>	<b>2</b>

Here is some general documentation for the freely-walking arena setup that was used to run the “Freely walking course control mechanisms screen” in 2025. This documentation includes information on how to design and run protocols, analyse the data, as well as the specifications of the arena used in experiments.

For the sake of clarity, this documentation will centre on how to run and analyse the specific protocol that was used in the screen experiments (`protocol_27.mat`). Other protocols that were run on this arena can be found within the `protocols` [folder](#) of the repository, but they are not documented here.

## 1 Designing and running a protocol

Patterns for the G3 arena can be generated using the `G4_pattern_generator_gui`, but for this screen all patterns and function were made from scratch using custom scripts and the protocols themselves are run through custom scripts that present the patterns using the `panel_com` class of functions from the `G4_Display_Tools` repository.

The scripts for making the different patterns can be found within the repository [here](#).

The scripts for the protocols themselves can be found within the repository [here](#). This folder contains a [subfolder](#) that contains the functions that are required to run the protocols.

## 2 Analysing the data

There are two levels to the analysis of the data from the ‘protocol\_27’ screen.

The first level is done for every run of the protocol (i.e. each individual vial of flies run) and is done by running the script `process_freely_walking_data()` ([code](#)). This function requires a string `date_to_analyse` which should be the name of the directory that was generated for the day’s experiments. It should be in the format ‘YY\_MM\_DD’. This function returns a number of figures and results files for each individual experiments (run of the protocol / vial of flies).

The second level is done after running the protocol for multiple vials of multiple strains and is done by running the script `process_screen_data` ([code](#)). This function requires a string `protocol` which is a string of the protocol number that you would like to process all of the data for, in this case `protocol = 'protocol_27'`. This function combines the data across all of the individual experiments and strains and creates timeseries plots comparing the behaviour of each strain of fly against the empty-split control flies.