

# Protocol 2

## Table of contents

### Quick summary:

More in-depth and feature-focused protocol. This protocol typically takes between 20-25 minutes.

- **Aim 1:** Determine higher resolution features of the cell's receptive field by using smaller flashes.
- **Aim 2:** Determine whether the cell displays directionally selective responses to bar sweeps in 16 directions.

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- **Overview:**

- Longer, high resolution probing of the cell's receptive field.
- Custom script design.
- Opens a pop-up at the beginning that asks the user to fill in the `peak_frame` from P1 and the side of the arena used for P1.
- This `peak_frame` value is then used to generate a protocol with the stimuli centred on the centre of the flash that elicited the greatest response in P1.
- These stimuli are presented within a 30 x 30 pixel area. The rest of the arena is set to the background intensity value.
- Only presents either dark or light stimuli. However, at the end of the protocol the `peak_frame` value that generates the protocol at the same location with the inverse contrast is returned so that the protocol can be run twice, once for each contrast if desired.

- **Location:** P2 is made de novo every time the function `generate_protocol2()` is run. A new folder of the format ‘yyyy\_MM\_dd\_HH\_mm’ is made within the the folder `C:\matlabroot\G4_Proocols\nested_RF_protocol2` that contains both the patterns, functions and experiment file `currentExp.mat` and the data that was recorded in the Log file.

**Stimulus parameters:**

**Protocol design:**

**Flash presentation:**

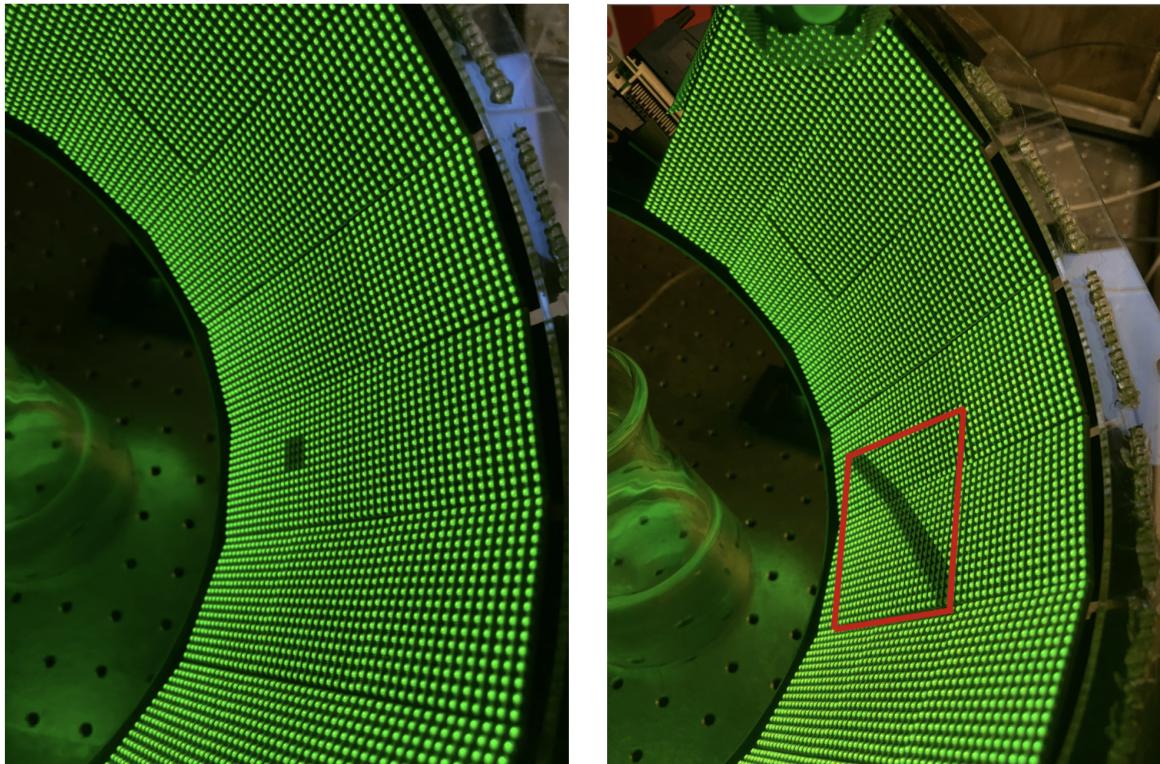


Figure 1: Figure 1 - Protocol 2 stimuli: Single dark 4 x 4 pixel flash (left) and 4 pixel wide bar (right) as presented in P2 on the G4 LED arena. These stimuli are presented within a 30 x 30 pixel area centred on the peak frame from P1.