BE-LIGHT

Improving biomedical diagnosis through light–based technologies and machine learning

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Collection of Retinal Records

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Abstract (for dissemination)	This dataset presents a comprehensive collection of retinal ganglion cell of mice ex vivo recordings obtained through multi-electrode array technology, comprising simultaneous recordings from 305 retinal ganglion cells in response to 149 unique natural movie stimuli. The data were collected to investigate efficient neural coding strategies in the retina, with particular emphasis on color processing mechanisms in naturalistic visual conditions.
Keywords	Retinal Records, Multi-Electrode Array (MEA), Light Stimulus, Color Encoding, Biomedical Diagnosis, Machine Learning

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EXECUTIVE SUMMARY

This deliverable presents a comprehensive dataset of retinal ganglion cell recordings obtained through multi-electrode array (MEA) technology. The dataset contains simultaneous recordings from 305 retinal ganglion cells responding to 149 unique natural movie clips, providing a total recording duration of 372.5 seconds. The dataset contains approximately 3.76 million spikes across all recorded cells, offering a substantial resource for investigating neural coding mechanisms in the retina.

The dataset has been collected to address fundamental questions about efficient coding in sensory systems, particularly focusing on colour processing and temporal coding strategies in retinal ganglion cells. This work directly contributes to the Be Light project objectives by providing empirical data for developing computational models of retinal function and advancing our understanding of sensory processing in naturalistic contexts.

INTRODUCTION

The retina represents the first stage of visual processing in the nervous system, transforming patterns of light into neural signals that are transmitted to the brain. Understanding how retinal ganglion cells encode visual information is crucial for multiple scientific and technological applications, including the development of retinal prosthetics, advancement of artificial vision systems, and fundamental understanding of sensory coding principles.

Traditional approaches to studying retinal function have relied heavily on simplified stimuli such as flashing spots, drifting gratings, or checkerboard patterns. While these stimuli have provided valuable insights into receptive field structure and basic response properties, they do not capture the complexity and statistical structure of natural visual scenes. Natural stimuli contain rich spatiotemporal correlations, diverse feature combinations, and temporal dynamics that are absent in simplified laboratory stimuli.

This dataset addresses this gap by providing recordings of retinal responses to natural movie stimuli. The use of dynamic natural scenes allows for investigation of coding strategies that may only be revealed under naturalistic conditions, including temporal coding mechanisms, efficient population codes, and adaptation to natural image statistics.

1. DATA DESCRIPTION

1.1.Overview

The dataset consists of two primary components: visual stimuli and neural responses. The visual stimuli comprise 149 unique natural movie clips, each lasting 2.5 seconds and presented at 60 Hz. The neural responses consist of spike times recorded from 305 retinal ganglion cells using multi-electrode array technology. Additional data include receptive field maps for all cells, obtained through separate mapping protocols.

Key Dataset Characteristics:

Total number of cells: 305 retinal ganglion cells
Number of stimuli: 149 non-repeated natural movie clips
Stimulus duration: 2.5 seconds per clip
Frame rate: 60 Hz (16.67 milliseconds per frame)
Spatial resolution: 72 by 72 pixels

1.2.Data Organisation

The dataset is organised into two directories:

Stimulus Data Directory (non_repeated_clips_folder)
Contains 149 MATLAB format files, one per stimulus clip. Each file includes the stimulus frames and timing information. File naming follows sequential numbering or descriptive conventions.

Response Data Directory (cells_folder)
Contains 305 MATLAB format files, one per cell. Each file includes spike times, receptive field masks, and receptive field coordinates. Files are named according to cell identification numbers (for example, cell_1004.mat).

1.2.1 Stimulus Structure

Each stimulus file contains the following variables:

clip_frames Variable

This variable stores the visual stimulus frames in a three-dimensional array with dimensions (5184, 150, 149).

The first dimension (5184) represents the flattened spatial dimension. The original stimulus has 72 by 72 pixels, which equals 5,184 pixels total. The spatial information is stored as a one-dimensional vector for efficient storage.

The second dimension (150) represents the temporal frames within each clip. With a frame rate of 60 Hz and a duration of 2.5 seconds, each clip contains exactly 150 frames.

The third dimension (149) represents the clip index within the complete stimulus set. This dimension allows efficient storage of metadata but note that for individual stimulus files, this dimension typically has size 1 or matches the clip number.

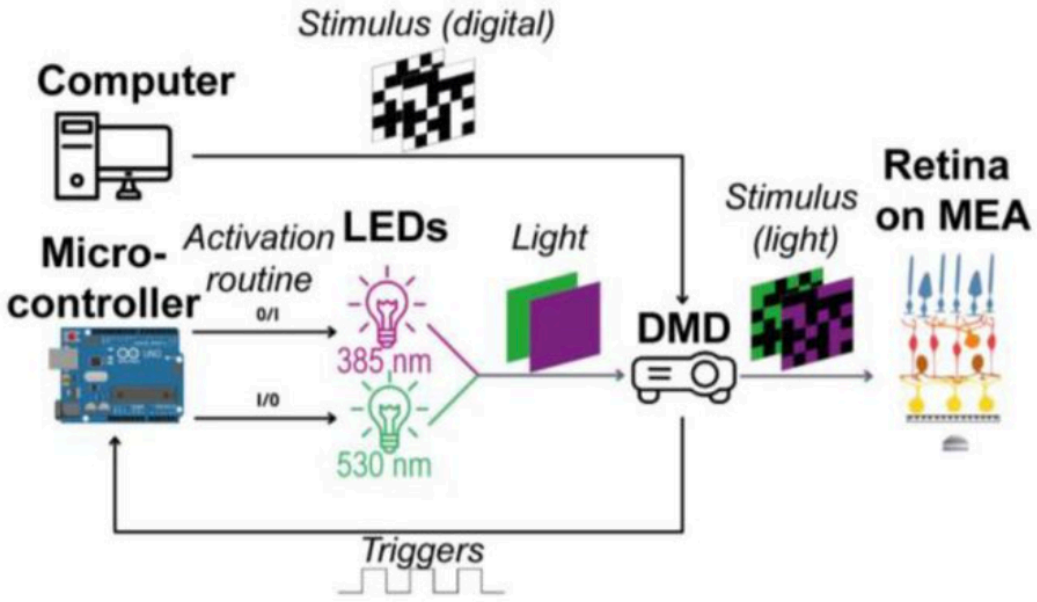
The data type is uint8 (8-bit unsigned integer) with values ranging from 0 to 255, representing grayscale or color intensity values.

To reconstruct the original two-dimensional image from the flattened format, the spatial dimension must be reshaped from 5184 elements into a 72 by 72 matrix.

time Variable

This variable provides temporal reference information with dimensions (1, 150).

The data type is float64 (double precision floating point) with values representing time in seconds. The time values range from 0.0 to 2.5 seconds, providing timestamps for



each frame within the clip.

The stimulus frames are stored in flattened format to optimize storage efficiency. The original spatial organization uses a 72 by 72 pixel grid, providing 5,184 pixels per frame. This resolution was chosen to match the spatial extent of the recorded retinal area while maintaining computational tractability.

To reconstruct the two-dimensional spatial structure from stored data:

In MATLAB: frame_2D equals reshape(clip_frames(:, frame_index, clip_index), 72, 72)
In Python: frame_2D equals clip_frames[:, frame_index, clip_index] reshaped to (72, 72)

Each pixel corresponds to a specific location on the retina, with the mapping determined by the optical magnification of the experimental setup. The spatial calibration and exact pixel-to-micron conversion depend on the specific optical configuration used during recording.

1.2.2 Response Structure

Each cell file contains the following variables:

spike_times Variable

This is the primary neural response data, stored as a one-dimensional array with dimensions (1, N) where N equals the number of spikes recorded from this cell.

Data type: float64 (double precision floating point)
Units: milliseconds
Reference point: Time zero corresponds to the onset of the first stimulus
Value range: 0 to approximately 4,247,000 milliseconds (372.5 seconds)

receptive_field_mask Variable

This variable provides spatial information about the receptive field location with dimensions (432, 432).

Data type: uint8 (8-bit unsigned integer)
Value range: Binary (0 or 1)
Interpretation: 0 indicates pixels outside the receptive field, 1 indicates pixels within the receptive field

The receptive field masks were obtained through separate mapping experiments using checkerboard or white noise stimuli. The spatial resolution (432 by 432 pixels) is higher than the natural movie stimulus resolution (72 by 72 pixels).

2.Data Acquisition

2.1.Experimental Set Up

In the schematic above, there is the experimental setup of the lab for Multi-Electrode Array (MEA) recordings with colour stimulation device (Ultraviolet and Green for mice). Two LEDs (385nm and 520nm) are modulated via a microcontroller, combined into a single beam using dichroic mirrors, and transmitted through an optical fibre to a Digital Mirror Device (DMD). The light is then focused onto the retina, positioned with the ganglion cell layer in contact with the MEA electrodes on the back focal plane of a microscope.

2.2. Data Processing

The raw MEA recordings underwent systematic processing to ensure data quality and reliability. Spike sorting was performed to isolate individual neuronal units from the raw electrode signals, with each identified unit assigned a unique cell identifier. The spike sorting process employed standard MEA analysis techniques, including threshold-based spike detection and template matching algorithm to distinguish spikes from different cells recorded on the same or neighboring electrodes.

Quality control measures were applied to ensure the dataset contains only well-isolated, stable recordings. Cells were included in the final dataset based on several criteria: consistent spike waveform morphology throughout the recording session, sufficient firing rate to enable statistical analysis (minimum average of approximately 0.1 Hz), and clear receptive field structure identifiable through reverse correlation analysis.

These criteria resulted in the final dataset of 305 high-quality retinal ganglion cell recordings.

The receptive field maps were generated using standard spike-triggered average analysis, correlating the spike times of each cell with the preceding stimulus frames. This reverse correlation approach reveals the spatial pattern of light sensitivity for each cell, providing essential information about the cell's location and spatial processing characteristics. The receptive field masks represent binarized versions of these maps, identifying the core region of visual space to which each cell responds most strongly.

3.SUMMARY

This deliverable presents a comprehensive dataset of retinal ganglion cell responses to natural movie stimuli, comprising recordings from 305 cells exposed to 149 unique video clips. The dataset provides approximately 3.76 million spikes collected over 372.5 seconds of total recording time, representing a substantial resource for computational neuroscience research into sensory coding principles.

The data are organized in a structured format with clear separation between stimulus and response components, facilitating computational analysis and model development. All stimulus files contain the visual frames and timing information, while response files include spike times and receptive field characterizations for each recorded cell. The use of natural movie stimuli enables investigation of neural coding strategies under ecologically relevant conditions, complementing traditional approaches based on simplified laboratory stimuli.

This dataset directly supports the objectives of the Be Light project by providing empirical foundations for developing and testing computational models of retinal function, particularly regarding efficient color coding and temporal processing mechanisms. The data have been prepared for public release on Zenodo, ensuring accessibility to the broader research community and promoting reproducibility and collaborative advancement of retinal neuroscience.