

# **ABR Peak Finder**

# Table of Contents

<b>1. Overview.....</b>	<b>2</b>
<b>2. The Algorithm.....</b>	<b>3</b>
<b>3. Keybindings.....</b>	<b>4</b>

# 1. Overview

---



## Introduction

This program is designed to facilitate the identification of threshold, P1-5 and N1-5 in an ABR waveform series and export this data. The default input/output formats used by the program are designed to work with the custom ABR file format used by the Eaton Peabody Laboratories. It is relatively straightforward to write your own import and export module if needed. Refer to the `peakio.py` file for documentation of what is required.

## Loading Data

Data can be loaded by opening a file directly, dragging it from the sidebar, or dragging its icon from the desktop. If you want to invert the waveform polarity, hold down control while dragging the file.

## Analysis

On load each waveform is bandpass filtered from 200 to 10,000 Hz to remove baseline shift as well as high frequency noise that interferes with the peak detection algorithm. To minimize phase shift, a first-order Butterworth filter is used to forward and reverse filter the waveform. An initial estimate of P1-5 is computed and presented for correction. It is recommended that you correct the location of P1-5 to your satisfaction before computing N1-5 as the algorithm relies on knowledge of P1-5 to produce the best possible estimate for N1-5. Even if you don't use this program to save threshold, it is important to specify it so that sub-threshold data is marked appropriately in the output file.

## Saving

Aside from bandpass filtering the raw data provided by the import module, no other pre or post-processing is done on the data. Current amplitude and latency of each point is saved, however, if the point is subthreshold (or if no threshold is provided), the latency is reported as a negative number.

## 2. The Algorithm

---

The algorithm computes all negative zero crossings (NZCs) of the first derivative, which identifies local minima and maxima in the function.

### 3. Keybindings

---

The current waveform is displayed as a thick, black line. Threshold waveform is specified by a dashed line. If a negativity or positivity is selected, it will be indicated by a white symbol. Negativities are indicated by triangles, positivities as squares. Red is P1/N1, yellow is P2/N2, green is P3/N3, light blue is P4/N4, and dark blue is P5/N5.

The following keybindings are used when processing a waveform series:

#### Waveforms

- **Up/Down arrows** – Select previous/next waveform in the series
- **P** – Toggles waveform polarity. Do this before any other data processing.
- **N** – Toggles normalized view of waveform.
- **+/- keys** – Increases/decreases scaling factor of waveform.

#### Peaks / Notches

- **Right/Left arrows** – Move a toggled peak left or right along the waveform. Movement of the peak will "snap" to estimated peaks in the waveform. To adjust the peak in fine increments, hold down the shift key simultaneously.
- **Number keys 1-5** – Select the corresponding peak on the current waveform. To select N1-5, hold down shift while pressing the corresponding number.
- **I** – Estimates N1-5 for all waveforms. If N1-5 is already estimated, recomputes the estimate.
- **U** – Updates guess for corresponding P or N of successive waveforms based on position of currently toggled P or N.

#### Threshold

- **Return** – Set threshold to current waveform.
- **T** – Estimates threshold using the correlation coefficients between responses to adjacent levels.
- **W** – Toggles display of threshold estimation details.

#### Analysis

- **L** - Toggles display of input-output function
- **X** – Clears analysis, restarts with initial peak guess.
- **R** - Restores last-saved analysis

#### Saving

- **S** – Saves amplitude and latency of peaks.
- **E** - Export filtered waveforms

The appropriate keys will repeat if you hold down the key, which may be useful when navigating through the waveforms or adjusting the location of a peak.