Zhen Lab

CaImg GUI Manual

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1 Setup and Installation

The software is available on GitHub. You can clone the repository and run the software by opening the .exe file. To clone the repository, open the Windows command prompt (or Mac terminal) and go to the directory where you want to have the software. Run the following in your command prompt (Windows users):

```
git clone https://github.com/Mohaddadnia/CaImg-Windows.git
```

Mac users can use the following:

```
git clone https://github.com/Mohaddadnia/CaImg-Mac.git
```

In addition, you can run the software by running the "CaImg.py" file using Python (version 3.x). To clone the code and run it with Python:

```
git clone https://github.com/Mohaddadnia/CaImg-GUI.git
```

To run the software through Python, ensure you have the required packages installed on your local machine. Running the following command in the Windows command prompt (or Mac terminal) will install all the required packages:

```
pip install -r requirements.txt
```

2 Usage

Once you open the software, you will see four different panels: "Signals", "IMFs", "Inputs", and "Fuzzy Logic". Each of these panels is designed for a specific part of the artifact correction pipeline, and here we explain each panel in detail.

2.1 Inputs

The "Inputs" panel is where you can specify the file that contains your data. You can also click the "Open" option from the "File" menu at the top of the software. Your data file should be formatted such that each signal is in a different column and the header of the column is the name/identifier of the signal. You will use this identifier to specify which of the signals is the GFP signal and which one is the RFP signal. Supported file formats are CSV (.csv), TSV (.tsv), Excel (.xlsx), and

	A	B	C	D
1	**AVB_GFP**	**AVB_RFP**	**AVA_GFP**	**AVA_RFP**
2	1180.677	758.2097	316.2593	732.6296
3	1001.42	776.2464	287.5221	662.469
4	936.942	801.5217	274.8761	617.531
5	947.7246	831.6377	280.6991	628.7345
6	874.7971	836.5507	277.7788	607.6283
7	868.9275	839.4928	264.1574	599.3519
8	728.6957	826.7536	247.8319	545.885
9	826.7681	832.029	250.3097	564.1593
10	750.1739	820.1884	272.9469	620.2035
11	748.3333	827.1884	239.4602	528.9381
12	723.7246	802.3913	255.1681	561.6726
13	653.5797	778.6377	271.9115	613
14	726.971	762.3623	271.354	620.9381
15	727.6087	752.2029	284.0463	644.0648

Figure 1: Sample data format from AVA and AVB neuron. Each signal must be in a different column and have the first row as its identifier. There can be as many recordings as you want in a single file, as long as they are each in their own separate column.

MATLAB (.mat). Below is an example of a file containing signals for both the AVA and AVB neuron:

After you have specified your file, the dropdown menus labeled ”GFP Signal” and ”RFP Signal” will allow you to select the identifiers that correspond to each signal. You will see each signal appear on the ”Signals” panel as it is selected. Once both signals are selected, the intrinsic mode functions (IMFs) will appear on the ”IMFs” panel. These are explained in the following sections.

2.2 Signals

The ”Signals” panel shows the recordings (GFP/RFP) along with the reconstruction. The top plot is the actual recording and the bottom one is the derivative of the GFP and reconstruction signals in order to assist with capturing the kinetics of the recording. is designed similar to a Matplotlib environment and, thus, has almost all functionalities available in a Matplotlib plot available. Hovering over each button will give you a one-sentence summary of the button’s functionality. Once the GFP and RFP signals are selected, you can use the ”Options” menu at the top of the software to apply normalization and/or plot reconstructions using other methods. The table below summarizes the functionality of each button in the ”Options” menu:

Button	Description
Show ratio	will produce and plot a new reconstruction by taking the ratio of the GFP to RFP signal
Show regression	will produce and plot a new reconstruction by removing the 'overlap' of the two signals using linear regression
Max normalize	will normalize all the signals in the "Signals" panel by dividing them by their respective maximum value
Norm normalize	will normalize all the signals in the "Signals" panel by dividing them by their respective Frobenius norm
Z normalize	will z normalize all the signals in the "Signals" panel
EMD parameters	allows you to adjust the parameters used to perform empirical mode decomposition
Choose colors	allows you to change the colors used for plotting the signals in the Signals panel

2.3 IMFs

The "IMFs" panel displays the intrinsic mode functions (IMFs) of the GFP signal. In brief, the sum of all these signals, and residuals, is equal to the GFP signal (you can check this by selecting all the available IMFs). Those shown in pink are the ones that are included in the current reconstruction shown in the "Signals" panel. You can click on each IMF to add or remove it from the reconstruction. Removing all the IMFs and the residuals from the reconstruction will give you a flat line. Below are the IMFs and the residual corresponding to the AVB signal.

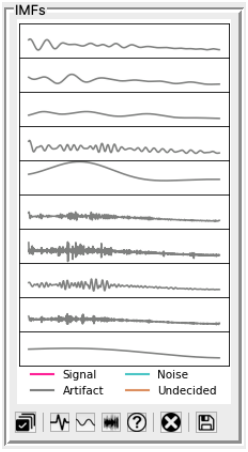

Figure 2: IMFs corresponding to the decomposition of a recording on the AVB neuron. Signals in pink are selected for reconstruction. You can add/remove IMFs to your reconstruction by clicking on each IMF.

You can use the buttons at the bottom of the IMFs panel to annotate your IMFs. Holding the mouse on each button will give you a short summary of what it does. With annotations, in addition to marking an IMF as an artifact or signal/activity, you can mark them as noise or undecided. This can save you time when making your reconstructions.

2.4 Fuzzy Logic

The "Fuzzy Logic" panel is where you can apply the Fuzzy system to your recording. To apply the system, simply click "Fuzz ..." and the reconstruction and the order of the IMFs will be updated. The IMFs will appear in the order of their selection scores. In other words, the IMF with the highest selection score (most important to the reconstruction) will be at the top. The slider allows setting the threshold for the fuzzy system. The threshold is the boundary above which the IMFs are selected. In other words, if the threshold is set to 0.5, IMFs with selection scores higher than 0.5 are selected for reconstruction. When the threshold is 0, all the IMFs are included and the reconstruction will be the same as the original signal, and when the threshold is 1, nothing is selected and the reconstruction will be a flat line.

2.5 Saving Results

Saving Session

You can save your current session with your reconstruction and your annotations in case you want to refer back to them in the future. To save your session, click on "File" in the top menu and click on "Save session". You will be asked to specify a path to which your session will be saved. Your session will be saved as a ".caimg" file format. To open your session, you can simply use the "Open" option from the "File" menu and choose your saved ".caimg" file.

Export Results

You can save your plots using the save button on the "Signals" panel. You will be asked to specify a path and the plot will be saved as a png file. To save your data and the corresponding reconstruction, you can use the "Save reconstruction as ..." button in the "File" menu at the top of the software. You will be asked to specify a path (make sure to include the file extension). You can save your reconstruction as a CSV (.csv), Excel (.xlsx), or a Numpy Array (.npy). Note that this method will save the current signals as they appear on the "Signals" panel. This means that if you have normalized the signals, they will be saved in their normalized forms. If you have the ratio and/or the regression reconstruction plotted, they will be saved too.

3 Appearances

3.1 Plotting Colors

You can customize the colors used for plotting the signals and reconstructions in the "Signals" panel. To change the colors, go to "Options" at the top menu bar and click on "Change colors". This should open a new window with the current color palette. In order to change any color, click on the "Change" button next to that color. Once you have selected your desired colors, simply click on the "Apply" button to update the "Signals" panel with the new colors. You can use the "Set as Defaults" button to set your desired color palette as the default color palette. In order to revert back to the original color palette, use the "Reset" button.

3.2 Themed Modes

There are two themed modes in addition to the default Light Mode:

- Dark Mode
- Colorblind-Friendly Mode

By default, the software will adapt your operating system's mode. In other words, if you use dark mode, it will open in dark mode, and if you use light mode, it will open in light mode. If you wish to change the theme, you can do so by going to the "View" menu from the top menu bar and selecting/unselecting a theme.

4 Reporting Issues

If you have any difficulties using the software and/or are receiving errors or any other issue, you can open an issue on our GitHub and we will get back to you as soon as we can. In addition, please do not hesitate to reach out to me at m.nia@mail.utoronto.ca if you have any questions.

5 Suggestions

If you have any suggestions that you think would improve the software, both in terms of technicality and accessibility, please forward your suggestions to me at m.nia@mail.utoronto.ca. Any suggestion would be appreciated.

Appendix A: Keyboard Shortcuts

Windows	MacOS	Description
Ctrl+O	⌘O	Open file
Ctrl+C	⌘C	Copy reconstruction to clipboard
Ctrl+S	⌘S	Export results
Ctrl+F	⌘F	Apply fuzzy logic
Ctrl+→	⌘→	Increase fuzzy threshold
Ctrl+←	⌘←	Decrease fuzzy threshold
Ctrl+↑	⌘↑	Add the next IMF to the reconstruction
Ctrl+↓	⌘↓	Remove the last IMF from the reconstruction
Ctrl+Shift+R	⇧⌘R	Show ratio correction
Ctrl+Shift+G	⇧⌘G	Show regression correction
Ctrl+Shift+Z	⇧⌘Z	Z-score normalize the signals
Ctrl+Shift+X	⇧⌘X	Max normalize the signals
Ctrl+Shift+N	⇧⌘N	Norm normalize the signals
Ctrl+Shift+E	⇧⌘E	Show EMD parameters
Shift+↓	⇧↓	Open the next neuron from the file (when name pattern is applied)
Shift+↑	⇧↓	Open the previous neuron from the file (when name pattern is applied)


CAIMG