

% created in January 2021, by Ho Nhu Y Nguyen

This dataset contains the data used in the article: “Reducing artifacts in photoacoustic imaging by using multi-wavelength excitation and transducer displacement”.

<https://doi.org/10.1364/BOE.10.003124>

All data files are saved under a name format as below:

“something\_x\_z\_theta\_wavelength\_time.rfe”

- phantom 1: something = phantom#1
- phantom 2: something = overlap
- *in vivo*: something = in-vivo

## 1. Figures in the paper

This part explains how to plot those Matlab figures used in the paper.

“z” and “wavelength” (in the file name) are the most important information in this processing step. In this work, **data files for transducer array displacement should be 6 files with 6 different z’s (in the file name) but with the same wavelength, data files for multi-wavelength excitation should be 8 files with 8 different wavelengths but with the same z.**

### 1.1. Figure 4

- Open script `out_of_plane_depth_behavior.m`
- Change parameters `x` and `a`, then run the script.
- You may modify the line width, and color of each curve

### 1.2. Figure 7(c)

- Run the script `paper_figures.m` with proper code for this figure

### 1.3. Figure 8

- Run the script `OPA_reflection_artifact.m`, select relevant data files of phantom 1 (multi-wavelength excitation)
- Run the script `paper_figures.m`. with proper code for this figure.

### 1.4. Figure 9

- Run the script `z_process_data_v2.m` and select relevant data files of phantom 1 (transducer array displacement)
- Run the script `paper_figures.m` with proper code for this figure.

### 1.5. Figure 10

- Run the script `z_process_data_v2.m` and select relevant data files of phantom 1 (transducer array displacement)
- Run the script `paper_figures.m` with proper code for this figure.

### 1.6. Figure 11

- Run the script `combine_methods.m` and select relevant data files of phantom 1
- Run the script `paper_figures.m` with proper code for this figure.
- You may change the location of the colorbar.

### 1.7. Figure 12

- Run the script `z_process_data_v2.m` and select relevant data files of phantom 2
- Run the script `paper_figures.m` with proper code for this figure.

### 1.8. Figure 13

- Run the script `z_process_data_v2.m` and select relevant data files of phantom 2
- Run the script `paper_figures.m` with proper code for this figure.
- You may relocate the colorbar.

### 1.9. Figure 14

- Run the script `OPA_reflection_artifact.m` and select relevant data files of this in vivo experiment
- Run the script `paper_figures.m` with proper code for this figure.

### 1.10. Figure 15

- Run the script `combine_methods.m` and select relevant data files of this in vivo experiment
- Run the script `paper_figures.m` with proper code for this figure.

### 1.11. Figure 16

- Run the script `combine_methods.m` and select relevant data files of this in vivo experiment
- Run the script `paper_figures.m` with proper code for this figure.
- You may change the location of the colorbar.

## 2. Videos in this paper

This part explains how to plot those visualizations used in the paper.

Videos are exported in the same folder with the data. You may use a video processing application to reformat the videos.

### 2.1. Visualization 1

- Run the script `z_process_data_v2.m` and select relevant data files of phantom 1 (transducer array displacement)
- Run the script `paper_videos.m` with proper code for this video.

### 2.2. Visualization 2

- Run the script `z_process_data_v2.m` and select relevant data files of phantom 1 (transducer array displacement)
- Run the script `paper_videos.m` with proper code for this video.

### 2.3. Visualization 3

- Run the script `z_process_data_v2.m` and select relevant data files of phantom 2
- Run the script `paper_videos.m` with proper code for this video.

### 2.4. Visualization 4

- Run the script `z_process_data_v2.m` and select relevant data files of this in vivo experiment
- Run the script `paper_videos.m` with proper code for this video.