

Optical Coherence Tomography Angiography (OCTA) Data Processing Guide

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Introduction:

This guide is for post data processing of OCTA which outputs the vascular structure. Please cite the following references^{1,2,3}:

1. Tang, J., Erdener, S. E., Sunil, S. & Boas, D. A. Normalized field autocorrelation function-based optical coherence tomography three-dimensional angiography. *J. Biomed. Opt.* **24**, 036005 (2019).
2. Tang, J. *et al.* Shear-induced diffusion of red blood cells measured with dynamic light scattering-optical coherence tomography. *J. Biophotonics* **11**, e201700070 (2018).
3. Tang, J., Erdener, S. E., Fu, B. & Boas, D. A. Capillary red blood cell velocimetry by phase-resolved optical coherence tomography. *Opt. Lett.* **42**, 3976 (2017).

Data acquisition

OCT-based repeat Bscan data acquisition, i.e. repeat Bscan once at each Y position. The data should be saved sequentially as a 1D array (ASCII int16) and named as: RAW-nk-nxRpt-nx-nyRpt-ny-iC, e.g. RAW-1024-001-00400-002-400-1.dat.

I. Input

```
% 1D array spectrum, nK*nXrpt*nX*nY, data format: ASCII int16
% nK: spectrum pixel (camera elements); nXrpt: Ascan repeat;
% nX: number of Ascans per Bscan; nY: number of Bscans for the whole volume
% NOTE: the raw data for the whole volume is usually very large, it's
recommended to process chunk by chunk
% PRSinfo: processing information
% PRSinfo.FWHM: Full width at Half Maxim, Amplitude, [transverse, axial], m
% PRSinfo.fAline: DAQ Aline rate, Hz
% PRSinfo.Lam: [light source center, wavelength bandwidth], m
% PRSinfo.Dim: [nz,nx,nyPchk,nTau]
% PRSinfo.g1_Start: start time for g1 calculation
% PRSinfo.g1_nt: number of time points for g1 calculation
% PRSinfo.g1_ntau: number of g1 time lag
% PRSinfo.intDk: OCT lambda to k space interpolation factor (calibration is
required)
```

Example data:

https://drive.google.com/a/bu.edu/file/d/1q9_F93_5p_pgmXIwzKZOCQ36m7sE95d2/view?usp=sharing
<https://drive.google.com/a/bu.edu/file/d/1nNzjB12JZFf4epRr4XSKhRYiT7FjCZT7/view?usp=sharing>
<https://drive.google.com/a/bu.edu/file/d/1dAwY56dSBoRLX246ALTeV3ZiV3dehrEH/view?usp=sharing>
<https://drive.google.com/a/bu.edu/file/d/1TUA9L170bLYQdrL6L9oiSkxae7XpV--E/view?usp=sharing>
<https://drive.google.com/a/bu.edu/file/d/1J3gG6HFBK2uVjDgCRHbRV6fvA2Ei9YHp/view?usp=sharing>

II. Output

```
% output:
% AG: [nz,nx,ny] OCT angiogram
```

I. CPU calculation-based sub-functions

```
% subFunctions:
% function [Dim, fNameBase, fIndex]=GetNameInfoRaw(filename0)
% function DAT= ReadDat_int16(filePath, Dim, iseg, ARpt_extract,RptBscan)
% function RR = DAT2RR(Dat, intpDk)
% function AG=RR2AG(RR, it0, ncorrect, z, K)
```

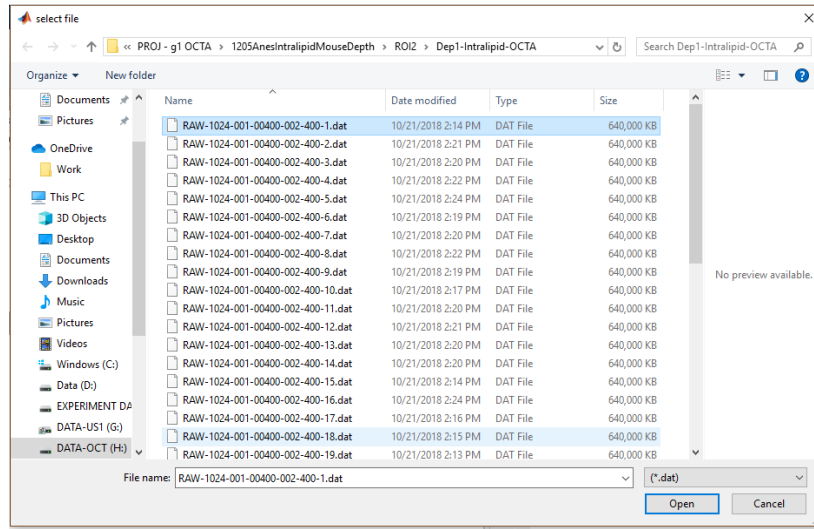
I. GPU calculation-based sub-functions

Note: the minimal GPU memory requirement is 16 GB.

```
% subFunctions:
% function [Dim, fNameBase, fIndex]=GetNameInfoRaw(filename0)
% function DAT= ReadDat_int16(filePath, Dim, iseg, ARpt_extract,RptBscan)
% function RR = DAT2RR_GPU(Dat, intpDk)
% function AG=RR2AG_GPU(RR, it0, ncorrect, z, K)
```

II. Main_OCTA data processing

III.1 select file



III.2 data processing parameter

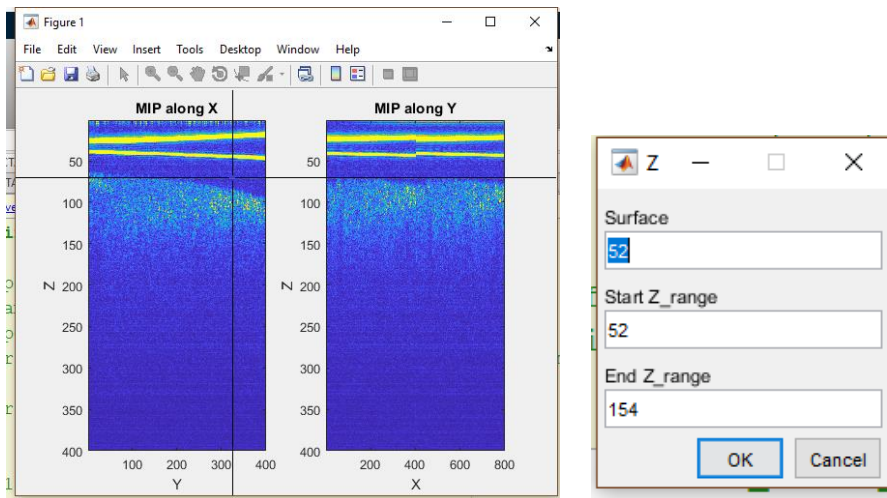
Specify number of Cscans (startFile+nFile to Load) to be processed. Double check the intDk, and voxel size.

The screenshot shows a dialog box with the following fields and values:

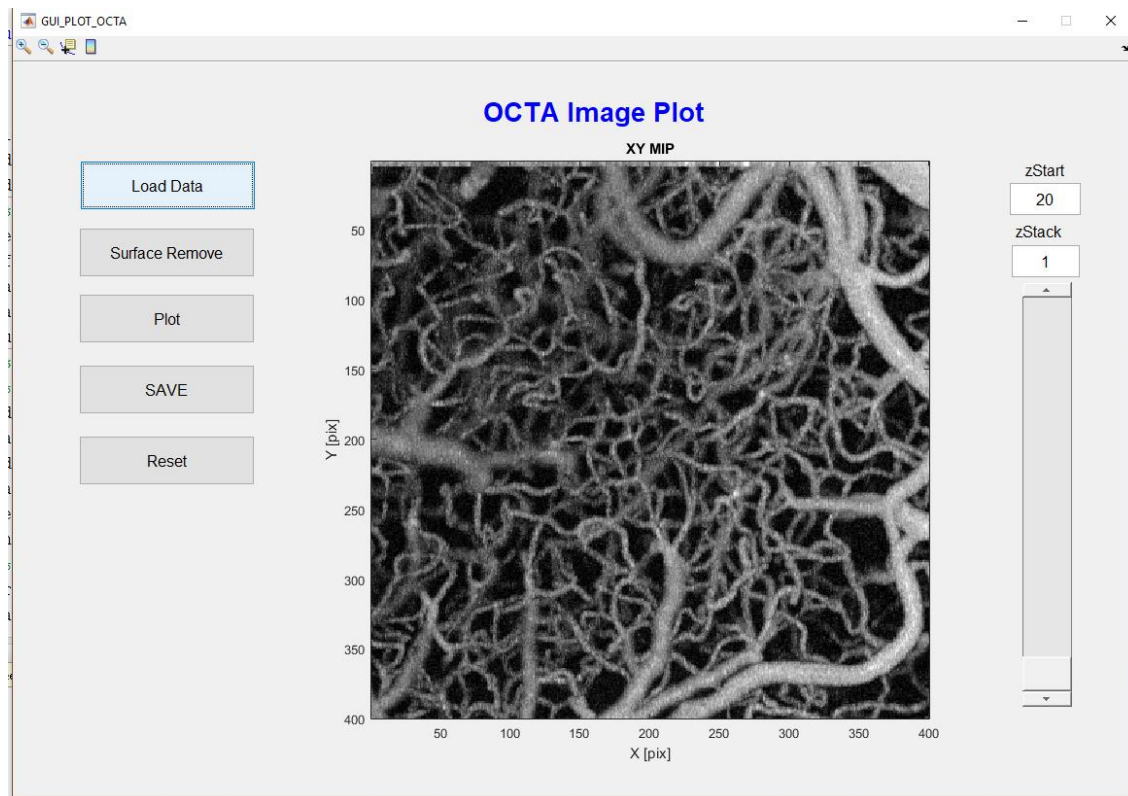
- startFile: 1
- nFile to Load: 10
- # of sub Spectrum (nk0=1024): 1
- intDk: -0.19
- dZ: 3.29
- dX: 1.5
- dY: 1.5

At the bottom are 'OK' and 'Cancel' buttons.

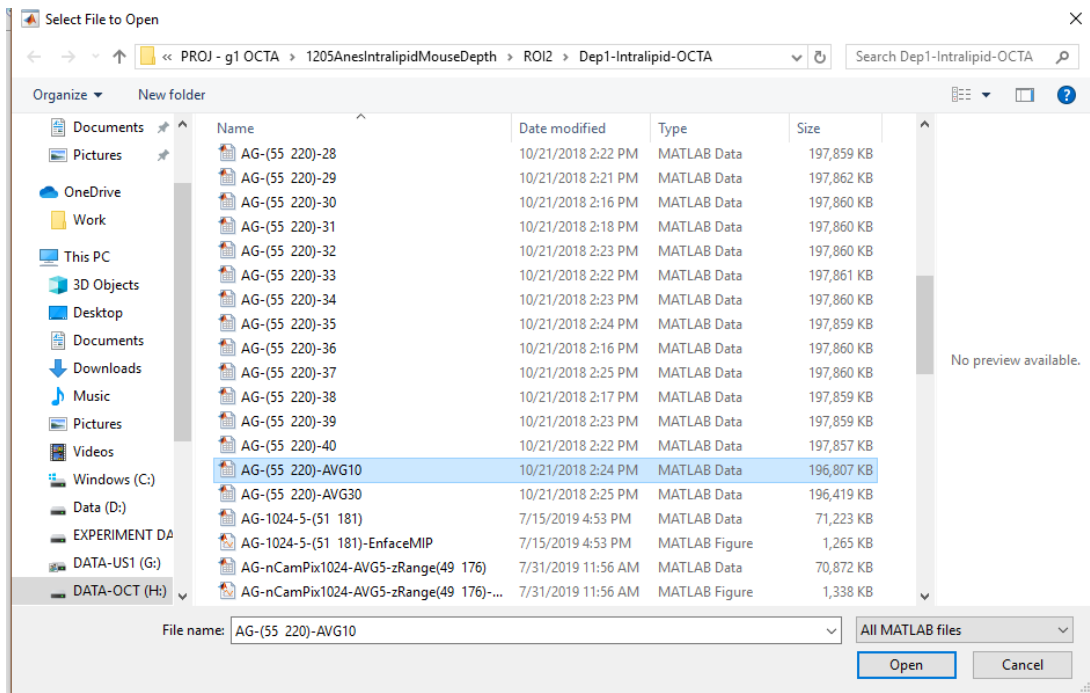
III.3 select axial range



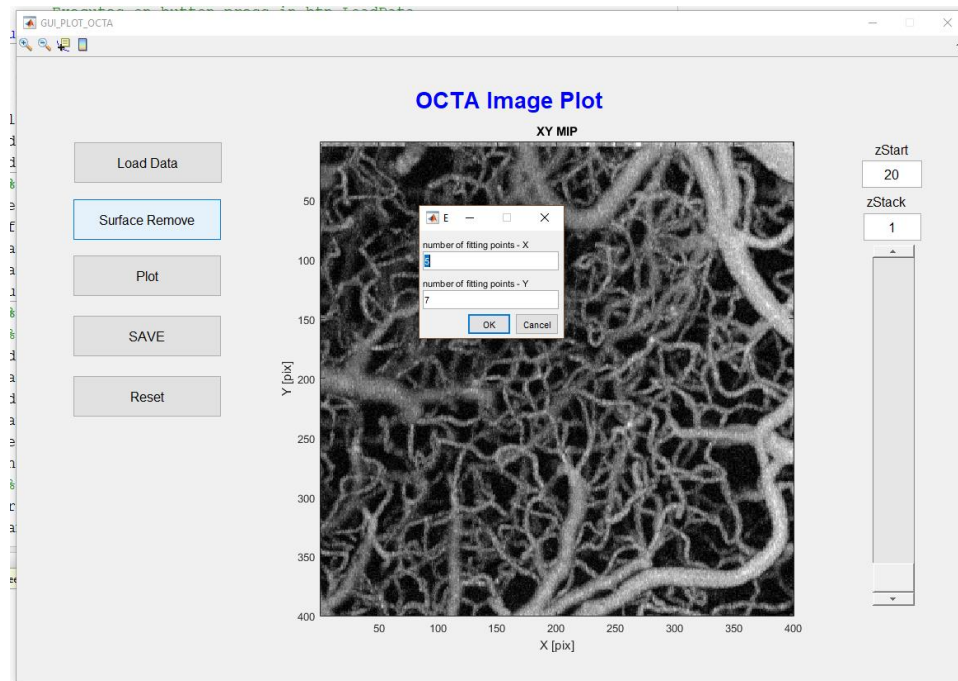
III.4 OCTA result plot (GUI_PLOT_OCTA)

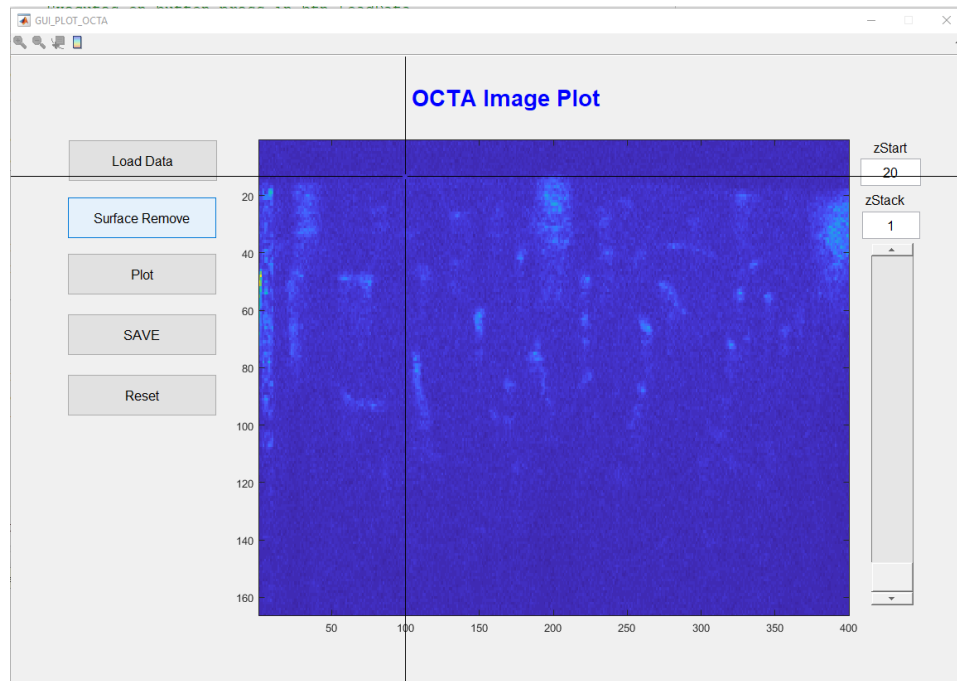


1. Load the saved AG data



2. Remove the signal above brain surface





3. Use the slider or zStart+zStack to check single or MIP (maxim intensity projection) en face plane.
4. Use 'Plot' to plot a MIP for certain depth range (set SideView(N:0; Y:1) to 0). Or plot XY, YZ, XZ, and MIP figures by set SideView(N:0; Y:1) to 1.