

Notes on x-ray data

Scott Trinkle

Last edited: September 5, 2018

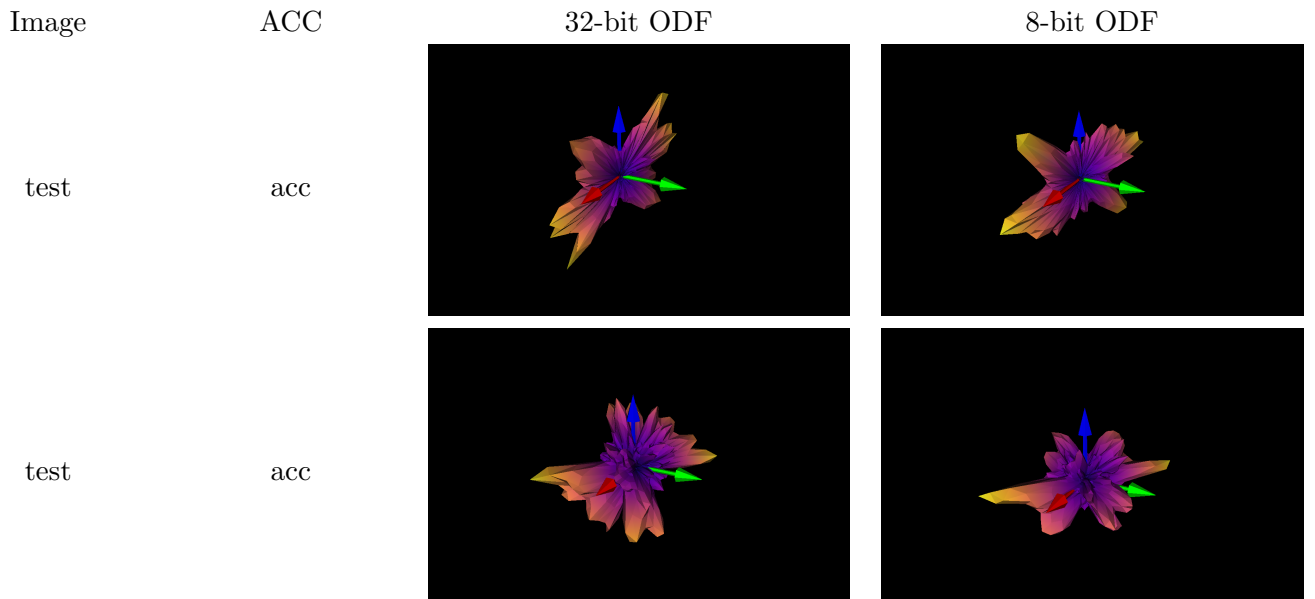
1 Introduction

The aim of these notes is to discuss and characterize the post-processing steps involved in preparing the reconstructed μ CT data for further analysis.

1.1 Data size reduction

The full resolution (1.2 μ m isotropic) μ CT data¹ is reconstructed with 32-bit float precision, with an image size of $11982 \times 11982 \times 13781$ voxels. A single slice is thus ~ 548 MB and the full volume is ~ 7.5 TB. The first family of post-processing steps attempt to reduce the data size. First, each slice is cropped to a 10096×6720 voxel field of view that just includes the extent of the brain volume. Next, the data values are rescaled from 32-bit floating point values to 8-bit unsigned integers.² These two operations reduce a single slice to ~ 68 MB, a reduction of $\sim 87\%$. A comparison of the pre- and post-processed data is shown in Figure ??.

Figure 1: Caption

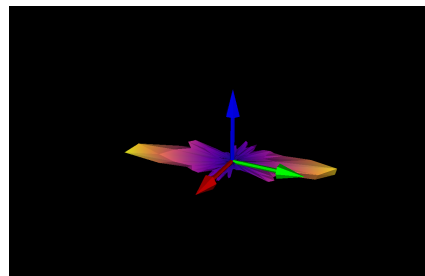
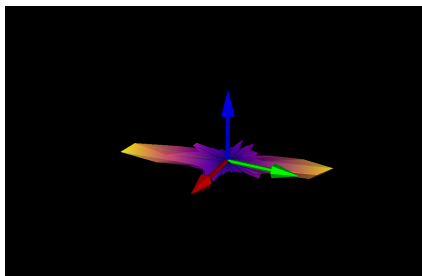


¹In these notes, I refer to what I am told is the “best” μ CT dataset that has a corresponding DW-MRI volume, located in `/data_raf/2017_07_22_WholeMouseMRI_5x_2k_phase35cm_gap31_exp30_newfocus/ recon_flatcorr_1x/recon_crop_8/` on globus.

²I am still communicating with Raf to understand how he does this rescaling. He claims that the rescaling causes the denoising, but I am able to better replicate his results after Gaussian filtering as well.

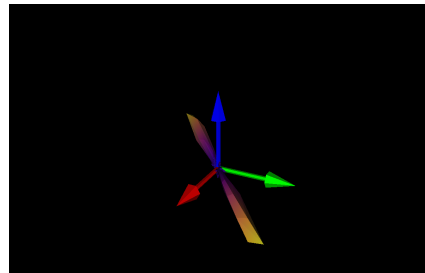
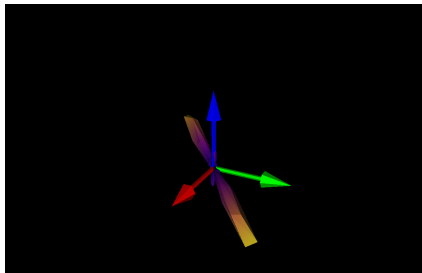
test

acc



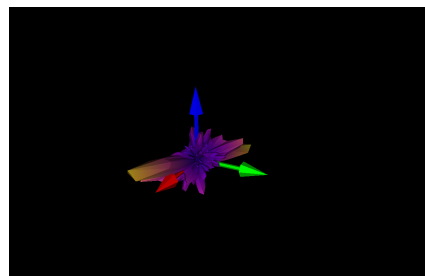
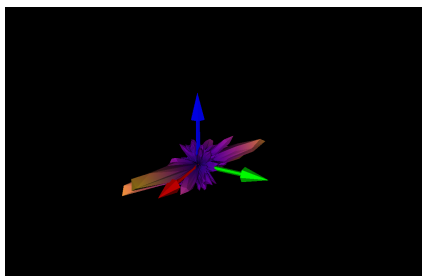
test

acc



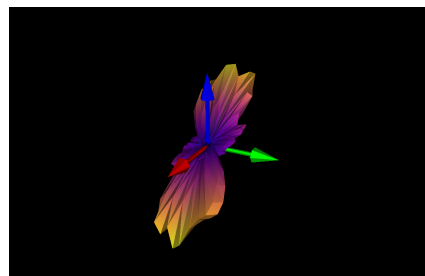
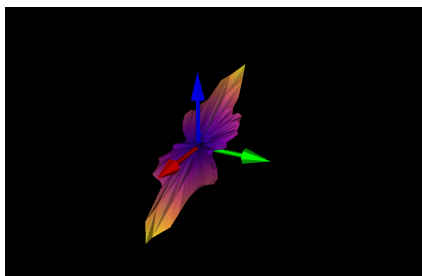
test

acc



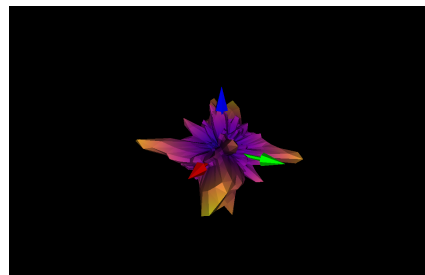
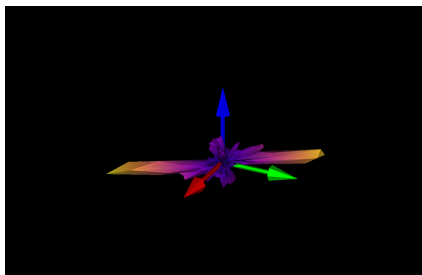
test

acc



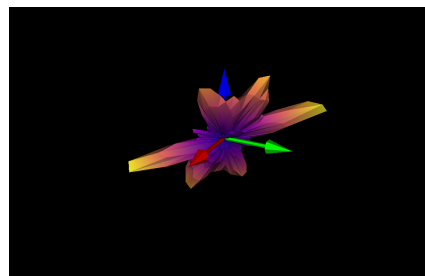
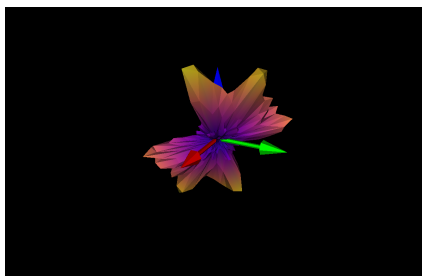
test

acc



test

acc



test

acc

