Notes on μCT data resolution

Scott Trinkle

Last edited: October 15, 2018

1 Introduction

In a recent group meeting, we discussed the idea of choosing the resolution of the acquired μCT data to optimize the calculation of ODFs and segmentation of white matter. The aim of these notes is to characterize the sensitivity of the μCT ODFs to the resolution of the data. My hypothesis is that while acquiring the data at a lower resolution will increase the accuracy and ease the computational burden of segmenting white matter tracts, this will be at the expense of ODF accuracy.

2 Methods

2.1 Downscaling and ODF construction

The same set of 225 ROI was used as in the previous notes detailing the effect of bit depth and rescaling. For this study, the original 32-bit data was used with no rescaling.

The native voxel size of the data is 1.2 μm. Each ROI was downsampled to four smaller voxel sizes: 2.4 μm (2x), 3.6 μm (3x), 4.8 μm (4x), and 6.0 μm (5x), using cubic spline interpolation. Structure tensor ODFs were then calculated from all five scales for each ROI. The optimized guassian filter widths used in the structure tensor pipeline (σ_d and σ_n, optimized in previous notes) were appropriately scaled to correspond to the same physical distance at each resolution. Orientation estimates were not thresholded by FA value or intensity before binning over 6500 uniform points on the sphere and expanding onto even, real spherical harmonics, with $L_{max} = 20$.

2.2 Comparison metrics

As in the bit depth notes, ODFs calculated at different scales were compared using the ACC, JSD, and RMSE of spherical harmonic coefficients. Additionally, the difference in generalized fractional anisotropy was computed, defined as

$$\Delta\text{GFA} = \text{GFA}_{ds} - \text{GFA}_0, \tag{1}$$

where GFA_{ds} is the GFA of the ODF calculated with downsampled data, and GFA_0 is the GFA of the ODF calculated with the original data.

3 Results

Figure 1 shows the overall trends of the various comparison metrics as a function of downsampling factor. All comparisons were done between the original 1.2 μm data and the downsampled data at various scales. The points correspond to the mean comparison metric values for all 225 ROI at each downsampling factor, and the error bars correspond to the standard deviations.

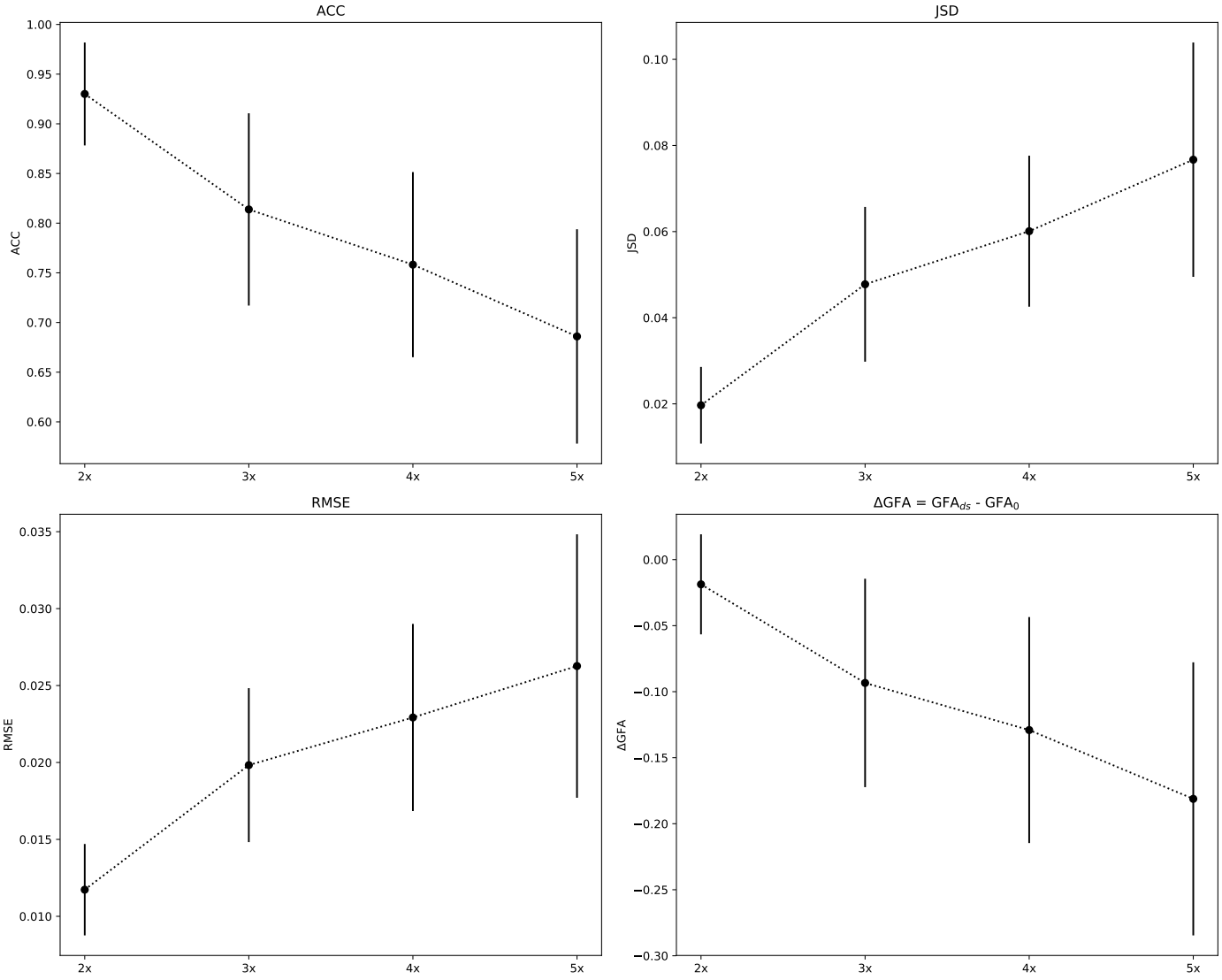

Figure 1: Comparison metric trends as a function of downsampling factor.

As expected, the comparisons become worse — i.e., the ODFs deviate more from the full-resolution "ground truth" — as the downsampling factor is increased. Full distributions of these comparison metrics are appended to these notes.

Important to note is that the ΔGFA tends to become more negative with more downsampling. This indicates that the ODFs become increasingly isotropic as we dicard more high-frequency content. Capturing anisotropic peaks in the ODFs is a fundamental task for all diffusion MRI reconstructions and forms the basis of all tractography algorithms.

Figure 2 gives a comparison of 1x and 2x ODFs for relatively high values of ACC. Though the shapes are generally similar, it is clear that there are discrepancies in the number and location of peaks. Even for the

ACC=0.95 case, the primary peaks are ~8° apart.

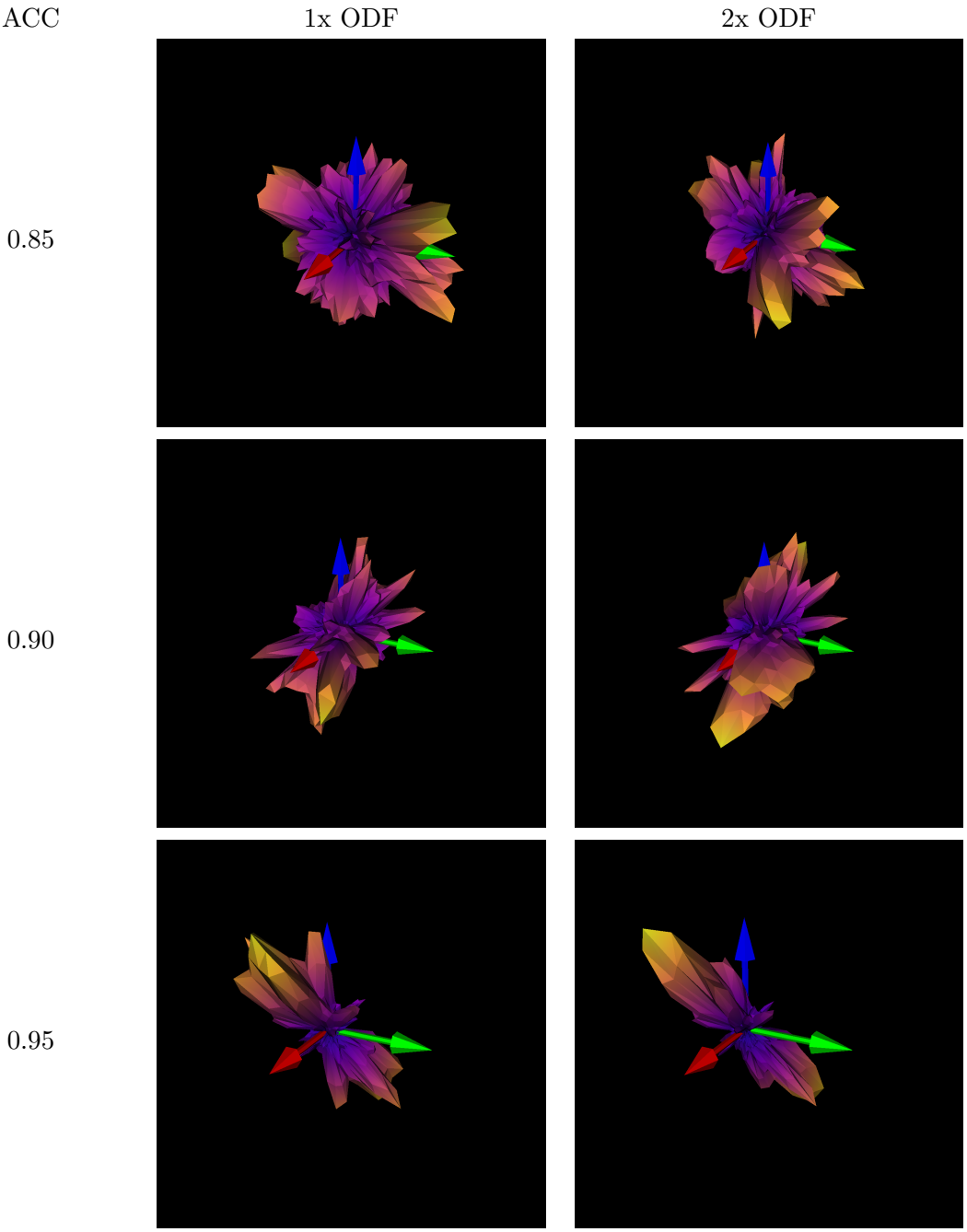

Figure 2: Sample ODFs with ACC

4 Conclusion

These results seem to indicate that much of the oriented structure in the μCT data is found in the high frequency content — that acquiring the data at a lower resolution will compromise the accuracy of the ODF.

A major issue that this potential strategy was brought up to address is the significant computational challenge of segmenting individual axon bundles throughout the high resolution dataset. Similar to our

discussion with the registration pipeline, however: I do not think we will ever need those bundles segmented at full resolution for our work. From what I understand, MRI tractography algorithms do not generate tracts near the ~1 μm resolution of the μCT data, so there will inevitably be downsampling of the μCT segmentation either way.

Accordingly, the general pipeline I propose is:

1. Acquire the μCT data at as high resolution as possible
2. Use the native resolution μCT data to calculate ODFs over MRI-voxel-sixed ROI
3. Calculate tractograms from either/both μCT and MRI ODFs
4. Downsample the μCT data to tractogram resolution and segment axon bundles for comparison

5 Appendix

Note that these comparison metrics tend to show less agreement and more variability with larger voxel sizes.

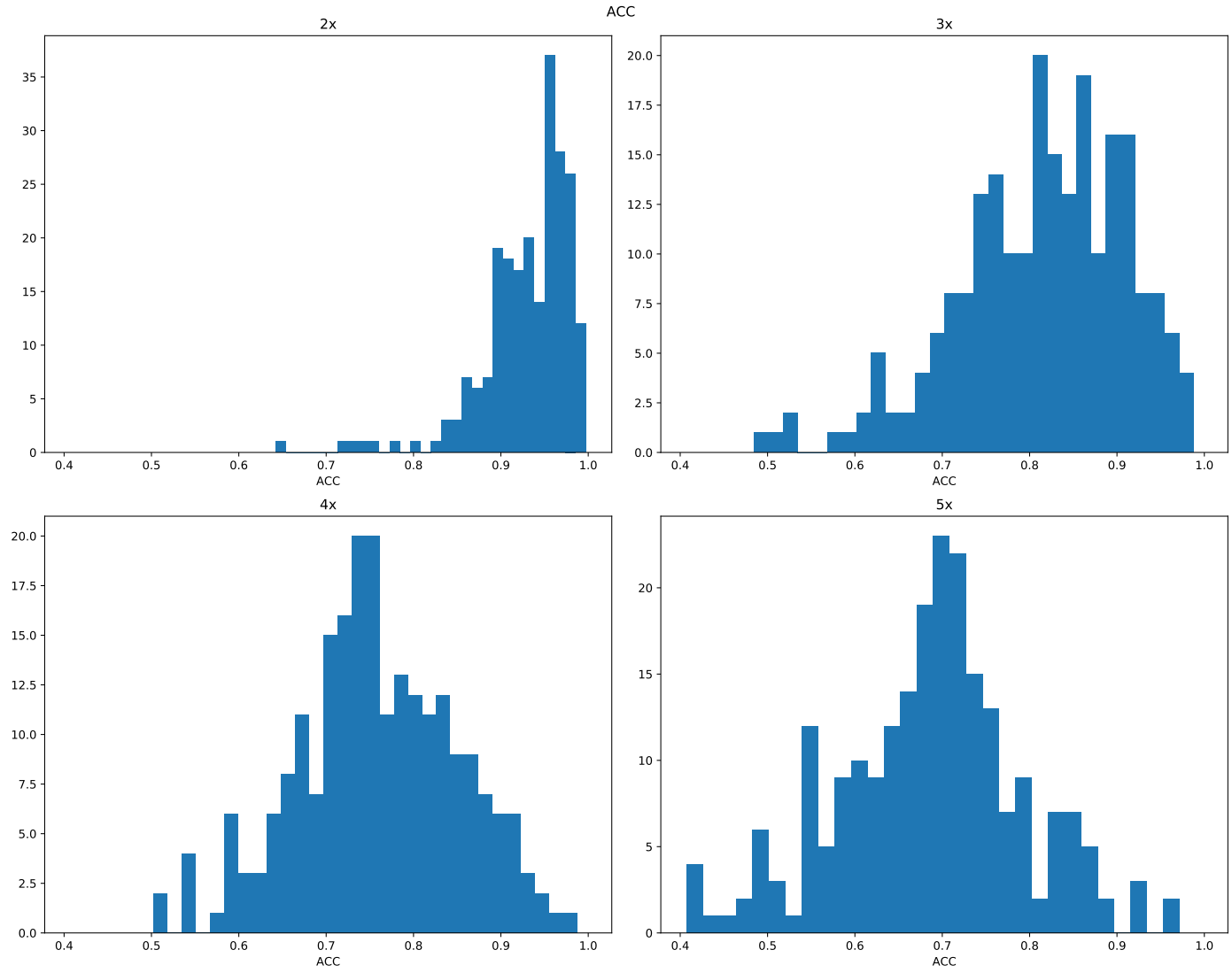

Figure 3: Full ACC distributions

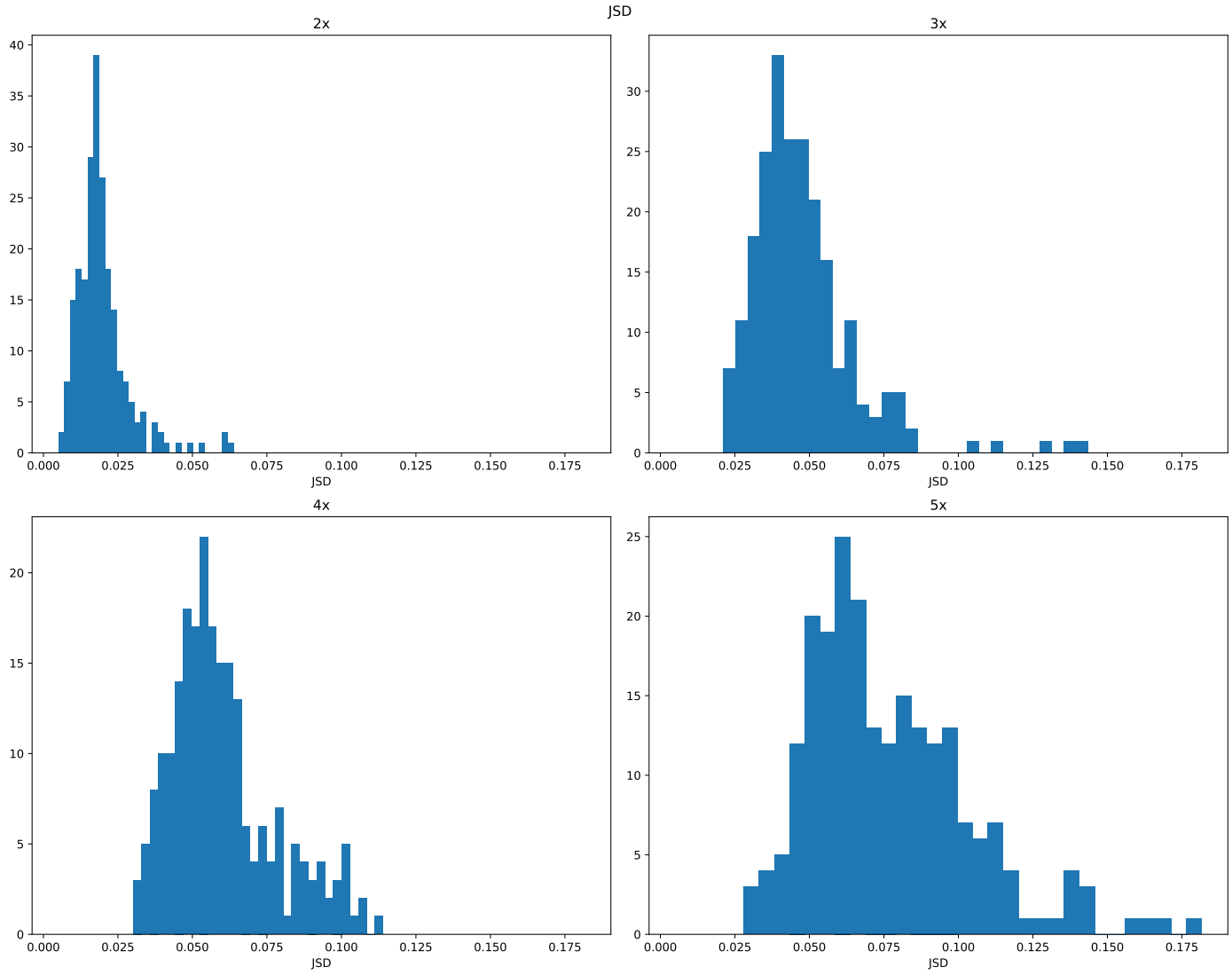

Figure 4: Full JSD distributions

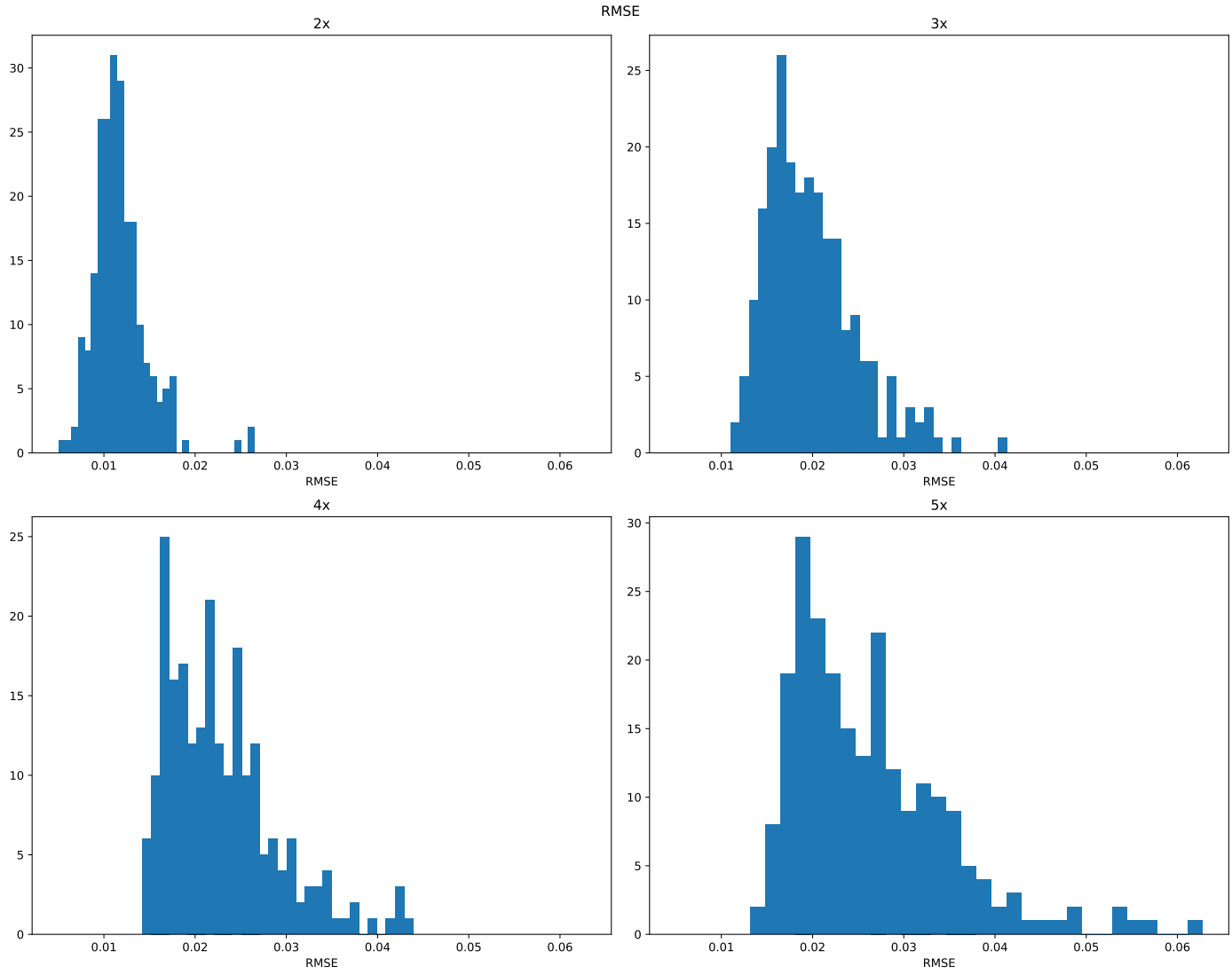

Figure 5: Full RMSE distributions

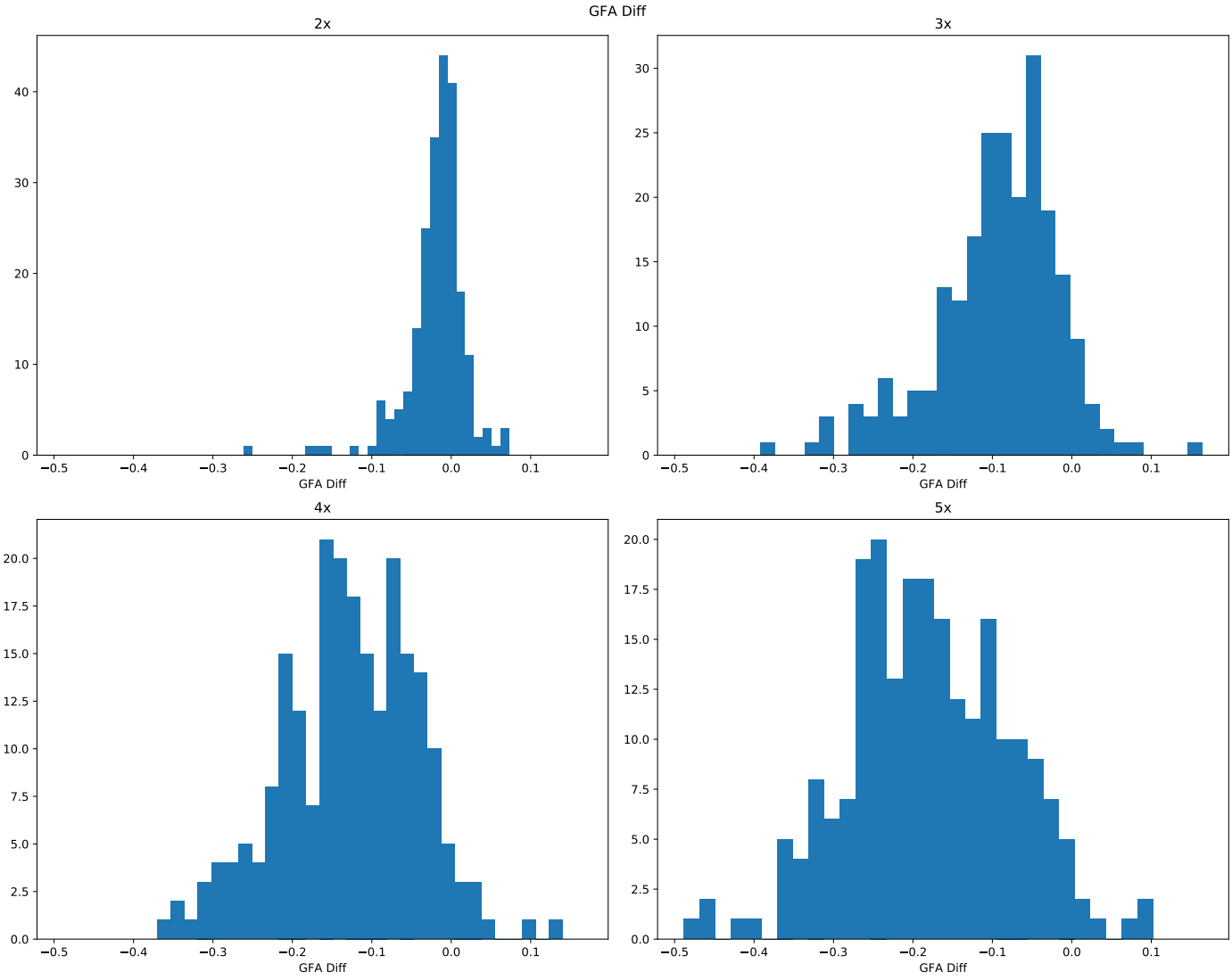

Figure 6: Full ΔGFA distributions