PreQual v1.0.8 (dtiQA v7 Multi)
Creation Date: August 27, 2022

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Run Date: 2023-07-05 23:28:43.552004

Project: SSBC
Subject: MS881355
Session: MS881355220321

Parameters:
- B-Value Threshold: 50
- Shells: [0 350 650 1350 2000]
- Run Denoise: False
- Run Degibbs: False
- Run Rician: False
- Run Prenormalize: True
- Topup B0s: First
- Try Synb0-DisCo: True
- Extra Topup Args:
- Eddy Mask: True
- Eddy B-Value Scale: 1.0
- Extra Eddy Args:
- Run Postnormalize: False
- Run N4 Bias Field Correction: True
- Run Gradient Nonlinearity Correction: False
- Mask Improbable Voxels: False
- Glyph Visualization Type: tensor
- Atlas Registration Type: FA
- Split Outputs: False
- Keep Intermediates: False

Preprocessing: Topup (RPE) + Eddy
Inputs (w/ PE direction and readout time):
- sub-MS881355_ses-MS881355220321_run-1_dwi (j+, 0.0716889)
- sub-MS881355_ses-MS881355220321_dir-PA_run-1_epi (j+, 0.0716889)
- sub-MS881355_ses-MS881355220321_dir-AP_run-1_epi (j-, 0.0716889)

Warnings (See "PreQual User Guide" at github.com/MASILab/PreQual for more information):

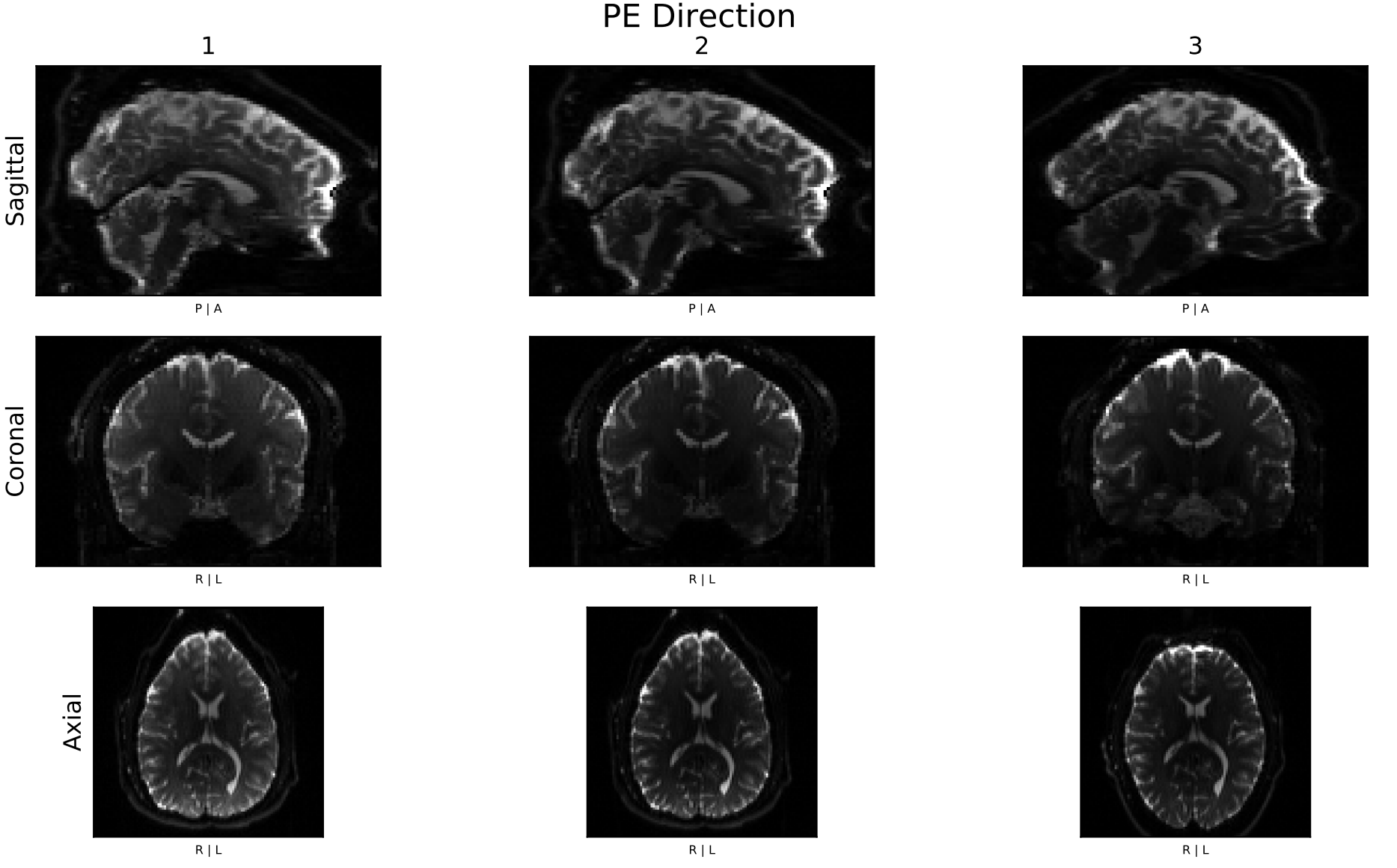
- All input volumes must have the same phase encoding axis, as input into this pipeline and as reflected above. Please see the PE Direction page of this PDF for more information.
- Both the sform and qform codes for sub-MS881355_ses-MS881355220321_run-1_dwi were non-zero. The NIFTI file was resaved with the sform affine overriding the qform.
- Both the sform and qform codes for sub-MS881355_ses-MS881355220321_dir-PA_run-1_epi were non-zero. The NIFTI file was resaved with the sform affine overriding the qform.
- Both the sform and qform codes for sub-MS881355_ses-MS881355220321_dir-AP_run-1_epi were non-zero. The NIFTI file was resaved with the sform affine overriding the qform.
- Eddy encountered an error while running and successfully reran when forced to run on non-shelled data, suggesting the input data was a non-shelled (i.e. DSI) image. Please note that eddy does not currently support DSI data and may produce spurious results. Please verify your data is shelled or that this behavior is expected.
- For SNR/CNR analysis, the number of unique b-values after preprocessing was not equal to the number of shells determined by eddy. B-values were matched to nearest supplied shell for analysis in an attempt to match eddy.
- b-values less than 500 or greater than 1500 s/mm2 detected. We recommend careful review of tensor fits prior to using them for purposes other than QA.

Methods Summary:

The diffusion data were preprocessed and quality-checked with the following pipeline built around the MRTrix3 [1], FSL [2], and ANTs [3] software packages. First, any volumes with a corresponding b value less than 50 were treated as b0 volume for the remainder of the pipeline. The images were then intensity-normalized to the first image and concatenated for further processing. FSL's topup and eddy algorithms were used to correct for susceptibilty-induced and motion artifacts and eddy currents and to remove outlier slices [4][5][6][7]. N4 bias field correction was then performed [8]. Lastly, the preprocessed data were fitted with a tensor model using the dwi2tensor function included with MRTrix3 using an iterative reweighted least squares estimator [9]. The quality of this preprocessing pipeline was then assessed qualitatively for gross errors and quantitatively analyzed using a three-step approach. In the first step, the preprocessed data were analyzed in accordance with the method outlined by Lauzon et al. [10]. The brain parenchyma without CSF were masked in a restrictive manner by using an eroded brain mask generated on the average b0 image using the bet2 function included with FSL [11]. Then, the tensor fits of the masked data were backpropagated through the diffusion model to reconstruct the original diffusion signal. The goodness-of-fit for the tensor model was then assessed using a modified pixel chi-squared value per slice per volume. In the second step, the tensor fit was converted to a fractional anisotropy (FA) image [12][13]. The ICBM FA MNI atlas with 48 white matter tract labels provided with FSL were then non-rigidly registered to the subject's FA image with the ANTs software package [14][15][16][17]. The average FA for each tract was then quantified and assessed for physiologic congruence. Lastly, the gradient orientations were visualized and checked using the dwigradcheck script included with MRTrix [18].

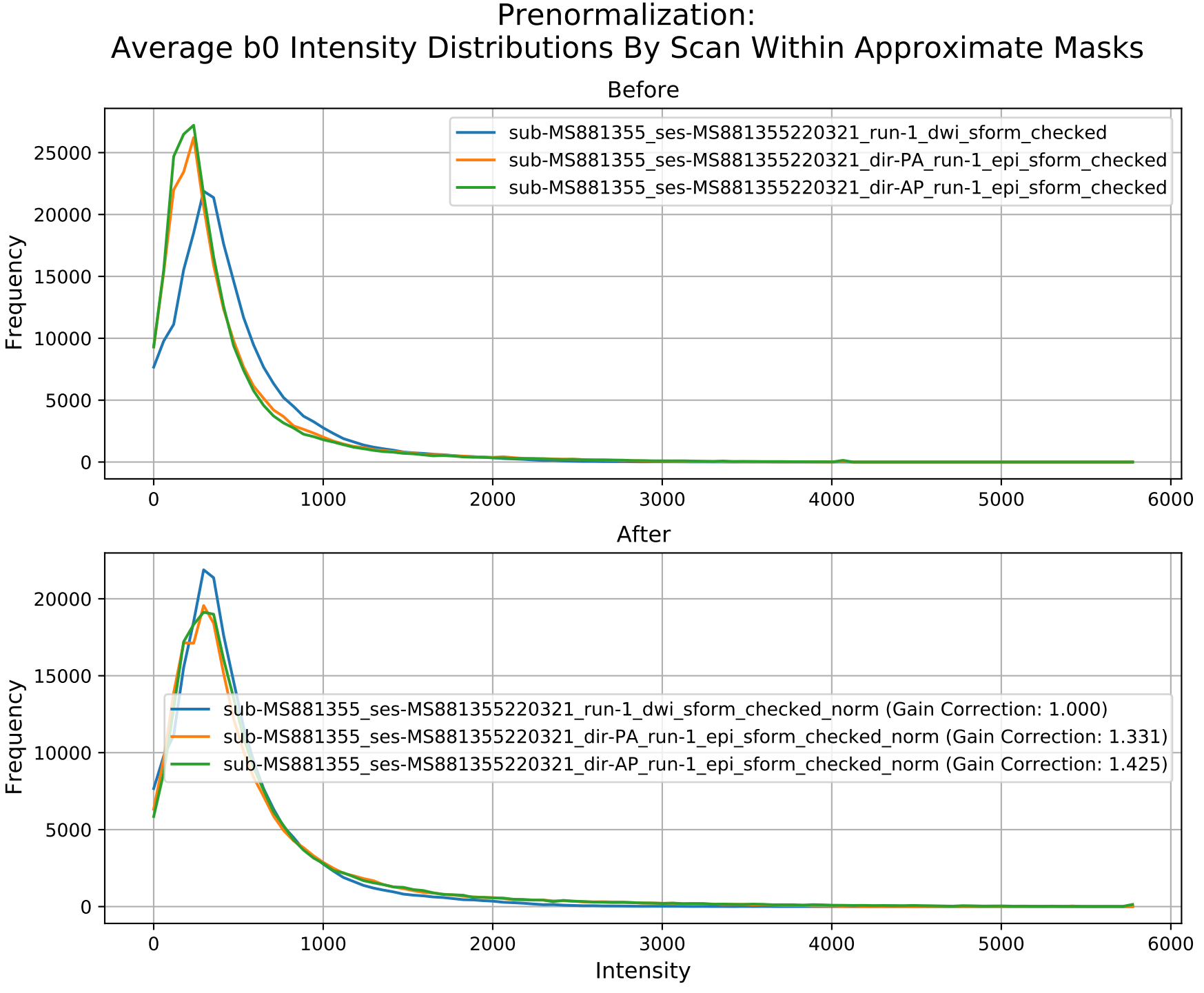
References:

[1] Tournier, J. D. et al. (2019). MRtrix3: A fast, flexible and open software framework for medical image processing and visualisation. NeuroImage, 116137.
[2] Jenkinson, M. et al. (2012). Fsl. Neuroimage, 62(2), 782-790.
[3] Tustison, N. J. et al. (2014). Large-scale evaluation of ANTs and FreeSurfer cortical thickness measurements. Neuroimage, 99, 166-179.
[4] Andersson, J. L. et al. (2003). How to correct susceptibility distortions in spin-echo echo-planar images: application to diffusion tensor imaging. Neuroimage, 20(2), 870-888.
[5] Smith, S. M. et al. (2004). Advances in functional and structural MR image analysis and implementation as FSL. Neuroimage, 23, S208-S219.
[6] Andersson, J. L. et al. (2016). An integrated approach to correction for off-resonance effects and subject movement in diffusion MR imaging. Neuroimage, 125, 1063-1078.
[7] Andersson, J. L. et al. (2016). Incorporating outlier detection and replacement into a non-parametric framework for movement and distortion correction of diffusion MR images. NeuroImage, 141, 556-572.
[8] Tustison, N. J. et al. (2010). N4ITK: improved N3 bias correction. IEEE transactions on medical imaging, 29(6), 1310-1320.
[9] Veraart, J. et al. (2013). Weighted linear least squares estimation of diffusion MRI parameters: strengths, limitations, and pitfalls. Neuroimage, 81, 335-346.
[10] Lauzon, C. B. et al. (2013). Simultaneous analysis and quality assurance for diffusion tensor imaging. PloS one, 8(4).
[11] Smith, S. M. (2002). Fast robust automated brain extraction. Human brain mapping, 17(3), 143-155.
[12] Basser, P. J. et al. (1994). MR diffusion tensor spectroscopy and imaging. Biophysical journal, 66(1), 259-267.
[13] Westin, C. F. (1997). Geometrical diffusion measures for MRI from tensor basis analysis. Proc. ISMRM'97.
[14] Mori, S. et al. (2005). MRI atlas of human white matter. Elsevier.
[15] Wakana, S. et al. (2007). Reproducibility of quantitative tractography methods applied to cerebral white matter. Neuroimage, 36(3), 630-644.
[16] Hua, K. et al. (2008). Tract probability maps in stereotaxic spaces: analyses of white matter anatomy and tract-specific quantification. Neuroimage, 39(1), 336-347.
[17] Avants, B. B. et al. (2008). Symmetric diffeomorphic image registration with cross-correlation: evaluating automated labeling of elderly and neurodegenerative brain. Medical image analysis, 12(1), 26-41.
[18] Jeurissen, B. et al. (2014). Automated correction of improperly rotated diffusion gradient orientations in diffusion weighted MRI. Medical image analysis, 18(7), 953-962.

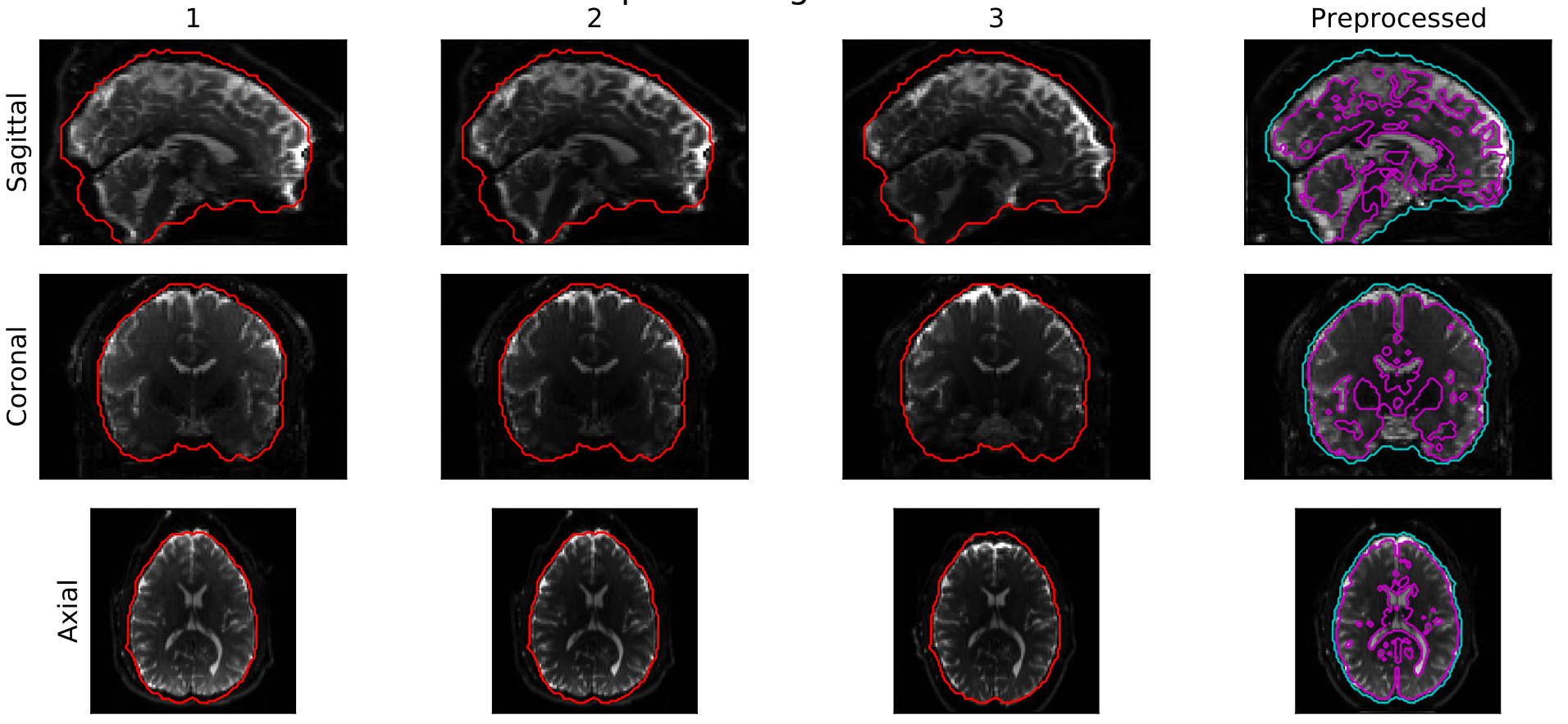


1) sub-MS881355_ses-MS881355220321_run-1_dwi_sform_checked (To A)
2) sub-MS881355_ses-MS881355220321_dir-PA_run-1_epi_sform_checked (To A)
3) sub-MS881355_ses-MS881355220321_dir-AP_run-1_epi_sform_checked (From A)

The supplied phase encoding direction for the input images was "j". Thus, the best interpreted anatomical axes for these images based on their affines are described to the left. Please ensure that these axes (direction agnostic) are interpreted to be the same and are visually distorted above for all images. It is an underlying assumption of this pipeline that all images be phase encoded on the same axis with varying direction as appropriate.

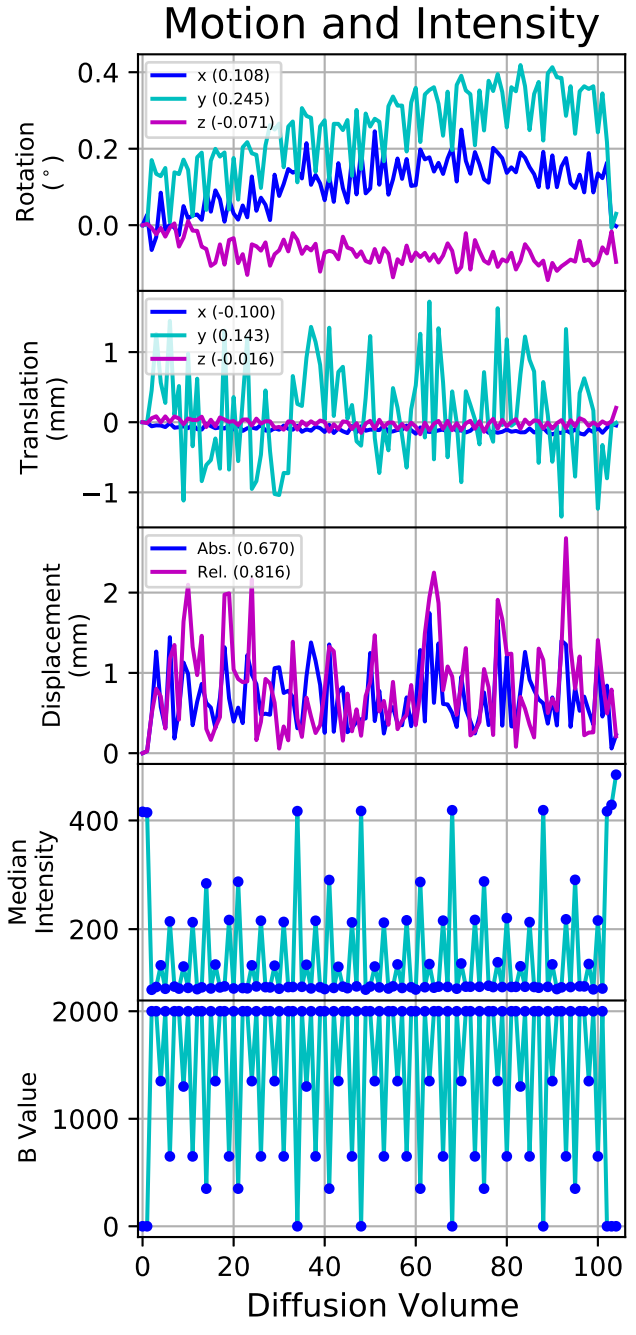

Prenormalization:
Average b0 Intensity Distributions By Scan Within Approximate Masks
Before
sub-MS881355_ses-MS881355220321_run-1_dwi_sform_checked
sub-MS881355_ses-MS881355220321_dir-PA_run-1_epi_sform_checked
sub-MS881355_ses-MS881355220321_dir-AP_run-1_epi_sform_checked
Frequency
0
5000
10000
15000
20000
25000
0
1000
2000
3000
4000
5000
6000
After
sub-MS881355_ses-MS881355220321_run-1_dwi_sform_checked_norm (Gain Correction: 1.000)
sub-MS881355_ses-MS881355220321_dir-PA_run-1_epi_sform_checked_norm (Gain Correction: 1.331)
sub-MS881355_ses-MS881355220321_dir-AP_run-1_epi_sform_checked_norm (Gain Correction: 1.425)
Frequency
0
5000
10000
15000
20000
0
1000
2000
3000
4000
5000
6000
Intensity

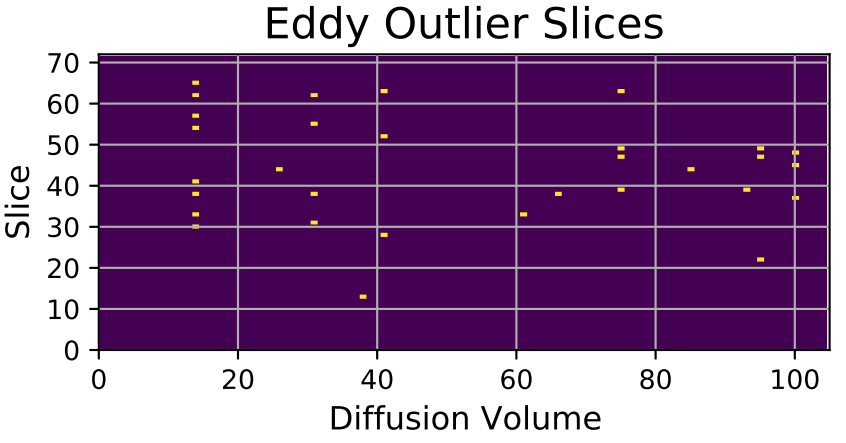
Preprocessing and Masks

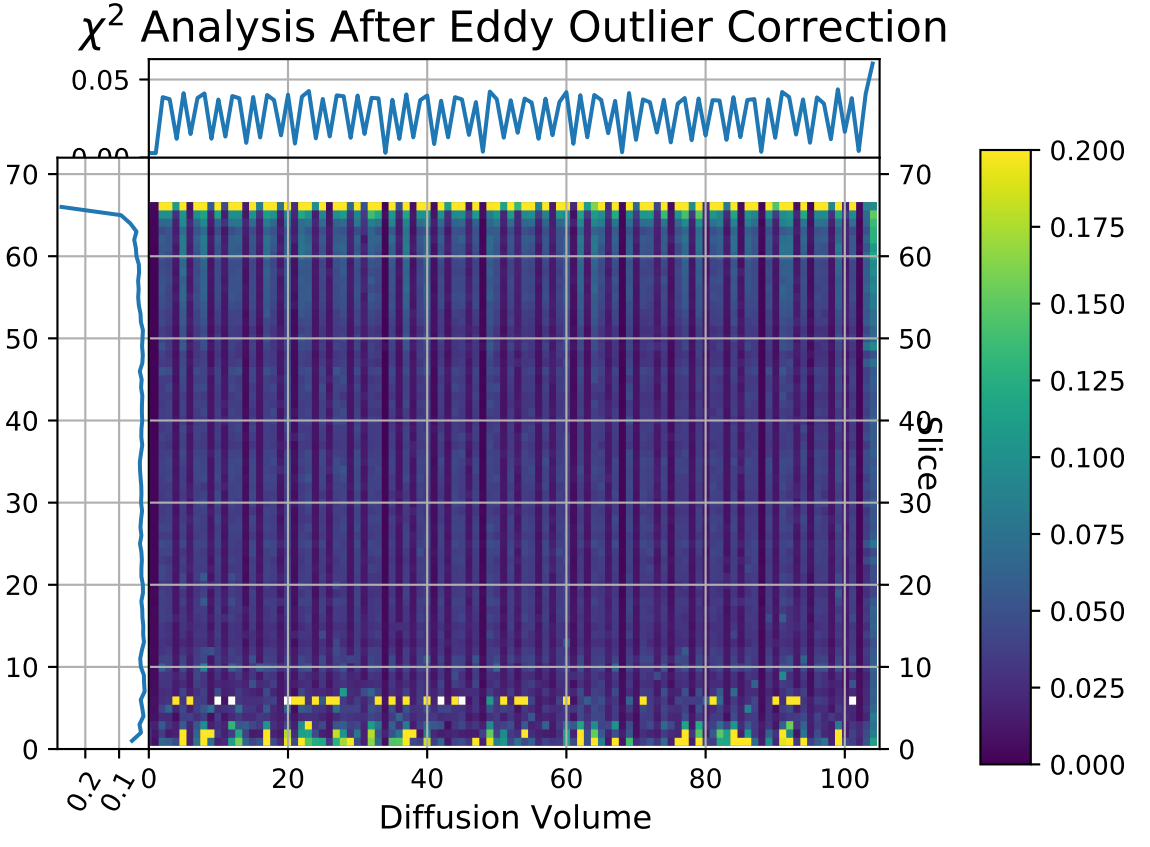


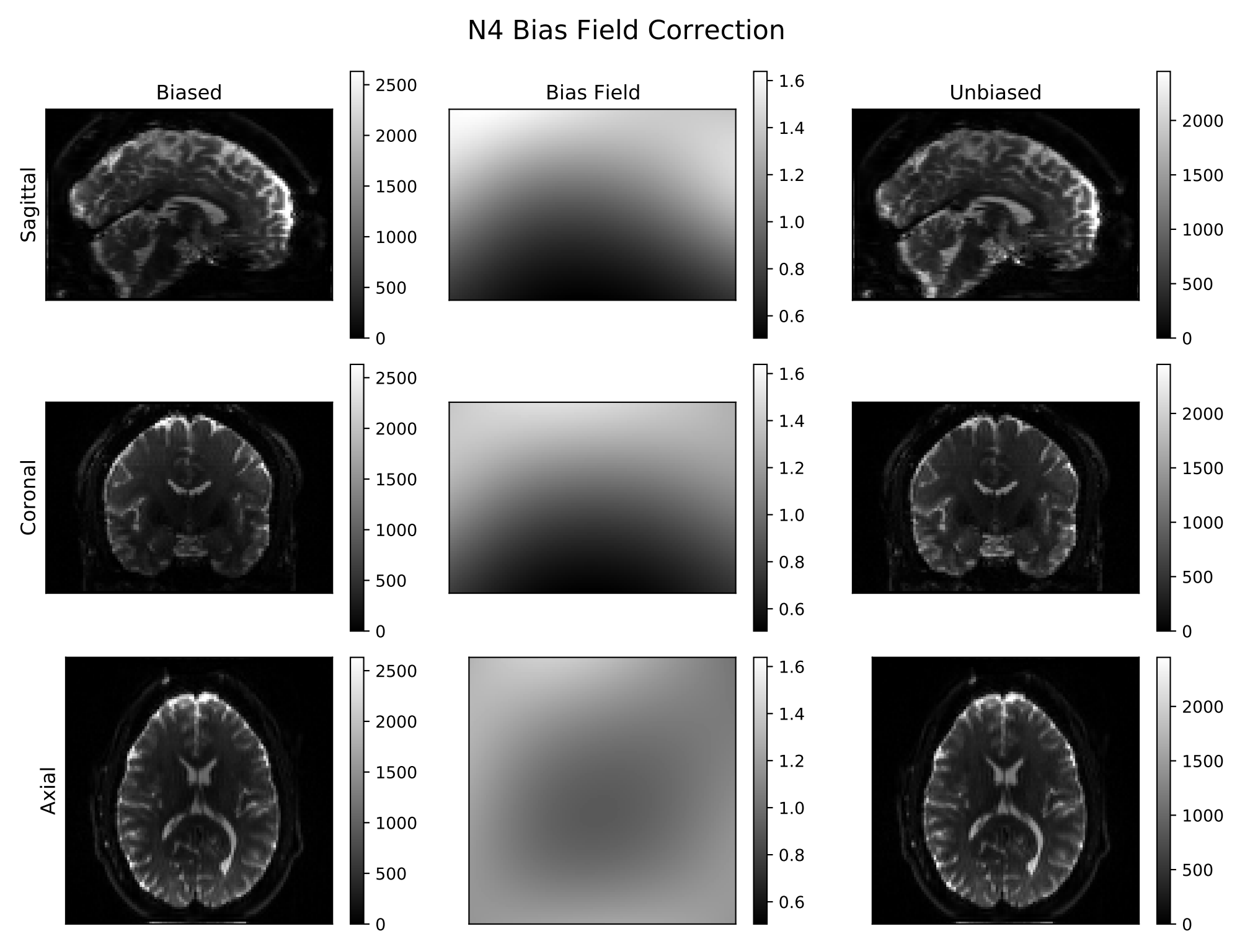
1) sub-MS881355_ses-MS881355220321_run-1_dwi_sform_checked
2) sub-MS881355_ses-MS881355220321_dir-PA_run-1_epi_sform_checked
3) sub-MS881355_ses-MS881355220321_dir-AP_run-1_epi_sform_checked

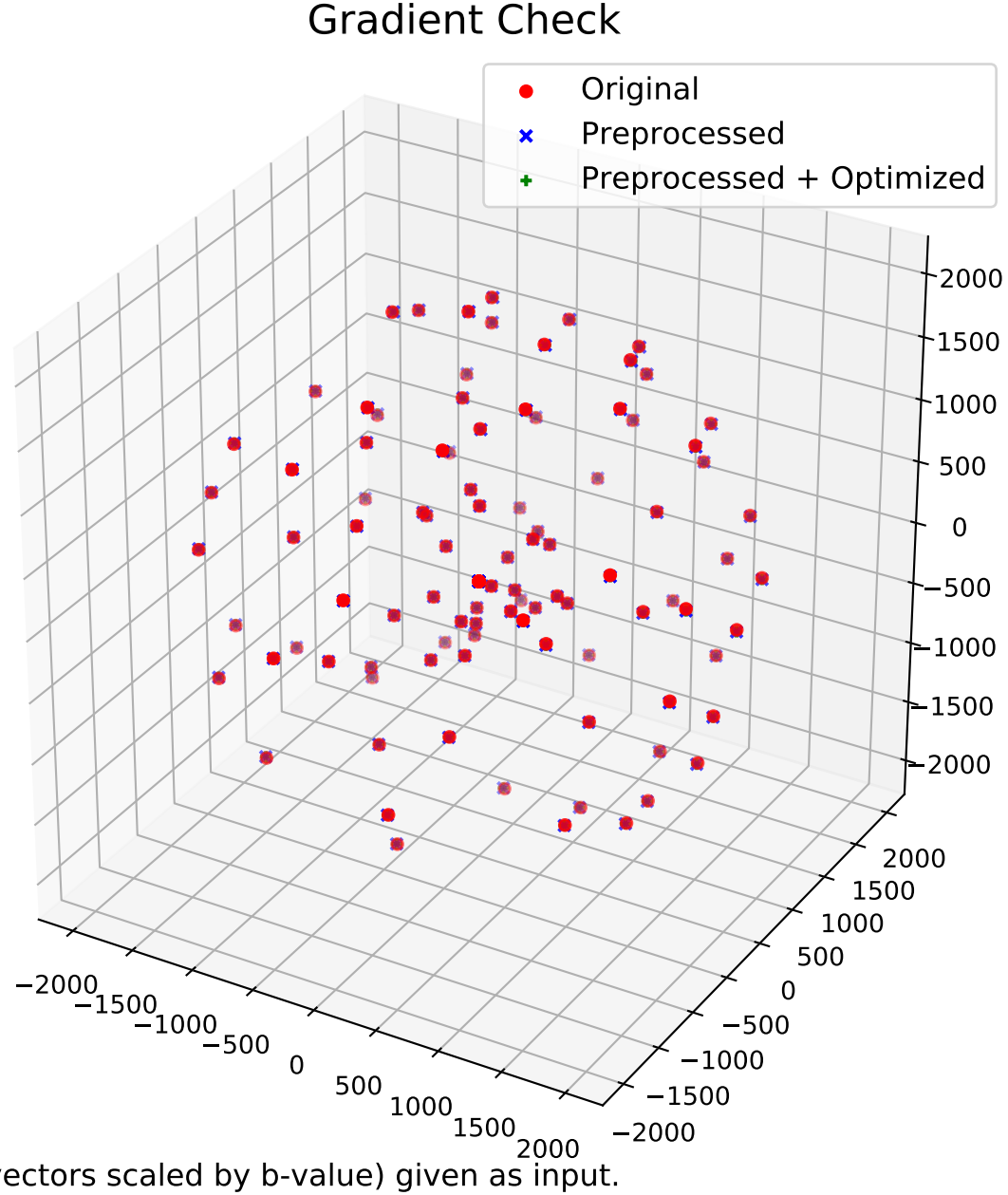
- Eddy Mask: If --eddy_mask is "on" (default), this is calculated on the averaged raw b0s if topup is not run and on the averaged topped-up b0s if it is. If --eddy_mask is "off", this mask is not applied and eddy is performed on the entire volume. This mask need only be approximate and is used for motion and eddy-current correction.
- Preprocessed Mask: This is calculated on the preprocessed averaged b0s. It is used for tensor visualization and other analyses (i.e. SNR and CNR calculations, gradient table checks, etc.) and is the basis for the chi-squared mask.
- Chi-Squared Mask: This is calculated from the preprocessed mask by subtracting the CSF and eroding the result. It is used to determine the voxels in which to perform the chi-squared analysis.


Motion and Intensity
Rotation (°)
x (0.108)
y (0.245)
z (-0.071)
Translation (mm)
x (-0.100)
y (0.143)
z (-0.016)
Displacement (mm)
Abs. (0.670)
Rel. (0.816)
Median Intensity
B Value
Diffusion Volume


Eddy Outlier Slices
Slice
Diffusion Volume


χ^2 Analysis After Eddy Outlier Correction
Slice
Diffusion Volume

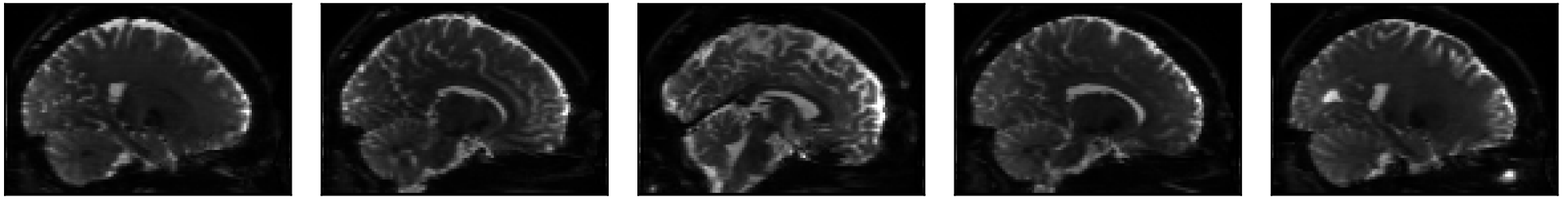

N4 Bias Field Correction
Biased
Bias Field
Unbiased
Sagittal
Coronal
Axial
2500
2000
1500
1000
500
0
1.6
1.4
1.2
1.0
0.8
0.6



- Original: Raw gradients (b-vectors scaled by b-value) given as input.
- Preprocessed: Gradients output and rotated by eddy. Often slightly different than the original gradients.
- Preprocessed + Optimized: Preprocessed gradients that have been sign and order permuted to produce the optimal tract length as determined by dwigradcheck in MRTrix3. Ideally identical to the preprocessed gradients. If not, this suggests an incorrect sign or axis permutation in the b-vectors. Tensor or vector glyph visualization in this PDF can help support this.

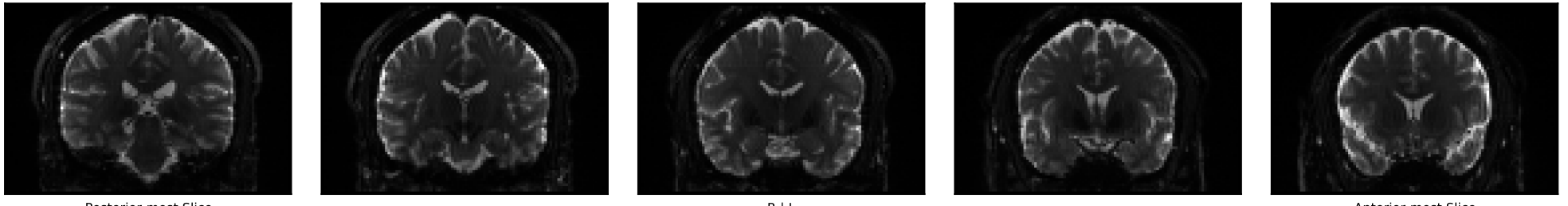
Preprocessed b0

Sagittal



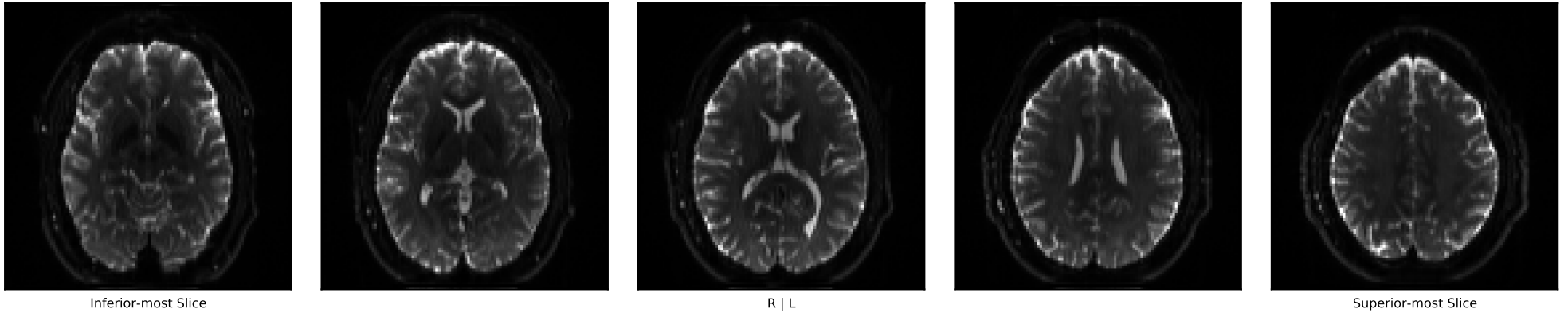
Right-most Slice | P | A | Left-most Slice

Coronal



Posterior-most Slice | R | L | Anterior-most Slice

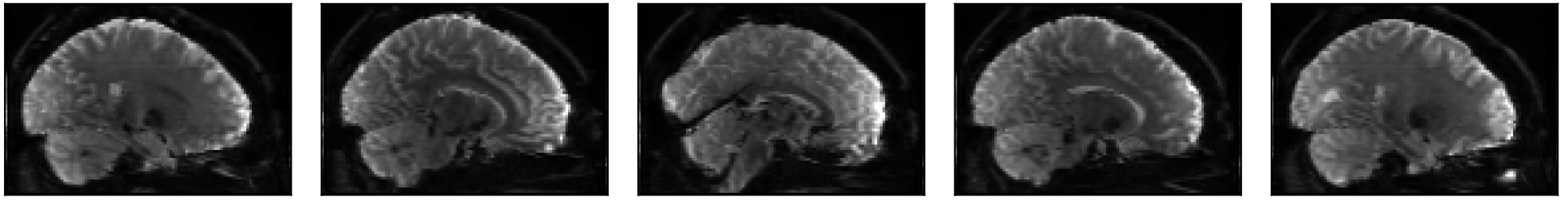
Axial



Inferior-most Slice | R | L | Superior-most Slice

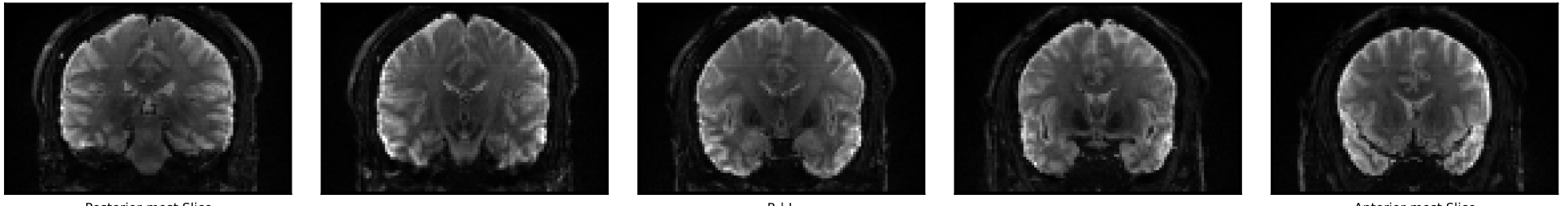
Preprocessed b350

Sagittal



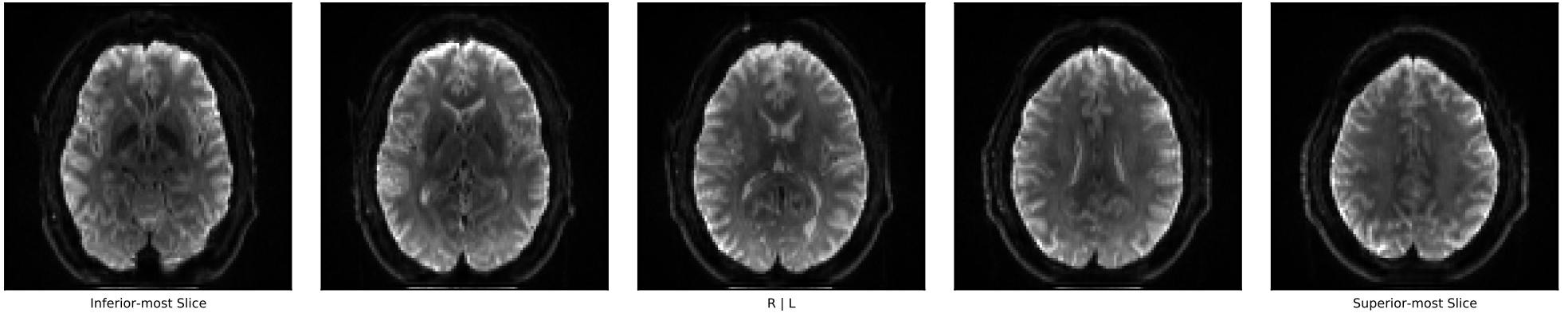
Right-most Slice | P | A | Left-most Slice

Coronal



Posterior-most Slice | R | L | Anterior-most Slice

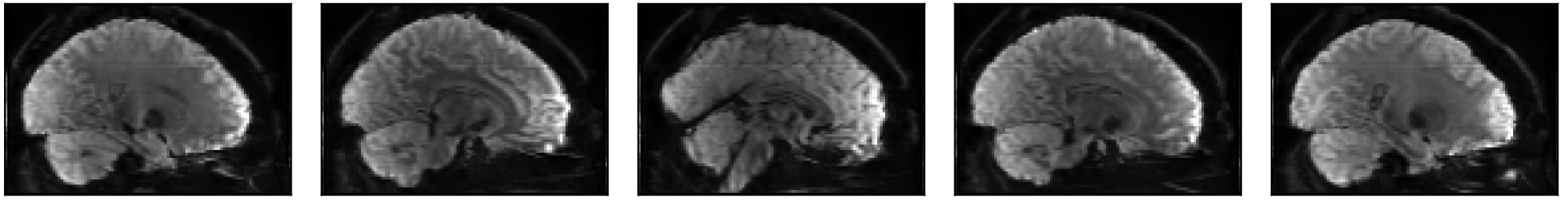
Axial



Inferior-most Slice | R | L | Superior-most Slice

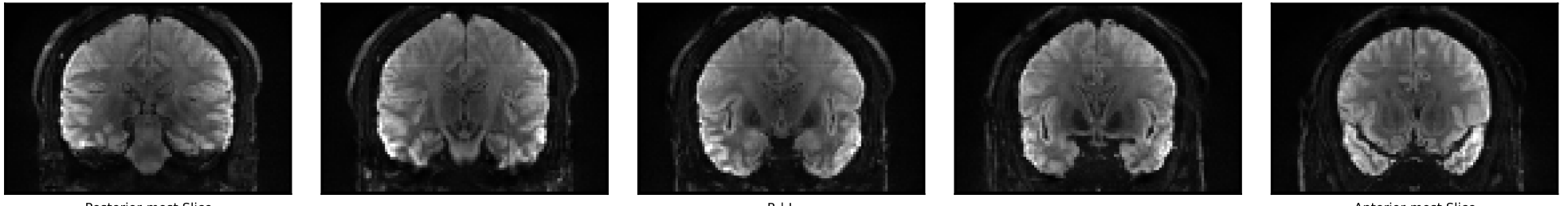
Preprocessed b650

Sagittal



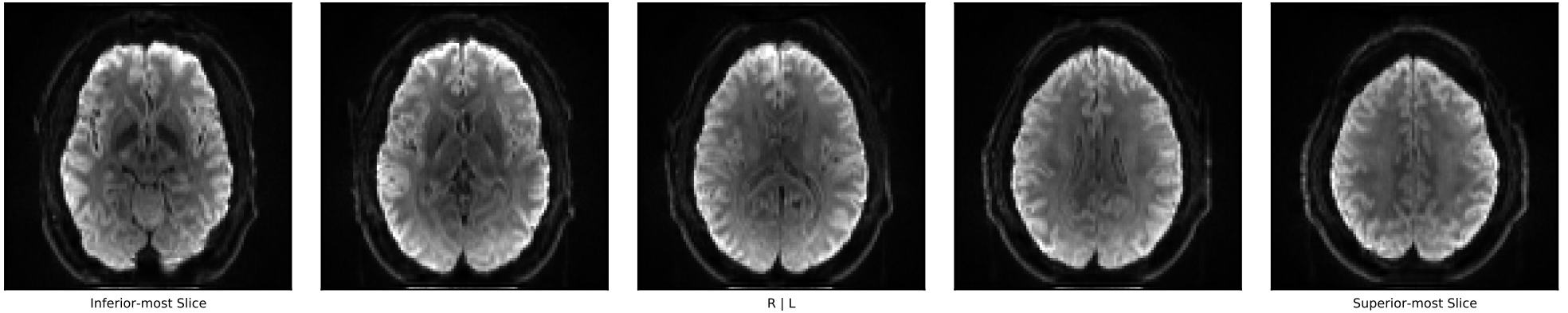
Right-most Slice | P | A | Left-most Slice

Coronal



Posterior-most Slice | R | L | Anterior-most Slice

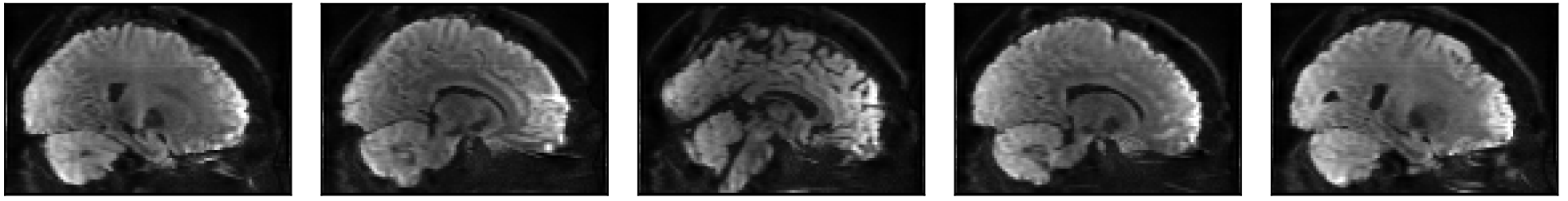
Axial



Inferior-most Slice | R | L | Superior-most Slice

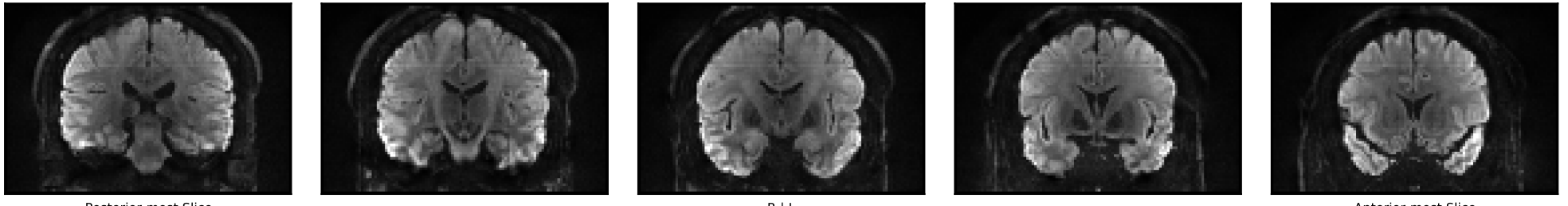
Preprocessed b1350

Sagittal



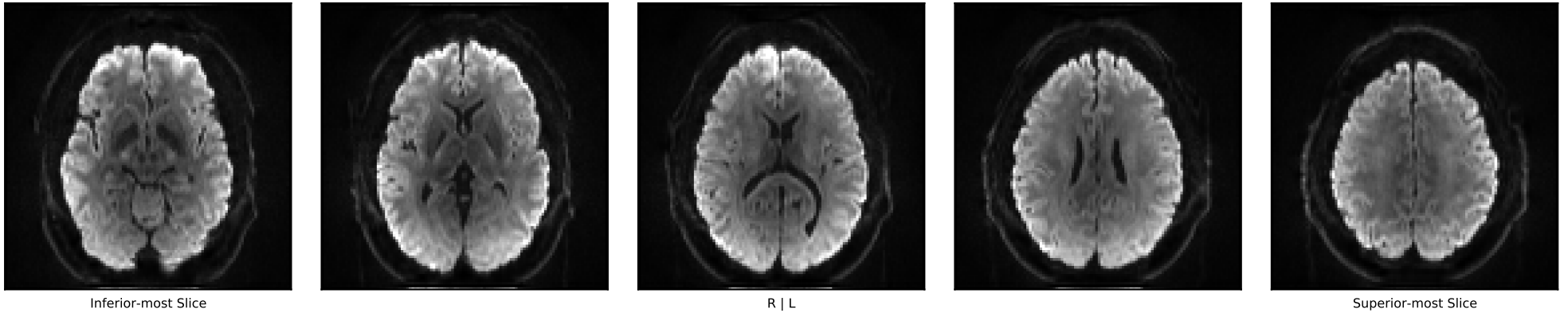
Right-most Slice | P | A | Left-most Slice

Coronal



Posterior-most Slice | R | L | Anterior-most Slice

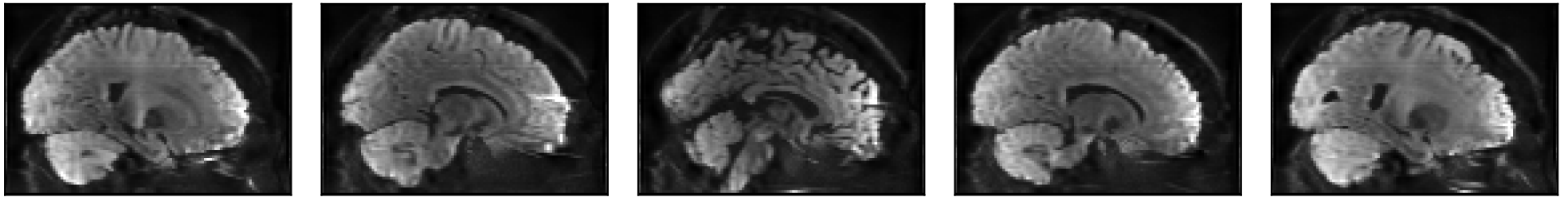
Axial



Inferior-most Slice | R | L | Superior-most Slice

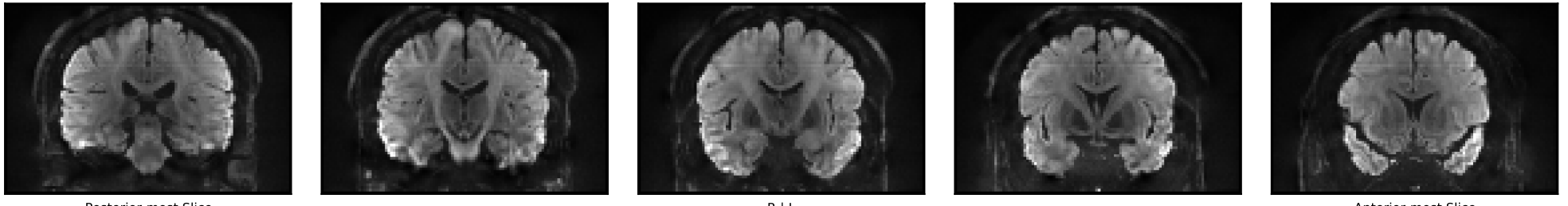
Preprocessed b2000

Sagittal



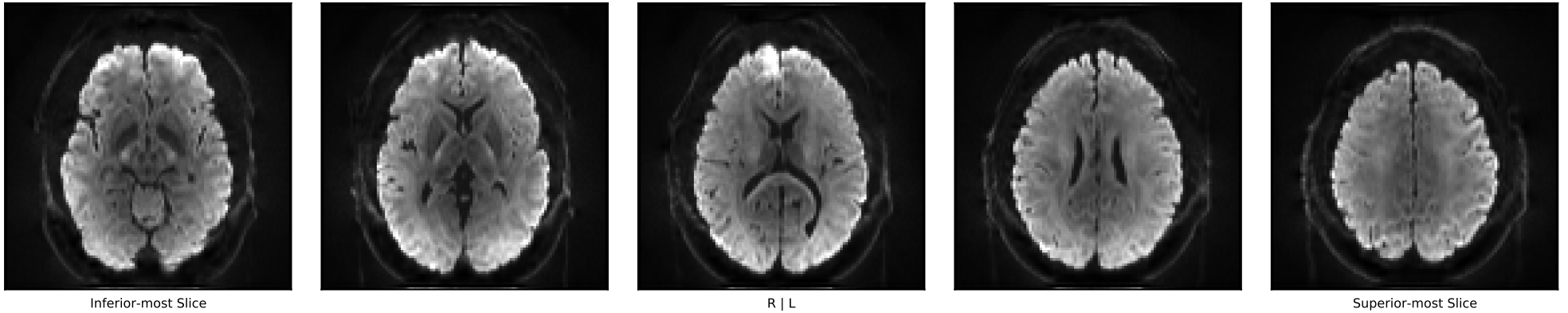
Right-most Slice | P | A | Left-most Slice

Coronal



Posterior-most Slice | R | L | Anterior-most Slice

Axial

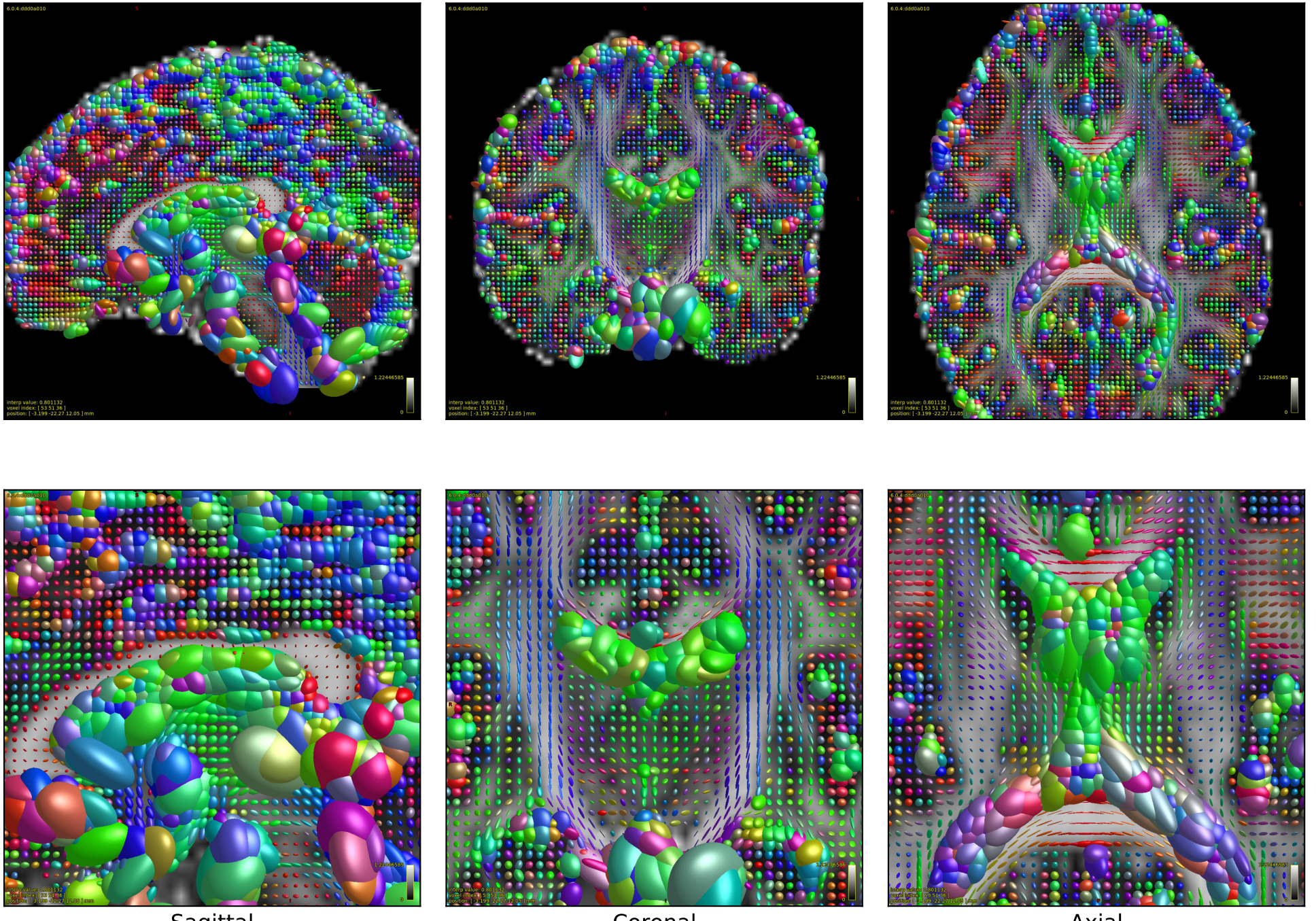


Inferior-most Slice | R | L | Superior-most Slice

Tensors (Non-physiologic Eigenvalues Omitted)

160 mm FOV

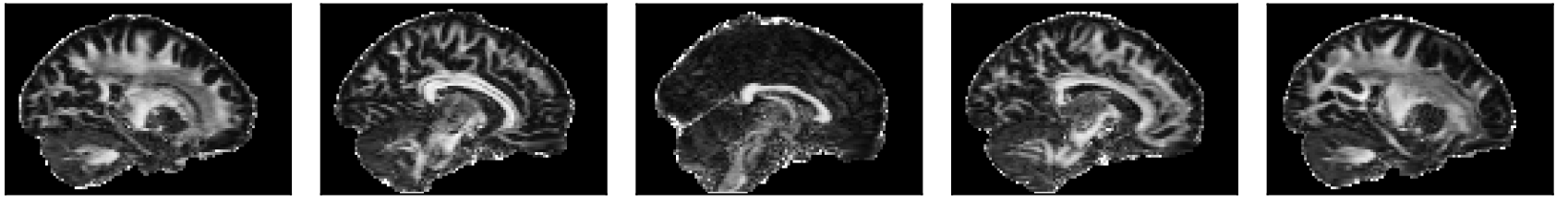
80 mm FOV



Sagittal Coronal Axial

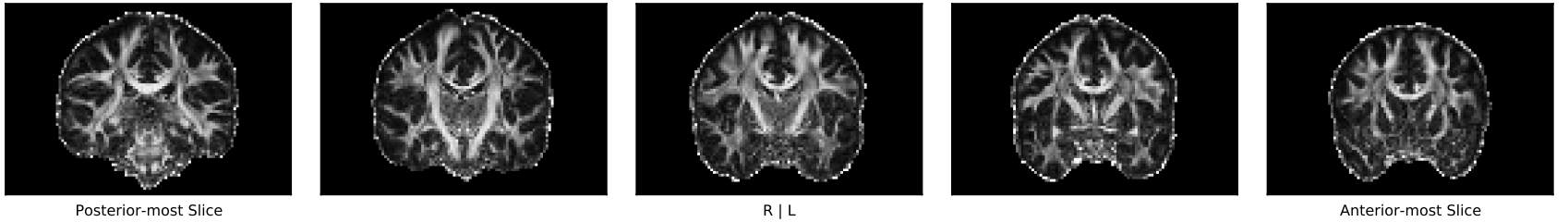
FA
(White matter should be bright)

Sagittal



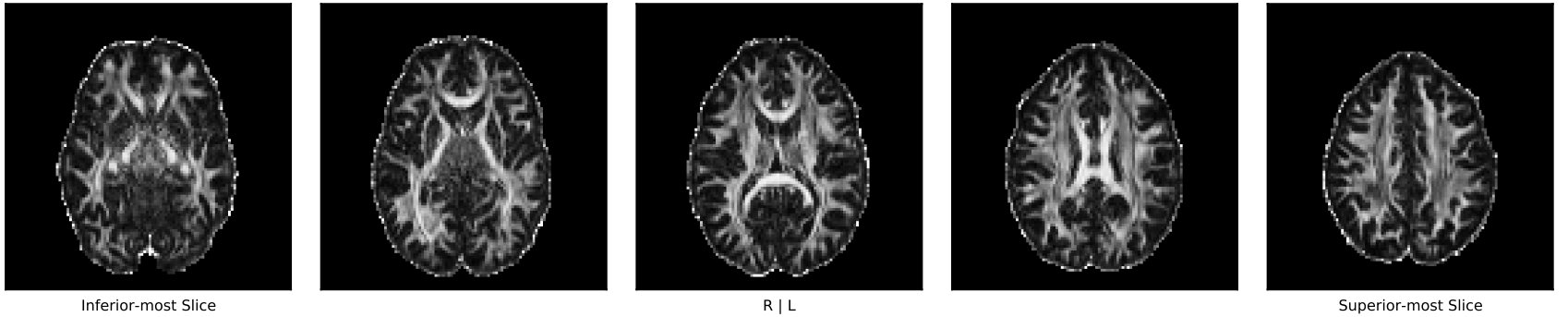
Right-most Slice | P | A | Left-most Slice

Coronal

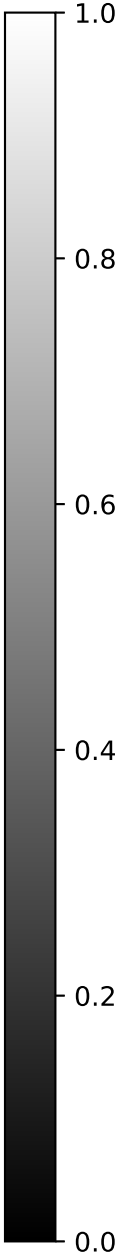


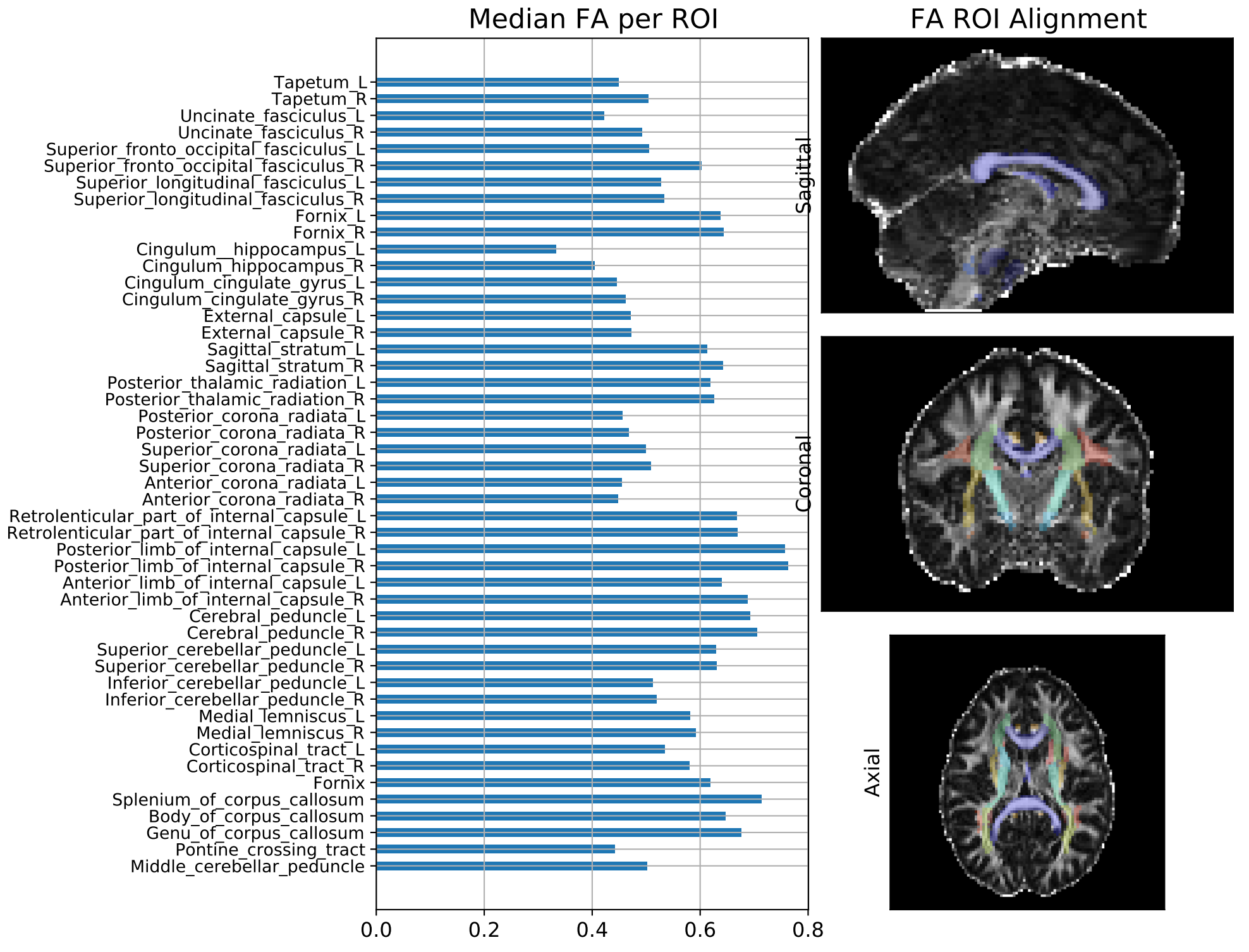
Posterior-most Slice | R | L | Anterior-most Slice

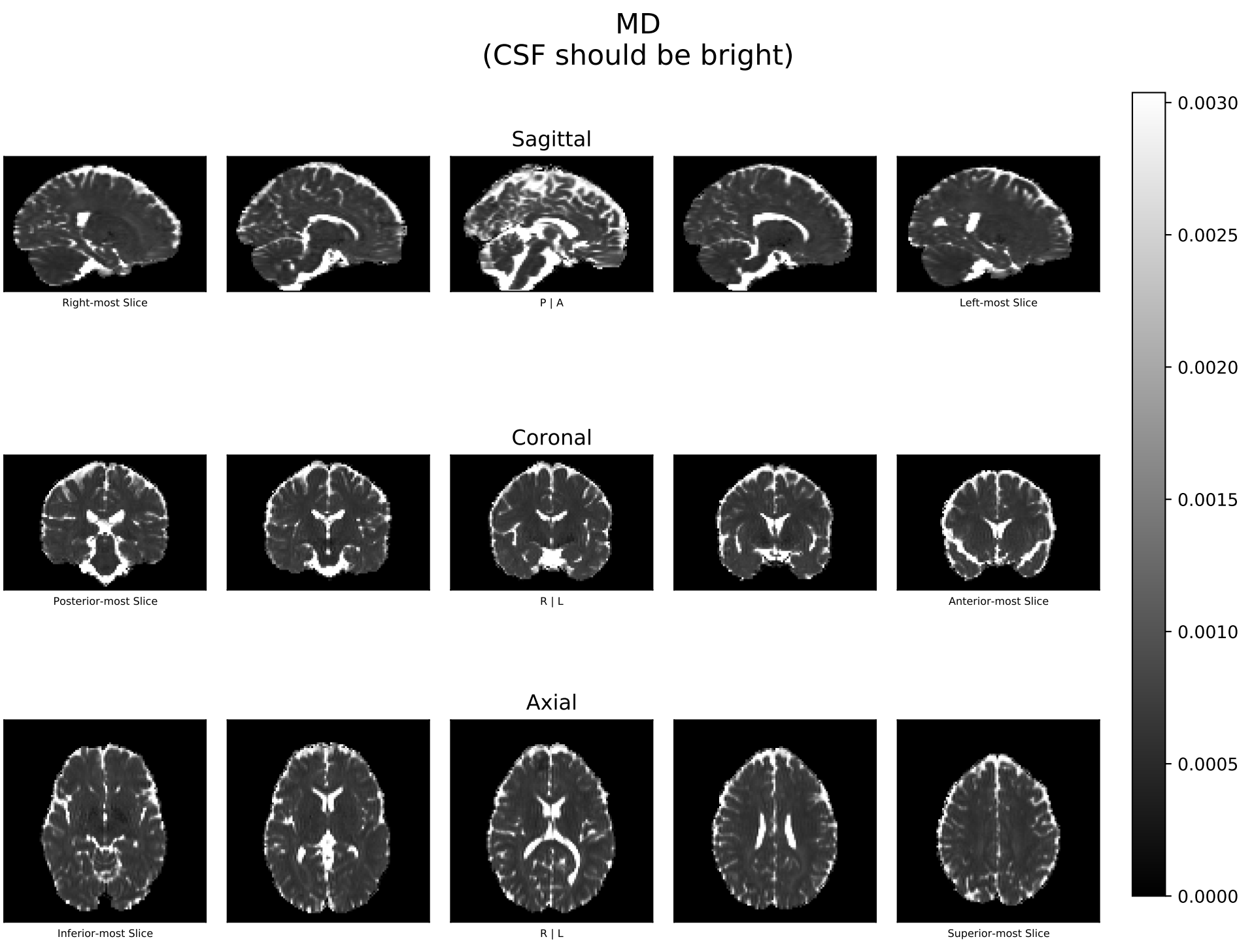
Axial



Inferior-most Slice | R | L | Superior-most Slice




Median FA per ROI
Tapetum_L
Tapetum_R
Uncinate_fasciculus_L
Uncinate_fasciculus_R
Superior_fronto_occipital_fasciculus_L
Superior_fronto_occipital_fasciculus_R
Superior_longitudinal_fasciculus_L
Superior_longitudinal_fasciculus_R
Fornix_L
Fornix_R
Cingulum_hippocampus_L
Cingulum_hippocampus_R
Cingulum_cingulate_gyrus_L
Cingulum_cingulate_gyrus_R
External_capsule_L
External_capsule_R
Sagittal_stratum_L
Sagittal_stratum_R
Posterior_thalamic_radiation_L
Posterior_thalamic_radiation_R
Posterior_corona_radiata_L
Posterior_corona_radiata_R
Superior_corona_radiata_L
Superior_corona_radiata_R
Anterior_corona_radiata_L
Anterior_corona_radiata_R
Retrolenticular_part_of_internal_capsule_L
Retrolenticular_part_of_internal_capsule_R
Posterior_limb_of_internal_capsule_L
Posterior_limb_of_internal_capsule_R
Anterior_limb_of_internal_capsule_L
Anterior_limb_of_internal_capsule_R
Cerebral_peduncle_L
Cerebral_peduncle_R
Superior_cerebellar_peduncle_L
Superior_cerebellar_peduncle_R
Inferior_cerebellar_peduncle_L
Inferior_cerebellar_peduncle_R
Medial_lemniscus_L
Medial_lemniscus_R
Corticospinal_tract_L
Corticospinal_tract_R
Fornix
Splenium_of_corpus_callosum
Body_of_corpus_callosum
Genu_of_corpus_callosum
Pontine_crossing_tract
Middle_cerebellar_peduncle
0.0
0.2
0.4
0.6
0.8
FA ROI Alignment
Sagittal
Coronal
Axial


MD
(CSF should be bright)
Sagittal
Right-most Slice
P | A
Left-most Slice
Coronal
Posterior-most Slice
R | L
Anterior-most Slice
Axial
Inferior-most Slice
R | L
Superior-most Slice
0.0030
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000