

Using an Anisotropic Diffusion Phantom and Bundle Analysis to Compare Diffusion MRI Protocols within and across Sites for Improved Sensitivity and Data Harmonization

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PreOperative
Performance

Introduction

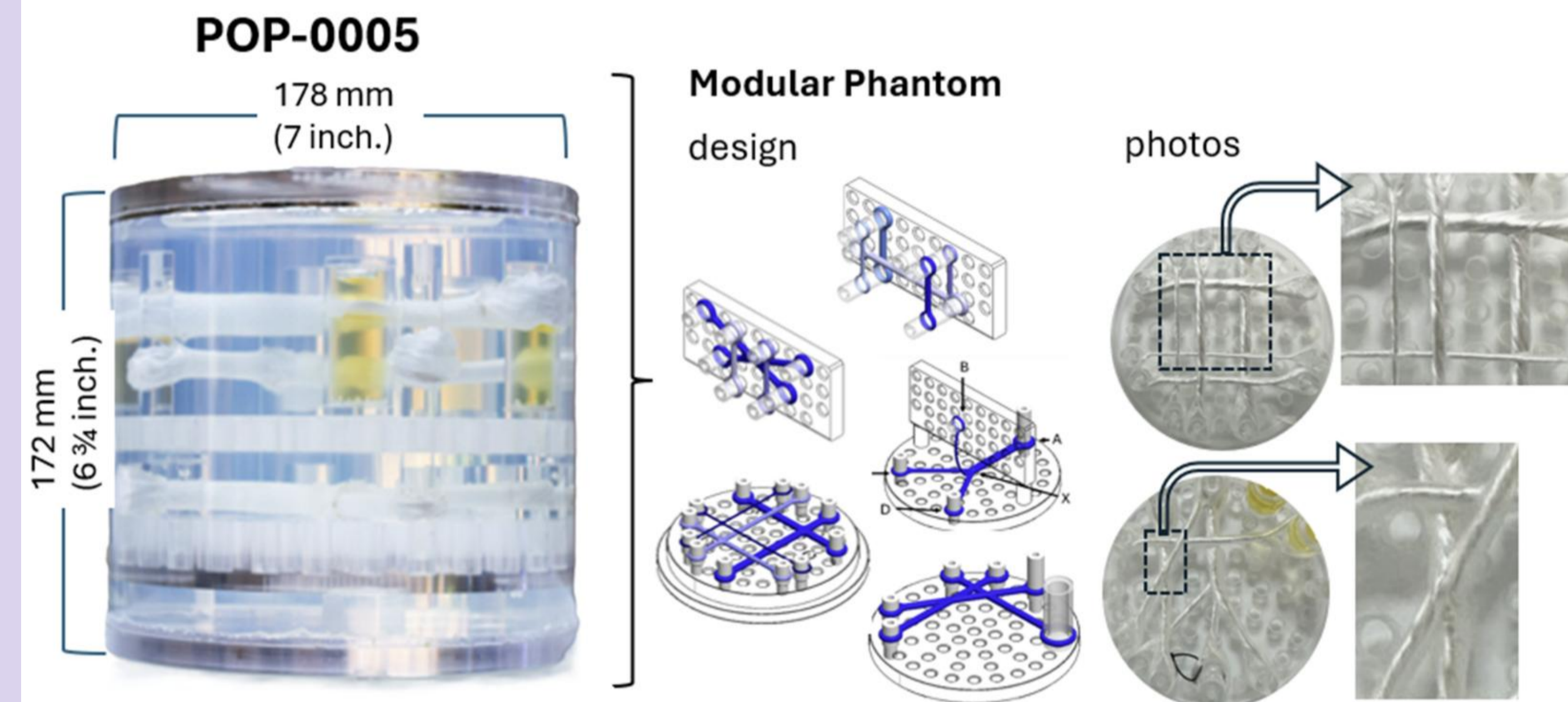
There is no gold standard for quantitative evaluation of DTI protocols. An anisotropic phantom can be used to develop an analysis pipeline that enables quantitative comparisons across protocols and vendors.

Main Goal

Compare various protocols/recon options within 3T scanner:

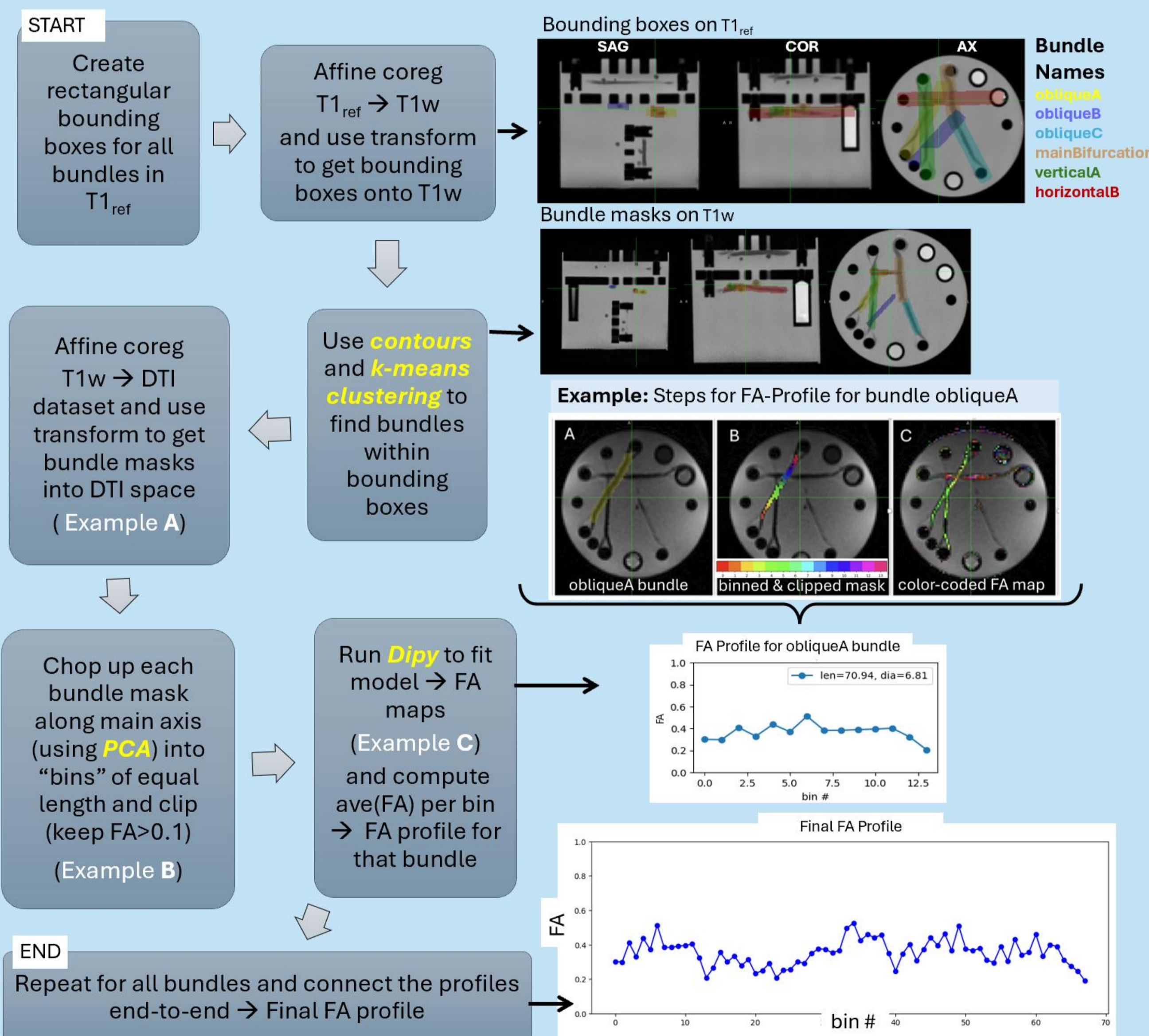
- ✓ Check effect of different TE/TR/SNR
- ✓ Check effect of AI denoising
- ✓ Check effect of 10-min fMRI before DTI

Compare matched protocol across vendors @3T



Methods

I. Image Processing : Python-based



Results

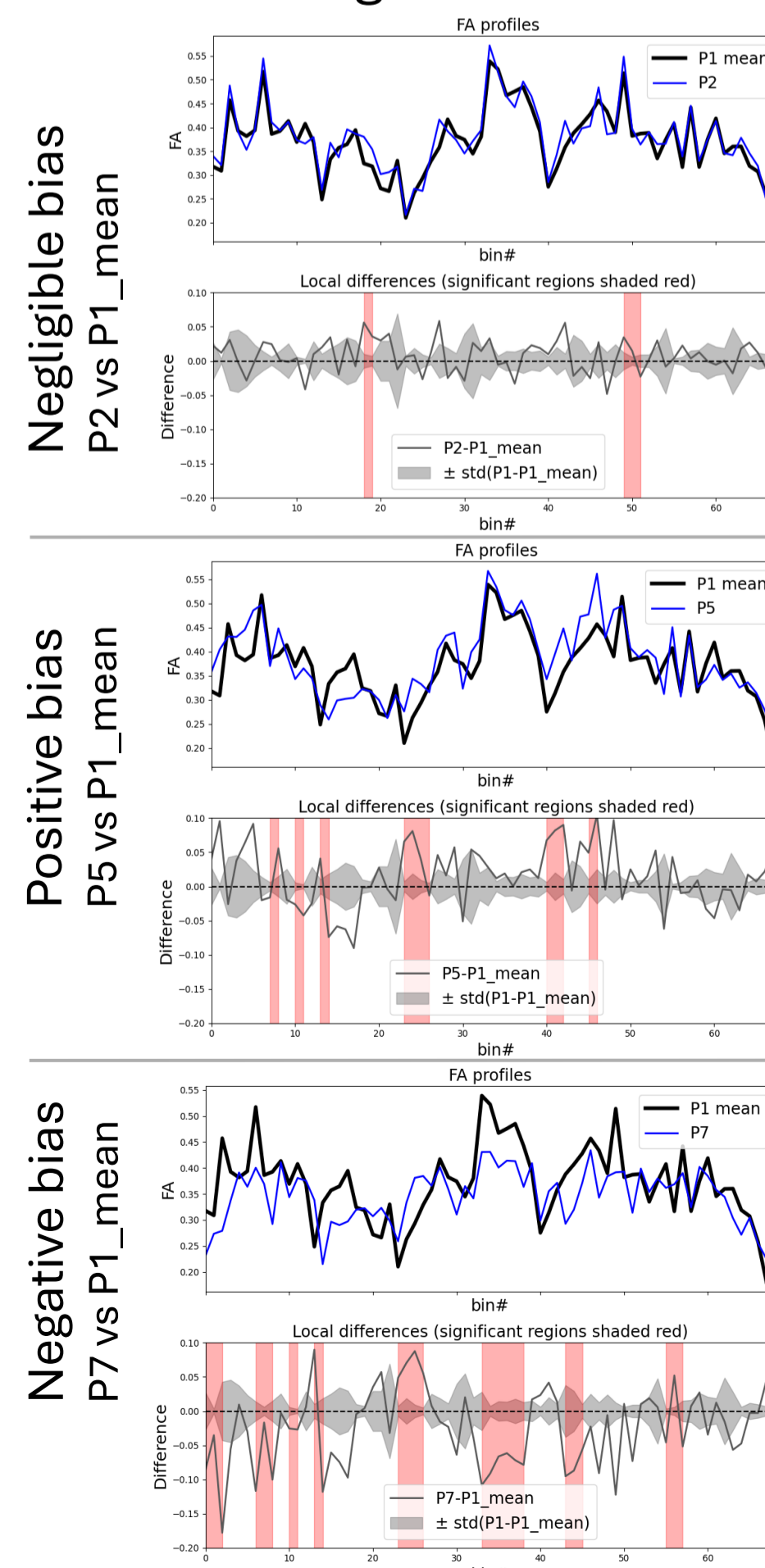
Biased differences - largest effects

Protocol	correlation	Bias_d	Effect_size_bias	Direction	p_bias	Bias_sig
P2	0.95	0.52	negligible	--	0.111	ns
P3	0.92	-0.75	negligible	--	0.111	ns
P4	0.90	-0.34	negligible	--	0.111	ns
P5	0.82	1.53	small	↑	0.111	ns
P6	0.86	-1.09	small	↓	0.111	ns
P7	0.64	-1.49	small	↓	0.111	ns

Absolute differences - largest effects

Protocol	AbsDiff_d	Effect_size_absdiff	p_absdiff	AbsDiff_sig
P2	2.62	moderate	0.111	ns
P3	2.47	moderate	0.111	ns
P4	3.62	large	0.111	ns
P5	5.3	large	0.111	ns
P6	4	large	0.111	ns
P7	5.06	large	0.111	ns

Localized significant effects: clusters



Methods

II. 3T Scans (GE Premier and Siemens Prisma)

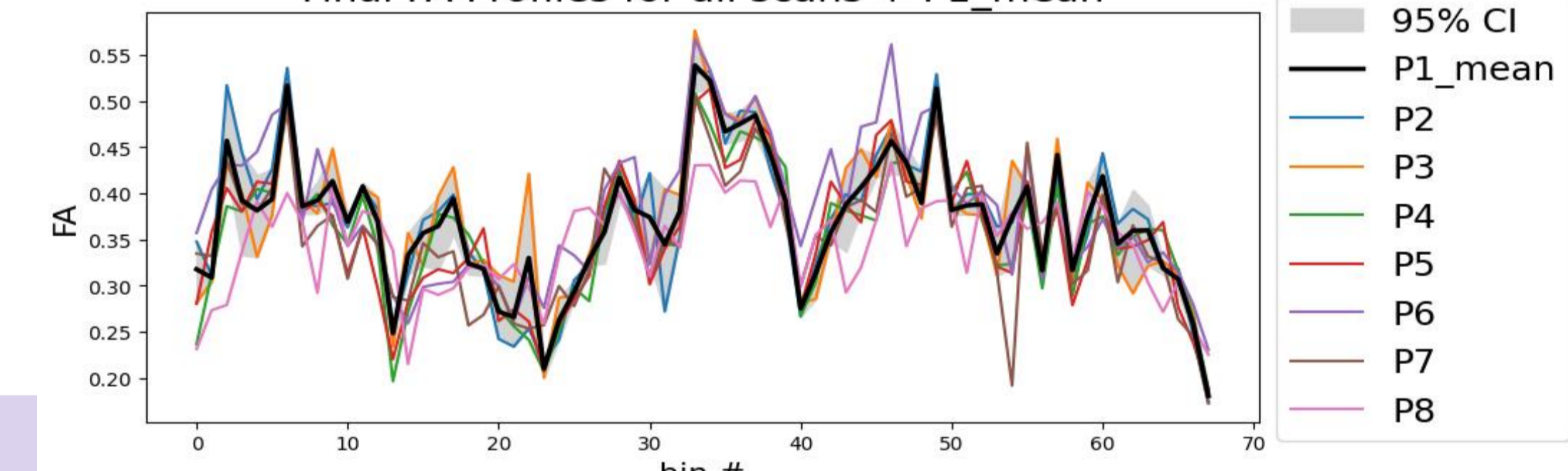
- P1 : GE-Protocol#1 scanned 3x repeated → P1_mean ± 95% CI
- P2 = GE-Protocol#1 + 3D Geometry Correction
- P3 = GE-Protocol #2
- P4 = GE-Protocol #2+ AI denoising
- P5 = GE-Protocol #3 after 10min fMRI + RTFA
- P6 = GE-Protocol #1 after 10min fMRI w/o RTFA
- P7 = Siemens Protocol #4

Scan Parameter	Protocol #1 (GE)	Protocol #2 (GE)	Protocol #3 (GE)	Protocol#4 (Siemens)
TE (ms)	80.5	57.0	57.0	71.0
TR (s)	11.3	10.0	10.0	9.9
Pixel BW (Hz)	1953	1953	1953	2170
Slice thickness (mm)	2.5	2.5	2.0	2.0
In-plane reso (mm ²)	.78 X .78	.78 X .78	.78 X .78	.78 X .78
# grad directions	32 (b=1000)	32 (b=1000)	32 (b=1000)	30 (b=1000)
# b=0	1	1	1	1

III. Data Analysis

- Bootstrap to get P1_mean ± 95% CI
- Use noise = stdev(P1-P1_mean)
- Compare P2-P7 to P1_mean:
 1. correlations for overall profile shape
 2. using permutation test to get null distribution of P1 → p_value
 3. using Cohen's effect size normalized to noise → d
- Compute for 2 differences:
 - a) mean of signed differences for bias detection
 - b) RMSE for overall differences in profile shape
- Look into clustered/localized effects

Final FA Profiles for all scans + P1_mean



Discussion

- Repeat scans of P1 showed consistency but due to N=3, not enough statistical power to detect significant differences across protocols (p_values > 0.05)
- All protocols scanned back-to-back on the same scanner without repositioning yielded **highly correlated Final FA Profiles** (r > 0.8) but even the Siemens scan gave r = 0.64, indicating **consistency in FA Profile shapes across protocols and scanners**
- Only 3 Protocols (P5, P6, P7) showed small bias effects: 1.0 < bias_d < 2.0, others were negligible suggesting that **Protocol#2 did not result in a significant bias in FA profiles relative to Protocol#1 (w/ and w/o AI denoising)**
- Scans run after the 10-min fMRI had small bias effects and large absolute difference effects that warrants further investigation
- The Siemens scan resulted in small negative bias effect relative to GE-P1 and a large absolute difference effect despite the thinner slices (2.0 mm vs 2.5 mm) which usually results in higher FA due to a reduction in partial volume effects (see P5 vs P1_mean), this warrants further investigation
- No consistent cluster locations were seen across scans

Conclusion

A new method to evaluate DTI protocols has been presented. This work presents a robust framework for identifying protocol parameters that drive sensitivity and for harmonizing DTI data across sites, supporting more reliable use of DTI in concussion research.

References

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