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The TL;DR

Background: Data have biases by collection site/scanner.
If we combine data from multiple sites, we need to correct for site bias.

Idea: Compress our data so that it is uninformative of site.
Desiderata:

"Find a representation z of x such that $I(z:s) - \lambda I(x:z)$ is minimal for tradeoff λ between compression and relevance."

Surprisingly, we can solve this optimization problem, giving us:

1. Site/scanner-invariant representations of images.
2. Reconstructed images with **bounded** info. about their original site/scanner.

Takehome Intution: Compression + Cond. Reconstruction → Harmonization

Details

We want a function from scan x to new scan x' that removes the original site information s and replaces it with s'.

Data Proc. Ineq.: Let $q : x \mapsto z$ and $p : z, s' \mapsto x'$. If $z \perp s$, then $x' \perp s$. Moreover,

$$I(x', s) \leq I(z, s)$$

So by reducing $I(z, s)$, we can remove site information.

Further, if we let p depend on a new s', we can attempt to map x to x' which has site information from s'.

Bound for $I(z, s)$

$$0 \leq I(z,s) \leq \underbrace{-\mathbb{E}_{x,s,z\sim q}[\log p(x|z,s)]}_{\text{Reconstruction}} + \underbrace{\mathbb{E}_x[\, KL[\, q(z|x) \,\|\, q(z)\,]\,]}_{\text{Compression}} - \underbrace{H(x|s)}_{\text{Const}}.$$

By minimizing this bound on $I(z, s)$ over q, p, we can learn a remapping function that tries to ``forget'' the original site variable, with a guarantee of the maximum amount of information retained.

DWI Specific Architecture
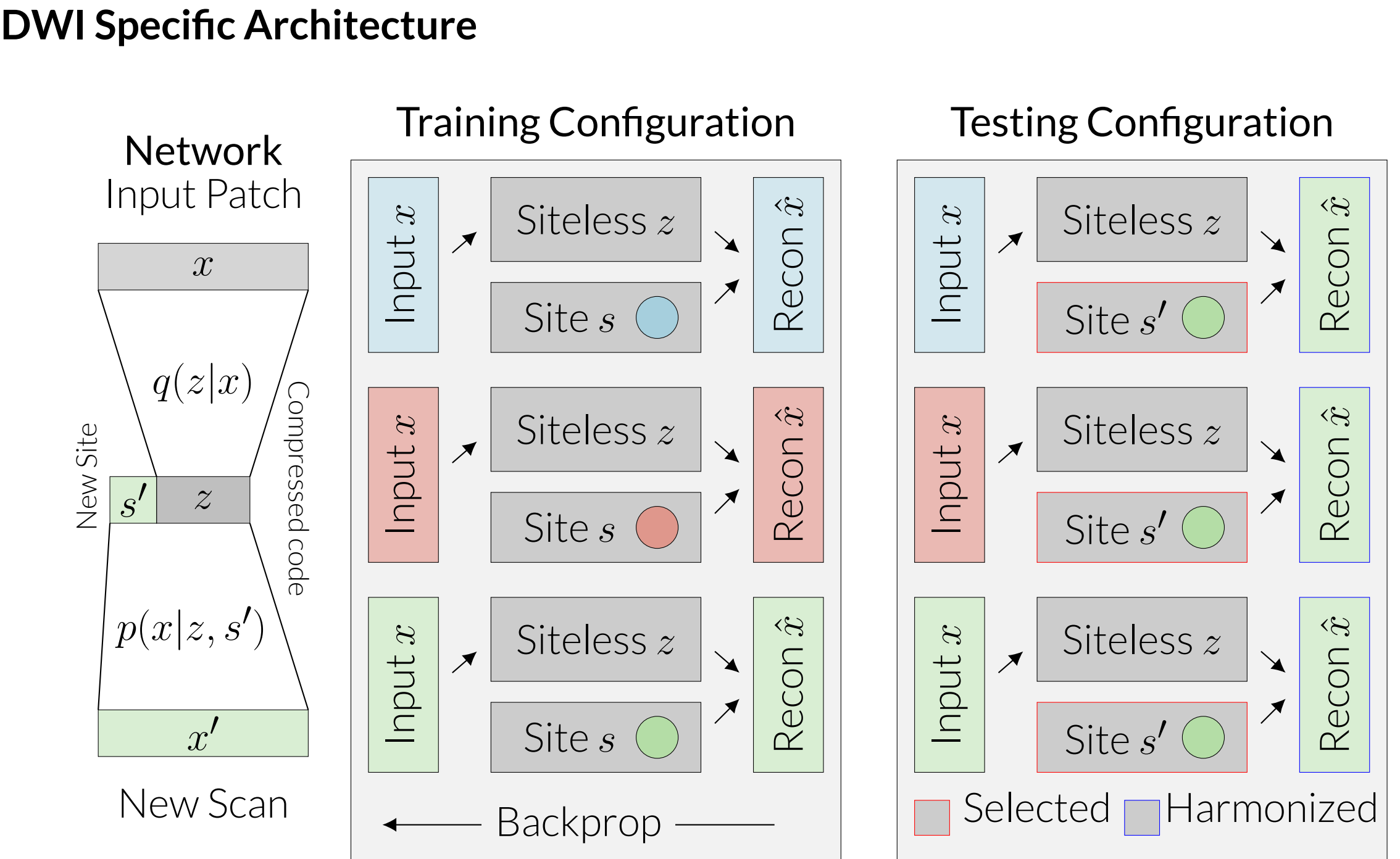
Data and Demonstration Experiments

We use the MICCAI CDMRI Diffusion Harmonization Challenge Dataset [2]:

- N=10 subjects scanned at all ``sites'', 8/2 Train-test split.
- All subjects Eddy and EPI corrected, then rigidly aligned. High spatial-resolution scans resampled to 2.4 mm isotropic.
- Projected to ℓ_2-minimal 8th order Spherical Harmonics basis using SVD.

Site Name	Scanner-type	Voxel Size (iso)	TE/TR	# Grad.
Prisma-30	Prisma	2.4 mm	89/7200 ms	30
Prisma-60	Prisma	1.5 mm	80/4500 ms	30
Connectom-30	Connectom	2.4 mm	89/7200 ms	30
Connectom-60	Connectom	1.2 mm	68/5400 ms	60

All scans collected two diffusion shells, $1200\frac{s}{mm^2}$ and $3000\frac{s}{mm^2}$, and at least 4 interspersed b_0 volumes, one with a reversed phase encoding.

Error Plot: Prisma-30 to Connectom-30

References
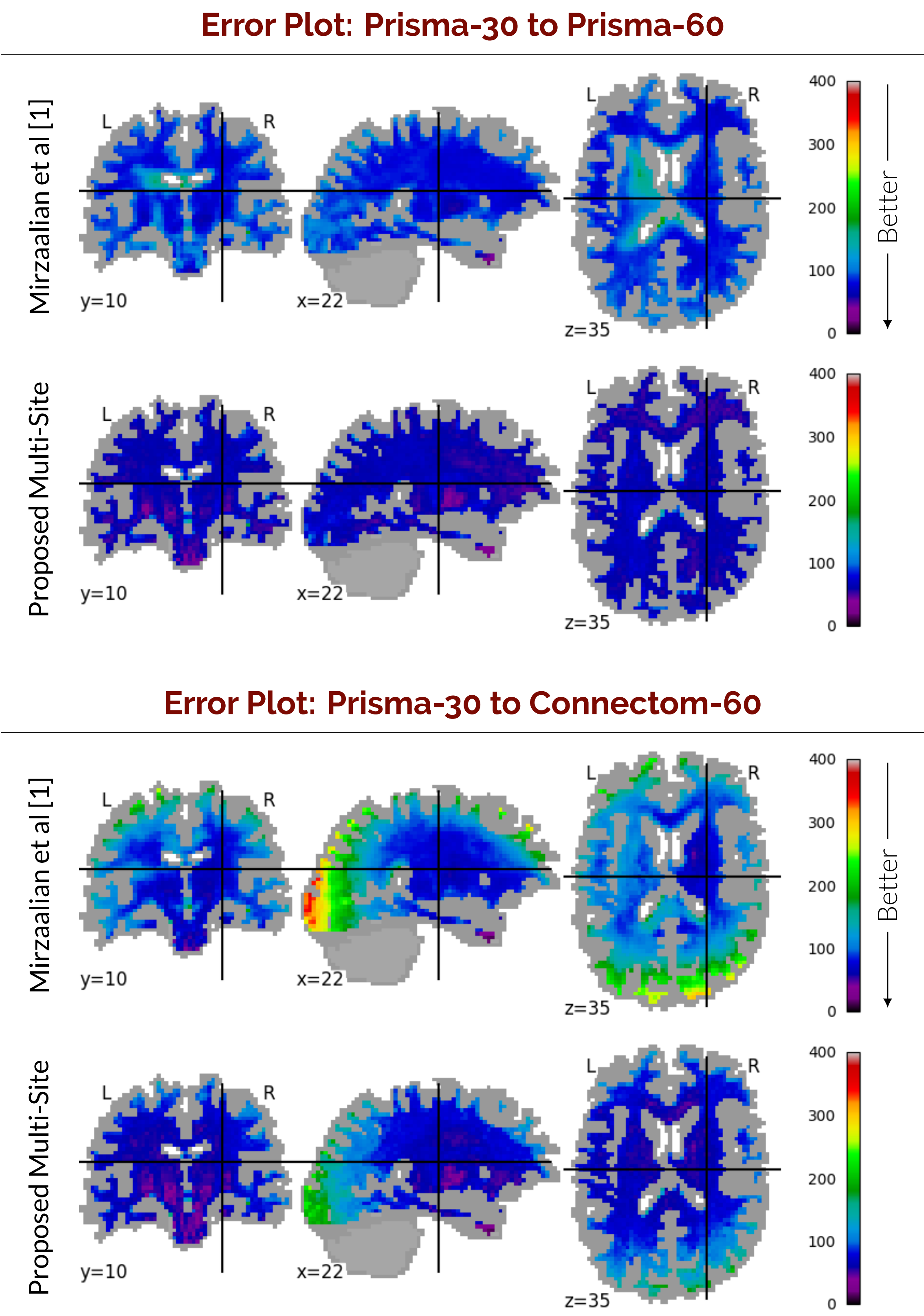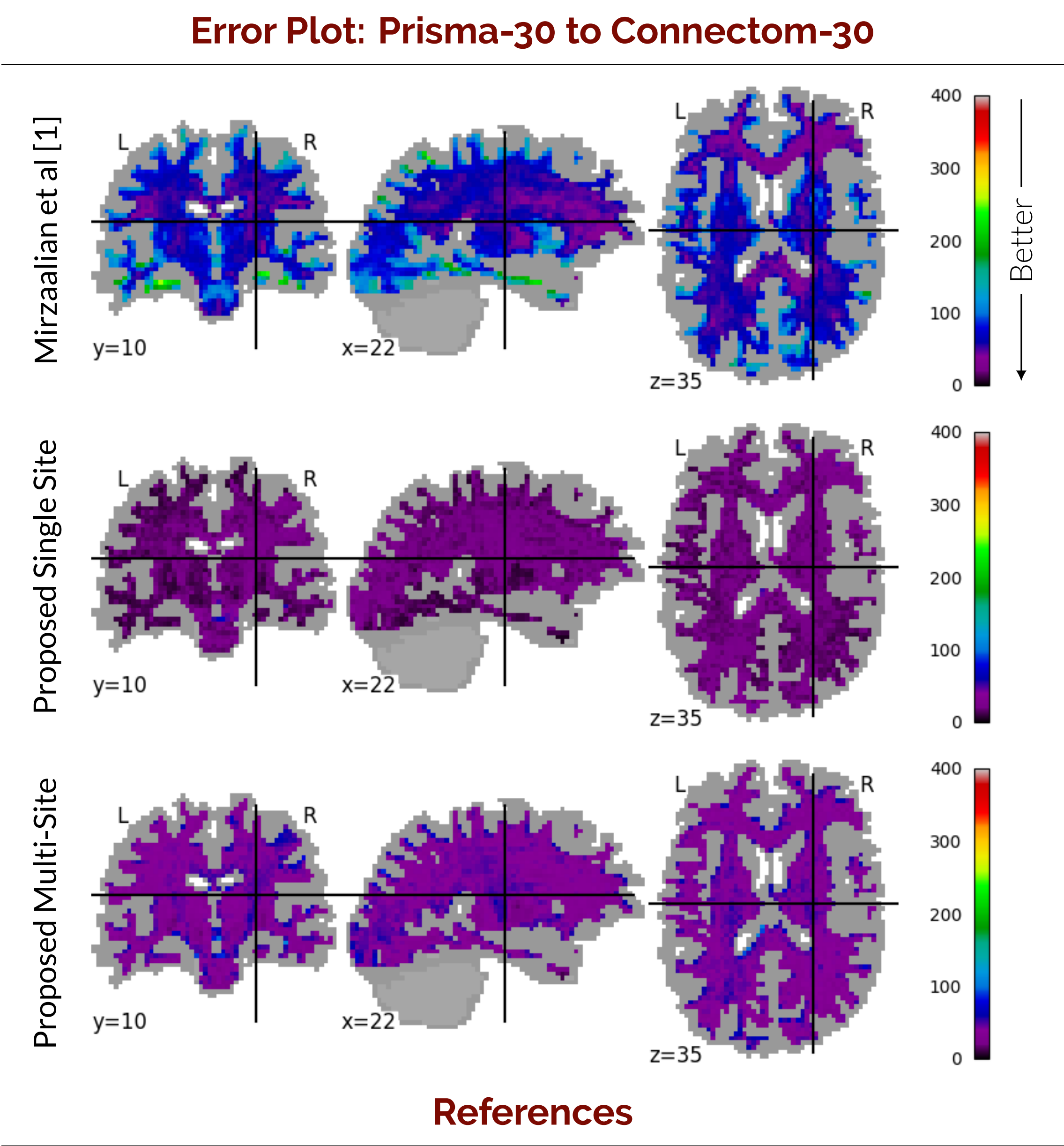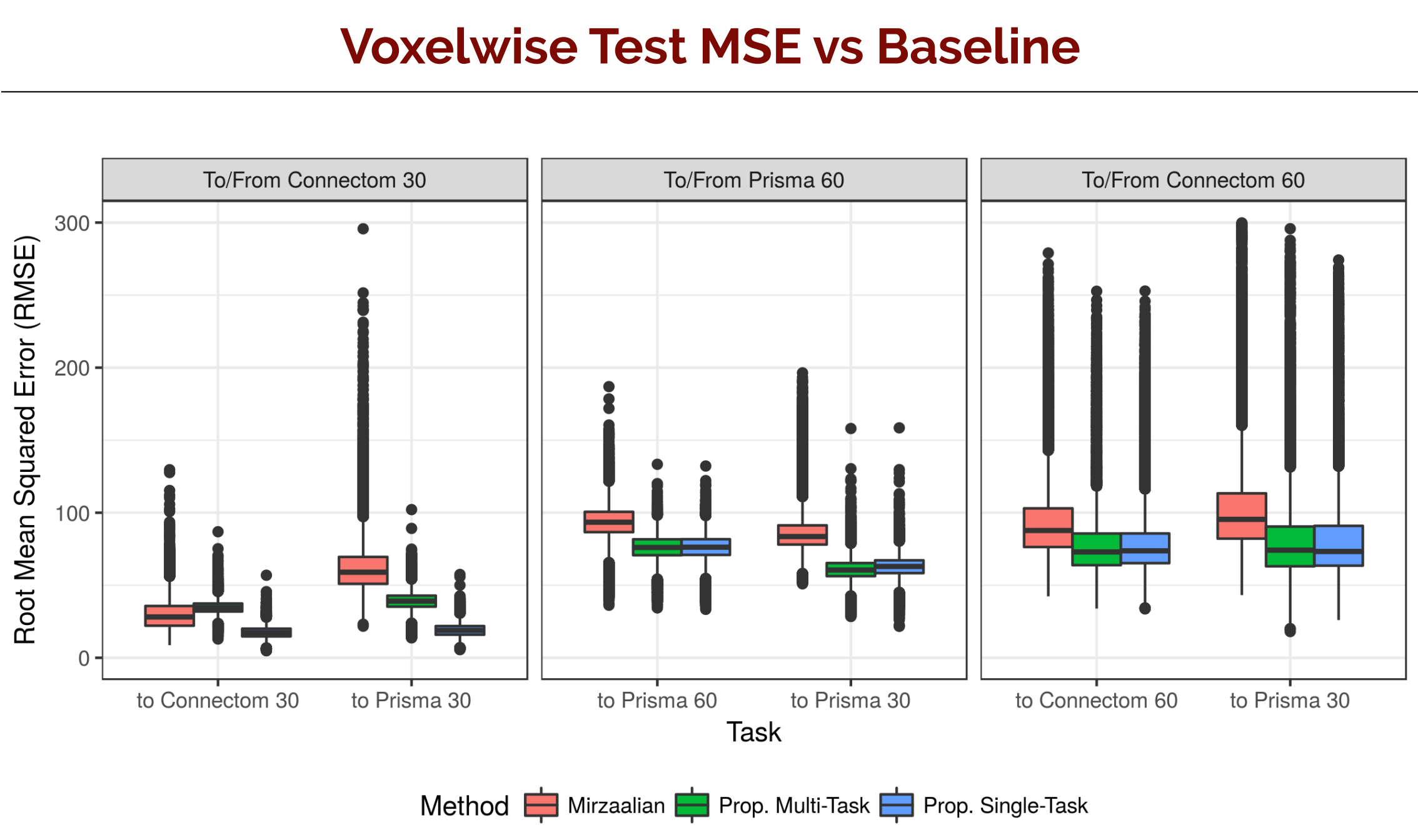
Please contact Daniel Moyer at `moyerd@usc.edu` for any questions/comments.

The Paper

[1] Hengameh Mirzaalian et al.
Multi-site harmonization of diffusion MRI data in a registration framework.
Brain Imaging and Behavior, 12(1):284--295, 2018.

[2] Lipeng Ning et al.
Multi-shell diffusion MRI harmonisation and enhancement challenge (MUSHAC): progress and results.

arxiv.org/abs/1904.05375

Voxelwise Test MSE vs Baseline

Error Plot: Prisma-30 to Prisma-60

Error Plot: Prisma-30 to Connectom-60