Multi-scanner Harmonization of Paired Neuroimaging Data via Structure Preserving Embedding Learning

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Background

- Combining datasets from multiple sites/scanners has been becoming increasingly more prevalent in modern neuroimaging studies.
- Problem: Despite benefits from growth in sample size by combining datasets, substantial variability associated with site/scanner-related effects exists which may inadvertently bias down-stream analyses (**Figure 1**).
- Harmonization is the task of removing scanner effects directly from image-derived measures (image-level harmonization) or the images (image-level harmonization).

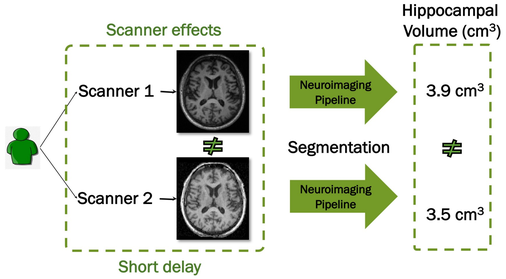


Figure 1. Example of scanner effects.

Contributions

In this work, we:

I. introduce the **first paired multi-scanner data on four different scanners**.

II. propose a **multi-scanner deep harmonization framework** called MISPEL (Multi-scanner Image harmonization via Structure Preserving Embedding Learning).

Paired Multi-scanner Dataset

- Acquisition: 18 subjects scanned on 4 different scanners with short delay (**Figure 2**).
- Preprocessing:

I. Non-linear registration to a T1-Weighted image atlas [1].

II. Spatial intensity inhomogeneity correction.

III. Skull stripping.

IV. Scaling.

These preprocessed images are referred to as RAW images and are input images for harmonization.

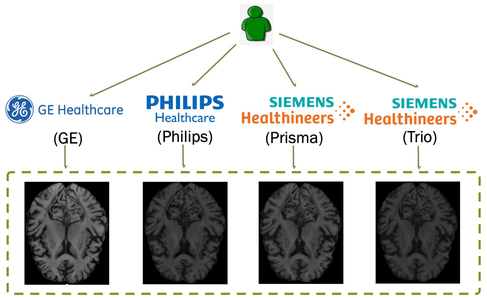
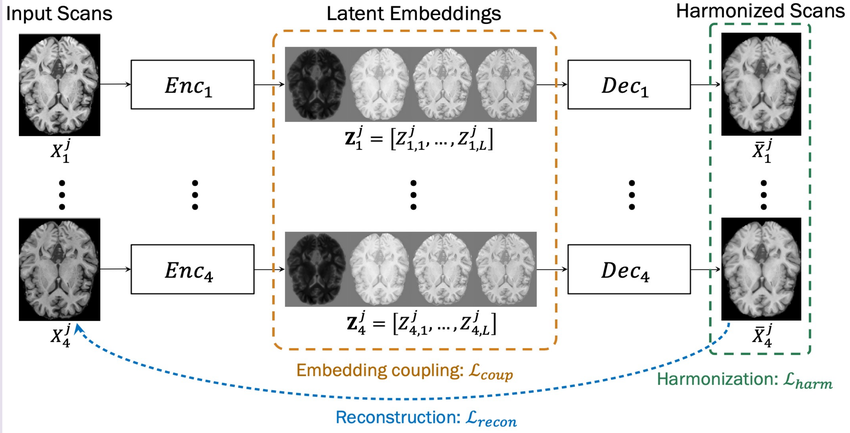


Figure 2. Paired multi-scanner dataset.

Method: MISPEL

- MISPEL: an image-level harmonization to preserve the structure of images.



Notations and loss functions:

Data: *N* axial slices (combined across all subjects) from each of *M* scanners.

Variables:

- i, j: Scanner and slice index, respectively
- l : Embedding's component index
- T_1, T_2: Max iteration for Steps 1 and 2
- X_i^j: Axial slice j from scanner i
- $Z_{i,l}^j$: Latent embedding l of X_i^j
- $\mathbf{z}_i^j$: L Latent embedding of X_i^j
- p: index for elements in $Z_{i,l}^j$
- $\bar{X}_i^j$: Harmonized X_i^j

Networks:

- Enc_i: Encoder U-Net for $\mathbf{z}_i^j \leftarrow Enc_i(X_i^j)$
- Dec_i: Decoder linear map for $\bar{X}_i^j \leftarrow Dec_i(\mathbf{z}_i^j)$

Loss functions:

- $\mathcal{L}_{recon}(X_{i=1:M}^j, \bar{X}_{i=1:M}^j) = \sum_{i=1}^{M} MAE(X_i^j, \bar{X}_i^j)$
- $\mathcal{L}_{coup}(Z_{1,l}^i, \dots, Z_{M,l}^i) = \frac{1}{LP}\sum_{l=1}^{L}\sum_{p=1}^{P} var\,(Z_{1,l}^i(p), \dots, Z_{M,l}^i(p))$
- $\mathcal{L}_{harm}(\bar{X}_{i=1:M}^j) = \frac{2}{M(M-1)}\sum_{i=1}^{M}\sum_{k=i+1}^{M} MAE(\bar{X}_i^j, \bar{X}_k^j)$
- $\mathcal{L}_{\textbf{Step 1}} = \lambda_1\mathcal{L}_{recon} + \lambda_2\mathcal{L}_{coup}$
- $\mathcal{L}_{\textbf{Step 2}} = \lambda_3\mathcal{L}_{recon} + \lambda_4\mathcal{L}_{harm}$

MISPEL Training Algorithm:

Procedure Step 1: Embedding learning
  for $t = 1, \dots, T_1$ or until $X_i^j \approx \bar{X}_i^j$ **do**
    for each slice j **do**
      for each scanner i **do**
        $\mathbf{z}_i^j \leftarrow Enc_i(X_i^j)$
        $\bar{X}_i^j \leftarrow Dec_i(\mathbf{z}_i^j)$
      end for
      Update $Dec_{i=1:M}$ and $Enc_{i=1:M}$ using $\mathcal{L}_{\textbf{Step 1}}$
    end for
  end for
end procedure (end Step 1)
procedure Step 2: Harmonization
  for $t = 1, \dots, T_2$ or until $\bar{X}_1^j \approx \cdots \approx \bar{X}_M^j$ **do**
    for each slice j **do**
      for each scanner i **do**
        $\mathbf{z}_i^j \leftarrow Enc_i(X_i^j)$
        $\bar{X}_i^j \leftarrow Dec_i(\mathbf{z}_i^j)$
      end for
      Update only $Dec_{i=1:M}$ using $\mathcal{L}_{\textbf{Step 2}}$
    end for
  end for
end procedure (end Step 2)

Results 1: Image Similarity

- Experiment: Comparing the similarity of RAW and MISPEL-harmonized images within pairwise combinations of scanners, using the structural similarity index measure (SSIM).
- The scanner effects were partially removed by images getting more similar (increased SSIMs) after the MISPEL harmonization (**Table 1**).

Methods	SSIM Between Scanners					
	GE-Philips	GE-Prisma	GE-Trio	Philips-Prisma	Philips-Trio	Prisma-Trio
RAW	0.75 (0.04)	0.78 (0.04)	0.78 (0.05)	0.81 (0.03)	0.81 (0.03)	0.87 (0.04)
MISPEL	**0.84** (0.04)	**0.85** (0.04)	**0.86** (0.05)	**0.87** (0.03)	**0.87** (0.03)	**0.91** (0.03)

Table 1. Mean (standard deviation) of SSIMs within pairwise combinations of scanners.

Results 2: Volumetric Similarity

- Experiment: Studying scanner effects and MISPEL harmonization on volumes of gray matter (GM) and white matter (WM) tissue types extracted by FSL FAST segmentation [2].
- Scanner effects appeared as dissimilarity of distributions of both tissues across scanners. Harmonization happened as distributions got more similar to each other (**Figures 3 and 4**).

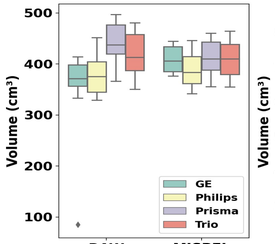


Figure 3. GM volumes.

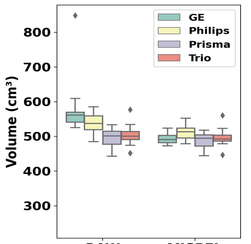


Figure 4. WM volumes.

Conclusions

- Scanner effects exist in our in-house paired multi-scanner dataset.
- MISPEL succeeded in harmonization of our data evaluated on image and volumetric similarity.

Acknowledgments

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Reference:

[1] Kenichi Oishi, et al. Atlas-based whole brain white matter analysis using large deformation diffeomorphic metric mapping: application to normal elderly and alzheimer's disease participants. Neuroimage, 2009.

[2] Y Zhang, et all. Segmentation of brain MR images through a hidden markov random field model and the expectation-maximization algorithm. IEEE Trans Med Imaging, 2001.

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