# A Hybrid Approach to Tissue-based Intensity Standardization of Brain MRI images

**Raghav Mehta, Jayanthi Sivaswamy**

Center for Visual Information Technology
International Institute of Information Technology, Hyderbad, India

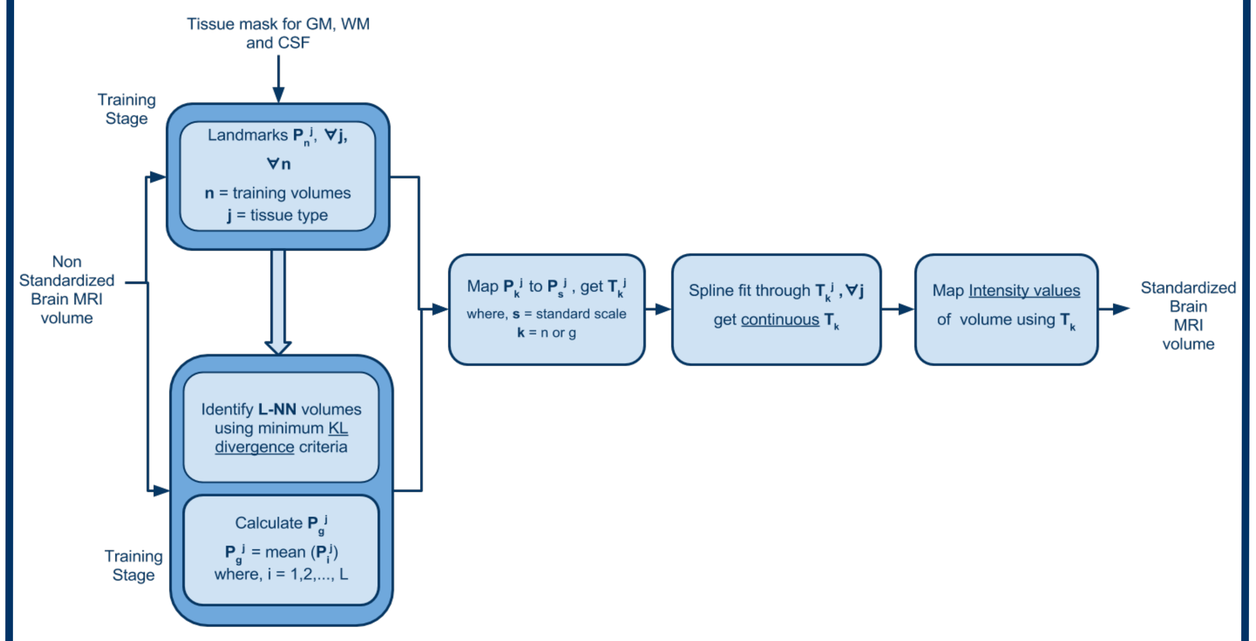
## 1. Introduction

- Segmentation and registration of MRI are critical to diagnosis of various neuro disorders.
- These tasks depend on intensity value of MRI, which varies across scanners, protocol, etc.
- A preprocessing step is required to address this variation.
  - This process is known as *Intensity Standardization* (IS).
- IS techniques are generally based on landmarks on histograms.

**Intensity Standardization**

| Without Tissue Information [2] | Proposed method | With Tissue Information [1] |
|---|---|---|
| Most Popular approach<br>Advantages:<br>• Based on percentiles of the *global histogram*<br>• No need for tissue segmentation<br>• Fast<br>Disadvantage:<br>• Tissue preservation not guaranteed | • Tissue labels required only for training phase<br>• IS of a new volume does not require tissue labels<br>• Tissue based percentiles derived from *nearest* pre-labelled volume<br>• Faster than [1]<br>• Performance is on par with [1] and superior to [2] | Recently proposed approach<br>Advantages :<br>• Based on percentiles of *tissue level histogram*<br>• Preserves tissue information<br>• Better performance than [2]<br>Disadvantages:<br>• Need for tissue segmentation<br>• Slow |

## 2. Method Overview




## 3. Training Stage

**Data**: A set of MRI $V = \{ I_n \}$ with tissue masks $\{ M_n^j \}$; $n = 1,..,N$ and $j = GM, WM \text{ and } CSF$; percentile $P_s^j$ of standard scale

**Processing steps**:

1) Calculate grey level histograms and corresponding percentiles for each tissue type $P_n^j$
2) Determine Transformation $T_n^j$, for every tissue type, by matching percentile landmarks $P_n^j$ to $P_s^j$
3) Derive continuous mapping $T_n$ for entire volume via spline-fitting through $T_n^j$

## 4.. Testing Stage

Given a non-standardized MRI volume $I_g$, IS involves the following:

1) Remap the intensity range of volumes $I_n \in V$ to that of $I_g$
2) Compute KL divergence (KLD) between $I_g$ and $V$
3) Find L nearest volumes by thresholding the KLD
4) Compute $P_g^j$ from landmarks of L training images

$$KLD(n) = KLD(h_n, h_g) = \sum_i h_n(i) \log\left(\frac{h_n(i)}{h_x(i)}\right)$$
$$h_x = Hist(I_x)$$

$$P_g^j = \sum_{i=1}^{L} W_i P_i^j, \quad \forall j$$
$$W_i = \frac{w_i}{\sum_{i=1}^{L} w_i}, \quad w_i = \frac{1}{KLD(i)}, \quad \forall i$$

5) Match $P_g^j$ to standard scale $P_s^j$ to get derive $T_g^j$
6) Interpolate to get continuous mapping $T_g$

## 5. Dataset and Preprocessing

- 8x3 (=24) T1 weighted volumes from different scanner manufacturers.
  - Data from scanners G and S were locally sourced; data from scanner P is from a public dataset.
- Denoising and Intensity Inhomogeneity correction (N3) was performed for all volumes.

| Scanner | TE (ms) | TR (ms) | TI (ms) | FA (°) |
|---|---|---|---|---|
| G | 4.2 | 10.2 | 450 | 15 |
| S | 2.9 | 2370 | 1000 | 7 |
| P | 4.6 | 9.83 | NA | 8 |

- Tissue segmentation generated using FAST tool of FSL toolbox

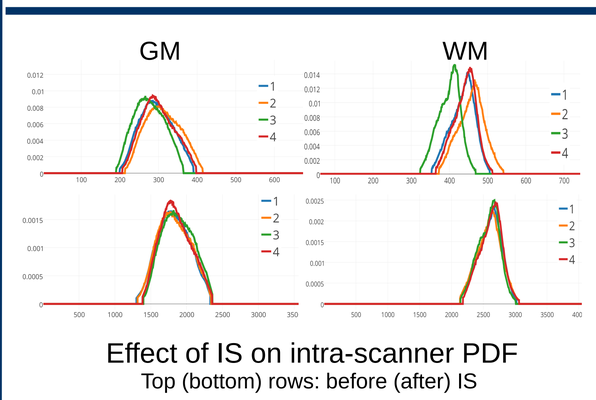
## 6. Quantitative Analysis

- The proposed method was validated using Jeffrey Divergence (JD) and statistics on Normalised Mean Intensity (NMI) values of whole dataset, with leave-one-out (LOO) approach
- Low JD is desirable
- $I_n^j(k)$ is the n[th] volume (after masking with $M_n^j$) from the k[th] scanner
- $n = 1,..,8;\ j = k = 1,2,3,$

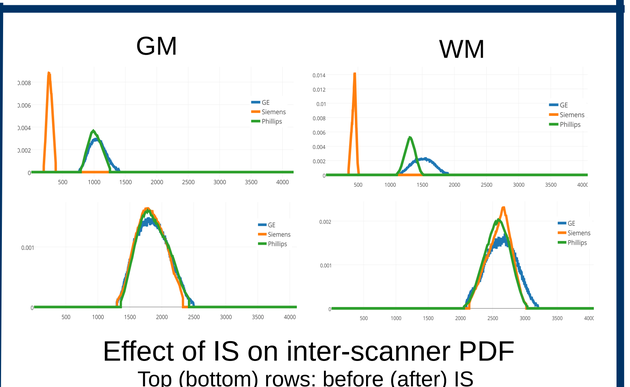
$$JD_{intra}(k, j) = \frac{1}{mn} \sum_n \sum_m JD(I_n^j(k), I_m^j(k))$$
$$m \neq n, \forall n, m \in k$$

$$JD_{inter}(k_a, k_b, j) = \frac{1}{mn} \sum_n \sum_m JD(I_n^j(k_a), I_m^j(k_b))$$
$$\forall n \in k_a, \forall m \in k_b$$

| | | Intra-scanner JD (in x $10^{-2}$) | | | Inter-scanner JD | | | NMI statistics (across all volumes) | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | G | S | P | G vs S | G vs P | S vs P | $\sigma_{NMI}$ | $\mu_{NMI}$ | % CV |
| CSF | Before IS | 7.99 | 6.06 | 2.04 | 1.25 | 0.28 | 1.10 | 0.0240 | 0.1444 | 16.621 |
| | [2] | 3.87 | 2.74 | 0.97 | 0.08 | 0.03 | 0.05 | 0.0127 | 0.2228 | 5.7001 |
| | ours | 3.53 | 2.40 | 0.87 | 0.04 | 0.03 | 0.04 | 0.0055 | 0.2506 | 2.1942 |
| | [1] | 3.50 | 2.35 | 0.84 | 0.03 | 0.02 | 0.03 | 0.0049 | 0.2412 | 2.0315 |
| GM | Before IS | 16.32 | 9.28 | 3.34 | 1.38 | 0.48 | 1.23 | 0.0305 | 0.2676 | 11.399 |
| | [2] | 7.70 | 3.54 | 2.28 | 0.15 | 0.08 | 0.05 | 0.0128 | 0.4129 | 3.1001 |
| | ours | 5.78 | 2.32 | 1.35 | 0.04 | 0.05 | 0.03 | 0.0094 | 0.4444 | 2.1152 |
| | [1] | 5.67 | 2.28 | 1.32 | 0.03 | 0.03 | 0.02 | 0.0084 | 0.4427 | 1.8974 |
| WM | Before IS | 19.53 | 8.71 | 3.46 | 1.38 | 0.88 | 1.25 | 0.0285 | 0.4049 | 7.0391 |
| | [2] | 7.56 | 5.25 | 2.95 | 0.44 | 0.25 | 0.14 | 0.0196 | 0.5792 | 3.3836 |
| | ours | 5.32 | 2.47 | 2.27 | 0.09 | 0.07 | 0.05 | 0.0119 | 0.6200 | 1.9193 |
| | [1] | 5.19 | 2.40 | 2.19 | 0.07 | 0.05 | 0.04 | 0.0106 | 0.6205 | 1.7082 |

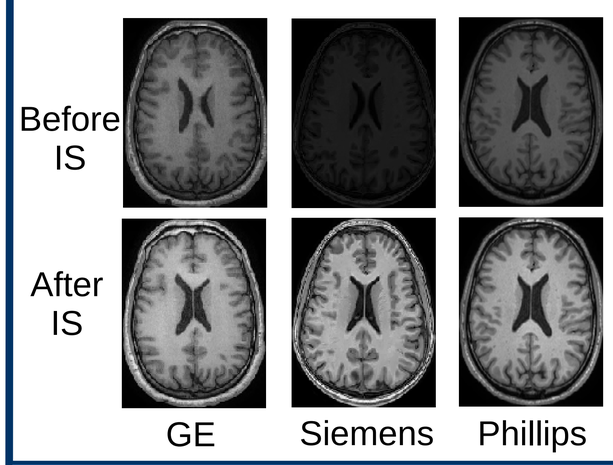



Effect of IS on intra-scanner PDF
Top (bottom) rows: before (after) IS

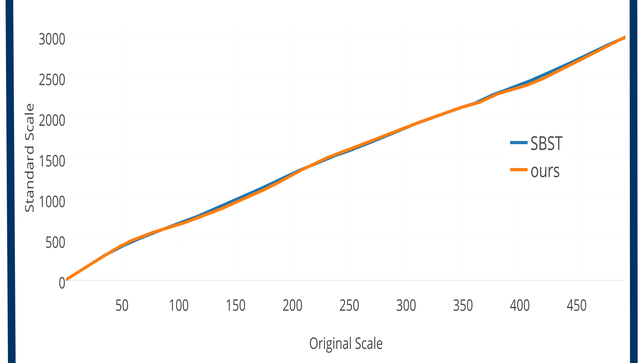



Effect of IS on inter-scanner PDF
Top (bottom) rows: before (after) IS

## 7. Qualitative Analysis




## 8. Mapping Function Comparision




Comparison of derived mapping function with (blue) and without (orange) tissue information

## 9. Reference

1) De Nunzio et al. "Robust Intensity Standardization in Brain Magnetic Resonance Images." Journal of digital imaging 28.6 (2015): 727-737

2) Nyúl et al. "New variants of a method of MRI scale standardization.", IEEE Transactions on Medical Imaging (TMI) 19.2 (2000): 143-150.

This work was supported by DST project: SR/CSRI/194/2013

ISBI 2016 - Prague, Czech Republic