Feather-Light Fourier Domain Adaptation in Magnetic Resonance Imaging

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Abstract. Generalizability of deep learning models may be severely affected by the difference in the distributions of the train (source domain) and the test (target domain) sets, e.g., when the sets are produced by different hardware. As a consequence of this domain shift, a certain model might perform well on data from one clinic, and then fail when deployed in another. We propose a very light and transparent approach to perform test-time domain adaptation. The idea is to substitute the target low-frequency Fourier space components that are deemed to reflect the style of an image. To maximize the performance, we implement the "optimal style donor" selection technique, and use a number of source data points for altering a single target scan appearance (Multi-Source Transferring). We study the effect of severity of domain shift on the performance of the method, and show that our training-free approach reaches the state-of-the-art level of complicated deep domain adaptation models. The code for our experiments is released3.

Keywords: Domain adaptation · MRI · Fourier Domain Adaptation · Test-Time Domain Adaptation

1 Introduction

Magnetic Resonance Imaging (MRI) has become an irreplaceable tool in healthcare thanks to its capacity to produce high-resolution scans without ionizing radiation. The widespread use of the modality has helped to accumulate large volumes of miscellaneous imaging data, which have been fueling development of machine- and deep-learning methods, aiming to mimic diagnostic decisions. However, the real-life deployment of these methods is often hindered by an issue known as Domain Shift, which originates from a possible difference in train (source) and test (target) distributions. This difference might occur whenever source and target datasets are acquired with different machines or research protocols, and entails a need for proper Domain Adaptation (DA) [4].

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3 https://github.com/kechua/Feather-Light-Fourier-Domain-Adaptation/
To this end, modern DA in medical imaging includes a plethora of shallow and deep models [4]. Existing shallow DA methods are somewhat rudimentary, requiring human-engineered features [21,22], and generally lagging in performance, while the deep ones are often heavy, slow, and barely interpretable (albeit accurate) [8,15,24].

One trait shared by all of the aforementioned methods is that they operate in the image space. It is only recently that the community has started to realize the potential of operating in $k$-space (also referred to as Fourier space or spectrum of an image) for tackling domain shift in MRI data with [11,10] being the only two studies we were able to find. This is surprising given that MRI is a modality that yields $k$-space data representation by design.

In $k$-space, specific spectral components are responsible for different properties of an image, e.g., the high frequency components accentuate the edges and enhance details, while the low ones control contrast and the large-scale content. Besides, it is known that the semantic information is mostly stored in the phase component of the spectrum. This suggests an efficient strategy for tackling DA via “mixing” the source and the target spectra. The purpose of this "mixing" (Fourier Domain Adaptation or FDA) is to transfer the style while preserving the patient-specific content, thereby compensating for the DA shift.

The idea is borrowed from the natural image domain [26] and adapted to MRI volumes, entailing a new “optimal style donor” selection module and a multi-source transferring routine (we use multiple source images when transferring the style to a given target image to further improve the performance).

We call our method feather-light because, unlike the modern go-to approaches, it does not involve any training, as we simply transfer the $k$-space components, characterizing the style of the source domain, to a target scan during the test time. Despite its simplicity, the method performs on par with complicated deep DA models, such as those based on Generative Adversarial Networks (GANs) [23]. Notably, the proposed method is also interpretable as it directly shows which style-carrying source frequencies alleviate the domain shift.

2 Related Work

A large part of Deep Domain Adaptation methods could be split into feature-level [2,13] and image-level approaches. Among the image-level ones, the majority exploit the idea of GANs [10,7,23] for eradicating the difference in distribution between images from various domains. GANs, however, are difficult to train, lack explainability and might produce undesirable artefacts, which pose an even greater problem in the medical imaging context.

Fourier Domain Adaptation (FDA) [26] provides a feasible alternative to GANs, as image-to-image translation, performed via low-frequency spectra components swap (amplitudes only), is simple, predictable and yet yields SOTA-level results on the natural images. This method has been adapted for the medical imaging, with the earliest application being mitigation of domain shift, appearing in the synthetic ultrasound images [17]. In [10] the authors applied FDA-based
augmentation technique for the cardiac MRI segmentation, with the novelty being swapping both amplitudes and phases, which apparently is not very stable and may lead to changes in the image semantics [25]. [11] applies FDA to federated learning in order to generate images exhibiting distribution characteristic of other clients, while [1] uses FDA as a proof-of-concept tool for obtaining ”poisoned” images, challenging for neural networks.

In [12] the authors solve automatic polyp detection task via combining feature-level adaptation with FDA, while further improving the FDA component with sampling ”matching” source and target image pairs. The closer a target image is to the source one in terms of cosine similarity of their deep ResNet-50 features, the greater is the ”match” probability. We note that adding an additional deep model to the pipeline makes it more complicated, while we strive for simplicity.

One dismissed idea in the FDA area is the one we propose to denote multi-source transfer, i.e., performing a number of $k$-space components swaps with a single target image and multiple source images followed by averaging of the down-stream task predictions for various versions of the changed target.

3 Method

We base our approach on the Fourier Domain Adaptation technique [26] and summarize it in Fig. 1. This method consists of swapping the low-frequency amplitudes of an image spectrum with those of another image, the style of which should be borrowed. As amplitudes of the low-frequency spectrum components are mostly related to the low-level image characteristics, defining the style, this procedure is expected to align the source and the target distributions, thus compensating for the domain shift between them.

While in [26], the source data is transferred to the target style, and the deep neural network is then trained on the $D^{s\rightarrow t}$ dataset, we note that in the clinical setting it would mean re-training the model for each new target domain (e.g., a new clinic), which might complicate certification and clinical deployment. Moreover, the target data (e.g., data from a hospital we need to adjust the model
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for) may appear to be scarce, which limits capabilities of the self-supervised training on target, another component of the original method.

Instead of $D^s \rightarrow t$, we focus on the $D^t \rightarrow s$ adaptation with a single source model used for various targets, which are transferred into the source style during the test time. Mathematically speaking, we carry out the following procedure:

$$t_{new} = f_{FDA}(s_i, t) = \mathcal{F}^{-1} \left( [M_\beta \circ \mathcal{F}^A (s_i) + (1 - M_\beta) \circ \mathcal{F}^A (t), \mathcal{F}^P (t)] \right).$$

The phase component of a spectrum remains intact, while the source style is injected with the low-frequency amplitudes we "cut out" with $M_\beta$ (Fig. 1).

As there is no additional training required, this setting is much more lightweight than the original one, but it is also more challenging in terms of reaching the optimal performance. To this end, we improve the method in the following ways:

- **We propose to carry out a multitude of $t \rightarrow s_i$ swaps (Multi-Source Transfer)** with the final result for slice $t$ calculated as
  $$\sum_{i=1}^{n_{MST}} net(f_{FDA}(s_i, t))/n_{MST},$$
  where $f_{FDA}(s_i, t)$ is the FDA procedure, performed on $s_i$ and $t$; $n_{MST}$ reflects the number of source slices used for the style transfer (after preliminary experiments we set $n_{MST} = 7$).
- **We design an approach for picking the optimal source slices**

The intuition behind the latter feature is that as swapping the spectral components inevitably leads to artefacts, we should minimize this detrimental effect by choosing source and target which are as close as possible in terms of their semantics. To do so, we assess the "closeness" with the Spectral Residual Similarity (SR-SIM) semantic similarity measure [27] (Fig. 2).

![Fig. 2. Multi-Source Transfer (MST) + SR-SIM source choice in the 2.5D fashion.](image)

We consider several approaches to the optimal source "style donor" search for the slices, belonging to the target scan. Firstly, we may average the similarity score between the corresponding slices in 2 scans, thus obtaining the scan-to-scan similarity score ($sim(s, t) = \sum_{i=1}^{n_{slices}} sim(s_i, t_i)/n_{slices}$). We then select for Domain Adaptation $n_{MST}$ most similar source scans (3D similarity).

We note that choosing the "style donors" on the scan level might introduce unnecessary constraint. Alternatively, source "style donors" for various $t_i$ slices
of the target scan \( t \) may come from different source scans. In this case, for \( i \in (1, n_{\text{slices}}) \) we look for the slices closest to \( t \), among \( (s_1^1, s_2^1, ..., s_{n_{\text{scans}}}^1) \) (2D). A natural extension to this approach is broadening this set to \( (s_1^1, s_1^2, ..., s_{n_{\text{scans}}}^2) \), which we refer to as 2.5D (Fig. 2). We set \( m = 2 \).

4 Experiments

4.1 Technical details

We conduct all the experiments on a public brain MR dataset called CC359 [20], which is formed of 359 scans and various masks, among which are the brain segmentation masks. The scans are produced by one of 6 MRI machines (Siemens, Philips, GE; 1.5T or 3T each), and thus fall into one of 6 domains of approximately equal size (60 or 59 scans). We perform affine registration of all the scans to MNI152 template using the FSL software [5, 6], and subsequently normalize voxel intensities to \([0, 1]\). We use the Surface Dice Score \([14]\) as it appears to be a more reliable indicator of the brain segmentation quality than the standard Dice Score \([19]\).

We solve the brain segmentation task with 2D U-Net with residual blocks, which we train for 100 epochs (100 iterations per epoch), using SGD optimizer with Nesterov momentum of 0.9, combination of BCE and dice losses (weighted with 0.4 and 0.6 coefficients), and learning rate of \(10^{-3}\), reduced to \(10^{-4}\) at epoch 80. We train the networks on \((256, 256)\) crops grouped in batches of 16 samples. The crops are sampled randomly at each iteration.

| Source domains | sm15 | sm3 | ge15 | ge3 | ph15 | ph3 |
|----------------|------|-----|------|-----|------|-----|
| sm15           | 0.90 ± 0.03 | 0.57 ± 0.18 | 0.83 ± 0.07 | 0.54 ± 0.18 | 0.78 ± 0.09 | 0.84 ± 0.03 |
| sm3            | 0.81 ± 0.04 | 0.90 ± 0.02 | 0.78 ± 0.03 | 0.63 ± 0.07 | 0.80 ± 0.05 | 0.78 ± 0.03 |
| ge15           | 0.61 ± 0.17 | 0.11 ± 0.06 | 0.90 ± 0.03 | 0.40 ± 0.16 | 0.51 ± 0.18 | 0.67 ± 0.15 |
| ge3            | 0.84 ± 0.03 | 0.44 ± 0.14 | 0.78 ± 0.07 | 0.91 ± 0.03 | 0.76 ± 0.1 | 0.78 ± 0.03 |
| ph15           | 0.83 ± 0.06 | 0.45 ± 0.1 | 0.87 ± 0.03 | 0.42 ± 0.17 | 0.91 ± 0.03 | 0.79 ± 0.03 |
| ph3            | 0.74 ± 0.12 | 0.40 ± 0.12 | 0.62 ± 0.12 | 0.39 ± 0.12 | 0.56 ± 0.12 | 0.88 ± 0.04 |

Table 1. Naive transferring (no Domain Adaptation applied).

We follow the methodology of the original Fourier Domain Adaptation (FDA) paper [26] with respect to the k-space swapping technique, with the notable difference of using the circular crop instead of the rectangular one, which is to take into account the radial symmetry of the spectrum components amplitudes.

4.2 Naive model transfer

Firstly, we consider a simple case of no Domain Adaptation applied. In this regard, we train 6 base models on the corresponding domains, designating all
but 2 source scans for training (these 2 are to ensure reaching the loss plateau when training). We then transfer these source-trained models to unseen domains, thus considering 30 source-target pairs. We calculate each transferred model performance on the target test set of 10 images. Besides, we also use 3-fold cross-validation to assess the model performance on the domain it was trained on.

As may be seen from Fig. 1, the magnitude of Domain Shift, i.e., the performance variability between the transferred model and the one which was initially trained on some domain changes significantly between the source-target pairs. As conducting subsequent experiments on all 30 source-target pairs is computationally prohibitive, we decide to concentrate on 3 clusters, representing severe domain shift, medium domain shift and the subtle one. We sort the source-target pairs by the metric decline magnitude, and pick 2 pairs per cluster from the top, bottom, and middle of this sorted list.

4.3 Choosing the optimal $\beta$

One of the most important FDA design choices is choosing the size of the swapping window $\beta$. Specifically for this purpose we designate another 10 target scans per source-target pair, on which the grid search over various $\beta$ values is performed. We consider 2 strategies of devising the optimal $\beta$, which correspond to 2 actual clinical set-ups:

- **Optimal per Pair.** Picking the $\beta$, which proved to be the optimal one for each source-target pair. This set-up is motivated by the scenario, in which at least some target domain data (e.g., data coming from a new clinical center) is available and labelled, and thus may be used for setting the optimal $\beta$, peculiar to this source-target pair.

- **Averaged Optimal.** Picking the $\beta$, based on the grid-search results, averaged over all pairs, which corresponds to a broader scenario of setting a single "standard" beta for all the pairs.

| Shift severity | No DA | Baselines | $\beta$ : aver. optimal | $\beta$ : opt. per pair |
|----------------|-------|-----------|--------------------------|--------------------------|
|                |       | Style | Cycle | Style | Fast | 3D | 2.5D | 2D | 3D | 2.5D | 2D     |
| severe #1      | 0.11  | 0.11  | 0.50  | 0.46  | 0.15 | 0.57 | 0.57 | 0.57 | 0.58 | 0.59 |
| severe #2      | 0.39  | 0.46  | 0.64  | 0.58  | 0.12 | 0.50 | 0.48 | 0.47 | 0.51 | 0.48 |
| medium #1      | 0.67  | 0.66  | 0.70  | 0.64  | 0.15 | 0.72 | 0.73 | 0.74 | 0.77 | 0.77 |
| medium #2      | 0.74  | 0.69  | 0.69  | 0.61  | 0.11 | 0.72 | 0.69 | 0.68 | 0.75 | 0.74 |
| subtle #1      | 0.84  | 0.85  | 0.60  | 0.41  | 0.17 | 0.81 | 0.81 | 0.82 | 0.83 | 0.83 |
| subtle #2      | 0.87  | 0.82  | 0.46  | 0.55  | 0.11 | 0.85 | 0.83 | 0.84 | 0.87 | 0.86 |
| average        | 0.60  | 0.60  | 0.60  | 0.54  | 0.14 | 0.7  | 0.68 | 0.69 | 0.72 | 0.71 |

Table 2. Comparison of the performance of various proposed methods with the baselines. *Style* is for StyleGAN [9], *Cycle* is for CycleGAN [23], *Fast* is for artistic stylization network [3].
### 4.4 Results and Discussion

As was discussed in Section 3, we consider 3 approaches to picking the "best" source slices, which we denote 2D, 2.5D, and 3D. Furthermore, in line with 4.3 we devise $\beta$ from the target validation set by means of either global averaging or averaging per pair. The corresponding results are presented in Table 2 in comparison with the SOTA-level baselines of CycleGAN [23], StyleGAN [10] and Style-Segor [13]. We also consider another light-weight baseline [3].

We perform the ablation study (Table 3), comparing (a) SR-SIM chosen sources + Multi-source transfer (MST) (b) Multi-source transfer (MST) (c) A "simple" swap.

| Shift severity | $\beta$ : averaged optimal | $\beta$ : optimal per pair |
|----------------|---------------------------|---------------------------|
|                | SR-SIM+ MST None           | SR-SIM+ MST None          |
| severe #1      | 0.57 | 0.41 | 0.40 | 0.59 | 0.57 | 0.53 |
| severe #2      | 0.47 | 0.42 | 0.41 | 0.48 | 0.41 | 0.41 |
| medium #1      | 0.74 | 0.78 | 0.76 | 0.77 | 0.78 | 0.76 |
| medium #2      | 0.68 | 0.69 | 0.65 | 0.73 | 0.69 | 0.65 |
| subtle #1      | 0.82 | 0.85 | 0.82 | 0.84 | 0.85 | 0.82 |
| subtle #2      | 0.84 | 0.85 | 0.84 | 0.86 | 0.85 | 0.84 |
| average        | 0.69 | 0.67 | 0.65 | 0.71 | 0.69 | 0.67 |

Table 3. The ablation study.

#### 2D vs. 2.5D vs. 3D. Interestingly, no significant difference could be observed between various SR-SIM-based source choice approaches. Subsequently, we concentrate on the 3D approach, as it appears to be both more intuitive and marginally better than the others.

**$\beta$: Averaged Optimal vs. $\beta$: Optimal per Pair.** Picking $\beta$ on target Validation set in a pair-wise fashion gives only a minor advantage over devising it from the averaged target validation $sDice(\beta)$ curve. Besides, the latter set-up does not require adjusting $\beta$ for a particular pair on a labelled subset of target data, and thus is more relevant in the clinical practice. Therefore, from now on we concentrate on the Averaged Optimal results analysis.

**Our method (3D; $\beta$: Averaged Optimal) vs. Baselines.** While our method is outperformed by CycleGAN on severe #2 pair and by StyleSegor on subtle #1 pair, it is the only one demonstrating good performance across all the data shift magnitude range, since GANs fail to preserve even the "naive" swap quality (no DA) in case of low domain shift and StyleSegor is barely improving the score in case of strong domain shift. Fast artistic image stylization [3], another light-weight method we consider as a baseline, does not demonstrate sufficiently good performance.

**Ablation Studies.** As could be seen in Table 3, both introducing Multi-Source Transfer and combining it with the SR-SIM-based source choice improves the score on average with the positive effect of the "smart" source choice substantial for the instances of severe domain shift.
In Fig. 3, we visually compare our approach with the baselines, considering the cases of severe (top) and subtle (bottom) domain shift. For illustration purposes, we apply the method to the middle-positioned slices. Notably, in case of severe domain shift GANs alter the appearance much more significantly, which might explain the decreasing score.

5 Conclusion

We present a novel Fourier-based Domain Adaptation method, which requires neither any training, nor incorporating any additional deep components into the pipeline. We consider various domain shift severity scenarios, and show that our method performs consistently across all of them, outperforming SOTA-level GANs in case of subtle domain shift. We note that the simplicity achieved ensures better explainability, and envision easier certification, as we avoid modifying the deep model in any way, but rather adapt an incoming image in a strictly defined fashion.

A limitation of this study is the blunt selection of the $k$-space low-frequency window, which could be improved by engaging intelligent search for the style-bearing spectrum components, such as presented in [18] for the supervised case, or by penalizing for the errors in the high-frequency part of the spectrum [16].
Another fundamental assumption we make is the separability of content and style, which is known to be true only partially [2]. Optimization of the k-space swapping pattern along with taking into account the intrinsic content-style coupling will be the subject of future work.

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Fig. 1. Dependence of the Multi-Source Transferring effectiveness on the number of the source slices. We set $n = 7$ as it proves to be the optimal value.

Fig. 2. Choosing the optimal $\beta$ value on validation set in both Averaged Optimal and Optimal per Pair scenarios. In case $\beta = 0$ is the global maxima, we set $\beta = 0.005$.
Fig. 3. Visual comparison of various approaches (in our method, $\beta=0.03$), tackling strong domain shift. Different slices of a single scan are considered.