# DomainATM: Domain Adaptation Toolbox for Medical Data Analysis
# – *Manual*

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In what follows, we introduce the workflow and usage of the Domain Adaptation Toolbox for Medical data analysis (DomainATM). The software and source code of DomainATM can be found online[1].

## A. *Prerequisite & Installation & Launch*

Before using the toolbox, the "image processing toolbox" and "statistics & machine learning toolbox" of MATLAB need to be installed.

After downloading the toolbox, click the file "DomainATM.mlappinstall" or click "Install App" in the "Apps" of MATLAB to install the toolbox. Within seconds, the installed toolbox will appear in the "Apps" of MATLAB. Click the icon of "DomainATM", then the toolbox will be launched, as shown in Fig. S1. To make the toolbox run correctly, it is suggested to change the current working directory of MATLAB to the directory of the toolbox.

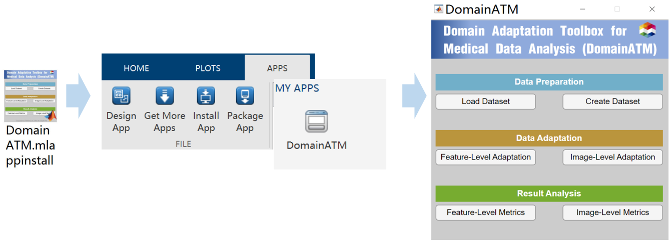


Fig. S1. Installation and launch of the DomainATM toolbox.

## B. *File Organization*

There are several subfolders in the directory of the toolbox, including: "data", "algorithms_feat", "algorithms_img", "evaluation", and "tools", as shown in Fig. S2. Specifically, the "data" subfolder is used to store real-world or synthetic medical datasets. The "algorithms_feat" and "algorithms_img" subfolders are used to store feature-level and image-level domain adaptation algorithms, respectively. The "evaluation" subfolder is used to store results generated by different domain adaptation algorithms. The "tools" subfolder stores functions used by the toolbox.

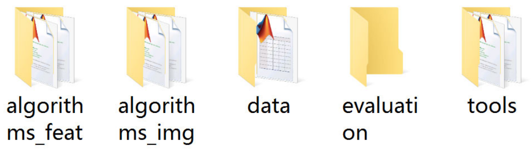
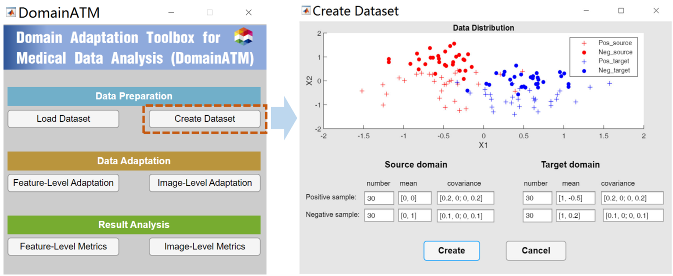


Fig. S2. Subfolders in the directory of the DomainATM toolbox.

## C. *Creating Dataset*

Click the "Create Dataset" button, then the dialogue for generating synthetic dataset will be popped up as shown in Fig. S3. Users can set the number, mean value, and covariance of positive/negative samples in source domain and target domain, respectively. Otherwise, default settings will be used. Click the "Create" button, then the created dataset will be visualized and automatically saved in the "Data" subfolder of the toolbox.



| | Source domain | | | Target domain | | |
|---|---|---|---|---|---|---|
| | number | mean | covariance | number | mean | covariance |
| Positive sample: | 30 | [0, 0] | [0.2, 0; 0, 0.2] | 30 | [1, -0.5] | [0.2, 0; 0, 0.2] |
| Negative sample: | 30 | [0, 1] | [0.1, 0; 0, 0.1] | 30 | [1, 0.2] | [0.1, 0; 0, 0.1] |

Fig. S3. Creating synthetic dataset for evaluation of domain adaptation algorithms using the DomainATM toolbox.

## D. *Loading Dataset*

To perform feature-level domain adaptation, the first step is to load the data into the toolbox. Both real-world medical datasets or synthetic datasets are stored in the "data" subfolder. Click the "Load Data" button and a file selection dialogue will be popped up. Select the data to be processed, then they will be loaded and automatically visualized in the user interface, as shown in Fig. S4.

To prepare the dataset for feature-level adaptation, it should be a *.mat* file that consists of the following three items. 1) **X**: source and target data, with each row representing a sample and each column representing a feature. 2) Domain label: a logical vector, with each element indicating that the

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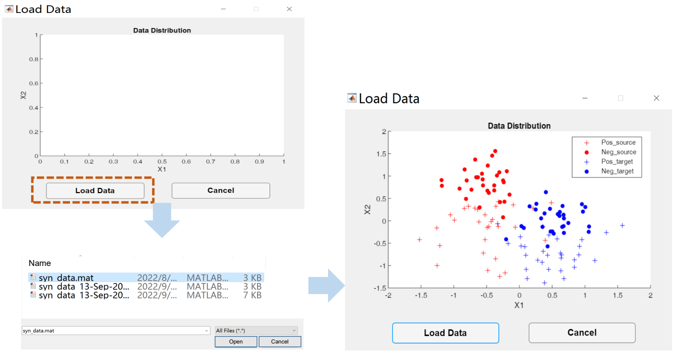
[1] https://mingxia.web.unc.edu/domainatm/

corresponding sample comes from the source domain (with the value of "1") or the target domain (with the value of "0"). 3) $\mathbf{Y}$: category labels for source samples and target samples. ("1" for positive samples, "2" for negative samples, "0" for unlabeled samples).



syn data.mat 2022/8/... MATLAB... 3 KB
syn data 13-Sep-20... 2022/9/... MATLAB... 3 KB
syn data 13-Sep-20... 2022/9/... MATLAB... 7 KB

syn_data.mat

All Files (*.*)

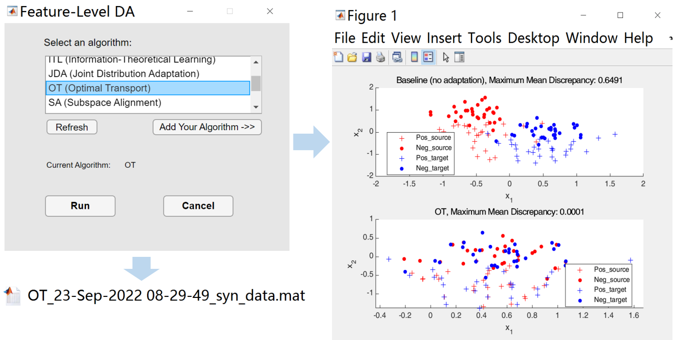
Fig. S4. Loading data into the DomainATM toolbox for further adaptation processing. After being loaded, the data distribution will be automatically visualized.

## E. *Performing Feature-Level Data Adaptation*

After loading the medical dataset (each sample is represented by features), users can run and test different domain adaptation algorithms. Click the "Feature-Level Adaptation" button, then the corresponding dialogue will be popped up. In the dialogue, all the available adaptation algorithms are listed. User can select one and then run it for the data that have been loaded already (if no data are loaded or no algorithm is selected, there will be a warning and nothing will run). After running, the data (in feature space) before and after adaptation will be saved in the "evaluation" subfolder (the result is named as algorithm + timestamp + dataset). Meanwhile, the data before and after adaptation will be visualized in the toolbox as shown in Fig. S5. Currently, the DomainATM includes nine built-in feature-level domain adaptation methods, with details introduced as follows.

1) Subspace Alignment (SA) [1]: The key hyper-parameter is the dimension of the shared subspace (default value is 2).
2) Correlation Alignment (CORAL) [2]: No hyper-parameters.
3) Transfer Component Analysis (TCA) [3]: The key hyper-parameters are the kernel type (default setting is "rbf") and subspace dimension (default value is 2).
4) Optimal Transport (OT) [4]: The key hyper-parameter is the regularization coefficient (default value is 0.01).
5) Joint Distribution Adaptation (JDA) [5]: the key hyper-parameters include kernel type (default setting is "rbf") and subspace dimension (default value is 2).
6) Transfer Joint Matching (TJM) [6]: The key hyper-parameters include kernel type (default setting is "rbf") and subspace dimension (default value is 2).
7) Geodesic Flow Kernel (GFK) [7]: The key hyper-parameter is the subspace dimension (default setting is 2).
8) Scatter Component Analysis (SCA) [8]: The key parameter is the dimension of the transformed space (default setting is 2).
9) Information-Theoretical Learning (ITL) [9]: The key hyper-parameters include subspace dimension (default value is 2) and regularization parameter (default value is 10).

Note that the TCA and GFK algorithms were implemented based on source code provided by Ke Yan[2]. The JDA and TJM algorithms were implemented based on source code provided by the authors[3]. The users can tune the parameters of each algorithm in their scripts in the "algorithms_feat" subfolder. In each script, parameters can be set in a section with the tips of "set your parameters here".



Current Algorithm: OT

OT_23-Sep-2022 08-29-49_syn_data.mat

Fig. S5. Selecting and running a domain adaptation algorithm for the loaded medical dataset. After running, the result will be saved as .mat data file in "evaluation" subfolder.

## F. *Evaluating Feature-Level Adaptation Algorithms*

After the processing of domain adaptation by a specific algorithm, the data before and after adaptation will be saved in the "evaluation" subfolder. Users can evaluate the adaptation performance by clicking the button of "Feature-Level Metrics". In the popped up dialogue, click the "Load Result" button, and then select and load the feature-level adaptation result of a specific algorithm. Then, the evaluation metrics will be automatically computed and displayed in the user interface. Meanwhile, the distribution of original data and adapted data will be visualized as shown in Fig. S6.

## G. *Performing Image-Level Data Adaptation*

To perform image-level domain adaptation, click the "Image-Level Adaptation" button, and the corresponding dialogue will be popped up. In the dialogue, select the source and target images, as well as the adaptation algorithm. After that, click the "Run" button to run the algorithm. With a few seconds, the adapted/harmonized source image will be displayed in the user interface. This process is illustrated in Fig. S7.

The DomainATM toolbox includes two built-in image-level domain adaptation methods. 1) Histogram Matching

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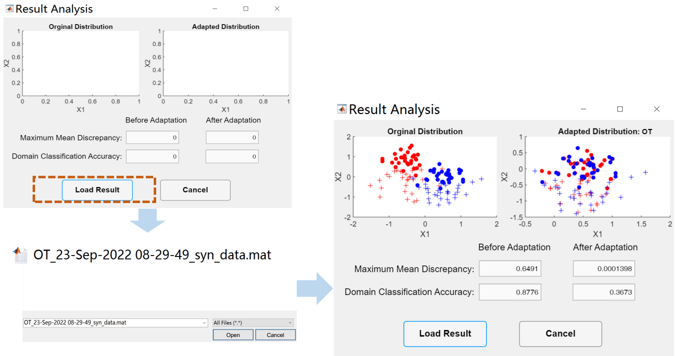
[2] https://github.com/viggin

[3] https://github.com/jindongwang

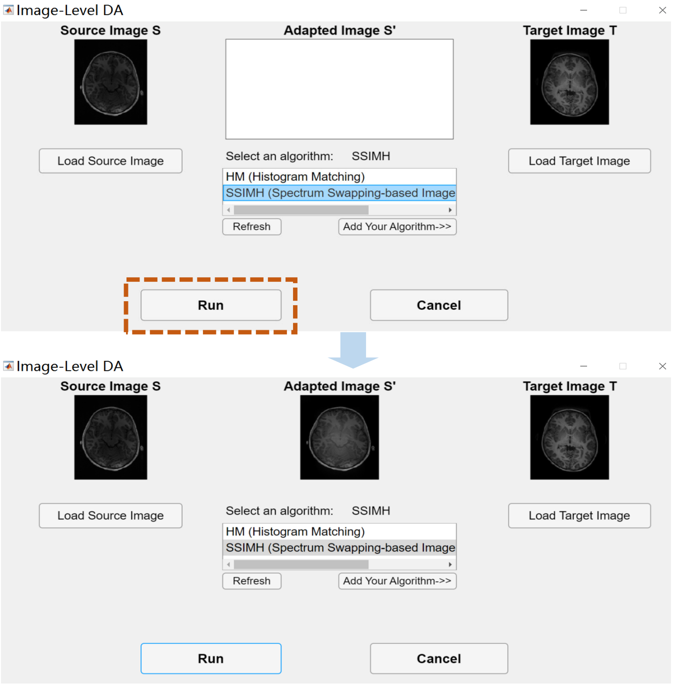


Maximum Mean Discrepancy: 0 | 0
Domain Classification Accuracy: 0 | 0

Maximum Mean Discrepancy: 0.6491 | 0.0001398
Domain Classification Accuracy: 0.8776 | 0.3673

Fig. S6. Evaluation of feature-level domain adaptation algorithms in the DomainATM toolbox. After loading the result (in .mat file), performance evaluation metrics before and after adaptation will be calculated, and the data distribution will also be visualized.

(HM) [10]: No hyper-parameters are needed for this method. 2) Spectrum Swapping-based Image-Level Harmonization (SSIMH) [11]: The key hyper-parameter is the threshold value for the range of low-frequency region for source and target image. The default value is set to 3 in the toolbox.



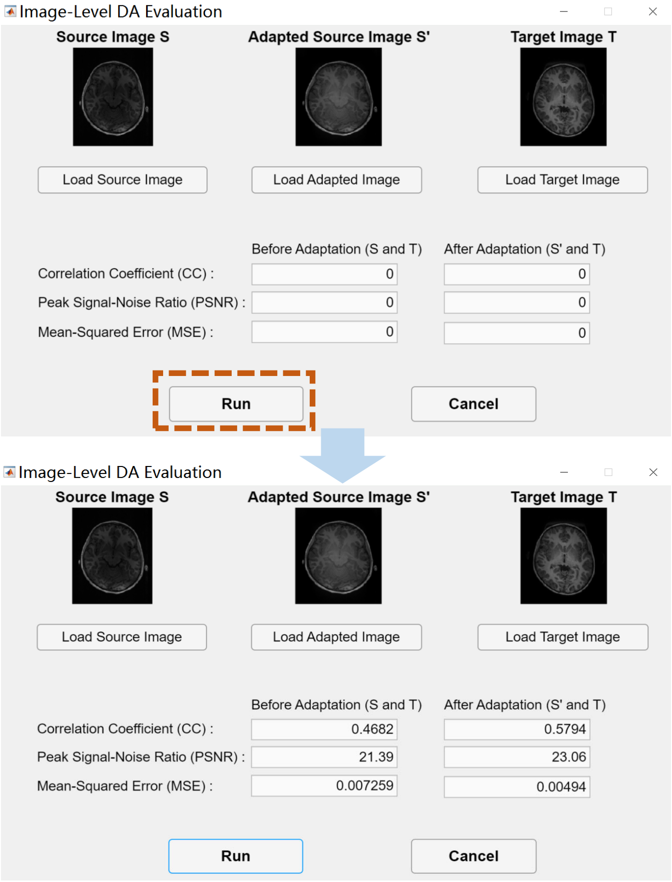
Select an algorithm: SSIMH

Select an algorithm: SSIMH

Fig. S7. Image-level domain adaptation by the DomainATM software.

## H. Evaluating Image-Level Adaptation Algorithms

When the image-level adaptation is finished, the adapted source image will be automatically saved in the "evaluation" subfolder. To assess the adaptation performance, click the "Image-Level Metrics". In the popped up dialogue, select the source image, target image and adapted/harmonized image, respectively. Please note that if the users have already loaded the source and target images via the "Image-Level Adaptation" module, these images will be automatically displayed in the dialogue of "Image-Level Metrics", and users do not need to load them again. Then click the "Run" button to run the evaluation. The metrics before and after adaptation will be calculated and shown in the user interface. This process is illustrated in Fig. S8.



| | Before Adaptation (S and T) | After Adaptation (S' and T) |
|---|---|---|
| Correlation Coefficient (CC) : | 0 | 0 |
| Peak Signal-Noise Ratio (PSNR) : | 0 | 0 |
| Mean-Squared Error (MSE) : | 0 | 0 |

| | Before Adaptation (S and T) | After Adaptation (S' and T) |
|---|---|---|
| Correlation Coefficient (CC) : | 0.4682 | 0.5794 |
| Peak Signal-Noise Ratio (PSNR) : | 21.39 | 23.06 |
| Mean-Squared Error (MSE) : | 0.007259 | 0.00494 |

Fig. S8. Evaluation of image-level domain adaptation by the DomainATM toolbox.

## I. Plugging Self-Defined Data Adaptation Algorithms

In real-world practice of medical data analysis, the users may want to develop their own domain adaptation algorithms. To cater to this demand, the DomainATM toolbox allows the users to add their own methods into the toolbox. In both of the dialogues for feature-level adaptation and image-level adaptation, the users can click the "Add Your Algorithm" button, which can guide the user to the subfolder to write their own scripts. All the algorithms should follow consistent input/output formats. After that, click "Refresh" button, the self-defined algorithm will be displayed in the toolbox. The users can select, use, and evaluate their customized algorithms just like all the other built-in algorithms as described above. Fig. S9 illustrates the operations.

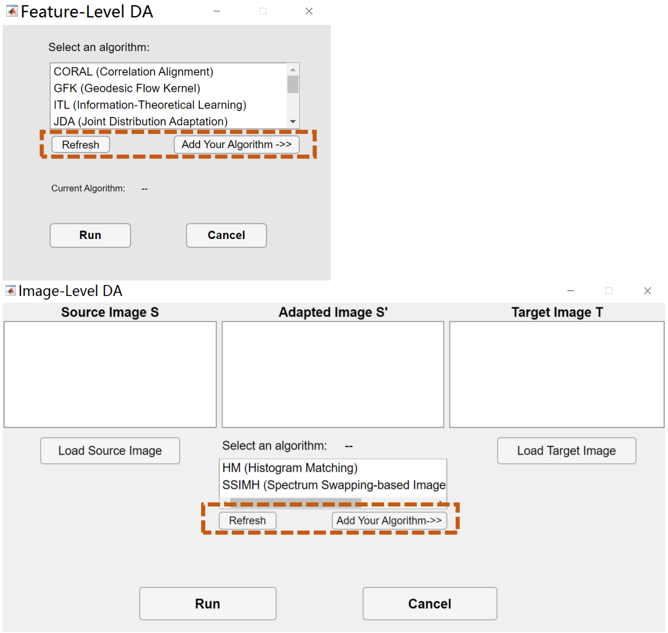


Fig. S9. Plugging self-defined domain adaptation algorithms into the DomainATM toolbox.

# REFERENCES

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