MRI Data Pre-processing for the PROSTATEx Challenge

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Introduction

Last year, our team participated in the PROSTATEx challenge conducted by the AAPM, SPIE and NCI. Our method performed well in both phase I and phase II of this challenge [1]. In addition to the deep learning and machine learning techniques we developed, the performance of our model could also be attributed to the proper data pre-processing. In this note, we aim to provide more details on the data pre-processing and to share our experience in preparing MRI data for deep learning studies.

A Short Introduction to MRI Data

There are various types of contrast in MRI, such as T1-, T2-, T2*-, and diffusion- weighted images [2]. Anatomical and functional information can be obtained using different data acquisition sequences. In this note, the data acquisition using a single MRI sequence is referred to as a "scan". There could be multiple "echoes" in a single scan. These echoes (3D volumes) can be assumed to be acquired simultaneously (in Fourier domain, i.e. "k-space"), and hence these echoes are naturally co-registered, reflecting the same anatomical region. But there could be change of the field of view (FOV) between different scans. Additionally, different imaging parameters may be used in different scans, which lead to different image resolutions, matrix sizes, and/or patient orientations. To cover a sufficiently large FOV within limited acquisition time, usually the imaging resolution is not isotropic.

MRI data are complex numbers, containing magnitude and phase components: $s = \mathrm{mag} \cdot \exp(i \cdot \mathrm{phase})$. Conventionally, only the magnitude images are used. The main reason is that phase images are more difficult to process and are often discarded, even though they contain useful information about in vivo tissue properties. The value range of magnitude images can be arbitrary, while the value range of phase images is proportional to -pi to pi. Any phase with bigger absolute value is wrapped into this range to form phase wraps. The extraction of the true phase value is done through phase unwrapping [3]. The MRI signal is dependent on the main magnetic field and the transmitting and receiving coils. Both magnitude and phase images can be affected by magnetic field inhomogeneity and coil sensitivity [4]. Hence, bias-field correction or background field removal is usually required to remove the low spatial frequency background [5]. The simplest form of background removal is high-pass filtering. In the PROSTATEx challenge, because we used relatively small ROI, we did not perform bias-field correction.

PROSTATEx Data Pre-processing

There were mainly two steps in the data pre-processing: interpolation and co-registration. In interpolation, the goal is to standardize the resolution of the images acquired in different scans. Depending on the purpose of the study, it might be advantageous to have isotropic resolution, especially when 3D slicing is

performed. In the PROSTATEx challenge, we rotated the volume centered at the lesion in 3D and used the central slice to capture the 3D information in a 2D slice. Hence, we first interpolated the images to 1mm isotropic resolution using linear interpolation.

In co-registration, the goal is to reduce the motion between different scans. There are multiple types of images, including T2 weighted images (collected in transverse, sagittal and coronal orientations), diffusion weighted images (DWI), apparent diffusion coefficients (ADC, calculated from DWI), K-trans (dynamic contrast enhanced MRI) etc. The other types of images were co-registered to the T2 weighted images through rigid body registration. We only used (transverse) T2WI, DWI, ADC, and K-trans (although ADC was derived from DWI, we decided to include both). To register Ktrans images to T2WI, it might be necessary to first truncate the values of Ktrans images, get the transformation matrix, and then apply the transformation to the original Ktrans data. Similarly, the same transformation matrix obtained from DWI can be used for the registration of ADC, since ADC and DWI are from the same scan.

After interpolation and co-registration, we performed an additional region growing using the provided lesion positions on DWI. Then the center of the lesion was calculated based on the region growing result. This step was to make sure that the lesion was at the center of the ROI. For each lesion, the volume centered at that lesion was rotated in 3D, and a 32x32mm^2 ROI was cropped from the central slice. Multiple 2D slices at different orientations were created for each lesion. Because we used multi-channel 2D slices in training, we performed the rotation and slicing for both train and validation data sets, since the 2D slices contain different 3D information. This is also a form of data augmentation. One small trick in the rotation and slicing was that we started with a slightly bigger ROI, performed the rotation, and then cropped the final 32x32 ROI. In this way, we can avoid introducing too much zeros or other filled values into the ROI. Once all the samples were generated, we checked the distribution of the values in each type of images, truncated the values at 99%, scaled the intensities to the range 0 to 255 and subtracted a constant mean value from each channel. Now all the channels corresponded to the same anatomical position and had similar value ranges with zero mean. Finally, the subjects were split into train and validation sets. Since we used Caffe for training the model, a total of 4 types of RGB images were generated by using different combinations of the MRI contrasts. For example, we used ADC, Ktrans and T2 as the RGB channels respectively and created the AKT input.

In fact, the most important step in data pre-processing was to check all the processed images and labels, before feeding them to the deep learning model. This quality assurance step is indispensable, because MRI data can be affected by various types of artifacts. While some artifacts could be reduced (e.g. background field), some artifacts are difficult to remove (low SNR, severe motion artifacts). When we were doing the co-registration, we failed to register the DWI data to the T2WI in a few cases, due to low SNR of the DWI (subjects 0011, 0052, 0177, 0192). For those data with very low SNR, it will be better to not use them at all.

The data pre-processing pipeline is illustrated in **Figure 1**. All the processing was done using MATLAB.

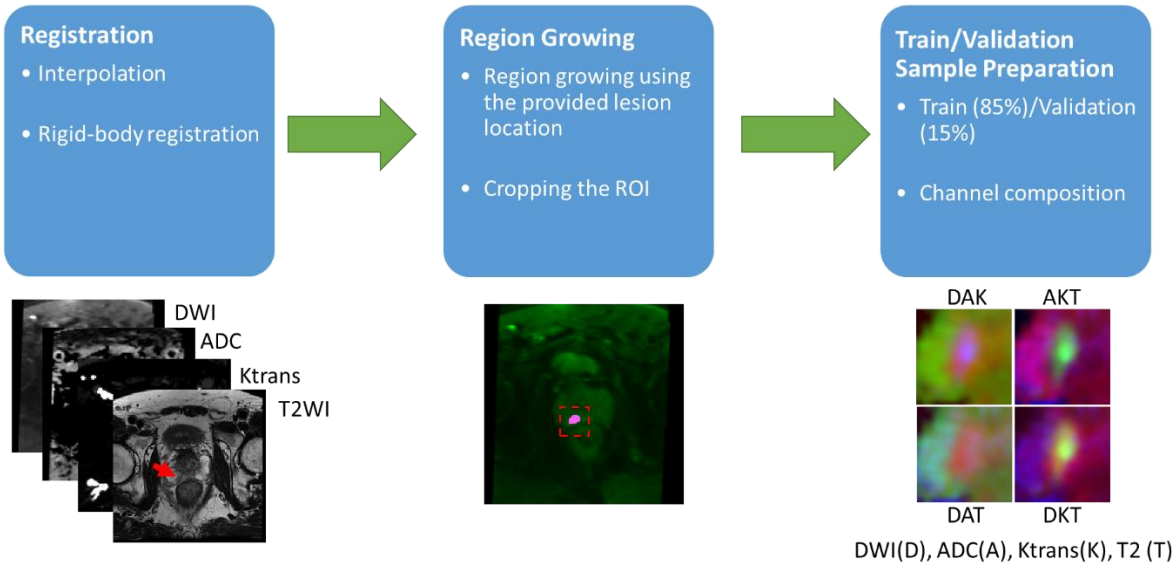

Figure 1. Data pre-processing steps.

Discussion and Conclusion

In this note, we discussed the data pre-processing for the PROSTATEx challenge data. The over-all goal of data pre-processing is to reduce the variation of the data (interpolation and co-registration), and to make different samples comparable (standardize the images, mean subtraction etc.). Together with the SPIE conference proceeding, we hope that these two documents provide sufficient details and useful guide for researchers who are interested in applying deep learning to MRI data.

References

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