MRI Diffusion Analysis Using TINA .

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Abstract

This document provides practical information for analysing diffusion MRI data. This includes both phantom calibration and clinical datasets from protocols A and B developed for the IMI project. Readers should refer to associated material and publications for technical details of the applied methods.

1 How to Use the Software for ADC Measurement from Clinical Diffusion Weighted MRI.

1.1 Introduction

This ADC measurement tool (TinaADCtool) can be applied to regions of interest for phantom or clinical data. The format of "DataInfo.txt" file for clinical data is partially different from that for the phantom data [1]. This file should be located in the current folder where the code is executed from.

There are a number of steps which need to be followed before one can run the software.

1.1.1 Data Preparations

Step 1: It is recommended that all dicom files are renamed (e.g. using soft links) so that each name includes all the information needed. An example renamed file name is: *'siteE-scanner1-v1-20120503-fasted-3b-image-G0-B1-N22'*. Here G0 refers to no diffusion gradient direction (protocol A), B1 refers to the first (smallest) non-zero b-value, and N22 refers to the slice number.

Step 2: Produce a 'DataInfo.txt' file containing all the information needed for the ADC measurement code to be executed. An example 'DataInfo.txt' file is as follows.

./ClinicalData/SiteE-V1
3
100.0
500.0
900.0
2
siteE-scanner1-v1-20120503-fasted-3b-image-G0-B1-N22
siteE-scanner1-v1-20120503-fasted-3b-image-G0-B2-N22
siteE-scanner1-v1-20120503-fasted-3b-image-G0-B3-N22
siteE-scanner1-v1-20120503-fasted-10b-gradients-image1-G1-B1-N22-roi-rect2-tissue.aiff
siteE-scanner1-v1-20120503-fasted-3b-image-G0-B1-N23
siteE-scanner1-v1-20120503-fasted-3b-image-G0-B2-N23
siteE-scanner1-v1-20120503-fasted-3b-image-G0-B3-N23
siteE-scanner1-v1-20120503-fasted-10b-gradients-image1-G1-B1-N22-roi-rect2-tissue.aiff

A second example 'DataInfo.txt' file is as follows (these are averaged motion-corrected image slices).

./ClinicalData/Protocol-B/siteE-scanner1-v1-20120503-fasted/MC-redone/tissue
3
100.0
300.0
500.0
1
renamed_slice3_b1_siteE-scanner1-v1-20120503-fasted-10b-gradients-image1-G1-B2-N22
renamed_slice3_b2_siteE-scanner1-v1-20120503-fasted-10b-gradients-image1-G1-B2-N22
renamed_slice3_b3_siteE-scanner1-v1-20120503-fasted-10b-gradients-image1-G1-B2-N22
siteE-scanner1-v1-20120503-fasted-10b-gradients-image1-G1-B1-N22-roi-rect2-tissue.aiff

Descriptions:

- Line 1: the path for the directory where the DW-MRI DICOM files exist.

- Line 2: the number of b-values (nb) for which image slices are available for the ADC fitting task (integer).

- Line 3 to 3+(nb-1): the actual values of b-values in increasing order from the top to the bottom (float numbers).

- Line 3+nb: the number of different slice locations (e.g. from the same volume) for which ADC measurements are required (ns)

- Line 3+nb+1 to 3+(2*nb): the names of the DICOM/AIFF image slices (for the first slice location chosen) corresponding to the b-values just listed and in the same order (i.e. the corresponding b-values increase from the top to the bottom). These names can simply be the original file names (renaming is not necessary). Note that the first file name is used by the software as the prefix for all the output file names (corresponding to that specific slice location). If these files are in aiff format, still no extension is needed (see the second example above).

- Line 3+(2*nb+1): the name of the corresponding 'aiff' binary mask file (with extension) as region of interest, with 1.0's inside and 0.0's outside the roi (.dat files, produced using ICR's in-house software ADEPT, are no longer used).

- If there are more than one slice location (ns < 1) for which ADC measurements are required, the last two items (nb b-value slices + their ROI file) are repeated ns times using appropriate file names.

1.1.2 Execution

Make sure you have prepared the "DataInfo.txt" file based on the guidelines given (and the example files) and is located in the right directory (if you use one of the example files make sure you rename it to "DataInfo.txt"). Also make sure that the image slices listed are actually the right ones in terms of slice location, b-value, etc using their DICOM headers. It is also important that the ROI files listed correspond to the image slices listed.

Step 3: The folder in which the output results will be written out is set by default to the folder 'output_files' inside the current folder (containing the code). Hence one needs to create such a folder before running the code if it does not exist. The text file of Results (one per slice location) in which ADC and S0 measurements and their corresponding errors are written out, provide the median values as well as the mean values corresponding to the ROI given.

Step 4:

- Compile and build the executable using 'make' command, and then run 'TinaADCtool -f adc' command to display 'DW-MR ADC Tool' window.

- The default selection for 'data protocol:' is 'A'.

- The default selection for 'image type:' is 'DICOM', but can be set to 'AIFF' if b-value image slices are aiff files.

- The default selection for 'ROI type:' is 'AIFF'.

- The default value for 'Ricean factor:' is 1.0, but can be set to other values as well depending on the case study. For instance, in case of pure diffusion it should be set to zero. It can be shown that, when comparing zero and non-zero values for Ricean factor, the difference in ADC measurement would be within few percent.

- Finally press 'measure ADC in clinical data (ROI)' button.

1.2 Manual annotation of tubes for phantom QA

If localisation of phantom tubes fails for any reason (such as ice clutter or image distortion), one can perform ADC measurements followed by phantom QA through manual annotation of tubes. To do this one needs to draw 5 individual circular regions of interest (inside the 5 tube regions) on an example image slice and save them as 5 aiff binary mask files. The name of each mask should correctly refer to the corresponding tube as in [2]. Next, in 'pgh_tool.c' file one should replace "float_mask#" with the new common part of the string used to name the masks drawn manually. Also before running the code for ADC measurement on the phantom, i.e. "measure ADC in the phantom", one should select 'Yes' for "manual annotation of tubes". Once the results are generated for three phantom image slices, the three path/filenames of the corresponding Results text files should be entered in the 'DataInfo.txt' file as input to the QA software as usual [2].

2 How to Use the Software for Local Rigid Alignment of Diffusion Weighted MRI.

2.1 Introduction

The current version of the alignment software works on a single slice location. This however may be extended to align the rest of the volume iteratively. There are a number of steps which need to be followed before one can run the software.

2.1.1 Data Preparations

Step 1: Rename all dicom files (e.g. using soft links) so that each name includes all the information needed. An example renamed file name is: *'siteE-scanner1-v1-20120515-fasted-10b-gradients-image1-G1-B1-N23'*. Here image1 refers to the first repeat (can vary between 1 to 4 or even 6), G1 refers to the first diffusion gradient direction, B1 refers to the first (smallest) non-zero b-value, and N23 refers to the slice number.

Step 2: Produce a 'DataInfoPB.txt' file containing all the information needed for the motion correction code to be executed. An example 'DataInfoPB.txt' file is as follows.

PB-MC
./ClinicalData/Protocol-B/siteE-scanner1-v1-20120515-fasted
siteE-scanner1-v1-20120515-fasted-10b-gradients

4
1
2
3
4

3
1
2
3

3
2
6
7

23
siteE-scanner1-v1-20120515-fasted-10b-gradients-image1-G1-B2-N23
siteE-scanner1-v1-20120515-fasted-10b-gradients-image1-G1-B1-N23-roi-rect2
siteE-scanner1-v1-20120515-fasted-10b-gradients-image1-G1-B1-N23-roi-rect2-tissue

- The first line only contains a file identifier (PB-MC).

- The second line contains the path to the folder where renamed files exist.

- The third line contains a common string including site name, scanner number, patient number, date of scan and the number of b-values available, with which all file names start.

- The next line is blank.

- The next line contains the number of repeats available for this scan session, followed in new lines by the actual numbers used to call different repeats.

- The next line is blank.

- The next line contains the number of diffusion gradient directions available for this scan session, followed in new lines by the actual numbers used to call different gradient directions.

- The next line is blank.

- The next line contains the number of b-values available for this scan session, followed in new lines by the actual numbers used to call different b-values.

- The next line is blank.

- The next line contains the slice number corresponding to the slice location to which motion correction is applied.

- The next line contains the reference slice file name.

- The next line contains the name of an 'aiff' file containing a rectangular region surrounding the region of interest. The pixel values in this file are not used, only the roi information is used to define ranges of loop counters.

- The next line contains the name of an 'aiff' file containing a binary mask region defining the region of interest with values of 1.0 for pixels included in and values of 0.0 for pixels excluded from the region.

2.1.2   Execution

Step 3: The folder in which the motion corrected image slices will be written out is set by default to the folder 'Results' inside the folder given on the second line of the 'DataInfoPB.txt' file as the location of renamed files. Hence one needs to create such a folder before running the code.

Step 4:

- Compile and build the executable using 'make' command, and then run 'TinaADCtool -f adc' command to display 'DW-MR ADC Tool' window.

- Here for 'averages per diffusion gradient:', choose between number of averages required. The default number is 4. This should be changed in the code if the number of repeats changes in the protocol, e.g. to 6.

- The 'reference type:' is usually set to 'DICOM', but can be any 'AIFF' file generated in Tina earlier.

- One can choose 'Yes' for 'align twice:' if they wish to use the motion corrected image slice as reference for a second round of motion correction.

- Set 'modify alignment:' to 'Yes' if you want the pattern of motion seen in the lowest b-value image (usually b=100) to be used for the rest of the b-value images.

- Finally press 'motion correction' button.

References

[1] Hossein Ragheb and Neil A. Thacker, "TINA Demo 004: The Pairwise Tool", *Tina memo* 2012-008, 2012, *http://www.tina-vision.net/docs/memos/2012-008.pdf*.

[2] Hossein Ragheb, Neil A. Thacker, David M. Morris and Alan Jackson, "Scanner Quality Assurance using the IMI QuIC-ConCePT Ice-Water Phantom (draft #2)", *Tina memo* 2014-003, 2012, *http://www.tina-vision.net/docs/memos/2014-003.pdf*.

[3] Hossein Ragheb, Neil A. Thacker, Jean-Marie Guyader, Stefan Klein and Alan Jackson, "Comparison of Local-rigid and Non-rigid Registration of Diffusion Weighted MRI for Improved Estimation of ADC", *Tina memo* 2014-006, 2014, *http://www.tina-vision.net/docs/memos/2014-006.pdf*.