predictMS - Short Introduction

This is a (very) short introduction to *predictMS* (**P**rofessional **R**emagen **D**iagnostic **I**mage **C**alculation **T**ool for **MS**), an application for the reconstruction of quantitative myelin and total water content, T1 and T2* maps using the approaches described in [1] and [2]. If you meet any problems or find new bugs, please contact neeb@rheinahrcampus.de

General remarks

Running executables of *predictMS* are available for Linux, Windows and Mac-OS X (tests were performed for Ubuntu, Windows Vista and Mac OS X 10.7.2, respectively). The current Windows version is 32 bit only while Linux and Mac executables are compiled for 64-bit systems. Furthermore, no GUI is yet available so that you have to run the application from a command line shell.

WINDOWS
As one of the goals was the development of a tool that is freely available and modifiable by anybody, we were consequently using free software during the development process. Thus, the Windows version is based on Cygwin (http://www.cygwin.com) and the gnu compiler collection. Therefore, users of predictMS should ideally have installed Cygwin before launching the tool. However, all necessary libraries are also included in the current release so that it is not absolutely vital to install Cygwin on your system, although recommended.

One of the (few) disadvantages of Cygwin is the occurrence of an annoying warning when using Windows path conventions such as *'C:\....'* The good new is, however, that you can switch them off by typing

```
set CYGWIN=nodosfilewarning
```

before launching *predictMS* as described below.

Preparation

LINUX/Mac
First, extract the zipped tarball predictMS.tar.gz to any location you like (e.g. /user/neeb/predictMS):

```
gunzip predictMS.tar.gz
tar -xzvf predictMS.tar
```

This will create a new Folder named *'predictMS'* which contains the current release of the tool.

Unzip the file predictMS.zip containing the current release of the tool to any location you like (e.g. C:\predictMS\).

Data acquistion and storage

1. The current version of the tool is still not very flexible with respect to data acquisition and storage. *predictMS* assumes that all data which are being transferred from the scanner are stored as DICOM file in a location (presumably on a filesystem) that can be accessed by *predictMS*.

2. A detailed description of the acquisition protocol is given in [2]. It is strongly recommended to acquire data according to the protocol specified there. The only exception applies to the number of echos acquired with the multi echo GE sequence. Here, we have tested data with both 10 echos (original version) and 8 echos (fast version). If you change the number of echos and/or echo spacing, T1, T2* and H2O reconstruction will very likely still give reliable results. However, the myelin water content mapping reconstruction is optimised to work with either 10- or 8-echo datasets. *predictMS* automatically detects the number of echo times and adopts the internal reconstruction/optimisation parameters accordingly. An example dataset of the 8 echo acquisition is included in the package (Folder *'ExampleData'*).

3. The full protocol consists of 6 datasets which have to be stored in DICOM format, each in its individual subfolder under a common folder which identifies the patient/subject. *predictMS* assumes that folders are named according to the following scheme (all names are case sensitive!):

- gre_lowflip → multiecho GE sequence with either 8 or 10 echo times for each slice (resulting e.g. in 400 images for an 8 TE acquisition of 50 slices). This dataset refers to the acquisition with 40° flip angle as described in [2].
- gre_lowflip_phase → the corresponding phase data (do not forget to enable the corresponding option your scanner console)
- gre_highflip → multiecho GE sequence with typically 2 echo times, which must be the same as the first two TEs of the gre_lowflip sequence. This dataset is required for T1 reconstruction and refers to the acquisition with 70° flip angle as described in [2].
- epi_body → EPI dataset of the same slices as the gre_* datasets, acquired with an flip angle of 90° and the BODY(!) coil for signal transmission AND reception.
- epi_highflip → EPI dataset of the same slices as the gre_* datasets, acquired with an flip angle of 90°, the head coil for signal reception and the body coil for signal transmission.
- epi_lowflip → EPI dataset of the same slices as the gre_* datasets, acquired with an flip angle of 30°, the head coil for signal reception and the body coil for signal transmission.

4. Some important practical hints for data acquisition:

- In order to assure that the signal has fully relaxed before the acquisition of any of the 3 EPI sequences listed above, please wait at least 30 seconds before starting each of the corresponding sequences. The acquisition scheme might therefore look like:
    1. gre_lowflip
    2. gre_highflip
    3. **30 seconds**
    4. epi_highflip
    5. **30 seconds**
    6. epi_lowflip
    7. **30 seconds (+ SWITCH TO BODY COIL)**
    8. epi_body

- Please fixate the head of you patient! As we try to measure all parameters quantitatively, motion free acquisitions are absolutely vital (if you like you can try how your myelin maps will look like if your subject moves during the measurement). Even though we are currently working on a scheme to correct for motion related artefacts, it's always better to prevent motion right from the beginning. Therefore, subject fixation is absolutely essential!
- Do not forget to switch to the body coil before the acquisition of the epi_body sequence (which should be the last sequence in you protocol).
- The current version is optimised for 3T imaging. If you acquire data on a 1.5T machine, some thresholds for segmentation need to be adapted. An automatic detection of the field strength is, however, not jet included in the current release. Therefore, 1.5T acquisitions should be interpreted with care!

5. Each individual acquisition (="patient dataset"), consisting of the six datasets mentioned above, should be stored in a separate folder. Imagine, e.g., that you have acquired data from 3 MS patients. In this case you should store the corresponding data in 3 folders which might be named, e.g.

LINUX/Mac

/user/neeb/myData/MS1/
/user/neeb/myData/MS2/
/user/neeb/myData/MS3/

WINDOWS

C:\myData\MS1\
C:\myData\MS2\
C:\myData\MS3\

Running predictMS

The good new is: you're almost done! Now you just need to create a text file which

lists (in separate line) the names of all Folders you would like to process. For the Linux/Mac example mentioned above, your text file might look like

```
/user/neeb/myData/MS1/
/user/neeb/myData/MS2/
/user/neeb/myData/MS3/
```

whereas the Windows file should contain the following three lines:

```
C:\myData\MS1\
C:\myData\MS2\
C:\myData\MS3\
```

An example of such a text file can be found in the 'etc' Folder. Store this text file at any location you like under whatever name you can think of (let's assume that the file has been stored under '/user/neeb/predictMS/myMSDataToProcess.txt' on a Linux/Mac machine or under 'C:\predictMS\myMSDataToProcess.txt' on a Windows system)

Now you're ready to launch predictMS.

LINUX/Mac
Open a terminal and cd to the path were *predictMS* is stored (e.g. /user/neeb/predictMS/bin/). Type, in a single line, the following text:

```
./predictMS  /user/neeb/predictMS/myMSDataToProcess.txt
/user/neeb/predictMS/etc/MyleinProcessingMatrix.txt RunInfo.txt RunResults.txt
```

Here, *'/user/neeb/predictMS/etc/MyleinProcessingMatrix.txt*' is a file you can find in the *'etc'* Subfolder of your predictFolder.

WINDOWS
Open a command line terminal (which typically can be found in the 'Accessories' at your start menu) and change you folder to the path where *predictMS* is stored. In the example above, where you have stored the downloaded package at C:\predictMS\, you should type:

```
cd c:\predictMS\bin
```

Now you can launch the tool by typing

```
predictMS.exe  C:\predictMS\myMSDataToProcess.txt
C:\predictMS\etc\MyleinProcessingMatrix.txt RunInfo.doc RunResults.doc
```

Here, *'C:\predictMS\etc\MyleinProcessingMatrix.txt'* is a file you can find in the *'etc'* Subfolder of your predictFolder.

The last two arguments are optional. If they are specified, some processing information (RunInfo.txt) and reconstruction results (RunResults.txt) are being stored.

Feel free to change the names or locations of those two files or omit them at all from the argument list.

predictMS creates a number of subfolders under each of the patient folders. Those subfolders contain both the reconstructed maps as well as correction factors which have been calculated during the different processing steps.

Please be patient during reconstruction! It takes approx. 1,5 hours on my dual-core Mac to process a single dataset! *predictMS* uses OpenMP (http://www.openmp.org) to distribute the processing tasks on as many cores as are available on your computer. Therefore, it is strongly recommended to use a multi-core machine whenever available.

Sources/Bugs

I have included all sources to the version released. Unfortunately, I did not find time yet to create configuration scripts that automate the building process. However, the code should compile with any decent compiler (I'm currently using gcc V4.2.1). *predictMS* depends on two open source projects which have to be bound to the sources during the linking stage:
   - Boost (http://www.boost.org)
   - GDCM (http://gdcm.sourceforge.net)

Please feel free to modify the code according to your own needs. If you have designed new classes or new functionality, I would be very glad if you could provide them as open source so that they can be included it in future releases. The same applies to bugs you might (definitely?!) find…

References

[1] V. Tonkova, V. Arhelger, J. Schenk, H. Neeb. Rapid Myelin Water Content Mapping on Clinical MR Systems. Z Med Phys (2012): http://dx.doi.org/10.1016/j.zemedi.2011.09.005

[2] H. Neeb, V. Ermer, T. Stocker, N.J. Shah. Fast quantitative mapping of absolute water content with full brain coverage. NeuroImage (2008). 42(3): 1094–1109