Working with the DICOM and NIfTI Data Standards in R

March 8, 2011

Associate Editor

General Comments

- Generating the pdf document from Sweave includes information on different machines (where the creation has been done). Thus the `audit.trail` in Fig.10 should be edit slightly in the final version (working directory).

  We're happy to do this on the final version of the manuscript.

Specific Comments

- Can the grey scale contrast be enhanced in the images?

  We have modified the `zlim` in Figures 3, 6 and 9.

JSS-specific Formatting

- `section` and `subsection` should be formatted in sentence style.

  Changed.

Reviewer #1

We would like to thank the reviewer for all his/her comments and suggestions.

Main Remarks

- The paper clearly describes what the packages can do. However, some questions raised my mind while reading the paper. How should you describe the users that are going the use the packages? And how did you implement their specific needs?

- For example 1: Suppose I am a practical researcher, which acquires imaging data to support a research question. Which functions would mostly provide in my needs?

  We have included a table that lists the major functions available in both the **oro.dicom** and **oro.nifti** packages.

- For example 2: Suppose I am a statistician that wants to use your package to enhance the statistical data analysis of imaging data. What are the main functionalities of header manipulation that I can use?

  See our answer to the previous question.

- Above questions are more or less addressed in the paper, but I think it should be better specified what the specific purposes of the packages are. I would like to suggest a description of the intended users in the introduction of the paper. Additionally, some

clear examples that are specifically intended for the described users would be highly beneficial for the clearness of the paper.

Thank-you for your questions and recommendations. We have added text in the introduction to address who should want to use the packages and how they might want to use the packages. In addition we have included a fuctional MRI (fMRI) example to illustrate how basic R functions can be applied to medical imaging data, once loaded into R using **oro.nifti**.

Minor Remarks

- section 2, 1st paragraph: DICOM abbreviation is already defined in the introduction

  This text has been removed.

- section2, 2nd paragraph: At the end you say that the fourth column of the DICOM format is not implemented. Why is this the case?

  The table of information was taken directly from the DICOM documentation. To the best of our knowledge there is nothing of value in the fourth column of Table 1.

- subsection 2.2: last sentence: extractHeader

  Changed.

Reviewer #2

We would like to thank the reviewer for all his/her comments and suggestions.

Major Points

- This brings me directly to the main criticism regarding this manuscript: There is no application of a statistical test or a linear modeling on imaging data. Instead, precalculated maps are loaded in chapter 3.7 to present overlay capabilities. One may ask why these libraries were just added to R? Furthermore, the authors stated in chapter 3.6, that (interactive) visualization is "however best performed outside of R". Again: Where is then the benefit of the library, when these things can be done outside of R more fluidly? I therefore strongly suggest adding at least a (real world) statistical example with image data, where R can show its outstanding performance in its field. This could convince the reader from the benefit they would have when using this library in R. The increased space requirements for that can then be saved at the expense of the detailed description of some (binary) internals of DICOM and ANALYZE/NIfTI.

  The main purpose of the **oro.dicom** and **oro.nifti** packages is to read and write NIfTI, ANALYZE and DICOM images, to manipulate data formats and to convert DICOM to NIfTI. From this, any statistical procedure in **R** can be used to analyze the images. As example, we added a section on the analysis of a functional MRI data set in Section 3.7.

Minor Points

- Page 2, Chapter 2, line 1: The first sentence is (somehow) redundant.

  Re-worded.

- Page 2, chapter 2, line 4: There are two two-byte (or 16 bit integer) sequences, not "two four-byte sequences" as mentioned, which form a tag.

  Changed.

- Page 2, chapter 2, line 7: Please, use "pixel data" instead of "data" enclosed in quotation marks. Besides that, this tag is not necessarily found (but surely most often) only at the end. There could be e.g. two of them: One with the data itself (at the end) and another one containing a thumbnail and embedded in a sequence (somewhere in the header).

  Changed.

- Page 2, chapter 2, line 12: The value representation string is only available when explicit encoding is used. Please reword.

  Re-worded.

- Page 2, chapter 2, line 14 and Table 1: Please use "Unlimited" or similar instead of "0".

  Added text in the table and body to emphasize this point.

- Page 5, chapter 2.1: The authors should clearly point out here, which kinds of DICOM objects can be accessed. I suppose that only monochrome images with 16 bit depth are supported. But the DICOM standard defines a lot more (RGB-colorized, JPEG- or JPEG2000-packed, .).

  Text has been added.

- Page 5, chapter 2.1, line 10: DICOM headers are encoded explicitly or implicitly, which is stated in the appropriate transfer syntax in the meta header. A strategy as "If the character string in bytes four and five do not correspond ." sounds to me a little bit too heuristic, but can accepted, if the meta header is not available..

  You make an interesting point, but I am not familiar with the meta header field that signifies "explicit" or "implicit" encoding. Could you please provide the (group,element) values for this field?

- Page 8, chapter 2.2, line 9: Typo: Write "extractHeader" instead of "extratHeader".

  Changed.

- Page 9, chapter 2.2, line 7: Because in MRI slices are not acquired at once, they also cannot have the same repetition time (TR). I suggest to change it to ". in a single repetition time (TR) frame .".

  Changed.

- Page 10, chapter 3, line 4: Analyze 7.5 might be the last known version of this file format, but "most recent" sounds like "actual", which is not true here: For Mayo

Clinics, the developer of the software ANALYZE, it is an obsolete format, superseded by AnalyzeAVW, which is much more flexible. It has survived in the scientific community for practical reasons and by early adoptions by SPM. Please, use another wording here, like "last available" or similar.

Text has been added and modified.

- Page 12, chapter 3.2, line 1: The voxel offset is already known for Analyze 7.5. It was possible (but only rarely used) to start with image information not from the beginning of the .img-file.

  Text at the end of the first paragraph has been modifed to include the case of "pairs of files" that occur under the ANALYZE and split NIfTI formats.

- Page 13, chapter 3.2, line 3 and page 14, chapter 3.3, line 8: This is not right. Following the radiological convention the radiologist looks into the brain from below, because the patient or volunteer is usually scanned lying head first and in supine position, and the feet point towards the radiologist. From this point of view, left and right are flipped. The neurological convention instead is oriented on the anatomy "as is" and uses therefore not a mirrored visualization.

  Thank-you for pointing this out, it appears that I have reversed my definitions. This has been corrected.

- Page 17, chapter 3.5, line 4: What does "ecode = 6" mean?

  Text has been added.

- Page 19, chapter 3.7, line 6 and Figure 7: The center of the crosshair does not point at the thalamus in the proper sense, because the thalamus is a paired structure and the main functional groups are situated left and right from the displayed mid-sagittal position.

  Modified.

- Page 22, chapter 4.1, line 5: "list(dcm =, datatype = 4, ." is truncated after "DIM ="

  We have not been able to find a way to impose line breaks in the `dput` command. We will most likely have to edit the final version of the manuscript to produce visually-pleasing output.

- Page 27: There is no URL for Mr. Thornton.

  This line has been removed from the manuscript.