Reviewer's report

Title: A cross-platform software tool for the generation of relaxation time maps in magnetic resonance imaging

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Reviewer: Einar Heiberg

Reviewer's report:

General comments
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The present manuscript is a software paper, and it is a well structured manuscript presenting a software tool for quantifying relaxation maps in magnetic resonance imaging.

The task of generating relaxation maps are neither novel or rocket science. However it is an important application and we present approach might work as a benchmark package for future software and also it can be used for education purposes, teaching students about relaxation and MRI. Furthermore, it seems that no other software is able do more than one kind of tissue quantification (at least as claimed by the authors).

Discretionary Revisions (which are recommendations for improvement but which the author can choose to ignore)

1. The source code is distributed under standard open source license (GPL), which is good and clearly stated (open access is a prerequisite for submission).

2. As being a non IDL user, I would have wanted more details on acquiring the IDL virtual machine. Preferably, I would also have like a standalone version of the software was made available (I vaguely remember that IDL can do this, but I might be wrong on this)

The need for standalone (again if possible) can be exemplified by me having large problems to get my account at the producer of IDL verified. It finally turned out that that particular page was incorrectly displayed using FireFox and this took me several days to find out. This is also the reason why this review was delayed. Many potential users of the software could potentially give up in this process. I acknowledge that is outside the control of the authors, but still is an important issue in the paper.

3. The web page on the project repository could be improved with the user manual available as a pdf file directly. This would also potentially allow more users to find the software since search engines would probably the index it.

4. Also consider releasing the user manual as a supplement of the paper. This would then also allow for a congruent snapshot between both the supplemented
source code and the user manual. Especially since that I hope that the software will continue to develop at the project homepage.

5. In the project homepage, please consider adding more details on how users can contribute to the software project. If software is not regularly updated, it will start to die away.

6. If the editor chose to accept this manuscript for publication also a link from the project page to the pdf file of this paper should be made.

7. When running the software, how come that one needs to specify the number of images to use in the image series. This is highly non intuitive. I might be wrong but I can not see any reason why the program can not automatically determine this. If this is for some particular reason, please make the error message somewhat clearer where this can be adjusted.

8. One thing that is missing (at least would be nice) in the software is the ability to zoom in the images. One could argue that this can be done in other post processing softwares to which one can export the images. However, this is not entirely true since it is nice to show the fitting curve for particular pixels, and they can be hard to point at in the original scale.

9. In the software the tab called T2, could perhaps be called T2(*) in analogy with the details in the paper.

10. In the software (as stated in the paper) pixels where the fitting process failed / was uncertain, then pixels are given zero value. It would be good if this was marked clearly in the colorscales so that uncertain pixels would stand out.

11. In the paper, no comparisons with existing techniques are done which is a clear drawback of the paper. For instance at least consider including a comparison with Thalassaemia tool, which is a (what I think a now commercially available software) for quantification of T2* in patients with iron overload. I also think that you can freely get an evaluation license of the software. Also CMRTool and CMR42 (if I remember correctly) do have parametric tissue maps and their software can be downloaded for evaluation purposes. Comparisons with these software's would highlight systematic differences, and the order of magnitude of potential differences. However, I do acknowledge that although the other suggested alternatives are commercial solutions their algorithms could be not be taken as ground truth data (perhaps with the exception of the Thalassemia tool, that seems to be very well validated).

12. The potential use of the software would increase significantly if also the used image examples were deposited on the web site. This would have the benefit of providing benchmark data for other future algorithms (that for instance will focus on computational speed etc). It is especially useful with the test data since other systems can then also be tested with data from multiple image sources. Also depositing data sets would also allow the use of the software for educational purposes, such as self studies, and literature reports of students studying MRI and quantification techniques.
13. Authors are encouraged to add a sentence in the paper that researchers that use this software should refer to this manuscript (if accepted for publication) when publishing scientific papers. This would gain not only the authors of this paper, but also the impact factor of the journal. Furthermore, it may also work as an information source that brings new users and usage of the software, when researchers read about it in other scientific journals.

14. The authors should consider adding the term “open source” in the title of the manuscript.

Minor Essential Revisions (such as missing labels on figures, or the wrong use of a term, which the author can be trusted to correct)

1. Page 4, last sentence, please include here the reference to the MOLLY sequence.

2. I believe that I have seen T2 quantification schemes were the flip angle value have been changed in the different acquisitions to get T2 values. If this is a standard technique, then this should at least be mentioned in the paper.

3. Bar graphs is not an acceptable method to visualize agreement between T1, T2, and T2* values with different methods as used in Figure 4. Please use Bland-Altman plots instead. Especially since it is definitely not clear that manual quantification would be the gold standard in this case. At the authors discretion also correlation plots can be included. In this case a line of identify should be included in the plot.

Major Compulsory Revisions (which the author must respond to before a decision on publication can be reached)

1. In the manuscript there are some annoying details that are incorrect/lacking. For instance I could not find any figure legends, and on Page 8, line 15 the sentence is incomplete. The authors are urged to carefully overlook the manuscript before submitting.

2. The description on how the software selects what types of mapping that should be performed depending of the input data needs to be improved. It is confusing for the reader, and one gets “black-box” feeling instead of an open source project approach were important details for the user are presented.

3. Implementation section (page 5-7), the presentation is not very clear to the reader. I strongly suggest dividing it into sections, for instance one for T2* mapping. Also how the software detects that a MOLLY sequence was used is not clearly stated in the paper.

Paper recommendation
I would recommend to accept this paper for publication, however only after a second review round.
**Level of interest:** An article whose findings are important to those with closely related research interests

**Quality of written English:** Needs some language corrections before being published

**Statistical review:** No, the manuscript does not need to be seen by a statistician.

**Declaration of competing interests:**

I would like to declare that I am the founder and CEO of Medviso AB, a company that produces the cardiac image analysis software Segment (http://segment.heiberg.se). The software is freely available to researchers, but sold for commercial purposes.