

Application for Round 3 QIBA Project Funding

Title of Proposal: Development of a Tool to Evaluate Software using Artificial DCE-MRI Data and Statistical Analysis		
QIBA Committee/Subgroup: MR / PDF-MRI		
NIBIB Task Number(s) which this project addresses: Task 3		
Project Coordinator or Lead Investigator Information:		
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Amount Requested:		

Project Description

Artificial data based on underlying pharmacokinetics and MR physics allows for the evaluation of the accuracy and performance of complex analysis software for dynamic contrast enhanced (DCE-) MRI and similar measurement techniques, such as diffusion weighted imaging (DWI) and native T1 mapping. Besides the creation of test data, it is important to evaluate and compare the results from the different software packages tested. This is especially relevant since the results will most likely show deviations, even for more or less identical implementations, resulting from the underlying numerics and differing initial values.

Consequently, it is not sufficient to simply compare the equality of parameter maps: a statistical comparison is needed, and we propose to build a tool to compare the results of parameter maps from different software packages with the reference parameter maps from the test data.

Therefore, we will provide a tool to compare results from software packages with the original artificial data using visualization of differences and statistical analysis.

The application will provide two different comparison methods:

1. Color-coded difference/ratio maps of result and simulated data.
2. Histograms, scatter-diagrams and box-plots between original and calculated parameters to allow a visual estimation of parameter differences and relations.
3. Statistical comparison of parameters
 - a. Student's t-test, Mann-Whitney-U test
 - b. Pearson and Spearman Rank Correlation to confirm linear dependency.
 - c. Covariance analysis for all parameters.
 - d. Principle component analysis between all parameters.
 - e. Least square linear and logarithmic model to identify linear constant variations for the algorithms, e.g., usage large and small vessel hematocrit, tumor T1.
 - f. Analysis of Variance (ANOVA).

The list of statistical methods is strongly depended on the incoming type of data and will be adapted to the requirements, if necessary.

The software will be build using the open source development environment Python, using the (also open source) extensions numPy, matPlotLib, and pyDicom.