PerfTool: A Software Platform for the Quantification of Dynamic Susceptibility Contrast Perfusion Imaging

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Introduction

Methods for deriving quantitative perfusion measurements are complex, often rely on a number of assumptions and are subject to intra- and inter-operator variability. It is difficult to compare and assess different arterial input function (AIF) identification and selection strategies because studies are often performed in limited simulation environments or the details of the algorithms are hidden from researchers within proprietary software packages.[1] Researchers often develop task-focused software programs to test new AIF or deconvolution routines, or simulations that are not able to accurately model real patient data. These programs are not designed to be extensible in order to test out other algorithms, nor do other researchers benefit from the labors exhausted on these programs. The software complexity of the human-computer interface required for AIF algorithms and other common tasks (*i.e.*, reading different medical image formats) are challenging and time consuming tasks that each researcher must independently solve for their particular research needs. To address these problems, we developed a comprehensive perfusion software package (PerfTool) that facilitates the analysis of relative and quantitative perfusion measures for both dynamic susceptibility MR and also bolus contrast CT perfusion data.

Methods

The Model-View-Controller (MVC) design pattern was used to separate PerfTool's user interface from the perfusion filters.[2] The core perfusion processing algorithms were written in C++ using the publicly available National Library of Medicine Insight Segmentation and Registration Toolkit (ITK) pipeline architecture,[3] as shown in Fig 1, and they are cross-platform. The user interface was developed with Xcode using objective-C and Cocoa frameworks (Apple Computer, Cupertino CA).

We developed a novel method to test different algorithms using data sets consisting of different simulated perfusion parameters. The test patterns were designed to be processed like regular perfusion data both offline for quantitative analysis and interactively for qualitative analysis (similar to television test patterns). For example, we used a simulated test pattern to compare standard SVD (sSVD) to a reformulated SVD (rSVD) implementation proposed by Smith *et al.*[4] that performs better in the presence of negative arterial tissue delays (ATD) (*i.e.,* the contrast agent arrives in the tissue signal before the selected AIF). To compare the performance of sSVD and rSVD, we generated a test pattern with known cerebral blood flow (CBF) values, shown in Fig 2a, for different mean transit times (MTT) and for both negative and positive ATD. From theory, CBF should not be affected by ATD (top-bottom direction of Fig 2a) while longer MTT corresponds with lower CBF.

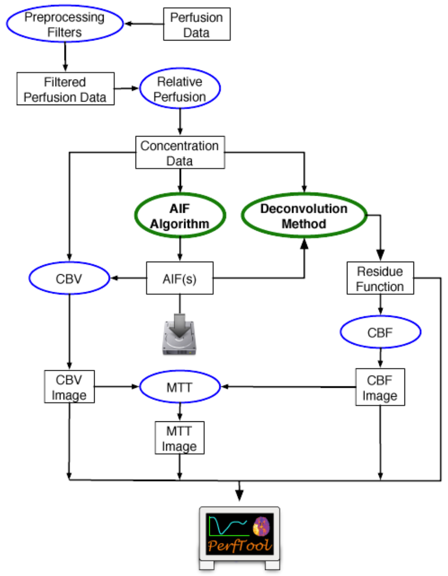

Figure 1: Perfusion Pipeline. The core perfusion processing of PerfTool is encapsulated using ITK's pipeline architecture. This allows researchers to focus on implementing new algorithms instead of focusing on time-consuming application details.

Results

The ITK pipeline architecture allowed us to implement different singular value decomposition (SVD) deconvolution techniques (sSVD, rSVD) and different AIF selection strategies (manual, user-assisted[5]) into PerfTool. The separation of the pipeline structure from the user interface using the MVC design pattern also allows perfusion processing to be performed automatically without the user interface using auto-AIF strategies.[6] On a dual 2.5 GHz PowerPC G5 (Apple), PerfTool can generate all relative and quantitative perfusion maps in 33 seconds for a perfusion sequence with 18 slices and 50 time points.

The simulated test patterns have enabled us to compare deconvolution algorithms qualitatively and quantitatively. Figs 2b and 2c show the resulting CBF patterns generated by PerfTool using sSVD and rSVD, respectively. sSVD is known to produce large CBF overestimations when the arterial-tissue delay (ATD) is negative.[4] The bright region at the top of Fig 2b (indicating high CBF) demonstrates this effect. Fig 2c shows that rSVD performs better for the negative delays.

Conclusion

PerfTool allows scientists to compare AIF selection strategies and deconvolution methods using both simulated test patterns (known results) and patient data (unknown results). The comprehensive functionality of PerfTool allows researchers to quickly see the effects of manipulating algorithm parameters. Processing the test pattern interactively with PerfTool provides unique insights into the performance of different algorithms as illustrated by our comparison between sSVD and rSVD. Isolating algorithms using ITK filters allows scientists to share new algorithms in order to enhance our ability to research perfusion. Also, the integration of ITK into PerfTool means that all ITK image processing algorithms are accessible to PerfTool. PerfTool will assist researchers in accurately evaluating perfusion quantification methods and enables these methods to be applied to clinical data for perfusion studies.

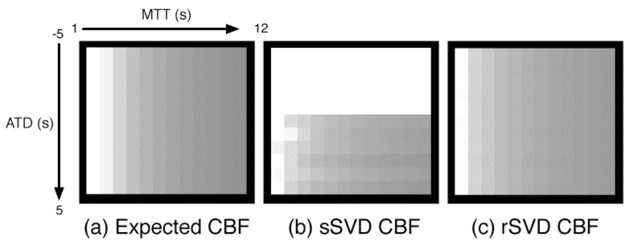

Figure 2: Example CBF test pattern. The simulated pattern (a) shows that in theory CBF is not affected by ATD (top-down direction). However, sSVD significantly overestimates negative ATD's as indicated by the bright region at the top of (b). rSVD performs better then sSVD for negative delays (c).

References

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