Myocardial Stress Perfusion Dynamic Signal Evaluation Algorithm Comparison

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INTRODUCTION Interpretation of MR first-pass perfusion images is limited due to poor signal-to-noise ratio and to the presence of artifacts. However, studies have shown that perfusion quantification can improve the diagnostic accuracy in ischemic disease. A simple approach to quantify myocardial perfusion uses dynamic signal (DS) upslope, based on averaging myocardial signal amplitude changes in a myocardial segment over a time series. While it has been repeatedly shown that a decrease in upslope is associated with myocardial perfusion defects, unfortunately, upslope estimation is sensitive to the artifacts due to respiratory motion, arrhythmias, fat or blood signal contamination, and fast imaging sequences. Model-based deconvolution methods can also be used to derive absolute perfusion by determining the relative intensity and timing of the DS segmental blood (as input function) and myocardial (as output function) signals. In order to systematically compare the performance of different perfusion quantification methods, we applied six algorithms to the same first pass stress and rest perfusion images of normal volunteers having the same endo- and epi-myocardial contours. Variation in regional estimates of flow reserve (FR), defined as the ratio of stress/rest upslope or absolute perfusion, was studied to see which algorithm would be more susceptible to artifacts based on the assumption that there is little variation in the FR among normal subjects.

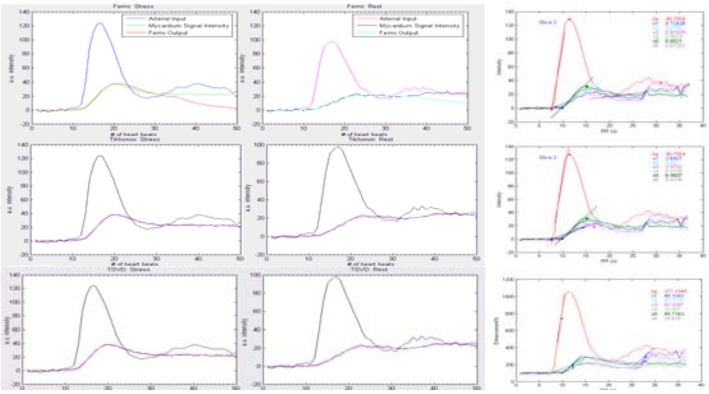
METHODS To ensure the normality of the perfusion data, volunteer recruitment was limited using the strict exclusion criteria of hypertension, diabetes, smoking, family history of cardiac disease, and EBCT coronary calcium score ≤ 20. Seven volunteers (ages: 18 to 67, 5 females) were enrolled after IRB approval. Using a saturation recovery TrueFISP technique, first pass perfusion studies after adenosine pharmacological stress and at rest were performed on a 1.5 T Sonata scanner (Siemens, Malvern, PA). A voxel spatial resolution of $1.9\times2.8\times8\text{mm}^3$ was achieved at 3 slices per heartbeat over 50 heartbeats using an acquisition time of 160ms per slice. Gadodiamide of 0.05mM/kg was injected, followed by a 15ml saline flush at 6ml/s during both the adenosine and then rest phases, with a 20-minute washout between contrast injections. Using MASS (Medis, Leiden, the Netherlands) software, the endo- and epi-myocardial contours were manually drawn in an image showing good myocardial contrast and then automatically propagated at each time point. The myocardium was divided clockwise into 6 equal segments using the anterior RV insertion as the reference (or starting) point. Mean signal intensities of all pixels in each myocardial segment at every time point were transferred to a customized program that used the time intensity curve to calculate upslope and absolute flow according to the following algorithms. The same algorithm was applied to ventricular cavity blood signal to calculate its upslope. Relative upslope of each myocardial segment is evaluated with each algorithm.

1. **Piecewise**: From start to end of the time series, segmental upslope was calculated for each time point by taking signal intensity from neighboring time points using least square means. The maximal relative upslope was selected as the largest upslope among all time series;
2. **Global**: Points at the peak and foot of the upslope were identified and all points in between were fitted to determine upslope;
3. **Constrained**: To select correct peak and foot values, two constraints were added to the global method: (a) myocardial peak values had to fall within 15 heartbeats after blood peak, and (b) myocardial foot values had to fall within 15 heartbeats after blood foot.
4. **Fermi**: To solve the deconvolution using blood as input and myocardial signal as output, a Fermi function was selected as the distribution of tracer residence times to search for the best fit of the DS curve for each myocardial sector;
5. **TSVD**: Truncated singular value decomposition is a numerical deconvolution regularization technique with less matrix components.
6. **Tikhonov**: Another regularized solution for numerical deconvolution based on minimization of the residual norm. (**)

The FR was determined as the ratio of stress to rest upslopes or perfusion. 3 out of total 126 sectors were excluded due to motion artifacts. Standard deviation (SD) was the variation of the mean among individuals. Coefficient of variation (CV) of each algorithm was calculated as SD/mean×100%.

RESULTS An example of a pair of DS and model produced fitting under stress (leftmost) and at rest (middle) of one sector are shown on the left as Fermi, TSVD, Tikhonov; while upslope calculation for one slice is shown on the right as global, constrained, and piecewise from top to bottom respectively in **Figure**. The mean, SD and CV of FR in 7 volunteers for each algorithm are shown in **Table**. The results of one-way ANOVA showed significant difference in mean FR among 6 methods; however, the mutual differences among the 3 model-based methods were insignificant, as well as between the global and constrained upslope methods. There was no significant difference in mean FR among slices (F=0.09, P=0.9178) and sectors (F=2.18, P=0.0543), but there was significant difference among individuals (F=8.21, P<0.0001). CV=13% was the lowest using the constrained method, but the mean FR was also low compared to model based methods, although higher than the other two upslope-based methods. The model-based methods showed similar CV and higher FR (than slope-based methods) that is closer to reference methods such as PET and invasive Doppler flow wire.

CONCLUSION Regional flow reserves vary with the algorithm chosen for upslope or perfusion evaluation. Results from a constrained algorithm showed mean flow reserve values closer to reference methods than both the Piecewise and Global algorithm with smaller CV, suggesting it might be the most useful algorithm in upslope approaches. Model based algorithms showed more consistent results.



Method	Mean	SD	CV
Global	1.75	0.36	0.21
Piecewise	1.22	0.23	0.19
Constrained	1.82	0.25	0.13
Fermi	2.91	0.49	0.17
TSVD	2.65	0.50	0.19
Tikhonov	2.44	0.48	0.20

**Koh TS, *et al*, IEEE Trans Med Imaging. 2004 Dec;23(12):15