COMPARISON OF FOUR TECHNIQUES THAT DIRECTLY USE RESIDUE FUNCTION CHARACTERISTICS WHEN ESTIMATING CEREBRAL BLOOD FLOW DURING DSC MRI STUDIES

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Introduction: Dynamic susceptibility contrast (DSC) studies involve deconvolution of the local tissue concentration signal $C_{VOI}(t)$ by an arterial concentration signal $C_a(t)$ to determine the residue function $R(t)$. The peak of $R(t)$ is used to generate cerebral blood flow CBF maps. Current filtering techniques to remove deconvolution enhanced noise are based on characteristics of the arterial signal $C_a(t)$ and lead to CBF estimates decreasing in accuracy as the tissue mean transit time (MTT) gets smaller (Fig. 1). *Our hypothesis is that CBF accuracy and CBF precision is improved by using filtering techniques based on characteristics of the residue function.*

Method and Results:

Method 1: Fig. 1 compares the CBF estimates from a standard time-invariant SVD approach (eigenvalue threshold (*Psvd*)) [1] with those obtained by directly multiplying the residue function's spectral components *R(f) = FFT(R(t))* by a window *W1(f)* based on the arterial signal spectral components $C_a(f) = FFT(C_a(t))$. Setting *W1(f) = 1* if $C_a(f)/C_a(0) > 0.2$, and 0 otherwise, generates a series of band pass filters [2] and provides essentially identical results to the standard SVD CBF estimates using *Psvd = 0.2*.

Method 2: A filter window based on the residue function spectral components allows removal of unnecessary noise when MTT is large (*R(f)* narrow). Setting *W2(f) = 1* if $R(f)/R(0) >$ *frac* and *0* otherwise leads to smaller error bars for large MTT when *frac = 0.2,* (Fig. 2) but the CBF accuracy is lost. Making *frac ~ 0.01* for large MTT restores the lost high frequency components of the residue function spectral components. This observation indicates that *Psvd ~ 0.01*, (very high SNR signals) would be needed to provide accurate SVD CBF estimates for tissues with small MTT (grey matter (MTT = 4 s) and white matter (MTT = 4.8 s) (c.f. [3]).

Method 3*:* The noise values at each point in the $C_a(t)$ and $C_{VOI}(t)$ sequences are statistically independent. Using alternate points in each data sequence permits the determination of two independent residue functions. Averaging the CBF estimates obtained after Fourier interpolating these low-resolution residue functions should provide a $\sqrt{2}$ improvement in CBF precision. Experimental limitations. e.g. signal aliasing, prevent this theoretical improvement from being totally achieved (Fig. 3).

Method 4: The previous methods rely on CBF estimates from a single noisy peak value. We suggest obtaining tissue MTT estimates (1) via a first moment calculation using multiple values derived from *R(f)* and (2) from multiple points along *R(t)* (after the residue function peak) using the noisy exponential analysis technique described by Smith and Buckmaster [4]. The latter approach includes a method for validating the assumption that a given clinical residue function is adequately described as having exponential characteristics. Averaging these MTT estimates from two different domain analysis techniques permits CBF estimates via CBF = CBV / MTT. As can be seen from Fig. 4, this new method greatly improves the accuracy of the CBF estimates. The CBF precision is determined by the combined errors from CBV and MTT determination. The existing implementation of this new approach results in a CBF precision lower than when the error bars from the other methods are scaled to correct for the CBF under-estimation present in those techniques.

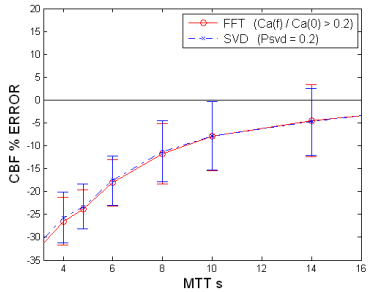

Fig. 1: **Method 1:** CBF estimates obtained by filtering the residue function using *W1(f) = 1* if $C_a(f)/C_a(0) > 0.2$ are equivalent to SVD results with *Psvd* = 0.2.

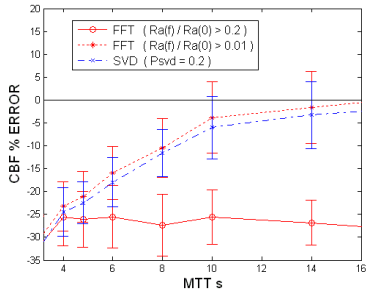

Fig. 2: **Method 2:** Using *W2(f) = 1* if $R(f)/R(0) >$ *frac* and *0* otherwise introduces CBF inaccuracies for large MTT unless *frac ~ 0.01*.

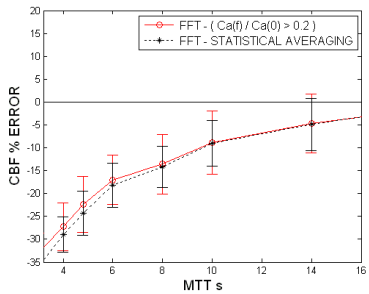

Fig. 3: **Method 3:** Minor improvements to CBF precision occur by using statistical techniques to allow averaging of multiple CBF estimates.

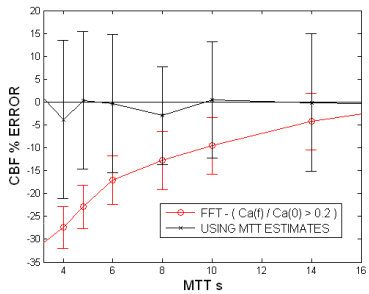

Fig. 4. **Method 4:** Using MTT estimates derived from multiple points on the residue function leads to increased CBF accuracy but lower CBF precision.

Conclusion: Four approaches for providing CBF estimates based on characteristics of the residue function are compared. A new technique using multiple points of the tissue residue function in time and frequency domains shows the most promise.

References: [1] Smith *et al.,* Mag. Reson. Med. 51:4, 631 -- 634, 2004. [2] Salluzzi *et al.,* Mag. Reson. Imag. 23:3, 481 -- 492, 2005. [3] Lui *et al.,* Mag. Reson. Med. 42:1, 167-172, 1999. [4] Smith and Buckmaster, J. Mag. Res. 17, 29 -- 33, 1975.