Methods for In-Line Calculation of Perfusion Parameter Images

R. Stollberger[1], F. Payer[2], C. Enzinger[2], F. Ebner[1], F. Fazekas[3]

[1]Radiology, Medical University of Graz, Graz, Austria, [2]Neurology, Medical University of Graz, Graz, Austria, [3]Neurology, Medical Uiversity of Graz, Graz, Austria

Introduction: The visualization and the determination of the cerebral tissue perfusion is of great importance for different diseases. With the frequently used bolus tracking technique [1] blood flow is typically derived from the tissue residue function (R(t)) calculated from the tracer tissue time curve and the arterial input function (AIF) by deconvolution. Several techniques have been proposed for deconvolution [e.g. 2, 3]. The most popular method is the truncated singular value technique (tSVD) [2]. However the whole procedure has several sources of errors. Additional to the problems associated with the different deconvolution techniques an important additional source of error exists in the correct determination of the AIF which is typically performed by experienced user.

In an explorative comparison of different techniques for perfusion analysis it was found that rCBF-images calculated without deconvolution by a special implementation of the maximum slope method (MSM) were almost identical to those calculated by SVD. To calculate relative perfusion images the MSM needs only the tissue signal time curve [4]. It is therefore a very interesting approach for a fast and automatic in-line calculation of rCBF images. In the present study the performance of the MSM was explored and compared it with the SVD deconvolution technique. Of specific interest was the influence of the different mean transit times (MTT) and different the contrast media bolus durations on the maximum slope method. Advanced temporal filters were explored to minimize the influence of noise.

Material and Methods: Simulations were performed for MSM and SVD deconvolution to check the influence of SNR, temporal resolution, MTT, AIF width and CBF on the performance of the techniques. To reduce the influence of noise on perfusion maps using MSM a Gaussian kernel, a polynomial filter [5] and PCA denoising [6] were applied. For comparison also unfiltered data were processed. The range of investigated CBF-values varied between 20 and 60 ml/(min 100 g), MTT varied between 3.4 and 9.2s and an exponential decay was taken as residue function. The AIF was constructed by using three different time shifted gamma-variate functions with FWHM from 8.5s to 15s for the first pass. The baseline SNR was varied between 24.5 and 192. The temporal resolution was set to 1.2, 1.4 and 1.7s (in accordance to our different scan protocols). To check the influence of the AIF delay in SVD processed in-vivo data, a Fourier Transform (FT) based deconvolution [2] was applied too. This method is shift invariant and for a specific filtering equivalent to block-circulant deconvolution [7]. A correlation analysis with a global bolus was performed to determine the distribution bolus lag-times. In vivo measurements were performed on two different 1.5 T Systems using either a segmented double echo sequence or a single shot GRE-EPI in combination with the GRAPPA technique and an acceleration factor of two. A dose of 0.2 mmol/kg body weight of contrast media was injected with 5 ml/s followed by a 30 ml saline flush. For clinical analysis data were taken from 25 consecutive patients with focal neurological symptoms, which had a MR perfusion scan in the applied scan protocol. The perfusion related parameter images of the different methods were independently classified by five readers.

Results: The simulations showed that appropriate pre-processing of the data is essential for the application of the maximum slope method. The best result was achieved for PCA based denoising (Fig. 1), however, polynomial-filtering showed an similar performance. For these filters the mean rCBF calculated by MSM was almost constant for a homogenous region and a baseline SNR of 192, 97, 41 and 24.5. The standard deviation of rCBF increases from 2.7% of mean CBF up to 10.1% for PCA denoising and from 4.3% up to 15.7% for polynomial-filtering (SNR from 97 to 24.6, white matter simulation). The comparison of MSM with SVD using noisless data showed for variations of the MTT from 3.4s to 8.1s perfusion changes of 26% for MSM and 24% for SVD (Δ=1.7s). Less influence was observed for a changing bolus width. For bolus durations (FWHM) ranging from 8.5s to 15s CBF changed by 17.% for MSM and by 12.4% for SVD. A clear disadvantage of the SVD method compared to the MSM is its known sensitivity for delay effects [8]. This influence is clearly depicted in the occipital region of the brain in Fig. 2. For regions with a delayed bolus (see t_lag) a general reduced perfusion is calculated by SVD. If the bolus delay insensitive Fourier method is used for deconvolution the resulting rCBF image is almost identical even in the occipital region to that calculated by MSM. The assessment of clinical investigation of 25 patients of rCBF images calculated SVD and MSM did not result in a significant differences for the perception of perfusion anomalies. The lag-time images produced by cross-correlation analysis were found to be extremely robust and the contained information is very similar to MTT maps derived from the residue function.

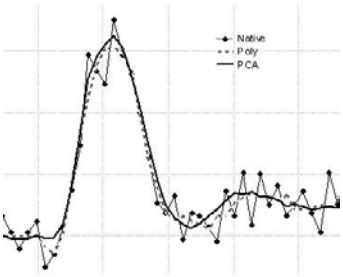

Fig. 1. Denoising in time domain using polynomial filtering and PCA

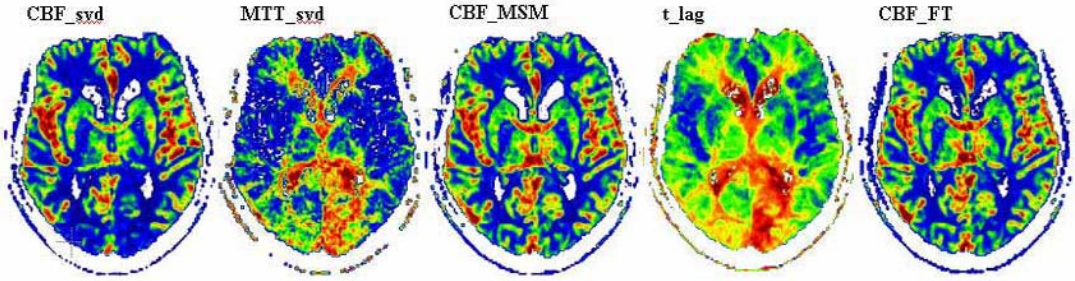

Fig.2. Hemodynamic parameter images of a stroke victim calculated by tSVD (rCBF_svd, MTT_svd), MSM (rCBF), correlation analysis (tlag) and Fourier deconvolution (rCBF_FT). No spatial filtering was applied.

Discussion: Although deconvolution methods should give the most reliable information about a specific haemodynamic status, it was found that perfusion maps using the maximum slope method show abnormalities with the same sensitivity. The maximum slope method is not influenced by delay effects and straightforward in application. Therefore it is a particular attractive method for automatic calculation of haemodynamic parameter images. This is also valid for the lag-time. The correct measurement of the AIF for clinically useful data sets is impeded by many adverse effects (Hct-dependent nonlinearities, partial volume effects, susceptibility dependent shifts, k-space filtering). Therefore, some calibration procedures are often applied additional to the deconvolution techniques. Such a calibration is also possible for the maximum slope method. Analogue to other techniques for perfusion imaging the MSM is sensitive for bolus dispersion. Further efforts are necessary for direct absolute quantification of CBF.

References:

1. Rosen BR, Belliveau JW, Vevea JM, et al. Magn Reson Med 1990;14:249–265.
2. Rempp KA, Brix G, Wenz F, Becker CR, Guckel F, Lorenz WJ, Radiology 1994;193:637–641.
3. Østergaard L, Weisskoff RM, Chesler DA, Gyldensted C, Rosen BR. Magn Reson Med 1996;36:715–725.
4. Miles KA, Br J Radiol 1991; 64:409-412.
5. Savitzky-Golay Filters, Numerical Recipes in C: The Art of Scientific Computing (2nd ed.), Cambridge University Press (1992)
6. Martel AL, Moody AR. The use of PCA to smooth functional MR images. In: Taylor CJ, Noble JA, Brady JM, (editors). Medical Image Understanding and Analysis, Oxford, UK: BMVA; 1997:13-16.
7. Wu O, Ostergaard L, Weisskoff RM, Benner T, et al., Magn Reson Med 2003 ;50(1):164-74.
8. Calamante F, Gadian DG, Connelly A, Magn Reson Med 2000;44:466–473.