# Robust and unbiased adaptive thresholding in SVD-based deconvolution of DSC-MRI perfusion data

S. P. Sourbron<sup>1</sup>, R. Luypaert<sup>1</sup>, M. Osteaux<sup>1</sup> <sup>1</sup>Vrije Universiteit Brussel, Brussels, Belgium

## **Synopsis**

SVD-based deconvolution of DSC-perfusion data requires the selection of a threshold parameter in order to regularize the solution. We extend three methods that are well-established in the literature on regularization to the context of pixel-by-pixel MRI perfusion quantification. We evaluate these methods in terms of image quality and sensitivity to abnormalities in CBF and compare them to fixed- and adaptive thresholding paradigms from the MRI literature. We conclude that the L-curve criterion combined with Tikhonov regularization shows promise as a robust and unbiased thresholding method.

# **Introduction**

Regularization methods for the deconvolution of DSC-MRI perfusion curves require the selection of a threshold which to a large extent determines the results [5]. The regularization method of choice in this field is Truncated Singular Value Decomposition (TSVD) with a fixed threshold (FIX) [1]. Recently it has become clear that the optimal threshold is dependent on tissue characteristics, SNR, dispersion and delay of the AIF [5]. An adaptive thresholding method (LIU) – custom made for DSC-MRI perfusion – has been proposed [3]. One possible drawback is that it neglects delay/dispersion effects, although these appear to be an important issue in TSVD [4]. On the other hand a number of methods are available from the literature on regularization which rely on very general assumptions only [2]. The three most common ones are evaluated in this work: the Discrepancy Principle (DP), the L-Curve Criterion (LCC) and Generalized Cross Validation (GCV). We apply them in combination with TSVD-regularization, and a 'smooth' version of the former called standard Tikhonov regularization (TIKH) [2].

### **Materials and Methods**

Perfusion experiments were performed with a double-shot multiple-slice gradient-echo sequence (TR/TE/0 899msec/30msec/40°, slice thickness 6.0 mm, 128\*128 pixels, FOV 230 mm, 20 slices, 40 time points). Subjects received 40ml of Gd-DTPA at 5ml/sec. An AIF was selected in the MCA and the images were deconvolved using TSVD- and TIKH-regularization with thresholds chosen pixel-by-pixel according to the five methods under consideration. Each time the overall mean threshold was calculated Among the cases treated we present here the results for one subject,



who showed increased Time To Peak (TTP) in the right hemisphere. A 6x6-pixel ROI was drawn on the region with hyperintense TTP and an identical one contralateral to it. Finally the ratio normal/abnormal CBF was calculated from these ROI's.

#### Results

The top row of the figure shows CBF-maps deconvolved with TSVD-regularization, the bottom row with TIKH-regularization. The columns represent the various thresholding methods. Color tables are the same for all the images. The table underneath lists numerical results for each of the techniques.

D-FIX
$\pm 0.00 \pm$
±1.06
H-FIX
$\pm 0.00 \pm$
±0.86

#### **Discussion/conclusion**

First, a qualitative inspection of the data shows clearly that the use of DP-, LCC- and GCV- thresholding is not advisable in combination with TSVD. The same conclusion holds for TIKH-DP. The DP can also be rejected on the grounds of its normal/abnormal CBF ratio, which is clearly unphysical. TIKH-GCV is acceptable in terms of image quality, but leads to extremely high CBF values due to the small thresholds it selects. Also, it seems rather insensitive to CBF-abnormalities. We are left with TIKH-LCC, which shows a good image quality except for some isolated, hyperintense pixels which blend in after optimisation of the algorithm. We note that it tends to produce slightly lower CBF values than both LIU- and FIX- thresholding. It is known to be an extremely robust technique [2] which is designed to seek a compromise between 'goodness of fit' and 'smoothness of the solution'. We conclude that it is a suitable candidate for an adaptive thresholding paradigm in DSC-MRI perfusion quantification.

# References

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