

A bootstrap approach to detect corrupted volume in ASL data

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TARGET AUDIENCE – Scientist and clinicians with interest in perfusion MRI

PURPOSE – Arterial spin labelling (ASL) is a technique that permits to estimate perfusion not invasively. The principle of this technique is to acquire images in two different conditions (label and control) and the difference of this two acquisition is used to estimate perfusion. Due to this difference the intrinsic SNR of ASL is low. Despite more reliable labelling technique has been proposed is still necessary to repeat the process and compute the average of a high number of repetitions to achieve a good SNR. This process can be affected by the presence of outliers in the data that could be caused by several artefacts or physiological tissue signal fluctuation. These outliers can highly impact estimation of perfusion introducing a bias. This work will present a method already successfully applied to Diffusion Tensor Imaging¹ to exclude corrupted volumes and achieve more reliable estimates of perfusion.

METHODS – The proposed method discards automatically corrupted volumes. To determine which volumes are to be discarded, a quality score (QS) is defined as follows. First, mean estimates for each voxel is computed by using a bootstrap approach, i.e., by removing volumes from the dataset for each estimate. Second, 95% confidence intervals (CI) for each voxel from the multiple mean estimates are computed. Third, QS is defined as the double integral of the CI distribution. We compute the initial QS using all volumes. Then QS is computed for the data excluding each volume, one at a time, and discard the volume associated with the maximum QS. We repeat this until the QS decrease. The proposed method has been tested on both simulated and real scenario.

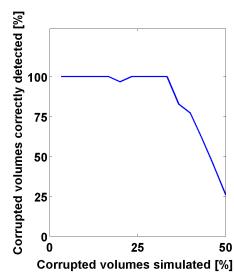


Fig. 1 Percentage of corrupted volumes correctly detected when 5% of total voxel are corrupted

SIMULATIONS – A 3D T1-weighted anatomical reference was segmented and a silico dataset of perfusion weighted images was built (80x80x30 voxel per volume). Perfusion level was addressed to Gray and White matter based on partial volume map obtained with the segmentation. The ratio between totally GM and WM perfusion level was set to 3. A constant SNR of 2 (calculated as $SNR = CBF_{GM}/\sigma_{NOISE}$) was hypothesized to add white noise to each perfusion volume. We tested our proposed rejection method on several different level of corruption: from 0 to 50% of volumes corrupted and changing the level of corruption for each volume, i.e. the percentage of corrupted voxel on the total (5%, 10%, 25%, 50%). Corruption was achieved randomly resampling the volumes and replacing the original voxel level with an outlier extracted from a uniform distribution symmetrically distributed out from 95% of CI of the noisy perfusion simulated dataset. The extreme of the distribution was chosen to be 2 times higher than 95th percentile of the original distribution and 2 times lower than the 5th. The number of corrupted volumes was quantified with the proposed method and the ratio between the numbers of true simulated corrupted volume was taken as a measure of performance. The method has also been applied to REAL DATA: 7 Healthy subjects (age 26±2.3) were scanned on a 3T Philips Achieva Scanner equipped with a 32 channels coil. A balanced pCASL labelling combined with multi-slice EPI single shot with following parameters were used: TE 16ms, TR 4.7s, labelling duration 1.8s, post-labelling delay 1.8s, two inversion pulses for background suppression purpose (1.89s and 3.22s after the pre-saturation pulse), 30 axial slices, voxel size 3x3x3mm³, SENSE acceleration factor 2.5, 30 label/control pairs for averaging, total time of acquisition of 4'45". The single label/control pairs were visually examined for performance evaluation purpose.

Subject	1	2	3	4	5	6	7
Manual	10	29,15	1,13	4,13,25	4,8,9,10,11,23,25	0	9
Auto	10	29	1,13	4,13,25	4,8,9,10,11,23	0	9
Matching	100%	50%	100%	100%	83%	0	100%
Non Matching	0	50%	0	0	17%	0	0

Tab. 1 Corrupted volumes individuated by visual inspection and with the proposed method. Matching and mismatching number volumes are reported as a measure of performance.

RESULTS – SIMULATIONS Percentages of volumes correctly identified as outliers and discarded from the average process for the lowest level of corruption (5% of total voxels) and for each number of corrupted volumes are reported in Fig.1. For this level of corruption the algorithm did not discard all volumes when the number of corrupted volume is more than 30% of the total. For other levels the algorithm was able to individuate all the corrupted volumes.

REAL DATA Percentage of matching between the visual examination and the proposed method is reported for each subject in Tab. 2, the total percentage of correct individuation of corrupted volumes was 84.6%. In Fig. 2 (up) is showed a typical uncorrected average perfusion image and the corrected average after discarding the corrupted volumes. Fig. 2 (down) reports a typical uncorrupted volume and a corrupted one (individuated by both the algorithm and visual inspection).

DISCUSSION – The method proposed was able to distinguish between corrupted and uncorrupted volumes on both simulated and real data. It was very conservative showing no false positive and a good global performance over very different level of corruption. It scores 88% over all the corrupted volumes on simulation and similar results were achieved on the real data set. This method is an alternative approach to other existing methods, like that proposed by Tan et al.² but, differently, it does not need any empirical threshold value to set. Our method is also different from the robust M-estimator approach proposed by Maumet et al.³, but differently, its performance evaluated on synthetic data is consistent also when using real data.

CONCLUSION – A novel method for corrupted volumes detection has been introduced. It uses a bootstrap like approach to exclude corrupted volumes based on a Quality Score index directly computed from the data. Outlier volume rejection operation should be performed on ASL dataset to avoid bias in estimated value of perfusion and this method is a valuable help to automatize the pipeline analysis.

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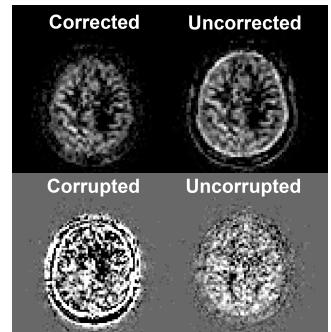


Fig. 2 Example of corrected perfusion map obtained with the proposal method and uncorrected one obtained with conventional averaging (subject #4). Typical corrupted and uncorrupted map (subject #2).