

Multi-parametric algorithm for the automated segmentation of brain vein

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Background: Cerebral vein analysis provides a fundamental tool to study neurovascular diseases. The assessment of vascular anatomy from a MR scan by means of manual segmentation of the cerebral veins is daunting and observer-dependent; therefore, automated approaches are actively sought for¹⁻³, as they also improve reproducibility.

Objectives: to present an algorithm for Multi-parametric Automated Vein Reconstruction (MAVERIC) that implements at once structural, morphological and relaxometric criteria of vein characterization to enhance classification accuracy.

Methods: A 3D double-echo spoiled gradient echo (TR=31ms, TE₁₋₂=[7.38;22.14] ms, resolution=0.5x0.5x1mm³, flip angle=13°) sequence was acquired once on 4 healthy controls, and twice on another subject, with head repositioning between the scans.

For each dataset SWI images (structural content), Vesselness (morphological information) and R2* (relaxometry) maps were derived. Based on the assumption that vein voxels have low SWI intensity, high Vesselness and R2* values, MAVERIC iteratively refines a vein mask by adding newly detected vessel voxels that satisfy the following criteria:

- SWI < mean(SWI) - 2.5 * std_dev(SWI)
- Vesselness > mean(Vesselness) + std_dev(Vesselness)
- R2* > mean(R2*)

Where the statistical moments were locally computed on a spherical moving window, excluding previously marked voxels. The exit condition for the iteration is verified when less than 1% of the voxels are added.

For each dataset, the performance of MAVERIC was compared to previous mono/bi-parametric^{1,4} (m/bPS) approaches by blindly grading on a 0-5 scale the accuracy of vascular tree depiction on 4 MIPped slabs (thickness: 20 mm). To assess inter-scan reproducibility, the difference between pre- and post-repositioning segmentations (S_{pre} and S_{post}) were expressed as Modified Hausdorff Distance⁵ (MHD) of the co-registered vein masks.

Results: m/bPS maps were never preferred to the corresponding MAVERIC maps in the test-sample. The mean accuracy scores were 4.44±0.51 for MAVERIC vs 3.38±0.62 for m/bPS. Comparison of S_{pre} and S_{post} showed a good overlap with a MHD of 0.33mm.

Conclusion: Combining information from SWI, Vesselness and R2* maps led to a reduction of false positives coupled to an improved detection of true positives, outperforming the m/bPS. The algorithm exhibits excellent inter-scan reproducibility, with a MHD that was well below the resolution of the used dataset.