Fully automated DWI-PWI mismatch quantification in acute stroke

Kartheeban Nargenthiraja¹, Lars Riisgaard Ribe¹, Kristina Dupont Hougaard^{1,2}, Josef Alawneh³, Tae-Hee Cho⁴, Susanne Siemonsen⁵, Josep Puig Alcantara⁶, Niels Hjort¹, Salvador Pedraza⁶, Jens Fiehler⁵, Norbert Nighoghossian⁴, Jean-Claude Baron³, Leif Østergaard¹, and Kim Mouridsen¹

¹Center of Functionally Integrative Neuroscience, Aarhus University, Aarhus, Denmark, ²Department of Neurology, Aarhus University Hospital, Aarhus C, Denmark, ³Department of Clinical Neurosciences, University of Cambridge, Cambridge, United Kingdom, ⁴Hopital Neurologique Pierre Wertheimer Creatis, Insa/UCBL, CNRS UMR5220 - INSERM U1044, Lyon I, France, ⁵Department of Neuroradiology, University Medical Centre Hamburg-Eppendorf, Hamburg, Germany, ⁶Department of Radiology-IDI, University Hospital Dr Josep Trueta of Girona, Spain

Introduction: Perfusion- and diffusion weighted MRI (PWI/DWI) is often used to identify patients who are likely to benefit from recanalization therapy [1]. The identification of PWI-DWI mismatch tissue, which is thought to represent potentially salvageable tissue, is however, highly subjective. Here, we present an algorithm which performs fully Automated Penumbra Segmentation (APS) based on PWI and DWI images, and compare automatically generated PWI-DWI mismatch mask to manually outlined masks performed by experts, in 168 patients.

Method: Patients and image acquisition:

We used a cohort of 168 acute ischemic stroke patients ($\mathcal{P}=70$) to evaluate the performance of APS in the multicenter study *I-KNOW* [2]. MRI was performed on several scanner types (GE Signa Excite 1.5 T, GE Signa Excite 3.0 T, GE Signa HDx 1.5 T, Siemens TrioTim 3.0 T, Siemens Avanto 1.5 T, Siemens Sonata 1.5 T, Philips Gyroscan NT 1.5 T, and Philips Intera 1.5 T). DWI was obtained for b-value 0 and = 1.000 sec/mm2. The PWI sequence (TE 30-50ms, TR 1500ms, FOV 24 cm, matrix 128x128, slice thickness 5mm) was obtained after an intravenous injection of Gadolinium based contrast (0.1 mmol/kg). Voxel-wise signal intensity time curves were converted to concentration-time curves, followed by gamma-variate fitting. *Algorithm: Perfusion lesion:* TTP maps were filtered by morphological grayscale reconstruction for automatic detection of lesion laterality. The TTP maps were then normalized relative to the mean TTP in the contralateral hemisphere and the map was reduced to contain only the ipsilateral hemisphere. The TTP seed point was defined as

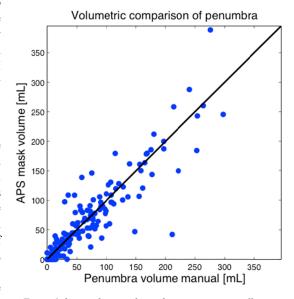


Figure 1 depicts the correlation between automatically and manually outlined mismatch volumes.

the voxel with maximum intensity. TTP maps were converted to binary maps according to the threshold TTP >4 seconds, and connected voxels were found by a connected component labeling algorithm. The cluster, which contained the seed point, was retained and considered as the TTP lesion. Finally, level-set algorithm was initiated to smoothen the scattered TTP lesion borders. *Diffusion lesion:* DWI images were filtered using morphological grayscale reconstruction. The level-set algorithm was initiated on the morphological grayscale reconstruction processed DWI images with an initial mask, which was derived by thresholding ADC maps at $600*10^{-6}$ mm²/sec. The mismatch = PWI_{lesion}–(PWI_{lesion}). *Comparison of automatic and manual mismatch outlining:* Four readers with extensive clinical experience within neuroradiology manually outlined the PWI and DWI lesions on TTP maps and DWI images. The APS outlined mismatches were compared with masks defined by agreement among three or more readers. To quantify the geometric and volumetric similarity between APS and manually outlined mismatches, we determined volumetric correlation and Dice coefficients (DC).

Results & discussion: The automatic determined mismatch volumes demonstrated good correlation with the manually outlined mismatch volumes $R^2 = 0.93$, see figure 1. The median difference in mismatch volume between manual outlining and APS approach was 2.1 mL (± 2SD: 61 mL). The median DC was 0.70 (0.46 - 0.77). The results indicate an excellent agreement between automatically generated and manually outlined mismatch masks. The performance of APS is highly encouraging in consideration of the number of patients and different scanner systems. The median processing time per patient was 21.4 seconds and this is a noticeably decrease in time, compared with visual assessment of multislice PWI and DWI images. Requiring no user intervention, this algorithm allows fast and reliable identification of tissue-at-risk, and we speculate this feature may aid not only fast, clinical decision-making, but also reduce the heterogeneity of inclusion criteria in multicenter

References:[1]Stroke, 1999, 30: 2230-7; [2] i-know-stroke.eu.

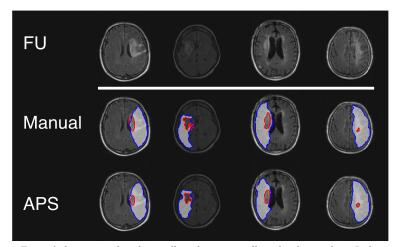


Figure 2 shows examples of manually and automatically outlined penumbras. Red contour is DWI lesion, blue contour is PWI lesion and the white-hatched area is the penumbra.