

## Significant MRI scanner model related differences in hemodynamic imaging: A secondary analysis of 174 dynamic susceptibility contrast MRI studies from the MR RESCUE clinical trial

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**Introduction:** MR RESCUE was a clinical trial that incorporated information from diffusion/perfusion MRI or CT perfusion to randomize acute ischemic stroke (AIS) patients to embolectomy or medical management based on favorable or unfavorable penumbral pattern as determined by MR RESCUE multivariate voxel-based predictive models. The primary hypothesis was that multimodal imaging, including MRI, could predict which AIS patients would benefit from mechanical thrombectomy. The trial was carried out at multiple centers and used multiple MRI scanner models. To our knowledge there has never been a study that comparatively investigated DSC MRI performance of different scanner models. This secondary analysis of the MR RESCUE MRI data focuses on absolute CBF as a stringent measure of DSC MRI perfusion imaging performance and evaluates whether scanner model performance differences are present in the MR RESCUE MRI data. An operational hypothesis is that hemodynamic readings from well perfused tissue contralateral to the hypoperfused hemisphere are comparable across patients. This study also evaluated whether there are scanner model related differences in CBF measured in the hypoperfused ipsilateral territory.

**Methods/patients:** 94 of 118 patients enrolled in MR RESCUE were randomized based on MRI (rather than CT) at 19 centers. Patients underwent a baseline imaging study that was used for randomization and a follow-up study done at a target time of 7 days. A total of 174 baseline or follow-up DSC MRI studies were available for evaluation. The regions used for arterial input function (AIF) sampling and the venous output function (VOF) sampling were manually identified in each study. Hemodynamic images were calculated by a single software package that used a standard truncated singular values decomposition approach with VOF scaling to compute CBF images. Brain masks and midline masks were manually drawn for each study. Well perfused contralateral tissue was defined as having  $T_{max} = 0$  and  $1.0 < CBV < 30.0$  ml per g. Ipsilateral hypoperfused tissue was defined only in baseline studies as having  $T_{max} \geq 6$  sec and  $0.0 < CBV < 30.0$  ml per 100 g. ANOVA (Kruskal-Wallis h-test) was used to identify scanner model related differences in the mean CBF in these two regions. This test requires at least 4 studies per scanner model. Scanner models used less frequently were not included leaving 178 studies.

**Results:** CBF readings taken from well perfused contralateral tissue in baseline and followup studies showed that a scale factor is needed to bring measured CBF values into the expected physiological range even when VOF correction for AIF partial volume sampling is used (Fig 1). Figure 2 provides scaled mean CBF readings (baseline and followup) from well perfused contralateral tissues. ANOVA shows a statistically significant difference in means ( $h = 43.0$ ,  $p < 0.001$ , 9 scanner models, 154 studies) in measured mean contralateral well perfused tissue CBF attributable to scanner model. This appears to be primarily due to an upward bias in CBF reported by GENESIS\_SIGNA scanner models. An evaluation of the mean CBF measured in ipsilateral hypoperfused tissue also showed a scanner model related bias ( $h = 20.9$ ,  $p = 0.002$ , 7 scanner models, 71 baseline studies) that is also related to CBF overestimation by GENESIS\_SIGNA scanner models. We have been unable to identify a reason that explains the bias. One possible explanation is that these scanner models slow the DSC time sampling rate without reporting this change in the DICOM record of TR, which is used by the analysis software as a measure of time resolution. In this regard the absence of a well-defined DICOM record for the DSC time sampling rate is a limitation. Figures 1 and 2 illustrate there is also substantial between patient variability that arises from clinical factors or from technical factors unrelated to scanner model.

**Discussion:** DSC MRI studies appear to be susceptible to bias introduced by the use of different scanner models. Future multicenter studies that use DSC MRI should take scanner model bias into consideration.

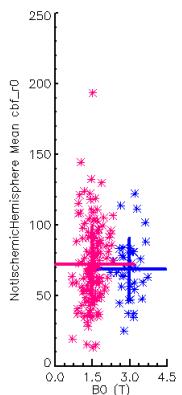


Figure 1: Unscaled mean CBF from well perfused contralateral tissue split by  $B_0$  (174 studies).

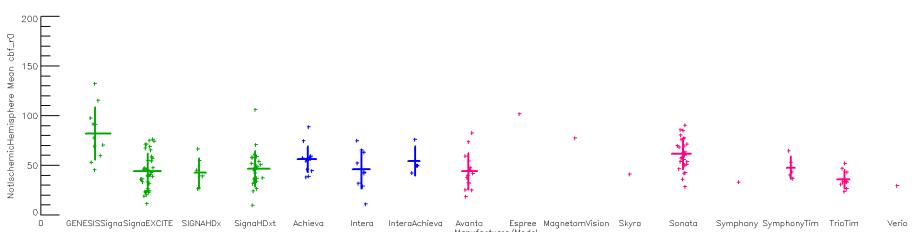


Figure 2: Scaled mean CBF (baseline and followup studies) from well perfused contralateral tissues split by scanner model for 174 studies (GE models: green, Philips models: blue, Siemens models: magenta). Means and standard deviations are shown by solid lines.