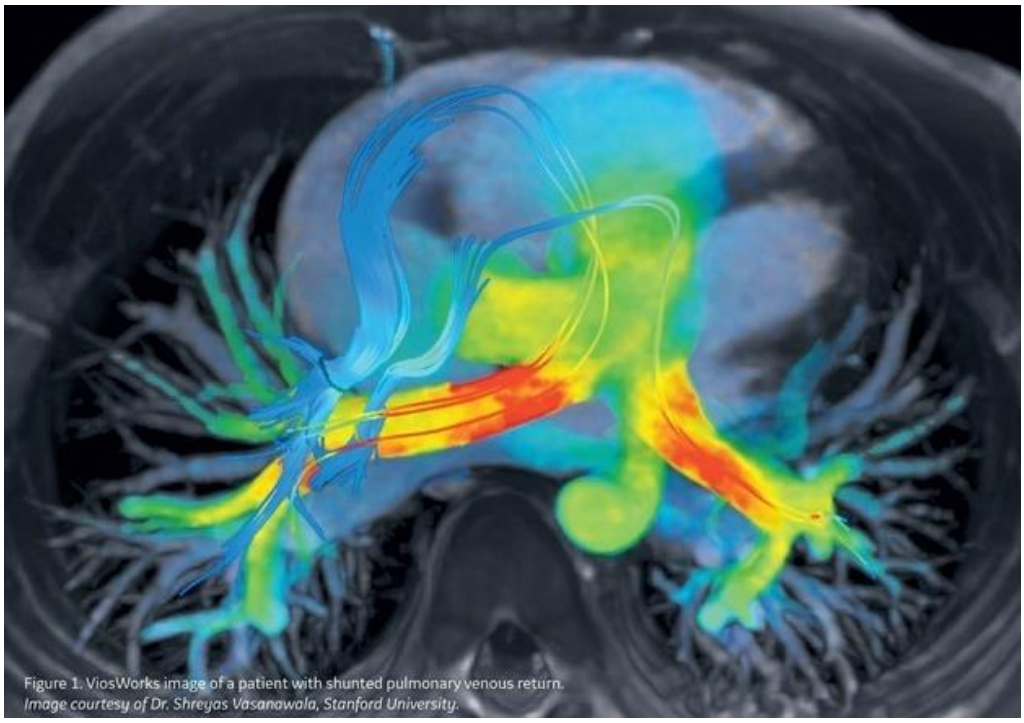

Figure 1. VIosWorks image of a patient with shunted pulmonary venous return. *Image courtesy of Dr. Shreyas Vasanawala, Stanford University.*

3T MR Research Program

Center for MR Research

University of Illinois at Chicago

TECH 2000 3T MRI RESEARCH FACILITY

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3T Research News

By Mike Flannery

The 3T MR Research Program always strives to keep our MR imaging capabilities in line with the most advanced technology. From time to time, this will require that we upgrade our current scanner to the next level of software. In the near future, we are preparing to upgrade our Harrison 3.0T MR750 scanner from the DV24.0 software to the next version of leading edge SIGNA Works software (DV26.0). The SIGNA Works software offers enhancements to exam workflow, applications, and advanced post processing that will impact both performance and imaging capabilities.

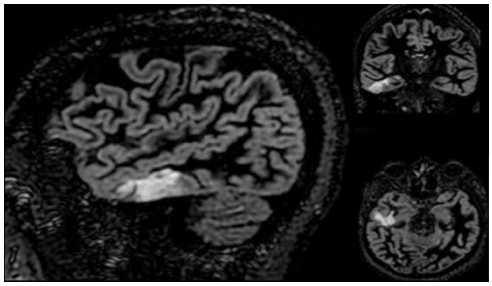
As a reminder, any studies that utilize custom pulse sequences (PSD) will need to be recompiled in order to be compatible with SIGNA Works software. If your study falls under this category, feel free to contact us here at the 3T MR Research Program to help address any questions or concerns in transitioning your study to the new software platform.

SIGNA Works

SIGNA Works is comprised both standard and advanced application portfolios. The standard SIGNA Works portfolio includes the following:

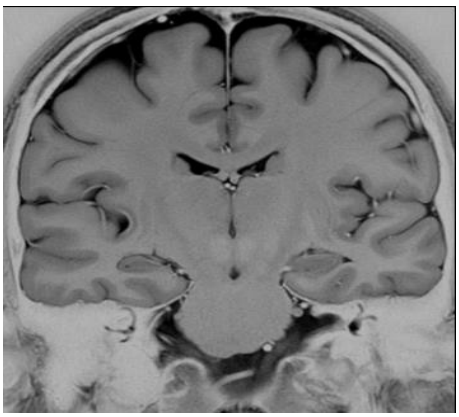
- NeuroWorks
- OrthoWorks
- BodyWorks
- CVworks

In particular, the NeuroWorks application includes an imaging suite optimized for imaging brain, spine, vascular and peripheral nerve anatomy. Two examples of these applications are CUBE DIR and PROPELLER MB. CUBE DIR, is a 3D volume sequence that allows for the suppression of CSF as well as gray or white matter for better lesion detection.



CUBE DIR showing temporal lobe lesion
Images courtesy of GE Healthcare

PROPELLER MB expands on the traditional PROPELLER sequence by utilizing a multi-shot blade technique that preserves tissue contrast and helps reduce motion artifacts. This new approach also allows for T1 FSE image contrast.



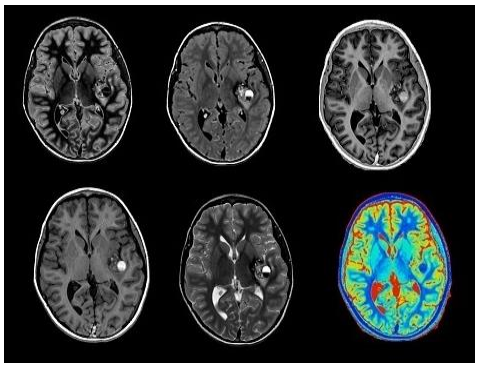
Coronal T2 PROPELLER MB (Inverted)
Images courtesy of GE Healthcare

The SIGNA Works advanced application portfolio includes the following:

- HyperWorks
- VIosWorks
- SilentWorks
- ImageWorks

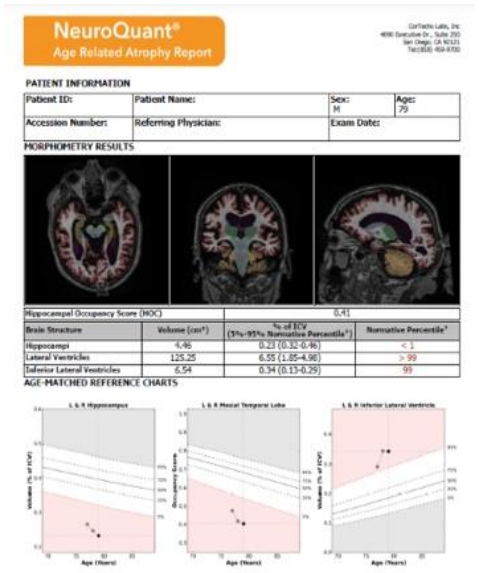
One unique application under the ImageWorks portfolio is MAGiC. The MAGiC (MAGnetic resonance image

Compilation) is a 2D FSE Multi-Dynamic (MDME) sequence that offers the ability to acquire multiple clinically useful image contrasts in a single scan. These would include T1, T2, Inversion Recovery (DIR, FLAIR,etc) and PD. This technique enables adjustment of TR, TE, and TI values after the exam completion in order to produce these desired image contrasts. Benefits from this technique would allow for a significant boost in productivity as well as freeing up additional time for advanced or repeated sequences.



DIR, FLAIR, PSIR (top) ,T1, T2 and T2 maps (bottom) acquired in one single scan
Images courtesy of GE Healthcare

NeuroQuant is another application within ImageWorks. This application allows for the volumetric quantification of brain structures and compares them to the accepted norms. This data would be useful to evaluate brain atrophy, hippocampal volume asymmetry, and brain development.



Some workflow enhancements worth noting include: Hz/Pixel calculation, Echo Spacing Display for FSE and EPI, automatic Navigator Tracker placement for free breathing body scans, Dual Shim Volume placement, and the Orchestra Algorithm which allows for faster image reconstruction.

Research spotlight

Muge Karaman, PhD

Dr. Muge Karaman received her Ph.D. in Computational Sciences at Marquette University in Milwaukee, WI. Dr. Karaman's research focus includes the following: 1) Application of fractional calculus formulation of anomalous diffusion processes in neural structures in order to investigate structural changes associated with progression, treatment, and regression of neurological disorders and 2) Development of computational statistical models for complex-valued fMRI. This issue highlights one of her recent publications on advanced diffusion imaging using higher *b*-values. Any investigators who are interested in applying her technique are encouraged to contact her at mkaraman@uic.edu.

Towards Glioma Grading Using Non-Gaussian Diffusion Imaging with a Continuous-time Random Walk Model and a Quantile Histogram Analysis

Introduction: Gliomas are the most common primary brain tumors in adults, spanning from grade I to IV according to the 2016 WHO guidelines. Glioma grade is typically determined by invasive surgical biopsy followed by histopathology analysis. This approach, however, may not always be feasible due to considerable surgical risks. While many imaging methods have been proposed to differentiate between low- (I and II) and high-grade (III and IV) gliomas, these techniques have limited success in determining individual grades. In this study, we demonstrate the feasibility of using a novel anomalous diffusion model, the continuous-time random walk (CTRW) model, with a quantile histogram analysis to differentiate Grade II (GrII), III (GrIII), and IV (GrIV) gliomas.

Methods: This study enrolled 103 patients with histopathologically proven gliomas, consisting of 2 patients with Grade I, 46 Grade II, 23 Grade III, and 32 Grade IV tumors. All patients were scanned on a 3T GE MR750 scanner with a 32-channel head coil. The MRI protocol included conventional MRI and DWI with 17 *b*-values (0 to 4000 s/mm²). The multi-*b*-value diffusion images were analyzed with the CTRW model, $S/S_0 = E_\alpha(-(bD_m)^\beta)$, where D_m is an anomalous diffusion coefficient, α and β are temporal and spatial diffusion heterogeneity parameters, respectively. A quantile histogram analysis, using the means of the first quartile of D_m, α, or β within the ROIs, was employed for group comparison and receiver operating characteristic (ROC) analyses.

Results: The higher-grade tumors showed lower values in all three parameters than the lower-grade tumors as shown in the figure. This observation was supported by the statistical significance (p-values<0.05) of the difference between GrII and GrIII, as well as between GrIII and GrIV groups. The CTRW parameters produced high performance metrics in differentiating GrII vs. GrIII and GrIII vs. GrIV gliomas with a sensitivity of 0.804 and 0.809, specificity of 0.714 and 0.645, accuracy of 0.776 and 0.730, and area under the curve of 0.773 and 0.755, respectively.

Conclusion: Our results represent an encouraging development from simply separating low-grade and high-grade as in the vast majority of diffusion MR studies. The quantile histogram analysis provides a "filter" for focusing on solid tumor regions without relying on precise ROI selections. This approach is also consistent with the current pathological practice of selecting the tissue from the worst part of the lesion. We have demonstrated that the combinations of the CTRW parameters are capable of differentiating glioma grades, pointing to a possible way for developing a non-invasive imaging-based glioma grading method without biopsies.

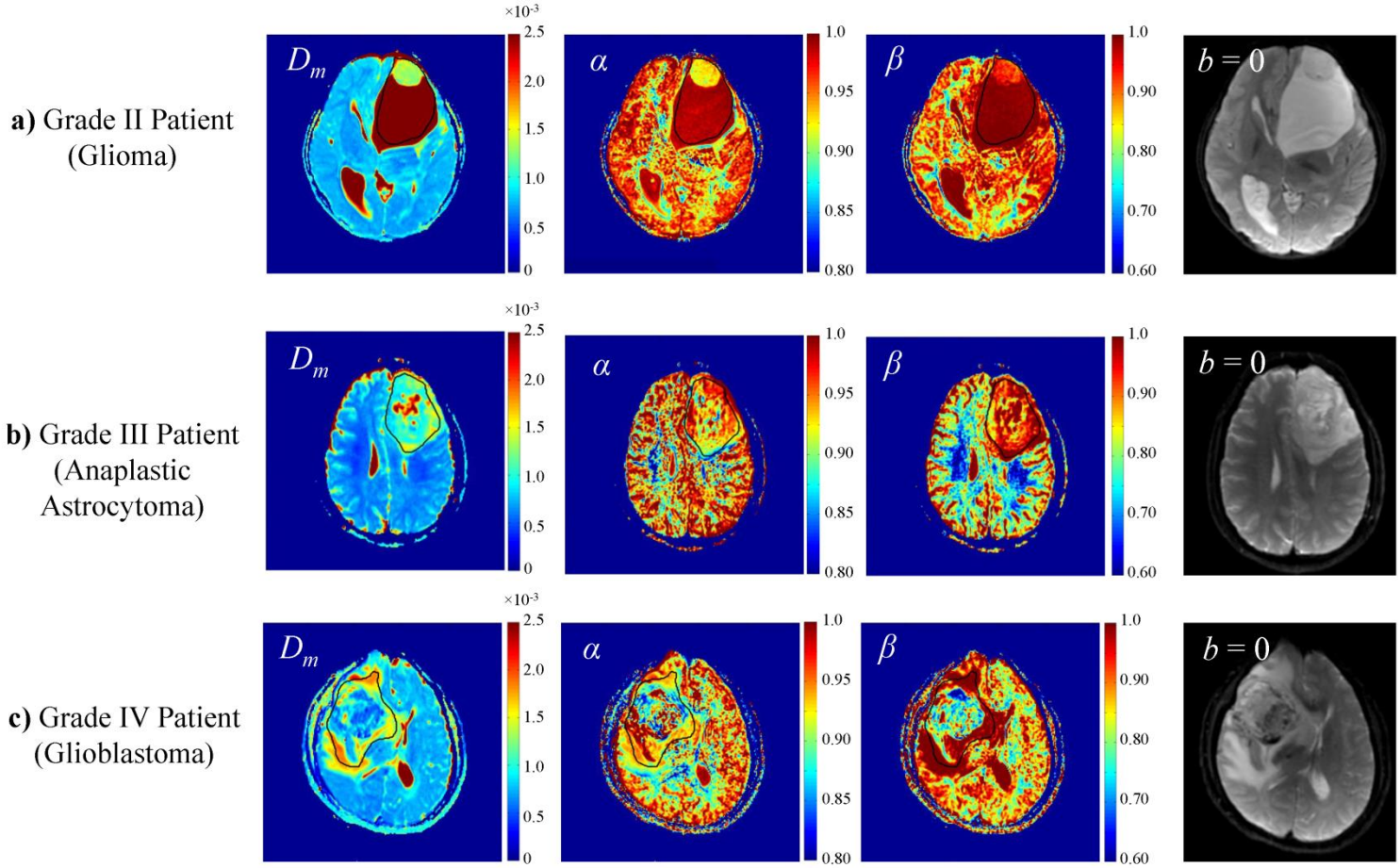


Figure: Maps of D_m, α, and β as well as b=0 image from a representative patient in each of the GrII (top row), GrIII (middle row), and GrIV (bottom row) groups. The ROIs are shown with black contours in the CTRW parameter maps. The CTRW parameter values of the solid tumor regions within the ROIs decreased progressively as the tumor grade increased.