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**COMPARING THE EFFECTS OF DIFFERENT PROCESSING PIPELINES ON
PRODUCING DIFFUSION METRICS**

Darshan Shimpi (Edward DiBella, PhD.)

UCAIR (Utah Center for Advanced Imaging Research)

Diffusion MRI is becoming increasingly popular due to its ability to non-invasively analyze and visualize areas of the brain, by tracking the motion of water molecules through tissue tracts. The technique has been used in the analysis of strokes, brain tumors, and white matter diseases, however, suffers from distortions which can alter the metrics utilized in clinical applications. Many post-processing methods, however, exist and are being increasingly utilized in pipeline sequences to generate results and data that are uncorrupted by distortion artifacts. With many pipelines being suggested and utilized, it is pertinent to find the most efficient pipelines and programs that can produce optimal image results.

In our work we compare the popularized Human Connectome Project Pipeline, to a recently developed pipeline from the University of Wisconsin-Madison, to test for efficiency in creating diffusion metrics. Testing was done by comparing the reproducibility of each pipeline in generating usable results from incomplete data subsets. Image quality metrics were then used to assess the difference between subset and full data parameter maps. The Wisconsin pipeline illustrated a 3% increase in structural similarity between subset maps and complete maps, along with other improved image metrics when compared to the HCP pipeline. The pipeline also processed data quicker than the HCP pipeline, suggesting a slightly more efficient approach in generating diffusion metrics for research purposes. Future experiments include creating our own pipeline to further increase efficiency, as well as developing deep learning networks to speed up post processing methods.