

DTI Working Group
Proposal to Harmonize DTI Measures for Genetic Analysis
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Diffusion tensor imaging (DTI) is a variant of standard brain magnetic resonance imaging (MRI) that is sensitive to fiber integrity and white matter microstructure. One of the most widely used and accepted DTI measures, fractional anisotropy (FA), evaluates the extent to which water diffusion is directionally constrained. FA, along with other DTI-based measures of fiber integrity has been consistently found to be highly heritable across several cohorts (CHIANG *et al.* 2009; JAHANSHAD *et al.* 2010a; JIN *et al.* 2011; KOCHUNOV *et al.* 2010; LEE *et al.* 2009).

DTI-based white matter abnormalities are widely reported in developmental and degenerative brain diseases (THOMASON and THOMPSON 2010) including Alzheimer's disease and mild cognitive impairment (FELLGIEBEL *et al.* 2004; NAGGARA *et al.* 2006), schizophrenia (CLARK *et al.* 2011), bipolar disorder (MAHON *et al.* 2010; SPROOTEN *et al.* 2011a), and autism (ALEXANDER *et al.* 2007; BARNEA-GORALY *et al.* 2004) to name a few.

Several specific genetic variants have also been associated with altered DTI measures throughout various parts of the white matter including *ApoE4* (BROWN *et al.* 2011; NIERENBERG *et al.* 2005; PERSSON *et al.* 2006; SMITH *et al.* 2008), *CLU* (BRASKIE *et al.* 2011), *BDNF* (CHIANG *et al.* 2011), *HFE* (JAHANSHAD *et al.* 2011), *ErbB4* (ZULIANI *et al.* 2011), *NRG1* (SPROOTEN *et al.* 2009), *DISC1* (SPROOTEN *et al.* 2011b), among others, making DTI-measures promising endophenotypes for identifying key genetic markers associated with structural differences in white matter pathways that may play a role in development and disease.

However, diffusion tensor images are subject to several sources of noise that can corrupt or bias measures of white matter integrity obtained, lead to uncertainties in measurements (ZHU *et al.* 2009) and cause additional sources of error when combining multisite data (ZHU *et al.* 2011). These can include spatial resolution of the images (ALEXANDER *et al.* 2001; JAHANSHAD *et al.* 2010b; KIM *et al.* 2006), the angular resolution (GIANNELLI *et al.* 2010; ZHAN *et al.* 2010), the ratio of the number of non-diffusion weighted gradients to diffusion-weighted gradients (JONES *et al.* 1999), the sampling scheme (HASAN *et al.* 2001; JONES 2004), the b-value(s) (CORREIA *et al.* 2009), among other sources of variations and artifacts. These parameters have even been shown to affect the correlations with disease progression in Multiple Sclerosis (LAGANA *et al.* 2010).

Without careful planning, combining data and identifying a reliable phenotype across different sites can involve biases, protocol effects, and sources of error beyond those seen in volumetric analysis of standard MRI.

We propose a DTI-working group for *phenotype harmonization* – to determine several measures computed from DTI images to serve as a phenotype for multi-site genetic analyses

- The working group is a methods development group to identify heritable, and reproducible, measures from diffusion images, with an easy-to-follow protocol that other sites can use

In response to substantial interest from David Glahn, Ian Deary, and Andrew McIntosh to develop image analysis protocols that could be applied across many sites to pool DTI datasets for genetic analysis, a preliminary teleconference was held to discuss overall interest, possible processing methods, initial phenotypes, and quality control considerations (November 17th, 2011).

The following people were on the call for the initial teleconference:

- UCLA: Paul Thompson, Neda Jahanshad, Omid Kohannim, Derrek Hibar, Jason Stein
- Edinburgh: Andrew McIntosh, Emma Sprooten
- Yale: David Glahn
- Brisbane: Margie Wright, Sarah Medland

To summarize the conclusions of the teleconference, the following main points were discussed:

- *Initial data:*
 - Queensland Twin Registry (PIs: Wright/Thompson) - ~700 Caucasian young adult (age 20-29) twins and siblings imaged with 27 directional gradients and ~550 of those also imaged with 94 directional high angular resolution diffusion imaging (HARDI)
 - ~840-850 large extended pedigrees of Mexican-American descent (PIs: Glahn/Blangero), wide age range imaged with 55 directional DTI
 - Lothian cohort (PI: I. Deary) LBC1936: >650 people scanned with DTI at 70 years of age imaged with 64 directional gradients
 - Bipolar Study (PI: Andrew McIntosh): Family based study of ~200 people (age 16-26) at high/low risk for BP based on family history scanned with 64 directional gradients.
- *Initial phenotypes to test:* It was decided to start cross-site comparisons by testing the stability of the following phenotypes, which have shown promise in terms of their heritability, reproducibility, and ease of measurement:
 - Full brain mean-FA from skeleton derived from the Tract-Based Spatial Statistics (SMITH *et al.* 2006) analysis
 - Emma Sprooten provided a TBSS protocol for the other sites to follow, if they have not already run TBSS
 - Mean FA from ROIs defined using the Johns Hopkins University white matter atlas (MORI *et al.* 2008)
 - Genu of the corpus callosum
 - Anterior internal capsule
 - The full corpus callosum (splenium, body and genu)

- Midsagittal corpus callosum mean FA, and mean diffusivity (MD)
- *Quality Control measures to be aware of:*
 - Intensity dropouts in images
 - Motion/ Eddy current or EPI distortions
 - Micro-strokes
 - Non-white matter regions artifactually skeletonized in TBSS

A full outline of minutes of the teleconference can be provided on request.

Parties interesting in joining the working group are welcome to contact **Neda Jahanshad** neda.jahanshad@loni.ucla.edu who will forward any related email to all group members.

In addition to a significant time commitment dedicated to discovery of stable and heritable phenotypes, we ask the following of any groups interested in joining:

- Diffusion tensor imaging and GWAS in a sizeable cohort, ideally 200+ individuals
- Images taken all with the same scanner/protocol and ideally at the same site.
- Images usable for test-retest reliability measures:
 - Either having subjects scanned twice, with a short time interval
 - Or subjects scanned multiple times at different scanning parameters

Interested parties with smaller datasets, or those unable to dedicate significant amounts of time and personnel to protocol development are welcome to sign-up for regular updates from the working group, and are encouraged to test any consensus protocol for feedback on ease of phenotype extraction, and reproducibility.

All groups interested in joining a full ENIGMA-DTI GWAS-MA (scheduled to start in a few months after protocol development efforts by the working group) are asked to email Neda (neda.jahanshad@loni.ucla.edu) with projected number of DTI scans, scanning parameters, and basic subject demographics

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