# Diffusion Kurtosis Imaging for the Human Connectome Project

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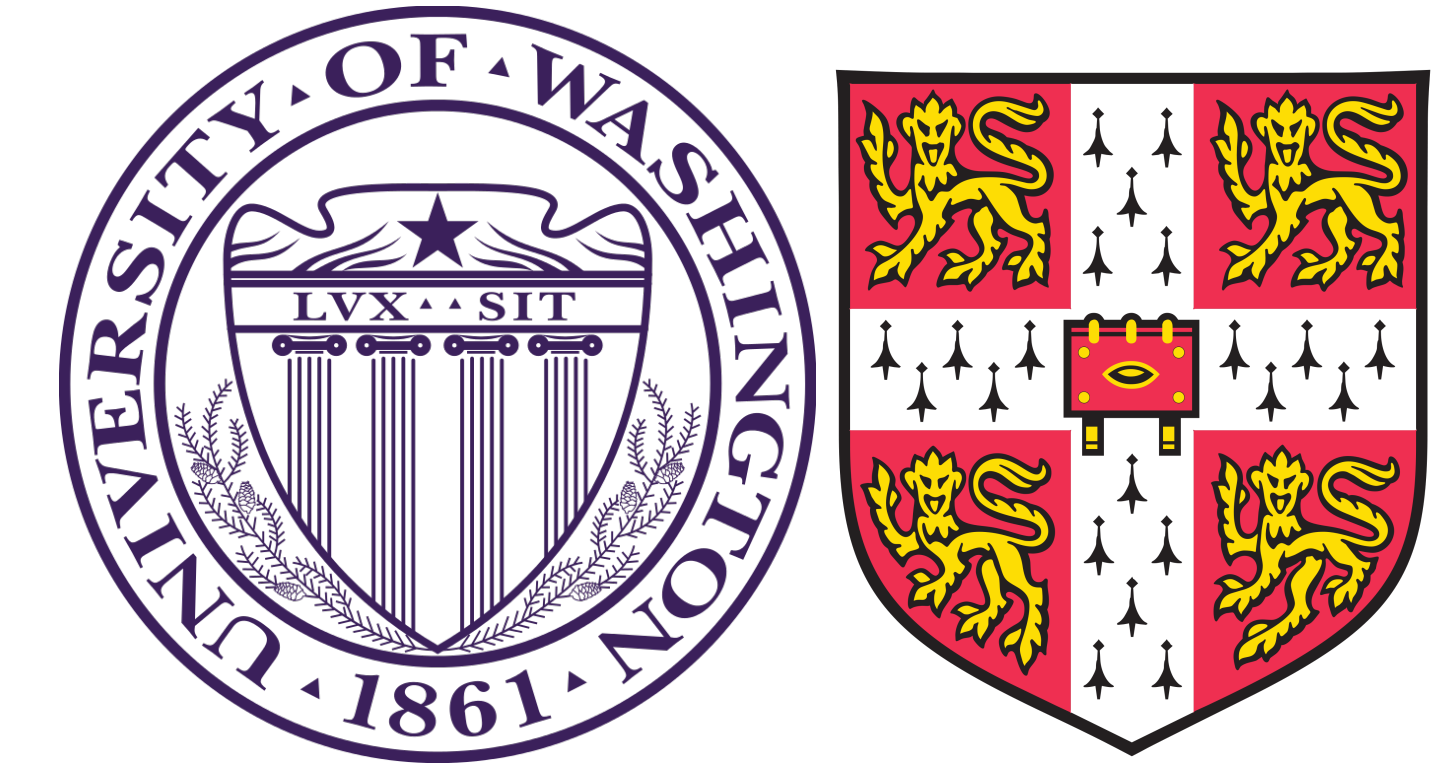
Introduction

The Human Connectome Project

Diffusion MRI (dMRI) measurements provide detailed information about human brain connectivity and microstructure *in vivo*. HCP is measuring high-quality multi-modal MRI data from 1,200 individuals and make these data publicly available [5]. It has already made measurements from approximately 900 subjects available through Amazon's Simple Storage Service (S3).

What model should we use to explain the data?

Diffusion Tensor Imaging (DTI): 6 parameters

Approximates diffusion in every voxel as a Gaussian distribution [1]:

$$S(\theta, b) = S_0 e^{\theta^T \mathbf{Q} \theta}$$

b is the **b-value**,
S_0 is the signal in the absence of diffusion gradient sensitization ($b = 0$)
Q is a positive-definite quadratic form:

$$\mathbf{D} = \begin{pmatrix} \sigma_{xx} & \sigma_{xy} & \sigma_{xz} \\ \sigma_{yx} & \sigma_{yy} & \sigma_{yz} \\ \sigma_{zx} & \sigma_{zy} & \sigma_{zz} \end{pmatrix}$$

Diffusion Kurtosis imaging (DKI): 21 parameters

DKI is an extension of DTI that accounts for non-Gaussian behavior in complex tissue, with many barriers to the diffusion process (cell membranes, myelin sheaths, etc.) [3]:

$$S(\theta, b) = S_0 e^{-bD(\theta) + \frac{1}{6} b^2 D(\theta)^2 K(\theta)}$$

$$D(\theta) = \sum_{i=1}^{3} \sum_{j=1}^{3} \theta_i \theta_j Q_{ij}$$

$$K(\theta) = \frac{MD^2}{D(\theta)^2} \sum_{i=1}^{3} \sum_{j=1}^{3} \sum_{k=1}^{3} \sum_{l=1}^{3} \theta_i \theta_j \theta_k \theta_l W_{ijkl}$$

W is a rank 4 tensor (3-by-3-by-3-by-3 matrix).

Diffusion Statistics

- Mean diffusivity (**MD**) characterizes the mean displacement of water molecules within a voxel.

- Fractional anisotropy (**FA**) characterizes the variance in diffusivity in different directions.

**Brain measurements that provide a close tie between brain tissue properties and behavior**.

Results

We compared DKI and DTI using *K-fold cross-validation*
We estimated model fit *accuracy* and model parameter *reliability*

Model accuracy

Cross-validated R^2: **A** Comparison of the full distribution in a single subject, and comparison of the median (dashed line) in all subjects for DKI (all b-values) and DTI (**B** all b-values, **C** only b=1,000 s/mm^2

**A**   **B**   **C**
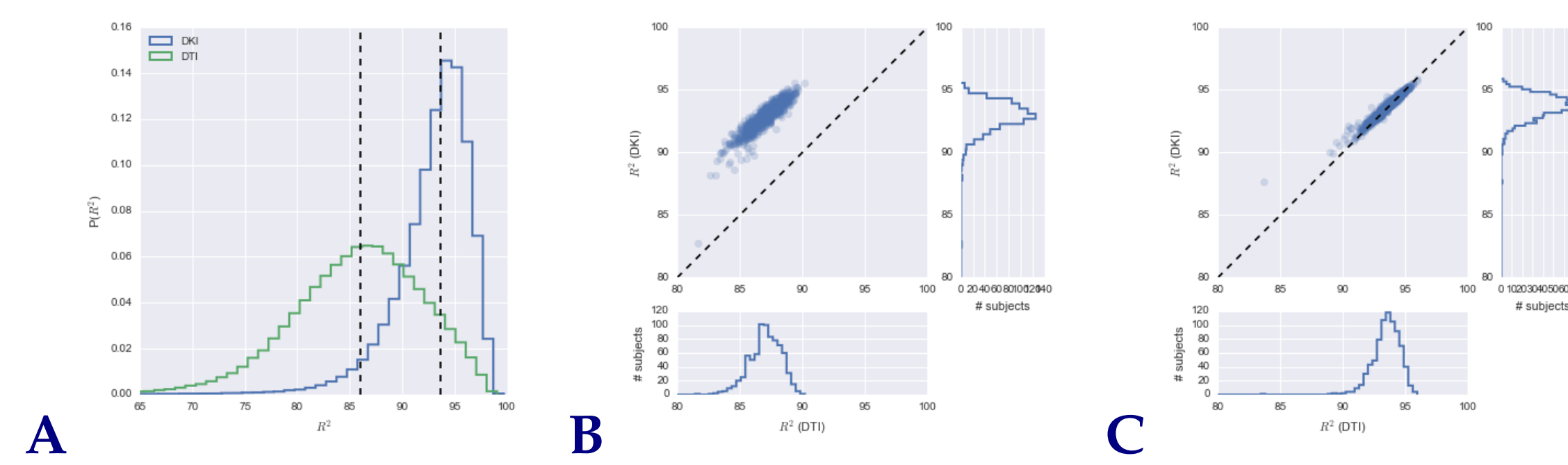
Parameter reliability

Parameter reliability is estimated by comparing diffusion-based statistics based on a difference in FA/MD between b=1000 and b=1000,2000 (DTI) or between b=1000,2000, b=1000,3000 (DKI). BIAS is the median difference between sub-samples VARIABILITY is the spread of differences (central 95% of the distribution)
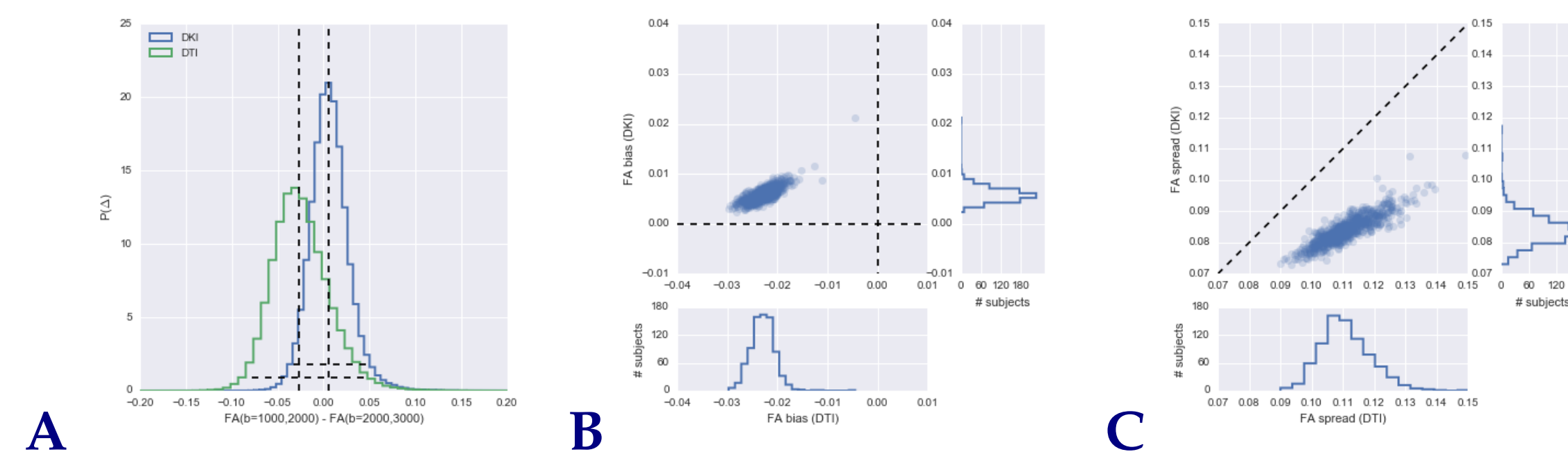
Mean diffusivity

A Single subject distributions. **B** Bias **C** Variability

A   **B**   **C**
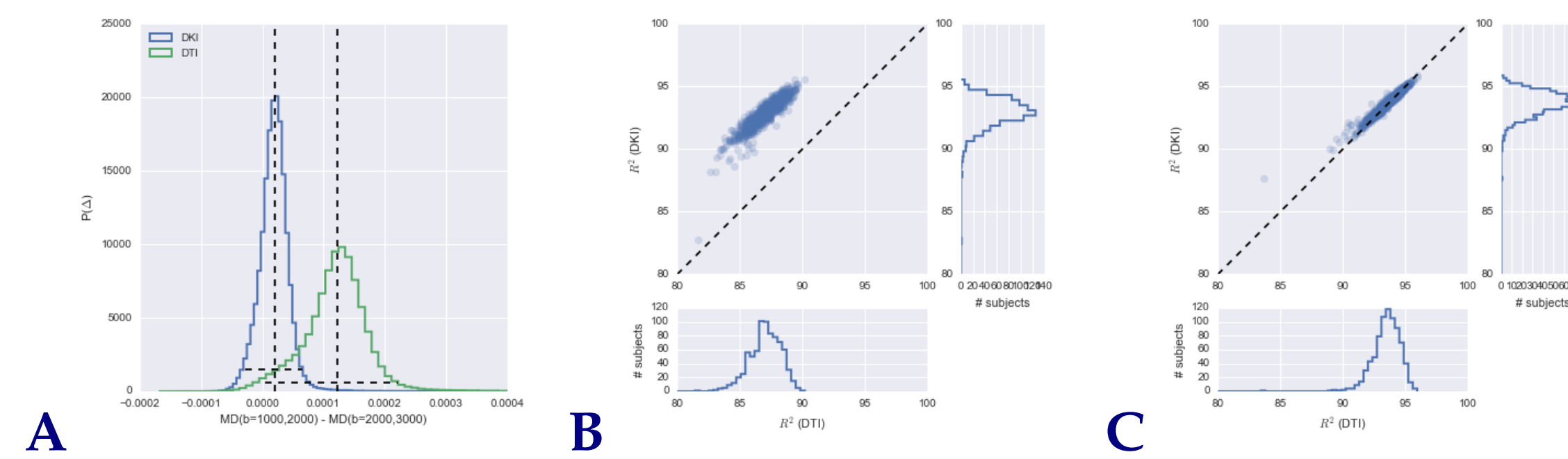
Fractional anisotropy

A Single subject distributions. **B** Bias **C** Variability

A   **B**   **C**

Materials and Methods

Data

Analysis

We used a 36-node Amazon Web Services compute cluster containing 36 nodes. AWS *r3.2xlarge* instances were used, optimized for memory-intensive applications: each instance has 8 vCPU, 61 GiB Memory and 160 GB SSD storage.
We used DTI and DKI implementations that are part of the DIPY open-source software library (http://dipy.org/) [2]. 5-fold cross-validation was implemented using DIPY's cross-validation module [4]
Computation was distributed using Apache Spark, an open-source parallel processing framework that coordinates computation across distributed clusters (http://spark.apache.org/). Because model-fitting requires large amounts of memory, each compute node ran one Spark worker.

Conclusions

- DKI more accurately fits the HCP data than DTI

- DKI statistics are more reliable than DTI statistics

- DKI has the additional benefit that it provides additional parameters that lend themselves to a richer biophysical interpretation of the signal.

References

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