QUANTITATIVE EVALUATION OF BIOPHYSICAL MODELS OF THE DIFFUSION WITH IN VIVO DATA BY ASSESSMENT OF THE GENERALIZATION ERROR

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PURPOSE.

- Biophysical models: describe the MR signal formation with a model whose parameters reflect the underlying biophysical mechanisms.
- Of crucial interest to characterize and compare tissue properties.
  - In disease: in vivo biomarkers for diagnosis, prognosis, tailored intervention and evaluation of success of therapy.
  - To study normal brain development.
- How to quantitatively evaluate various generative models? An open question.

Common approach

- Estimation of the generalization error:
  - Leave-one-out: low bias but high variance.
  - K-fold cross validation: lower variance but higher bias.
  - Better approach:
    - Bayesian Information Criterion (BIC)
      - Akaike Information Criterion (AIC)
        - Asymptotically optimal (Unlike BIC).
    - But F is unknown

HYPOTHESIS: A BIOPHYSICAL MODEL THAT WELL CAPTURES THE UNDERLYING BIOPHYSICAL MECHANISMS OUGHT TO ACCURATELY PREDICT THE SIGNAL FOR NEW GRADIENT DIRECTIONS AND STRENGTHS.

ASSESSMENT OF THE GENERALIZATION ERROR.

RESULTS

- We evaluated five biophysical model of the diffusion.
- CUSP65 acquisition - FOV=240mm, matrix-size=128x128, 68 slices, resolution=1.8x1.8x2mm³, TE=78ms, TR=10.1s, ~12min acquisition time.
  - Provides a large number of different b-values between 1000s/mm² and 3000s/mm² with low TE and high SNR.
- Generalization error estimated with B=300 bootstrap iterations.

- Fig.a - DTI is the worst predictor of the diffusion signal.
- Fig.b - NODDI provides a lower generalization error in regions of crossing and close to the cortex because models the fascicle dispersion in each voxel and accounts for freely diffusing water.
- Fig.c - 1T+iso better predicts the signal than NODDI. This is likely because a number of parameters are fixed in NODDI (fixed parallel diffusivity, no radial diffusivity).
- Fig.d - Accounting for the heterogeneity of each compartment (DIAMOND) slightly improves the generalization error in regions of crossings.
- Fig.e - Accounting for each fascicle in each voxel and accounting for the compartment heterogeneity leads to the smallest generalization error.

CONCLUSION

- Novel framework to achieve quantitative evaluation of biophysical models of the diffusion with in-vivo data.
- Characterizes how well each model predicts unseen data.
- Identify the model that best captures the underlying biophysical mechanisms for the data at hand.