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Deep learning microstructure estimation of developing brains from diffusion MRI: a newborn and fetal study

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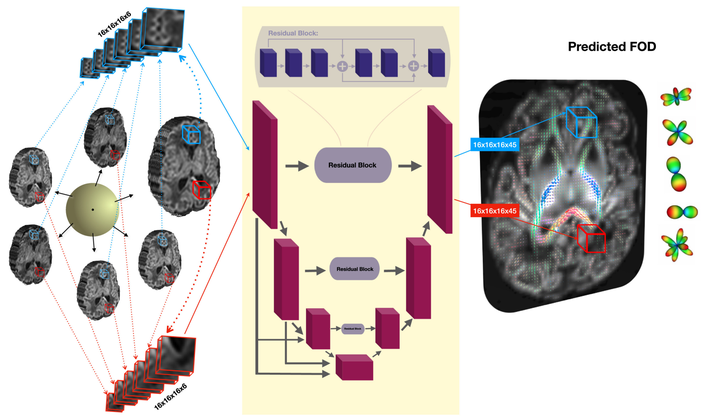
Context & Summary

- Diffusion MRI (dMRI) is the tool of reference for studying brain white matter in vivo and non-invasively:
  - Large number of measurements required for state-of-the-art models[1] to estimate microstructure with fiber orientation distribution functions (FODs)
  - Few measurements available for newborn and fetal populations because of acquisition time constraints
- ***Aim:*** Circumvent the problem using deep learning on high quality datasets (i.e. developing human connectome project, dHCP[2]) with few samples (6-12)
- Validated results on research (dHCP) and clinical datasets (Boston Children's Hospital) of newborns and fetuses, with histology.

Materials & Methods

1. Newborn network (DL_n)

- Trained on 16^3 patches of spherical harmonics (SH) representation of 6 b0-normalized uniform[3] diffusion samples to predict 45 SH FOD coefficients from multi-shell multi-tissue constrained spherical deconvolution (MSMT-CSD)[1] using 300 multi-shell measurements
- *Trained* on 109 **dHCP** subjects and *tested* on 320 **dHCP** quantitatively and 15 **BCH** qualitatively ([27-45] weeks of b=1000 s/mm^2).



The proposed framework to predict FODs in the SH domain (SH-L_{max} order 8). The network takes 3D input patches from 6 diffusion measurements and outputs patches of SH coefficients.

2. Preterm network (DL_f)

- Similar to DL_n in training but using 12 b0-normalized directions
- *Trained* on 58 pre-term ([27, 38] weeks, b=400 s/mm^2) **dHCP** subjects
- *Tested* on 11 **BCH** fetal subjects ([24,39] gestational weeks, b=500 s/mm^2)

3. Evaluation

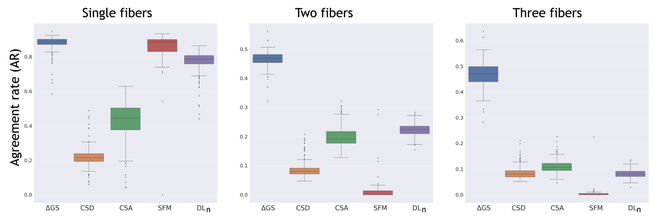
- Comparison with three classical methods (Constrained spherical Deconvolution, CSD[4], Constrained Solid Angle, CSA[5] and Sparse Fascicle Model, SFM[6]) and two deep learning methods (Multilayer Perceptron, MLP; CTtrack)[7,8] in the agreement rate in the number of estimated fibers, the angular error and the apparent fiber density[9]
- Splitting the ground truth into two disjoint gold standard subsets of 150 measurements and computing within-ground truth consistency (ΔGS)

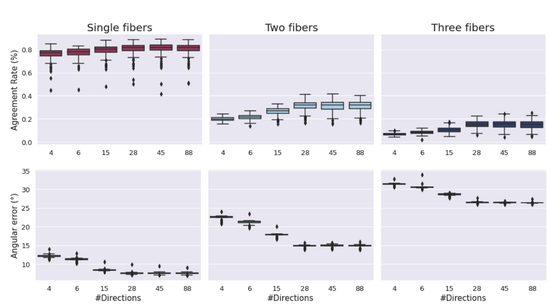
BCH dHCP

Results

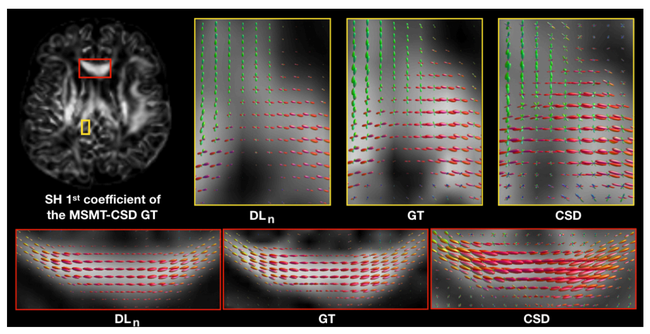
1. Newborns of dHCP

- Low agreement rate within the ground truth for multiple fibers
- Levels on par or superior performance of DL_n to state-of-the-art classical methods using significantly less (~21-43 times) measurements
- Lowest error for our method in approximating the apparent fiber density (AFD)
- No notable improvement above 28 directions





Method	b-values (s/mm^2)	M	Angular error		
			Single fibers	Two fibers	Three fibers
DL_n	$\{0, 1000\}$	7	10°(±0.2)	20°(±0.3)	30°(±0.1)
CSD	$\{0, 2600\}$	148	7°(±0.2)	16°(±0.3)	27°(±0.1)
CSA	$\{0, 400, 1000, 2600\}$	300	43°(±0.3)	37°(±0.1)	35°(±0.1)
SFM	$\{0, 400, 1000, 2600\}$	300	42°(±0.6)	37°(±2.0)	35°(±4.0)
ΔGS	$\{0, 400, 1000, 2600\}$	150	6°(±0.1)	14°(±0.1)	25°(±0.1)

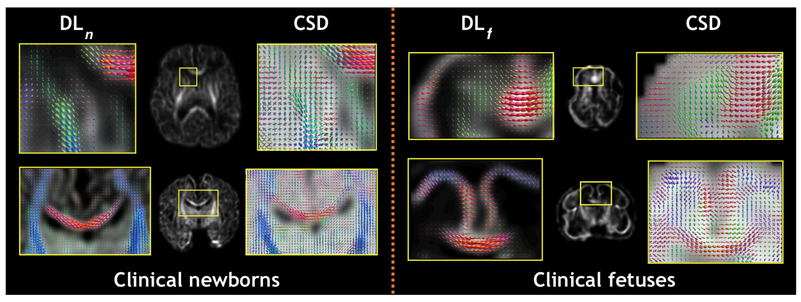


Qualitative comparison between the deep learning method DL_n, the MSMT-CSD ground truth and CSD in two brain regions of a newborn dHCP subject.

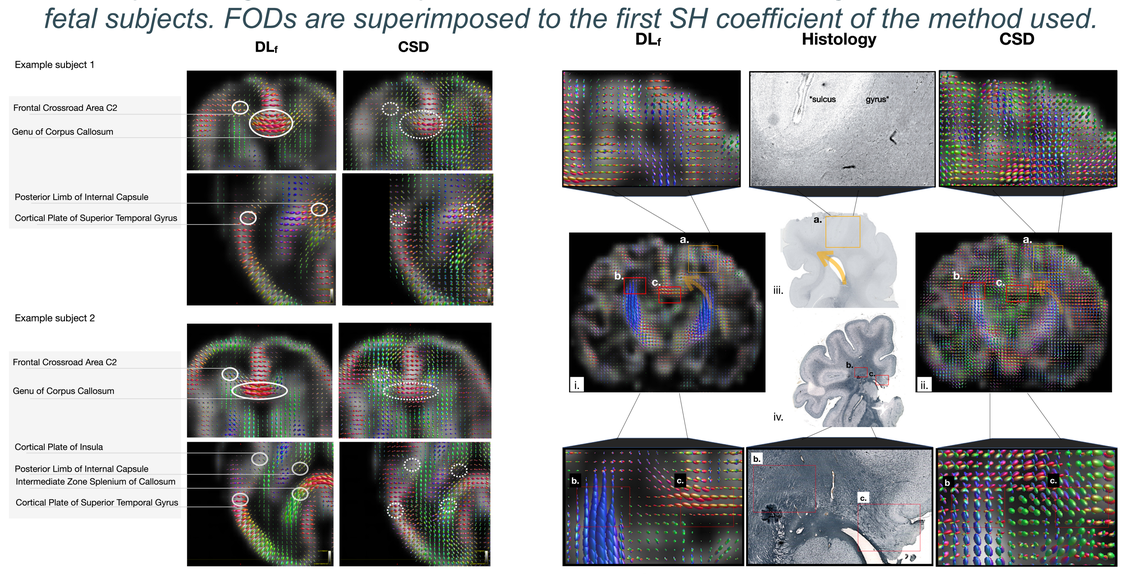
- DL_n outperformance over the voxel-wise baseline deep learning methods [7,8]

Method	b-values (s/mm^2)	M	Agreement rate (Angular error)			AFD error
			Single fibers	Two fibers	Three fibers	
DL_n	$\{0, 1000\}$	7	77.5% (10°)	22.2% (20°)	8.0% (30°)	0.178 (±0. 083)
MLP	$\{0, 1000\}$	7	74% (16°)	15.5% (28°)	7.7% (32°)	0.398 (±0. 104)
CTtrack	$\{0, 1000\}$	7	74.5% (16°)	16.8% (25°)	4.4% (32°)	0.263 (±0. 105)

2. Clinical newborns and fetuses of BCH



The deep learning method compared to CSD in different brain regions for newborn and fetal subjects. FODs are superimposed to the first SH coefficient of the method used.



- The model DL_n generalized to clinical newborns' data despite the scanner and protocol domain shifts. Similarly to DL_f to the clinical fetal data despite the anatomy, scanner and protocol domain shifts
- Compared to CSD, low amplitude FODs for the deep learning models in isotropic regions, where white matter fiber bundles are not expected

Conclusion

- Deep learning can successfully predict FODs using a small number of measurements by leveraging neighbouring information and high quality datasets. This has the potential of contributing to scanning time reduction with more than an order of magnitude and can highly benefit anatomical reconstruction of non-cooperative cohorts such as neonates or fetuses [10].

REFERENCES [1] Jeurissen et al., Neuroimage 2014; **[2]** Hutter et al., MRM 2018; **[3]** Skare et al., JMR 2022; **[4]** Tournier et al., Neuroimage 2004; **[5]** Aganj et al., MRM 2010; **[6]** Rokem et al., PloS one 2015; **[7]** Karimi et al., Neuroimage 2021; **[8]** Hosseini et al., Neuroinformatics 2022; **[9]** Raffelt et al., Neuroimage 2012; **[10]** Kebiri et al., Medical Image Analysis 2024.

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