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C8: Fast, fully automated MRI-based measurement of the human corpus callosum

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Mind & Brain at UC Davis

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Abstract

C8 measures midsagittal cross-sectional thickness and area of the human corpus callosum from high-resolution T1 in vivo MR images that have been preprocessed using affine normalization and tissue segmentation [1].

Areas are computed for geometrically defined callosal compartments [2]. Thickness is sampled along a median line within the corpus callosum (CC) according to three methods of spacing.

The performance was tested and showed C8 (nitrc.org/projects/c8c8) producing consistent, reliable callosal measurement estimates comparable to those from manually-segmented callosa and from the literature.

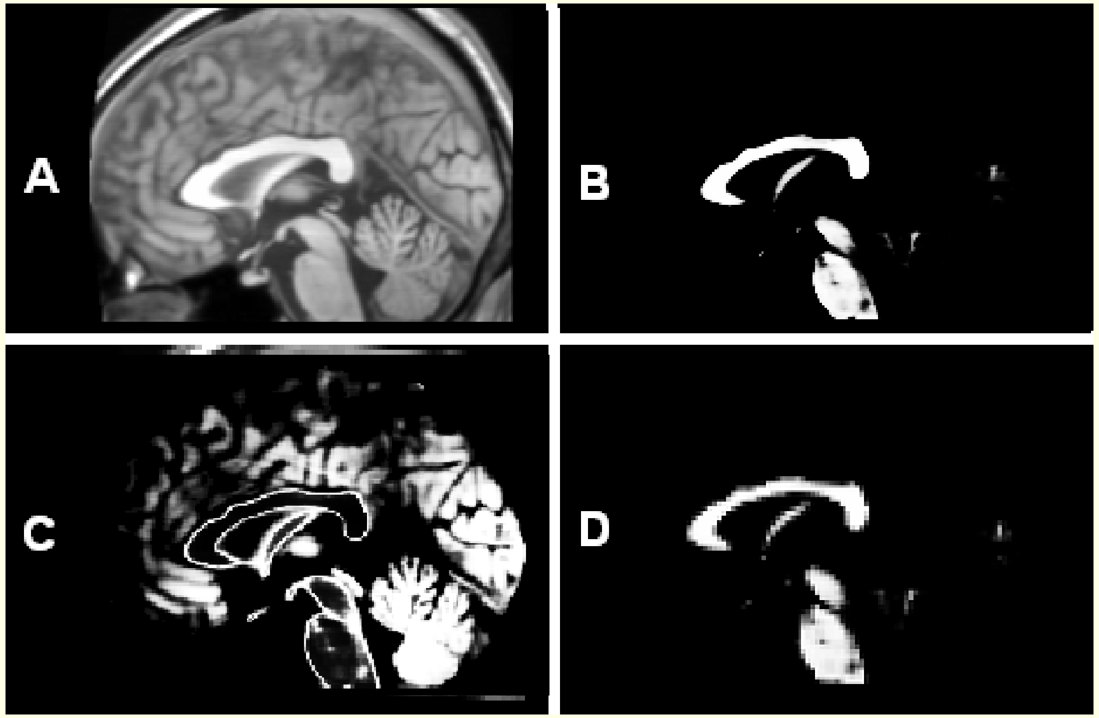
C8 was applied to 1231 FCP [4] public database images to explore demographic, CC, and overall brain size relationships. C8 was also applied to the OASIS [3] database to explore specific callosal/cortical correlations.

Preprocessing

<u>Preprocessing</u>: Standard tissue segmentation and affine normalization (SPM, FSL, …) of T1 images.

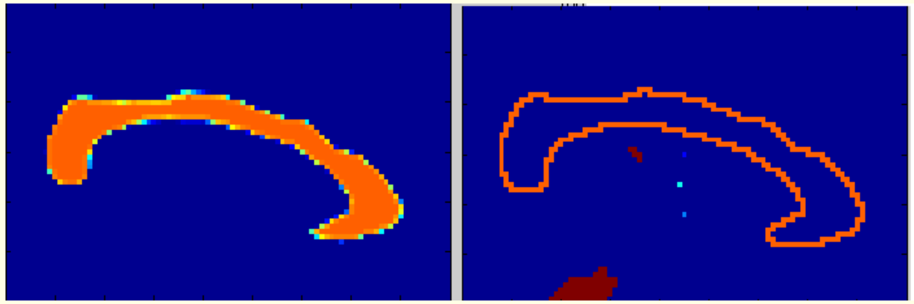
Useful to have high quality (in-plane) whole brain T1 images and high quality segmentation (extensive sampling, good intensity normalization).

Quality of normalization is not important (rotation & translation is adequate, even manual).



C8 Callosal Identification

1) Find CC by probing WM from superior side, then grow cluster(s) based on threshold.
2) Identify boundary of cluster(s)
3) Remove Fornix
    a) Remove WM not in some medial-lateral path
    b) Eliminate isolated clusters
    c) Remove inferior “branches” of main cluster
4) Recompute for several para-midsaggital slices

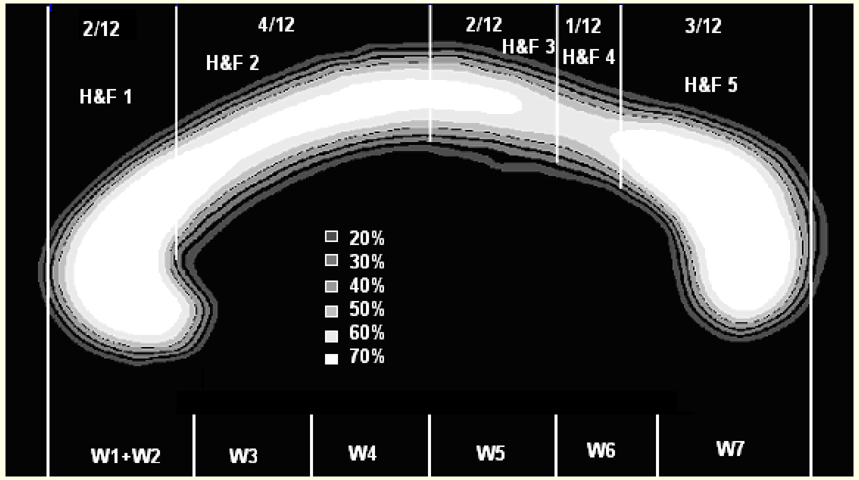


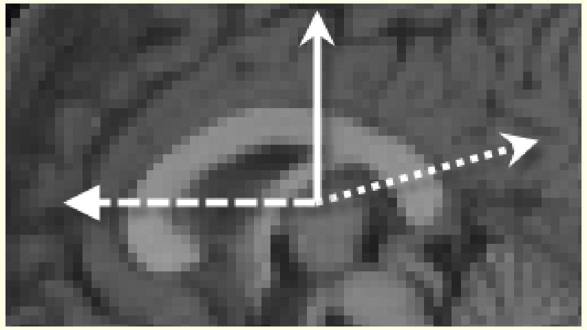
C8 Callosal Parcellation

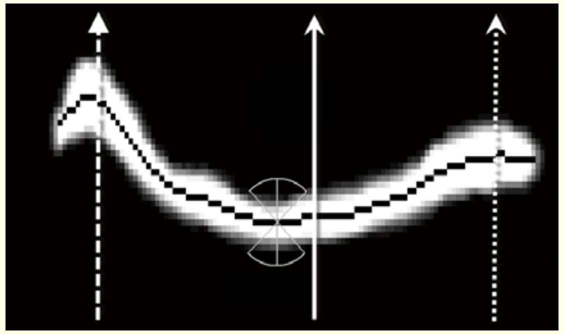
Break up CC lengthwise into geometric compartments [1]: Witelson and Hofer & Frahm.

“Straighten” CC by using central pivot and defining equal-angularly spaced lines (3 shown) for resampling

Define mesial line as the weighted median location of the WM segmentation values (smoothed by using surrounding locations) on the straightened MSCC WM.





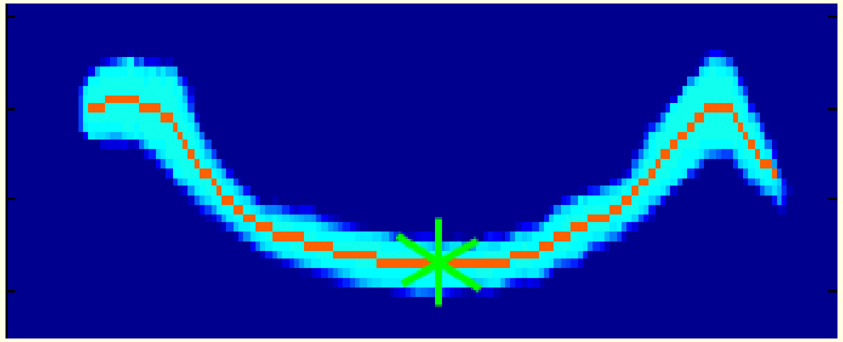


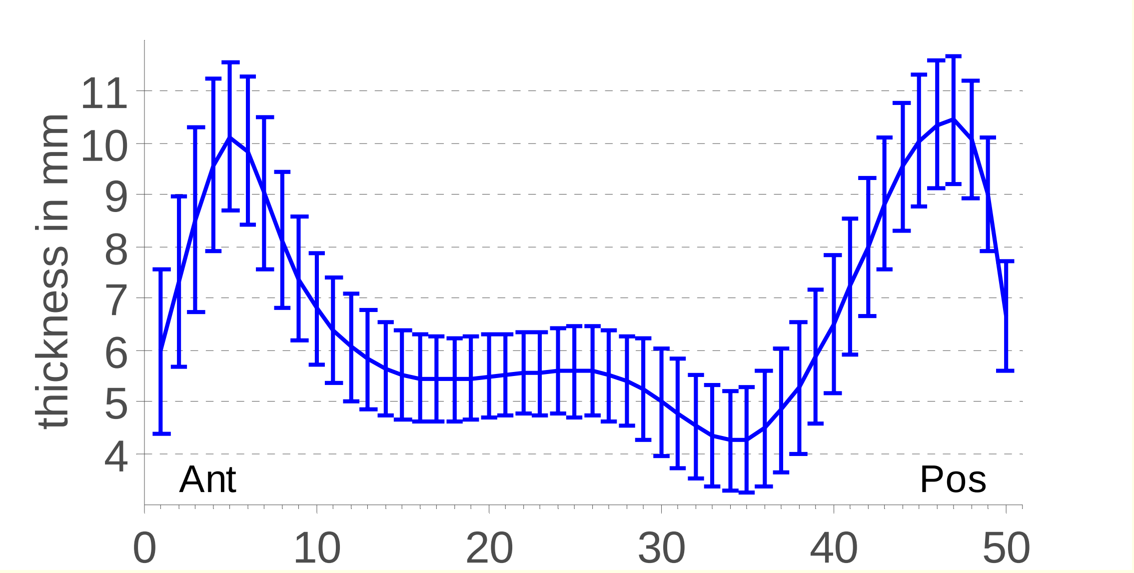
C8 Callosal Measurements

Thicknesses defined as shortest line segment WM sums passing through a medial line point.

Areas defined as total sums of WM segmentation values within geometric partitions.

Values computed in MNI space and recalculated for native space by inverting affine transformation for each 2D area or line segment.





OASIS-152 [3] Thickness Means

Area: Comparison to Literature

Study		W1+W2+W3	W4+W5	W6	W7
OASIS database analysis (n=152, age: 23.2 ± 4.2) using C8	2 mm	240 ± 36 mm^2	128 ± 25 mm^2	49 ± 13 mm^2	162 ± 30 mm^2
	1 mm	243 ± 36 mm^2	130 ± 21 mm^2	50 ± 12 mm^2	166 ± 23 mm^2
(Jäncke et al., 1997) n=54, age 27.8 ± 5.2		274 ± 34 mm^2	162 ± 24 mm^2	66 ±12 mm^2	186 ± 31 mm^2
(Bermudez and Zatorre, 2001) n=136, age: 24.6 ± 4.8		294 ± 34 mm^2	169 ± 12 mm^2	67 ± 14 mm^2	190 ± 27 mm^2
(Luders et al., 2003) n=30, age: 23.3 ± 3.9		254 ± 38 mm^2	149 ± 11 mm^2	57 ± 13 mm^2	191 ± 29 mm^2
(Luders et al., 2006a) n=60, age: 23.9 ± 4.7		235 ± 39 mm^2	117 ± 14 mm^2	44 ± 11 mm^2	177 ± 34 mm^2
(John et al., 2008) n=23, age=30.1 ± 5.1		260 ± 37 mm^2	151 ± 25 mm^2	252 ± 29 mm^2	

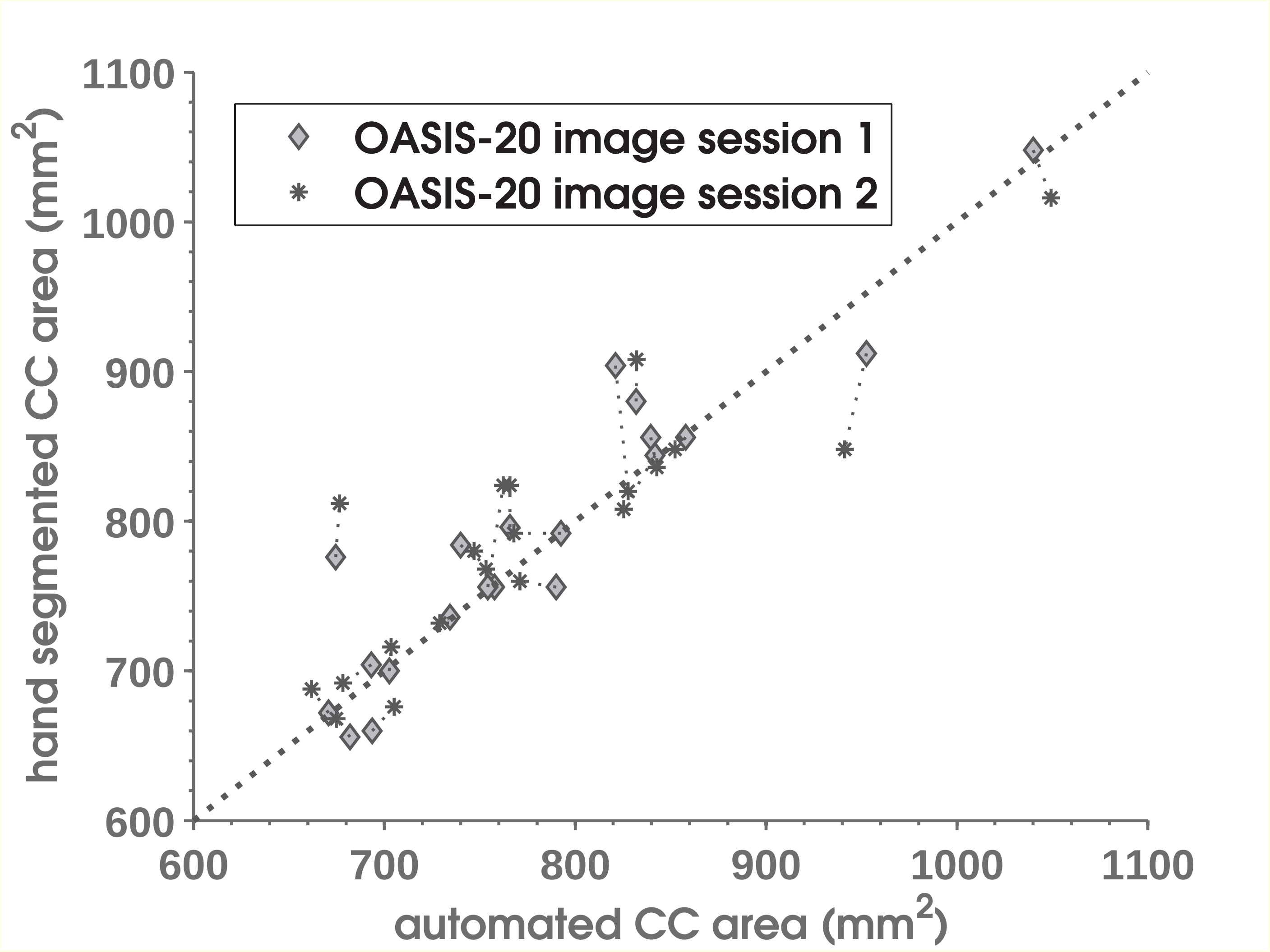
Corpus Callosum Witelson partition area measurements (mean ± std dev) of young, normals for OASIS-152 vs. previous similar populations.

Area: Comparison to Hand Segmentation

OASIS-20 are 20 OASIS young normals who underwent repeated scans.

Hand-segmenting done using MRIcron’s ROI tool, on anonymized images prior to C8 computations.

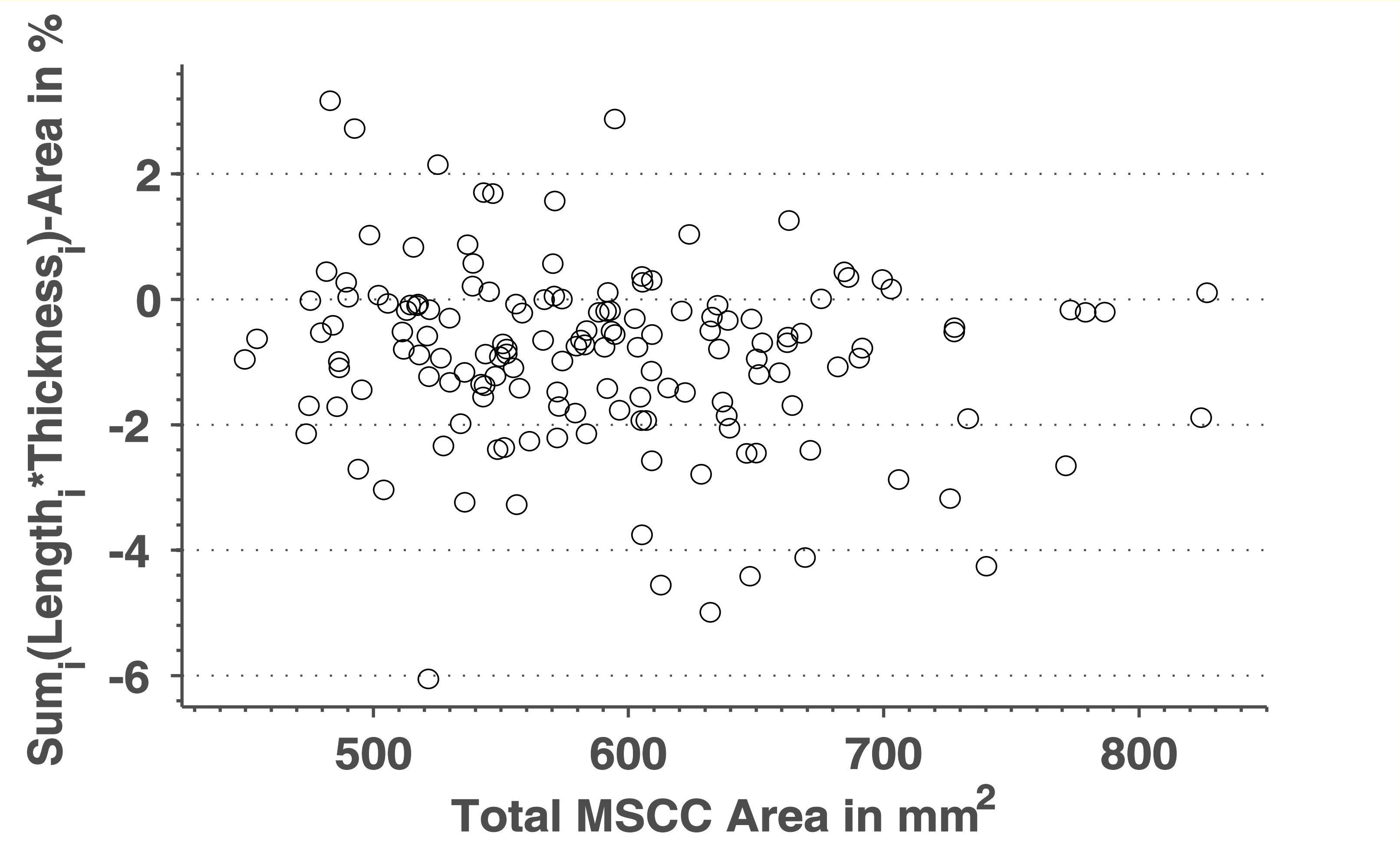
Repeat scans connected by dotted lines.



Area/Thickness Consistency

Total area of the CC compares well with the sum of local areas, i.e. the sum of medial line local lengths x local thicknesses.

Slight underestimate of thicknesses, with a small total area correlation with the discrepancy.



Repeated Scans and Robustness

OASIS-20 repeated scan mean absolute differences for both thickness and area using segmentations of two voxel sizes.

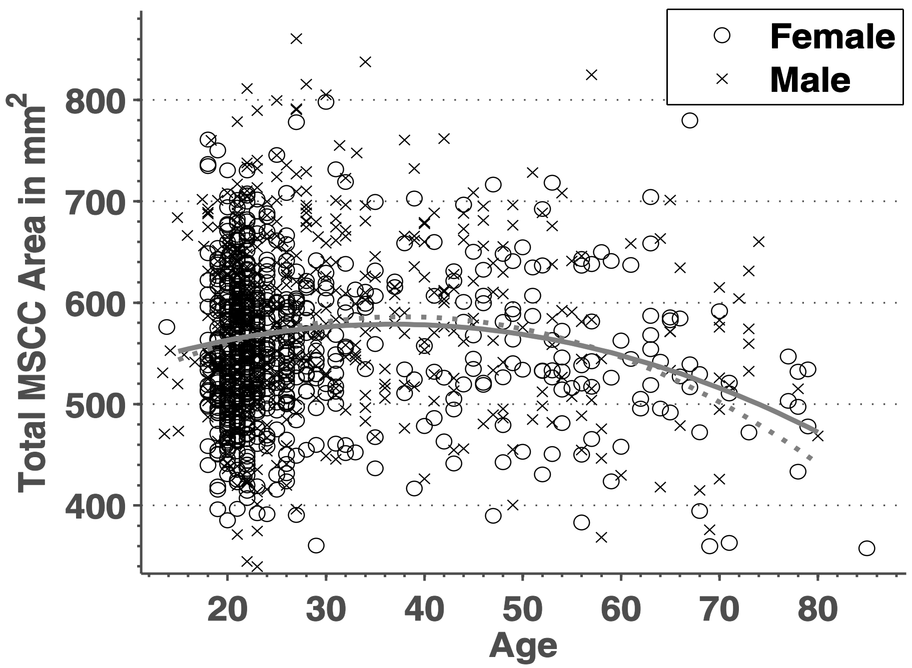
		H&F 1	H&F 2	H&F 3	H&F 4	H&F 5
Thickness variation	1 mm	4.2%	2.0%	4.2%	4.0%	3.9%
	2 mm	4.3%	2.5%	6.3%	6.7%	5.1%
Area variation	1 mm	5.3%	4.9%	5.8%	6.2%	1.4%
	2 mm	6.5%	6.6%	6.1%	4.8%	2.7%

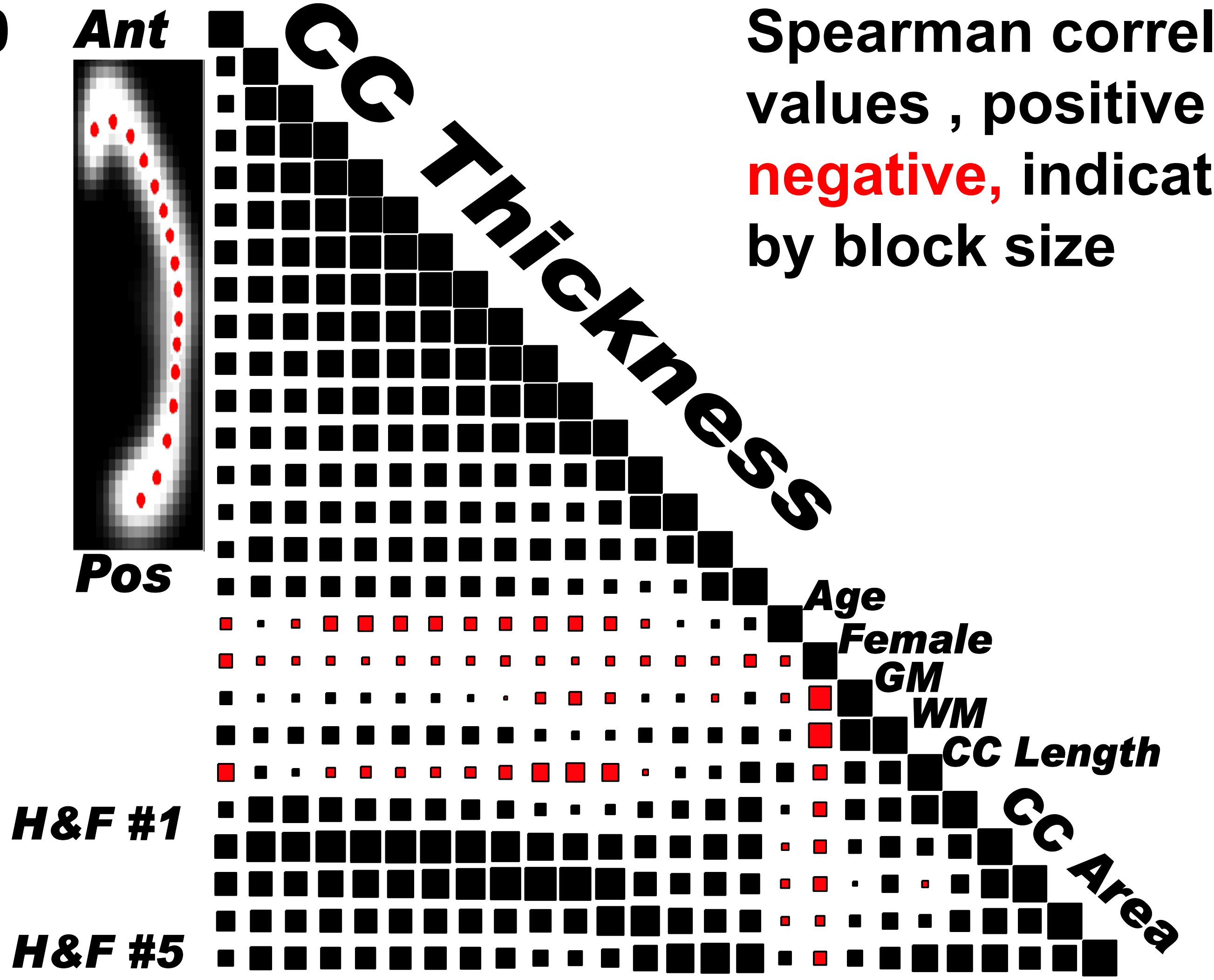
Segmentation Algorithm		H&F1	H&F2	H&F3	H&F4	H&F5
SPM5 *spm_segment*	mm^2	149 ± 23	163 ± 29	61 ± 12	28 ± 7	188 ± 27
	mm	6.19 ± 0.96	5.52 ± 0.73	4.99 ± 0.94	4.25 ± 0.96	6.65 ± 1.38
EMS (MRF) *ems_segment*	mm^2	144 ± 22	146 ± 27	55 ± 11	25 ± 7	178 ± 26
	mm	5.58 ± 0.92	5.06 ± 0.72	4.54 ± 0.91	3.87 ± 0.94	6.11 ± 1.41
FreeSurfer *mri_segment*	mm^2	145 ± 25	161 ± 34	62 ± 14	29 ± 9	188 ± 32
	mm	6.06 ± 0.96	5.43 ± 0.80	5.09 ± 1.00	4.38 ± 1.11	6.67 ± 1.40

OASIS-152 young normal mean areas and thicknesses using different segmentation algorithms. Hofer & Frahm partitions.

Basic callosal relationships

1231 T1 images from the 1000 Functional Connectome Project image database [4] were used to study demographic, brain size, and callosal, relationships.

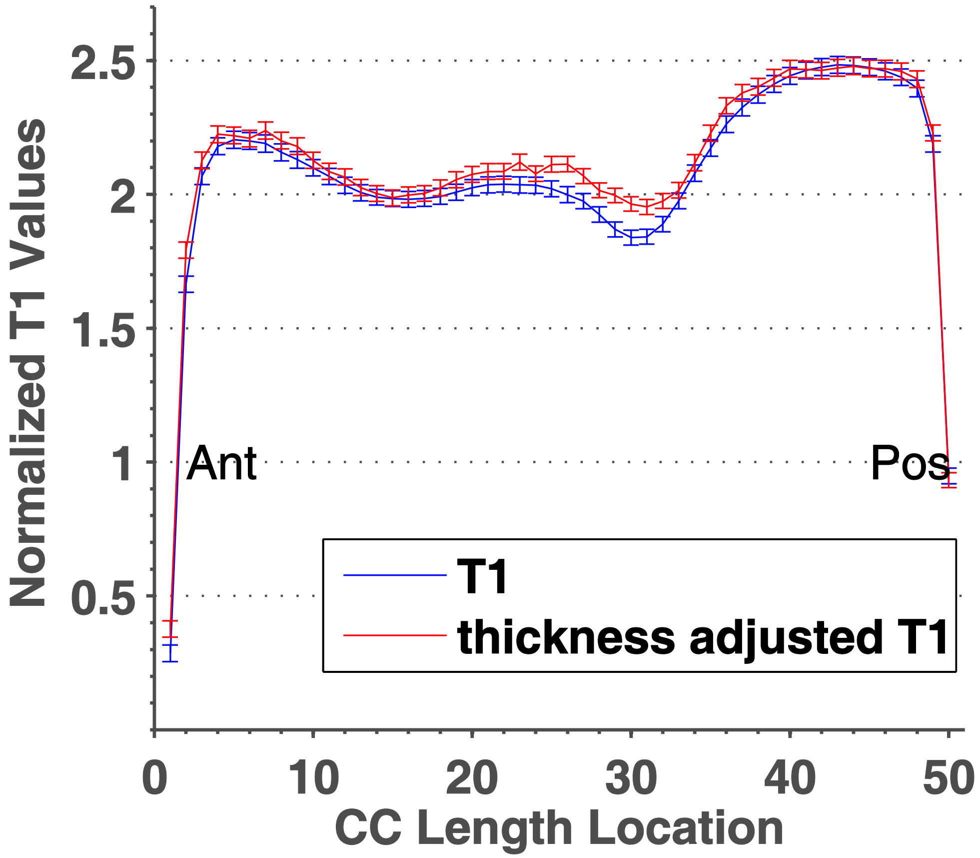




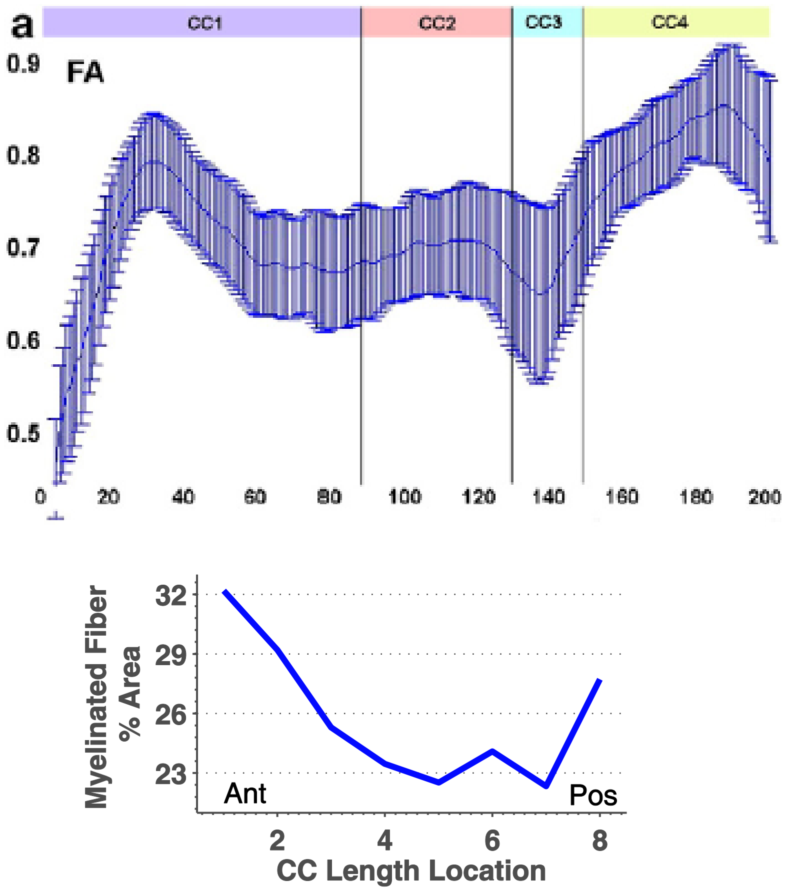
Spearman correlation values , positive and negative, indicated by block size

Normalized T1 Values

1231 images from the 1000 Functional Connectome Project image database [4] had T1 image values sampled along the median line at 50 points, normalized by T1 values in lateral ventricle CSF, and adjusted by scanner.



T1 values were adjusted by thickness separately at each point along the CC to control for susceptibility.

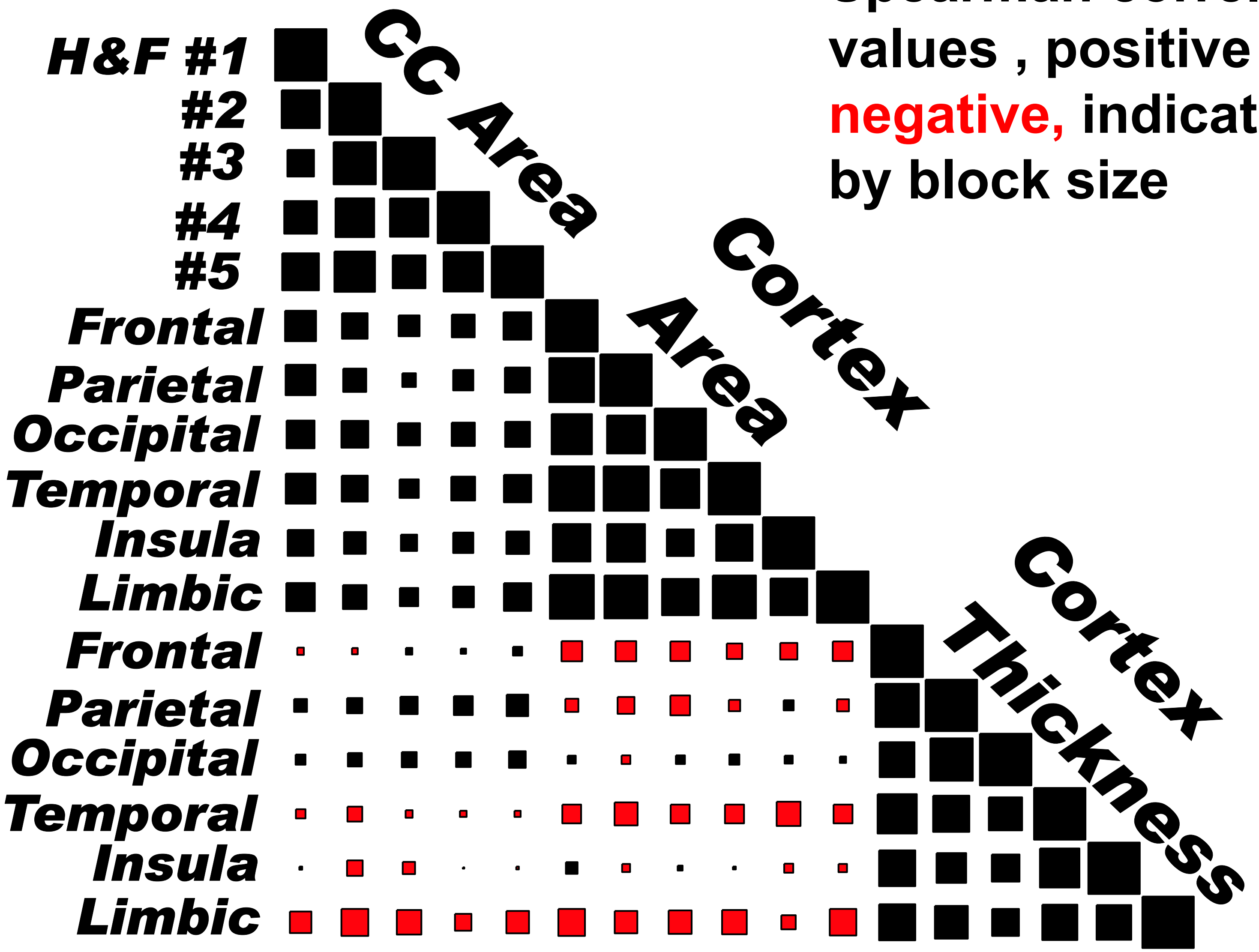


Top: FA values along the MSCC from [5].
Bottom: Postmortem myelination [5]

Callosal/Cortical Correlations

138 young normal high-res T1s (1.5T, age mean 26, 67 F) added to 152 OASIS young normals (3T, age mean 23, 82 F), processed using FreeSurfer for lobar cortical areas and cortical thicknesses.

Correlations have age, gender, and scanner partialed out.



Spearman correlation values , positive and negative, indicated by block size

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[1] Herron et al., SfN 2010, San Diego (www.ebire.org/hcnlab).

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