Human cortical areas are sparsely connected: Combining histology with diffusion MRI to estimate the absolute number of axons

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Abstract The tracts between cortical areas are conceived as playing a central role in cortical
information processing, but their actual numbers have never been determined. Here we estimate the
absolute number of axons linking cortical areas from a whole-cortex diffusion-MRI (dMRI) connectome,
calibrated using the histologically-measured callosal fiber density. Median connectivity is estimated as
~2,700 axons between cortical areas within-hemisphere and ~540 axons interhemispherically, with
axons connecting functionally-related areas surprisingly sparse. These results challenge models that
require direct transmission of detailed information between cortical areas, rather suggesting that
cortical integration mainly relies on the extremely dense local connections.

Introduction

The major tracts connecting cortical areas have long been central to models of information-processing

in the human brain [1]. Such models have been refined and applied to development and disease with

the advent of diffusion-MRI or dMRI, [2]. However, dMRI only provides *relative* connectivity, not the

absolute number of axons. Relative connectivity is very useful in many circumstances but more

constraints would be possible if the absolute number of axons connecting different cortical areas

could be estimated. We find that routinely observed widespread functional synchronization belies a

surprising small absolute number of long range axons connecting functionally-related areas.

Materials and Methods

The basic principle of our method is very simple. Given a dMRI-based measure of total

interhemispheric connectivity in arbitrary units and the physical number of axons traversing the corpus

callosum, the conversion factor between the two can be obtained by dividing the first by the second.

Specifically, we started with the total interhemispheric tractography strength reported in our dMRI

connectome of the Human Connectome Project (HCP) cohort [3]. For each individual, the cross-

sectional area of the corpus callosum was obtained using the standard FreeSurfer structural MRI

pipeline [4]. Multiplying this number by a histologically ascertained callosal fiber density [5] yields an

estimate of the number of axons traversing an individual's corpus callosum. Dividing this count by

individuals' interhemispheric dMRI streamline value yields the conversion ratio from the arbitrarily-

scaled dMRI metric to the absolute number of axons. Note that this procedure does not at all depend

on the scale of the dMRI metric, requiring only that it be proportional to absolute number of fibers.

This proportionality has been observed in a comparison of dMRI and retrograde tracing in macaques

[6]. Therefore, while the ratio itself is study-specific, the procedure can be applied to any dMRI

tractography method or parameter set. It only requires that the dMRI method return a continuous

distribution of connectivity values and have reasonably similar sensitivity to callosal and ipsilateral fiber

tracts. For detailed methodology, see S1 Appendix: Extended Methods.

Results

Our previous dMRI study [3] includes estimated tractography streamlines among all 360 parcels of the

HCP-MMP1.0 atlas [7] for each of the 1,065 individuals in the HCP dMRI cohort. The sum connectivity

between the 180 left hemisphere cortical parcels and the 180 right (180^2 parcel pairs) constitutes the

total callosal connectivity, on average 1.25x10^8 streamlines. Comparing linear regressions of distance-

matched log-transformed streamlines, we found no difference between the slope or intercept of inter-

and intrahemispheric connections; within the common distance domain a paired r-test showed no

difference in correlation, p = 0.58. Based on our assumed fiber density of 1.6x10^5 axons/mm^2 [5] and

measured callosal cross-sectional area (mean = 689.45mm^2), we estimate this cohort to have 1.1x10^8

callosal fibers on average. The mean quotient between these two quantities is 0.87 axons-per-

streamline, a ratio specific to the dMRI methodology and parameters used.

Applying the conversion factor to the inter-parcel connectivity from our prior study yields an

estimate of the absolute number of axons connecting different cortical areas (*Figure 1A*), 1.05x10^9

axons in total. Axons are approximately log-normally distributed among non-adjacent parcel pairs,

with adjacent pairs having disproportionally high axon counts (*Figure 1B*). The total count of a parcel's

axons to or from all other areas is much less variable when normalized by the parcel's area (*Figure 1*

D,E). Multiplying the total number of fibers by the effective fiber cross-sectional area (the inverse

callosal packing density, 6.2×10^{-6} mm^2/axon) yields 6.6×10^3 mm^2 of cortex or 3.7% of the total white-

gray interface. Note that the effective axonal area includes myelin, supporting cells and intercellular

space in addition to the axon proper. The percent of fiber-allocated cortical area is quite similar to the

~4% of total cortical fibers Shülz and Braitenburg estimated [8] are contained in the corpus callosum

and long fascicles. The remaining ~95% of the cortical gray-white interface area is likely occupied by

the short range U-fiber system which is difficult to assess with dMRI.

The volume of hemispheric white matter (WM) occupied by axons between cortical parcels is equal

to the sum of all axons' lengths multiplied by their cross-sectional areas. The mean fiber tract lengths of

connections were taken from our prior dMRI analysis [3]. For the effective cross-sectional area of axons

we again used the inverse of the callosal fiber density [5]. So calculated, the volume occupied by

cortico-cortical and hippocampo-cortical fibers is 4.3×10^5 mm^3, or about 96% of the total MRI-assessed

WM volume. This implies that the number of long-range fibers cannot be larger than our estimate

unless the callosal fiber density measurement is mistakenly low. The remaining WM volume may seem

insufficient for connections with subcortical structures. However, the major subcortical structures

known to communicate with the cortex (thalamus, amygdala, striatum, nucleus basalis, locus coeruleus,

etc.) contain, in sum, less than 1% of the number of cortical neurons [9,10]. Even under the unlikely

assumption that all excitatory thalamic neurons project to all cortical parcels proportionally to their

area, their axons would only comprise ~4% of the total WM volume.

Discussion

Our estimation of the absolute number of axons interconnecting cortical areas depends on

assumptions of callosal axon packing density, proportionally between the number of axons connecting

two areas and dMRI tractography for the areal pair, and approximate parity between dMRI sensitivity to

inter- and intra-hemispheric connections. Although there are only two reports of axonal density in the

corpus callosum, they are consistent with each other and with reports of axonal density of

intrahemispheric tracts. Our study relies on the data reported by Aboitiz et al. [11], because it is the

most systematic count of which we are aware. There is one later study, Liewald et al. [12], which

provides a value only slightly lower, 1.23×10^5 vs 1.6×10^5 axons/mm^2 after correction for tissue

shrinkage. And because this study was primarily a survey of axon diameter with packing density only

incidentally recorded, it is conceivable that density values derived from could be small underestimates.

Mis-estimated tissue shrinkage is possible but likely to be <10% and callosal areas were measured with

a well-validated and widely-used method [4]. Concerning dMRI- to-axon-count proportionality, it has

been shown in macaques that there is a strong linear correlation between dMRI-traced streamlines and

the number of fibers identified with retrograde tracers connecting regions the cortex [6]. We found a

similar, though understandably weaker, correlation among homologous connections between human

dMRI and macaque histology in our prior study [3].

Furthermore, we found little difference between distance-matched dMRI connectivity for callosal

versus ipsilateral connections (*Figure 1C*). If callosal axons were more easily detectable, this would be

reflected as an upward displacement of the blue trace above the green trace across the entire distance

domain, which is not evident. This parity is perhaps unsurprising because over most of their

trajectories, inter-hemispheric fibers are subjected to the same crossing fiber issues as intra-

hemispheric. Specifically, the corpus callosum is a distinct tract for only about 15-35 mm, but its fibers

range in length up to about 300 mm. Of course, short interhemispheric trajectories are dominated by

the callosal segment, and long by the intrahemispheric segments. Generally, the proportion of their

trajectories that are within the callosum is roughly proportional to their length. Consequently, if there

were enhanced detection of callosal fibers as streamlines by dMRI, the green trace in figure 1C would

be expected to be elevated primarily at short fiber lengths, resulting in a noticeably steeper slope for

the blue than the green trace, which again is not observed. These data support the applicability of the

scaling factor derived from interhemispheric fibers to intrahemispheric fibers.

While we derive a single dMRI-to-axon count factor, it is possible that the true conversion ratio

varies somewhat among connections due to local microstructural differences other than axon count

such as axon caliber, packing density, or myelination. However, the major fasciculi (including the

corpus callosum) have similar axon calibers and packing densities [12], as expected given that

different sections of the same long-range fibers contribute to the composition of several fasciculi. More

generally, packing density is a function of local cellular interactions, especially oligodendrocytes, and

because these are the same in the corpus callosum and intrahemispheric white matter, the *a priori*

expectation is that packing density would be similar, as histological data supports. Myelination has

only a modulatory effect on dMRI-detected anisotropy, with most of the effect derived from axonal

membranes [13]. Nevertheless, microstructural variation in dMRI-to-axon count ratio is a possible

source of noise in our estimate. We evaluated the effects the potential mis-specification of these critical

parameters on our estimates of axonal connections and found that they would result in only modest

changes of axonal connectivity. For example, using the alternative value for callosal axon packing

density (1.23×10^5 [14] rather than 1.60×10^5 axons/mm^2 [11]) decreases the estimated number of

axons between Wernicke's and Broca's areas from 25,310 to 19,310; assuming a 75% [15] rather than

65% linear shrinkage coefficient [11] increases the estimated number of axons from 25,310 to 33,690.

Thus, our basic conclusions seem to be robust within plausible ranges of these parameters.

The simple scaling factor we derive here permits some interesting quantitative estimates which may

inform models of cortical neurophysiology. For example, the connections between Wernicke's and

Broca's areas are thought to integrate receptive and expressive aspects of language, but there are only

~25,000 axons between the core cortical parcels in these regions (parcels 44 and PSL), fewer than the

number of words in a college student's vocabulary [16]. Areas distant from the hippocampus, notably

the dorsolateral prefrontal cortex, may be connected to it by <10 axons/mm^2 (*Figure 1F*). On a global

scale, we estimate the total number of inter-areal axons as 1.05×10^9, implying that <5% of the

~11.5×10^9 cortical pyramidal cells [17] project outside their area (because only half of the axons are

efferent). Furthermore, since 51% of those are to adjacent areas, <2.5% of pyramidal cells project

beyond the adjacent parcel. This sparse long-range connectivity is consistent with its exponential fall-

off measured with dMRI in humans and histologically in other mammals [3,18].

These constraints encourage consideration of models of cortical function where connections are

dense but mainly local. Neural models with multiple paths between cortical neurons due to numerous

short connections can show long-range covariance and even synchrony [19,20], and these have been

observed experimentally in humans [21]. In such models, cortical locations interact through activation

of multi-synaptic pathways rather than direct connections, and the key to connectivity is physiological

selection under multiple constraints rather than anatomical projections. Lastly, it is useful to note that

these quantitative considerations are radically different in other species, where the smaller number of

cortical neurons and shorter inter-areal distances allow greater connectivity between cortical areas, as

well as a larger proportion of subcortical connectivity.

Figure 1. The number of axons connecting interconnecting the 360 cortical parcels of the HCP-

MMP1.0 atlas. (A) Connectivity matrix of intrahemispheric axon counts, averaged across the two

hemispheres. Parcels are ordered into 10 functional networks. (B) Histograms showing the distribution

of inter- and intrahemispheric pairwise axon counts. Physically adjacent and non-adjacent parcel pair

intrahemispheric histograms are stacked. Median connectivity is ~2,700 axons between cortical areas

in the same hemisphere, and 540 interhemispherically. (C) dMRI connectivity as a function fiber tract

distance. Pairwise values averaged within 15 fiber-length bins. Shading shows bootstrapped 95%

confidence intervals. (D-F) axons counts and densities averaged across the two hemispheres and

196 visualized on the left fsaverage template cortex. (D) total axons connecting each parcel to all others. (E)

197 axons connecting each parcel to all others, normalized by the reference parcel's area. (F) axons

198 connecting the hippocampus to the rest of the cortex, normalized by the area of the cortical parcel,

199 shown in log scale.

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208 **Data availability**

209 The processed data used in this study are available at https://doi.org/10.5281/zenodo.4910310. Datafiles are in

210 Matlab v7.3 format. The Human Connectome Project's raw imaging data and FreeSurfer outputs may be

211 downloaded from https://db.humanconnectome.org.

212
213 **Code availability**

214 The main standalone analysis Matlab code used in this study is available at

215 https://doi.org/10.5281/zenodo.4910310. Additional non-standalone supporting code will be made available

216 upon request.

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S1 Appendix: Extended Methods

Diffusion MRI

The dMRI connectivity data used to estimate inter-parcel axon totals was described in our prior report

[1] whose data are available in full at https://doi.org/10.5281/zenodo.4060485. Preprocessed imaging

data for 1,065 healthy young adults were retrieved from the Human Connectome Project WU-Minn

consortium 1200 release [2] (https://db.humanconnectome.org). We segmented the cortex into 180

parcels per hemisphere following the HCP-MMP1.0 atlas[3] and performed probabilistic tractography

using the probtrackX tool [4] from FSL [5] using tractography parameters detailed in our prior report

[1]. This analysis yielded a 360 x 360 dMRI connectivity matrix for each subject which provided the

example data for applying the method presented here. For probtrackX-derived connectivity, the raw

unit of dMRI connectivity strength is the number of streamlines connecting seed and target regions.

The absolute magnitude of this metric is arbitrary as it scales with the number of samples drawn from

the probability distribution of diffusion parameters in each voxel, in our analysis 5,000. Note that the

method described here is largely agnostic to the dMRI methodology, provided it returns a continuous

connectivity metric and has relatively equal sensitivity to callosal and ipsilateral connections.

Cross-sectional area of the corpus callosum, white matter volume, and parcel areas

The HCP WU-Minn consortium 1200 release [2] includes the standard outputs from the FreeSurfer

`recon-all` pipline [6]. With default parameters, this pipeline labels the 1 mm^3 voxels of the `aseg.mgz`

volume which contain the corpus callosum with a fixed 5mm lateral extent. Dividing the number of

callosum-label voxels by 5 yields an estimate of its cross-sectional area, in mm^2. The total white matter

volume is reported in the `aseg.stats` output of `mri_segstats`. Parcel areas and adjacency were

determined [7] on triangular mesh of each subject's reconstruct white matter surface, or white matter –

gray matter interface (`?h.white`).

Estimate of callosal fiber density

Our estimate of callosal fiber density was based on the electron microscopy (EM) study of Aboitiz

and colleagues [8] who reported a fiber density of 38 per 100 μm^2 or $1.6x10^5$ axons/mm^2 after

accounting for 65% linear tissue shrinkage after fixation. This is concordant with their finding of

$1.57x10^5$ axons/mm^2 as measured with light-microscopy in twenty brains as well as the $1.23x10^5$ non-

exhaustively counted axons per mm^2 reported in a more recent EM study [9] of callosal axon diameter

in two brains [9], assuming the same degree of tissue shrinkage.

Distance matched Intra- vs. Interhemispheric dMRI connectivity

One assumption of the method described in this report is that the dMRI tractography methodology

has approximately similar sensitivity to callosal and ipsilateral connections. This is difficult to determine

without ground truth connectivity, as intra- and interhemispheric connections may have true

anatomical differences. Nevertheless, we examined distance-matched intra- vs interhemispheric

connections (Figure 1*C*) and found no statistical evidence that they are different. Pairwise connections

were averaged in 15 distance bins, log-transformed and linear fits obtained for intra- and

interhemispheric connections. For the overlapping distance domain, the intrahemispheric slope is -

0.30, 95% confidence interval = [-0.33 -0.26] with an intercept of 6.18 [5.91 6.45] and the

interhemispheric slope is -0.26 [-0.29 -0.24] and intercept of 5.93 [5.72 6.14]; the 95% confidence

intervals of both parameter are overlapping. In addition, a paired r-test of correlation differences [10]

failed to reject the null hypothesis, $p = 0.58$. The parity between distance-matched intra- and

interhemispheric connections also holds when the linear fit is obtained for over the entire distance

domain, with an intrahemispheric slope and intercept -.31 [-0.33 -0.28] and 6.24 [6.01 6.46],

respectively; -.28 [-0.30 -0.25] and 6.00 [5.78 6.23] for interhemispheric connections.

<u>Estimating axon counts and axon volume from dMRI</u>

From the histological estimate of callosal fiber density, MRI-derived measures of callosal cross-

sectional area and white matter connectivity, the conversion factor between dMRI connectivity and

physical axons can be estimated as follows:

Eq. 1.1 $N_{callosum} = A_{callosum} * D_{callosum}$

Eq. 1.2 $C_{axon} = \frac{Ncallosum}{M_{dMRI}}$

Where $A_{callosum}$ is the cross-sectional area (mm^2), $D_{callosum}$ is the assumed fiber density (1.6x10^5

axons/mm^2) of the corpus callosum, $N_{callosum}$ is the estimated total number of callosal fibers, M_{dMRI} is the

magnitude of dMRI callosal connectivity, in our case, the number of tractography streamlines, and C_{axon}

is the conversion factor from dMRI to physical fibers (axons/streamline).

In addition to connectivity strength, or number of streamlines, the dMRI tractography analysis also

yields a mean streamline length for every parcel-pair connection. After converting dMRI connectivity

strength to physical axon count as described above, the total volume of the estimated axons can be

calculated as follows:

Eq. 2.1 $WM_{volume} = \sum_{i=1}^{Npair} l_i * n_i * C_{axon} * \frac{1}{D_{callosum}}$

Eq. 2.2 $WM_{volume} = \sum_{i=1}^{Npair} l_i * n_i * \frac{A_{callosum}}{M_{dMRI}}$

Where WM_{volume} is the estimated axonal white matter volume (mm^3) and N_{pair} is the total number of

parcel pairs. l_i and n_i are the length (mm) and number of dMRI streamlines in the ith parcel pair. Eq. 2.1

can be simplified into Eq. 2.2 by substituting Eqs. 1.1 and 1.2 into 2.1.

Parcel ordering

The parcel ordering and the ten functional networks shown in Fig 1*A* were defined in our previous

report [1] and were modified from twelve networks identified by Ji and colleagues in a resting-state

fMRI study on the HCP cohort [11].

Thalamocortical fiber volume estimation

The scope of our previous dMRI tractography study [1] was confined to corticocortical (including

cortico-hippocampal) connectivity. In order to estimate the total volume of thalamocortical axons, we

assumed a total axon count of 22.6x10^6 as reported by histological count [12] and allocated these

axons to cortical parcels in proportion to their area. The inverse callosal packing density was used for

effective cross-sectional area, as with corticocortical connections. To estimate the length of

thalamocortical fiber tracts, for each parcel i, we first identified the thalamic voxel nearest to parcel's

centroid. We then used the interparcel fiber tract length [1] from the centroid of parcel i to the

identified parathalamic parcel centroid. To this figure we added the Euclidean distance from the

parathalamic centroid to the nearest voxel of the thalamus, ensuring that estimated thalamocortical

fiber tract length is always non-zero. As with corticocortical connections, the total white matter volume

of each connection was estimated by taking the product of the number of axons, the effective cross-

sectional area, and the estimated fiber tract length (Eq. 2).

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