SUPPLEMENTARY MATERIAL**:**

Methods:

1) Gray matter and white matter segmentation

In order to obtain probabilistic gray and white matter maps, we employed an extension of the software Statistical Parametric Mapping (SPM) entitled "Clinical Toolbox". The Clinical Toolbox was developed by our group¹, with the intent to optimize the segmentation and registration of brains with distorted anatomy due to large lesions (e.g., post ischemic necrosis after stroke). It utilizes a cost-function approach 2 to normalize the brain into the standard stereotaxic space (MNI space), which signifies that a manually defined mask of the stroke necrosis site (drawn by one of the authors - Bonilha) is used to weigh tissue influence on normalization.

The Clinical Toolbox employs SPM's unified normalization-segmentation subroutines to yield probabilistic gray and white matter tissue maps $\frac{3}{2}$, which are subsequently used to guide subsequent connectivity assessment steps. The gray and white matter regions corresponding to the location of the stroke lesion were excluded from the resulting probabilistic tissue maps.

Linear and non-linear normalization parameters were applied to a Brodmann Areas (BA) ROI Atlas in standard space - distributed with MRIcro⁴, and the probabilistic map of gray matter (in native T1 space) was segmented into a map of cortical BA ROIs.

To enable the registration of the tissue maps (including the ROI segmented gray matter map) into DTI space, native volumetric T2 weighted image was linearly co-registered onto the native T1 image. Since tissue contrast is comparable between B0 and T2 images, the registered T2 image was linearly co-registered onto the B0 image using FMRIB's Linear Image Registration Tool (FLIRT). The transformation matrices were then applied to the map of segmented cortical ROIs and to the white matter probabilistic tissue map, yielding cortical ROIs and white matter maps in DWI space.

2) Fiber tracking and connectome reconstruction.

Probabilistic tractography was used to define the number of white matter streamlines connecting cortical regions, which were separately defined according to an anatomical atlas. This step was iteratively performed until the connectivity between all possible pairs of cortical regions was determined. The connectivity information was then compiled in a connectivity matrix, providing a two-dimensional representation of the brain connectome. These steps are explained in detail below.

Structural connectivity was obtained by applying FDT's probabilistic method for fiber tracking⁵⁻⁷. Probabilistic tractography was performed on diffusion data after voxel-wise calculation of the diffusion tensor. FDT's BEDPOST was used to build default distributions of diffusion parameters at each voxel. Probabilistic tractography was obtained using FDT's probtrackx with 5000 individual streamlines drawn through the probability distributions on principal fiber direction. We chose to employ probabilistic tractography in this study, since it is theoretically capable of accommodating intra-voxel fiber crossings $5, 8$.

The cortical ROIs corresponding to the BA were used as seed regions for tractography. For each subject, we calculated the connectivity between cortical ROIs i and j defined as the number of probabilistic white matter streamlines arriving at j when i was seeded, averaged with the number of probabilistic streamlines arriving at i when j was seeded. The step was iteratively repeated to ensure that all BAs were used as seed regions. Once all iterations were completed, a connectivity matrix A was constructed, where each entry A_{ii} corresponded to the weighted connectivity between structures i and j, also referred to as the link between nodes i and j. Since the number of streamlines between i to j, and j to i were averaged, the connectivity matrix was symmetrical with respect to its main diagonal.

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Legends for Supplementary Materials

Supplementary Table 1- demographic information and language performance for all subjects included in this study.

Supplementary Table 2- summary of linear regression models.

Supplementary Figure 1- this figure demonstrates the structural connectomes from all subjects. The rows and columns of each matrix correspond to Brodmann Areas (BA). The left quadrant of each matrix illustrates connections within the left hemisphere, while connections within the right hemisphere are illustrated in lower right quadrant. The scale bar demonstrates the link-wise strength, which corresponds to the log of the number of streamlines connecting the ROIs (corrected based on ROI volume and distance travelled by the streamlines).

Supplementary Figure 2- two-dimensional circular diagrams demonstrating the brain network configurations from all subjects. Each node corresponds to a different Brodmann Area (BA) (as indicated by the adjacent number). Only links above the 95% link-weight percentile are shown. The color of the node represents the percentage of the ROI that was damaged by the stroke (in accordance with the colorbar).

Supplementary Table 1

Legend: F=female; M=male; W=white; B=black; WAB-AQ= Western Aphasia Battery Aphasia Quotient; SP = Semantic Paraphasias; PP= Phonemic Paraphasias; New = New items correctly named after treatment.

Supplementary Table 2

Legend: PNT improvement = treatment-related improvement in the naming; WAB-AQ= Western Aphasia Battery Aphasia Quotient; NSW= Normalized small worldness; SE = Standard Error; T= T-statistic; p= p value.

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log (streamlines)

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