***eLife’s* transparent reporting form**

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see [EQUATOR Network](http://www.equator-network.org/%20)), life science research (see the [BioSharing Information Resource](https://biosharing.org/%22%20%5Ct%20%22_blank)), or the [ARRIVE guidelines](http://www.plosbiology.org/article/info%3Adoi/10.1371/journal.pbio.1000412) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

The sample size for each species was comparable to that of most recent comparative studies (Eichert et al, 2020; Balezeau et al, 2020; Roumazeilles et al, 2020). We tried to include as much available data as possible in our experiments. The subject information for each species can be found in the sections of “Human data, Chimpanzee data, and Macaque data”.

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
* If you encountered any outliers, you should describe how these were handled
* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

The parcellation results of the human inferior parietal lobule (IPL) generated in this study were retested using high-resolution 7T MRI dataset from the Human Connectome Project Dataset (HCP) and conventional clinical MRI dataset. The parcellation results of the chimpanzee IPL were retested using high-resolution ex-vivo MRI data. The parcellation results of the macaque IPL were retested using high-resolution ex-vivo dataset and another low-resolution in-vivo MRI dataset.

Criteria for exclusion/inclusion of macaque data was whether it is a macaque (Macaca mulatta) or not. Criteria for exclusion/inclusion of chimpanzee data was the resolution of MRI data. More information can be found in the sections of “Human data, Chimpanzee data, and Macaque data”.

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Linear regression was performed to investigate the allometric relationship across species. The p-values were reported and all of them were less than 0.001. ANCOVA was used for comparisons across the two regression slopes between hemispheres. This information can be found in the section of “Statistical analysis and Allometric scaling and structural asymmetry of IPL subregions”.

For the vertex-wise analysis, a one-sample t test was performed for each species using PALM, with 5000 permutations, and the Cohen's d were reported. This information can be found in the section of “Statistical analysis and Connectional asymmetries of IPL subregions”.

For the volumetric, ROI-wise, and tract-wise analysis, a two-sided Wilcoxon signed-rank test was performed for each species. This information can be found in the section of “Statistical analysis and Connectional asymmetries of IPL subregions”.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Human data were selected from the Human Connectome Project Dataset (HCP).

Chimpanzee data were available from the National Chimpanzee Brain Resource (NCBR)(http://www.chimpanzeebrain.org/).

Macaque data (*Macaca mulatta*) were downloaded from OpenNeuro website (http://openneuro.org/datasets/ds001875/versions/1.0.3).

This information can be found in the sections of “Human data, Chimpanzee data, and Macaque data”

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

The resulting maps (including the parcellation map of the inferior parietal lobule and the vertex wise statistic map) from this study will be made publicly available. Anyone is welcome to download it from <https://github.com/LuqiCheng/IPL_Connectional_Asymmetry>.