

Comparative quantitative analysis reveals preserved structural connectivity patterns in the human and macaque brain



Alexandros Goulas^{1*}, Matteo Bastiani^{2,3*}, Gleb Bezgin⁴, Alard Roebroeck², Peter Stiers¹

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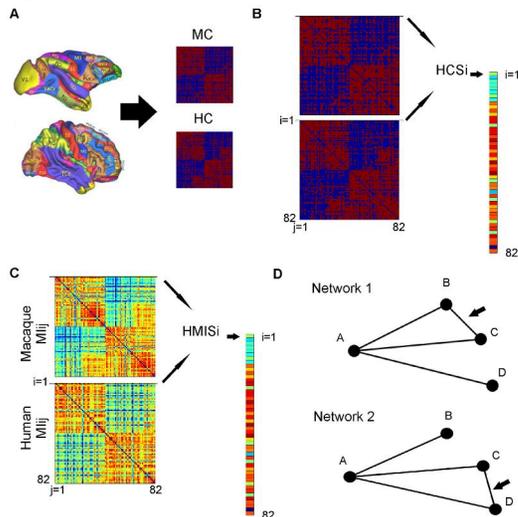
1 Department of Neuropsychology and Psychopharmacology, Maastricht University, Maastricht, The Netherlands 2 Department of Cognitive Neuroscience, Maastricht University, Maastricht, The Netherlands 3 Institute of Neuroscience and Medicine – 4, Forschungszentrum Juelich GmbH, Juelich, Germany 4 Rotman Research Institute, Baycrest Centre, Toronto, Canada *Equal contribution and correspondence: alexandros.goulas@maastrichtuniversity.nl matteo.bastiani@maastrichtuniversity.nl

Introduction

- The brain is a complex network. The connectivity of each region constrains its function.
- Large scale connectivity can be used as a guide to cognition [1-3].
- The macaque brain functions as a model but evolutionary changes might render extrapolations to the human brain inaccurate. Direct testing of the preservation of the connectivity of assumed homologues is needed [4].
- Our goal: Quantitative whole brain approach to assess connectivity pattern preservation and topological properties of the macaque and human brain at the systems level.

Materials & methods

- The human connectome (HC) was estimated from 5 healthy subjects (1 female) with dwMRI. Preprocessing, model fitting and multi-direction local probabilistic tractography as described in [5].
- The macaque connectome (MC) was assembled from the CoCoMac database. The Regional Map was used as a parcellation scheme (Fig. 1 A) [6].
- Similarity of the MC and HC assessed with the Edit Distance (ED) (eq. 1). Region wise preservation of connectivity: Homologue Connectivity Similarity (HCS) (Fig. 1 B eq. 2) and Homologue Matching Index Similarity (HMIS) (Fig 1 C eq. 3) indexes [7].
- Tracing the structural backbone in the two species: rich club coefficient (eq. 4).
- Significance of results: randomization statistics.



$$ED(A, B) = \sum_{i,j} |A_{ij} - B_{ij}| \quad (1)$$

$$HCS_i(A, B) = \frac{A_i \cap B_i}{A_i \cup B_i} \quad (2)$$

$$MI_{ij} = \frac{X_i \cap X_j}{X_i \cup X_j} \quad (3)$$

$$HMIS_i(MI_A, MI_B) = r(MI_{A_i}, MI_{B_i})$$

$$\varphi(k) = \frac{2E_{>k}}{N_{>k}(N_{>k} - 1)} \quad (4)$$

Fig 1. Graphic representation of the analysis pipeline and the network metrics used.

Results

MC and HC are significantly similar (ED=0.303, $p < 0.001$).

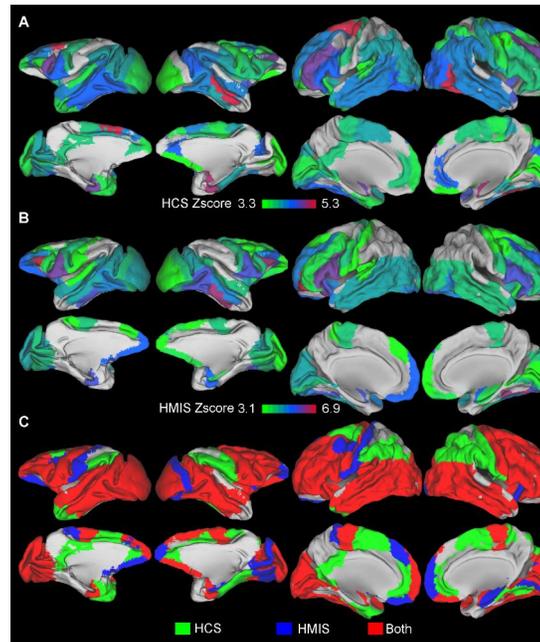


Fig 2. Preservation of connectivity as indicated by A. HCS and B. HMIS C. Summary ($p < 0.05$ Bonferroni)

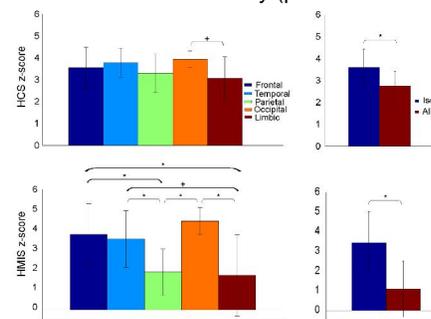


Fig 3. Summary of results based on lobe and cortical type ($p < 0.05$ *Bonferroni +Uncorrected).

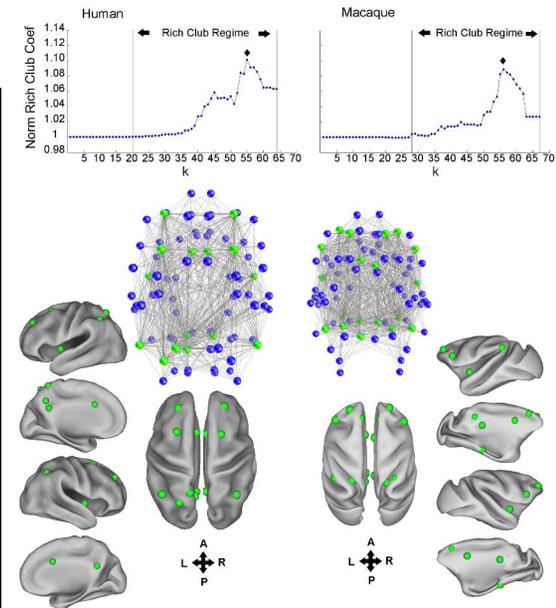


Fig 4. Rich club structure (green nodes/regions) in the HC and MC ($p < 0.0001$). The structural backbone significantly overlaps between the two species ($p < 0.0001$).

Conclusions

- MC and HC as a whole are significantly similar.
- Region wise analysis reveals similarities, but also some discrepancies.
- A common structural backbone preserved across primate evolution.

References

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