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

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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 preservance of the connectivity of assumed homologues is needed [4].
- Our goal: Quantitative whole brain approach to assess connectivity pattern preservance 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-directional 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 preservance 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.

Results

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

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