The morphological evolution of the primate brain revealed by alignment of the cortical sulci

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Introduction

Comparing the brains of different species based solely on anatomy is a challenging task, particularly for the highly variable regions such as the cortex. On the other hand, a meaningful comparison of species can provide insight into the evolutionary processes that led to the human brain.

We propose and demonstrate a methodology for quantifying anatomical differences between human (*homo sapiens*), chimpanzee (*pan troglodytes*), and gorilla (*gorilla gorilla*) brains, based on a non-linear registration technique that uses the cortical sulci as explicit landmarks.

Methods

The methodology consists of three successive steps, which are described below.

1. Construction of a template brain for each species

A template brain of each species (human, chimpanzee, and gorilla) is constructed by averaging coregistered anatomical scans of a population of subjects.

The template used for **humans** is the well-known MNI ICBM152 asymmetric 2009c template (Fonov 2011). The T1-weighted template was processed using BrainVISA/Morphologist (Fischer 2010, see www.brainvisa.info) in order to compute a grey–white–CSF segmentation, and to extract geometric objects that represent the cortical sulci (Fischer 2012).

The template **chimpanzee** brain was constructed from whole-brain in vivo T1-weighted anatomical scans of 30 captive chimpanzees acquired in a 3-tesla MRI scanner. All subjects are part of the National Chimpanzee Brain Resource (www.chimpanzeebrain.org). All procedures used with the chimpanzees were approved by the local institutional animal care and use committee.
All 30 chimpanzee scans were processed with the BrainVISA/Morphologist segmentation pipeline to extract their cortical sulci. The sulci were then labelled by two of the authors (A. S. and O. F.), who worked together until a consensus was reached. The labelling used a subset of the human nomenclature used in Morphologist (Perrot 2011), with the notable addition of the lunate sulcus, which is very deep and stable in chimpanzees, but has no reliable match in human brains. These 30 brains were nonlinearly coregistered using the DISCO+DARTEL pipeline (Lebenberg 2018). In this pipeline, the DISCO method (Auzias 2011) is used first, in order to compute a deformation of every subject into an average space where the major sulci are aligned. This provides a good initialization for DARTEL (Ashburner 2007), which improves the coregistration by maximizing the overlap of tissue classes. The total deformation fields were finally applied to the intensity-normalized T1-weighted scans in order to bring them into the average space and build an average template. This template was processed using Morphologist, yielding a representation of the average sulcal pattern of these 30 chimpanzees.

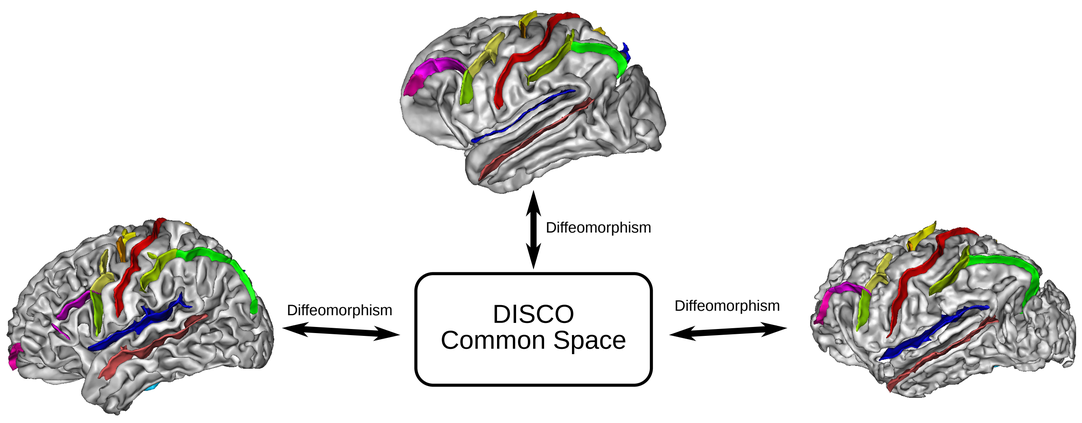
The template **gorilla** brain was constructed using exactly the same methodology as for the chimpanzees, based on whole-brain anatomical scans of 18 *post-mortem* specimens of gorilla brains acquired in a 7-tesla MRI scanner.

2. Extraction of the cortical sulci for each template brain

Each of the three templates was segmented using the BrainVISA/Morphologist pipeline in order to automatically extract a geometric representation of its cortical sulci, then the main sulci were labelled manually. The result of this process is shown on **Figure 1**.

3. Non-linear coregistration of the templates and deformation-field morphometry

We then applied the DISCO method (Auzias 2011) to coregister the templates of the different species. This method estimates a smooth, diffeomorphic deformation for each species template, that brings all three templates into a common space, where the coregistration of the sulcal crest lines and bottom lines is optimized.



For this process we selected only the major sulci that are found unambiguously in all three species (see the complete list in **Figure 1**), and postulated the homologies between them based on their morphological similarity. Note that in order to optimize the anatomical relevance of the cross-species deformations over the whole brain, the sulci should ideally be distributed evenly across the whole brain surface. However, the chosen sulci also need to be well-defined and unambiguous : as a result, some regions are less constrained than the rest of the brain because we chose to exclude some sulci because of high inter-individual variability (e.g. the superior part of the frontal lobe, the occipital lobe), inter-species variability (e.g. the occipito–temporal junction where humans lack a reliable lunate sulcus), or issues of segmentation quality (the inferior temporal lobe).

We then extracted the pairwise deformation fields between the species templates, by composing the deformation fields to/from the common space estimated by DISCO. These deformation fields encode the total deformation that must be applied to the brain of a source species in order to map its sulci onto the corresponding sulci of a target species. For visualization, we calculated the **determinant of the Jacobian** of the deformation fields. This value quantifies the local amount of expansion (>1) or contraction (<1) in each point of the brain, between two given species. It is represented in **Figure 2** for all three pairs of species, projected onto the grey–white interface of the source species.

Results

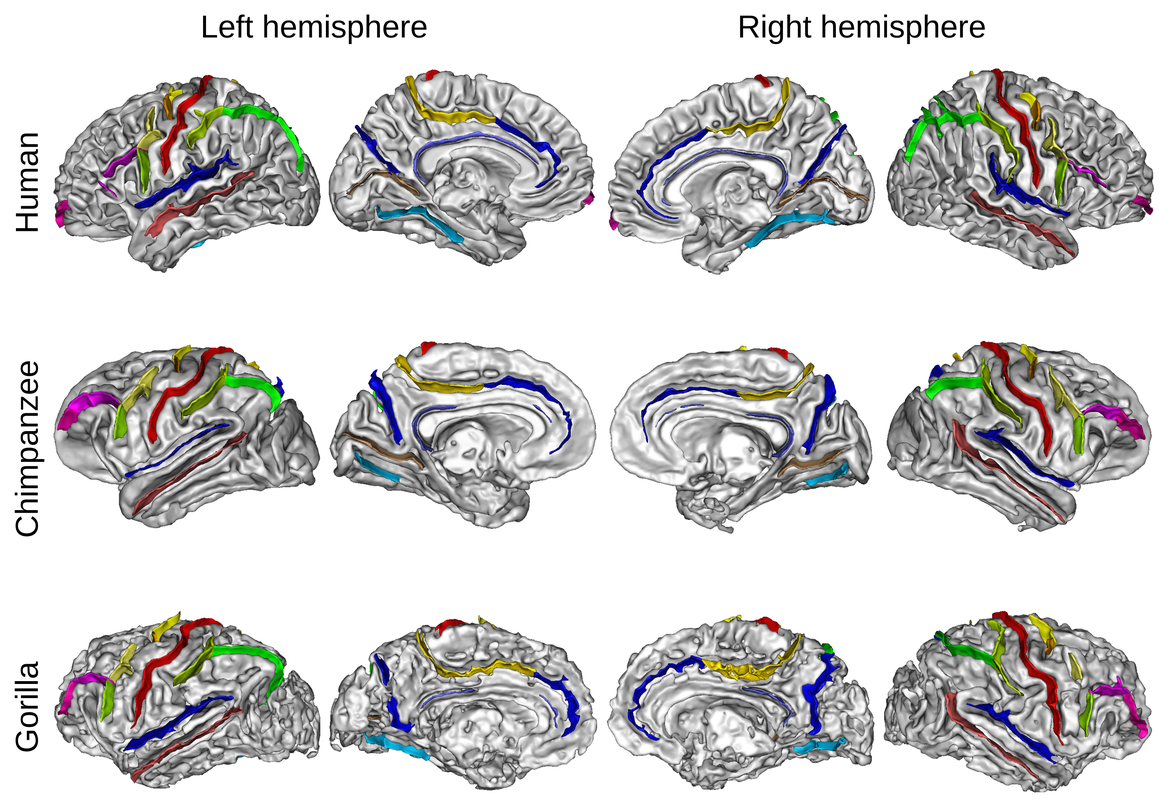


Figure 1: Each row shows the template that is used to represent one of the species. For each template the grey–white surface segmented by Morphologist is shown, as well as the sulci that were used in the interspecies registration.

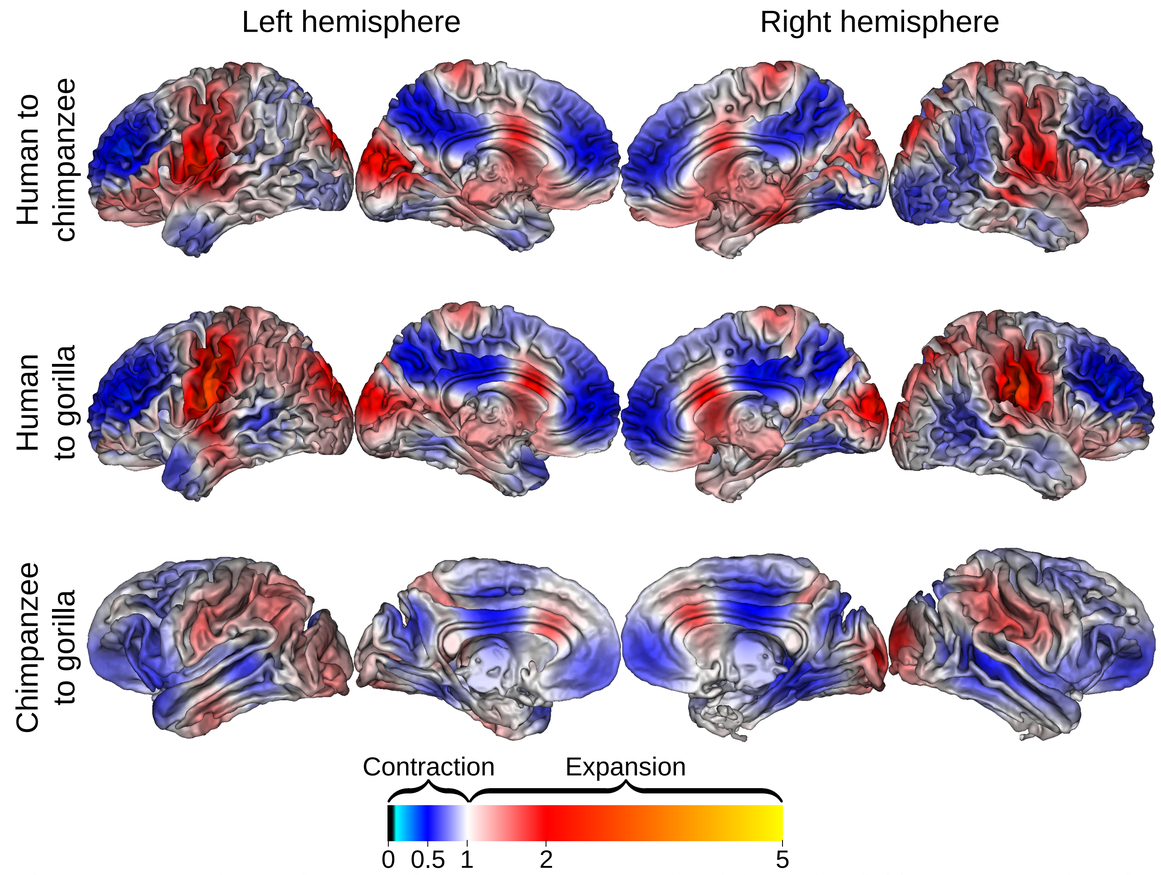


Figure 2: Determinant of the Jacobian of the cross-species deformation fields, represented on the grey–white surface of the source species. Values smaller than 1 (blue) represent regions that are relatively smaller in the target species than in the source species. Conversely, values larger than 1 (red) represent regions that are relatively larger in the target species than in the source species.
It should be noted that all templates are put to the scale of a human brain by applying an affine transformation as part of the template construction. The expansion/contraction coefficients are therefore computed *between affinely normalized brains*, which explains that some regions have an exansion coefficient larger than 1, even though their absolute volume is smaller in the target species (e.g. the pre-central and post-central regions).

Conclusions

Deformation fields are rich objects, which can be analyzed in many ways. We confirm the potential of this method by replicating a well-known pattern: the higher associative areas (frontal and parietal lobes) are shown to be far more developed in humans than in other primates; and conversely for the primary areas.

This method also has the potential to give quantitative results, e.g. to quantify the evolution of the volume of a given brain area across species, provided that the anatomo-fonctional homology between species is verified locally.

References

Ashburner, J. (2007). A fast diffeomorphic image registration algorithm. NeuroImage, 38(1), 95–113. https://doi.org/10.1016/j.neuroimage.2007.07.007
Auzias, G. et al. (2011). Diffeomorphic Brain Registration Under Exhaustive Sulcal Constraints. IEEE Transactions on Medical Imaging, 30(6), 1214–1227. https://doi.org/10.1109/TMI.2011.2108665
Fischer, C. et al. (2012). Morphologist 2012: The new morphological pipeline of BrainVISA. Proceedings OHBM 2012
Fonov, V. et al. (2011). Unbiased average age-appropriate atlases for pediatric studies. NeuroImage, 54(1), 313–327. https://doi.org/10.1016/j.neuroimage.2010.07.033
Glaunès, J. et al. (2004). Diffeomorphic matching of distributions: A new approach for unlabelled point-sets and sub-manifolds matching. In CVPR (Pp. 712–718). Los Alamitos: IEEE Comput. Soc.
Lebenberg, J. et al. (2018). A framework based on sulcal constraints to align preterm, infant and adult human brain images acquired in vivo and post mortem. Brain Structure and Function, 223(9), 4153–4168. https://doi.org/10.1007/s00429-018-1735-9
Perrot, M. et al. (2011). Cortical sulci recognition and spatial normalization. Medical Image Analysis, 15(4), 529–550. https://doi.org/10.1016/j.media.2011.02.008

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