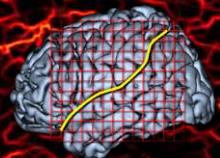# Optimizing automated preprocessing streams for brain morphometric comparisons across multiple primate species

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INTRODUCTION

MR techniques have delivered images of brains from a wide array of species, ranging from invertebrates to birds to elephants and whales. However, their potential to serve as a basis for comparative brain morphometric investigations has rarely been tapped so far (Christidis and Cox, 2006; Van Essen & Dierker, 2007), which also hampers a deeper understanding of the mechanisms behind structural alterations in neurodevelopmental disorders (Kochunov et al., 2010). One of the reasons for this is the lack of computational tools suitable for morphometrci comparisons across multiple species. In this work, we aim to characterize this gap, taking primates as an example.

METHODS

Using a legacy dataset comprising MR scans from eleven species of haplorhine primates (Rilling & Insel, 1998), we tested different automated processing streams (cf. Fig. 1), focusing on denoising and brain segmentation. Newer multi-species datasets acquired on one scanner are not currently available, so our experiments with this decade-old dataset (which had a very low signal-to-noise ratio by contemporary standards) can serve to highlight the lower boundary of the current possibilities of automated processing pipelines. After manual orientation into Talairach space, an automated bias correction was performed using CARET (Van Essen et al., 2001) before the brains were extracted with FSL BET (Smith, 2002) and either smoothed by an isotropic Gaussian Kernel, FSL SUSAN (Smith, 1996), an anisotropic diffusion filter (Perona & Malik, 1990), an optimized Rician non-local means filter (Gaser & Coupé, 2010), or not at all. Segmentation of the brains was performed separately by either FSL FAST (Zhang, 2001) without atlas priors, or using an Adaptive Maximum A Posteriori Approach (Rajapakse et al., 1997). Finally, the white matter surface was extracted with CARET, and inspected for anatomical and topological correctness.
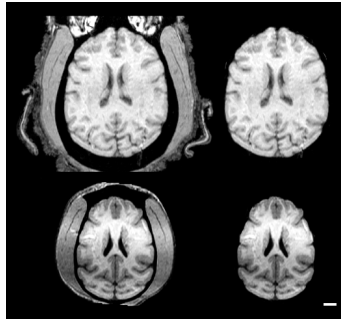

Fig. 1: Brains before (left) and after (right) brain extraction with FSL-BET. Top row: Chimpanzee. Bottom: Capuchin monkey (scanned with a different coil on the same scanner). Scale bar: 1 cm.

Denoising	Segmentation
None	**FSL-FAST** MRF neighbourhood beta value number of iterations iterations for bias correction field smoothing
CARET -volum-blur	
FSL-SUSAN	
anisotropic diffusion	**MINCNUMAP** Number of iterations for anisotropic diffusion filter
Rician NL-MEANS	

Fig. 2: ???

- frontal lobe
- parietal lobe
- temporal lobe
- occipital lobe
- sylvian fissure
- hindbrain (brainstem & cerebellum)

Fig. 3: ???

RESULTS

All of the noise reduction approaches resulted in better segmentations compared to the original images, but these improvements did not translate readily into

Bias correction by means of CARET did generally not have significant effects on the quality of the segmentation, though it interfered with brain extraction in some cases. The reasons for this are that some of the key assumptions of the algorithm were only partially applicable to non-human species, namely that neither size nor centre of gravity differ greatly between head and brain. Additionally, the histograms vary across species, thus affecting the thresholding used to seed the surface growing algorithm. Figure 2 shows that noise reduction was generally necessary but could be achieved by simple isotropic filtering, with anisotropic filtering (SUSAN, diffusion filter) providing no or little improvement. While none of the tested segmentation methods performed uniformly well in all 11 species, performance could be improved by reducing the noise contained in the original images, and by deviating systematically from the default parameters recommended for processing human brains (Figure 3). Nonetheless, all of the non-human segmentations required topology correction and - often considerable - manual cleanup.
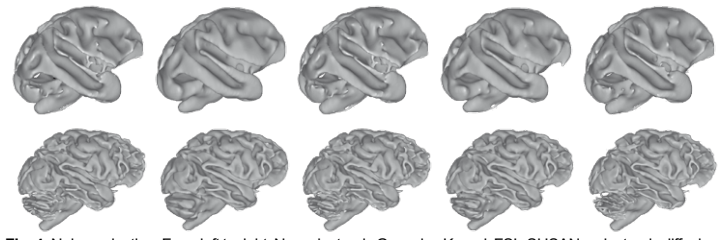

Fig. 4: Noise reduction. From left to right: None, isotropic Gaussian Kernel, FSL-SUSAN, anisotropic diffusion filter. Top row: Chimpanzee. Bottom row: Capuchin monkey.
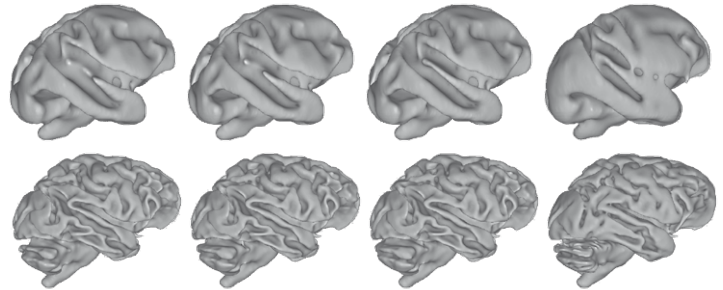

Fig. 5: Comparison of segmentation algorithms. First three from left: FSL FAST with 400+200, 200+100 and 400+200+200+100 iterations for bias correction field smoothing. Right: Adaptive Maximum A Posteriori Approach (AMAP). Top row: Chimpanzee. Bottom row: Capuchin monkey.

CONCLUSIONS

Automated processing pipelines for surface-based morphometry still require considerable adaptations to reach optimal performance across brains of multiple species, even within primates. However, most contemporary datasets have a better signal-to-noise ratio than the ones used here, which provides for better segmentations and cortical surface reconstructions. Considering further that cross-scanner variability is well below within-species differences (Stonnington, 2008), the prospects look good for comparative evolutionary analyses of cortical parameters. In order to succeed, however, computational efforts on comparative morphometry depend on high-quality imaging data from multiple species being more widely available.

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Zhang, Y. (2001), Segmentation of brain MR images through a hidden Markov random field model and the expectation maximization algor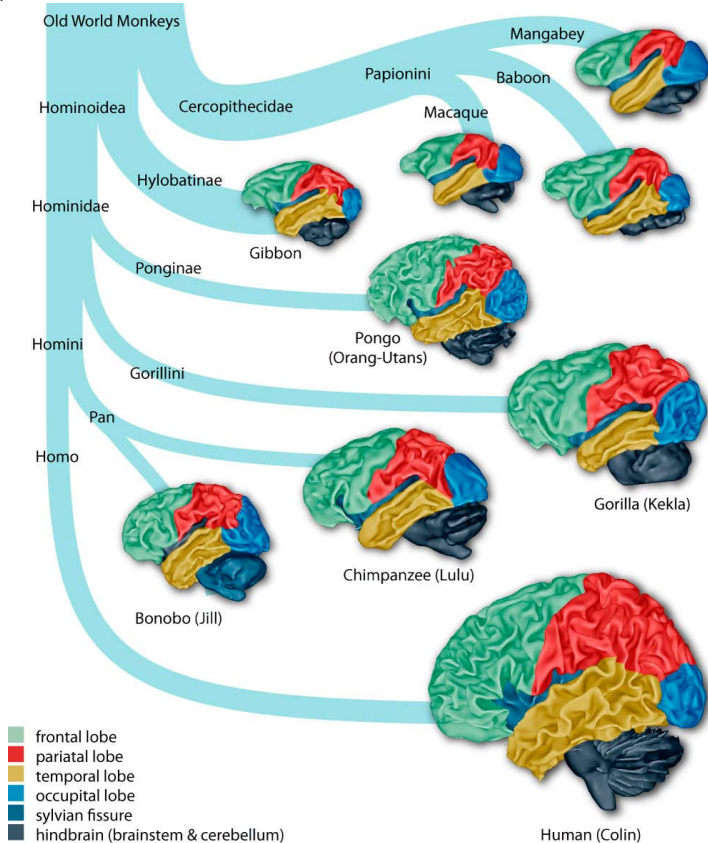ithm, IEEE Trans Med Imaging, vol. 20, no. 1, pp. 45-57.