

Relating PLI Data Across Scales

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Introduction

Polarized light imaging (PLI) [1, 2] enables scanning of individual histological human brain sections with two independent setups: a large-area polarimeter (LAP, object space resolution: $64 \times 64 \mu\text{m}^2/\text{px}$) and a polarizing microscope (PM, object space resolution: $1.6 \times 1.6 \mu\text{m}^2/\text{px}$). PM images are of high resolution (HR) containing complex information, whereas the LAP provides low resolution (LR) overview-like data. The information in an LR image constitutes a composition of the information contained in its HR equivalent [5]. Our goal is to directly relate measured HR to LR data of the same object, avoiding artificial intermediate steps.

Material and Methods

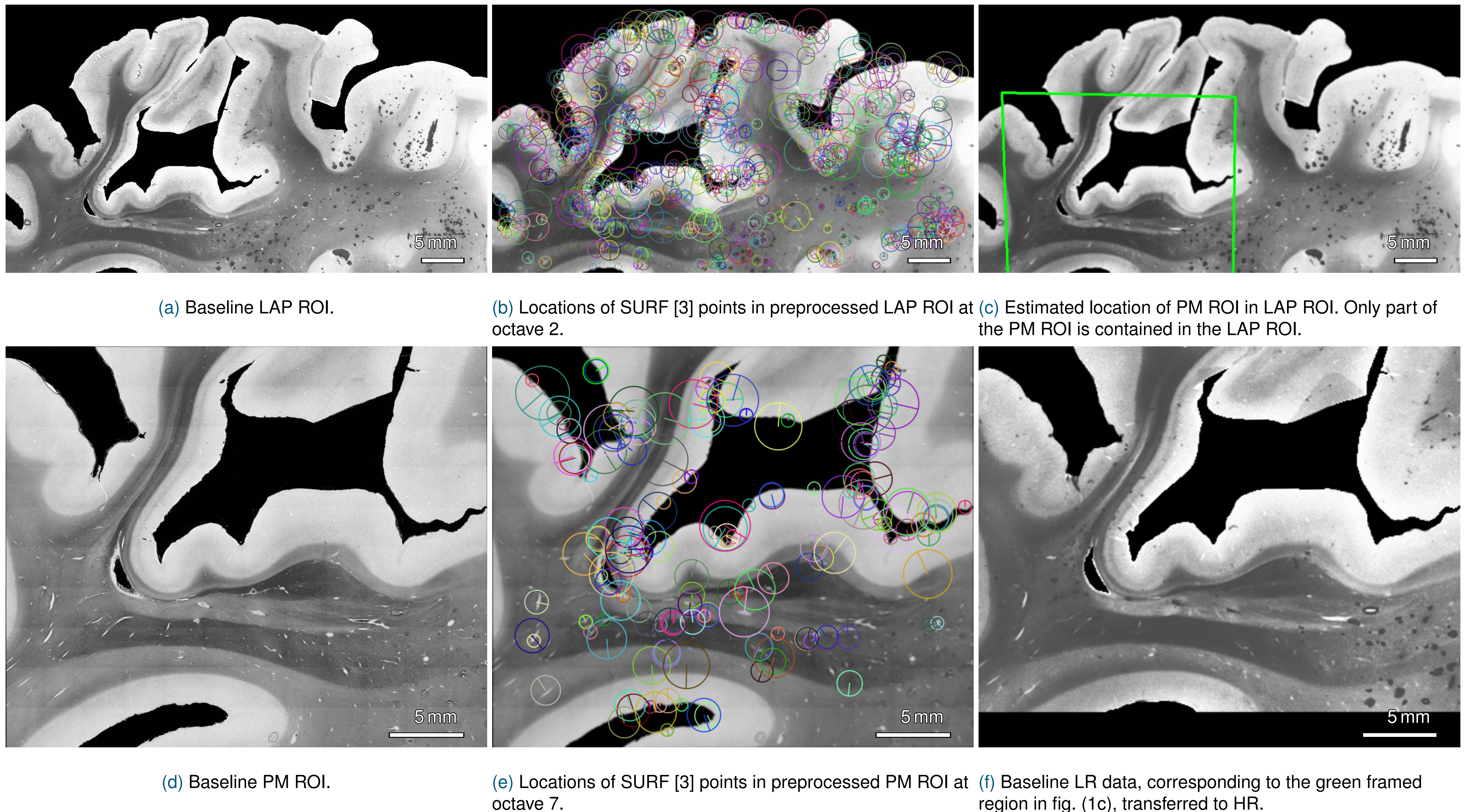


Figure 1: All images show the average light intensity, that is transmitted through a thin brain slice [1, 2], and depict a region from the human occipital pole. The images were manually segmented. Figs. (1b), (1c) and (1e) are smoothed by a Gaussian kernel suitable for noise reduction and adapted to each resolution. Locating the PM ROI in the LAP ROI used a homography estimated by RANSAC [4] from feature point pairs matched by FLANN [6].

Results and Discussion

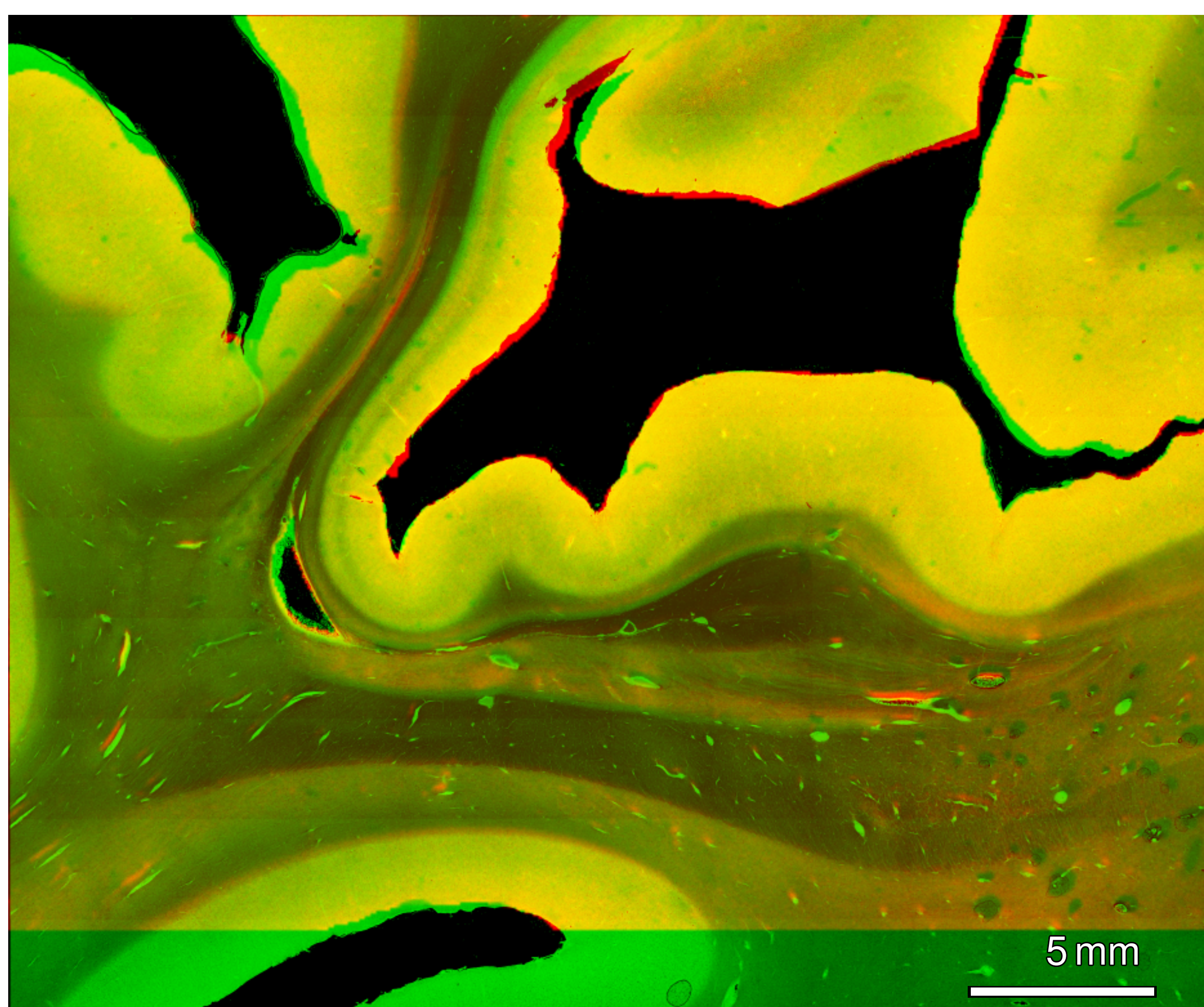


Figure 2: Sum image of normalized PM data (labeled green) and normalized transferred LAP data (labeled red).

The experiments were performed with one HR ROI (figure (1d)), one LAP ROI (figure (1a)) and one LAP image. Localization of the HR ROI in the LR ROI is plausible (figure (1c)), while localization of the HR ROI in the LAP image fails, because the matched feature point positions in HR and LR do not correspond. Numerical and feature point matching inaccuracies become evident in figure (2). We plan to improve the algorithm and to obtain complete HR data sets for further exploration of the method's performance.

References

- [1] Markus Axer, Katrin Amunts, David Gräßel, Christoph Palm, Jürgen Dammers, Hubertus Axer, Uwe Pietrzyk, and Karl Zilles. A novel approach to the human connectome: ultra-high resolution mapping of fiber tracts in the brain. *Neuroimage*, 54(2):1091–1101, Jan 2011.
- [2] Markus Axer, David Gräßel, Melanie Kleiner, Jürgen Dammers, Timo Dickscheid, Julia Reckfort, Tim Hütz, Bjoern Eiben, Uwe Pietrzyk, Karl Zilles, and Katrin Amunts. High-resolution fiber tract reconstruction in the human brain by means of three-dimensional polarized light imaging (3d-pli). *Frontiers in Neuroinformatics*, 5(34), 2011.
- [3] Herbert Bay, Tinne Tuytelaars, and Luc Gool. Surf: Speeded up robust features. In Aleš Leonardis, Horst Bischof, and Axel Pinz, editors, *Computer Vision – ECCV 2006*, volume 3951 of *Lecture Notes in Computer Science*, pages 404–417. Springer Berlin Heidelberg, 2006.
- [4] Martin A. Fischler and Robert C. Bolles. Random sample consensus: a paradigm for model fitting with applications to image analysis and automated cartography. *Commun. ACM*, 24(6):381–395, June 1981.
- [5] Jan J. Koenderink. The structure of images. *Biological Cybernetics*, 50(5):363–370, 1984.
- [6] Marius Muja and David G. Lowe. Fast approximate nearest neighbors with automatic algorithm configuration. In *VISAPP International Conference on Computer Vision Theory and Applications*, volume 1, pages 331–340, 2009.

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