Ultra-high resolution atlas-based segmentation of GPi for deep brain stimulation in Parkinson's disease

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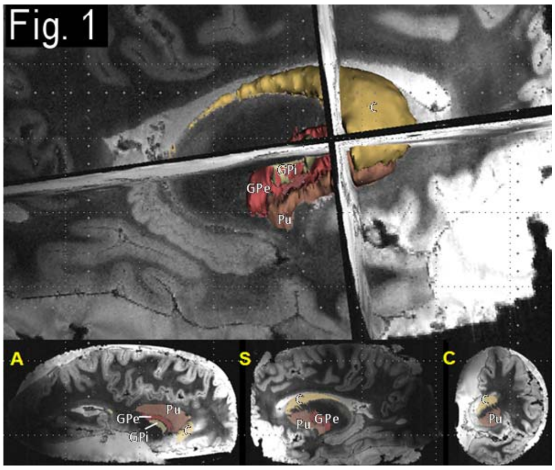
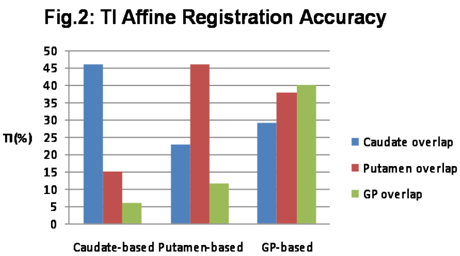
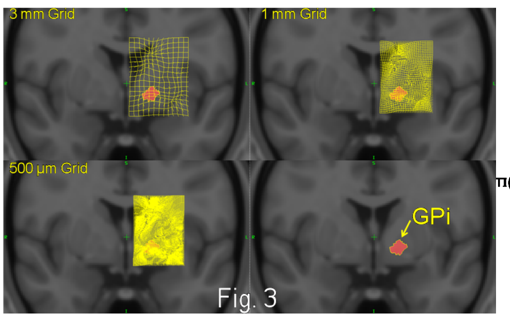
Introduction: Parkinson's disease (PD) is the second most common neurodegenerative disease and more than 4 million people worldwide are affected. The early symptoms and signs of PD, namely rest tremor, bradykinesia and rigidity, are related to the progressive loss of nigrostriatal dopaminergic neurons [1]. Deep brain stimulation (DBS) of the internal part of the globus pallidus (GPi) and the subthalamic nucleus (STN) have shown to significantly improve the motor symptoms of advanced PD patients who are no longer responsive to drug therapy. A process that helps significantly the neurosurgical DBS procedure is the accurate identification of these small structures using a pre-operative MRI. Currently, this is done by direct visualization, which is intrinsically limited because of the poor contrast and resolution of the clinical routine images [2]. To optimize this process we can use detailed information derived from high resolution human brain datasets on which the GPi and/or the STN are well defined. Herein we used a high resolution human brain dataset on which we segmented the GPi. Subsequently we used these data in an atlas-based segmentation procedure to outline the GPi on the pre-operative low resolution images of patients affected by PD. The mapping of the atlas on the pre-operative low-resolution MRI will provide a highly accurate anatomical detail that can be useful for the targets localization.

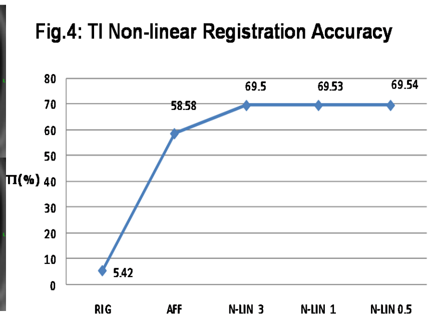
Methods: A normal brain hemisphere was selected for the construction of the high resolution MRI-based atlas. A T2* MRI was acquired as follows: 100 μm^3 isotropic resolution, TR/TE/flip=40ms/20ms/20°, 1600×1100×896 matrix [3]. The contours of the target nucleus (GPi) and the surrounding nuclei (caudate, putamen and the external part of the globus pallidus GPe) were manually outlined on the high resolution dataset. Fig. 1 shows the 3D model of the basal ganglia and the axial, the sagittal, and coronal views of the segmented structures. The 1 mm^3 resolution MNI152 MRI (Montreal Neurological Institute, McGill, USA) has been used as low-resolution image. The caudate and the putamen were manually segmented also on this dataset, while the globus pallidus was segmented as an unique structure without discerning between its internal and external parts that will be automatically segmented by the atlas warping and the subsequent label propagation. The registration of the atlas on the low-resolution images was performed by an affine and a non-linear surface-based registration. The corresponding meshes were generated by directly triangulating the homologous structures segmented on both the atlas and the MNI152. Then we registered the meshes using a multiresolution FFDs registration algorithm based on B-splines, which was formulated by Rueckert et al. [4, 5]. This algorithm manipulates a shape by embedding it into a subsequently refined volumetric mesh, which defines a continuous deformation field through a set of B-splines basis functions. For each location in the reference shape, the corresponding locations in the individual shapes are found to obtain an optimal match. The corresponding optimal deformation field is obtained by minimizing the sum of squared differences (SSD) between corresponding points. The accuracy of the transformation is measured by the root mean square error (RMSE). Herein we compared the performance of different registration strategies. First we performed an affine surface registration by aligning each segmented structure separately: the caudate nucleus, the putamen and the entire globus pallidus. Then, a non-linear registration algorithm based on multiple nuclei was applied. The non-linear registration was applied in a multi-resolution fashion by manipulating an underlying mesh of B-spline control points. The control points act as parameters of the FFDs and the degree of deformation which can be modeled depends essentially on the resolution of the mesh of control points. Once the different transformations were estimated, the manual labels of the GPe and GPi were transformed according to those and propagated on the MNI152 template. The performance of each procedure were then evaluated by quantifying the overlap between the propagated labels and those manually outlined by the anatomist. For each segmentation, we computed the false positive (FP), false negative (FN) and true positive (TP) counts. The Tanimoto index (TI) was estimated to benchmark the different types of registration [6]. The index is close to 100% for very similar segmentation and is near 0 for complete misclassification.





Results:
For each structure the overlap metrics were calculated after the caudate-based (C), the putamen-based (P) and the GP-based registrations as shown in Fig. 2. For each structure the TIs show high values (in %) for caudate, putamen and GP when registration is GP-based (green bars). In Fig. 3 the results of the non-linear registration are presented. The resulting deformed grids and the deformation fields are shown at three different resolution levels. We obtained a RMSE of 492 µm, 450 µm and 432 µm for the 3 mm, 1 mm and 500 µm resolution levels respectively. TI for the non-linear registration increased significantly as we moved from a rigid to an affine and a non-linear registration with different resolution grids (Fig. 4)





Conclusions: We propose a high resolution atlas-based segmentation procedure to discriminate the GPi on the pre-operative low resolution images. Surface non-linear registration based on multiple nuclei prove to benefit accuracy in segmenting the target of interest. Our preliminary results on localizing the GPi are encouraging and we expect that the high resolution and the optimized contrast of the atlas may allow us to discriminate other DBS target structures such as the STN in a way similar to the atlas-based segmentation procedure described for the GPi.

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