Multi-structure Registration Allows Group Interpretation of Midbrain Iron Content in Parkinson's

Jingyun Chen[1], Ali R. Khan[1], Christian Denk[2], Shawna Galley[3], Alexander Rauscher[2], Martin J. McKeown[3], Mirza Faisal Beg[1]

[1] School of Engineering Science
Faculty of Applied Science
Simon Fraser University
8888 University Drive
Burnaby, BC, Canada V5A 1S6

[2] UBC MRI Research Centre
Room M10 Purdy Pavilion
2221 Wesbrook Mall
Vancouver, BC
Canada V6T 2B5

[3] Brain Research Centre
2211 Wesbrook Mall
Vancouver, BC
Canada V6T 2B5

J. Chen: jingyunc@sfu.ca
A. R. Khan: akhanf@sfu.ca
M. F. Beg: mfbeg@ensc.sfu.ca
S. Galley: shawna.galley@gmail.com
M. J. Mckeown: mmkeown@interchange.ubc.ca
C. Denk: ch.denk@gmail.com
A. Rauscher: rauscher@phas.ubc.ca

Introduction

Midbrain iron deposition imaged on susceptibility weighted imaging (SWI) magnetic resonance (MR) sequence is a potential biomarker for Parkinson disease (PD)[1]. Accurate registration of SWI images to a template image allows assessment of common spatial patterns of iron deposition.

Challenges for Accurate Registration:

➢T1-MR images alone are usually not sufficient due to low intrinsic contrast.

➢SWI images do not offer adequate anatomical contrast except for a few structures such as the red nucleus (RN).

Solution:

A hybrid "multi-structure" approach that jointly incorporates T1 images and manual binary segmentations of midbrain structures in the SWI images concurrently.

Method

Data acquisition:

➢The T1 and SWI images are obtained on a 3 Tesla scanner equipped with a head-coil (3DT1TFE CLEAR, TR = 7.716ms, TE = 3.56ms, flip angle = 8, FOV = 256x170x200mm).

➢19 PD subjects (15 male, 4 female, 17 right-handed, mean age=64 years, SD=9), and 18 age-matched normal control subjects are obtained.

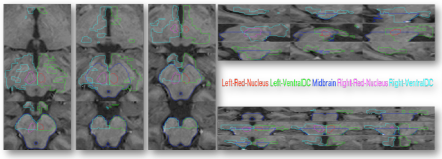
Binary segmentation:

➢T1 images registered to SWI images using FLIRT.

➢Red nucleus (left and right) manually segmented on SWI images.

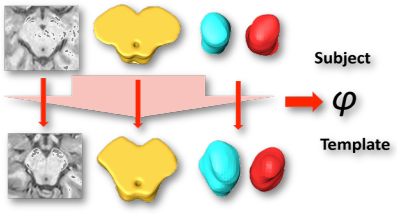
➢Midbrain areas manually segmented on registered T1 images.

➢The left and right ventral diencephalon (VentralDC) segmented by Freesurfer on original T1 images.



Three-step registration:

1. Affine registration of T1 images to SWI images with FLIRT.
2. Boundary box containing midbrain neighborhood cropped.
3. High dimensional non-rigid registration within the boundary box with multi-structure Large Deformation Diffeomorphic Metric Mapping (LDDMM)[2].



References:

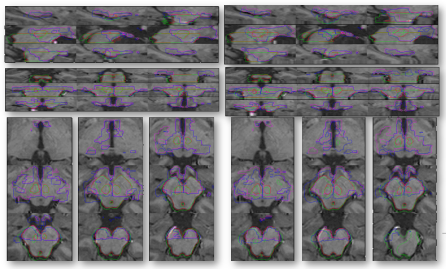
[1] Martin, W.W.R., Wieler, M. and Gee, M. (2008), 'Midbrain Iron content in early Parkinson disease. A potential biomarker of disease status', *Neurology*, vol. 70(2), no. 16, pp. 1411-1417

[2] Khan, A., Beg, M. F. (2009) 'Multi-structure whole brain registration and population average', *Proceedings of the IEEE Engineering in Medicine and Biology Society Conference (EMBC)*, pp. 5797–5800

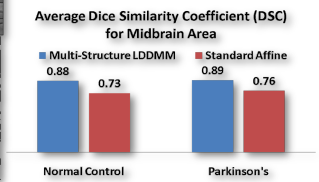
Results

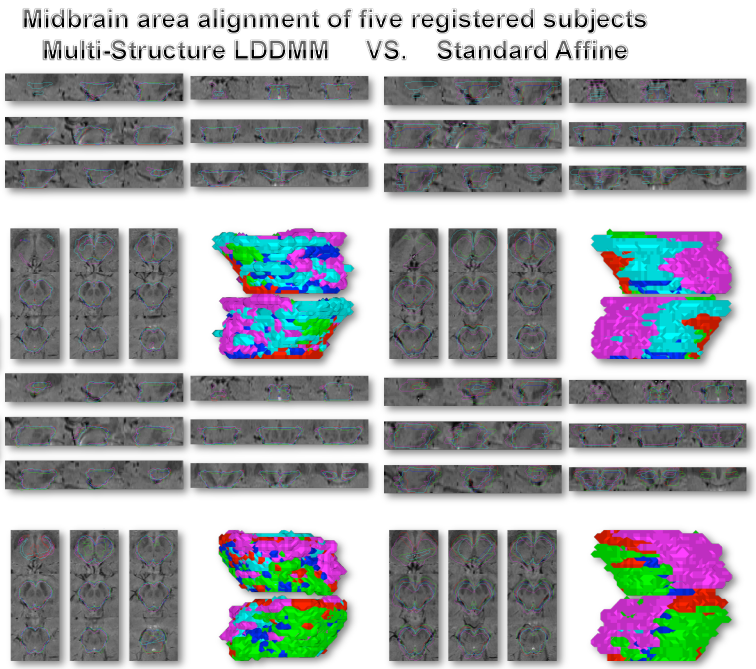
Multi-structure LDDMM registration using T1 image and binary segmentation of midbrain, red nucleus and ventral DC as channels. T1 as background, outline colors defined as follow:

Target-Midbrain Target-RedNucleus Target-VentralDC
Template-Midbrain Template-RedNucleus Template-VentralDC



$$DSC(A,B) = 2\frac{V(A \cap B)}{V(A) + V(B)}$$





Conclusions

We propose a novel method of using multiple concurrent streams of anatomical information for the registration of complex brain areas such as the mid-brain. For both PD and control subjects, the multi-structure LDDMM method improved alignment of structures on, within, and near midbrain areas, thus providing more reliable registration of SWI images for localizing group difference of midbrain iron content.