NON-LINEAR IMAGE REGISTRATION OF BRAIN MRI IMAGES AND MEASUREMENT OF ATROPHY

BiomedIQ
Biomedical Image Quantification

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Abstract

Why? Accurately quantifying atrophy in brain.

How?

Step 1: Whole Brain Segmentation on baseline ← Freesurfer

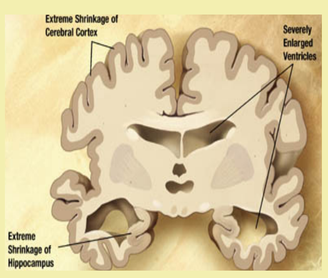
Step 2: Multi-scale Nonlinear Deformation from Baseline to Follow-up

Step 3: Estimate the volume change per voxel from the deformation field

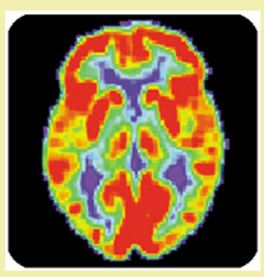
And? We apply these methods on publically available subjects from the Alzheimer's Disease Neuroimaging Initiative (ADNI) data and present statistics on several ROI's

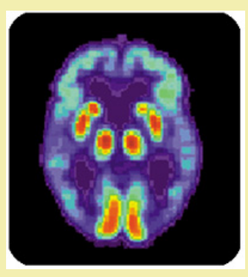
Alzhiemer's: Alzheimer's disease is an irreversible, progressive brain disease that slowly destroys memory and thinking skills.

Data: Baseline and 12 month follow-up 1.5 T T1-weighted MRI volumes of a subset of 101 ADNI database were analyzed: 24 normal controls (NC), 29 MCI, and 48 AD.



AD disease


Normal PET


AD PET

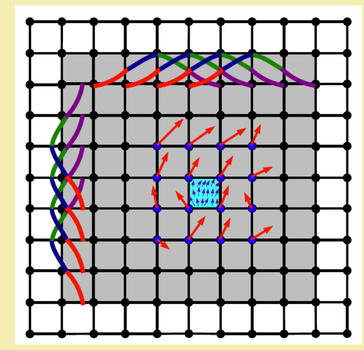
Materials and methods

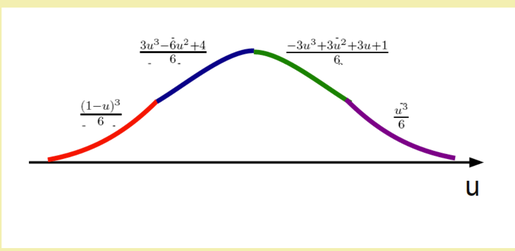
Rigid: Translation and rotation

Non-Rigid: Cubic B-Splines

Similarity Measure: Normalized Mutual Information (NMI)

Evaluation points: Every 3rd voxel, every voxel in ROI in the last level.


B-spline grid

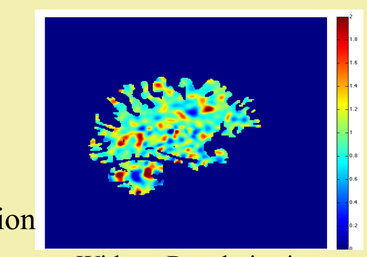


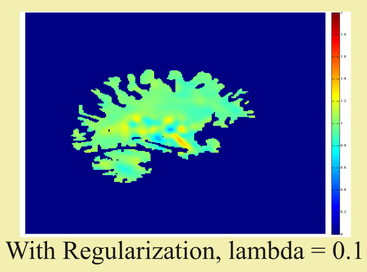
Cubic B-spline formulation

Regularization: A simple gradient of motion in neighborhood control points is used.

$$S(\phi)=|\nabla\phi|^2$$

Why Regularize? ill-posed problem, unique solution


Without Regularization

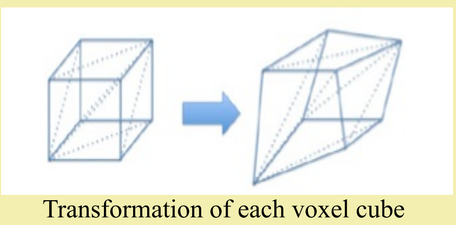

With Regularization, lambda = 0.1

Atrophy computations:

Each vertex of a cubic voxel is pushed through the transformation and the volume of the deformed triangulated cube is computed.

In 3 dimensions, the computation take the form,

$$J f(x,y.z) = \left|\frac{\partial Y}{\partial x}.\frac{\partial Y}{\partial y}\times\frac{\partial Y}{\partial z}\right|$$


Transformation of each voxel cube

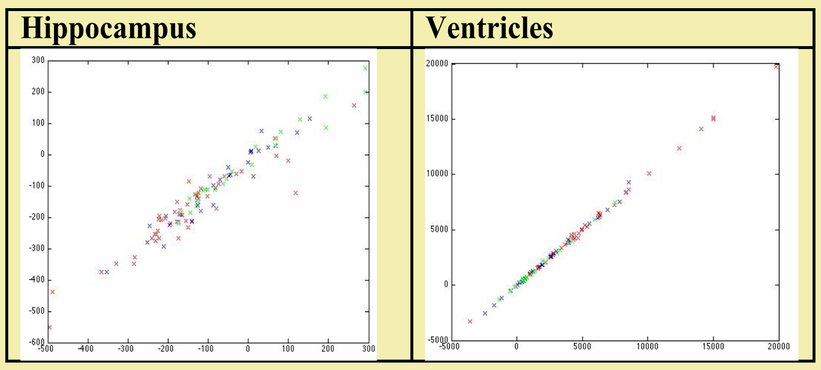
Efficacy tests

Comparison of registration based and freesurfer static pipeline based methods in separating the cognitive groups using non-parametric testing (Wilcoxon's ranksum).

	Hippocampus	Ventricles
Registration based	NC=0.2±2.06 MC1=1.3±2.11 AD=2.9±2.9 MCI>No=0.069 AD>MCI=0.0095 AD>No=0.000114	NC=-4.6±4.0 MCI=-6.7±13.04 AD=10.9±6.6 MCI>No=0.45783 AD>MCI=0.06949 AD>No=0.000101
Freesurfer	NC=1.00±7.04 MC1=0.9±5.6 AD=4.7±7.3 MCI>No=0.356 AD>MCI=0.018259 AD>No=0.003552	NC=-4.2±5.2 MCI=-8.5±15.8 AD=13.2±6.7 MCI>No=0.44103 AD>MCI=0.07158 AD>No=0.00015

Bias Estimates

Swap Analysis



R>0.96 R>0.99

Conclusions: The algorithm developed has been able to successfully separate the control and AD groups. The algorithm is fairly consistent in backward registration.

References

[1] D. Rueckert, L. I. Sonoda, C. Hayes, D. L. G. Hill, M. O. Leach, and D. J. Hawkes, "Nonrigid registration using free-form deformations: Application to breast MR images," *IEEE Trans. Med. Imag.*, vol. 18, pp. 712–721, Aug. 1999.
[2] Fischl, B., Salat, D.H., Busa, E., Albert, M., Dieterich, M., Haselgrove, C., van der Kouwe, A., Killiany, R., Kennedy, D., Klaveness, S., Montillo, A., Makris, N., Rosen, B., Dale, A.M., 2002. Whole brain segmentation: automated labeling of neuroanatomical structures in the human brain. Neuron 33 (January), 341–355.