An automated AI-based framework for putamen volume measurement in Multiple System Atrophy

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We present a fully-automated, end-to-end workflow for putamen volume and volume change estimation in a computationally efficient, scalable manner with advantages for clinical trial deployment.

The **putamen is a well-established biomarker in Multiple System Atrophy** (MSA) used to assess disease progression and potential efficacy of interventions.

As such, the estimation of accurate and robust volume and volume change measures in this region, in a scalable and consistent manner, is highly important for deployment as clinical trial endpoint.

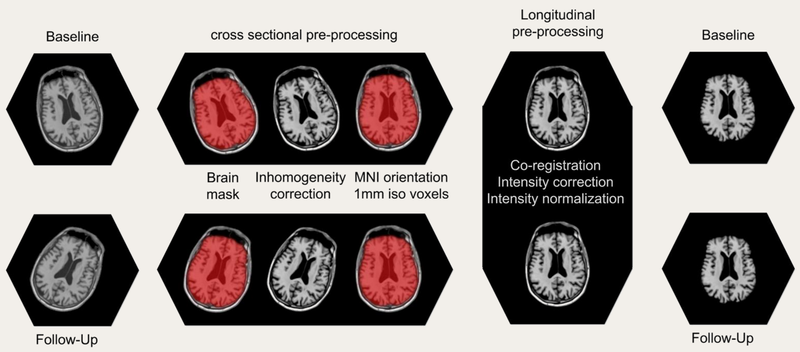
Here we present **a fully automated, end-to-end workflow for estimation of cross-sectional volume and volume change in the putamen using two techniques based on deep-learning.**

We retrospectively analysed 300 T1W images from MSA patients (both cerebellar and parkinsonian subtype – MSA-C = 171 and MSA-P = 129 respectively) from the M-STAR study. No healthy controls were included, and analysis was performed on the pooled placebo and treatment groups.

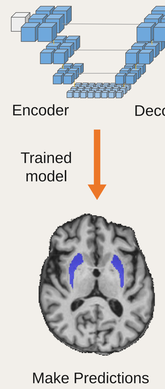
Cross-sectional segmentations of structural MR images and putamen volumes were obtained with a 3D convolutional neural network (CNN) employing a U-net like architecture.

To measure **longitudinal volume change** we trained a CNN to perform non-linear registration of serial MR image pairs. Volume change measures were obtained from integration of the **Jacobian determinants** within baseline putamen segmentations.

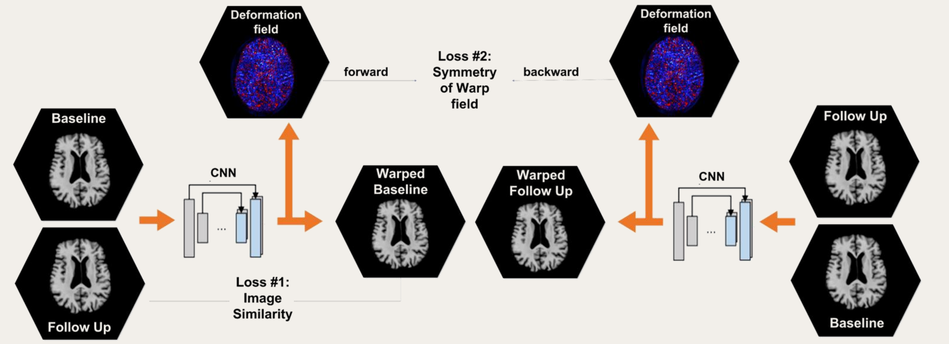
Pre-processing



Cross-sectional Putamen Volume

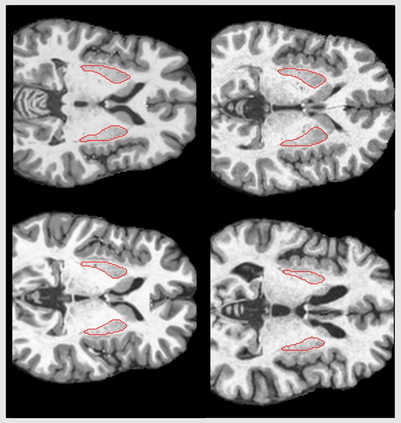


Longitudinal Putamen Volume Change



Cross-sectional Putamen Volume

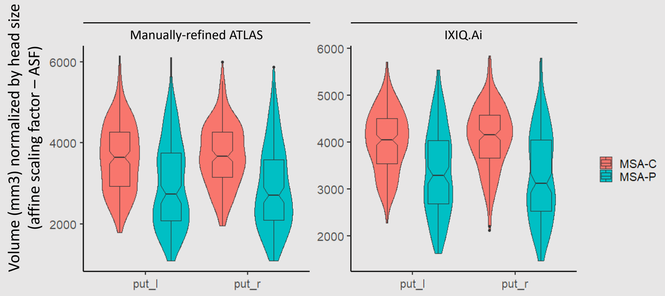
Example segmentations



Baseline putamen volume was compared between clinical groups, estimated with:

1. Manually-refined multi-ATLAS-based
2. CNN-based segmentations (IXIQ.Ai)

Both methods reported **significant differences between MSA-C and MSA-P (p< 0.001*)**



* GLM models were adjusted for age, sex, site and total UMSARS

Longitudinal Volume Change

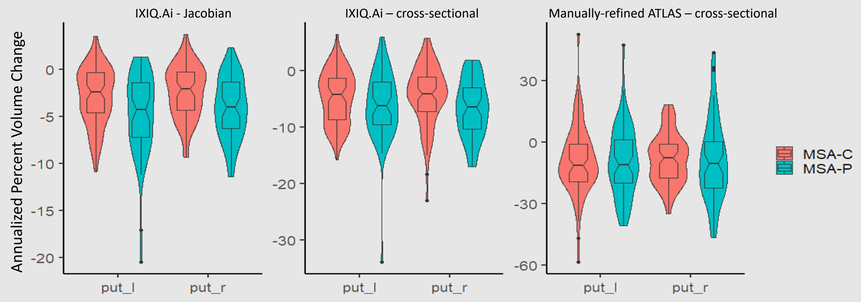
Putamen percentage atrophy over 1 year was compared between:

1) manually-refined ATLAS segmentations at all timepoints

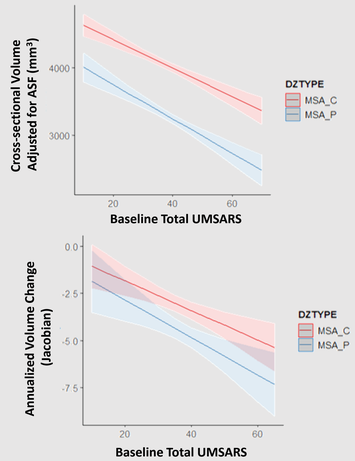
2) IXIQ.Ai cross-sectional segmentations at all timepoints

3) The IXIQ-Ai - Jacobian method with CNN baseline segmentations

Longitudinal change measured using IXIQ.Ai – Jacobian showed significant group discrimination (p < 0.01*), but not cross-sectional segmentations at both timepoints for either IXIQ.Ai or ATLAS segmentations (all p > 0.05*)



Sensitivity to Disease Stage



IXIQ.Ai cross-sectional and longitudinal methods further show good sensitivity to disease stage as described by total UMSARS at baseline in both MSA-C and MSA-P subtypes.

Conclusion: Our fully-automated IXIQ.Ai methods provide estimates of volume and volume change sensitive to disease subtype and progression in MSA.