Fully-automatic Al segmentation of subcortical regions Weatheritt J¹, Joules R¹, Rueckert D² & Wolz R^{1,2} ¹IXICO plc, London UK [²Department of Computing, Imperial College, London, UK



Introduction. Putamen volume change is used as a biomarker to track the development of Huntington's disease (HD) and monitor the potential effect of interventional treatments. Therefore, accurate volume calculations, obtained via segmentations, are of utmost clinical importance. Putamen segmentation is challenging, due to unclear region boundaries. We present a fully-automated approach that performs at state of the art for an HD population.

Neural Network Method

A neural network (CNN) is a set of operations, loosely modelled on the human brain, that by repeated exposure to 100s of examples of labelled data, learns how to predict anatomical regions at the pixel level.



Data. The CNN is trained and validated using semi-automated labels from 170 subjects from an AD cohort¹ (ADNI) and 25 subjects from an HD cohort respectively. Qualitative results are shown on further data sets labelled below.



Results There is no change in model performance between training (AD) and test (HD) populations – despite a large change in volume. On the validation data set, we compare the model to LEAP³, P-LEAP (optimised for putamen), MALPEM and Freesurfer.

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One subject close to median dice overlap (DSC) for all methods

Conclusions. The deep learning method is shown to perform at state of the art for an HD population – after being trained on an AD population. Further, the algorithm is seen to generalise well to different data sets – comprised of different disease groups and scanner settings.

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