## Human thalamic structure segmentation with universal SHape Interpolation using the Radon Transform (uSHIRT)

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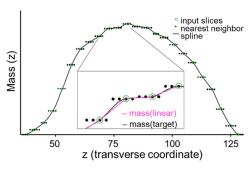
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TARGET AUDIENCE: Developers of image processing pipelines; scientists interested in image processing and morphology.

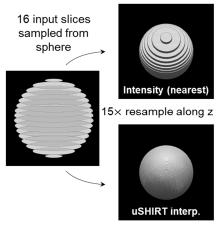
**INTRODUCTION:** The thalamus has been of increasing interest in neurological disorders due to its involvement in sensory and motor signal relay and the regulation of consciousness and sleep <sup>1,2</sup>. Various methods have been proposed to estimate thalamic volume, including automatic segmentation, visual segementation with manual drawing of 2D contours, and stereological methods <sup>3</sup>. However, lack of anatomical accuracy and highly labor-intensive methods make the thalamus a very difficult target for structural analysis. In addition, intensity interpolation of anatomical mask shapes creates difficulties for Fig. 1. Example mass function and various coregistration, reslicing and editing masks in different planes. Our aim is to generate anatomically correct region of interest (ROI) shapes using the proposed universal Shape Interpolation using the Radon Transform (uSHIRT).

The uSHIRT algorithm can take the place of ubiquitous intensity interpolation methods (e.g. trilinear, sinc) as we described previously <sup>4</sup>, allowing rapid resampling of arbitrary, naturally shaped anatomical masks. The uSHIRT method proposes an advancement based on a mass-smoothness constraint using a straightforward procedure. In this study, we tested the capability to interpolate arbitrary complex shapes firstly using test images, and secondly using manually delineated thalamus segmentations of the human brain.

**METHODS:** The uSHIRT algorithm was implemented based on our previously described algorithm<sup>4</sup>. In uSHIRT, radon transformed projections are blended using a mesh between arcs, with a distance coefficient that determines the relative location along legs of the arc mesh. In order to introduce a spline, we first measure the area (2D sum) of each slice, the input mass function, and then we stipulate an output (target) mass function (Fig. 1). The mass function of a sphere is precisely a parabola, and thus we specify a bounded, low-order polynomial spline as the interpolant for the output mass function. The spline must be bounded, as overshoot would lead to unbounded arc mesh segments. The target mass function can be satisfied by

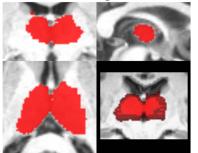


interpolant splines.



**Fig. 2.** The comparison between Intensity interpolation (top, right) and uSHIRT shape interpolation (bottom, right) using a sphere (left) as test input.

## **Automatic Segmentation**



## uSHIRT with 22 input slices

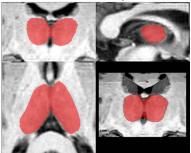


Fig. 3. Automatic segmentation of the thalamus using FreeSurfer (left) and uSHIRT resampling (right).

calculating new distance coefficients, which are themselves functions of the axial (z) dimension. Conveniently, the output mass function can be obtained without taking the inverse radon transform. In a first pass, the output mass is measured with a linear coefficient series. Then, the corrected coefficient series is obtained using a 1D interpolation step. This operation comprises a one-time loopback over the radontransformed data. The tested speed of our uSHIRT code on a Linux desktop computer, with image size  $256 \times 256$ , was roughly 10 slices/second.

**RESULTS AND DISCUSSION:** A test shape

(Fig. 2) was obtained by sampling a spherical solid at every 15 slices. Nearest neighbor interpolation, and uSHIRT results for this shape, are shown in Fig. 2. Segmentations of the thalamus are shown in Fig. 3. Automatic segmentation (FreeSurfer) is shown at left, and manual segmentation at 22 slices, followed by uSHIRT interpolation, is shown at Fig. 3. Whole-thalamus volume results were 16373 mm<sup>3</sup> using FreeSurfer and 11428 mm<sup>3</sup> using manual segmentation with

REFERENCES: [1] Zivadinov et al, Radiology 2013. [2] Minagar et al, Neurology 2013. [3] Keller et al, Neuroinformatics 2012. [4] Adany et al, PISMRM 2014. This work is partly supported by NIH (S10RR29577, UL1TR000001) and the Hoglund Family Foundation.