

# NeuroShape Manual

Version 0.9

[neuroshape.neuroimaging.ch](http://neuroshape.neuroimaging.ch)

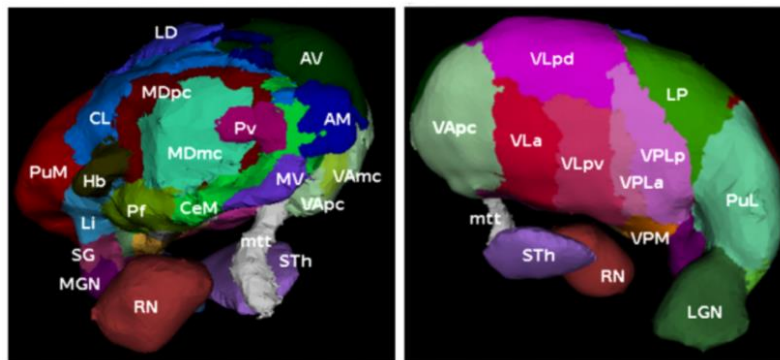
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## Overview

Conventional neurosurgical targeting commonly relies on transferring stereotactic coordinates from an atlas to the patient's anatomical space using linear correspondences between reference points in the atlas and CT or MRI images. Such reference points are, for example, the anterior and posterior commissures in the midline. The linear transfer of coordinates offers only a limited flexibility in faithfully localizing common neuroanatomical targets, such as for image-guided thalamotomy or deep brain stimulation, and the direct visualization of target structures is not currently possible with conventional clinical MRI.

NeuroShape is an extension to the popular medical image analysis software Slicer 3D. The concept of the NeuroShape software is to use known correspondences between predictor and target structures from a statistical shape model (SSM) atlas of the human thalamus to provide target models for neurosurgical targeting that match the patient's anatomy. Predictors are structures that are visible on targeting images, such as the macroscopic thalamus outlines visible on the pre- or intra-operatively acquired MRI. Instead of reference landmarks, NeuroShape therefore uses volumetric, 3D meshes as predictors. The remaining, unobservable part of the thalamus anatomy is predicted using the correspondences stored in the SSM atlas. Neurosurgical target structures typically represent the unobservable geometry, such as the ventrolateral posteroventral (VLpv – or Vim) nucleus.



The neuroanatomical atlas used in the NeuroShape software is based on the multiarchitectonic analysis of 7 thalami (illustrated above) as described in the works of Krauth et al., 2010 and Morel, 1997, and on the implementation of this atlas as a statistical shape model.

## Licensing

NeuroShape is freely available for academic purposes. However, you need to obtain a specific license to use the “Morel Thalamus Atlas”. Licensing is managed by the secretariat of the Computer Vision Laboratory, ETH Zürich, Switzerland. Please contact the secretarial office of Professor Gabor Székely and Professor Luc van Gool to get more information:

**Email:** [biwiadm@ee.ethz.ch](mailto:biwiadm@ee.ethz.ch)

If you use NeuroShape in your research, please cite the following references:

Krauth A, Blanc R, Poveda A, Jeanmonod D, Morel A, Székely G. A mean three-dimensional atlas of the human thalamus: generation from multiple histological data. *Neuroimage*. 2010 Feb 1;49(3):2053-62.

Jakab A, Blanc R, Berényi EL, Székely G. Generation of individualized thalamus target maps by using statistical shape models and thalamocortical tractography. *AJNR Am J Neuroradiol*. 2012 Dec;33(11):2110-6.

## Installation

### Downloading the software

As of 1/2/2018, the NeuroShape software is only available through individual requests. Please contact the project team:

Dr. Andras Jakab, [andras.jakab@kispi.uzh.ch](mailto:andras.jakab@kispi.uzh.ch) and Prof. Dr. Orcun Goksel

And please acquire a license for the “Morel Thalamus Atlas” with the procedure described on page 3.

### Compiling from source code

The NeuroShape software can be downloaded by executing:

```
git clone https://git.ee.ethz.ch/zgoey/neuroshape.git
```

To build and install the software on an Ubuntu machine (16.04 LTS):

cd into the directory neuroshape, execute the bash script install.sh (issue ./install.sh on the command line):

```
bash install.sh or ./install.sh
```

To build and install the software on a Windows 10 machine:

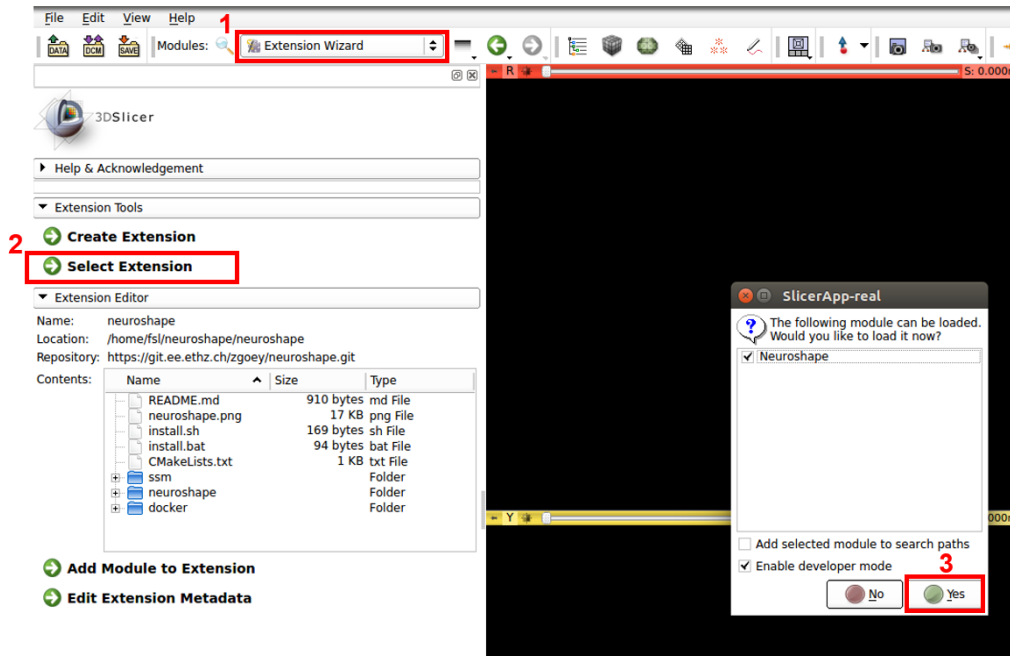
1. download and install cmake (<https://cmake.org/download/>) and add it to the system path (see option in installer)
2. download and install Visual Studio 2013 Community Edition (<http://go.microsoft.com/?linkid=9863609>)
3. download and install 7-Zip (<http://www.7-zip.org/download.html>), and add it to the system path (by hand)
4. execute the batch script install.bat

On other platforms, the content of install.sh and install.bat can be used as a guidance on how to build and install neuroshape.

Note: this project contains ssm as a subproject.

## Installing the Slicer 3D extension

To use NeuroShape, you must install a compatible version of Slicer 3D. NeuroShape has been tested with the stable release of Slicer 3D version 4.6. Select the module **Developer Tools / Extension Wizard**, then click on **“Select Extension”**. In the directory selection window, select the directory that contains the “neuroshape” directory in your NeuroShape installation:

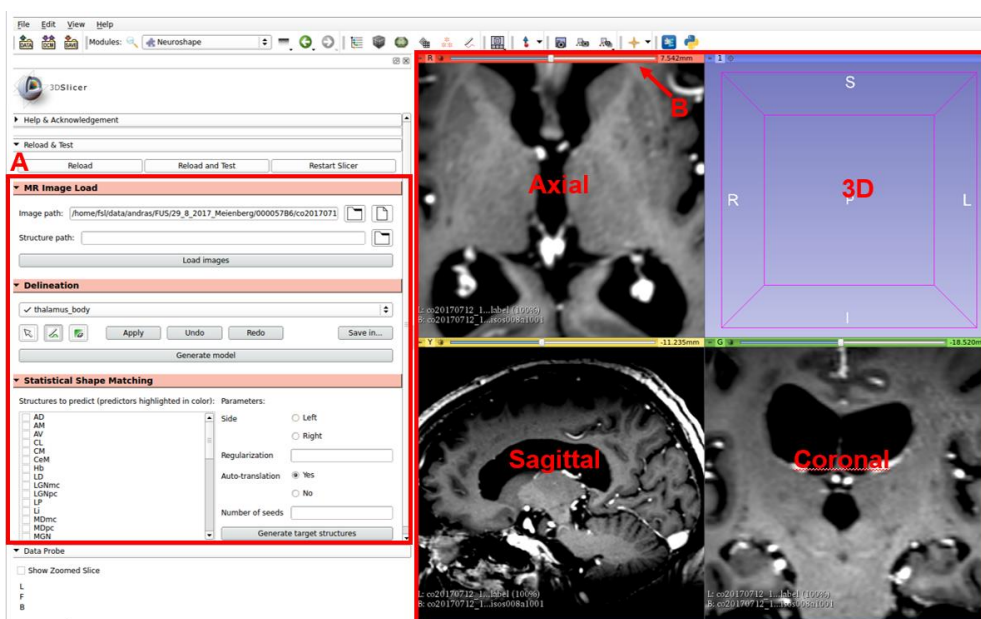


## Usage

Many steps of the NeuroShape work-flow rely on Slicer 3D functions. For tutorials and trainings on how to use Slicer 3D, please visit the following websites:

<https://www.slicer.org/wiki/Documentation/Nightly>

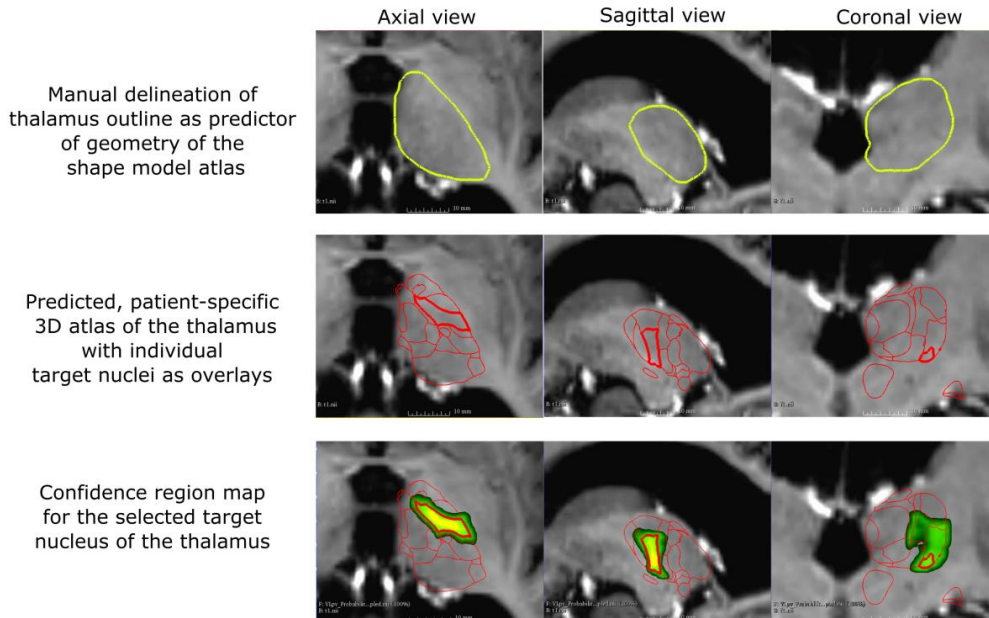
<https://www.slicer.org/wiki/Documentation/4.6/Training>



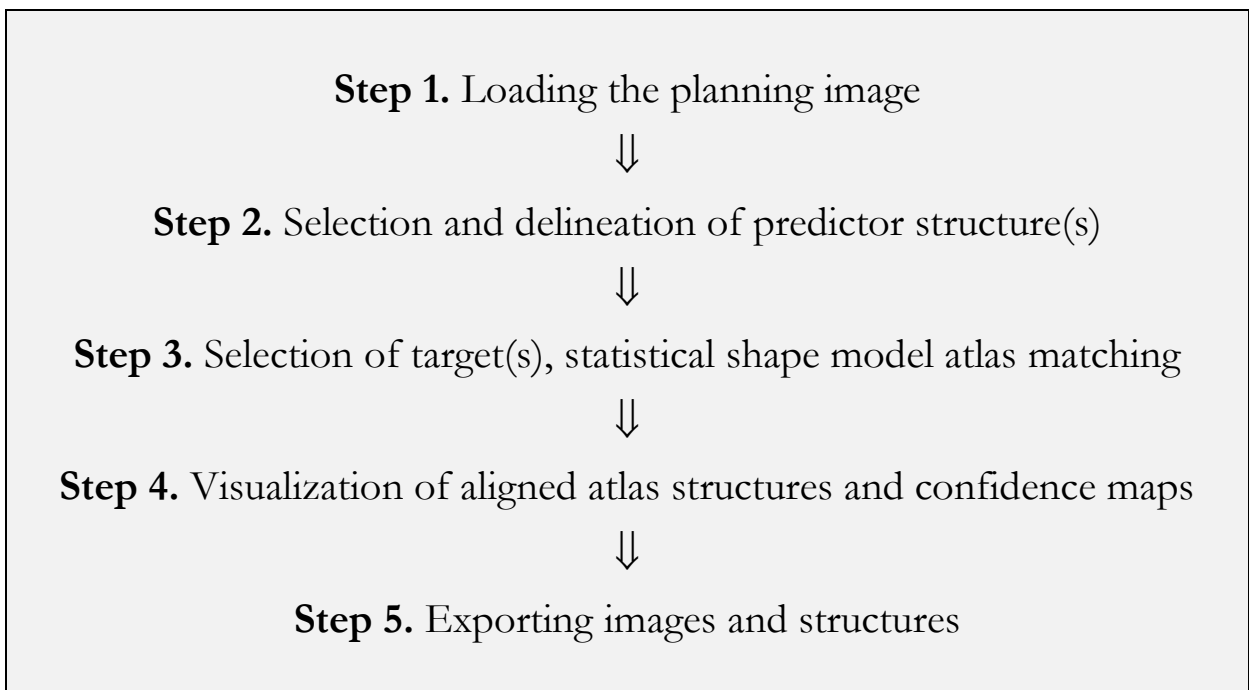
Overview (A): NeuroShape extension. (B) View manipulation tools.

## Overview of the NeuroShape work-flow

The NeuroShape work-flow requires a baseline planning image on which the user annotates visible reference structures, such as the visible (macroscopic) thalamus outline. This image is typically the pre-operative 3DT1 or T2 image, or in case it is available, intraoperatively acquired MRI. CT is not currently recommended due to the difficulty in locating the borders of subcortical structures.

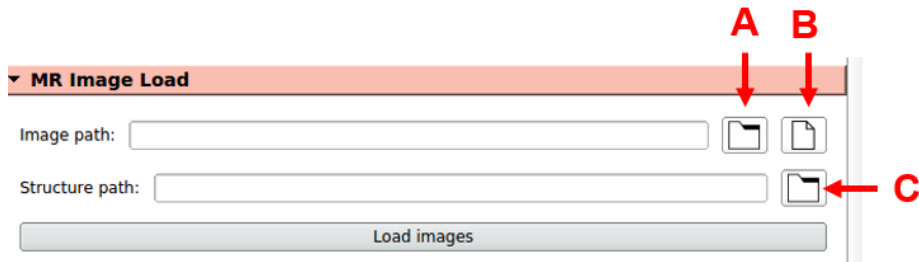


The following flow-chart summarizes the steps of the NeuroShape tool:



## Step 1. Loading the planning image

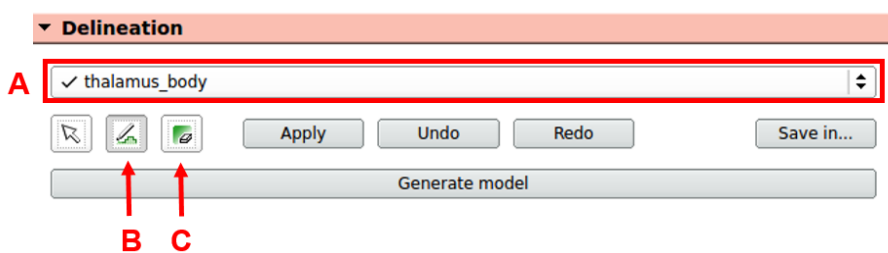
**Module “MR Image Load”.** Two options are available: **(A)** loading an entire directory of DICOM images that corresponds to one image series, and **(B)** loading individual images. Currently, NeuroShape forces the .nii.gz (NifTI, gzip compressed) image format if the single-image option is chosen. The user can also re-load previously saved annotated structures in this step **(C)**. By pressing “**Load images**”, the selected planning images and/or previously saved annotated structures will be loaded.



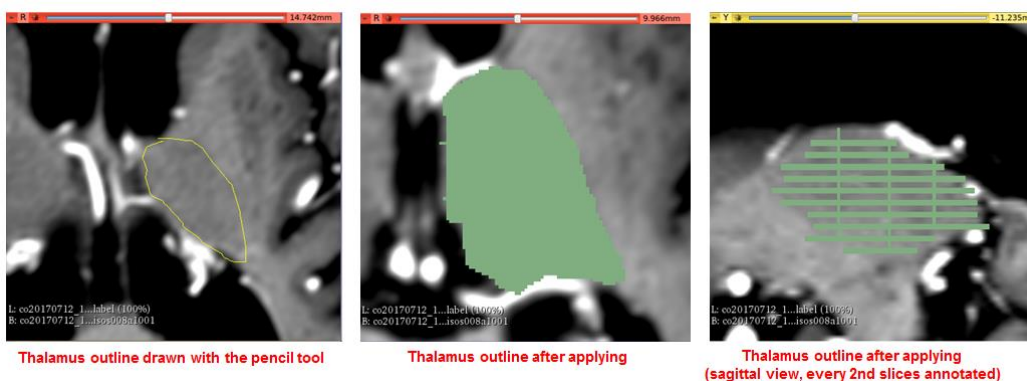
## Step 2. Selection and delineation of predictor structure(s)

**Module “Delineation”.** NeuroShape requires one or more, predictor structures to align the SSM atlas to the patient’s anatomy. While the user has full freedom in defining individual predictor structures and combine them, it is recommended that structures are used that are reliably and completely visible on a given type of image. For example, the gross thalamus outlines are clearly distinguishable from neighboring structures at, and above the level of the AC-PC plane on T1- and T2-weighted MRI.

First, the user selects a structure to be annotated from a drop-down list **(A)**. The MRI-visible gross thalamus outline is named as “thalamus\_body”. Then a simple pencil tool is available for delineation **(B)**. The eraser tool **(C)** works identically to the pencil tool, with the only difference that it will create shapes with a label value of zero:



You can “apply” your currently drawn 2D shape by pressing enter or clicking on the **Apply** button, this will make it a part of a 3D label map. The complete volume has to be covered slice-by-slice or by delineating every 2<sup>nd</sup> slices. Example annotation of the visible thalamus outlines:



After the first structure has been completely delineated, the user can select the next structure from the same list, if needed, which would create a blank label map image (the previous annotation gets saved automatically). You can resume delineating another structure by selecting its name in the drop-down menu in the Delineation module.

Next, when the user finished annotating all the required predictor structures, the button “**Generate model**” creates a merged 3D object from all of the previously delineated structures.

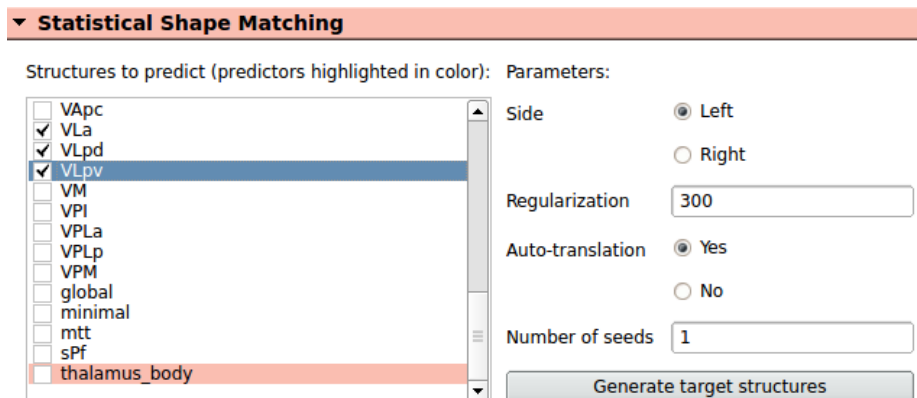
NeuroShape performs a sequence of simple morphological operations once the user has finished delineating all visible structures: the annotation is interpolated by using a morphological opening filter and spatial smoothing with a kernel of 1.5 mm. For this reason, it is enough for large structures to only draw their outlines in every second or third slices (for example, in case of the visible thalamus borders), after the morphological processing, the missing in-between slices will be filled up by interpolation.

### Step 3. Selection of target(s) and statistical shape model atlas matching

**Module “Statistical Shape Matching”.** This window consists of two parts. On the left, a list displays a list of all the structures in the thalamus atlas. The structures that have been delineated and for which models have been generated in Step 2. are highlighted in color.

The same list is then used to select target structures that the user wants to see during the neurosurgical planning process.

First, the user selects one or more target structures from the list. In the following example, the thalamus\_body has been delineated (color highlight), and the VL<sub>a</sub>, VL<sub>pd</sub> and VL<sub>pv</sub> (=VIM) nuclei will be generated as target models.



Next, the user configures the SSM matching process by using the right side of the module.

“**Side**”: the hemisphere of the predictor and target structures has to be selected. It is highly recommended that the delineated predictors and targets are in the same hemisphere.

“**Regularization**”: this parameter affects the shape matching process: lower regularization means more freedom during the alignment, the resulting shape will conform more to the predictor structures, but will be less similar to the “real” geometries stored in the atlas. By default, a value of 100 to 300 is recommended.

“**Auto-translation**”: this controls if an initial transformation (3 degrees of freedom of translation) is performed to match the atlas to the predictor structures. The default recommended value is “Yes”.

“**Number of seeds**”: NeuroShape enables confidence maps to be calculated for each structure. More seeds mean better estimation of the uncertainty associated with the matching, however, for



initial testing a value of 1 is also possible. The computational time is proportional to the number of seeds.

The target structures and confidence maps are generated by pressing the “**Generate target structures**” button. Computational time with seed value 1 is around 20-30 minutes. During this time, Slicer 3D is unresponsive and may appear to be frozen.

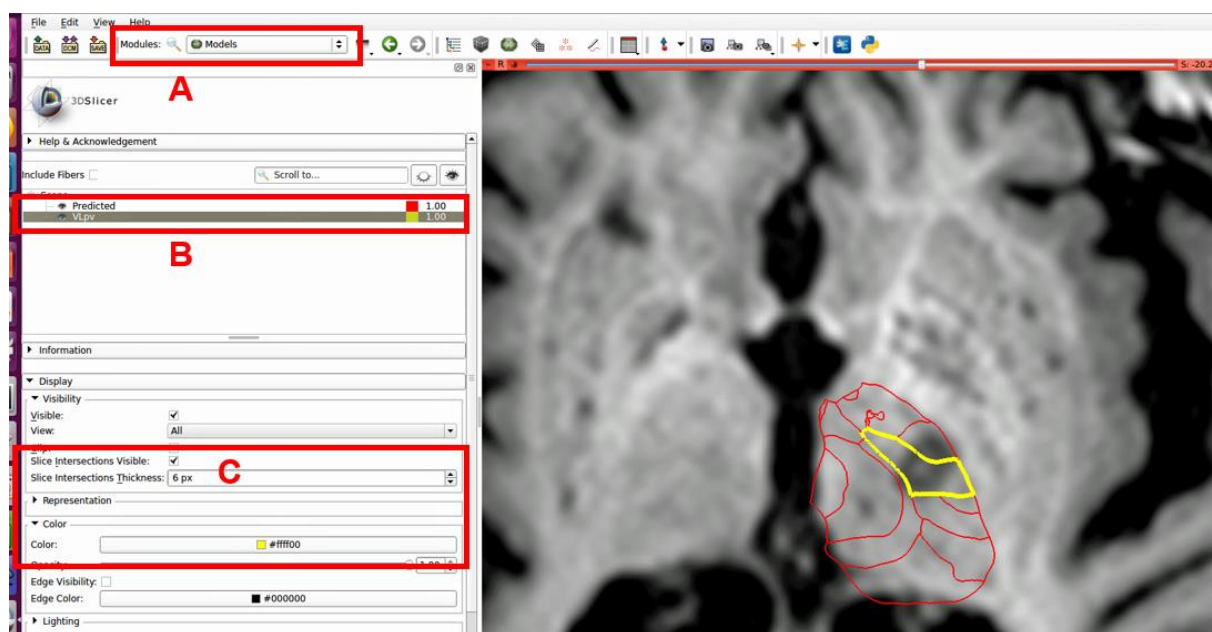
#### Step 4. Visualization of aligned atlas structures and confidence maps

In the “Data” module in Slicer 3D, the user can check all the structures, while in the “Models” module, the user can change the display properties of the individual target and predictor structures.

After running Step 3. the following structures are stored in Slicer 3D:

- the predicted global thalamus model
- the predicted thalamic nuclei selected by the user
- the confidence maps for the predicted thalamic nuclei selected by the user

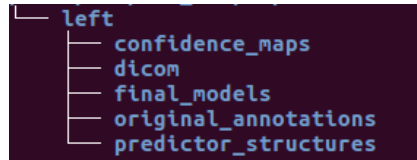
The resulting target structures are stored in .vtk file format and the individual nuclei are named after the nomenclature defined on page 11. of this manual. Besides this, a global thalamus model (named: **Predicted**) is also always calculated. This is a merged model of all thalamic nuclei in the atlas. For visualization purposed within Slicer 3D, the user can make them visible as outlines fused with the planning MRI. First, open the module “Models” in Slicer (**A**), select the Predicted (global model) and/or the target nucleus (**B**), tick on the “Slice intersections Visible” display property of the corresponding entry (**C**):



**Confidence maps:** each selected target structure is also saved as a confidence map. In these images, the value of each voxel corresponds to the confidence of the SSM-matching process (value between 0 and 1). This can be overlaid with the original planning image, and exported in any image formats, including DICOM.

## Step 5. Exporting images and structures

Export from NeuroShape is possible in two ways. By selecting the output folder in Step 3, the resulting structures (3D objects and confidence map images) and the predictor structures are saved in the following sub-directories within the selected directory (example for left-sided thalamus):



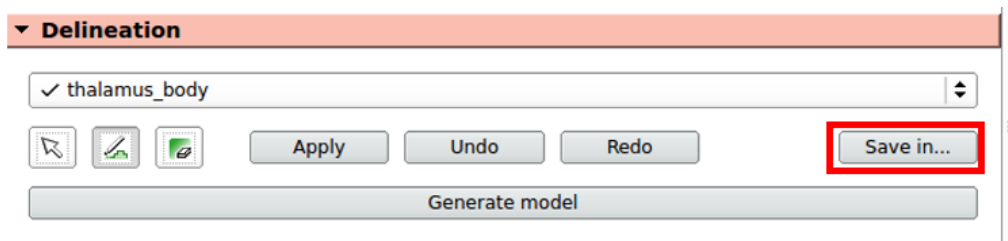
However, the “Data” module in Slicer 3D allows the user to save all structures and maps separately in any format that Slicer 3D supports.

**DICOM Export:** Slicer 3D supports DICOM export function, which is used in case of the automatic output option. However, the DICOM images are anonymized and the DICOM tags corresponding to the image modality, patient or acquisition settings are blank. By default, the confidence maps of the selected output structures are saved into separate DICOM directories.

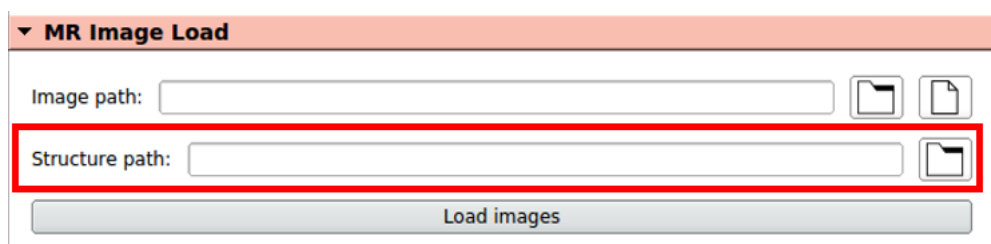
This way, the predicted target structures can be imported to other software, such as in BrainLab.

## Saving and loading intermediate results

The user can save the delineations in the “Delineation” module by pressing the button “Save In”



NeuroShape relies on the predefined nomenclature of how files are named, therefore file names should not be changed, and no additional image files should be stored in this directory.



Previously saved structure annotations can be reloaded in the “MR Image Load” module, “Structure path” option.

## Usage notes

### Thalamus atlas nomenclature

The NeuroShape nomenclature is based on the Morel Atlas of the Human Thalamus and Basal Ganglia (Morel, 2007). The definition of these structures and their relationship to the thalamic nuclei in different nomenclatures (e.g. Schaltenbrand and Wahren) is given in the book and the referred articles. The program uses the following abbreviations to refer to these structures:

AD	Anterodorsal nucleus	PuL	Lateral pulvinar
AM	Anteromedial nucleus	PuM	Medial pulvinar
AV	Anteroventral nucleus	Pv	Paraventricular nuclei
CL	Central lateral nucleus	RN	Red nucleus
CM	Centromedian nucleus	SG	Supragenulate nucleus
CeM	Central median nucleus	STh	Subthalamic nucleus
Hb	Habenular nucleus	VAmc	Ventral anterior nucleus, magnocellular division
LD	Lateral dorsal nucleus	VAPc	Ventral anterior nucleus, parvocellular division
LGNmc	Lateral geniculate nucleus, magnocellular layers	VLa	Ventral lateral anterior nucleus
LGNpc	Lateral geniculate nucleus, parvocellular layers	VLpd	Ventral lateral posterior nucleus, dorsal division
LP	Lateral posterior nucleus	VLpv	Ventral lateral posterior nucleus, ventral division (corresponds to VIM)
Li	Limitans nucleus	VM	Ventral medial nucleus
MDmc	Mediodorsal nucleus, magnocellular division	VPI	Ventral posterior inferior nucleus
MCpc	Mediodorsal nucleus, parvocellular division	VPLa	Ventral posterior lateral nucleus, anterior division
MGN	Medial geniculate nucleus	VPLp	Ventral posterior lateral nucleus, posterior division
MV	Medioventral nucleus	VPM	Ventral posterior medial nucleus
Pf	Parafascicular nucleus	mtt	Mamillothalamic tract
Po	Posterior nucleus	sPf	Subparafascicular nucleus
PuA	Anterior pulvinar	“Global”	All nuclei
PuI	Inferior pulvinar	“thalamus_ body”	Thalamus outlines + MGN

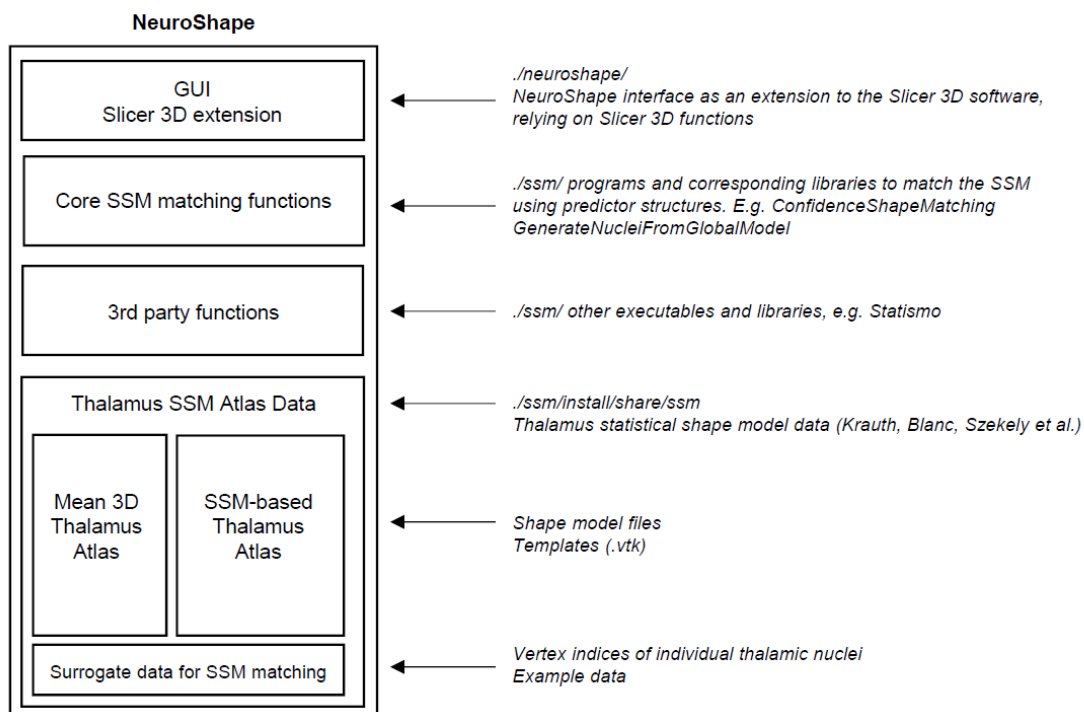
## Transfer of results to BrainLab

The predicted thalamic nuclei can be imported into BrainLab by converting them to DICOM format. By default, NeuroShape converts the confidence maps to two images (1) a combined image that contains the original planning image and the 90% confidence outline of the predicted target nucleus, (2) the confidence map of the predicted target nucleus on a black background.

These DICOM images should have identical dimensionality to the original planning image, therefore the fusion and visualization in BrainLab or other software should be straightforward. Importing the images into PACS is not recommended, as the tags (metadata) are not exported and left blank.

## Program structure and auxiliary functions

NeuroShape is an extension to Slicer 3D which merges annotation functions, SSM-matching functions (Blanc et al.) and the SSM-based atlas (Krauth et al., Morel) of the human thalamus into one package.



NeuroShape uses python system calls to execute the “core SSM” functions. These command-line functions are found in the neuroshape installation directory `/ssm/install/bin`

**ConfidenceShapeMatching:** main executable used for SSM alignment. Creates a global thalamus model (in .vtk format) that contains all predicted nuclei)

**GenerateNucleiFromGlobalModel:** splits up the global thalamus model into individual nuclei.

**MeshToLabelImage\_Template:** projects .vtk format meshes to images, “voxelization” of the resulting nuclei.

**ProbabilityOfPointInsideStructure:** generates probability maps (confidence regions) from the individual thalamic nuclei.

## Known issues

**No models generated in case of too small annotations:** the user should annotate at least 2-3 slices for each structure. Some structures (e.g. Hb) might be too small, and an error message is displayed after pressing the “Generate models” button.

**Unable to load planning image in case of “unsorted” DICOM directories:** it is recommended that the user selects a DICOM directory in which only one image type is stored (sorted DICOM). Please check how your images have been exported from the scanner.

**Slicer 3D is hanging during Step 3:** this part takes a considerable time to finish, and during this time, Slicer 3D is unresponsive, thus it may appear to be hanging (grayed-out screen). This is expected behavior and the user should wait 20-30 minutes to see the results.

## Credits

### NeuroShape Slicer 3D interface

Ms. Zoé Goey, Computer Vision Laboratory, ETH Zürich, Switzerland

Dr. András Jakab, Center for MR-Research, University Children’s Hospital, Zürich, Switzerland

Prof. Dr. Orcun Göksel, Computer Vision Laboratory, ETH Zürich, Switzerland

Prof. Dr. Gábor Székely, Computer Vision Laboratory, ETH Zürich, Switzerland

### SSM core functionality

Dr. Rémi Blanc, Computer Vision Laboratory, ETH Zürich, Switzerland

### Morel Thalamus Atlas

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Dr. Anne Morel, University Hospital Zürich, Switzerland

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