

# *Medtronic*

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StealthViz User Manual (original) >>

**VA scan types**

CT	4:1.0
T1	3:8:1.0
F3 (cubic FLAIR)	5500:1.0
DTI (3 mm)	6000:3.0
DTI (2 mm)	7000:2.0

Loading CDs on Stealth Station – always use “Unstructured DICOM” format.

**HDH scan types**

DTI	10900:2.0 or 11000:2.5
T1 wo	1800:1.0
T1 w	2000:1.0
FGATIR	3000:1.0
F3 (cubic FLAIR)	5000:1.0
SWI	20:28:1.5

## **StealthViz**

StealthViz implements a fast version of the Fiber Assignment by Continuous Tracking (FACT) algorithm licensed from Johns Hopkins Univ. It is a deterministic algorithm.

**HELP DESK**

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[dl.navstealthvizsupport@medtronic.com](mailto:dl.navstealthvizsupport@medtronic.com) or you can call the Tech Support hotline at 1-800-595-9709 (Ask for Brittany, Dani, or Ben).

## **Imaging Protocols for StealthViz Software**

To perform fiber tracking with the StealthDTI module of the StealthViz application software, you need an anatomical scan and a set of diffusion-weighted scans. For the anatomical scan, image the patient using the general instructions for the cranial application in the Medtronic Imaging Protocols document (9732379). Follow the additional instructions for the diffusion-weighted imaging protocols below.

### **Specific Requirements for Diffusion-Weighted Scans**

StealthDTI can accept diffusion-weighted scans from scanners manufactured by:

- GE
- Siemens
- Philips

Oblique scans are supported using the latest scanner software offered by GE or Siemens.

- If you are using a Phillips scanner, turn off the “Overplus” option.
- If you are using a Siemens scanner plus DICOM/Mosaic, check the “Rotate gradients if applicable” box before you load the exam into the StealthDTI software.

The StealthDTI module of StealthViz does not support averaging of the diffusion weighted images. Only protocols with a single B0 are supported.

### **Scan Transfer**

Archive the exam from the scanner to a CDR in non-volumetric DICOM format. StealthDTI does not support Siemens' mosaic format or Philips PAR/REC format. Alternatively, you may transfer the exams electronically to the StealthViz planning station via a DICOM network.

### **Assistance**

For questions about the StealthDTI Imaging Protocols or for information about using scanners from manufacturers not listed above, contact your local Computer-Assisted Surgery Specialist or call Medtronic Navigation for technical support at (+1) 800.595.9709 or (+1) 720.890.3200.

## **IMPORT Datasets**

### **IMPORT tab**

- [File] (in toolbar) → Import DICOM → choose from drop-down menu “user/people/exams” → select exam volume (only imports one at the time) → OK → “Convert” → “Close tab” in the left panel → click “Query” (new dataset appears on the list)
- select exam(s) → “(Add to) view”
- saved sessions on that dataset are displayed in the lower right window; may choose “Show Most Recent Sessions”.

## **MERGING (FUSING)**

### **A METHOD**

- make sure both exams are visible on fusion display.
- activate “fusion registration” toolbar ([View] → Show toolbars)
- click “Auto Registration” button → “Accept Registration”  
N.B. sometimes need to “Align centers” and do provisional “Manual Registration” to get as close to ideal merge as possible and then use “Auto Registration”

### **B METHOD**

[Tools] (in toolbar) → Coregistration

## **SEGMENTATION**

Materials = (Segmentation) Objects

- two objects cannot overlap (one voxel cannot be assigned to two separate objects).
- “MPR view” window does not show R or L labels (H: create object and check it in VIEW tab).

Ctrl-Z – undo steps (unlimited)

### MATERIALS list (top right)

**EXTERIOR** – all voxels not assigned to objects

“Eye” icon – display or hide object

“Lock” icon – lock object to prevent accidental editing

“Select” – to select that object (object gets red overlay).

- right-click on object (in the list) for visualization options.

### SELECTION area (on the right)

vs. SELECTION menu in toolbar

**Current slice** vs. **All slices** – actions on current axial slice vs. on entire object.

“Eraser” – to deselect object (it does not erase object!).

“Recycle (update)” – selection becomes new selected region (if selection touches previous selection then unselected voxels from old selection will be deleted).

“Plus”, “Minus” – selected areas are added / deleted from previous selection.



vs.



- toggle display (one or three MPR views)

### TOOLS area (on the right)

“Arrow” (pick region) – click and drag selection area (holding SHIFT allows to rotate it)

“Brush” – selects area by brushing (area below lets to change brush parameters)

N.B. to erase – use “Brush” and hold CTRL

“Lasso” – select by lasso

“Auto trace” works like magnetic lasso

“Freehand” with ALT leaves attachment points

“Magic wand” – select using histogram (click in area of interest and then adjust histogram) – excellent for selecting fMRI activation region

“Blow” – selects by selective blow

### SEGMENTATION TIPS

- 3D objects are associated with one anatomical exam, so if you want to see all 3D objects at the same time, make sure you do segmentation when the same anatomical exam is chosen as primary dataset when you do segmentation or later, when you view 3D objects (if you will choose different anatomical exam as primary, 3D objects won't be on the list)

N.B. when anatomical exam is chosen as primary dataset (in VIEW tab), then SEGMENTATION tab will also show it; if you want to use different exam for segmentation (e.g. fMRI), choose it using SEGMENTATION (in toolbar) → Grey image → fMRI exam;

if needed fMRI is greyed out, it means it wasn't fused with anatomical exam; for merging do not use “Auto Registration” (as there is not enough anatomical data in fMRI to fuse),

instead look if fMRI activation regions sit in appropriate place on anatomical exam (in fusion display mode) and then just click “Accept Registration”

- use “Blow” then fine-tune with “Brush”, Ctrl+
- make selections every few slices then: SELECTION (in tool bar) → INTERPOLATE\*  
N.B. when done, click “Plus” to make selection an object (or to add to existing object)  
\*interpolates in one axis (vs. WRAP – interpolates in all 3 axes)

### BEST ANATOMICAL EXAMS FOR SEGMENTING

(always verify with FA map):

- cerebral peduncle** – FGATIR
- red nucleus** – CUBE FLAIR, SWI (FGATIR does not show)
- thalamus** – FGATIR

### How to work on existing 3D object

- SEGMENTATION tab.
- SEGMENTATION in toolbar → Gray Image → select primary anatomical (reference) exam – you will see outline of existing 3D objects (associated with this anatomical exam).
- now use regular selection tools (e.g. brush) and ADD (+) or DELETE (-) selections from existing 3D object (make sure that object is selected in “Objects” area).

### How to merge two separate objects

(even from two separate datasets as long as they associated with same anatomical exam)

- Segment one dataset, then go to another dataset (as another grey image) – you still will see outlines of previously created 3D object; stay on the same object (in “3D objects” toolcard) and keep segmenting and adding with “+” to 1<sup>st</sup> object.
- If already have two separate objects: select 1<sup>st</sup> object (in “3D objects” toolcard click “Select” next to 1<sup>st</sup> object’s name); then highlight 2<sup>nd</sup> object’s name (in “3D objects” toolcard) and click “+” – this way selected voxels (from 1<sup>st</sup> object) will become assigned to 2<sup>nd</sup> object. Now can delete 1<sup>st</sup> object now.

### How to subtract voxels from existing 3D object

Highlight object’s name (in “3D objects” toolcard) → select image area and click “-” (or “minus” on keyboard)

Easiest way to select entire separate object (e.g. one of fMRI activation areas that stands alone) – use

button 

### TUMOR segmentation

SEGMENTATION tab with anatomic exam loaded (i.e. primary exam is MRI with tumor visible)

- “3D objects” area (upper right): New → rename by double-click
- using TOOLS (e.g. “Blow” → “Brush”, Ctrl+) mark tumor on every 2<sup>nd</sup> slice
- SELECTION (in toolbar): Interpolate (tumor acquires selection red)
- SELECTION (area on the right): click “+” (make sure “All slices” is selected) – tumor becomes object

VIEW tab → “3D object” toolcard tab – select “Surf” at tumor object (tumor must be visible now in 3D; if not, go to “Display” toolcard tab and pull histogram right arrow to the right – skull becomes more transparent)

### Convert fMRI to 3D object

- make sure primary exam is anatomical exam (and not fMRI) that you will use for intraop navigation
- SEGMENTATION tab (SEGMENTATION in toolbar → Gray Image → select fMRI)
- on histogram to move both sliders as far left as possible – makes activation region maximally visible.
- use “Magic Wand” tool → click on fMRI region → move histogram slider:
  - right – as far right as possible
  - left – just to the left of data values
  - (fMRI region should become selected)
- [New] → (+) to add to object

## DTI TENSOR PREPARATION

IMPORT tab (lower left) → select (using CTRL) MRI, DTI → “Add to view”

VIEW tab – make sure anatomic exam is primary dataset (but no need to merge any exams)

TOOLS (in toolbar) → DTI tensor preparation – will open 4-step dialog:

### 1. Gradient assignment

- background masking (eliminates air – represented in blue) – move slider to  $\approx 50-300$  – must remain no blue on brain (blue in ventricles and sinuses is OK)
  - same background mask is applied to all gradients (may check by clicking each gradient on the list)
- check that color boxes on the left of each gradient are green or yellow (if red – means patient moved – exclude gradient by unchecking it)
- optional – check “Smooth Raw Input Data” – reduces noise

### 2. Gradient registration (registers individual gradients to B0)

- usually gradients are aligned so leave default “Identity” registration type (if misalignment was detected, change from “Identity” to “Auto”); if using 2 mm slice thickness, then MRI scanning takes longer – may use “Auto” to readjust for patient movements.
- if all look OK → “Verify All Registrations”

### 3. Coregistration (registers gradient dataset to anatomical exam)

- confirm that reference exam is anatomical exam that you will use in surgery
  - N.B. fMRI has only activation regions map (not enough info for coregistration) – must be premerged with anatomic exam on another system
- select B0 and change “Identity” to “Auto”
- for other exams may leave “Identity” (but check if they merged correctly; if not then change “Identity” to “Auto” – system will fuse)
- “Verify All Registrations”

### 4. Tensor computation

- FA, DEC, ADC must be checked (all other only for research purposes)
  - Default values:
    - FA 0.20
- “Compute”
- DEC (Directionally Encoded Colors) map is automatically shown overlaid on anatomic exam
- DEC is also known as RGB:

- red – fibers left-right (red heart on left)
- green – fibers anterior-posterior (being “green” means moving forward)
- blue – vertical fibers (towards blue sky)

## DTI FIBER TRACKING (TRACTOGRAPHY)

- use “DTI fiber tracking” toolcard (lower right)
  - N.B. check if DTI (DEC, FA, ADC) are fused properly with anatomical exam!
- drag crosshair to seeding region → “Add” – selection box appears:
  - a) choose 3D object (instead of selection box) in drop-down menu
  - b) modify selection box: drag or rotate borders (zooming helps), shift box with SHIFT+click&drag
- “Compute” – fibers will appear
  - N.B. check “Auto” (next to “Compute”) – draws fibers in real time as you change parameters.

### How to filter tract

- use “Mid Region” and “End Region” – can use another box or segmentation object (e.g. fMRI activation region)

At the very end\* may “Crop” unnecessary fibers

\*if you change anything afterwards, fibers will be regenerated and will need crop again

### TRACTOGRAPHY PARAMETERS

More Options → Dialog:

**Seed Density** (default 1.0) – how many seed points will be generated in each mm<sup>3</sup>; ↑ (up to 5.0) – more fibers.

**Max. directional change** (default 45 degrees); ↑ (up to 180 degrees) - more fibers.  
 for pyramidal – use 60° (if internal capsule looks too thin, increase to 90°)  
 for rubrothalamic – use 45°

**Min. fiber length** (default 20.00); ↑ - less fibers (eliminates short spurious fibers).

**3D object distance** (default 2.0) – safety margin when generating 3D object from fiber tracts; OK to decrease to 0.0

**MPR Line Depth** (default 5.0)

**FA start value** 0.20; ↓ - more fibers (may try 0.0 to start from lateral motor cortex).

**ADC stop value** 0.10; does not change number of fibers.

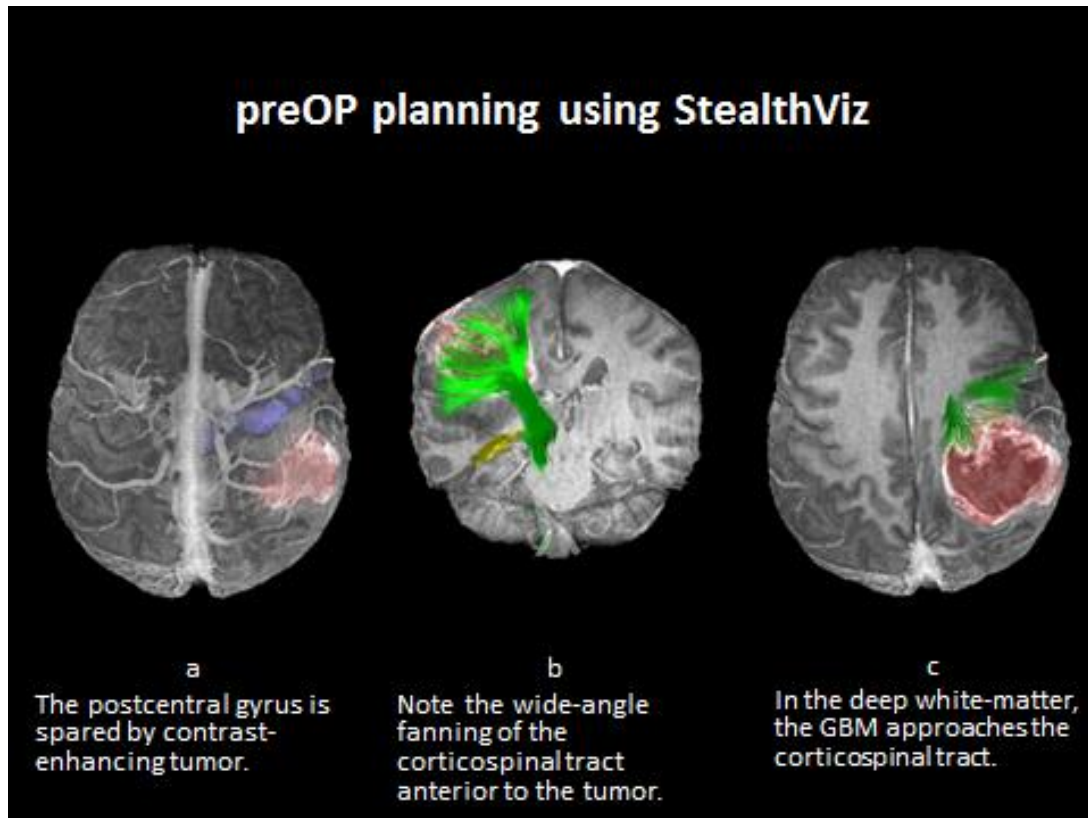
### CONVERT TRACT INTO 3D OBJECT

- check “MPR” next to tract name (on “DTI fiber tracking” toolcard)
- check “Surf” next to tract name (on “3D Object” toolcard)
  - N.B. can make object (tract) less puffy by decreasing “3D Object distance” to 0 (“More Options” → “Dialog”)

### PYRAMIDAL TRACT

The ability to see the lateral/inferior reaching tracts on CST can be difficult and may be dependent on the quality of your DTI scans.





Put either a start or end region along the motor strip (see the purple bit on the leftmost image).

It can help to rotate the crosshairs to orient the lines along the motor strip and then turn on the end region and stretch the box to cover the motor strip. Alternately, you could use modeling tools in segmentation to create a contoured 3D model of the MS and then use that for the start/end region.

Then you can increase the seed density and max directional change in more options > dialogue box (found at bottom right in fiber tracking menu).

This should show the lat/inf fanning portion of CST along with some crossing fibers so you will likely need to crop extraneous areas to achieve a result looking like the picture above.

## RESEARCH TOOLS

Add-on >>

---

I didn't mean for you to type the ellipses (...) - that was just a lead in to the next lines with the commands.  
Thanks, Bruce

Also, you'll need a space after a command like "mount"

---

### NEW

Hi Viktor,

Sorry again for failing to follow up. Please try the revised sequence below – it adds logging in as “superuser” to give you extra permissions

Save attached file to a USB stick.

Start up StealthViz on the planning station, insert the USB stick, wait about 10 seconds, and then press F9 once to mount it.



Press Alt+F9 to minimize the stealthviz screen.

Right click and select New Window

Then type the following

```
su
```

```
;subrosa; (password)
```

```
ls /mnt/USB and check to see that the xml file is there
```

```
if the above fails, type mount /dev/sdb1 /mnt/USB and repeat above
```

```
cd /opt/Medtronic/StealthViz-1.3/examine_local/hanging-protocols (note that you can type  
the first few characters of a word and then hit the Tab key to autocomplete the word)
```

```
cp /mnt/USB/*.xml system
```

press F10 to unmount the USB stick and then you can remove it.

Double click the StealthViz icon to maximize it.

Log out and then log back in to stealthviz.

View a scan (do not load a previous Session – this won't work for previous Sessions)

There should now be a tab called "Statistics" beside the fiber tracking tab.

If not, click on the Protocol menu at the top of the screen, and let me know which one has a checkmark beside it

And then follow the remaining steps in the original email below

Thanks,

Bruce

## OLD

Hi Viktor,

Sorry again for the delay in getting this to you

The attached file will turn on the Statistics functionality in StealthViz. Please try the procedure below and let me know if you need any help – we could facetime or something similar.

Save attached file to a USB stick.

Start up StealthViz on the planning station, insert the USB stick, wait about 10 seconds, and then press F9 once to mount it.

Press Alt+F9 to minimize the StealthViz screen.

Right click and select New Window

Type ...

```
ls /mnt/USB and check to see that the xml file is there
```

```
if the above fails, type mount /dev/sdb1 /mnt/USB and repeat above
```

```
cd /opt/Medtronic/StealthViz-1.3/examine_local/hanging-protocols (note that you can type the first few characters  
of a word and then hit the Tab key to autocomplete the word)
```

```
cp /mnt/USB/*.xml system
```

press F10 to unmount the USB stick and then you can remove it.

Double click the StealthViz icon to maximize it.

Log out and then log back in to StealthViz.

View a scan (do not load a previous Session – this won't work for previous Sessions)

There should now be a tab called "Statistics" beside the fiber tracking tab.

If not, click on the Protocol menu at the top of the screen, and let me know which one has a checkmark beside it

Go through the normal process to create fiber tracts or 3D models of areas of interest.

On the View tab, with the Statistics toolcard open, click on Compute

There will be one row per 3D model, with the stats within that volume from the Primary exam. You can click/drag the divider to widen that panel temporarily.

**If you need to calculate the statistics based on different datasets (e.g. if you want average FA within a fiber tract):**

One limitation is that every time you change the Primary exam to something different (e.g. to FA or ADC to calculate statistics on them), the previously created 3D models disappear (they are associated with whatever was Primary when they were created). If you want to have the same 3D model be used with multiple datasets, you will have to do something like:

create a 3D model (check the MPR box to make a fiber tract be a 3D model)

use File, Save 3D Objects to save a Hybrid exam to a directory on disk (should be able to create a new directory in /opt/mnav/StealthViz-1.3/examine\_local to put them in)

use File, Import DICOM and find and load that Hybrid back into StealthViz – it will become a new series under the same patient

Then, for each dataset you want to calculate stats on

make the dataset you want to create stats on be the Primary, (e.g. FA or ADC)

and make the Hybrid be the Overlay

use Tools, Coregistration to make sure they're merged (will likely be Identity) and checkmark Verified

in Segmentation tab, use Segmentation menu, Gray Image to switch to the Hybrid, and segment (usually with thresholding) the 3D model again (it will now be associated with the new Primary)

in the View Tab, click Compute on the Statistics toolcard

all of this probably gives you an indication of why this functionality isn't enabled by default ... **we have also seen issues if you save a Session and then come back in later and try to use the statistics, so try to do all your work in one session.**

Let me know how it goes and feel free to ask for help.

Thanks,

Bruce

### **Bruce Leggett**

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**LET'S TAKE HEALTHCARE  
FURTHER, TOGETHER**

## **SAVING/EXPORTING**

StealthViz exports/saves 3D objects in Mach rainbow color map – objects can be colored in the Medtronic applications.

- make separate sessions and separate hybrid exams for each tract – fibers (tracts) can intersect but one voxel can belong only to one 3D object in same session (and, thus, hybrid exam).

There is no straightforward way to export sessions (which contain the fiber tracts as fiber lines) between systems with SV on them.

If you right click on the tract name in the DTI tool card, it does let you save the tract in a format (\*.am AmiraMesh) that enables you to transfer it to Amira. But, there's no way to import that into another copy of StealthViz.

Thanks, Bruce

### FILE → SAVE 3D OBJECT

– save to **CD/USB**

**USB** – mount with F9 → create new folder on USB → save.

**CD** – first need to save exam locally (Look in: opt/Medtronic/StealthViz-1.3/examine\_local/saved\_results – create new folder here [e.g. “Patient DTI”] and go into it → OK → Save – exam will be saved to this folder) → then burn CD (click F11 – opens CD burning window → select patient, etc.)

### FILE → EXPORT 3D OBJECT

– send to **Stealth Station directly (over network)** or save on **local hard drive**; click OK/accept – will save to the directory where FrameLink / Cranial MACH can find it.

N.B. select “Burn Hybrid” (will save 3D objects fused with anatomical exam)

### EXPORT tab

Only exports snapshots!

- select needed snapshot → Save
- may choose USB: insert USB → press <F9> to mount → Save → press <F10> to unmount