

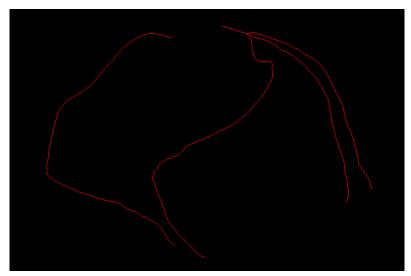
Slicer3 Training Tutorial Centerline Extraction of Coronary Arteries in 3D Slicer using VMTK based Tools

Daniel Haehn Fetal-Neonatal Neuroimaging & Developmental Science Center Children's Hospital Boston

> Updated for Slicer3 Version 3.6 by: Ana K. Ortiz Modeling and Simulations Engineer Open Source Medical Software Corporation



Learning Objective

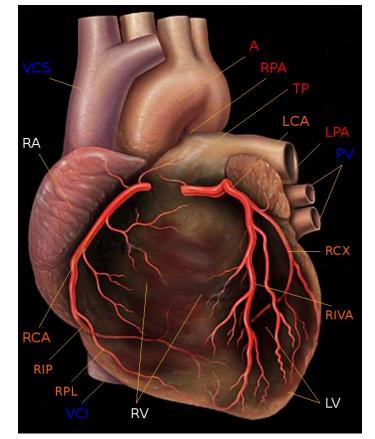


Guiding you step by step through the process of centerline extraction of Coronary Arteries in a cardiac blood-pool MRI using VMTK based Tools.









Human Heart with Coronaries, Author: Patrick J. Lynch (1999), Creative Commons License

Coronary heart disease (CHD) is the leading cause of death in high-income countries and one of the main causes of death worldwide*.

The primary cause for CHD is atherosclerosis of the coronary arteries and is called coronary artery disease (CAD).

The extraction of the central lumen line (centerline) of coronary arteries is helpful for visualization purposes, stenosis quantification or further processing steps.

* WHO Fact Sheet 310: http://www.who.int/mediacentre/factsheets/fs310/en/index.html





This tutorial requires the installation of the **Slicer3** software and the tutorial dataset. They are available at the following locations:

• Slicer3 download page (Slicer 3-3.6.3-2011-03-04-win32.exe)

http://slicer.org/pages/Special:SlicerDownloads

Slicer Downloads	
This is the download page for compiled versions of the 3D Slicer software. If y	ou are looking for the source code, please click here.
LICENSE AGREEMENT	
Please read the Slicer License Agreement before downloading any binary re	eleases of Slicer.
DOWNLOADS	
Type of download: Operating System:	March 2011: Slicer 3.6.3 released to download, select stable releases and your platform
File to download: Slicer3-3.6.3-2011-03-04-win32.exe	
Download	

• Tutorial MRI data (3 files)

http://www.na-mic.org/Wiki/index.php/File:TutorialVMTKCoronariesCenterlinesMRI_Data_Winter2010AHM.zip

Disclaimer: It is the responsibility of the user of Slicer to comply with both the terms of the license and with the applicable laws, regulations, and rules.



Overview

Installing VMTK in 3D Slicer The Pipeline Loading Data Extracting the ROI Vesselness Filtering Level Set Segmentation **Centerline Computation** Results References Acknowledgements

slides 6-12 slide 13 slides 14-19 slides 16-28 slides 29-38 slides 39-51 slides 52-62 slides 63-68 slide 69 slide 70



Installing VMTK in 3D Slicer





Installing VMTK in 3D Slicer

	3D Slicer Version 3.5 Alpha 1.0 🛛 🕚
Exte	ensions Management Wizard
-	This wizard lets you search for extensions to add to 3D Slicer, download and install them, and uninstall existing extensions. You will need a network connection to access remote extension repositories.
	🔳 Find & Install 📃 Uninstall 📃 Either
	Change extensions install path:/home/hype/Slicer3hype
	Delete zip files from temp. dir. (optional):
	Where to search: http://ext.slicer.org/ext/trunk/10201-linux-x86
	Click "Next"
	Back Next > Finch Cancel



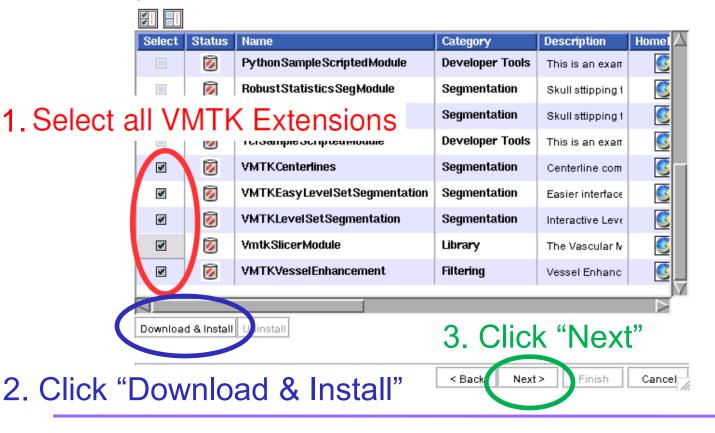
Installing VMTK in 3D Slicer

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X 3D Slicer Version 3.5 Alpha 1.0

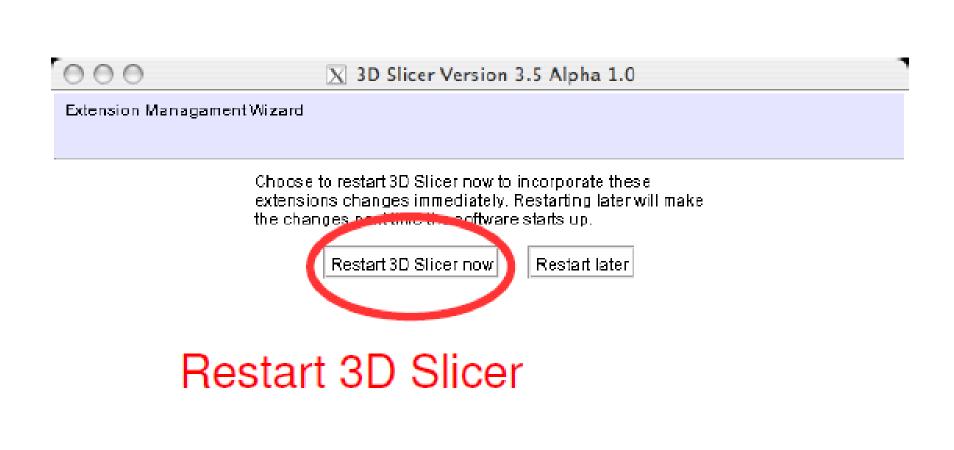
Extension Management Wizard

Select extensions, then click uninstall to remove them from your version of 3D Slicer, or click download to retrieve them.









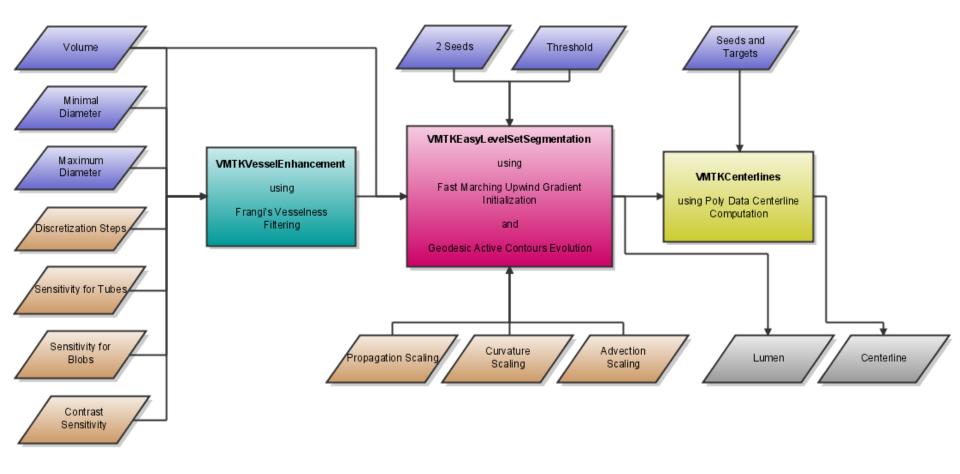
3DSlicer

Installing VMTK in 3D Slicer

Slicer Version 3.5 Alpha
earch modules 🔀 🔂 🔝
The VMTK Extensions appear in the modules selector (1) inside the category "Vascular
Modeling Toolkit"



The Pipeline





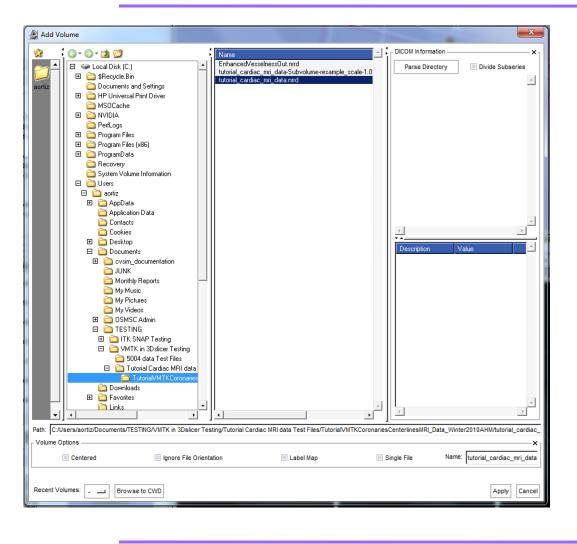
Loading Data

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	Close Scene	Ctrl-W			
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To load the tutorial data, choose the "File" menu (1) and select "Add Volume..." (2)



Loading Data



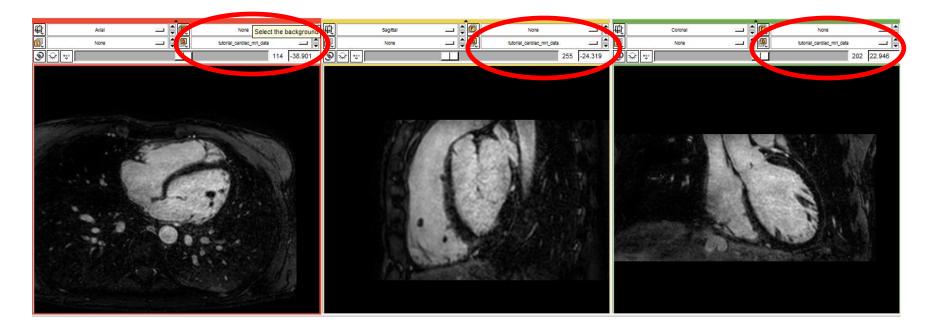
Select the file "tutorial_cardiac_mri_d ata.nrrd" and press Apply.

Repeat this for the other two files: "tutorial_cardiac_mri_d ata-Subvolumeresample_scale-1.0.nrrd" and "EnhancedVesseIness Out"



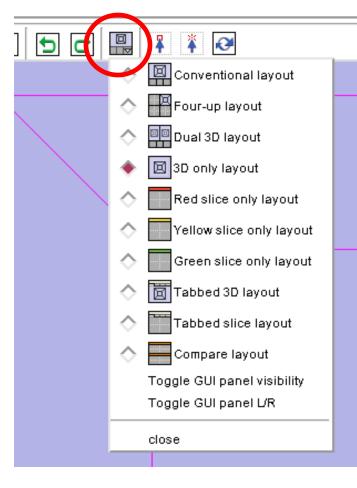


Make sure you are viewing the "tutorial_cardiac_mri_data.nrrd" data by selecting that file on each slice window as shown.





Viewing Data



The layout selector will allow you to choose the desired window(s) of interest for viewing. Start off with the "Conventional layout"

Your layout preference will depend on the task that you are performing. You might want to use the "Red slice only layout" for segmentation or the "3D only layout" for centerline computation



Active Volume

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Use the modules selector (1) to navigate to the "Volumes" module (2)



Active Volume

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File Edit View Window Help Fee	dback	
Modules: Volumes	Eearch modules	🛗 🟠 🛍
3DSlicer		
Help & Acknowledgement		<u> </u>
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Image Orientation: From File 💻		
Label Map Single File		
Apply	Previous Next	
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▲ Display		
Lookup Table:	Grey 🔺	
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Volume Window Level Pr	esets:	
Window/Level: Manual	2488.3 1249.1	
Threshold: Off	0 2488.3	
🗹 Update Histogram Inte	eractively	
[0, 2488.3] × [0, 1]		-

Make sure that the **Active volume** is the "tutorial_cardiac_mri_data" file.

You will need to make sure that you have the correct data file as the **Active Volume** at each step: Extracting ROI, Vesselness Filtering, Level Set Segmentation, and Centerline Computation.



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File Edit View Window	Color	
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Load	Transforms	
Select Volume File	VolumeRendering	
	✓ Volumes	
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w	Vascular Modeling Toolkit	Create a DICOM Series
		Dicom to Nrrd Converter

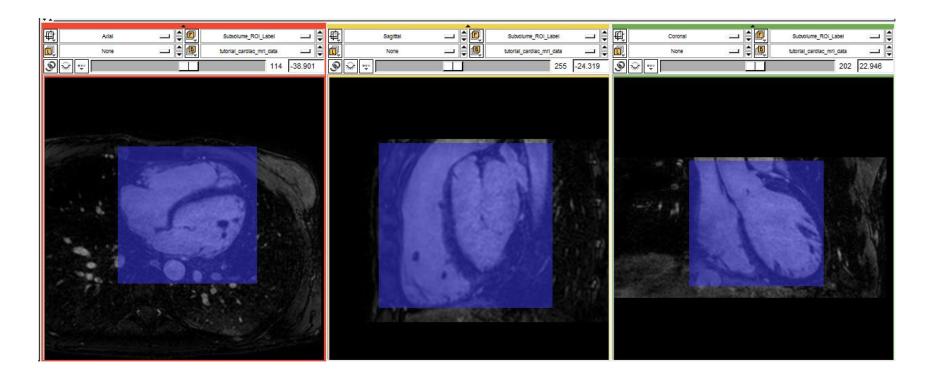
Use the modules selector to start "CropVolume" under the "Converters" menu



And the set of the set
lelp Feedback
1. Make sure the "Input
Volume" is the tutorial data
Create New MRMLROINode
Output volume: ResampledSubvolume Edit Properties
Input spacing scaling constant 1
Isotropic voxel size for output volume
Interpolation type: 🔲 Nearest Neighbor 🔳 Linear 🔲 Cubic
Do ROI resample
R0: Create New MRMLROINode R0! visibilit Rename Cutput volume: ResampledSubvolume Input spacing scaling constant 1 Delete Interpolation type: Nearest Neighbor

3. Create a new volume as the "Output Volume"

3DSlicer



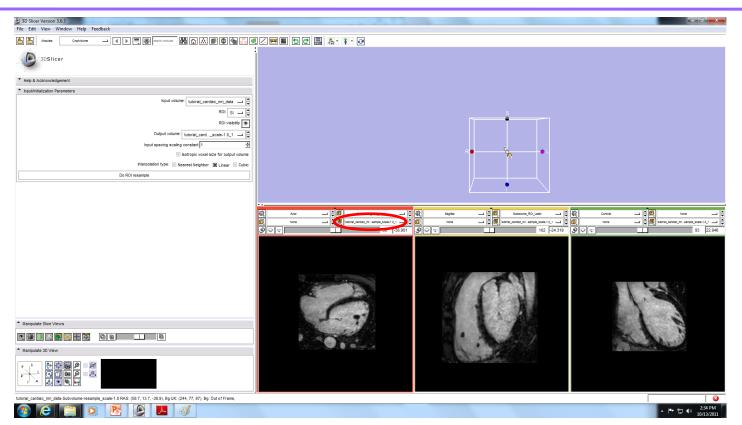
Now click around the heart in the slice views to select the subvolume. The selection is shown in transparent blue above.



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File	Edit	View	Window	Help	Feedback										
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Click "Do ROI resample" to extract the subvolume.





Your red, yellow, and green slice windows should now show the subvolume. If not...

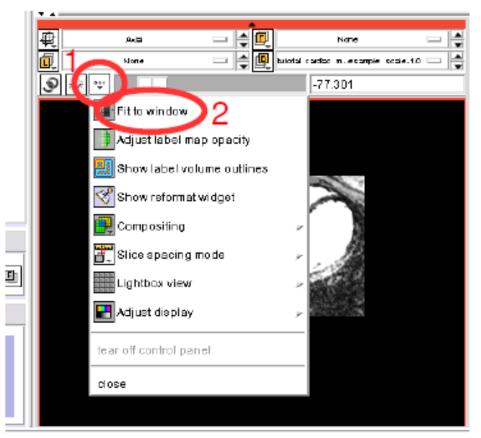


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					Rename
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If not, you should be able to change the data in view to the subvolume that you extracted, "tutorial_cardiac_mri_data-subvolume-resample_scale-1.0_1".

Alternatively, you can use the subvolume that you initially loaded, "tutorial_cardiac_mri_data-subvolume-resample_scale-1.0".





Fit the volume to the window by using the options icon (1) and selecting "Fit to window" (2)



Change Active Volume

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Use the modules selector (1) to navigate to the "Volumes" module (2)



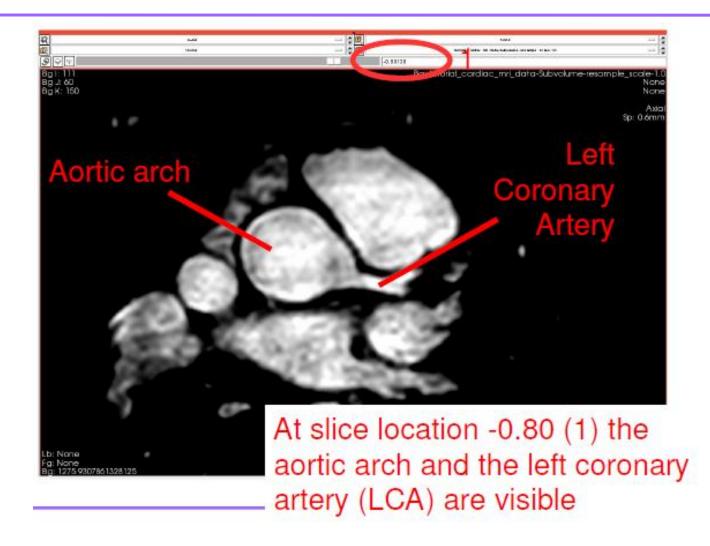
Change Active Volume

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▼ Help & Acknowle	dgement	
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📄 Select Volum	o File	
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Volume Window Le	evel Presets:	
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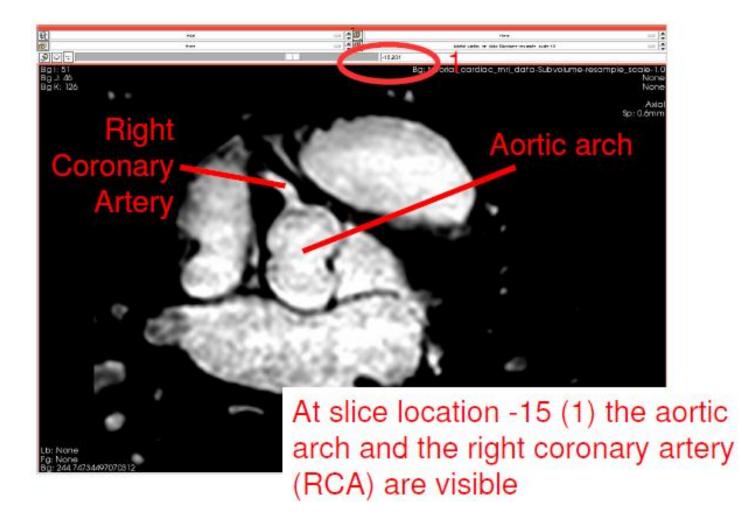
1. Be sure the subvolume that you selected for viweing, either the "tutorial_cardiac_mri_datasubvolume-resample_scale-1.0_1" or the "tutorial_cardiac_mri_datasubvolume-resample_scale-1.0" is the Active Volume.

2. If you adjust the Window/Level setting to 1082 and 1257 you get a better visualization







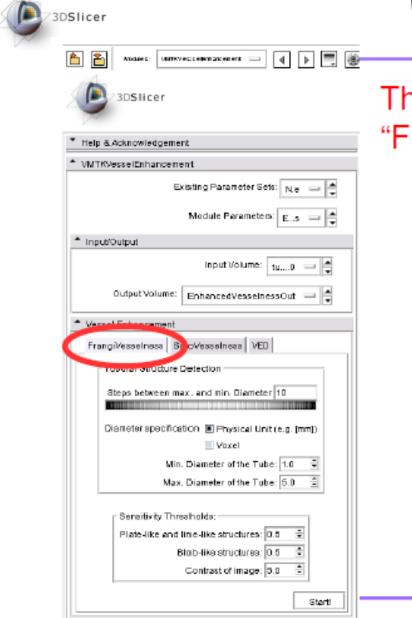




Vesselness Filtering

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	Measurements	
	Models	
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	Developer Tools	
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1	Diffusion Weighted	
2	Vascular Modeling Toolkit 👌	VMTKBranchSplitting
1804	ene (close current)	VMTKCenterlines
score (close current)		VMTKEasyLevelSetSegmentation
ene (to current)		VMTKNetworkExtraction
		VMTKVesselEnhancement
or a	data directory	

Navigate to the VMTKVesselEnhancement module under the "Vascular Modeling Toolkit" Menu using the modules selector



Vesselness Filtering

This panel appears. Switch to "FrangiVesselness".



Vesselness Fl	iltering
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3D Slicer Version 3.6.3			
File Edit View Window Help Feedback			
Modules: VMTKVesselEnhancement			
3DSlicer			
Help & Acknowledgement			
▲ VMTKVesselEnhancement			
Existing Parameter Sets: N.e 🔜 🗨			
Module Parameters: Es			
 Input/Output 			
Input Volume: tutorial_cardscale-1.0_1			
Output Volume: EnhancedVInessOut1			
Vessel Enhancement			
FrangiVesselness SatoVesselness VED			
Tubular Structure Detection:			

1. Select the desired subvolume as your "Input Volume"

2. Make sure that the "Output Volume" is a new file with the file name starting with "EnhancedVesselnessOut..." and NOT any other file that would potentially be overwritten



Vessel	ness	Filte	ring

Input Volume: tutorial_cardscale-1.0_1				
Output Volume: EnhancedVInessOut1				
Vessel Enhancement				
FrangiVesselness SatoVesselness VED				
- Tubular Structure Detection				
Steps between max. and min. Diameter 10				
Diameter specification Physical Unit (e.g. [mm])				
Voxel				
Min. Diameter of the Tube: 0.1 뢎				
Max. Diameter of the Tube: 2.0				
Sensitivity Thresholds:				
Plate-like and line-like structures: 0.3 🗧				
Blob-like structures: 500 🖨				
Contrast of image: 500 🜩				
Start!				

1. Enter "0.1" (unit: mm) as the minimal diameter of tubular structures to detect

2. Enter "2.0" (unit: mm) as the maximum diameter of tubular structures to detect

3. Choose a low threshold of "0.3" to detect line-like rather than plate-like structures

4. *A* higher threshold of "500" limits the detection of bloblike Structures

5. The contrast of the vessels in comparison to the background in the tutorial data is very high, so set a higher threshold of "500" to detect only well visible structures



Vesselness Filtering

* Vessel Enhancement	
FrangiVesselness SatoVesselness VED	
Tubular Structure Detection	
Steps between max. and min. Diameter 10	
Diameter specification 🔳 Physical Unit (c.g. [mm])	
Min. Diameter of the Tube: 0.1 🖃	
Max. Diameter of the Tube: 2.0 🕃	
Censitivity Thresholds:	
Plate-like and line-like structures: 0.3 🚔	Click "Start!"
Blob-like structures: 600 🖃	
Contrast of Image: 500 🚍	
Starti	



Vesselness Filtering

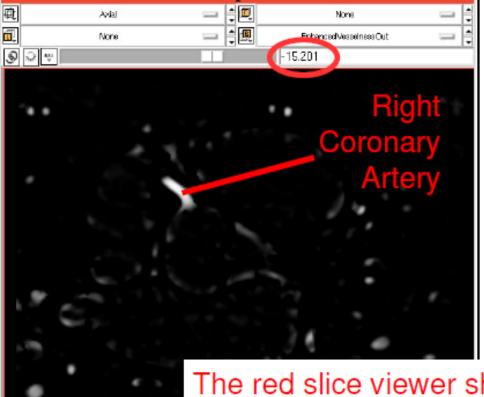
After you Click Start, the software may appear as "Not responding". Don't worry, it should still be working!



In fact, any time you click on a button to perform a task, the software may appear as not responding, but should be performing the task indicated.



Vesselness Filtering



The red slice viewer shows the vesselness filtered volume. The enhanced tubes are visible (f.e. at slice location -15).



Level Set Segmentation

All Modules	
Color	
Data	
Editor	
Fiducials	
Measurements	
Models	
ROI	
SlicerWelcome	
Slices	
Transforms	
VolumeRendering	
Volumes	
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Wizards	
Informatics	
Registration	
Segmentation Quantification	
Diffusion	
IGT	
Filtering	
Surface Models	
Converters	
Endoscopy	
Developer Tools	
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Diffusion Weighted	
Vascular Modeling Toolkit	VMTKBranchSplitting
	VMTKGenterlines
\langle	 VMTKEasyLevelSetSegmentation
	VMTKNetworkExtraction
	VMTKVesselEnhancement
L	

Navigate to the VMTKEasyLevelSetSegmen tation module under the "Vascular Modeling Toolkit menu using the modules selector

3DSlicer	evel Set Segmentation
Moder: MEssyLevelSetSegmentation • Help & Acknowledgement • VMTKEasyLevelSetSegmentation Existing Parameter Sets: N.e • Input/Output Input/Output Input/Output Input/Output Input/Output Input/Output Input/Output Input/Output Initialization Output Volume: VMTKEvolutionOut Initialization Initialization Initialization Initialization Initialization Istarti * Evolution Iess inflation Istarti * Evolution Iess inflation Istartion	This panel now appears. The Level Set Segmentation process consists of two steps: Initialization and Evolution

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3DSlice	er			4
 Help & Acknowledg 	ement			-
 VMTKEasyLevelSet 	Segmentation			
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Input/Output				
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Initiali	zation Output Volu	me: VMTKInitia	Edit Properties Delete	
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0.143	Thres	holding	1	
<u>ц</u>			Start !	
Evolution				
Method I Geodes	c Active Contours			

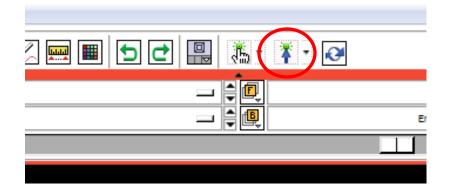
1. Select the "EnhancedVesselnessOut" volume as the "Input Volume"

2. Use the "Source Seeds" selector to "Create New Fiducial List"

3. Make sure that both "Output volumes" are new files that begin with
"VMTKInitialization..." and
"VMTKEvolution..." and NOT existing files that can potentially be overwritten

4. Deactivate "Use Volume Rendering" because Polydata is needed later





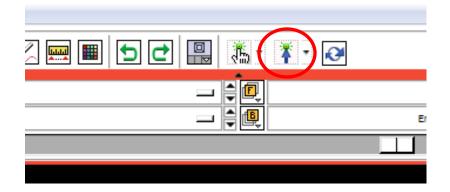
Switch to "Place mode by using the icon in the toolbar shown above.





Click inside the RCA on the red slice viewer to place one seed point (f.e. at slice location -15)





Change to switch to "Place" mode again!

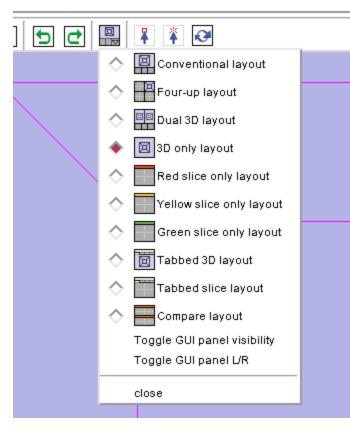




Click inside the LCA on the red slice viewer to place one seed point (f.e. at slice location -0.80)

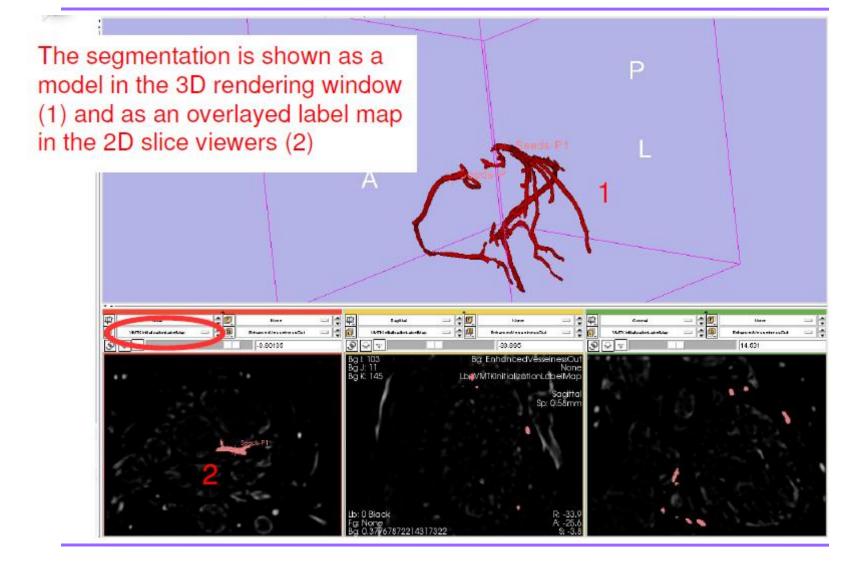
3DSlicer	evel Set Segmentation
3DSlicer	
Help & Acknowledgement	-
 VMTKEasyLevelSetSegmentation 	
Existing Parameter Sets: N.e	
Current Parameter Sets:	
Input/Output	
Input Volume: EnhancedVesselnessOut	5. Set a lower threshold of "0.143"
Source Seec V None	
Target Seeds (optio	_
Edit Properties	6. Click "Start!
Initialization Output Volume: VMTKInitia Delete	
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Initialization	
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0.143 Thresholding 1	
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Evolution	
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If you are not already in "Conventional Layout," switch to conventional layout to see the 3D rendering of the model you just created!







And also :: The EasyLovelS at Segments also - 4 🕨 📃 🚳 reach module : 🛗 🚠 🖾 🚳 🚳	I [:
3DSlicer	
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VMTKInitializationOut	
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Evolution Output Volume: VMTKEvolutionO	
U	
Use the "Input Volume" sele	ctor (1) to
Thresholding set the extracted subvolume	(2) as the
input for the evolution stage	
input for the evolution stage	



Evolution		
Method I Geodesic Active Contours		
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more inflation <-> less inflation	0	
less curvature <-> more curvature	70	
more attraction to ridges <-> less attraction to ridges	100	
Iterations: 10	4	
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1. The initialization is already close to the edges of the vessels so no inflation in needed

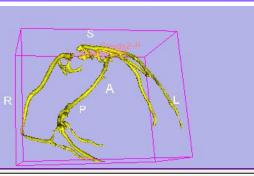
2. To get a smooth surface a higher curvature weight of "70" is important

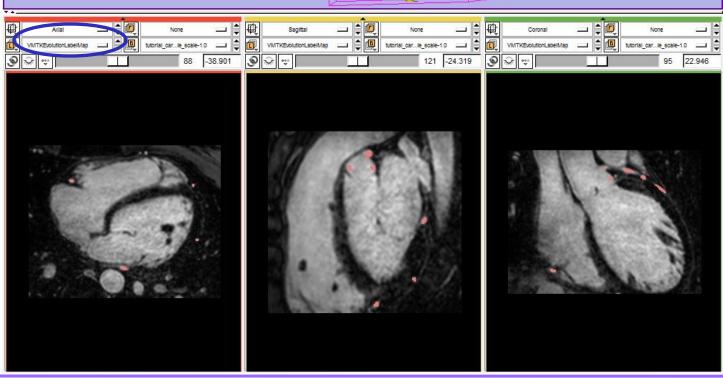
3. To attract the segmentation to the gradient ridges a high attraction weight of "100" is necessary

4. Now Click "Start"!



The result is shown as a yellow model in the 3D rendering window and as an overlayed label map in the 2D slices







All Modules	1	
Color		
Data		
Editor		
Fiducials	hter	
Measurements		
Models		
ROI		
SlicerWelcome		
Slices		
Transforms		
VolumeRendering		
Volumes		
Wizards		
Informatics		
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	VM VM	ALasyLevelSetSegmentation
	VMT	KNetworkExtraction
70	VMT	KVesselEnhancement

Navigate to the VMTKCenterlines module under the "Vasculas Modeling Toolkit" using the modules selector

National Alliance for Medical Image Computing



Centerline Computation

3DSlicer
Help & Acknowledgement
* VMTKCenterlines
≜ Input
Input Model: VMTKCenterlinesPrepOut 🖃 🗬
▲ 1. Preparation Step
Preparation Step Output Model: VMTKCenrepOut
[]
2. Centerlines Computation
Source Seeds: Seeds 🔤 🗬
Target Seeds: Seeds 🔤 🗬
Centerlines Output Model: VMTKCenterlinesOut 📼 🛋
Voronoi Diagram: VMTKVoronoiOut 📼 🚔
Get Centerlines!
3. Export To File
▼ 4. Import From File

This panel now appears.

The Centerlines extraction consists of two steps: Model preparation and Centerline Computation

National Alliance for Medical Image Computing



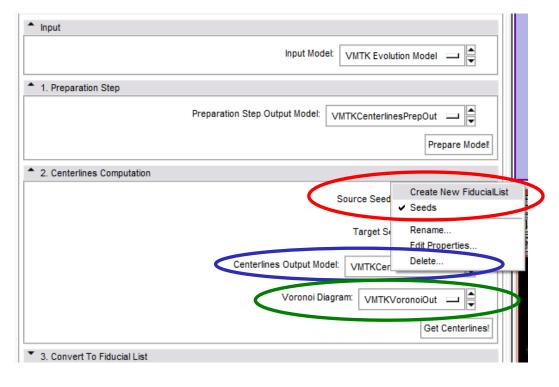
VMTKCenterlines		
▲ Input		
	Input Model: VMTK Evolu	ution Model
1. Preparation Step		
Preparation Ste	p Output Model: VMTK Initializa	Create New Model VMTK Initialization Model VMTK Evolution Model VMTKCenterlinesOut
2. Centerlines Computation		Rename
	Source Seeds	Edit Properties Delete
	Target Seeds:	Seeds2
Center	rlines Output Model: VMTKCent	terlinesOut 💷 🚔
paration Step Output Model:	VMTKCenterline	esPrepOut 💷 🖡
		Prepare M

1.Set the "VMTKEvolution Model" as the "Input Model"

2. "Create New Model" for the Preparaton Step Output Model. This will create a model called "VMTKCenterlinesPrepOut"

3. Click "Prepare Model!" The blue model in the 3D Rendering Window turns green





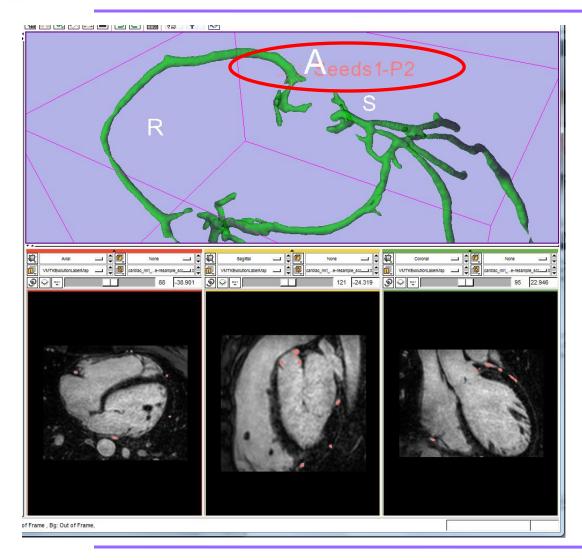
1.Use the "Centerlines Computation" panel to delete the "Seeds" FiducialList and "Create New FiducialList." This will create a fiducial list named "Seeds1"

2. "Create New Model" for the Centerlines Output Model. This will create a model called "VMTKCenterlinesOut"

3. "Create New Model" for the Voronoi Diagram. This will create a model called "VMTKVoronoiOut"

DON'T CLICK "GET CENTERLINES!" YET

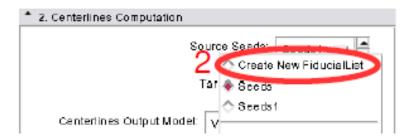




Place a Seed in the 3D Rendering Window directly on the green model where the desired Centerline path will start

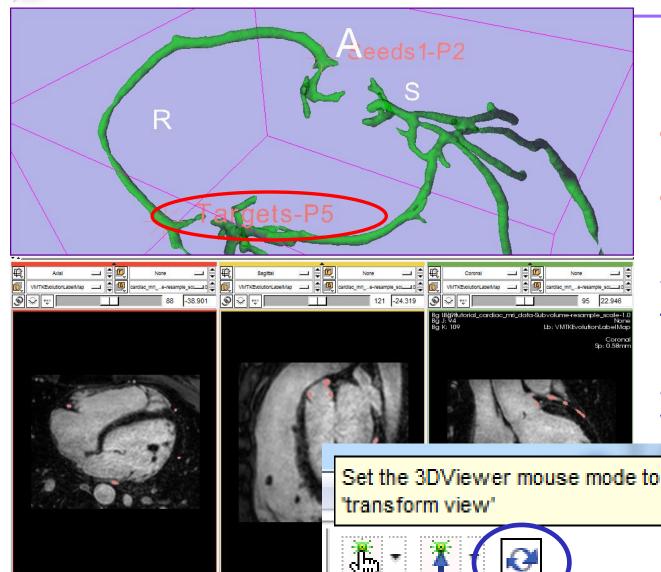


* z.c	enterlines Computation
	Source Seeds: Seeds 🗖 🚽
	Target Seeds: Seeds 💻 🚔
	Centerlines Output Model: TratkCenterlinesOut 😑 🖃



Use the "Target Seeds" selector (1) to create a new Fiducial list (2)

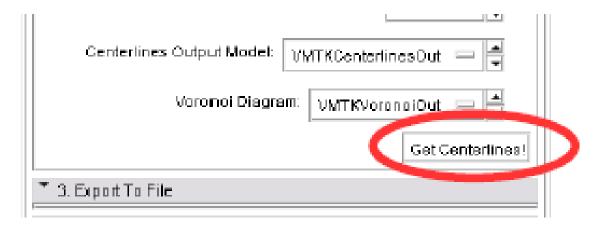




Place a "Target" Seed in the 3D Rendering Window directly on the green model where the desired Centerline path will end.

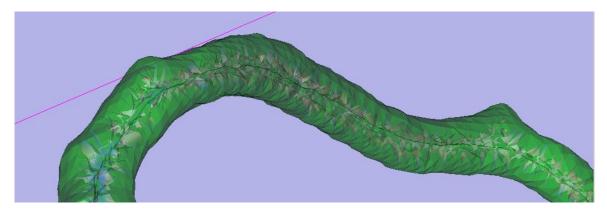
You can switch to Transform mode to rotate the model and place the seeds where desired





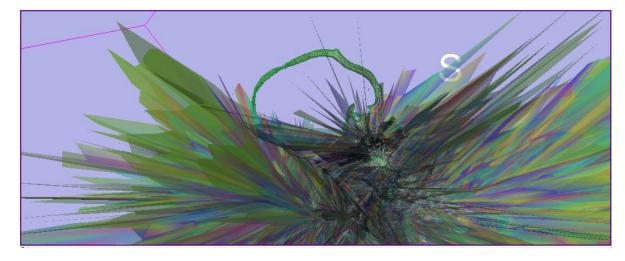
Click "Get Centerlines!"





You should have gotten a centerline for the selected path and a Voronai diagram for the entire segmented area. It looks like figure 1.

If you got something that looks like figure 2, then something went wrong when computing the Voronoi diagram. We can just delete or make the voronoi diagram invisible for now....



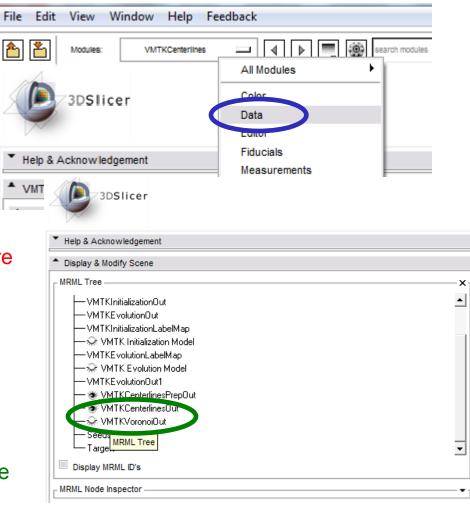


2. Centerlines Computation	Source Seeds:	
	Targ Create New Model VMTK Initialization Model VMTK Initialization Model VMTK Evolution Model VMTK Evolution Model Voronoi Diagram: VMTF VMTK VMTKCenterlinesOut VMTK VMTK Voronoi Diagram: VMTF Rename Een Properties	
3. Convert To Fiducial List	Delete	

You can delete the Voronoi diagram by opening the "Voronoi Diagram" menu under the Centerlines Computation panel. Make sure the "VMTKVoronoiOut" file is selected and choose delete

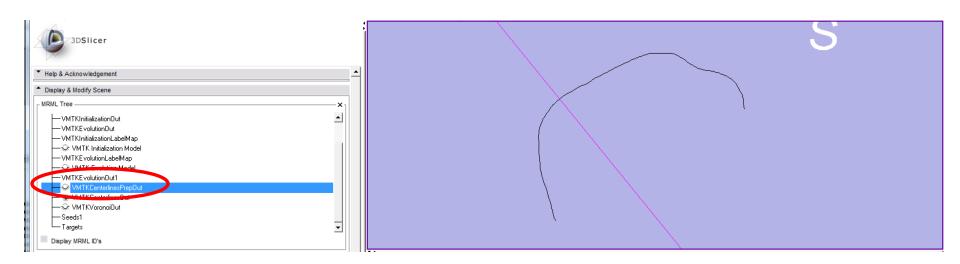
If instead you want to make the Voronoi diagram invisible open the "Data" module.

Then scroll down on the "Display & Modify Scene" Panel and click on the eye next to the "VMTKVoronioOut" file to close the eye and make it invisible.









You can also turn off the VMTKCenterlinePrepOut model to see just the Centerline path that you created in the 3D rendering Window.



2

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Module s:



3DSlicer
Heip & Acknowledgement
Display & Modify Scene
MRML Tree X Scene View Camera VMTKCenterlinesPrepOut VMTKCenterlinesOut VMTKCenterlinesImport EnhancedVesselnessOut VMTKInitializationOut VMTKEvolutionOut L UMTKInitializationLabelMap Display MRML ID's

Date

4

►

All segmentation parts are available as MRML nodes in the current scene. The "Data" module shows the MRML tree.

In general you can come back to the data module at any time to turn on and off segmentation parts conveniently.



Saving Files

Save :	Scene and Unsaved Data					2	
Save So	ene & Data Options					×1	
	Change Destination for AI Selected: 🛅 C/Users/Jacriz/Documenta/TESTNG/VITK in 3Disicer Testing/						
Tele 1	Node Name	Node Type	Node Status	File Format	File Name	Data Directory	
	(Scene Description)	(SCENE)	Modified	MRML (.mml)	SlicerScene1.mml	C:/Users/aprtiz/Documents/TESTING/VI/TK in 3Dislicer Testing	
	tutorial_cardiac_mri_data-Subvolume-resample_scale-1.0	Volume	Not Modified	Pick format for saving	Select Directory	Im In If Files/Tutoria/MI/TKCoronariesC	
	EnhancedVesselnessDut	Volume	Not Modified	NRRD (.nmd)	2 0 0	st Files/Tutoria/VIITKCoronariesC	
	VMTKInitializationOut	Volume	Not Modified	 (nmd) 		Contacts	
	VMTKEvolutionOut	Volume	Not Modified	NRRD (.nmd)		Cookies	
	VMTKInitializationLabelMap	Volume	Not Modified	NRRD (.nmd)		Carl Desktop	
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	VMTK Evolution Model	Model	Not Modified	Poly Data (.vtk)		C Mankhiji Reports	
	VMTKEvolutionOut1	Volume	Not Modified	NRRD (.nmd)	1	C My Pictures	
	VMTKCenterlinesPrepOut	Model	Not Modified	Poly Data (.vtk)		My Videos OSMSC Admin	
	VMTKCenterlinesDut	Model	Not Modified	Poly Data (.vtk)		🖻 🧰 TESTING	
	VMTKVoronoiDut	Model	Not Modified	Poly Data (.vtk)		E Contracting	
	Seeds1	FiduciaList	Not Modified	Fiducial List CSV (.fcsv)		🗀 5004 data Test Files	
	Targets	FiduciaList	Not Modified	Fiducial List CSV (.fcsv)		Control Cardiac MRI data Test Files Control Cardiac MRI data Test Files Control Cardiac MRI data Test Files	
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						OK Bancel	
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	Save Selected Cancel						

- 1. Now is a good time to save your work...when saving, select all of the files that you would like to save
- 2. Select the directory that you would like to save the checked files in.
- 3. Click "OK"
- 4. Then Click "Save Selected"



Saving Files

* 3. Export To File		
Add description headers		
Invert coordinates (IJK<->NIFTI)		
Export details		
	Export	3
 4. Import From File 		

The VMTKCenterlines module supports the export of extracted Centerlines as clouds of points to the filesystem.

To export details like the maximum inscribed sphere radius activate the checkbox (1), choose a destination (2) and click "Export!" (3).



Make sure that, when you choose a destination and enter a file name, you include the file extension type to save as a ".dat" file



Saving Files

🛓 centerline.dat 209595 _3.5754_35524 _2.75525325507 1.35627795835 53563.0 53155.0 0.755 -43.5243453979 23.6248474121 -2.82282710075 1.3566731071 83156.0 74764.0 0.076 -43.5672912598 23.6453384291 -2,84163999557 1.34768368553 83687.8 74764.0 8.848 -44.3442382812 23.8746795654 -3.11588931084 381434156682 83626.0 83606.0 0.0 2905764 73 8921318264 3 132454 -44,6662406921 23,9847869873 -3,34564328194 1,31296327481 B1841.0 B1841.0 0.0 -44.7168263862 24.8884348755 -3.36283813553-4 **21391.8 B4189.0 8.6**6 - -----45.0116713379 24.0653190613 -3.4202637672 1.36677139288 2024 0 8.0 -45.1805003325 24.092821239 -3.53823828697 1.420-02318.9 82318.0 0.0 -45.3257182966 24.1287387739 -3.57551217879 1.44477739523 67865.0 67865.0 0.8 -45.3494758686 24.1336631775 -3.5815183854 1.45831551176 82928.8 82938.8 8.72 -45.4883161621 24.1486834393 -3.61397314872 1.45145492922 59494.8 82928.8 8.872 -45.5894927979 24.1538124884 -3.6366481781 1.45485727223 82684.0 82699.0 0.104 -45.8841552734 24.2133865356 -3.7817223835 1.45863325172 82693.0 82693.0 0.0 -45,9728851318 24,2313556671 -3,73139214516 1,46847186443 54875.8 54875.8 8.8 -45.9736822949 24.2315886256 -3.73163154741 1.475319183 54875.8 81328.8 8.992 -46.1253738403 24.3120250702 -3.77564024925 1.47537432912 B1328.0 B1328.0 0.0 -46.2832869397 24.3918942878 -3.82611846924 1.46898955773 B1335.8 B3671.0 8.576 -46.5725859589 24.5875893482 -3.93619441986 1.45986542314 B3675.8 B3671.8 8.736 -46.5947151184 24.5178642273 -3.94453848786 1.47386688327 83672.8 83675.8 8.852 -46.6676940918 24.5478801727 -3.9686293602 1.47718453004 83732.0 83732.0 0.0 -46,7952346802 24,5904388428 -4,00715827942 1,48037306238 63731.0 63728.0 0,312 -46.8497428894 2 -47.119468689 24 -47.4573402485 2 -47.7022323608 2 -**17.7317488483** 2 -48.2851288667.2 -48.295879364 25

ANA: I HAVE NOT **CHECKED** TO SEE IF **FILES WERE SAVED** CORRECTLY

-48.3784751892 Z -48,4057388306 2 -48.4948959351 2 -48.6587486267 2 -48.765625 25.28

The exported file includes the world coordinates (1) of the Centerlines and also the Maximum Inscribed Sphere Radius (2) for each point.

-48.8883724976 2



Luca Antiga, Marina Piccinelli, Lorenzo Botti, Bogdan Ene-Iordache, Andrea Remuzzi, and David A Steinman. An image-based modeling framework for patient-specific computational hemodynamics. *Med Biol Eng Comput*, 46(11):1097–1112, Nov 2008.

V. Caselles, R. Kimmel, and G. Sapiro. Geodesic active contours. In *Proc.* Fifth International Conference on Computer Vision, pages 694–699, 20–23 June 1995.

Alejandro F. Frangi, Ro F. Frangi, Wiro J. Niessen, Koen L. Vincken, and Max A. Viergever. Multiscale vessel enhancement filtering. In *Lecture Notes in Computer Science*, volume 1496, pages 130–137. Springer-Verlag, 1998.

J. A. Sethian. Level Set Methods and Fast Marching Methods: Evolving Interfaces in Computational Geometry, Fluid Mechanics, Computer Vision, and Materials Science (Cambridge ... on Applied and Computational Mathematics). Cambridge University Press, 2 edition, 6 1999.



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