

# The Vascular Modeling Toolkit: A Python Library for the Analysis of Tubular Structures in Medical Images

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## Software

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## Summary

Vascular disease is the leading cause of death in the developed world (Benjamin et al. 2018). There is a wide body of evidence demonstrating that the geometric structure and layout of the vascular network has a major impact on hemodynamics and the associated severity / progression of vascular diseases such as heart attack, stroke, and aneurysm rupture (Luca Antiga 2002, L. Antiga et al. (2008)). Analysis of diagnostic medical scans designed to highlight vascular structures (such as CT Angiography or MR Angiography) allows for the detailed characterization of these structures *in vivo*. Such analyses generate quantitative measures which can be used in order to understand both disease characteristics across a population, and the efficacy of potential treatments (Piccinelli et al. 2009, L. Antiga et al. (2008)).

The **Vascular Modeling Toolkit (VMTK)** is a collection of python-wrapped C++ methods which enable the efficient segmentation, geometric characterization, network analysis, hemodynamic modeling, and visualization of vascular structures from medical images. Image segmentation is performed via a 3D gradient based level set algorithm which is initialized from user defined seeds. Surface editing, mesh generation, and geometric characterization is largely automated, relying heavily on the centerline definitions calculated from segmented structures. User interaction is facilitated by a unique system of unix-inspired **pypes**. This interface allows for the composable creation and execution of entire analyses from simple terminal commands, providing a flexible framework for high-level coding, both from the user's and from the developer's point of view.

VMTK is a mature package with an active development team and user community. It can be used via its standalone interface, included as a Python or C++ library, or as an extension to the medical image processing platform 3D Slicer (Kikinis, Pieper, and Vosburgh 2014). It has received over 400 citations in scientific publications since its first release in 2004 (L. Antiga et al. 2008). The library relies upon two major open source frameworks for building highly performant and well validated image analysis algorithms and visualizations: the Visualization Toolkit (VTK) and the Insight Segmentation and Registration Toolkit (ITK). Thorough tutorials and documentation are available on the project webpage: [www.vmtk.org](http://www.vmtk.org).

## VMTK In Action

### Generating a Surface from an Image via Level Set Evolution

Segmenting a complex vascular tract comes down to selecting the endpoints of a branch, letting level sets be attracted to gradient peaks with the sole advection term turned on,

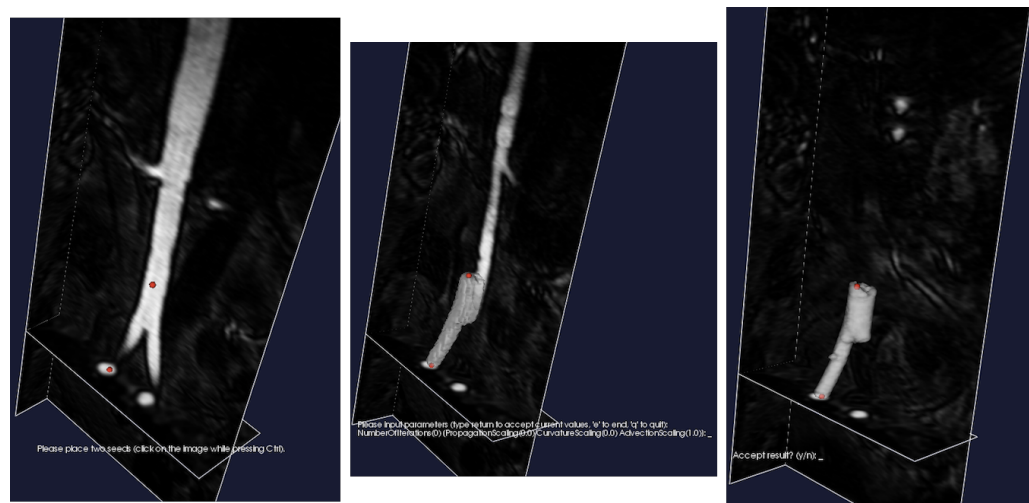


Figure 1: levelset segmentation

repeating the operation for all the branches and merging everything in a single model.

```
vmtklevelsetsegmentation -ifile foo.dcm --pipe vmkmarchingcubes -i 0.0
--pipe vmtksurfacewriter -ofile foo.vtp
```

The process of placing seeds on an image (left), initializing an isosurface from the seeds using the colliding fronts methods (center), and finally evolving the isosurface through the level set equations (right).

## Generating Centerlines from a Surface

Centerlines are determined as the paths defined on Voronoi diagram sheets that minimize the integral of the radius of maximal inscribed spheres along the path, which is equivalent to finding the shortest paths in the radius metric.

```
vmtkcenterlines -ifile foo.vtp -ofile foo_centerlines.vtp
```

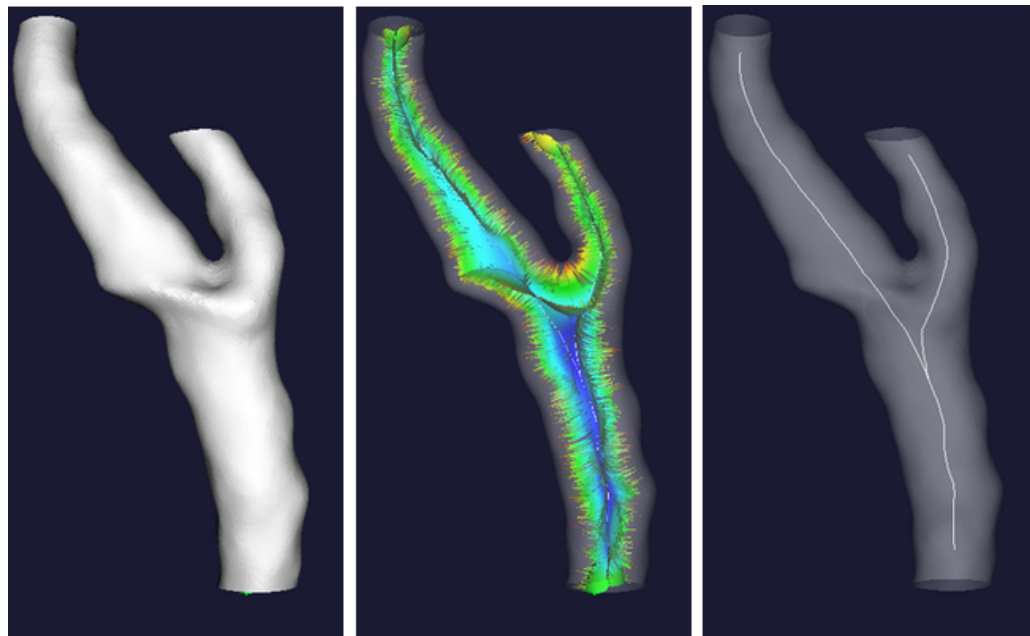
The input surface representation (left), a visualization of the internal subset of the voronoi diagram where each sheet represents a maximum inscribed sphere radius centered at some point in the surface (center), the centerline extracted from the voronoi diagram rendered as in its position within the input surface (right).

## Splitting a Surface from its Centerlines

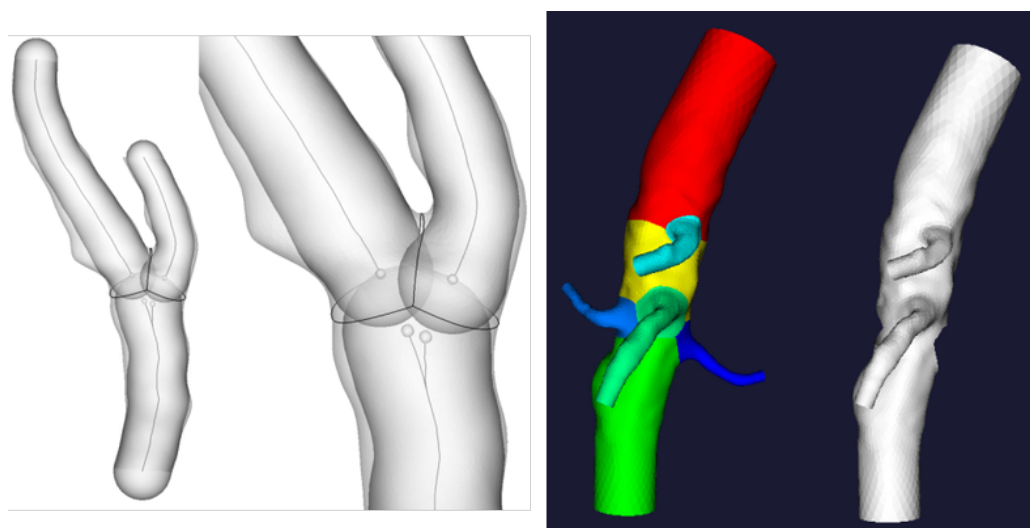
Surface properties can be analyzed, and the surface can be split by analyzing the surface-centerline tube containment relationships.

```
vmtksurfacereader -ifile foo.vtp --pipe vmtkcenterlines --pipe vmtkbranchextractor
--pipe vmtkbranchclipper -groupids 0 -insideout 1 -ofile foo_sp.vtp
```

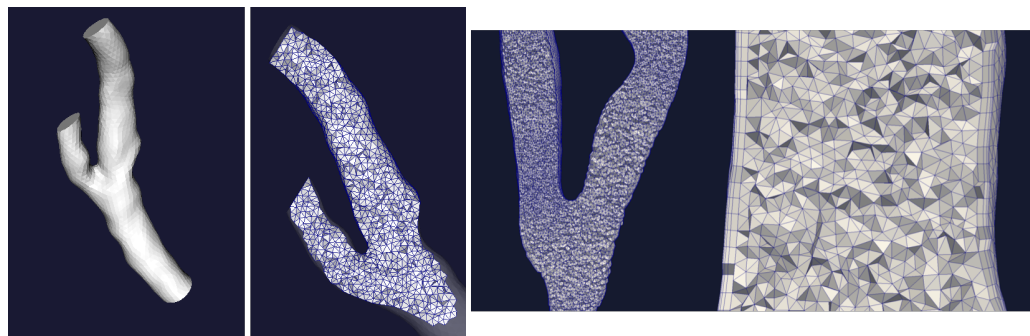
Illustration of the centerline-surface tube containment relationships (left), visualization of the surface being split into independent groups based on the surfaces membership in a centerline tract/group (right).



**Figure 2:** centerline generation



**Figure 3:** centerline splitting



**Figure 4:** mesh generation

## Generating a Volumetric Mesh from a Surface

Tetrahedral, mixed tetrahedral, and boundary layer meshes can be generated from a surface and its centerlines.

```
vmktsurfacereader -ifile foo.vtp --pipe vmtkcenterlines --pipe vmtkdistancetocenterlines
-useradius 1 --pipe vmtkmeshgenerator -elementsizemode edgelengetharray
-edgelengetharray DistanceToCenterlines -edgelengethfactor 0.3 -boundarylayer
1 -ofile foo.vtu
```

The input surface representation (left), a visualization of the internal mesh (center), a visualization of a boundary layer internal mesh (right).

## Composable Scripting With Pypes

Pypes is the glue among vmtk scripts. It allows new scripts to be written easily and have a common interface, but, most of all, it allows single vmtk scripts to interact with each other, making VMTK modular and flexible. Pypes can be used from the command line, a python interpreter, or from the custom PyPePad user interface

The VMTK PyPePad user interface.

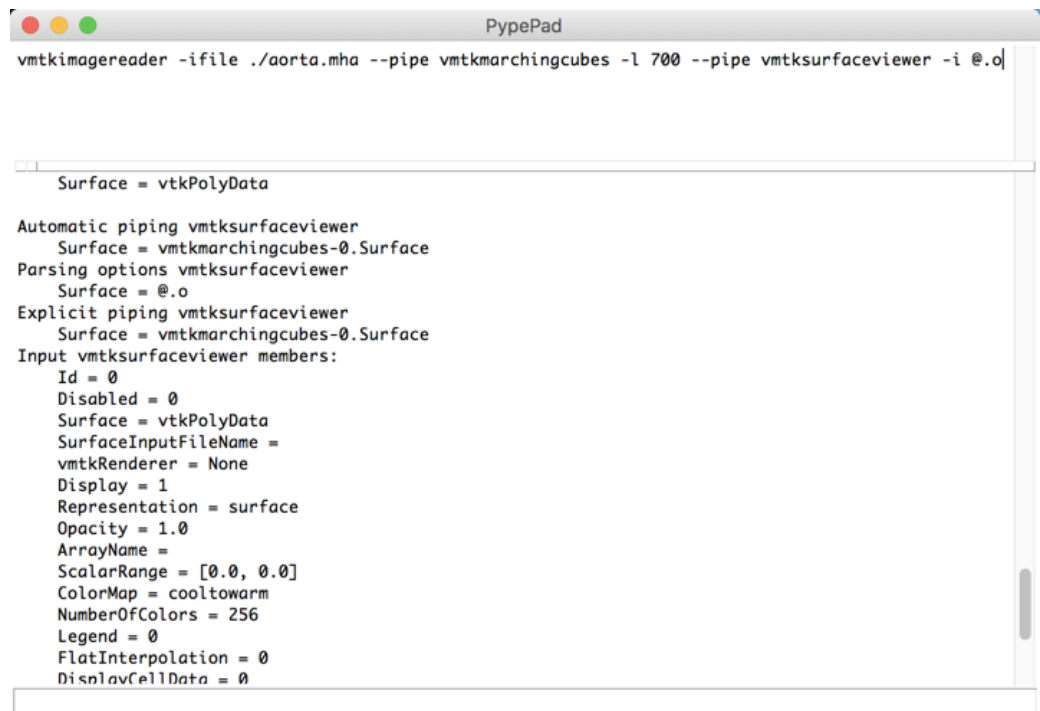
## Acknowledgements & Funding

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## References

Antiga, L., M. Piccinelli, L. Botti, B. Ene-Iordache, A. Remuzzi, and D. A. Steinman. 2008. "An Image-Based Modeling Framework for Patient-Specific Computational



```
vmtkimagereader -ifile ./aorta.mha --pipe vmtkmarchingcubes -l 700 --pipe vmtksurfaceviewer -i @.o

Surface = vtkPolyData

Automatic piping vmtksurfaceviewer
  Surface = vmtkmarchingcubes-0.Surface
Parsing options vmtksurfaceviewer
  Surface = @.o
Explicit piping vmtksurfaceviewer
  Surface = vmtkmarchingcubes-0.Surface
Input vmtksurfaceviewer members:
  Id = 0
  Disabled = 0
  Surface = vtkPolyData
  SurfaceInputFileName =
  vmtkRenderer = None
  Display = 1
  Representation = surface
  Opacity = 1.0
  ArrayName =
  ScalarRange = [0.0, 0.0]
  ColorMap = cooltowarm
  NumberOfColors = 256
  Legend = 0
  FlatInterpolation = 0
  DisplayCellData = 0
```

**Figure 5:** pyperpad

Hemodynamics.” Journal Article. *Med Biol Eng Comput* 46 (11):1097–1112. <https://doi.org/10.1007/s11517-008-0420-1>.

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