

## RELEASE NOTES - AMIRA 6.4.0, SEPTEMBER 2017

---

### Amira 6.4.0

3D Data Visualization and Analysis Software for Life Sciences

Dear Amira User,

With this document we would like to inform you about the most important new features, improvements, and changes in this version of Amira. Please read these Release Notes carefully. We would appreciate your feedback regarding this version. If you encounter problems, but also if you have suggestions for improvement, please report them to [fei-sw-support@fei.com](mailto:fei-sw-support@fei.com). We would like to thank you in advance for your efforts.

September 2017, the Amira team

**IMPORTANT:** The Amira 6.4 licensing mechanism has been upgraded to FlexNet Publisher 11.14. If you are using floating licenses managed by a FlexNet license server, make sure you have installed version 11.14.0 or higher of the FlexNet tools on your system. For more details and download links, please refer to <http://www.fei-software-center.com/support/flexnet-server-doc/>.

## CONTENTS

Contents.....	2
Amira - Enhancements and new features .....	3
New feature .....	3
Enhanced features .....	3
Bio-Formats - Enhancements.....	4
Enhanced features .....	4
XImagePAQ   Amira Cell Biology – Enhancements and new features .....	5
New modules.....	5
Enhanced features .....	6
Amira Cell Biology edition – Enhancements and new features .....	8
XWind extension.....	9
New feature .....	9
New module .....	11
New XPoreNetworkModeling extension .....	12
New separation method dedicated to arbitrary pore space .....	12
Generation of a pore network model .....	13
Visualization.....	13
Pore network model filtering.....	15
Intersection percentage computing .....	15
Properties calculation .....	16
New XVolumeCorrelation extension .....	17
Avizo for FEI - Enhancements and new features .....	18
Licensing.....	19
Operating systems .....	19
Solved issues .....	20

## AMIRA - ENHANCEMENTS AND NEW FEATURES

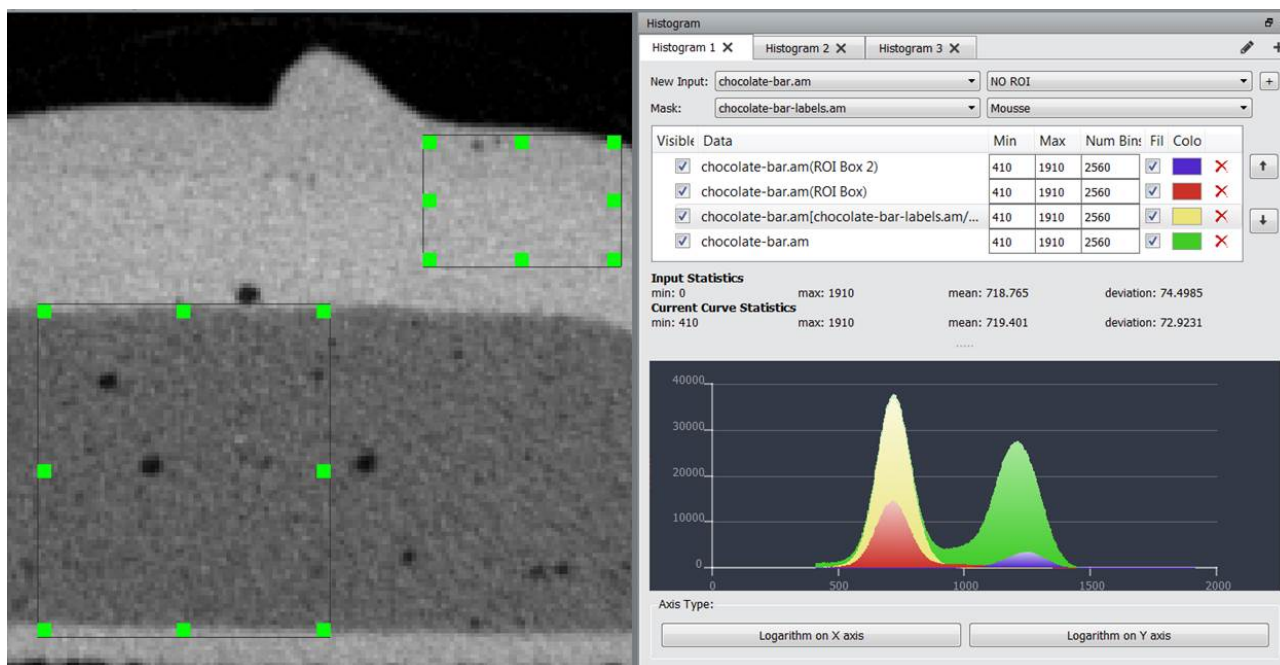
### NEW FEATURE

#### HISTOGRAM AND CORRELATION PANELS

This release includes two new panels available from the Window menu:

The **Histogram Panel** allows displaying the distribution of multiple measures in the same window and comparing them with various graphical options (e.g., REV evaluation by comparing multiple histograms of a given image within various ROI boxes). In addition, multiple tabbed histogram windows can be created in the panel. Typical inputs include images, spreadsheets, label analyses, spatial graphs and pore network models.

The **Correlation Panel** allows plotting a given measure against another one. Multiple correlations can be added and compared with various graphical options (curve, histogram, marked curve, markers, impulse). In addition, multiple tabbed correlation windows can be created in the panel. Typical inputs include spreadsheets, label analyses, spatial graphs and pore network models.



### ENHANCED FEATURES


















#### SEGMENTATION WORKROOM ENHANCEMENTS

A **Recolor Materials** menu entry in the **Segmentation** menu of the **Segmentation Workroom** was added that changes the color of identically colored adjacent labels in order to make them **visually distinguishable**.

## FILAMENT WORKROOM ENHANCEMENTS

The **Filament Workroom** was enhanced to reflect the state of the 'Show' column selected in the **Label Window** in both the **3D Viewer** and the **2D Slice Viewer**.

To improve visibility of selected labels in the **Label Window** of the **Filament Workroom** across different platforms and desktop environments, label highlighting has been changed from bold face to a red font color.

Name	Color	Show	Location
Identified_Graphs		<input checked="" type="checkbox"/>	GRAPH
Graph0		<input checked="" type="checkbox"/>	
Graph1		<input checked="" type="checkbox"/>	
Graph2		<input checked="" type="checkbox"/>	
Graph3		<input checked="" type="checkbox"/>	
Ranks		<input checked="" type="checkbox"/>	SEGMENT
Rank1		<input checked="" type="checkbox"/>	
Rank2		<input checked="" type="checkbox"/>	
Rank3		<input checked="" type="checkbox"/>	
Rank4		<input checked="" type="checkbox"/>	
Rank5		<input checked="" type="checkbox"/>	
Rank6		<input checked="" type="checkbox"/>	
Rank7		<input checked="" type="checkbox"/>	
Rank8		<input checked="" type="checkbox"/>	
Rank9		<input checked="" type="checkbox"/>	
Rank10		<input checked="" type="checkbox"/>	
Rank11		<input checked="" type="checkbox"/>	

## BIO-FORMATS - ENHANCEMENTS

### ENHANCED FEATURES

## BIO-FORMATS ENHANCEMENTS

**HDR and Multi-channel support:** The **Bio-Formats Reader** has been enhanced to enable import of **High Dynamic Range** image data stored as RGB fields with 16 bits per channel and **multi-channel** fields stored with an RGB field per channel. To improve memory efficiency, only those channels that store actual data will be imported as a multi-channel field.

**Large Slices Support:** The **Bio-Formats Reader** was enhanced to enable import of 2D images of **up to 4GB**.

**Very Large Data Management:** The **Bio-Formats Reader** has been enhanced to enable the direct conversion of images in any file format supported by Bio-Formats to the Amira native LDA data format for **out-of-core data** management. This enables users to visualize images larger than the system memory and to utilize the full feature set that the XLVolume extension offers. This conversion requires the XLVolume extension.

*Note: Conversion of double precision floating values and 32-bit unsigned integers is currently not supported.*

### NEW MODULES

#### THRESHOLD BY CRITERION

Threshold by Criterion performs a thresholding with a criterion on an image. If the result of computation is true, output pixel will be set to 1, 0 otherwise. Possible criteria are:

- "less-than"
- "less-or-equal"
- "equal-to"
- "greater-or-equal"
- "greater-than"
- "not-equal-to"

#### MARKER-BASED WATERSHED INSIDE MASK

The region of interest that the **Marker-Based Watershed** tool is executed on, can now be limited by an arbitrarily defined mask in the form of a **binary mask**. In addition, this module integrates the steps of landscape image creation with watershed segmentation.

#### INTENSITY AUTO CLASSIFICATION

The module is a non-supervised classification tool performing an **automatic segmentation of multi-channel images** into a given number of classes. This command applies a k-means clustering method considering each pixel as an observation vector. In this way the number of channels of the input image corresponds to the dimension of the vectors.

- Choose K vectors that will represent the centers of K classes.
- For a subset of S, sort its vectors in all the classes in function of a distance (which can be Euclidian, Tanimoto, scalar or Mahalanobis).
  - Move the center of the smallest class in the direction of the biggest one.
  - Recalculate the classes with the new centers.
  - Iterate until a good repartition of the vectors is achieved.
- Sort all vectors of the set S in the K classes to obtain the result classification.

where S, the size of the subset, is a parameter of the algorithm, and K is the number of classes to obtain.

### BOX FILTER

The performance of the filter has been optimized.

**Compatibility note:** When used with the Auto Scale option enabled, the output type is no longer upgraded (an 8-bit input now gives an 8-bit output). If the Auto Scale option is disabled, the output type is still upgraded.

### MEDIAN FILTER

The filter now offers a parameter to specify the kernel type.

The *Iterative* mode enables the former mode of the median filter. This algorithm repeats iteratively a median filter on a square window with a size of 3 x 3. This algorithm converges quickly and applying more than three iterations doesn't change the result significantly. As a consequence the main drawback of this algorithm is to be ineffective when a large window size is required.

The *Square/Disk* and *Cube/Ball* modes perform a real median filter on the full size of the window. These modes are performed by an optimized algorithm that offers improved performance.

The gain of performance is especially noteworthy in the 3D case. For small kernel size in 2D, the prior mode (iterative) is recommended.

### IMAGE GRADIENT

The module now offers the options *Prewitt* and *Sobel* for computing the gradient in 2D and 3D. These modes are the simplest algorithms for computing a gradient. The benefit of these operators is to be very efficient and fast to compute. Prior to this version a kernel size of `_3x3` was proposed only with the 2D gradient. It is equivalent to the *Prewitt* operator.

### AUTO THRESHOLDING

The module now offers an option to define the input range. The mode *other* corresponds to the prior mode, which was not adapted by default when the dynamic range of the input image was greater than 256 gray levels. The new mode *min-max* allows a default behavior suitable for use with `ost` grayscale images.

### LABEL ANALYSIS

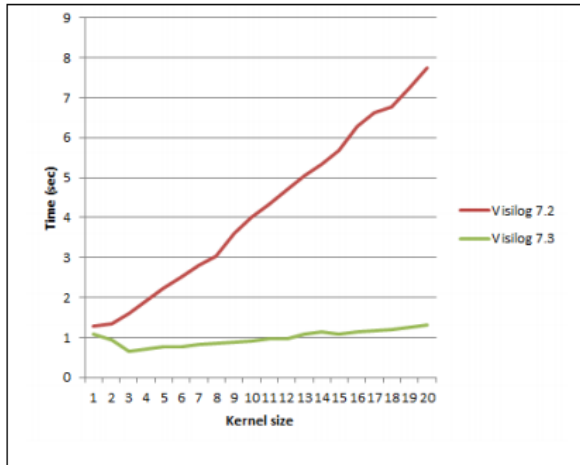
**New measure - Thickness3d:** The Length3d measure, also known as the Feret's longest diameter, represents the major diameter. The Breadth3d measure the primary minor diameter is the largest diameter orthogonal to Length3d. The new measure Thickness3d is the secondary minor diameter and largest diameter orthogonal to both measures Length3d and Breadth3d.

The related ThicknessOrientPhi and ThicknessOrientTheta measures express the orientation of this secondary minor diameter.

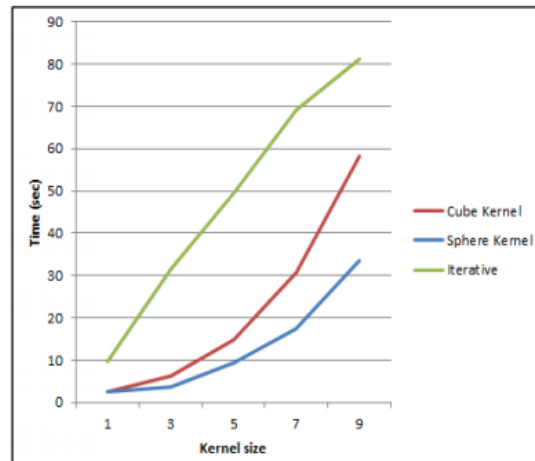
**Measure Improvements:** The number of Feret diameters has been limited to 100 in 3D. It is now possible to set this value to up to 3000 Feret diameters. For efficiency and file size reasons, only some predefined configurations are allowed for a number of diameters greater than 100: 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000, 1500, 2000, 2500 and 3000 diameters. If an intermediate value is set, the higher predefined value is retained.

Precision and capacity has been improved to 64-bit for large data analysis with the following measurements:

- Area
- Area3d
- Volume
- Volume2
- Volume3d



Scalability comparison of box filter on a 512x512x512 image (boxfilter3d)



Scalability comparison of median modes on a 512x512x512 3D dataset

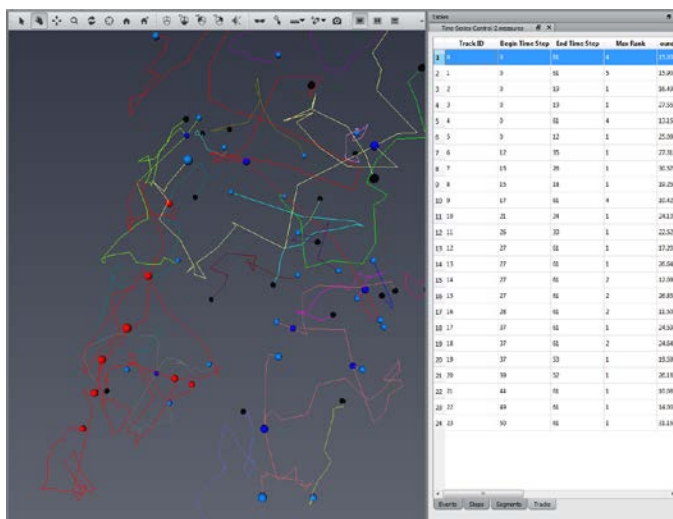
## AMIRA CELL BIOLOGY EDITION – ENHANCEMENTS AND NEW FEATURES

Launched with Amira 6.3, the Amira Cell Biology Edition aims at helping researchers to understand living cells and their processes. This Edition packages the standard Amira application, the XImagePAQ advanced image processing and quantification extension, the Bio-Formats reader, the XTracing extension and a new, comprehensive set of time series processing, object tracking and analysis tools.

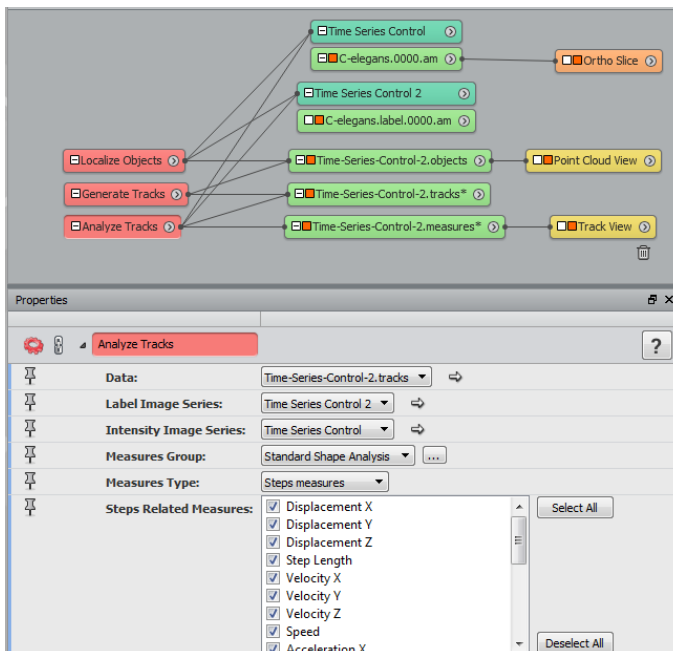
Amira version 6.4 brings important improvements to Bio-Formats (read above) and to the object tracking tools.

### OBJECT TRACKING ENHANCEMENTS

The **Analyze Tracks** module has been enhanced with a **result locator**. This enables locating the results for a particular track, segment or event by left clicking on the different elements in the 3D viewer. This will highlight the selected element in the viewer and the corresponding row in the data spreadsheet. To select an entire track instead of a segment or event, a Shift + Left Click is required. This locator also works in the opposite direction; a left click on a row in the spreadsheet highlights the element in the 3D viewer.



The **Analyze Tracks** module has been enhanced to allow selecting **only the motility-related measures of interest**, instead of computing all available measures. In addition, it now enables the selection and computation of all intensity and shape measures available in **Label Analysis** to be applied to each tracked object at each time step. For this, the module requires the original time series of intensity images and a corresponding time series of label images as secondary inputs.

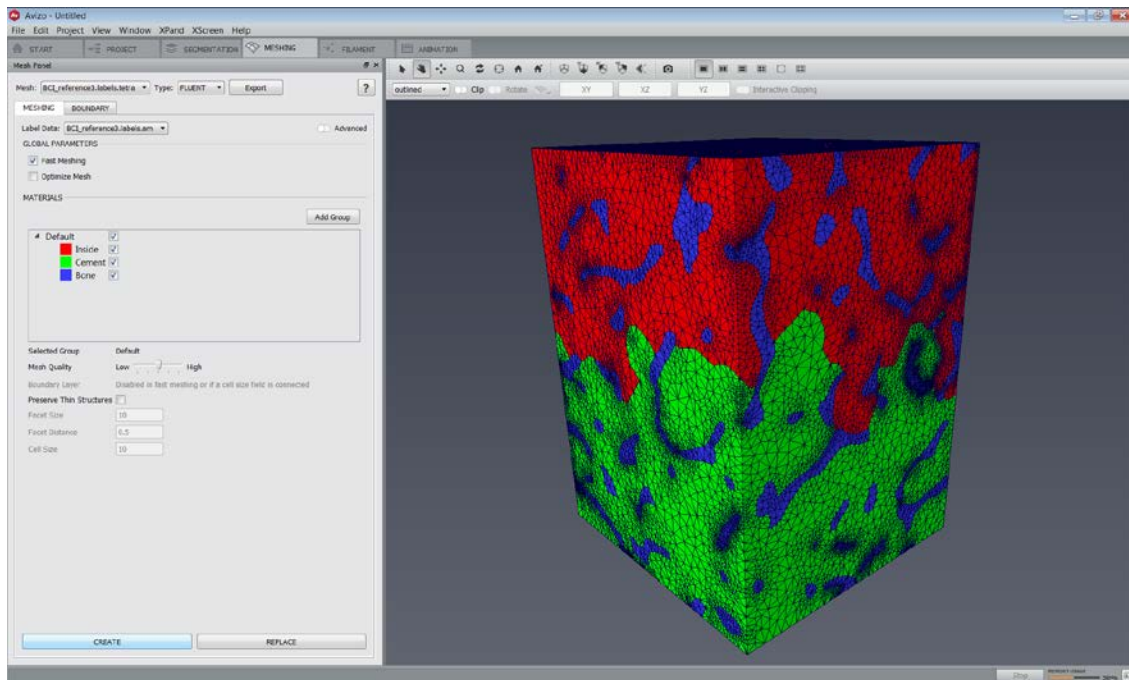




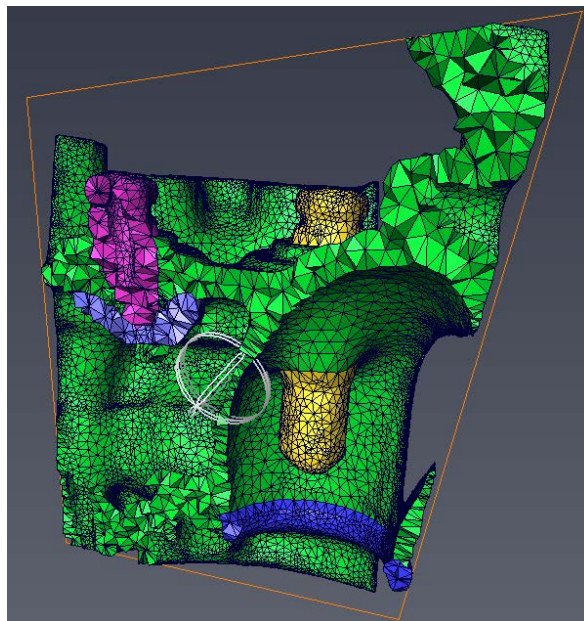
### NEW FEATURE

XWind now includes a totally new meshing workroom that permits very fast production of very high quality 3D meshes suitable for collaboration with CFD/FEA solvers.

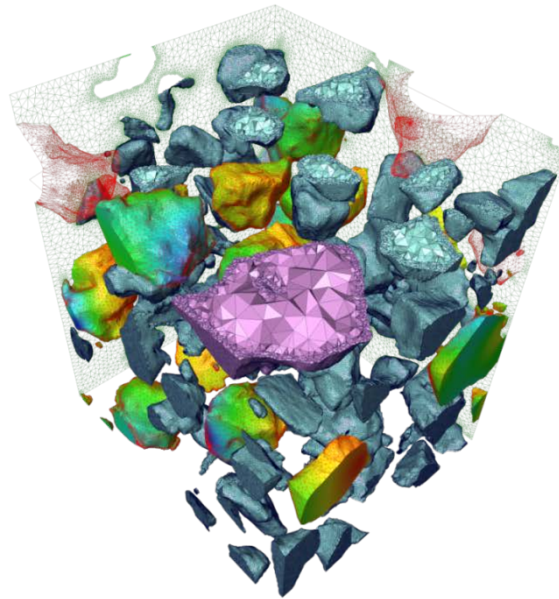
- Automatically create tetrahedral mesh from label data within a dedicated meshing workroom:



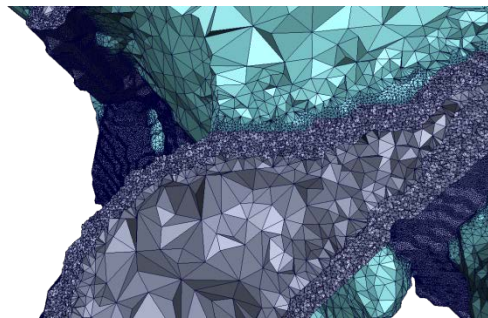
- Dedicated mesh inspection tools:



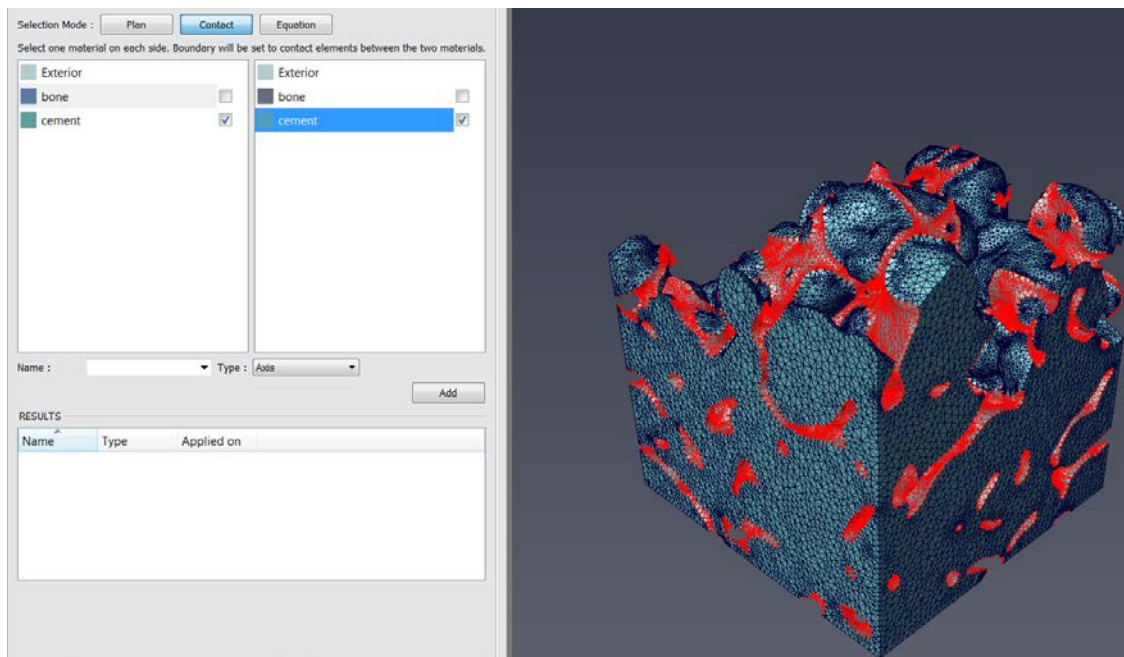
- Mesh any topology with any number of materials with mixed sizing element:



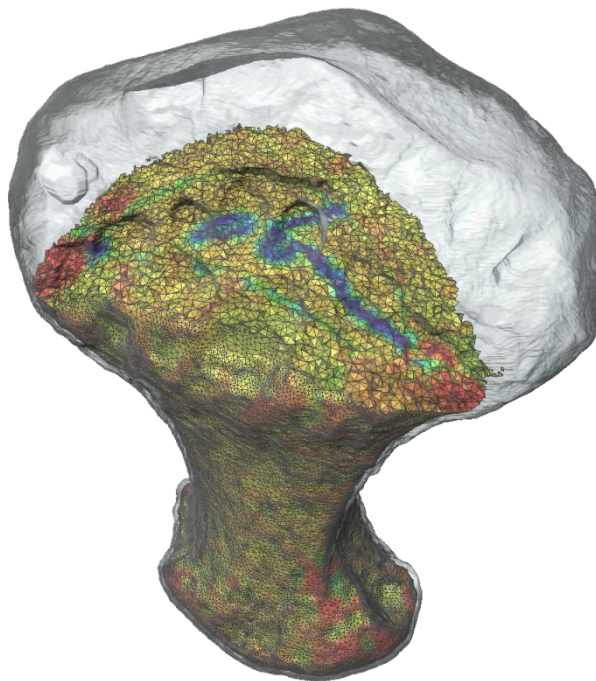
- High quality meshing with conforming interfaces and topology preservation
- Fast Robust Meshing Engine for large dataset
- Fine user control over sizing element and regions through image fields
- Boundary layer support:



- Thin structure preservation
- Interface smoothing
- Set boundary conditions with visual feedback:



- Optimization methods for reducing/removing slivers
- Export to all major solver (NEW: including COMSOL Multiphysics®)
- High quality display with multiple overlaid data:



## NEW MODULE

### GENERATE TETRA MESH

**Generate Tetra Mesh** creates a volumetric tetrahedral mesh. Its input is a description of a 3D volume by a label. The meshing engine is based on Delaunay refinement and is the same engine used in the new meshing workroom.

## NEW XPORENETWORKMODELING EXTENSION

The new **Pore Network Modeling** extension allows accessing different statistics from a labeled and separated pore space 3D image. The statistics include distribution of the following parameters:

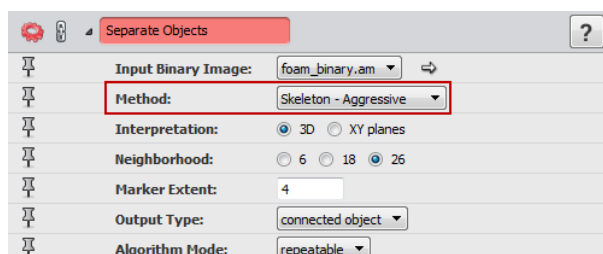
- Pore volume
- Pore area
- Pore equivalent radius
- Pore center of gravity
- Pore coordination number (number of connected neighbors)
- Intersection percentage between pore network model and original pore space
- Throat area
- Throat equivalent radius
- Throat channel length
- Throat connection (id of pore 1, id of pore 2)

The extension also allows reading pore network code from the *Pore Network Node-Link* data format.

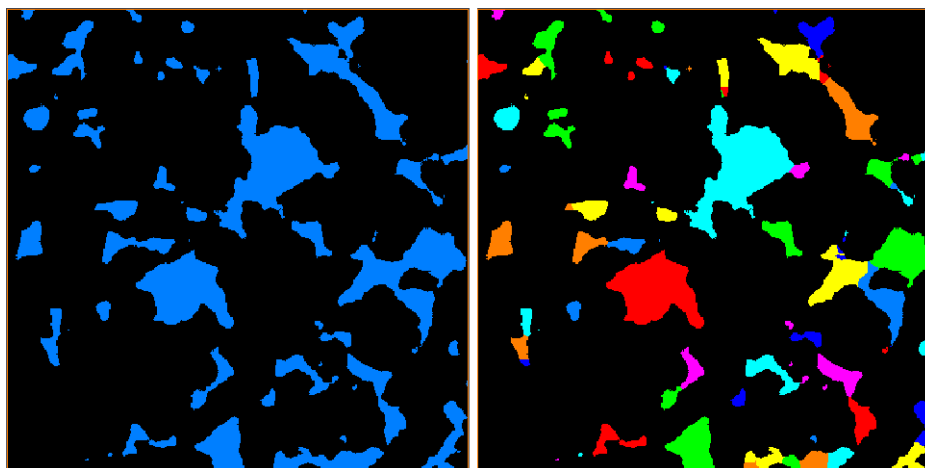
From a labeled image representing a separated pore space, a pore network can be generated. It contains the network code and can be used with several dedicated modules for visualization, filtering, etc.

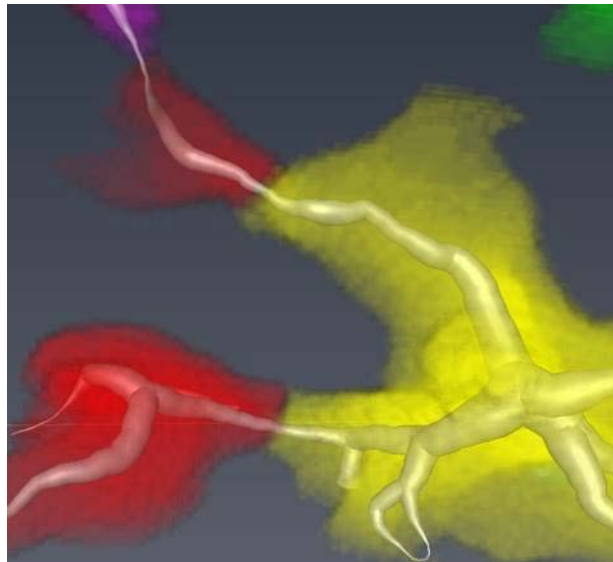
## NEW SEPARATION METHOD DEDICATED TO ARBITRARY PORE SPACE

A pore space can be separated into a set of connected and labeled pores using the **Separate Objects** module. The **Pore Network Modeling** extension provides an optimized mode for arbitrary pore shapes (*Skeleton – Aggressive*). Spherical pores can still be separated using the default mode (*Chamfer – Conservative*).



This method generates a label field using a separation algorithm based on watershedding and skeletonization, which carefully separates pores at throat centers.





## GENERATION OF A PORE NETWORK MODEL

The **Generate Pore Network Model** module generates a pore network model from a separated and labeled pore space. The extracted pore network model contains the following statistics:

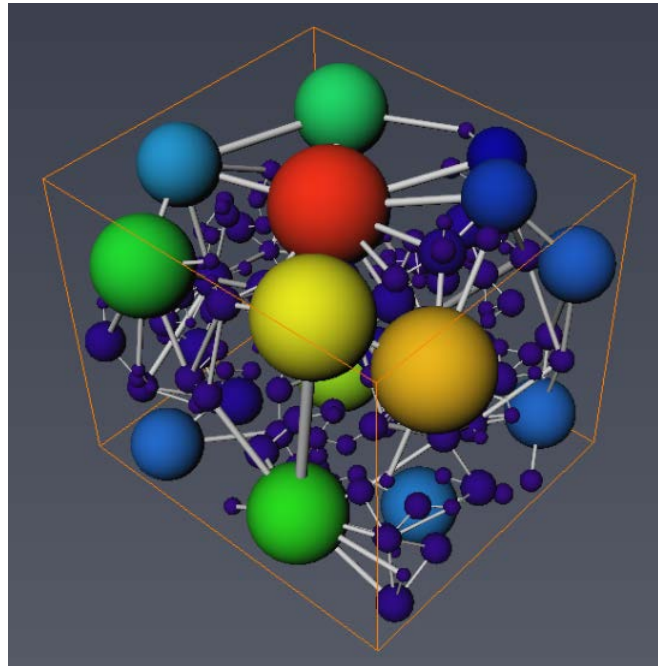
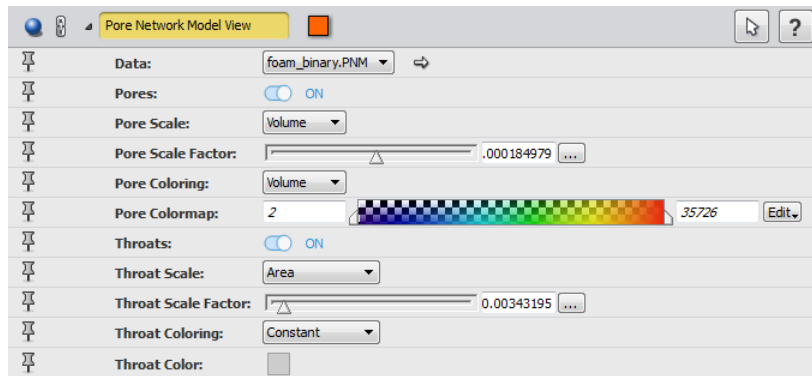
- Number of nodes
- Number of throats
- Coordination number
- Throat equivalent radius
- Throat channel length (defined as distance from pore to pore centers)
- Pore volume
- Pore equivalent radius

	Pore ID	Volume	Area	EqRadius	LabelID	X Coord	Y Coord	Z Coord	Coordination Number
1	0	6182	1943.84	11.3854	1	12.1655	6.9264	10.3928	2
2	1	32004	5852.38	19.6957	2	46.5946	18.0579	13.7421	5
3	2	4506	1554.4	10.2463	3	76.9585	8.97847	5.62406	4
4	3	12638	3338.99	14.4498	4	105.767	10.6916	12.1898	4
5	4	79	146.159	2.66183	5	124.57	1.12658	4.63291	0
6	5	5807	2522.17	11.1503	6	12.5557	30.1362	4.74514	4
7	6	30558	6072.47	19.3945	7	83.2811	42.305	12.6139	10

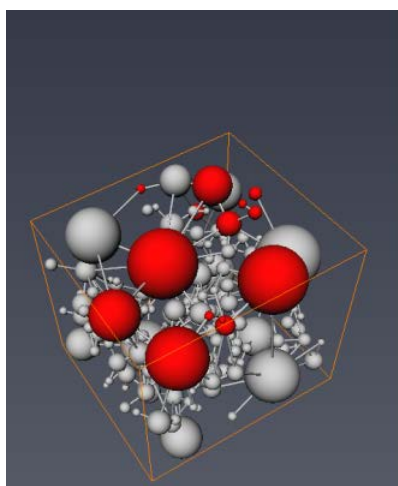
## VISUALIZATION

The **Pore Network Model View** module is a visualization module for a pore network model. *Pores* are displayed using spheres, and *Throats* are displayed using cylinders. Each of them may be colored or scaled according to their attributes.





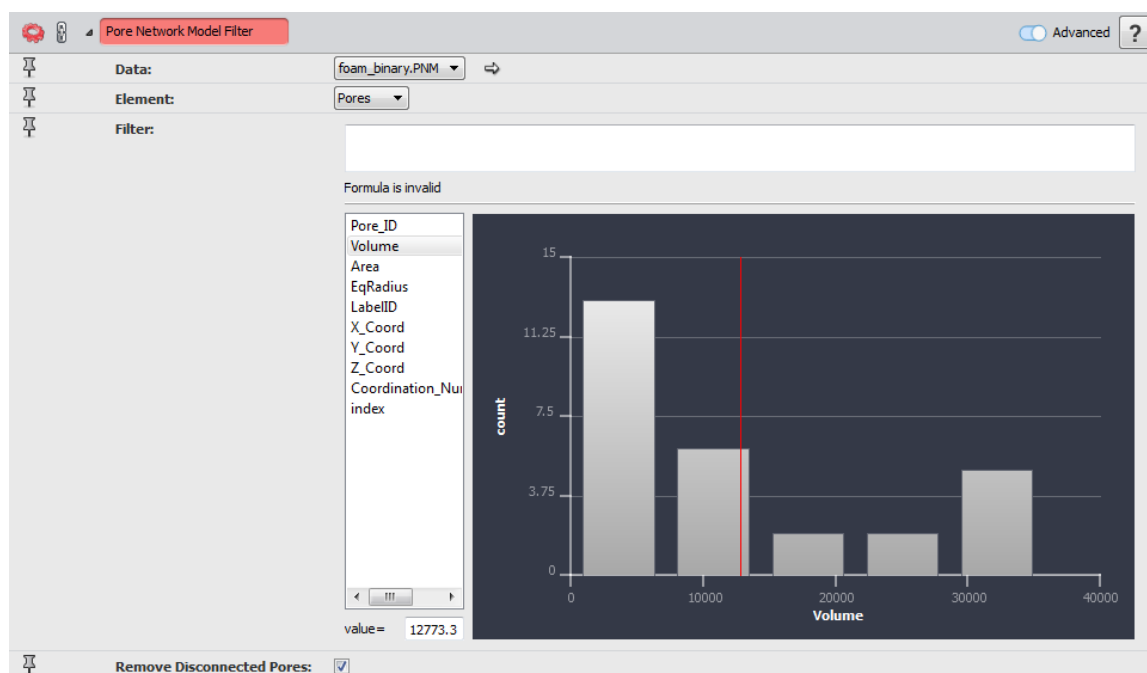
The network code can be displayed as a spreadsheet in the Tables panel. This spreadsheet has two tabs, one for pores and one for the throats. *Pores* and *Throats* can be highlighted by selecting them in the pore network model inner spreadsheet.



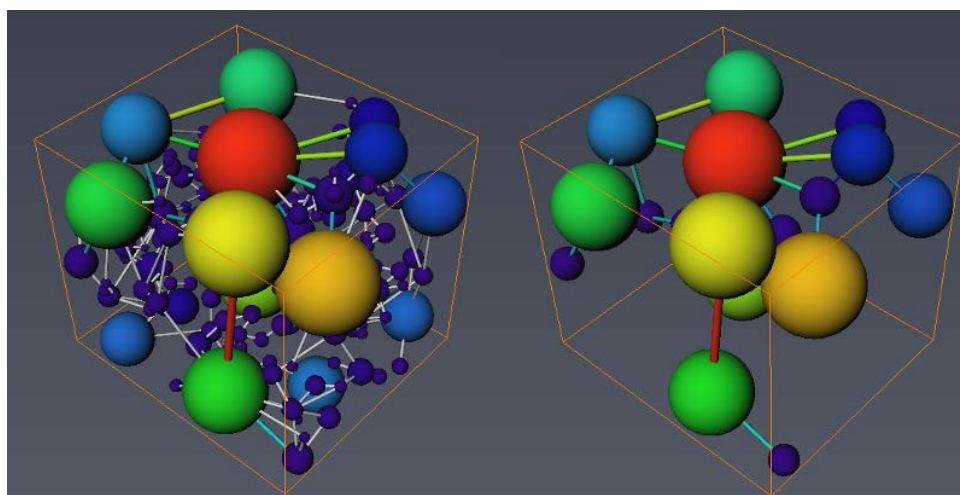
	Pore ID	Volume	Area	EqRadius
1	0	0.0780831	1.22915	0.265149
2	1	0.36192	3.39577	0.442087
3	2	0.137864	1.8568	0.32047
4	3	0.00497395	0.150073	0.105894
5	4	0.00123118	0.0697584	0.0664881
6	5	0.227976	2.9301	0.378966
7	6	0.0134125	0.870604	0.147392
8	7	0.540863	4.71242	0.505436
9	8	0.00509241	0.146202	0.106728
10	9	0.392019	3.23963	0.454018
11	10	0.00184343	0.109115	0.0760641
12	11	0.702889	4.64731	0.551568
13	12	0.0356069	0.616192	0.204087
14	13	0.00127244	0.0578862	0.0672227
15	14	0.0140966	0.950393	0.149856
16	15	0.000537724	0.0350506	0.0504456
17	16	0.00379867	0.121044	0.0967939
18	17	0.00159853	0.0676121	0.0725344

## PORE NETWORK MODEL FILTERING

The **Pore Network Model Filter** module filters a pore network model based on a user-specified formula. It will remove all the elements whose value does not fulfill this filter formula. Only one type of element, *Pores* or *Throats*, can be filtered at a time.

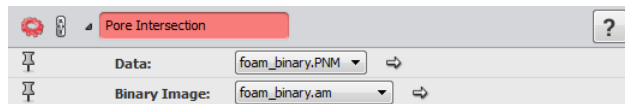


This module generates a new pore network model containing only the pores and throats resulting from this filtering. An option allows removal of all the disconnected pores in a second process.



## INTERSECTION PERCENTAGE COMPUTING

The **Pore Intersection** module compares a pore network model with a binary image in order to compute an intersection percentage for each sphere representing the pores and their representation in the binary image. The *Volume* of the pore network model attribute is automatically used for the intersection computation.



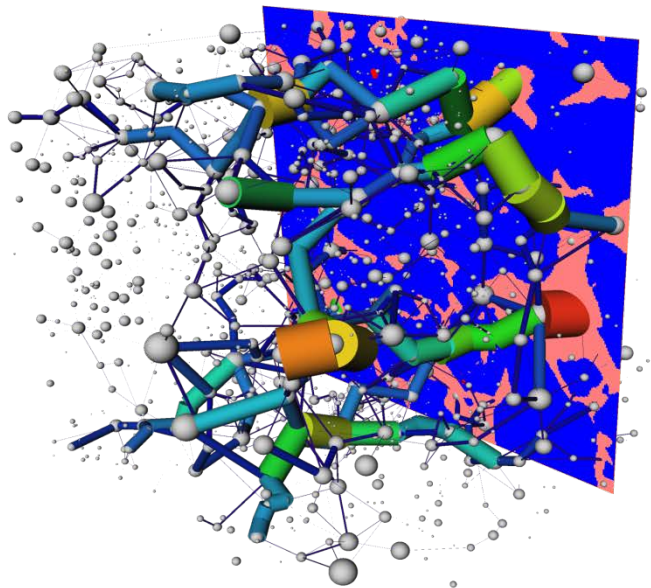
A copy of the pore network model is generated as a result. The intersection percentages computed are added in a new *Pores* attribute.

	Pore ID	Volume	Area	EqRadius	LabelID	Intersection	X Coord	Y Coord	Z Coord	Coordination Number
1	0	6182	1943.84	11.3854	1	68.2789	12.1655	6.9264	10.3928	2
2	1	32004	5852.38	19.6957	2	77.1997	46.5946	18.0579	13.7421	5
3	2	4506	1554.4	10.2463	3	63.4044	76.9585	8.97847	5.62406	4

## PROPERTIES CALCULATION

The **Pore Network Modeling** extension allows for additional property computation, helping to characterize material samples even further.

- **Absolute Permeability** (including flow rate per throat property in PNM)
- **Tortuosity** (based on velocities)



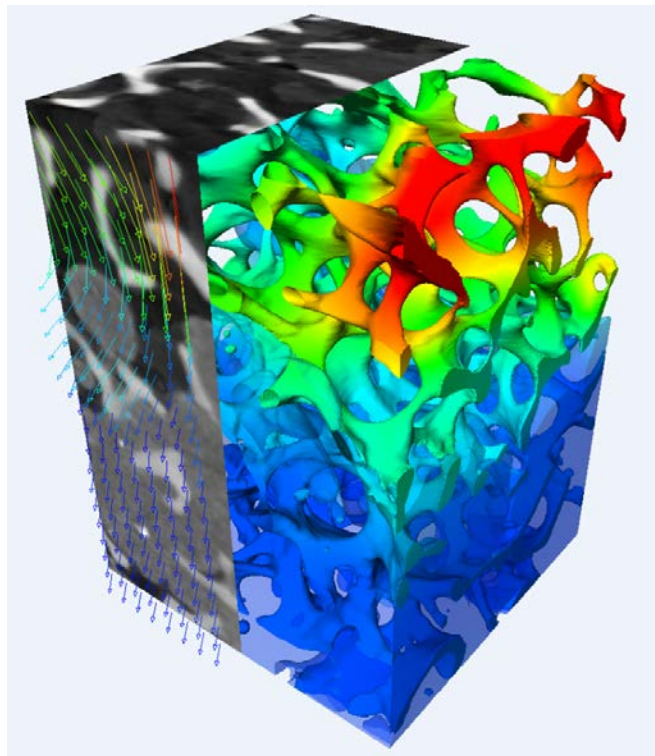


## NEW XVOLUMECORRELATION EXTENSION

The Amira XVolumeCorrelation extension provides Digital Volume Correlation (DVC) techniques to compute 3D full-field continuous displacement and strain maps from volume images acquired during a deformation process of an object. The user inputs two images and a mesh that will be used to measure the displacement and strain maps.

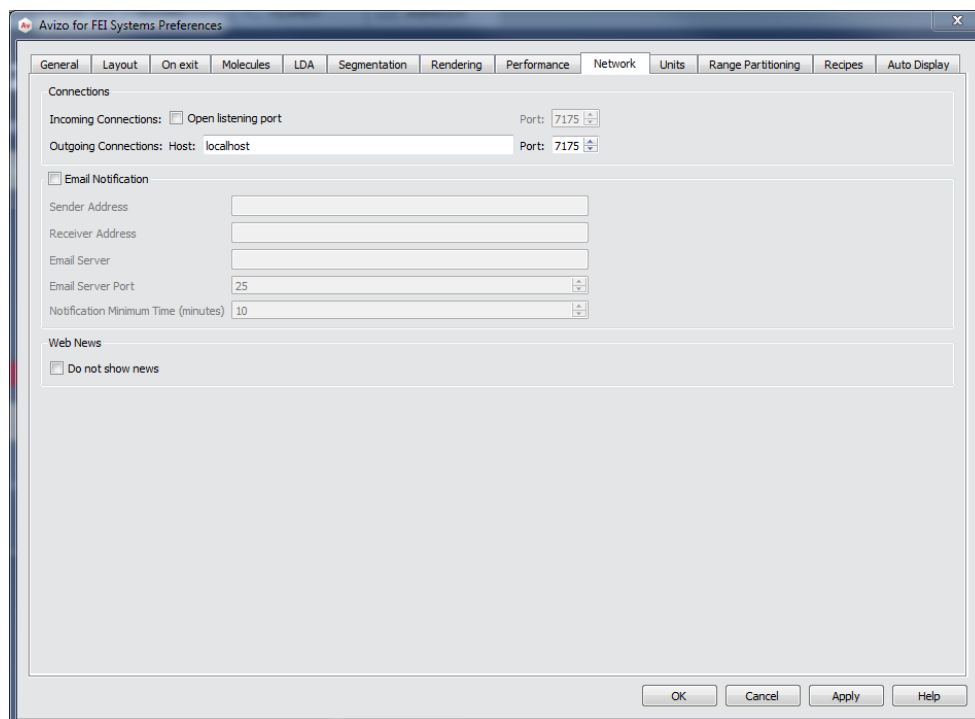
The extension can, for instance, be used to visualize and quantify deformation-induced microstructural changes during dynamic processes, such as localization phenomena induced by heterogeneities or thermal expansion mismatch between materials. Furthermore, the output displacement field can be used to enrich a numerical simulation by using measured boundary conditions, or to optimize this simulation by comparing numerical and measured data.

- The extension includes two DVC algorithms (a traditional subset-based approach and a more robust FE-based continuous approach) implemented in a user-friendly interface that can be used independently or together to tackle, for instance, phenomena where large deformations are expected.
- Powerful combination with Amira quantification modules.
- Powerful combination with XWind meshing tools for setting up simulation with displacement and strain coming from real experiments.



### AVIZO-MAPS BRIDGE

Incoming/outgoing connections between Avizo and MAPS can now be defined through the Preferences dialog.



## LICENSING

The Amira 6.4 licensing mechanism has been upgraded to FlexNet Publisher 11.14. If you are using a FlexNet license server, make sure you have installed version 11.14.0 or higher of the FlexNet tools on your system. For more details and download links, please refer to <http://www.fei-software-center.com/support/flexnet-server-doc/>.

## OPERATING SYSTEMS

Amira 6.4 runs on:

- Microsoft Windows 7/8/10 (64-bit).
- Linux x86\_64 (64-bit). Supported 64-bit architecture is Intel64/AMD64 architecture. Supported Linux distribution is Red Hat Enterprise Linux 6 and Red Hat Enterprise Linux 7.
- Mac OS X El Capitan (10.11) and macOS Sierra (10.12).

In order to add custom extensions to Amira with Amira XPand, you will need:

- Microsoft Visual Studio 2013 (VC12) Update 4 on Windows.
- gcc 4.4.x on Red Hat Enterprise Linux 6 and Red Hat Enterprise Linux 7.
- Currently, Amira XPand support is not available for Mac OS X El Capitan (10.11) nor macOS Sierra (10.12). It will become available again once Clang support has been completed.

## SOLVED ISSUES

Amira 6.4 provides many enhancements and solutions to known problems, including the following:

Align Slices	58999	The Align Slices module could not be connected to a 2D image. This has been fixed.
Arithmetic	59217	When using Arithmetic module with different input types, using logical expression on label values could produce wrong results on the label borders. This has been fixed. <b>Note that this fix impacts the following modules' computation: MarkerBased Watershed Inside Mask, 2D-Histogram Segmentation, Watershed Segmentation.</b>
Animation Director	56012	The Stop Watch icon was not displayed on animated ports in some cases. This has been fixed.
	52823	The video quality of an MPEG movie created by the Animation Director or the Movie Maker could be degraded. This has been fixed.
ANSYS / Abaqus export	23268	Material names are now managed for a mesh exported to ANSYS or Abaqus.
Auto Skeleton	59309	In some cases, nodes could be created outside of the bounding box during skeletonization. This has been fixed.
Auto Thresholding	43728	With interpretation mode set to XY, only the first slice was thresholded. This has been fixed.
Create Label Colormap	39651	Create Label Colormap module and makeColormap Tcl command now generate colormaps with Exterior material color fully transparent.
Crop Editor	44427	Crop editor would fail when applied to a multi-channel field data with a Volume Rendering visualization. This has been fixed.
	52286	After the ROI List function was used, the voxel size of the cropped image was slightly different from that of the uncropped image. This has been fixed.
Bio-Formats	42827	Bio-Formats reader is now able to read slices bigger than 2GB. Note: To handle slices larger than 4GB the XLVolume and Experimental extensions are required.
	57954	Some multi-channel files could not be loaded on Mac OS using Bio-Formats reader. This has been fixed.
	55821	Bio-Formats reader is now able to read TIFF file with time step information as Time Series.
	43377	Bio-Formats reader is now able to load multi-channel CZI.
	42615	Bio-Formats reader is now able to load images that contain multi-channel RGB data.
B-Spline	58008	When the Curve Editor was used on a B-Spline, the Curve Editor display remained even after the Curve Editor was switched off. This has been fixed.  Note that now when using the curve editor, a Line Set view is automatically attached to the B-Spline.
Colormap port	57125	The "Auto Adjust To" option behavior has been reworked in order to avoid inconsistency.
Compute Secondary Structure	55795	A project containing the result of "Compute Secondary Structure" could not be reloaded successfully. This has been fixed.
Curved Slice	57880	The module uses now the nearest-neighbor interpolation for label images.

DICOM reader	57271	DICOM files could sometimes be rendered with an inconsistent size. This has been fixed.
	43302	Reloading DICOM files from a directory path that contains non-ASCII characters would fail. This has been fixed.
Dual Beam 3D Wizard (Amira for FEI only)	60119	Reloading a saved project containing the Dual Beam 3D Wizard was not working properly. This has been fixed.
	44384	On Mac OS, the Crop Editor was not working properly. This has been fixed.
Eval On Lines	58559	The Thickness computation resulting from an Eval On Lines module was not correct with a float field input. This has been fixed.
	36110	After Eval on Lines was applied to spatial graph, the spatial graph was not updated. This has been fixed.
Export data	60741	It is now possible to export data greater than 2GB to ASCII format.
Extract Image	30507	Auto-refresh is no longer enabled by default when the module is created.
	31692	The module is no longer tightly connected with its Data in the Project View.
Filament Editor	43638	If the option Edit/Preferences/Rendering/Raycasted spheres was activated, it was not possible to pick a node in a spatial graph displayed in the Filament Editor. This has been fixed.
	56325	The Filament Editor documentation has been updated to add available Tcl commands description.
Fluent file format	42554	Material names are now managed in exported .cas file.
Generate Surface	52918	The Generate Surface algorithm, being multi-threaded, could generate different results on different machines. A new advanced option <i>Algorithm Mode</i> has been added to the module: with <i>repeatable</i> option the algorithm will be mono-threaded and always give the same results, whereas with <i>fast</i> option the algorithm will be multi-threaded and results will be machine dependent.
Generate Tracks	59668	Minimum values have been set for the following ports to prevent computing inconsistent results: Min.Track.Len minimum value is now 2, and Time Window minimum value is now 1.
Grid View	60371	Enabling cell filtering using Grid View module was not working properly. This has been fixed.
Image Statistics	62313	Projects containing an Image Statistics and its result were not loaded properly. This has been fixed.
Interactive Thresholding	55102	Results wouldn't be recomputed when the module data source was changed. This has been fixed.
Label Analysis	35837	Results have been improved to support large data.
	58922	The computation with some large label fields could lead to artifacts. This has been fixed.
Label measures	36490	Label measures have been improved to support large data.
LDA Expert Settings	58677	Fixed resolution was not taken into account when doing snapshots from a script. This has been fixed.
License Manager	34841	Deactivating extensions in offline mode caused an error message. This has been fixed.
Localize Objects	55880	This module can now use Time Series of 2D images as input to compute the tracking.
Match Point Clouds	55619	The module's computation was not working properly. This has been fixed.
MATLAB	59254	A new version of the MATLAB writer (.mat) is available. This allows export of MATLAB files larger than 2GB.

<b>MRC reader</b>	61183	It is now possible to read all MRC files, with and without the extended FEI header. All versions 2000 and 2014 are supported. Note that MRC files that don't follow the FEI description of extended headers will not load.
<b>Multi-Channel</b>	58599	Removing one of the channels would modify the range of the other channels. This has been fixed.
	57876	Multi-channel field does not accept connections to data sources that are controlled by a Time Series Control anymore.
<b>Multiplanar viewer</b>	40022	Offscreen rendering snapshot didn't scale the image correctly. This has been fixed.
<b>Ortho Slice LDM</b>	27570	Ortho Slice LDM is now correctly updated after input voxel size modification.
<b>Preview</b>	58588	The preview management in the Properties Area could slow down the application when the selected data object had inconsistent properties. This has been fixed.
<b>Process Time Series</b>	56953	It is now possible to select a Spreadsheet as input of the module.
<b>Python</b>	51462	A new section Python Limitations has been added to the Python documentation. Please refer to the documentation for further details.
<b>Quick Probe</b>	59191	Quick Probe tool used on an Ortho Slice now works properly when the Ortho Slice input data is changed.
<b>Recipes (Amira for FEI only)</b>	57288	Play buttons are now available only for steps that can be played again in the current run.
	59416	Ports values of snapshot on Pore Network Model were reset at each recipe run. This has been fixed.
	57188	Saving a recipe could modify its name. This has been fixed.
<b>Resample</b>	57254	16-bit label input data objects are now correctly managed by the Resample module.
<b>Save/Load</b>	59216	Loading a project containing an Avizo As Large Disk Data object from a path containing space characters was not working properly. This has been fixed.
<b>Script Object</b>	56023	With the release of Avizo 9.2 many modules have been reworked with respect to their user interface, which required changing names and types of ports. As a consequence, scripts and script objects written for earlier versions of Avizo than 9.2 would in many cases no longer work. To account for this, a backward compatibility mode has been implemented. Please refer to the documentation (section Versioning of Script Objects and backward compatibility) for more information.
<b>Segmentation Editor</b>	59945	When a new label field was selected, the default viewer layout was restored (one single viewer). This has been fixed.
<b>Spatial Graph Statistics</b>	57758	Computation on large Spatial Graph could lead to abnormal RAM consumption. This has been fixed.
	40592	The values for mean length and mean radius are now computed by averaging the mean Curved Length and Mean Radius of each segment.
<b>Stacked Slices</b>	44202	Stacked slice of series consisting of 8-bit images can now be read as 'Stacked Slices as Large Disk Data'.
<b>Standard View</b>	61588	Clicking in one of the 2D viewers was not repositioning the crosshair. This has been fixed.
<b>Surface View</b>	59755	Interacting with the Colormap port in constant color mode was making the port disappear. This has been fixed.
	62389	Attaching a Surface View to a surface with no material would fail. This has been fixed.

<b>Temporal Spatial Graph</b>	55258	The export command wouldn't export the Event Type values. This has been fixed.
<b>Thickness Map</b>	58121	Displaying the Thickness Map result with a Volume Rendering was not working properly. This has been fixed.
<b>Trackball</b>	58009	The interactivity with the measurement tool and editors such as Crop Editor was disabled after the camera trackball was manipulated. This has been fixed.
<b>Transform Sequence</b>	36717	Up and Down buttons have been removed from the module's properties.
<b>Tridexterity View</b>	23137	Tridexterity View now works for ML4210-ML552 screens.
<b>TXM reader</b>	59052	The display scale on TXM data could be inconsistent. This has been fixed.
<b>Viewers layout</b>	60407	Some viewer layout Tcl commands were not working properly. This has been fixed.

Our team is continually focused on solving as many issues as possible to make your experience of Amira as satisfactory as possible. To this purpose, we would appreciate your feedback regarding this version. If you encounter problems, or if you have suggestions for improvement, please report them to [fei-sw-support@fei.com](mailto:fei-sw-support@fei.com).