thermoscientific

Release notes

Amira–Avizo Software

Version 2020.2

3D data visualization and analysis

The aim of this document is to inform you about the most important new features, improvements and changes in this version of Thermo Scientific™ Amira-Avizo™ Software.

Please read these Release Notes carefully.

We would appreciate your feedback regarding this version. If you encounter any problems or have any suggestions for improvement, please do not hesitate to contact us at FRBOR.3d_hotline@thermofisher.com.
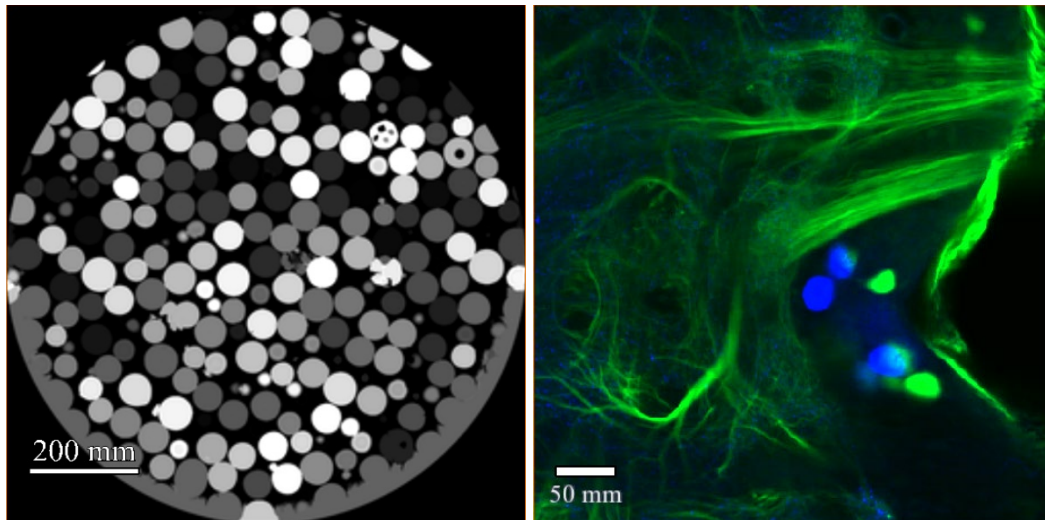
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Avizo Software Lite and Amira Software: Enhancements and new features

Scale Bar

The 2D ScaleBar module has been made compatible with LDAOrthoSlice. It can now be used with any orthoslice and any type of data, including RGB images, multi-channel, or large data.

An option in the properties now enables the legend to be written above the scale bar.

Relabel By Track ID – Amira Software for Cell Biology

A new module, Relabel By Track ID, allows you to relabel a Time Series of segmented objects to match their corresponding Track ID. This enables the visualization of the results of the object tracking step using Slices or Voxelized Rendering. The Object Tracking Tutorial has been updated to explain how to use this new module.
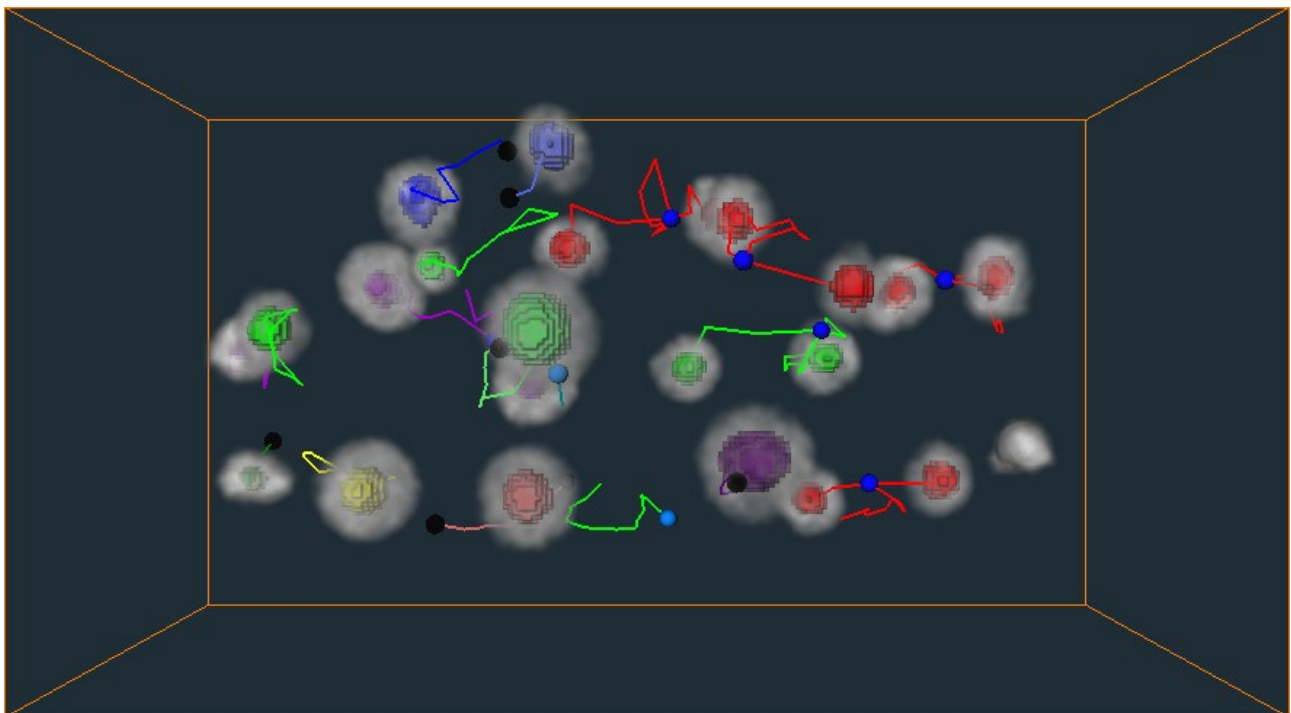
Compatibility note: In order to use this new module with old projects, it is necessary to recompute the Generate Tracks step. The module has been slightly modified to increment the track ID by 1 and insert an empty track on the Track ID 0. This modification allows the same colors to be used when displaying the relabeled objects and when displaying the track segments colored by their Track ID when using Track View.

A new xtra has also been published to show how to best use this module and the others for tracking objects: https://xtras.amira-avizo.com/xtras/cell-detection-and-tracking

This xtra shares a set of add-ons for easily performing cell tracking throughout a time series.

Molecule DNA-RNA Visualization – Amira XMolecular

This module visualizes the typical ladder structure of double-stranded DNA or single-stranded RNA structures. Each strand consists of multiple nucleotides with four different base types (Adenin, Cytosine, Guanine, and Thymine for DNA and Adenine, Cytosine, Guanine, and Urazil for RNA). The backbone part of the nucleotide will be shown as a strand with an elliptical cross section and the bases as elliptical cylinders with different patterns at the ends, called sticks.

Instead of the sticks, you can also visualize the sugar rings of the backbone in combination with the single-ring pyrimidines or the double-ring purines of the bases. The module provides several coloring modes that color either the DNA/RNA specific properties or general molecular properties.

In order to use this module, you need a graphics card that supports geometry shaders.
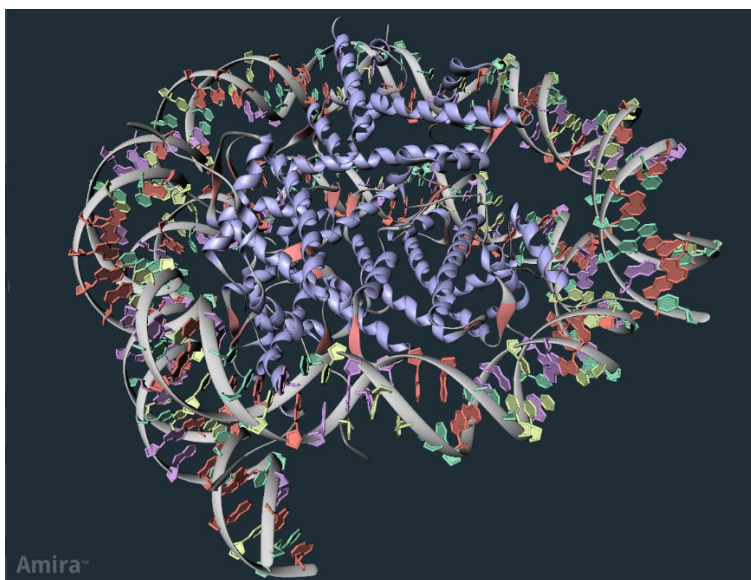
Visualization of DNA and secondary structures of a nucleosome.

N. Lindow, D. Baum, M. Leborgne, H.-C. Hege (2019). Interactive Visualization of RNA and DNA Structures. IEEE Transactions on Visualization and Computer Graphics, vol. 25, no. 1, pp. 967-976.

New option: Multiple Hypothesis Tracing for module Trace Correlation Lines – Amira XTracing / Avizo XFiber

A new option, Multiple Hypothesis Tracing, is available in the module Trace Correlation Lines. This allows for more robust results to be obtained, especially in the context of dense fibers and low data contrast, at the cost of increased computation time. It is accessible from the Advanced Parameter settings.
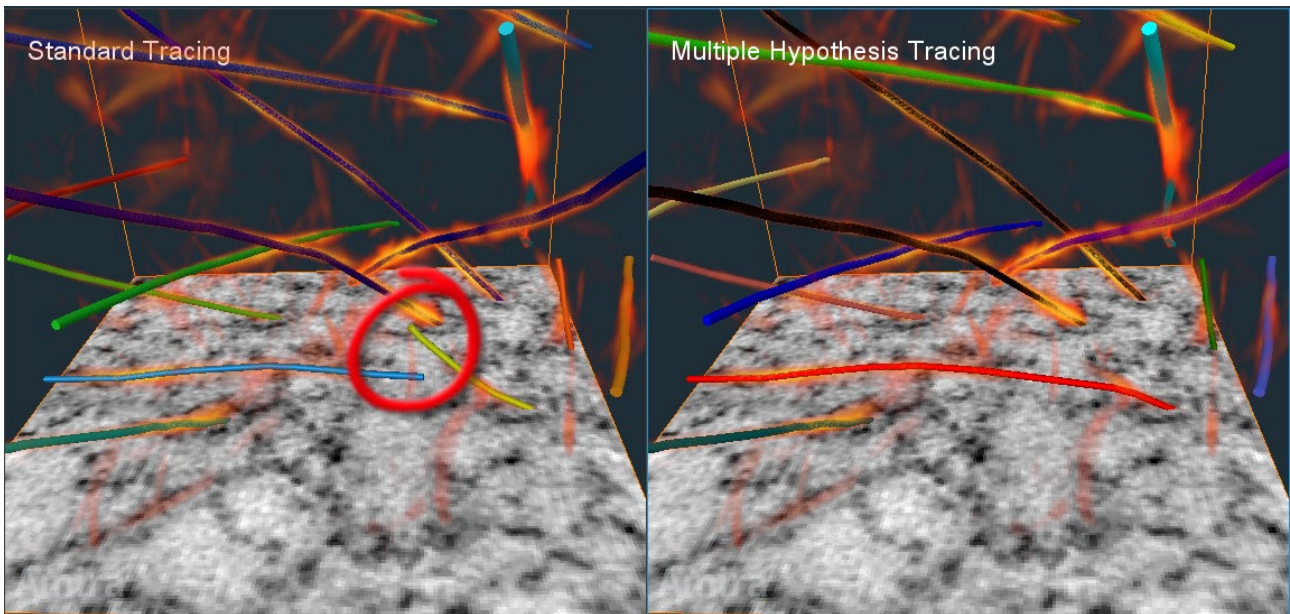
Tracing of microtubules in electron tomography images, with and without Multiple Hypothesis Tracing. The orange volume rendering displays the correlation field, whereas colored tubes show the traced centerlines.

Friman, O., Hindennach, M., Kühnel, C., Peitgen, H.-O. (2010). Multiple hypothesis template tracking of small 3D vessel structures. Medical Image Analysis, 14:160-171

Python

$AMIRA_LOCAL or $AVIZO_LOCAL are now supported as search paths for Python Script Objects. See the paragraph *Resource File* in the chapter *Automating, Customizing, Extending > Python Documentation > Script Objects* for more details.

Trial Watermark

Amira-Avizo Software Trial version displays a watermark of "Trial Version" on top of the 3D Viewer. This watermark is removed upon activation of the license.
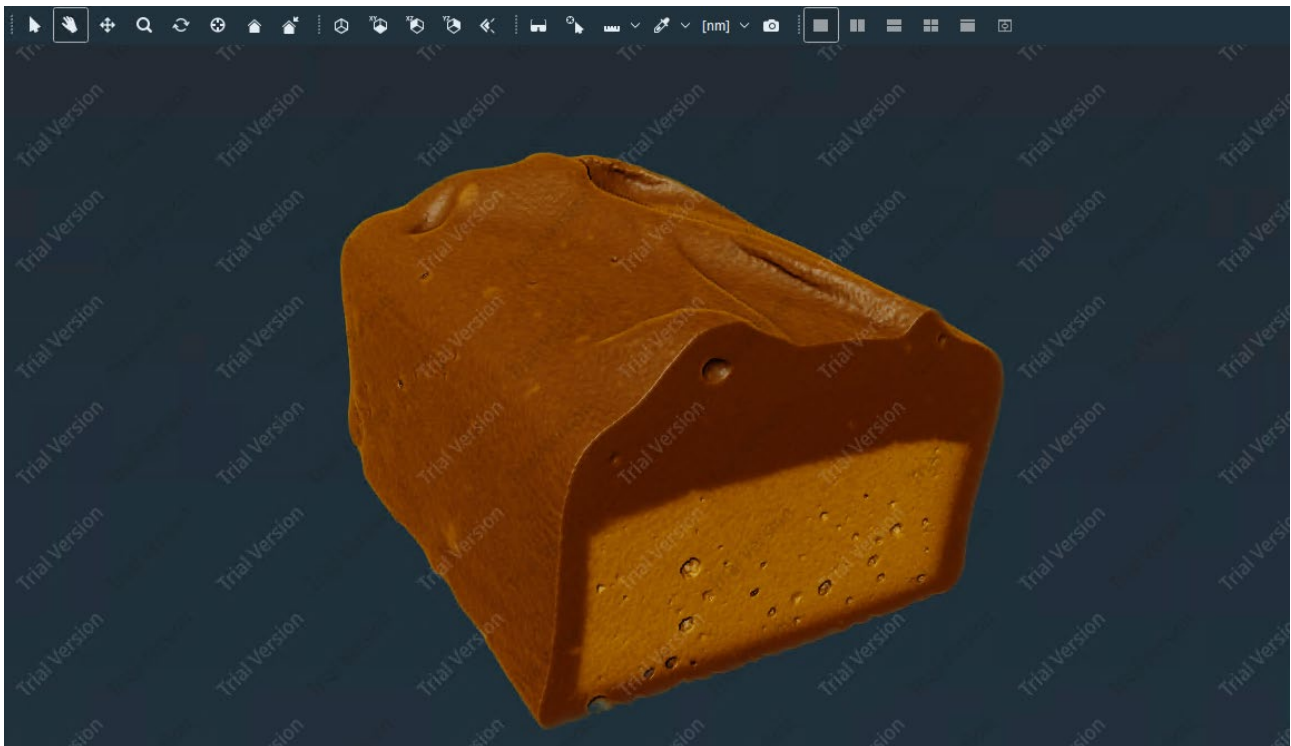
Compatibility notes

- Deprecated ports: Documentation section *Automating, Customizing, Extending* has been re-organized, and a new section has been added to document how to upgrade old projects, recipes or other custom resources when upgrading to a new version of Thermo Scientific™ Amira™ or Avizo™ Software.

- Amira Software for Cell Biology - module Generate Track: To use the new module, Relabel By Track ID, with old projects, it is necessary to recompute the Generate Tracks step. The Generate Tracks module has been slightly modified, to increment the track ID by 1, and inserting an empty track on the Track ID 0. This modification allows the same colors to be used when displaying the relabeled objects, and when displaying the track segments colored by their TrackID when using Track View.

End of support

- XScreen support has been discontinued starting with Avizo-Amira Software version 2020.1. The feature will be removed from products in next version.

- Microsoft Windows 8 support will be discontinued starting with next version, only Microsoft Windows 10 will be supported.

Operating systems

Amira-Avizo Software version 2020.2 runs on:

- Microsoft Windows 8/10 (64-bit). Windows 8 support will be discontinued starting with next version.

- Linux x86 64 (64-bit). Supported 64-bit architecture is Intel64/AMD64 architecture. Supported Linux distribution is CentOS 7.
- macOS Mojave (10.14) and macOS Catalina (10.15). The application runs on macOS Catalina (10.15) with a known limitation : the application cannot run in debug mode.

Avizo Software 2020.2 for Industrial Inspection runs on:

- Microsoft Windows 8/10 (64-bit). Windows 8 support will be discontinued starting with next version.

To add custom extensions with Amira-Avizo XPand extension, you will need:

- Microsoft Visual Studio 2013 (VC12) Update 4 on Windows
- gcc 4.8.x on Linux CentOS 7
- XCode7 or greater on macOS

Solved issues

Colormap	AA-22233	Sometimes the labels colormap was changed when a saved project was reopened. This has been fixed.
DICOM	AA-22557	Sometimes the DICOM import would only load a subset of the slices, now the whole stack loads properly.
Digital Volume Correlation	AA-21834	Digital Volume Correlation Mesh Generation could generate inconsistent nodes, the Mesh Generation algorithm has been reworked.
Meshing	AA-22407	The Label Data selection port now only displays label data compatible with the mesh generation (2D label data are filtered).