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Specification Sheet

Amira – Base Package

The base package is required for all applications of Amira. It provides advanced modules for general 3D/4D analysis and visualization. When multidimensional data needs to be processed and explored, this package offers a rich set of powerful tools with intuitive graphical user interfaces to get detailed insight into complex data sets. Besides high visualization requirements, this package satisfies the needs to advanced analysis and process of clinical or preclinical image data, nuclear data, optical or electron microscopy imagery, and all types of multidimensional image. Several modules are also provided to prepare presentations, demos and movies. The basic package contains the powerful Segmentation Editor and the Multi-planar Viewer.

Analysis

- Material statistics
- Volume and surface measurement
- 2D/3D linear measurement and annotation
- Co-localization analysis
- Arithmetic operations
- Densitometry
- Surface analysis
- Integration of MATLAB® engine (Windows and Linux only)
- Network statistics

Visualization

- Orthogonal, oblique, and curved slicing
- Shaded multi-resolution volume rendering
- Surface rendering
- Isolines and isosurfaces
- Multi-channel image visualization
- Image fusion
- Height field and bump slicing
- Orthogonal projections
- Visualization of traced filaments
- 3D ROI selection
- Clipping and cutting
- Visualization of time lapse data
- 3D+MPR viewer to explore complex data sets

Processing

- Image filtering
- Surface generation
- Image segmentation
- Slice alignment
- Automatic and manual registration
- Volume and image sampling
- Volume cropping
- Direct volume edit
- Surface editing
- Data type conversion
- Scripting
- Fusion in 3D MPR viewer
- Automatic and manual registration in 3D MPR viewer

Presentation

- DemoDirector for authoring complex animations
- High quality demos
- Movie generation
- Various 3D stereo display modes
- Auto stereoscopic display support
- 2D and 3D annotation

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Editors

- **Segmentation Editor** interactive and semi-automatic tools for 3D image segmentation
- **Multi-planar Viewer** to view up to two data sets simultaneously in a 3+1 MPR viewer
- **CameraPath Editor** to create a camera path using keyframes for animations and movies
- **Color Dialog** graphical interface for defining a color value
- **2 Colormap Editors** to modify the RGBA values of a discrete colormap
- **Curve Editor** creates and edits curves
- **Digital Image Filters** to apply standard image processing filters
- **Image Crop Editor** to crop 3D images, change bounding box, and voxel size
- **Landmark Editor** to add, move, or delete markers in a landmark set
- **LineSet Editor** to select, create, modify, and delete polylines
- **Parameter Editor** to add, change, or delete attributes of a data object
- **Surface Simplification Editor** to reduce the number of triangles of a surface
- **Surface Editor** to modify triangles, remove intersections, assign boundary ids
- **Transform Editor** to translate, rotate, or scale any 3D data object
- **Plot Tool** graphical interface for displaying 2D plots
- **Demo Manager** graphical interface to manage and control demos

Customization

- **Amira Script Object** Amira script objects are custom modules with user-defined GUI elements (ports) written in the Tcl command language.

Import/Export

File Format	Extension	Read/Write
Amira Script Amira Tcl script	hx	rw
AmiraMesh Format Amira's native general purpose format	am	rw
AmiraMesh, StackedSlices and Raw data as LargeDiskData	ldd, ldm	rw
Analyze 7.5 3D image data with separate header file	hdr	rw
AnalyzeAVW contains 2D and 3D medical image data	avw	rw
BMP uncompressed Windows bitmap format	bmp	rw
DXF Drawing Interchange Format for AutoCAD 3D models	dxl	rw
EPS (Encapsulated PostScript) for 2D raster images only	eps	w
HTML Hypertext document format	html	r
Hoc Hoc file reader of morphometric models for NEURON environment	hoc	rw
HxSurface Amira's native format for triangular surfaces	surf	rw
Icol ASCII format for colormaps with alpha channel	icol	rw
Interfile format used in nuclear medicine, based on Analyze 7.5	img/hdr	r
JPEG 2D image format with lossy compression	jpg	rw
LargeDiskData access image data blockwise	ldd	rw
MATLAB Binary MATLAB matrices	mat	rw
MATLAB M-files MATLAB script	m	rw
Nifti successor of the popular Analyze 7.5 format	nii/img/hdr	rw
Open Inventor standard file format for 3D models	iv	rw
PNG portable network graphics format for 2D images	png	rw

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Import/Export (cont'd)

File Format	Extension	Read/Write
PNM simple uncompressed 2D image format	pnm	rw
PSI ASCII format for 3D points and associated data values	psi	rw
Ply Stanford triangle format for points and surfaces	ply	rw
Raw Data binary data as a 3D uniform field	raw	rw
SGI-RGB 2D image format with run-length encoding	sgi/bw/rgb	rw
STL simple format for triangular surfaces, no connectivity	stl	rw
Stacked-Slices info file grouping together 2D images	info	rw
SWC interchange format for neuroscience	swc	rw
TIFF standard format for 2D and 3D image data	tif/tiff	rw
Tecplot Tecplot ASCII and Binary file reader	tec/plt	rw
VRML virtual reality markup language for 3D models	wrl	rw
Vevo Raw Images 2D and 3D ultrasound images from Visual Sonics' Vevo 770	rdb/rdi	r

Supported Platforms

- **Windows 32-bit, Windows 64-bit** - Windows XP/Vista/7, 32-bit and 64-bit editions
- **Mac OS** - MacOS X 10.5 (Leopard)/10.6 (Snow Leopard)
- **Linux** - Red Hat Enterprise Linux 5.0 for x86_64 or compatible

System Requirements

A processor (CPU) supporting SSE2 instruction set is required.

A graphics card with hardware accelerated texture mapping capabilities and OpenGL support is required. Some visualization modules, i.e. the highest quality volume rendering, require graphics hardware with vertex and fragment shader support, as well as installation of the most recent graphics drivers.

Note: Amira and all its extension options are intended for research only and not for diagnosis or treatment of patients.

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Mesh Option – Surfaces, 3D grids, and vector fields

The Mesh Option offers advanced features for scientists working with complex surface analysis, volume reconstruction using tetrahedral grids, vector field visualization, and complex tensor computation. This package is designed especially for Finite Element Modeling (FEM), for computational analysis of 3D regular fields, tensors, and 3D fluid dynamics simulations.

Main features

- Surface editing
- Tetrahedral and hexahedral grid visualization
- Tetrahedral grid generation
- Grid analysis and refinement
- Grid parameterization
- Conversion from tetrahedral to hexahedral grids and vice versa
- Boundary condition visualization
- Vector field visualization
- Planar and surface LIC (line integral convolution)
- Tensor computation
- Tensor visualization
- Out-of-core tensor computation
- Animated illuminated streamline visualization
- Animated cone plot visualization
- Ribbon visualization
- Stream surface

Editors

- **Grid Editor** to edit and simplify tetrahedral grids

Import/Export

File Format	Extension	Read/Write
Abaqus stores geometry and data values of unstructured grids	inp	w
AVS Field stores data defined on regular grid	fld	raw
AVS UCD Format stores unstructured cell data	inp	raw
FIDAP NEUTRAL stores FEM meshes and solution data	ascii fmt	r
Fluent-UNS contains FEM meshes, boundary ids, solution data	hdr	raw
Hypermesh used by Altair HyperWorks FEM software	hm/hmascii	raw
IDEAS universal format describes FEM grids and simulation data	unv	raw
Plot 3D Single Structured stores curvilinear grids and associated data	p3d	raw

Platforms

Windows 32-bit, Windows 64-bit, Mac OS, Linux

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Microscopy Option – Readers and tools for microscopy

The Microscopy Option is the comprehensive option for visualization of microscopy data. It includes specific readers for microscopy data as well as a powerful 3D image deconvolution suite. The Microscopy Option comes with several examples and step-by-step tutorials to easily learn how to enhance images with filters and deconvolution process. This option includes the Filament Editor.

Main features

- Microscopy file readers
- Deconvolution
- Z-Drop correction
- Tool for bead measurements
- Background image and flatfield correction
- Fourier transform
- Automatic and interactive filament tracing
- Filament network labeling and editing
- Filament network automatic hierarchy and loop detection

Editors

- **Filament Editor** to extract, modify and label neuron and vessel networks (including features of the Skeletonization Option)

Import/Export

File Format	Extension	Read/Write
Bio-Rad Confocal simple uncompressed format for 3D image stacks	pic	r
Leica 3D TIFF contains 3D image data and meta data	tif	r
Leica Binary 3D image stacks, time series, and meta information	lei	r
Leica Image 3D image stacks, time series, and meta information	lif	r
Leica Slice Series contains list of 2D TIFF files or raw data and meta	info	r
MRC MRC file format for electron microscopy	mrc/rec	rw
Metamorph STK special TIFF variant for 3D image stacks	stk	r
Olympus OIB/OIF binary file format (windows only)	oib/oif	r
Zeiss LSM 3D raster image format	lsm	r

Platforms

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Neuro Option – Medical image analysis for DTI and Brain Perfusion

This option offers specialized modules to analyze medical images obtained from CT or MR imaging. Diffusion weighted MR imaging (DWI) is used to image the rate of water diffusion in tissues like brain or muscle. This option allows the user to compute the apparent diffusion coefficient (ADC), fractional anisotropy (FA), and directionally encoded color (DEC) maps. Diffusion tensor imaging (DTI) aims at localizing and visualizing fiber tracts in the human or primate brain and is supported by several modules. Brain perfusion analysis is supported based on tracking a contrast bolus in a time series of MR or CT images.

Main features

- Fiber tracking supporting several stream-line based algorithms
- Fiber separation into fiber bundles based on user defined source and destination regions
- Computation of tensor fields from an arbitrary number of diffusion weighted MR images
- Generation of test data for tensor field and gradient weighted image stack analysis
- Computation of diffusion weighted maps like ADC, FA, relative anisotropy (RA), and DEC
- Eigenvalue decomposition of tensor fields
- Supports both CT and MR bolus tracked images
- Computes mean transit time (MTT), cerebral blood flow (CBF), and cerebral blood volume (CBV)
- Manual selection and export of arterial/venous functions from perfusion time series
- Tracer delay time corrected
- Computation based on deconvolution

Platforms

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Very Large Data Option – Explore data sets larger than 8 GByte

The Very Large Data Option allows Amira to display large data sets that exceed the available main memory, e.g., on computers with only a small amount of RAM or when using a 32-bit operating system. Using volumes of interest and multi-resolution techniques, the Very Large Data Option overcomes these limitations and allows interactive visualization and processing of large data volumes. Depending on the available resources, this option allows exploration of image volumes greater than 8 GByte, and has been successfully tested with data sets larger than 300 GByte.

Main features

- Interactive visualization with orthogonal/oblique slicing, volume- and isosurface rendering
- Fast disk access to sub-regions and sub-samples
- Optimal image quality based on available hardware resources
- Automatic refinement of displayed images
- Import/export based on native file format (LDA VolumeViz)

Platforms

Windows 32-bit, Windows 64-bit, Mac OS, Linux

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Molecular Option – Visualize complex molecular structures and properties

This option combines Amira's strong capabilities for 3D data visualization, such as hardware-accelerated volume rendering, with specific tools for molecular visualization and analysis, such as molecular surfaces, sequence alignment, configuration density computation, molecule trajectories, and more. The Amira Molecular Option comes with self-running demos and step-by-step tutorials for the most common molecular visualization tasks.

Main features

- Secondary structure extraction and visualization
- Molecular trajectory computation and visualization
- Potential field computation
- Pseudo-electron density computation
- Molecule labeling
- Molecule surface computation
- Align molecule and sequences
- Pareto-optimal set computation
- H bond computation and visualization
- Ribbon, tube, cartoon chain visualization
- Dynamic visualization
- Configuration density evaluation
- Mean-molecule computation

Editors

- **Molecule Attribute Editor** allows editing of attributes of groups contained in a molecule
- **Molecule Editor** allows you to change geometry and topology of a molecule

Import/Export

File Format	Extension	Read/Write
AMBER Assisted Model Building with Energy Refinement format	top/crd/vel	r
AMF Amira Molecule Format	amf	rw
DX APBS DX electrostatic field file	dx/apbs	r
GROMACS Groningen Machine for Chemical Simulations format	gro/top/trr	rw
MDL MDL file format saving chemical structures	sdf	rw
PDB protein data base file format	pdb	rw
PHI Congen PHI Electrostatic field file	phi	r
PSF/DCD (CHARMM) file format used by CHARMM	psf/dcd	r
Tripes file format used to save Tripes Sybyl mol2 molecules	mol2	rw
UniChem file format used by the UniChem molecular software	uni	rw
ZIB Molecular format developed as molecular exchange	zmf	rw

Platforms

Windows 32-bit, Windows 64-bit, Mac OS, Linux

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Skeletonization Option – Reconstruct and analyze networks

This free-of-charge option supports reconstruction and analysis of vascular, dendritic, and fracture networks. It combines specific micro-detailed image mosaic management with advanced automatic and semi-automatic tools for reconstruction of a 3D vessel network from confocal microscopy or synchrotron image acquisition. The Skeletonization Option delivers a unique set of features for the researcher who works at studying and analyzing neurons or micro-vascular networks.

Main features

- Automatic skeletonization tools
- Distance mapping
- Thinning
- Smoothing
- Support for bricked data (mosaic)
- Radius histogram

Platforms

Windows 32-bit, Windows 64-bit, Mac OS, Linux

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Quantification+ Option – Extract quantitative information

The Quantification+ Option delivers high-level tools for obtaining and visualizing advanced quantitative information on 3D images. This option offers the whole range of software tools needed to perform automated segmentation, convolution, object separation, and to extract statistical and geometrical information.

Main features

- Interactive and automatic thresholding
- Interactive and automatic labeling
- Equalization, standardization, and look-up table (LUT) modification
- Arithmetic and linear combination
- Logical operation
- Erosion and dilatation
- Fill holes and remove edges
- Distance, maxima and local minima computation
- Watershed algorithm for labeling
- Thinning, thickening, and geodetic propagation
- Workflow for object separation
- Geometric measurements
- Radiometric measurements
- Complex filtering

Platforms

Windows 32-bit, Windows 64-bit

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Developer Option – Extend Amira through C++ development

The Developer Option allows you to extend Amira by developing custom data types, visualization or processing modules, and input/output routines through a well-documented C++ API. The object-oriented language together with the open design makes this option the ideal answer to specific technical requirements.

Main features

- Provides the C++ header files needed to compile and develop custom extensions
- Offers a development wizard (assistant) to simplify code development
- Build and test new modules for computation, I/O, and visualization
- Based on a number of industry standard libraries (OpenGL®, Open Inventor™, Qt®)
- Comes with the Open Inventor graphics libraries for creating new Amira visualization modules
- The unique object-oriented interface provides maximum flexibility also for developers with basic experience in C++ coding
- Expert programmers can easily include new graphical user interface (GUI) elements based on Qt, even without having the Qt libraries installed
- Requires a C++ development environment such as Microsoft Visual Studio on Windows or a C++ compiler on UNIX systems.

Platforms

Windows 32-bit, Windows 64-bit, Mac OS, Linux

Supported Compilers

In order to add custom extensions to Amira using the Developer Option, a C++ compiler is also required. The following C++ compilers are supported:

- **Windows** – 32-bit: Microsoft Visual Studio 2005 (VC++ 8);
64-bit: Microsoft Visual Studio 2008 (VC++ 9).
- **Mac OS X** - 10.5 (Leopard): gcc 4.0.x; 10.6 (Snow Leopard): gcc 4.2.x.
- **Linux** - gcc 4.1.x.

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Virtual Reality (VR) Option – Display 3D data in immersive environments

The Amira VR Option enables advanced data visualization and analysis with large tiled displays as well as immersive VR configurations like CAVEs. The VR Option supports efficient multi-threaded rendering on multi-pipe systems and distributed rendering on cluster systems at optimal performance with minimal bandwidth requirements. It also supports active or passive stereo, edge blending, head tracking, and 3D interaction for using Amira capabilities with a true immersive experience.

Main features

- Full immersive 3D interaction
- Support for single and multiple screens
- Support for single and multi-pipe rendering
- Support for graphic clusters
- Flexible customization for specific display geometry
- Supports passive and active stereoscopic displays
- Supports auto-stereoscopic displays
- Head-tracking
- Support for tracked hand-held 3D input devices
- Control functionality via user interface
- Control of 2D user interfaces with 3D devices (virtual mouse)
- Scriptable using Tcl

Platforms

Windows 32-bit, Windows 64-bit, Linux

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DICOM Option – Read and write DICOM files

Beside the import and export potentials of Amira, this free-of-charge option offers an extended capability to read and write DICOM images using a clear user interface. This option includes also a module to “push” (save) the DICOM data set on a remote server. These features are especially useful in a medical research environment.

Main features

- **DICOM Push** to save data on a remote DICOM node

Import/Export

File Format	Read/Write
ACR-NEMA predecessor of the DICOM format for medical images	r
DICOM export medical image export	w
DICOM import standard file format for medical images	r

Platforms

Windows 32-bit, Windows 64-bit, Mac OS, Linux

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Specialized Readers

Amira contains many built-in import capabilities, which allow the user to quickly access and analyze data coming from a large variety of sources. The CATIA, IGES, and STEP readers allow visualization of data from CAD applications. Coupled with the Amira VR Option, these readers bring CAD models to immersive visualization and collaborative environments.

Import/Export

File Format	Read/Write
CATIA5 Computer Aided Three-dimensional Interactive Application V5	r*
IGES Initial Graphics Exchange Specification	r*
Madymo Madymo kinematics format	r*
Madymo Time -history output from Madymo	r*
Radioss Mecalog Radioss format for simulations	r*
SEG-Y Society of Exploration Geophysicists format	r*
STEP Standard for The Exchange of Product data	r*

*) In addition to purchasing the respective license, the specialized readers require the installation of additional software that will be made available by Visage Imaging. Please contact our support hotline at amirasupport@visageimaging.com for more information.

Platforms

Windows 32-bit, Windows 64-bit