



# Introducing MIPAV

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Imaging is essential to medical research and clinical practice. Biologists study cells and generate three-dimensional (3D) confocal microscopy datasets; virologists generate 3D reconstructions of viruses from micrographs. Radiologists identify and quantify tumors from Magnetic Resonance Imaging (MRI) and Computed Tomography (CT) scans.

Neuroscientists detect regional metabolic brain activity from Positron Emission Tomography (PET) and functional MRI (fMRI) scans. Analysis of these diverse image datasets require sophisticated quantification and visualization tools. Until recently, 3D visualization and quantitative analysis of an image dataset could only be performed on expensive UNIX workstations with customized software.

Because of technological advancements, medical image visualization and analysis can now be performed on an inexpensive desktop computer that is equipped with the appropriate software applications.

This *User's Guide* explains how to use one of these software applications: Medical Image Processing, Analysis, and Visualization (MIPAV). Researchers use MIPAV to extract quantitative information from image datasets of various medical image modalities. The MIPAV application can run on virtually any platform, including Microsoft Windows, Solaris, and the Macintosh Operating System (Mac OS).

This chapter provides information on the characteristics of the product:

- Platform independence
- Supported image types
- Ability to visualize image datasets of two or more dimensions
- Volume of interest (VOI) segmentation and analysis methods
- Ability to accommodate customized user-created plug-ins

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## Platform independence

Much research at NIH requires the segmentation, quantification, and visualization of 2D, 3D, and 4D image datasets. Researchers analyze images of varied imaging modalities, such as microscopy, microarray data, X-ray, CT, MRI, fMRI, and PET. Factors such as personal preference, data requirements, software limitations, and precedent have led to a heterogeneous distribution of computer platforms, among which are personal computers executing Windows or Linux, Macintoshes, and workstations by SGI, Sun Microsystems, or Hewlett-Packard. To analyze an image dataset, researchers may use several software applications. If each software application is platform specific, researchers may need access to several platforms to analyze a single image dataset. This often reduces efficiency while simultaneously increasing lab costs. MIPAV has been designed to help researchers increase efficiency and reduce costs by providing them with a flexible tool that can operate on virtually any platform. Researchers can use MIPAV by itself or in concert with other image processing and visualization tools.

The MIPAV application is platform independent because it is written in Java, which is an object-oriented, interpreted, programming language that

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was developed by Sun Microsystems. Java source code is compiled into the bytecode, which is machine-level code that is compiled specifically for the Java Virtual Machine (VM). There are versions of the Java VM for different platforms. The same program (bytecode) can run on any of those versions. If researchers run a Java program on a Windows 2000 platform, the bytecode is interpreted by the Java VM that has been specifically designed for the Windows 2000 platform. If the same program is run on a Solaris platform; the bytecode is then interpreted by the Java VM that was specifically designed for the Solaris platform.

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**Note:** The correct version of the Java VM can be downloaded from the MIPAV web site <http://mipav.cit.nih.gov> along with the MIPAV installation program.

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## Supported image types

Before image dataset analysis and quantification can be performed, an application must be able to read and write image datasets in industry-standard formats. Conformance to accepted standards, such as DICOM, ensures compatibility with present and future applications and medical equipment. This protects researchers' investment in hardware and provides flexibility in reaching their goals.

MIPAV supports over 20 different industry-standard image formats including: DICOM, TIFF, Analyze, and RAW (a complete list appears in Appendix C: "Supported formats" on page 627). MIPAV reads and writes images in both big and little endian formats.

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## Visualization of images

The visualization of datasets with two or more dimensions is an important aspect of image dataset analysis and research. The ability to visualize the orientation, locality, or progression (time) of structures in clinical and nonclinical datasets can be vital to researchers. Confocal microscopy, CT, and MRI are examples of imaging modalities that are comprised of multiple adjacent cross-sectional image datasets that can be combined to form a 3D volume dataset. MIPAV allows researchers to visualize datasets using a

variety of presentation formats, including lightbox, triplanar, cine, and animate. Once researchers display the image dataset, they can adjust the lookup table (LUT), apply prepackaged pseudo-color LUTs to highlight structures of interest, control the magnification level, adjust the transfer function, and more.

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## Volume of interest (VOI) segmentation and analysis

Another significant research activity is the quantification of data from image datasets. Although the visualization of image data is important, the actual quantification of the data is typically required to evaluate the researchers' hypothesis. Researchers must be able to identify regions-of-interest (ROIs) and/or volumes-of-interest (VOIs).

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**Note:** An ROI is used in the context of 2D image datasets. VOI usually describes the analysis of volume data for datasets with more than two dimensions. This document uses the term VOI to represent both ROI and VOI.

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*Image segmentation* is the process of identifying connected regions of images as members of a common group. In the medical field, physicians must routinely identify (i.e., segment) structures in medical image datasets to facilitate the treatment of patients. For example, many researchers who study the brain are interested in the segmentation of gray matter, white matter, and cerebrospinal fluid in MR images. The quantification of important attributes, such as volume, of various tissue types enables researchers to better understand, diagnose, monitor, and treat neurobehavioral disorders.

There are a multitude of image dataset segmentation methods; the choice of segmentation algorithm depends on the image data type and task. Automatic segmentation methods are desirable because they require little user interaction, which is subject to operator error and subjectivity. However, in practice automatic methods sometimes fail and require manual VOI correction (adjustment of the boundary that identifies the region). Thus, in MIPAV, researchers have the choice to automatically, semiautomatically, and manually segment VOIs. Contours can be manually edited, grouped, and copied to other slices in the dataset. MIPAV also offers a variety of

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mask-generation methods. Researchers can manually paint a mask or use one of several algorithms.

MIPAV also allows researchers to perform statistical calculations on masked and contoured VOIs. Statistical results can be saved to an ASCII text file and imported to another program, as needed.

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## Extensibility with Java plug-ins

A typical analysis and visualization application can be designed to meet a broad range of researcher requirements. Many components of image dataset processing, analysis, and visualization techniques are general and can be applied to many types of data. However, many datasets also require unique functionality to meet special requirements. MIPAV allows researchers, who have the programming resources, to add a customized Java plug-in to the application. To program a plug-in, researchers must have a strong understanding of the underlying structure of the application's software design.

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**Note:** This *User's Guide* presents information on how to add and remove plug-ins from the MIPAV application. It also indicates the statements that must be included in the source code to allow the plug-in to interface properly with MIPAV. However, in-depth information is not included in this guide. If you need more information, check the MIPAV web site <http://mipav.cit.nih.gov> for the e-mail address for technical support (Figure 1).

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JHU Medic



Johns Hopkins University **MedIC** have built plug-ins for MIPAV, focusing on modifying images to use Talairach co-ordinates.

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### About MIPAV

- [Feature listing](#)

#### What is MIPAV?

The MIPAV (Medical Image Processing, Analysis, and Visualization) application enables quantitative analysis and visualization of medical images of numerous modalities such as PET, MRI, CT, or microscopy. Using MIPAV's standard user-interface and analysis tools, researchers at remote sites (via the internet) can easily share research data and analyses, thereby enhancing their ability to research, diagnose, monitor, and treat medical disorders.

MIPAV is a [Java](#) application. This allows a user to run MIPAV on any Java-enabled platform such as Windows, UNIX, or Macintosh OS X.

#### Goals for MIPAV

MIPAV is to meet the following goals:

- To develop computational methods and algorithms to analyze and quantify biomedical data;
- To collaborate with NIH researchers and colleagues at other research centers in applying information analysis and visualization to biomedical research problems;
- To develop tools (in both hardware and software) to give our collaborators the ability to analyze biomedical data to support the discovery and advancement of biomedical knowledge.

#### Need for MIPAV

Imaging has become an essential component in many fields of bio-medical research and clinical practice. Biologists study cells and generate 3D confocal microscopy data sets, virologists generate 3D reconstructions of viruses from micrographs, radiologists identify and quantify tumors from MRI and CT scans, and neuroscientists detect regional metabolic brain activity from PET and functional MRI scans. Analysis of these diverse types of images requires sophisticated computerized quantification and visualization tools. To support scientific research in the NIH intramural program, CIT has made major progress in the development of a platform-independent, n-dimensional, general-purpose, extensible image processing and visualization program.

This page last reviewed: March 14, 2007

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**Figure 1. MIPAV home page**

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## Sampling of MIPAV's features

MIPAV provides ready-made, general-purpose tools that meet the majority of requirements of many researchers. Researchers can use MIPAV to perform a variety of tasks. The following list shows a sampling of the tasks that researchers can performed with the program. These tasks and others are addressed in volumes 1 and 2 of this *User's Guide*.

- Visualize files and create new image dataset files
- View and modify the attributes of an image dataset, including DICOM and VOI information
- Adjust the display of an image dataset file and adjust magnification settings
- View DICOM overlays and protect patient privacy using the anonymize feature
- Send and receive image dataset files to and from databases via DICOM-compliant servers
- Contour VOIs using manual, semi-automatic, and automatic methods
- Generate graphs and calculate statistics on VOIs
- Generate and adjust histograms and LUTs using customized or preset options
- Run sophisticated, predefined algorithms, and generate logs
- Blend two image datasets and adjust opacity levels of the alpha channels so overlapping areas can be studied
- Create new plug-ins to further customize the analysis of data
- Save transformation, LUT, and VOI data, and apply them to other image datasets
- Print image dataset files, intensity profiles, statistical data, algorithmic logs, and debugging log data
- Create black and white, grayscale, and pseudo-color masks