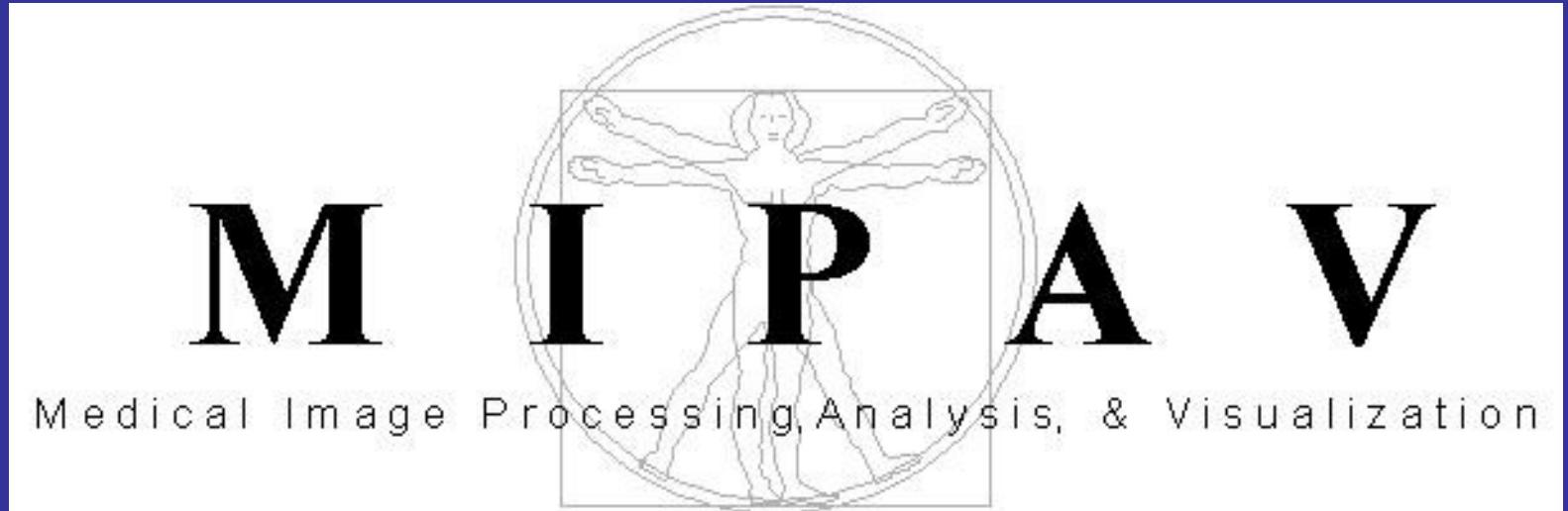




Plugins



<http://mipav.cit.nih.gov>





Medical Image Processing, Analysis & Visualization & Plugins

Evan McCreedy

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Biomedical Imaging Research Services Section (BIRSS)

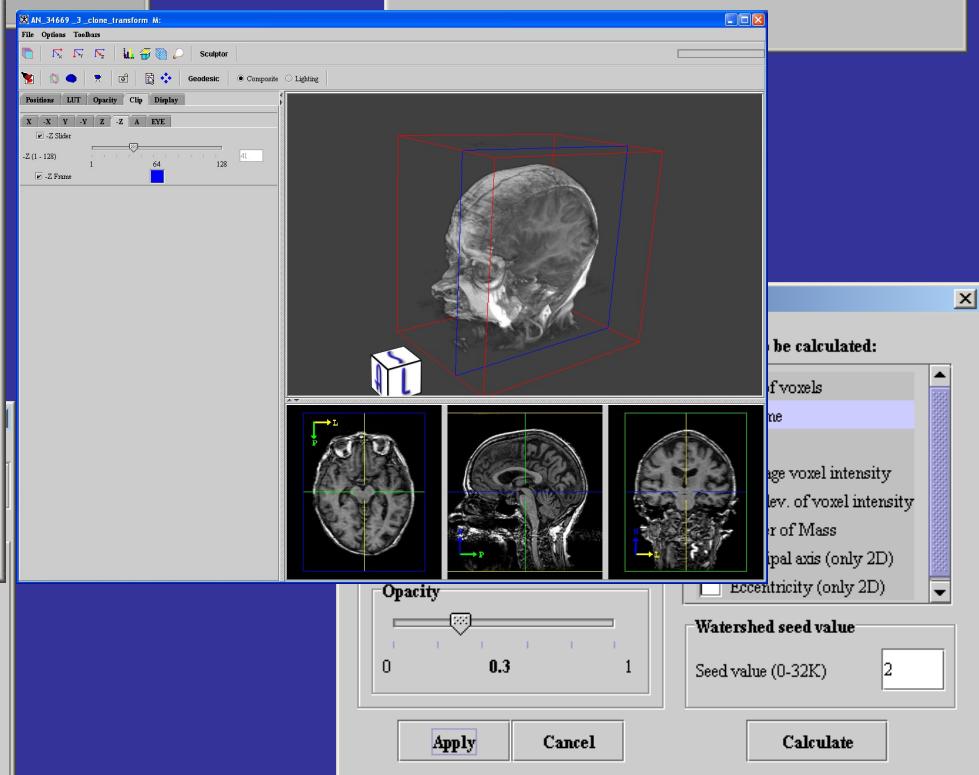
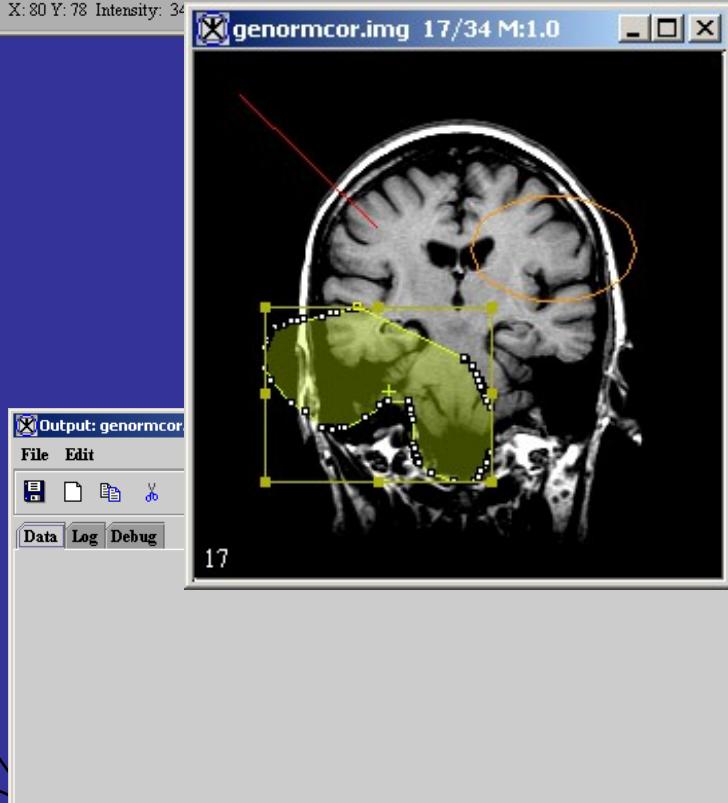
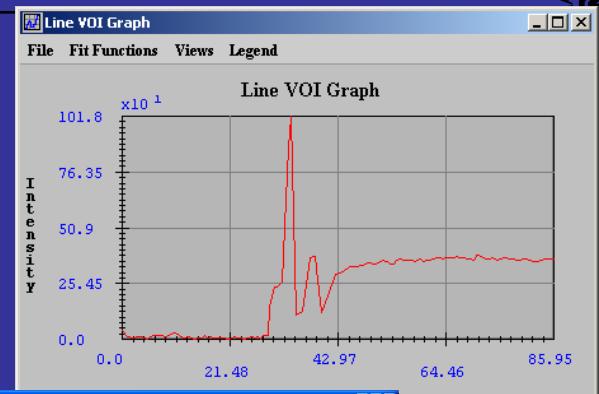
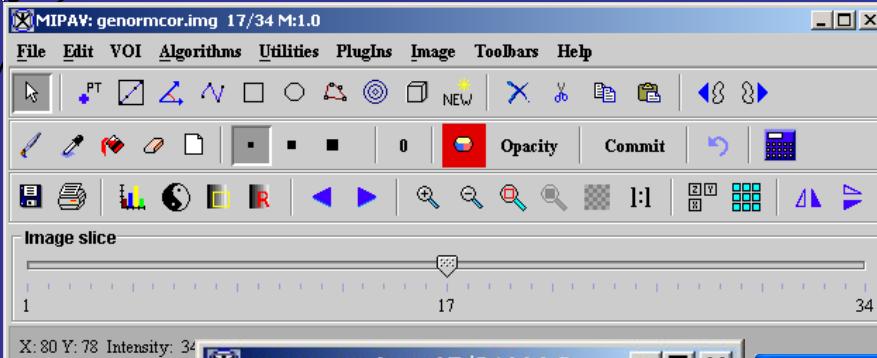
Imaging Sciences Laboratory
Division of Computational Bioscience

Center for Information Technology

(301) 496-3323

<http://mipav.cit.nih.gov>







Functional Overview

GUI

Views – with data fusion

2D planar,
“Lightbox”,
Cine (movie),
Multi-planar,
3D tri-planar,
Surface render, (supports 3D texture
mapped volume rendering)
Volume render

VOIs

32K
Manual and
automated
contouring

Algorithms

Filtering
Segmentation/classification
Measurement/quantification
Registration/fusion
Utilities
Plugins

S
c
r
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&
P
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g
s

Data (Image) types: n-dimensional structure

(boolean, byte, unsigned byte, short,
unsigned short, int, long, float, double, Complex, ARGB)

PACS

DICOM 3.0:
Query/Retrieve, Catcher

File types

(Raw, Analyze, DICOM 3.0, GE, Siemens, Bruker, Interfile,
Micro cat, MINC, MRC, FITS, Cheshire, AFNI, TIFF, JPEG, GIF,
BMP, AVI, QuickTime, Biorad, Ziess LSM510, **XML**, and more)





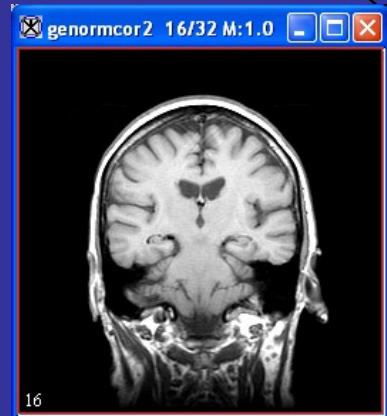
Code Snapshot

```
int destExtents[] = new int[2];
destExtents[0] = image.getExtents()[0]; // X dim
destExtents[1] = image.getExtents()[1]; // Y dim

// Make a result image of Unsigned byte type
resultImage = new ModelImage(ModelStorageBase.UBYTE, destExtents, "Result Image", null);

int length = destExtents[0] * destExtents[1];
for (int i = 0; i < length; i++){
    destImage.set(i, i%256);
}

ViewJFrameImage imageFrame;
ModelLUT LUTa = new ModelLUT(ModelLUT.COOLHOT, 256, dimExtentsLUT);
imageFrame = new ViewJFrameImage(resultImage, LUTa, new Dimension(610,200), userInterface);
```





Major Algorithms Supported

- **Algorithms**

- Filters: Gaussian blurring, gradient magnitude, Laplacian, curvature, other higher order derivatives, median, anisotropic diffusion, coherence-enhance diffusion, isotropic diffusion, wavelet, unsharp masking, etc.
- Image Calculator (add, subtract, multiply, divide, AND, OR, XOR)
- Registration
 - Landmark – least squares, thin-plate splines for both 2D and 3D datasets
 - AIR 5.07 and AFNI
 - Automatic 2D/2.5D/3D registration intra/inter patient, intra/intra modality
 - multi-resolution, user selectable DOF, user selectable cost function (correlation ratio, normalized cross correlation, least squares, mutual information.
- Image transformations or resample with nearest neighbor, tri-linear, 3rd, 4th bSpline, Sinc, 3rd, 5th, 7th order Lagrangian, etc.
- Surface extraction with decimation
 - Adaptive skeleton climbing
 - Marching cubes
 - Marching tetrahedrons
- Skull striping
- Classification – Fuzzy c-means
- Watershed
- Morphological filters (open, close, erode, dilate, etc)
- Active contour methods (GVF etc.)





Download and Setup

1. <http://mipav.cit.nih.gov/download>
2. Fill in form
3. Install (e.g. installMIPAV.exe)

Screenshot of a Netscape browser window showing the MIPAV download page. The URL in the address bar is <http://mipav.cit.nih.gov/download/>. The page content is as follows:

We are making test-builds available, in addition to the regular release versions found here. The [test-build download page](#) has more information about why one might be interested and the risks associated with getting a test-release.

Please fill in all items since this is used to determine further development of MIPAV.

The latest release version is 1.14

Name (required)
Email (required)
Address
Institute or Center Not at the National Institutes of Health, Maryland, USA
Platform Installation Instructions

Windows

- Turn off virus scanner. Windows virus scanners often prevent proper download. Be sure to restart your virus scanner after the download, feel free to scan the MIPAV installer then.
- After downloading, double-click `installMIPAV.exe`
- The on-screen instructions should be descriptive.

`md5sum: 5ccb53c184a53dcfd8d272108171e357`

Linux

- After downloading open a shell and, `cd` to the directory where you downloaded the installer.
- At the prompt type: `sh ./installMIPAV.bin`

`md5sum: faef18a36850f224426960c7f07ceeb`

Solaris

- After downloading open a shell and, `cd` to the directory where you downloaded the installer.
- At the prompt type: `sh ./installMIPAV.bin`

`md5sum: 6a52d4a2052b91a4546d72d7e337ec70`

Macintosh **Macintosh OS X** only Please be aware that this version is currently being tested, and may not be completely functional.
MIPAV uses [Java 1.4](#) or higher, additionally, many functions will not work without [Java WebServices](#), including the use of all of MIPAV's XML-format images. Surface rendering is unavailable without [Java 3D](#) and [Java Advanced Imaging](#). Unfortunately, both WebServices and Java3D/JAI, require that Mac OS 10.3 (Panther) be installed.
1. Download and install [Java 3D](#) and [JAI](#).
2. Install WebServices.

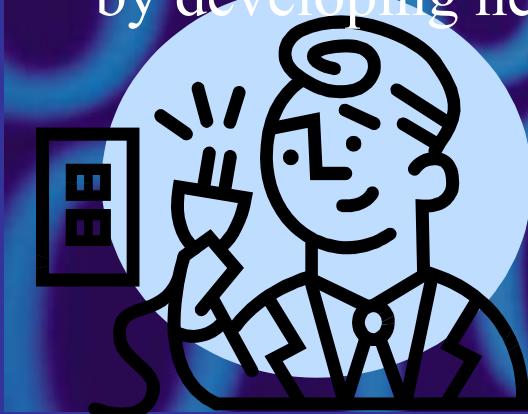
1. Download the [UNIX](#) version of [Java WebServices](#).
2. Java Web Services default installation directory is your home directory, and if you change it so other users on your Macintosh can access MIPAV, you may. Within /Library/Java/WebServices is a good location. Remember





Scripting & Plugins

- Scripts - Automation of MIPAV functions applied to a group of datasets to increase efficiency and productivity
- Plugins – Ability to add unique functionality to MIPAV by developing new algorithms using MIPAV's API





Plugins

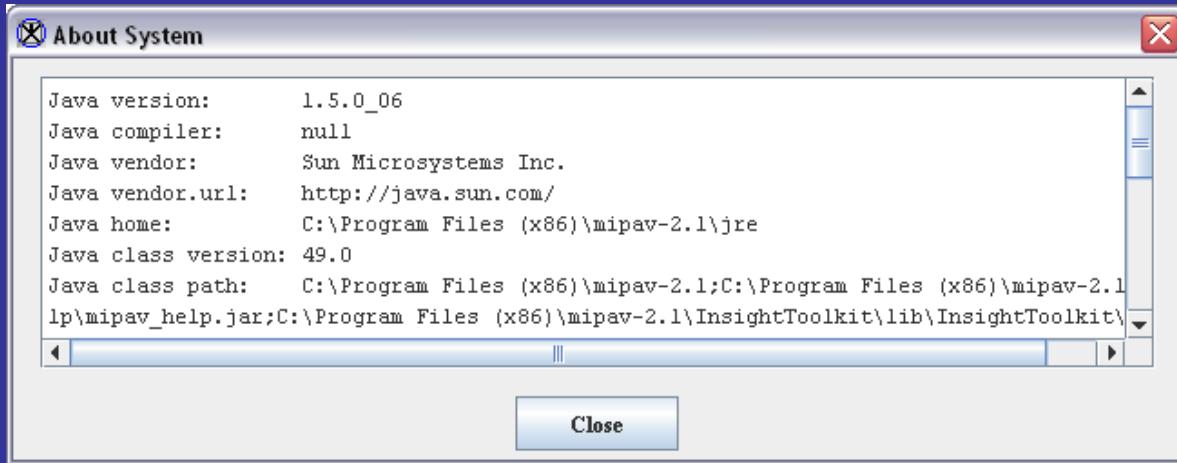
- Pure Java/MIPAV plugin
 - Unique functionality.
- MIPAV to C, system call, Python, Perl etc.
- MIPAV to ITK (a C++ imaging library).





Plugins

- Four steps to building a plugin
 - 1. Determine type of plugin (usually Algorithm)
 - 2. Determine Java version to use
 - Use the same version javac as MIPAV (Help -> About Java)
 - 3. Write the plugin
 - 4. Compile the plugin





Plugins

- PlugInAlgorithm – Develop new functionality and ability to call functions already in MIPAV.
- PlugInFile – Develop files readers to support unique file formats. Rarely used since MIPAV supports numerous file formats.
- PlugInGeneric – Generic plugins that do not require an open image
- PlugInView – Develop new visualizations of datasets.





Plugins

- To build a plugin, three files are typically required:
 - PlugInFoo.java
 - interface to MIPAV and the plugin
 - PlugInDialogFoo.java
 - invokes the dialog to get user supplied parameters – can be hidden when no parameters are required
 - PlugInAlgorithmFoo.java
 - The actual algorithm to be implemented. It can be a mixture of calls to MIPAV's API, C programs, Perl, ITK, etc.





Plugins - Location

- Stored for each user in \$home/mipav/plugins
 - Windows - C:\Documents and Settings\user_name\mipav\plugins
 - Unix/Mac - usually /home/user_name/mipav/plugins
 - Note: By default, the home directory of the user who installed MIPAV is used. If you are running plugins as a different user, set the classpath before running mipav:
 - % CLASSPATH=\$HOME/mipav/plugins/ /path/to/mipav





Plugins - MIPAV API

<http://mipav.cit.nih.gov/documentation/api/>

The screenshot shows a Mozilla Firefox window displaying the MIPAV API Documentation at <http://mipav.cit.nih.gov/documentation/api/>. The page is titled "gov.nih.mipav.model.algorithms (MIP...)" and includes navigation links for Overview, Package, Class, Tree, Deprecated, Index, and Help. A sidebar on the left lists "All Classes" and "Packages". The main content area displays two sections: "Interface Summary" and "Class Summary". The "Interface Summary" section contains entries for [AlgorithmInterface](#) and [AlgorithmOptimizeFunctionBase](#). The "Class Summary" section lists numerous algorithm classes with their descriptions, such as [AlgorithmAGVF](#) (Snake-like algorithm derivative), [AlgorithmAHE](#) (algorithm to apply an adaptive histogram to an image), [AlgorithmAHFLocal](#) (algorithm to apply an adaptive histogram to an image), [AlgorithmArcLength](#) (algorithm calculates the arc-length of a B-spline fit to user-defined control points), [AlgorithmAutoCorrelation](#) (Reference: Digital Image Processing, Second Edition by Rafael C.), [AlgorithmAutoCovariance](#) (let $\text{del}(x,y) = \langle i(x,y) - \bar{i} \rangle$ where the angle brackets are used to denote a spatial average), [AlgorithmBase](#) (Base abstract class for algorithms), [AlgorithmBrainExtractor](#) (A class for segmenting the brain from a 3D MRI), [AlgorithmBrainBoundaryAttention](#) (This class provides an implementation of a second method for segmentation of the brain from a 3D MRI, as opposed to the BET algorithm implemented in AlgorithmBrainExtractor), [AlgorithmBrainSurfaceExtractor](#) (Smoothing of VOI using 1 iteration of B-Splines), [AlgorithmBSnake](#) (Snake-like algorithm derivative using B-Splines), [AlgorithmBSpline](#) (Fourth-order B-spline for 1-3D lines and 2D surface), [AlgorithmColorizationEM](#) (An optional registration may be performed before colocalization), [AlgorithmColorizationRegression](#) (This algorithm creates a 2D histogram from 2 colors of a single image or from 2 black and white images and uses an orthogonal line fit of the histogram data to generate a correlation line thru the histogram), [AlgorithmConstPowellOpt3D](#) (Runs Powell's method for a 3D image), [AlgorithmConstPowellOptBase](#) (Powell's Method), [AlgorithmConstrainedCAR3D](#) (Runs Powell's method), [AlgorithmCrop](#) (Convolves kernel with a 2D or 3D image - only pixels where the kernel is completely contained in the image are), and [AlgorithmConvolver](#).



Plugins - Documentation

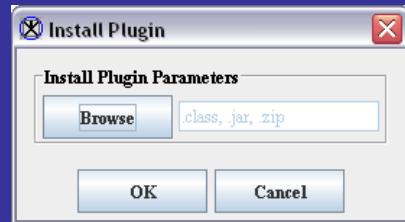
- Plugin development documentation
 - http://mipav.cit.nih.gov/documentation/userguide/volume1/MIPAV_PlugIns.pdf
- Using ITK from MIPAV
 - http://mipav.cit.nih.gov/documentation/techguides/TechGuide2_UsingInsightToolkit.pdf
- This presentation will be posted at
 - <http://mipav.cit.nih.gov/documentation/presentations/> in the next couple of weeks.





Plugins – Installing

- Installation of a simple plugin (Plugins -> Install Plugin)



Copies files

- Chosen .class files, or the contents selected of jar/zip files into the directory
 - \$home/mipav/plugins
- When MIPAV starts, it parses this directory and builds the plugins menu.

Note:

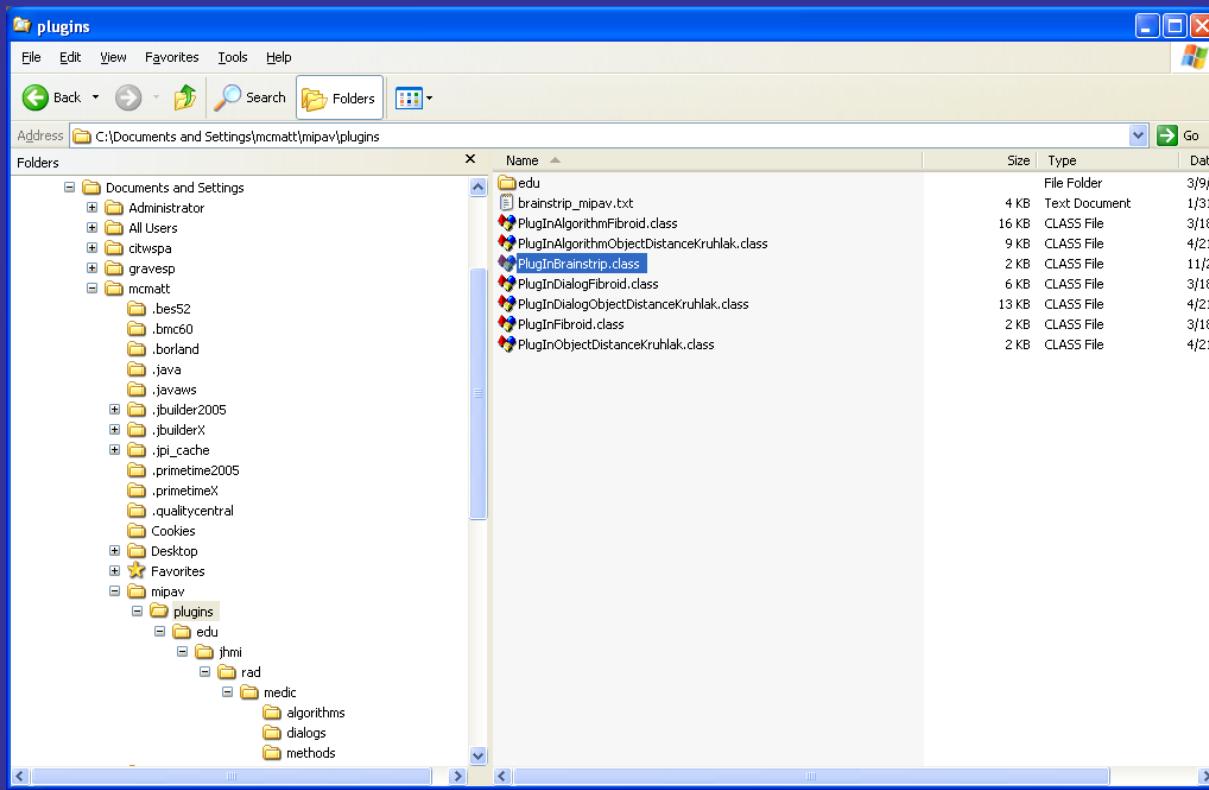
Simply use the OS's tool for coping the files into the directory listed above is also acceptable. The user will be required to restart MIPAV to have the new plugin appear in the menu.





Plugins – Installing

- Installation of a complex plugins
 - Medic Talairach plugin





Plugins – Installing Lab

- Install
 - PlugInCT_MD.class
 - PlugInDialogCT_MD.class
 - PlugInAlgorithmCT_MD.class





Medic Plugins

<http://medic.rad.jhmi.edu/download/public/index.shtml>

The Medic plugins are being ported to be compatible with the 3.0.0 release of MIPAV. 3.0.0-compatible versions of their plugins are expected soon.





Plugins

```
• package gov.nih.mipav.plugins;  
  
• import gov.nih.mipav.model.structures.*;  
• import gov.nih.mipav.view.*;  
  
• import java.awt.*;  
  
• public interface PlugInAlgorithm extends PlugIn {  
  
•     /**  
•      * run  
•      * @param UI          MIPAV main user interface.  
•      * @param parentFrame Frame that displays the MIPAV image.  
•      *           Can be used as a parent frame when building dialogs.  
•      * @param image        Model of the MIPAV image.  
•      * @see  ModelImage  
•      * @see  ViewJFrameImage  
•      */  
•     public void run (ViewUserInterface UI, Frame parentFrame, ModelImage image);  
  
• }
```





Plugins – Hello World

```
import gov.nih.mipav.plugins.*;      //needed to load PlugInAlgorithm / PlugInView / PlugInFile interface
import gov.nih.mipav.view.*;
import gov.nih.mipav.model.structures.*;

import java.awt.*;
import javax.swing.*;
```





Plugins - Example

```
• import gov.nih.mipav.plugins.*;           //needed to load PlugInAlgorithm / PlugInView / PlugInFile interface
• import gov.nih.mipav.view.*;
• import gov.nih.mipav.model.structures.*;
•
• import java.awt.*;
•
• /**
• * This is simple plugin for the University of Maryland to simple segment an image based on CT Hounsfield units
• *
• * @see PlugInAlgorithm
• */
•
• // This is a Algorithm type of PlugIn, and therefore must implement PlugInAlgorithm
• // Implementing the PlugInAlgorithm requires this class to implement the run method
• // with the correct parameters
• public class PlugInCT_MD implements PlugInAlgorithm {
•
• /**
• * Defines body of run method, which was declared in the interface.
• * @param UI          User Interface
• * @param parentFrame Parent frame
• * @param image        Current ModelImage - this is an image already loaded into MIPAV. Can be null.
• */
• public void run (ViewUserInterface UI, Frame parentFrame, ModelImage image) {
•
•     if (parentFrame instanceof ViewJFrameImage)
•         new PlugInDialogCT_MD (parentFrame, image);
•
•     else
•         MipavUtil.displayError ("PlugIn CT_MD only runs on an image frame.");
•     }
• }
```

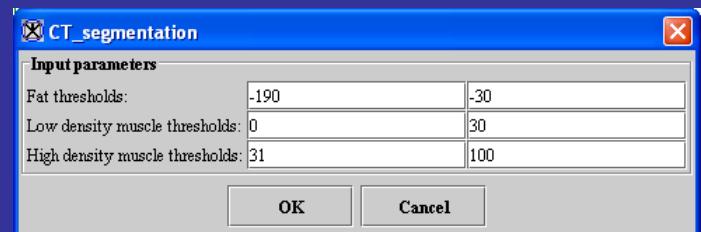




Plugins - Dialog

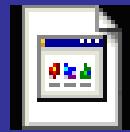


PlugInDialogCT_MD.java





Plugins - Algorithm



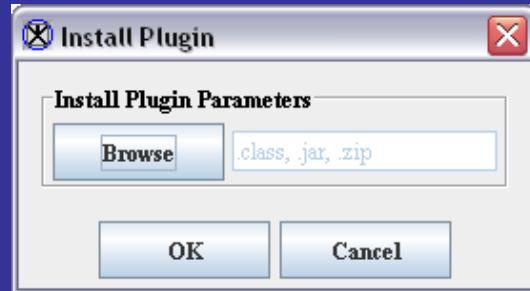
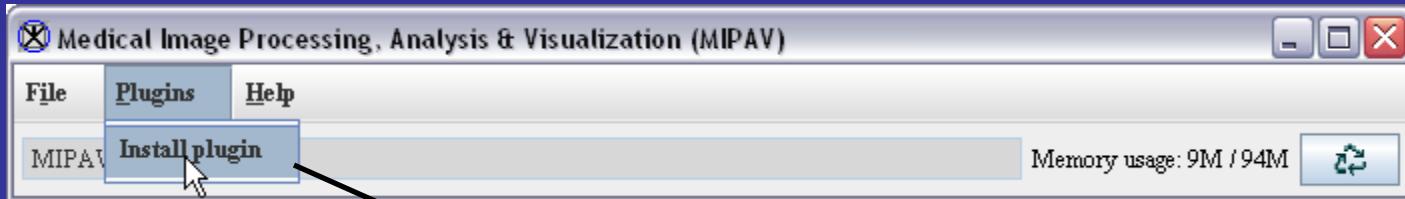
PlugInAlgorithmCT_MD.java

Simple algorithm to segment an image based on Hounsfield values





Plugins - Installing



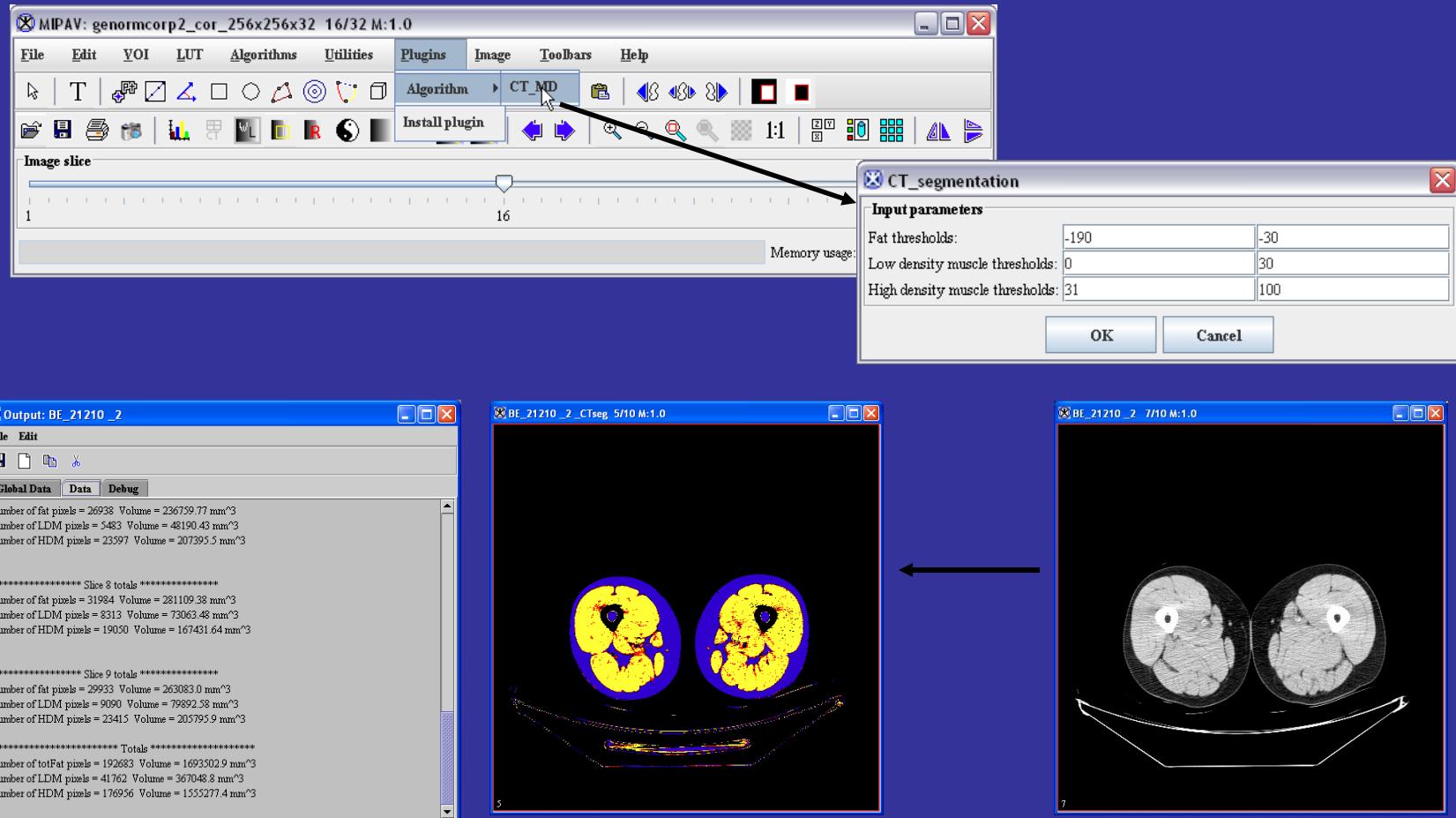
Be sure to select the files to be moved into the user's directory (e.g. PlugInFoo.class, PlugInDialogFoo.class and PlugInAlgorithmFoo.class).

** This is nearly the same as manually copying the files into the user's directory.





Plugins - Executing





Plugins to system calls

```
•     if (os != Preferences.OS_MAC) {  
•         int response = JOptionPane.showConfirmDialog(this, "Restart MIPAV to apply memory changes?",  
•                                         "Restart needed",  
•                                         JOptionPane.YES_NO_OPTION, JOptionPane.INFORMATION_MESSAGE);  
•         if (response == JOptionPane.YES_OPTION) {  
•             if (os == Preferences.OS_WINDOWS) {  
•                 // "./mipav.exe" could be replaced with a precompiled c++ program for example.  
•                 Runtime.getRuntime().exec("./mipav.exe");  
•             }  
•             else {  
•                 Runtime.getRuntime().exec("../runmipav");  
•             }  
•             System.exit(0);  
•         }  
•     }
```





Setting up development environment

- To build a new plugin for MIPAV, the user must first install a build environment, alter the PATH environment variable, and compile the plugin files.
 - Install the **Java 2 SDK version 1.5**.
 - Install **Apache Ant 1.6.X**.
 - Add JAVA_HOME to your environment, pointing to the directory where the SDK is installed (e.g. C:\Program Files\Java\jdk1.5.0_06).
 - Add ANT_HOME to your environment, pointing to the directory where Ant is installed (e.g. C:\Program Files\apache-ant-1.6.3).
 - Add the bin directories under ANT_HOME and JAVA_HOME to your PATH environment variable (e.g. add - %JAVA_HOME%\bin;%ANT_HOME%\bin to the end of PATH).





Setting up development environment (continued)

- Retrieve our **example Ant build file** and place it in the same directory as the plugin .java files you want to compile.
- Alter the dir.mipav and dir.jdk properties within the build.xml to point to the directory where MIPAV and the SDK are installed, respectively.
- Type in "ant compile" (without quotes) into a terminal window (e.g. cmd on Windows or xterm on unix platforms).
- BUILD SUCCESSFUL should appear at the end of the Ant output.
- Copy the .class files that Ant produced into MIPAV's plugin directory (C:\Documents and Settings\username\mipav\plugins or /home/username/mipav/plugins).
- Install the plugin file using MIPAV (Plugins -> Install Plugin).





Build XML example

```
<!-- build file for MIPAV plugin class -->
<project basedir=". " default="compile" name="mipav_plugin">
    <property name="dir.mipav" value="c:\\Program Files\\mipav\\\"/>
    <property name="dir.jdk" value="c:\\Program Files\\Java\\jdk1.5.0_06"/>
    <target name="init">
        <tstamp/>
        <path id="build.classpath">
            <pathelement path="${dir.mipav}"/>
            <pathelement location="${dir.mipav}/InsightToolkit/lib/InsightToolkit/InsightToolkit.jar"/>
            <fileset dir="${dir.mipav}">
                <filename name="*.jar"/>
            </fileset>
        </path>
        <property name="build.cp" refid="build.classpath"/>
    </target>
```





Build XML example (cont)

```
<target name="compile" depends="init">
    <echo>classpath: ${build.cp}</echo>
    <javac debug="true" deprecation="true" description="Builds MIPAV" verbose="no"
        listfiles="yes" nowarn="no" fork="true" memoryInitialSize="220M"
        memoryMaximumSize="1000M" id="mipav build" source="1.4"
        target="1.4" destdir"." srcdir"." compiler="modern">
        <classpath refid="build.classpath"/>
    </javac>
</target>
<target name="clean" depends="init">
    <delete>
        <fileset dir=".">
            <include name="**/*.class"/>
        </fileset>
    </delete>
</target>
</project>
```





Modify Plugin Lab

- Edit PlugInHello.java
 - Change the message from “Hello World!” to:
“Hello ” + image.getImageName() + “!”
- Compile PlugInHello.java using the plugin build.xml
- Install the generated PlugInHello.class into MIPAV
- Open an image
- Run the Hello plugin





Summary

- Plugins
 - Unique functionality using MIPAV API
 - Can be used to call C, System, Python, JPython, Perl, etc. programs





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M I P A V

Medical Image Processing, Analysis, & Visualization

