

# MIPAV



MEDICAL IMAGE PROCESSING AND VISUALIZATION

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





# Scripting MIPAV and the Java Image Science Toolkit

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# MIPAV Team

## Employees

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## Fellows

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## Contractors

Alexandra Bokinsky, Geometric Tools Inc. (Visualization)

Olga Vovk, SRA International Inc. (Technical Writing)

## Alumni

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# Extensibility

## Plugins and Scripts

- **Plugins**
  - Written in Java using the MIPAV API.
- **Scripting**
  - Use MIPAV to record and save function(s) applied to image dataset(s)
  - Apply the script to any number of image datasets using the ‘Run script’ dialog.
  - Apply the script to any number of image datasets from the command line.





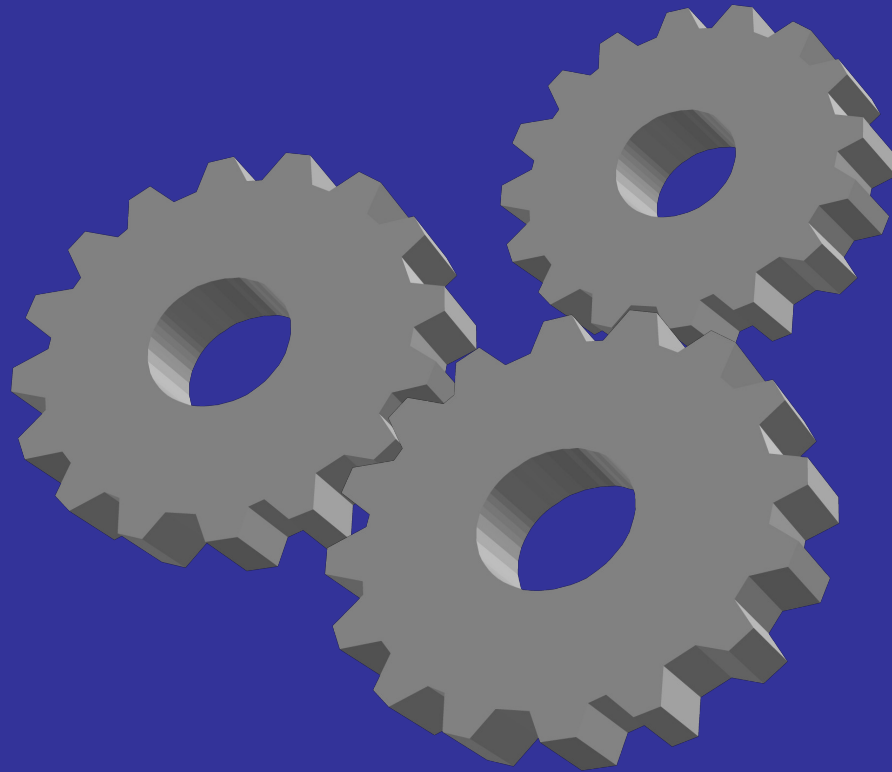
# Usability

- **Most NIH intramural researchers not interested in software-development:**
  - they want a GUI for interactive work
- MIPAV provides:
  - a GUI driven application for user-interaction;
  - scripts to automate repetitive functions;
  - plugins for customized functionality;
  - command line input for batch processing.





# Scripting

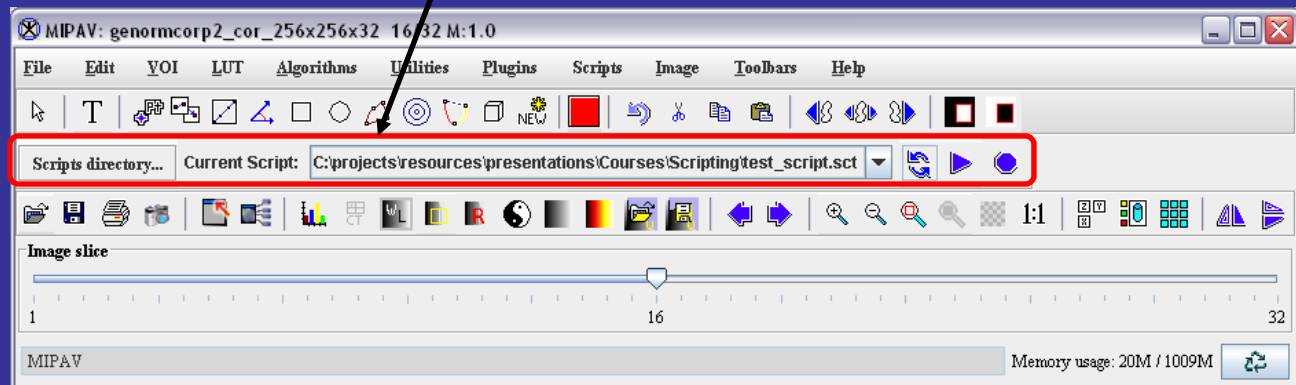
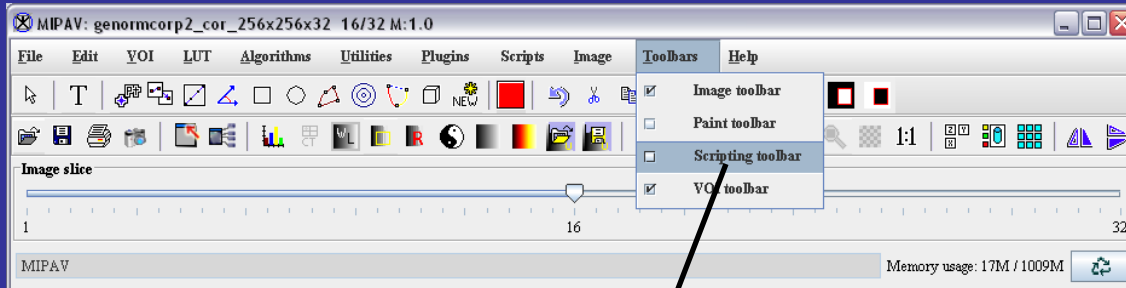


# Scripting (Macros)

- Automation of functions applied to a group of datasets
  - Increase efficiency and productivity
- MIPAV does NOT require learning a new scripting language.
  - Record and execute scripts via MIPAV's GUI.
  - Scripts can also be executed from the command line to process images from another program or script.



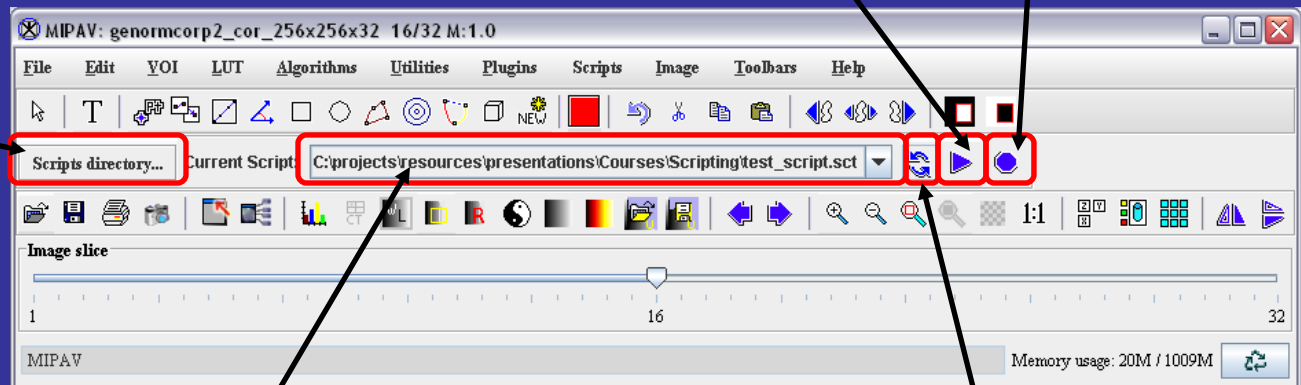
# Scripting





# Scripting

Allows the user to select the directory used for scripts



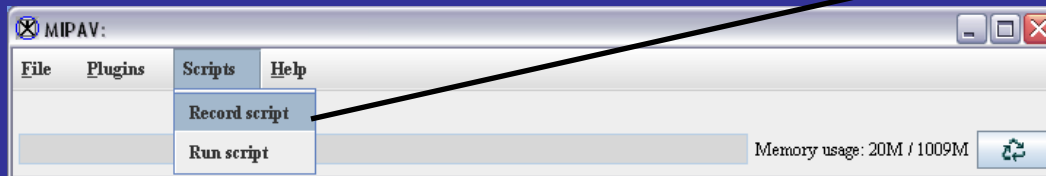
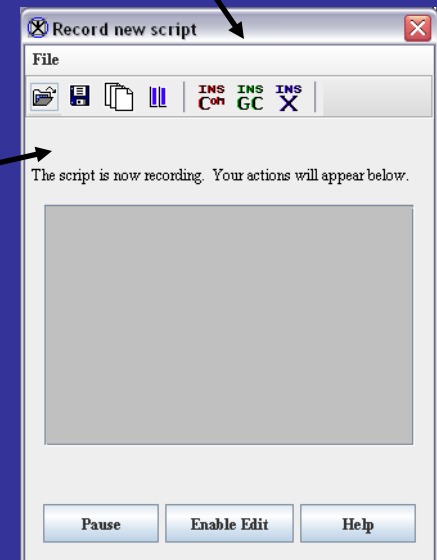
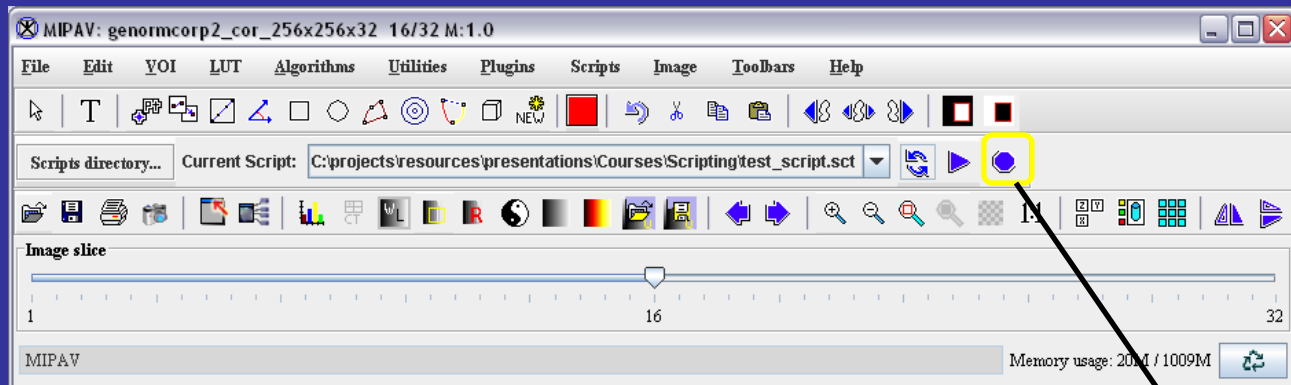
Run script

Record script

List of scripts found in the script's home directory. The usual suffix is ".sct".

Refresh the list of scripts.

# Script Recording



# Recording A Script

Resets the script recorder

Inserts a comment into the script

Inserts a command to recover memory

Opens script file

Saves script file

Pauses script recording

Inserts an exit command to quit MIPAV. Used in scripts that will be run from the command line.

Allows manual editing of the script. For advanced users.





# Scripting Features

- Arbitrary ordering of parameters allowed
- Parameter labels to facilitate parameter editing
- Script execution dialog
- More robust error messages



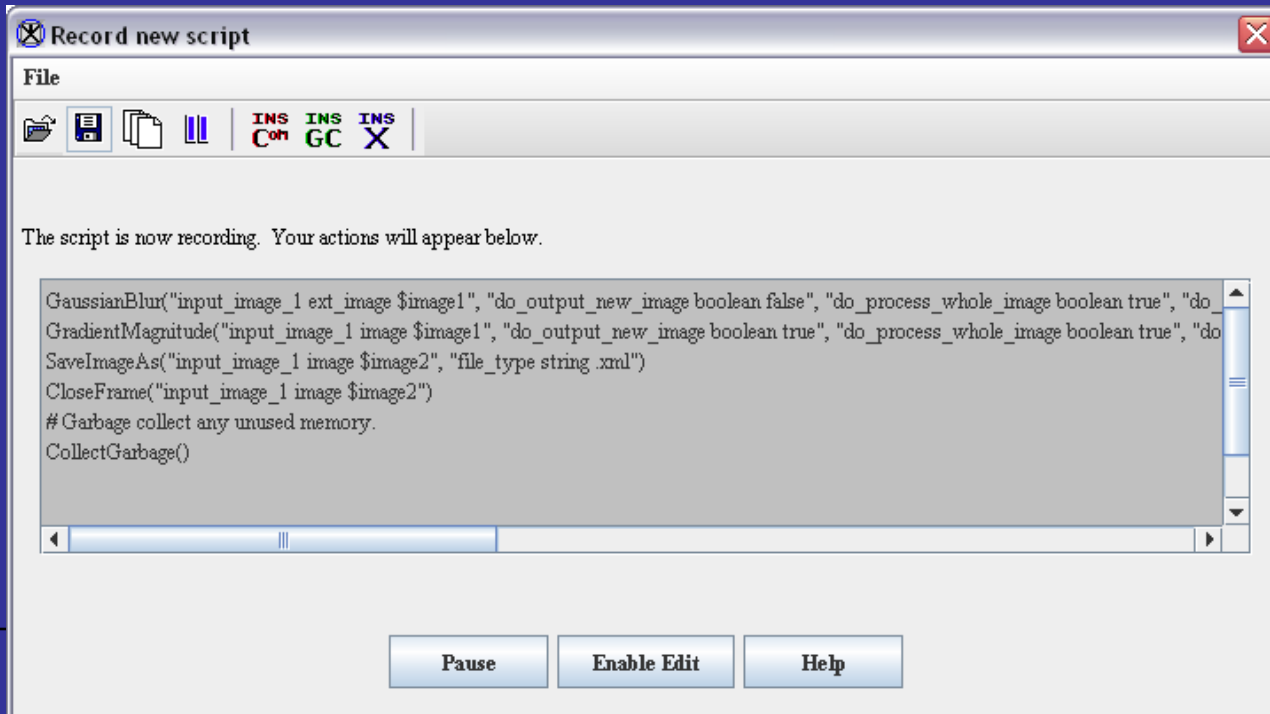
# Script Example

- GaussianBlur(“input\_image\_1 ext\_image \$image1”,  
“do\_output\_new\_image boolean true”,  
“do\_process\_whole\_image boolean true”, ...)

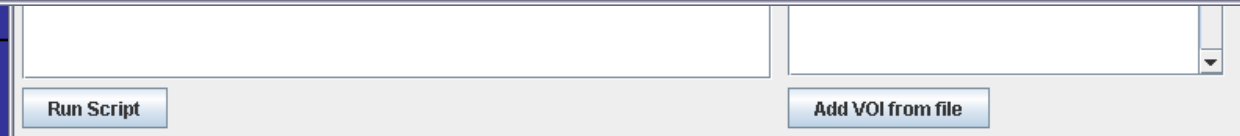
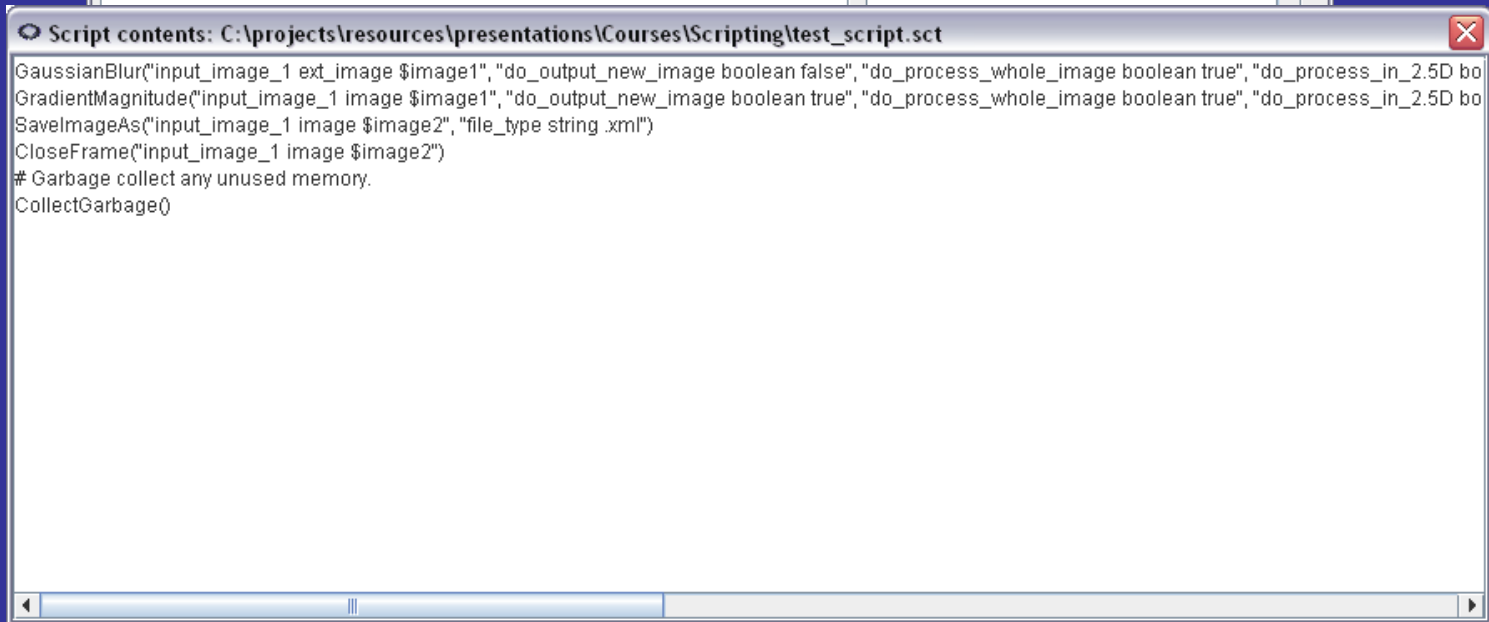
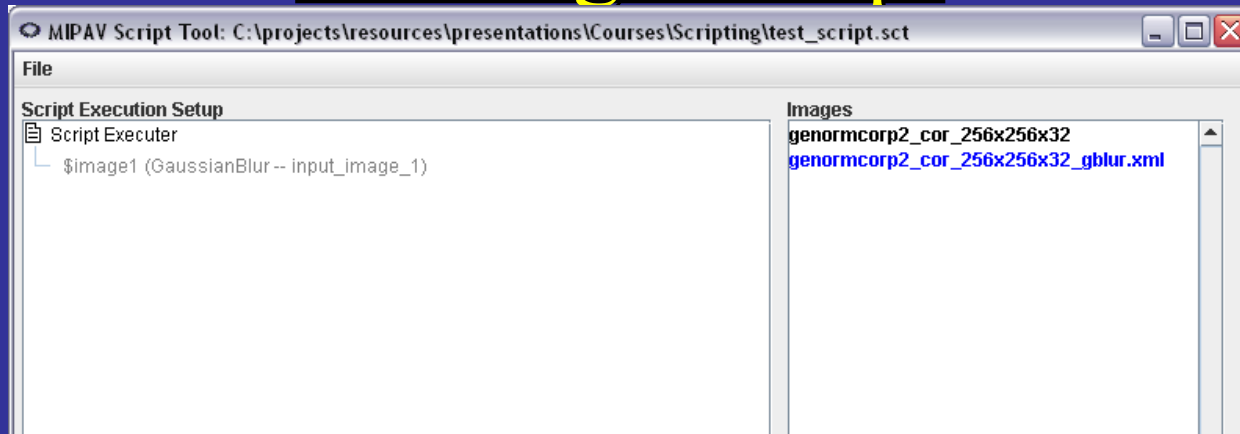


# Script Lab

1. Open an image
2. If an algorithm is to operate using a VOI, the VOI must be loaded from disk using VOI > Open VOI > Open VOI
3. Start script recording
4. Run the algorithms in the order specified
5. Save the script when done



# Running a Script





# Running a Script

The screenshot displays the MIPAV Script Tool interface. The title bar reads "MIPAV Script Tool: C:\projects\resources\presentations\Courses\Scripting\test\_script.sct". The interface is divided into several sections:

- File:** A menu bar at the top left.
- Script Execution Setup:** A tree view showing the script execution process. It includes a "Script Executer" folder, a "\$image1 (GaussianBlur -- input\_image\_1)" node, and a sub-node "(run-1) genormcorp2\_cor\_256x256x32".
- Images:** A list of image files, with "genormcorp2\_cor\_256x256x32" and "genormcorp2\_cor\_256x256x32\_gblur.xml" listed.
- Add image from file:** A button located below the Images list.
- VOIs from selected image:** A list box for viewing VOIs from the selected image, currently empty.
- Add VOI from file:** A button located below the VOIs list.
- Run Script:** A button at the bottom left of the main window.





# Running a Script

The screenshot displays the MIPAV Script Tool interface. The title bar reads "MIPAV Script Tool: C:\projects\resources\presentations\Courses\Scripting\test\_script.sct". The interface is divided into several sections:

- File:** A menu bar at the top left.
- Script Execution Setup:** A tree view showing the script execution process. It includes a "Script Executer" folder containing a "\$image1 (GaussianBlur -- input\_image\_1)" node. Under this node, there are two sub-nodes: "(run-1) genormcorp2\_cor\_256x256x32" and "(run-2) genormcorp2\_cor\_256x256x32\_gblur.xml".
- Images:** A list box on the right side showing two image files: "genormcorp2\_cor\_256x256x32" and "genormcorp2\_cor\_256x256x32\_gblur.xml". The second file is selected.
- Add image from file:** A button located below the Images list.
- VOIs from selected image:** An empty list box located below the "Add image from file" button.
- Add VOI from file:** A button located below the "VOIs from selected image" list.
- Run Script:** A button located at the bottom left of the interface.



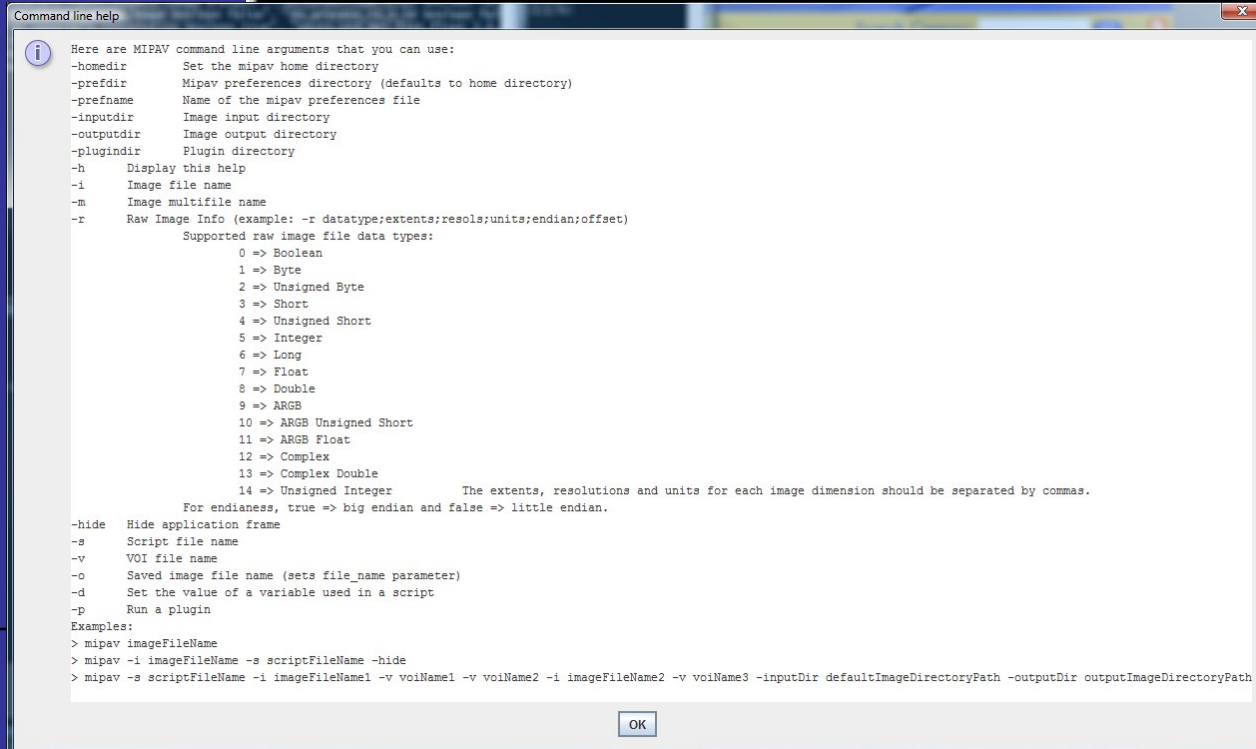
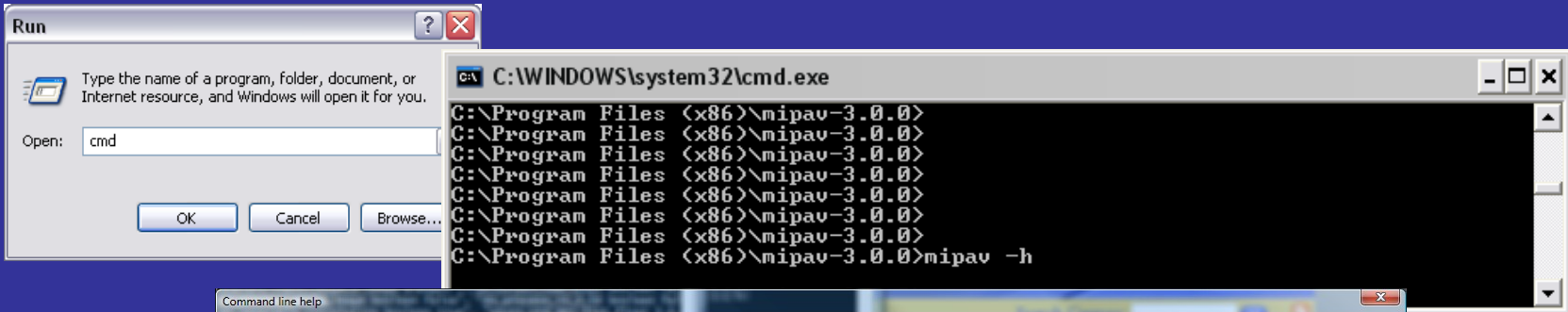


# Scripting from the Command Line

- MIPAV can be called from scripts (Perl, batch, shell scripts, etc.)

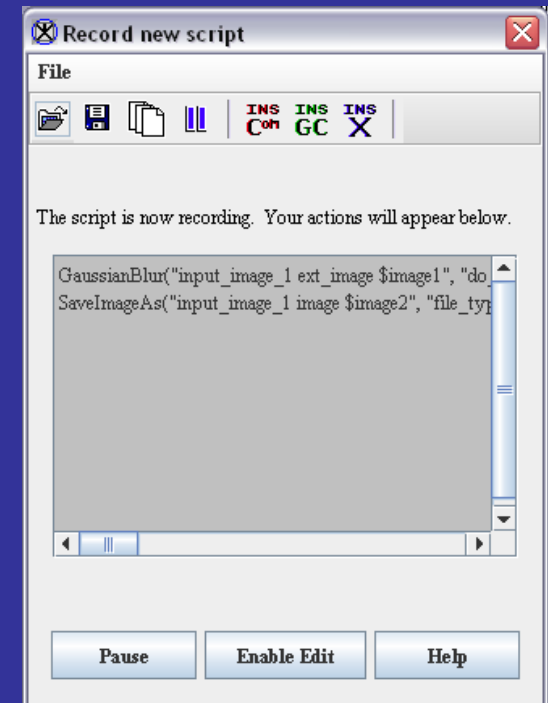


# Calling a Script from the DOS command line



# Writing a Script for Batch Processing

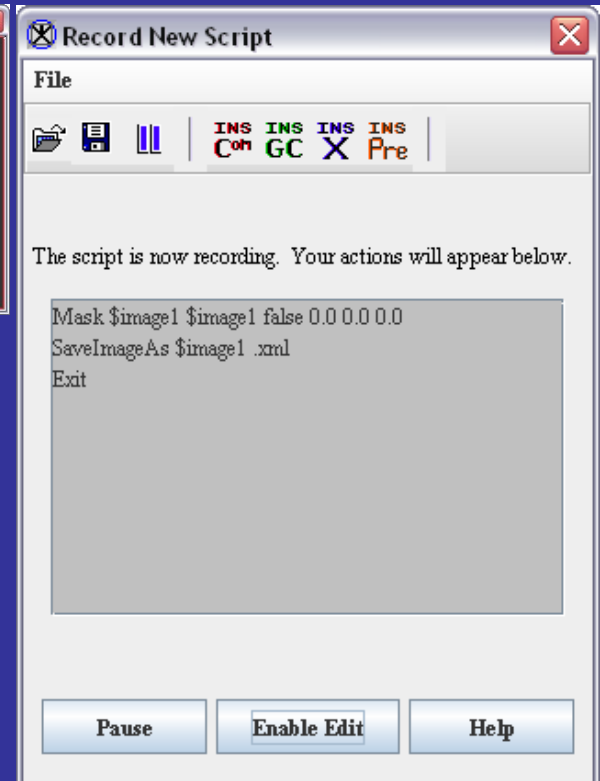
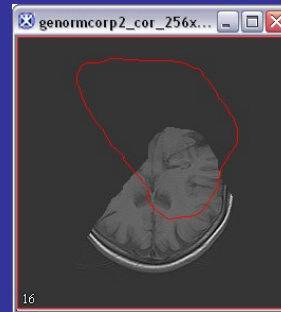
- Do not record loading VOIs into the script – we load these from the command line with the -v option
- Don't forget to “**Save As...**” before finishing
  - -o options saves the result image using the user provide string.
    - E.g. “-o outputFileName”
- Optionally, add an **Exit()** command to the end of the script
  - An **Exit()** will be automatically added to the end of a script executed with the -hide command



# Writing a Script for Batch Processing – Lab

## Classroom Lab

1. Open an image
2. Open a VOI
3. Start script recording
4. Mask the image
5. Save result image as...
6. Save as new script when done – call it *example.sct*



# Batch Processing with MIPAV

- From the command line:
  - We can call MIPAV to run the script we have recorded
  - We can call a batch script or shell script to run a MIPAV active script
  - Windows:
    - Batch scripts (.bat files)
    - Cygwin (<http://www.cygwin.com/>)
    - ActivePerl
  - Linux/UNIX/Mac OS X
    - Shell scripting (bash, tcsh, zsh, etc.)
    - Perl
    - Python



# Lab for Batch Processing with MIPAV

1. Open the command shell
2. At the command prompt:

```
mipav -s example.sct -i image.xml -v voi.voi
```

Note: Runs the script just once on the given image



# Batch Processing with MIPAV

Multiple images can also be processed through the use of scripting:

```
@echo off

rem usage: loop_xml.bat image_directory script voi_file
echo processes xml files in a dir with a mipav script, using a voi

for %%f in (%1\*.xml) do "C:\Program Files (x86)\mipav\mipav" -i %%f -s %2 -v %3
```

Similar scripts are even easier to write in shell scripts and Perl programs.







# Command Line Notes

- Use the `–hide` option to prevent the MIPAV GUI from showing up.
- The `–m` option should be used to open multi-file images (such as DICOM volumes).
- Use the `–help` option to learn about other command line switches





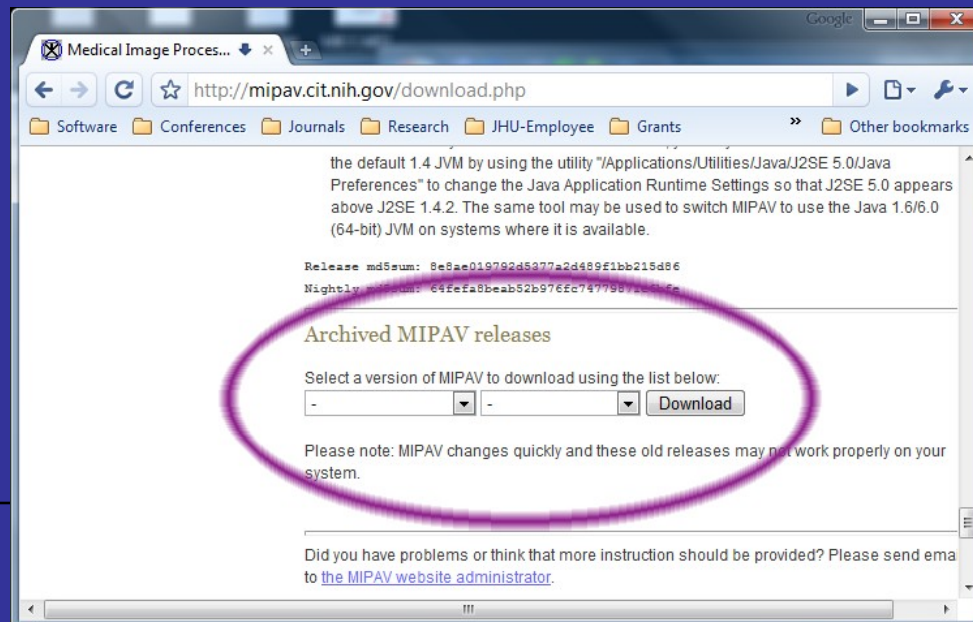
# Java Image Science Toolkit

- Originally developed at Johns Hopkins, now also supported by Vanderbilt (LGPL license)
- Created as a set of MIPAV extensions & plugins
- Main features
  - Automated GUI generation for application plugins
  - Graphical image processing workflow layout tools
  - Command line interfaces
- <http://www.nitrc.org/projects/jist>



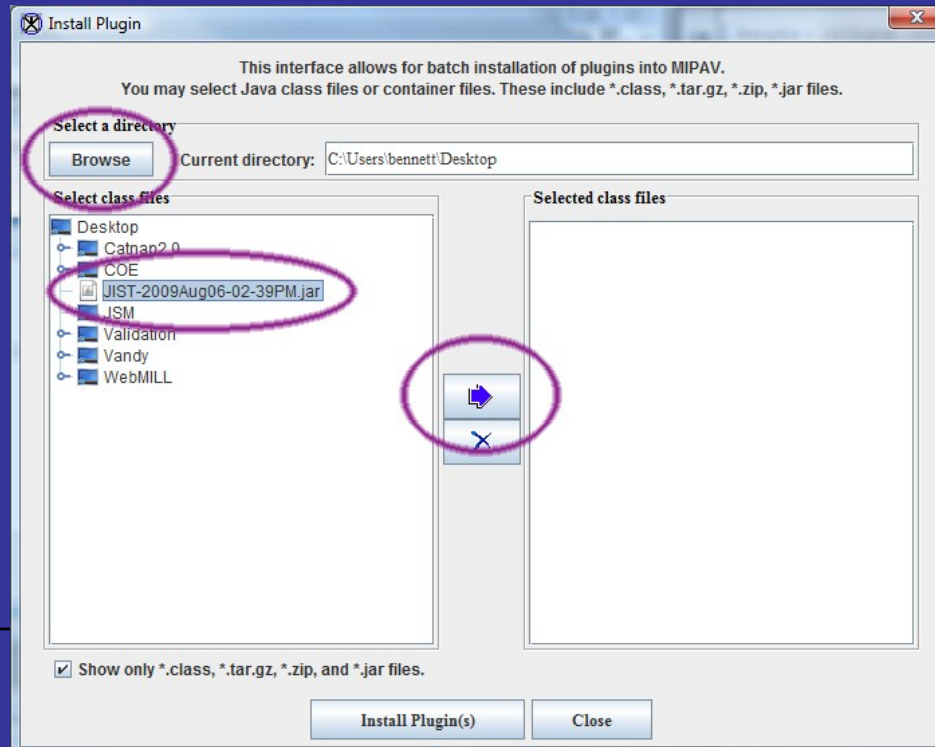
# Installing JIST

- Install MIPAV
  - Download & install the MIPAV version compatible with the release of JIST you will be using
  - Latest release of JIST works with MIPAV 5.3.1



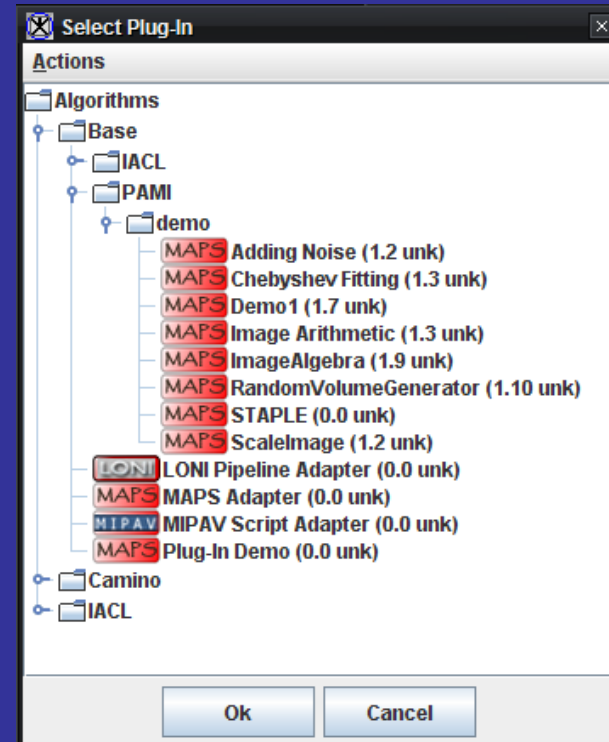
# Installing JIST (cont.)

- Download the JIST jar file
- Use MIPAV's Plugins -> Install plugin dialog



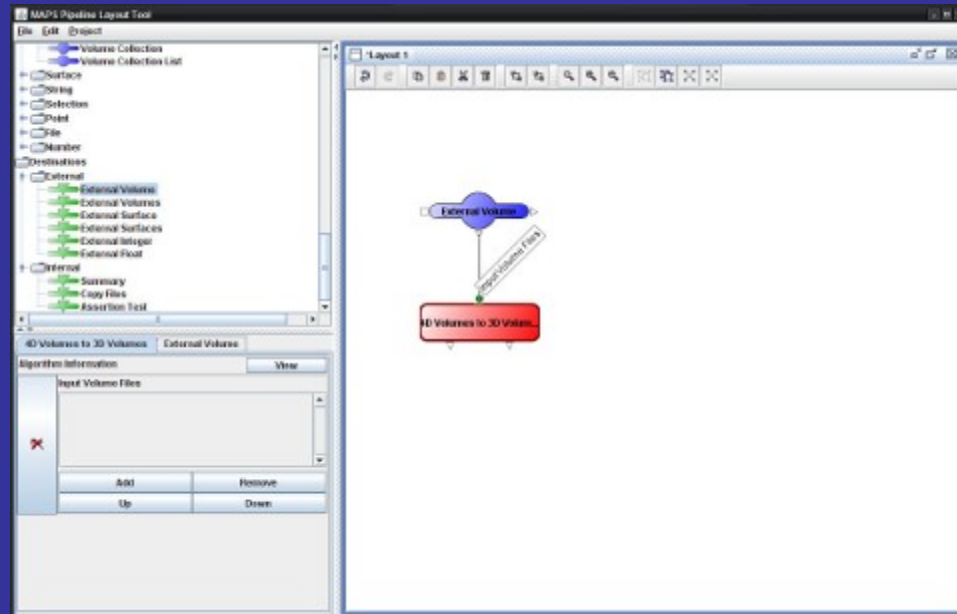
# JIST Plugin Selector

- Useful for running or debugging a single JIST module



# JIST Layout Tool

- Connects JIST modules together to create image processing workflows
- GUI interface



# JIST Process Manager

- Run from the Layout Tool or standalone
- Executes layouts and displays status

The screenshot shows a window titled "Process Manager [localhost - Test1.maps]" with a "Scheduler" tab. The window contains a table with the following data:

Experiment	Module	Algorithm	Priority	Time (Actual)	Memory Used / Al.	Status	Progress
.0000.A	4D Volumes to 3D Volumes	AlgorithmVolumeFileCollectionF	1	- / -	- / -	READY	
.0001.A	4D Volumes to 3D Volumes	AlgorithmVolumeFileCollectionF	2	- / -	- / -	READY	
.0002.A	4D Volumes to 3D Volumes	AlgorithmVolumeFileCollectionF	3	- / -	- / -	READY	

At the bottom of the window, there is a status bar that reads: "Scheduler Stopped: Succeeded (0) Failed (0) Pending (0) Queued (0) Total (3) Elapsed Time (Actual: - / CPU: -)"



# JIST Lab

- Get JIST from <http://www.nitrc.org/projects/jist>
- Install JIST
- Create a simple workflow
  - Choose a MIPAV algorithm (e.g., Median filter)
  - Select the input image for the module
  - Output the result image to an External file





# M I P A V

Medical Image Processing, Analysis, & Visualization





Thank you!

