

LesionTOADS User Manual

LesionTOADS is a software for simultaneous tissue classification and WM/MS lesion segmentation of MR brain images. It segments the multichannel MR images based on both intensity and atlas information.

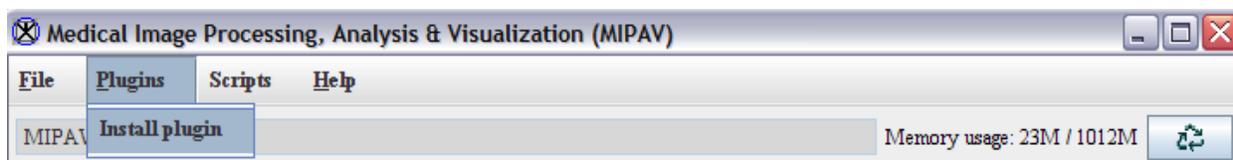
This manual contains information about required mipav commands, lesionToads installation and running.

Installation:

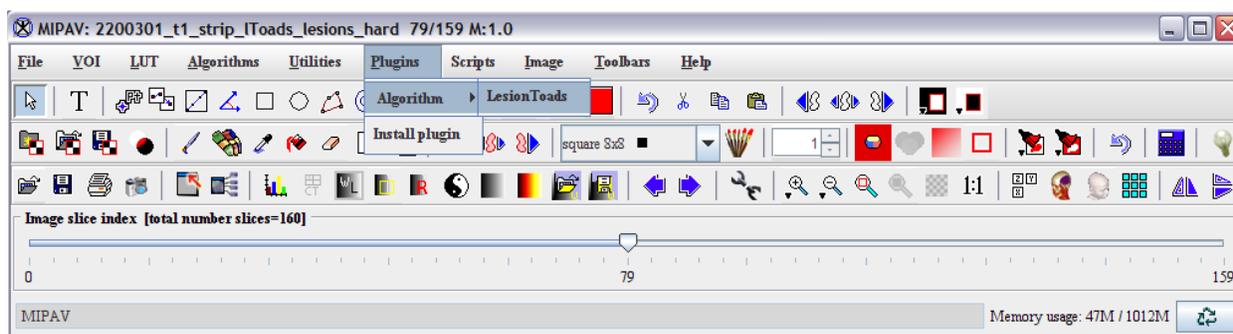
LesionTOADS is distributed as a plugin to MIPAV software developed by NIH. MIPAV is a free software with a variety of options for both visualization and processing of the medical images and it is compatible with most of file formats including Analyze, NIFTI, DICOM, etc. It can be downloaded from www.mipav.cit.nih.gov .

After downloading MIPAV you can easily install LesionTOADS as follow:

- 1) Run mipav.
- 2) Choose Install plugin from Plugins menu.

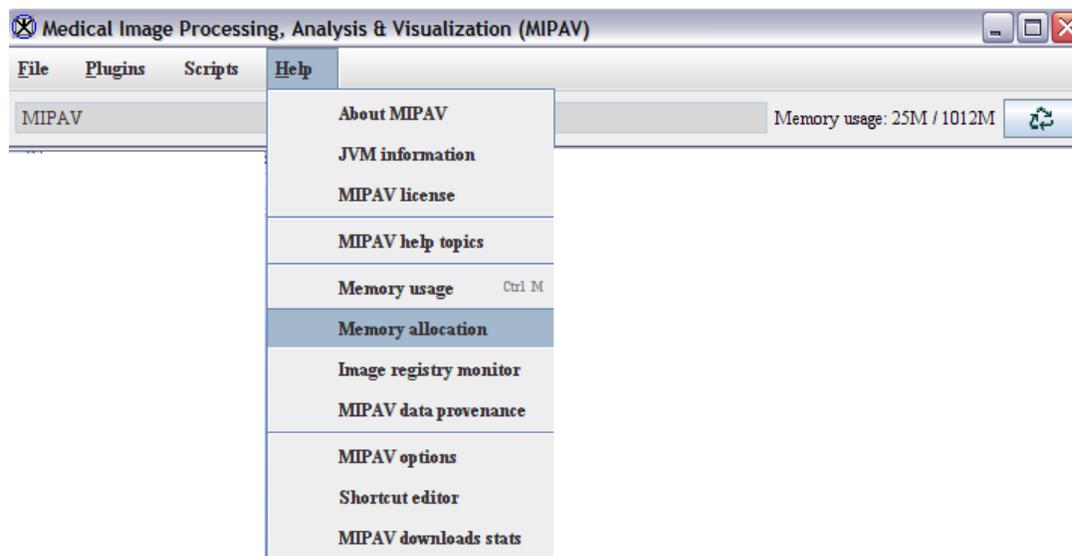


- 3) In the opened dialog locate where LesionTOADS.jar is saved using browse and click on OK button.
- 4) Now exit MIPAV and rerun it.
- 5) Now open an image. Under Plugins menu, choose Algorithms and from that you can run LesionTOADS.



Running LesionTOADS:

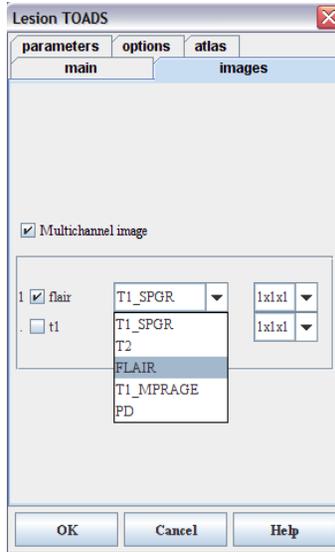
Before running LesionTOADS, note that based on the resolution of the input files, you should allocate enough amount of memory to mipav. We recommend allocating at least 2.5 GB. To change the memory settings in MIPAV, choose Memory allocation under Help menu. Note that you should the units for memory assumed to be megabytes. If you change the memory setting, you should rerun MIAPV to these changes take effect.



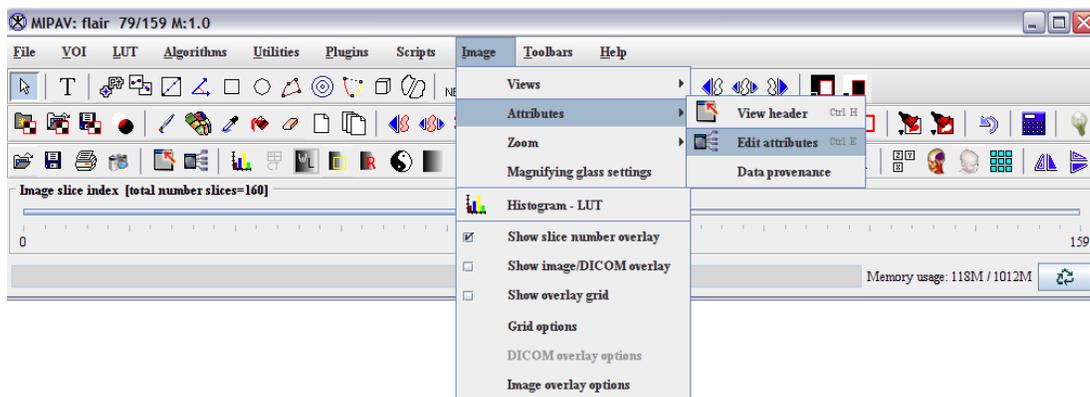
Note that you should the units for memory assumed to be megabytes. If you change the memory setting, you should rerun MIAPV to these changes take effect.

To run LesionTOADS, first open the images you want to be processed. After this, choose LesionTOADS from Algorithms under Plugins menu.

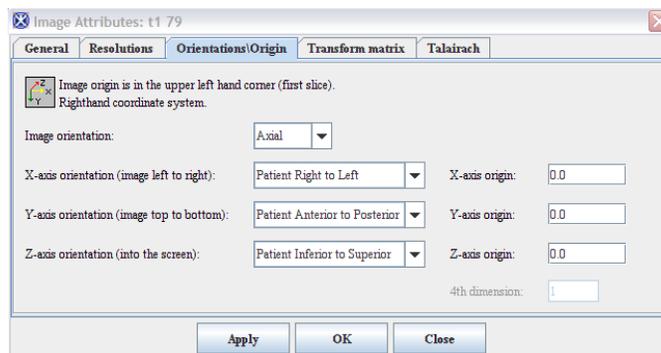
Input Images: First step is to choose the input images you want to be processed and select their pulse sequence. You can choose any open images as input there is no limitation on the number of input images. But the algorithm is optimized for T1+FLAIR input images. From “images” panel first check the images you would like the algorithm use as its input images, and then select the image pulse sequence (not that there is a different option for T1_MPRAGE and T1_SPGR).



Important Remark : Make sure that the orientation of the input images are correct. To check this, active the input image and then from “Image” menu choose “Attributes” and then select “Edit attributes” (or use Ctrl+E).



A window called “Image attributes” will be opened. On this window, click on “Orientations\Origin” panel. This panel shows you the current file orientation. If it is wrong or there is no orientation associated with the image, correct it, hit ok and then save the image (Ctrl+S, or from File menu choose save).



Atlas files: LesionTOADS use statistical and topological atlases. The needed atlases are provided with the software release. With the atlas files, there is also a “?.txt” file that will be used as the input to the algorithm. After downloading atlas files unzip them and make sure the “?.txt” be in the parent directory to the atlas files. For example if you the atlases are in “/home/lesionToads/atlas/” the ?.txt file should be located at “/home/lesionToads/”. From the “atlas panel” choose Load and locate the ?.txt file. There are two atlas parameters for LesionTOADS. “Atlas scale” rarely need to be changed. “Atlas coefficient” controls the effect of statistical atlases on the segmentation. Although the default value should work for most of the cases, based on the image contrast or amount of noise, one can increase it (range : 0.1 - 2).

Output Images: LesionTOADS has several output options. From the “main panel” you can choose one of these output options:

1. Classification: Outputs hard classification of tissues and lesions in two separate files. To understand the representative id of each structure, refer to the atlas file. In front of each structure in the atlas file, there is a number which shows the id of each tissue in the hard segmentation. Lesions are included in cortical WM in the hard tissue segmentation but their hard segmentation is outputted in a separate file.
2. Class+member: Outputs of the “classification” option plus the fuzzy membership function for each structure.
3. Cruise inputs: inputs required for our cortical reconstruction software called cruise (it is downloadable from (<http://medic.rad.jhmi.edu/downloads>))
4. Dura removal inputs: inputs required for our dura removal software (distributed upon request)
5. All images: Outputs of “class+member” option and the field inhomogeneity correction coefficients.

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