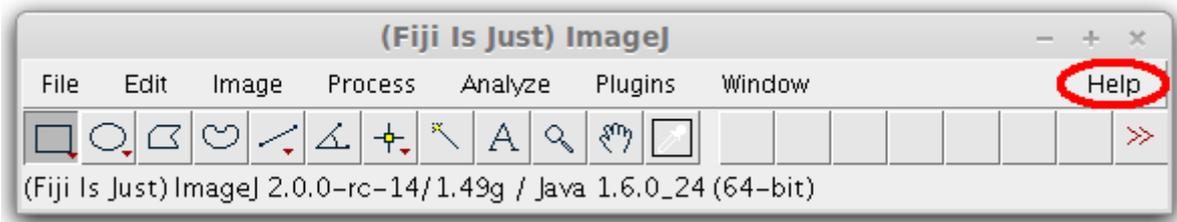# *Beth Israel Plugin*

## Quick User Guide

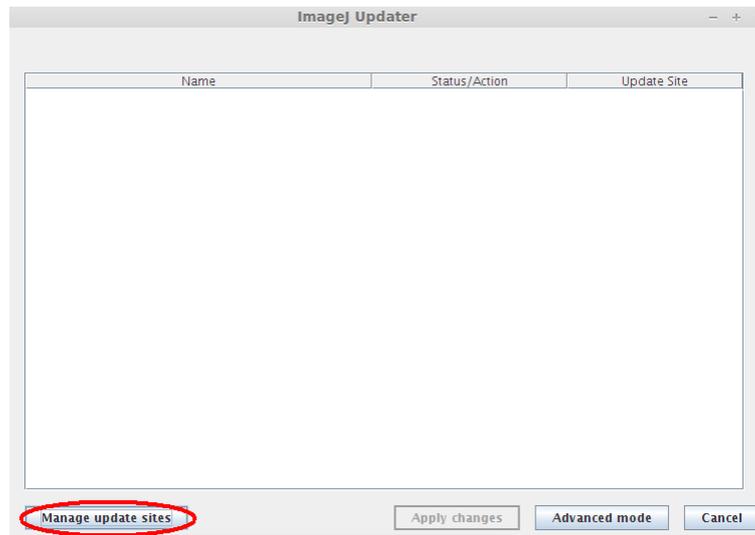Installation / DICOM reading / PET-CT viewer / Metabolic Tumor Volume

# Installation

The installation process is dead easy, just follow those few steps :

- Download and install FIJI (Fiji Is Just ImageJ) for your operating system :
http://fiji.sc/#download

- Run FIJI and go to "**Help**" and "**Update**..."



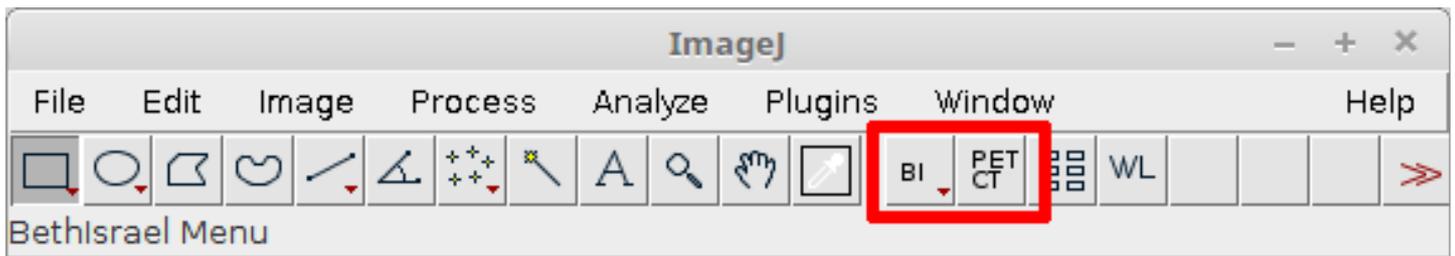- Click on "manage update site"



- On the list select "PET-CT" and click "close"



You will be asked to stop and restart FIJI, once this done your Beth Israel PET/CT viewer will be properly installed. Moreover, the software will propose auto-update at each new release.

# Quick Access buttons



After restarting Fiji you will see these two buttons to access the main applications of the software.
"BI" is a quick access to DICOM reading softwares (Read From CD / BI Database)
"PET/CT" to open manually the PET/CT viewer (images have to be loaded first in Fiji like described under).

# Reading your DICOM files

The software includes a DICOM parser and reader, you just have to set the directory of your DICOM files. Once this is done the software will scan your DICOM files and show you a proper visualization of your patients and image sequences. (See demo on youtube or the French demo.)

- At startup, "Read From CD" will automatically start, go to "setup" (red) to chose your image directory (you can also access "Read From CD" through File => import => Read From CD).
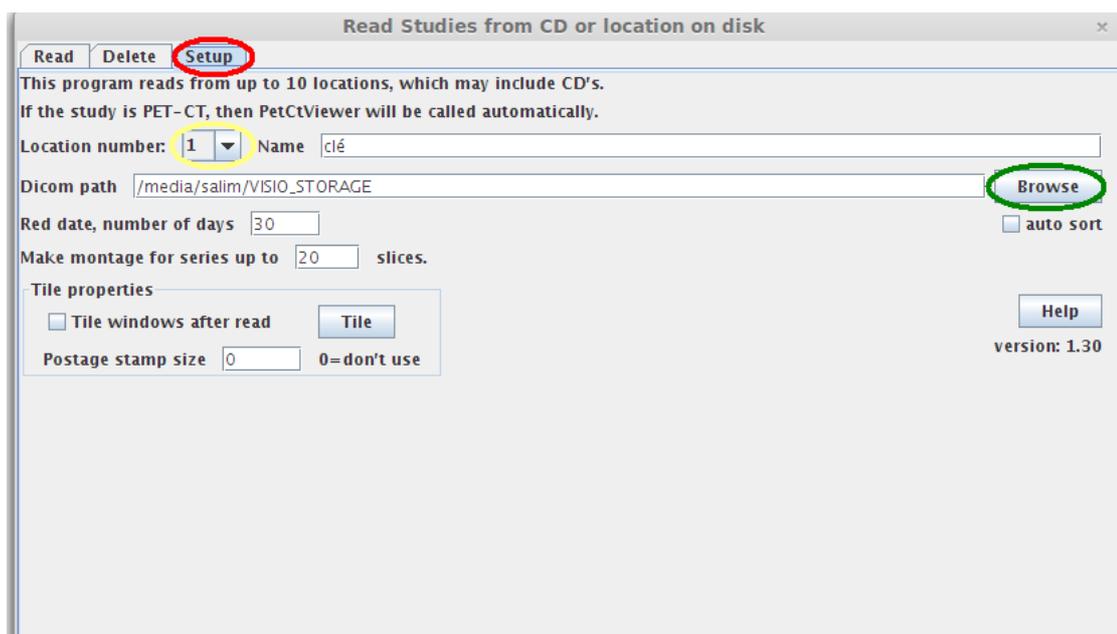


- Set your DICOM path with the "browse" button (green). You can set multiple locations (yellow) if you have multiple directories (just change the location number to set all your needed directories)

- Click on the "Read" tab and push the "Read" (red) button to scan your files. Patients name will be shown.

You can double click on a patient name to open all sequences of this patient or look at the available studies (green) to choose the sequences you want to analyze.

Please note the buttons on the bottom (blue), they allow you to switch from one directory to another.
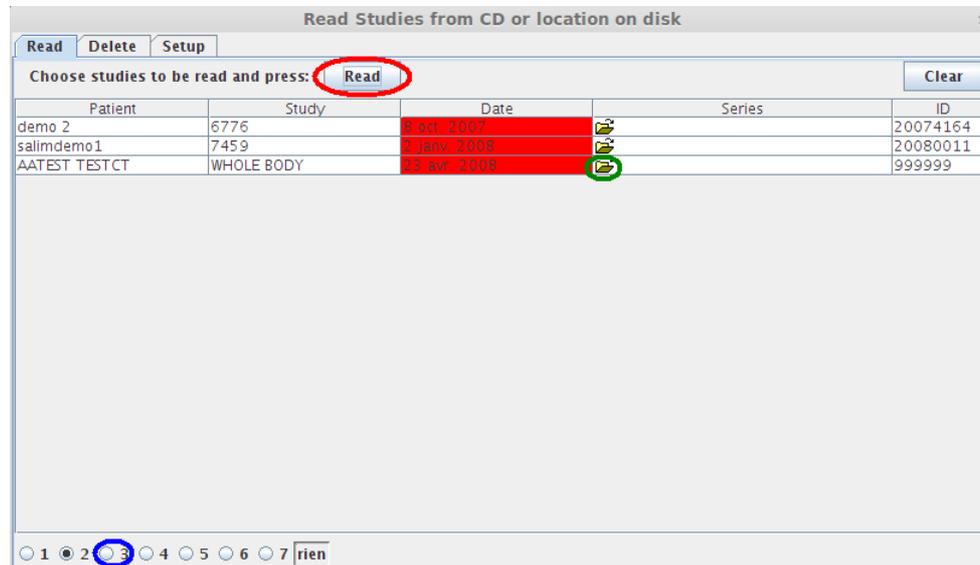


You can select manually each series using the "ctrl" button, if you selected 1 corrected attenuated + 1 CT serie and press "Read", the PET/CT viewer will open automatically. Otherwise, you can load the needed series in Fiji and open manually the PET/CT viewer with the quick access button (as seen before).

# Warning : DICOM format

The 2 available presentations of DICOM files are supported by the DICOM reader :
- The hierarchical structure : Each series has to be in a separate subfolder
- The flat structure : All DICOMs are in the same folder and a DICOMDIR is available in the root folder (set the root folder in Read from CD where the DICOMDIR is located)

A usual error is trying to read a flat structure while the DICOMDIR is missing, in this case you should import the messy DICOM dataset to a DICOM software like the free and open source Orthanc server (see our documentation on Orthanc or contact us for help).

Compressed DICOMs are not directly supported by Fiji but you can read them with Orthanc Server which will uncompress the DICOM on the fly to be read in Fiji (see our documentation on Orthanc or contact us for help).

Lastly, if you see error messages during the DICOM reading process, please contact us (Ilan.Tal@gmail.com and Salim.Kanoun@gmail.com), it will signify that we should increase the compatibility of our DICOM reader, we will ask you to send us one DICOM sample of your files to update our software. You will contribute to extend the DICOM compatibility for the community.

# PET-CT Viewer

Here is a short presentation of the interface of the PET/CT Viewer :
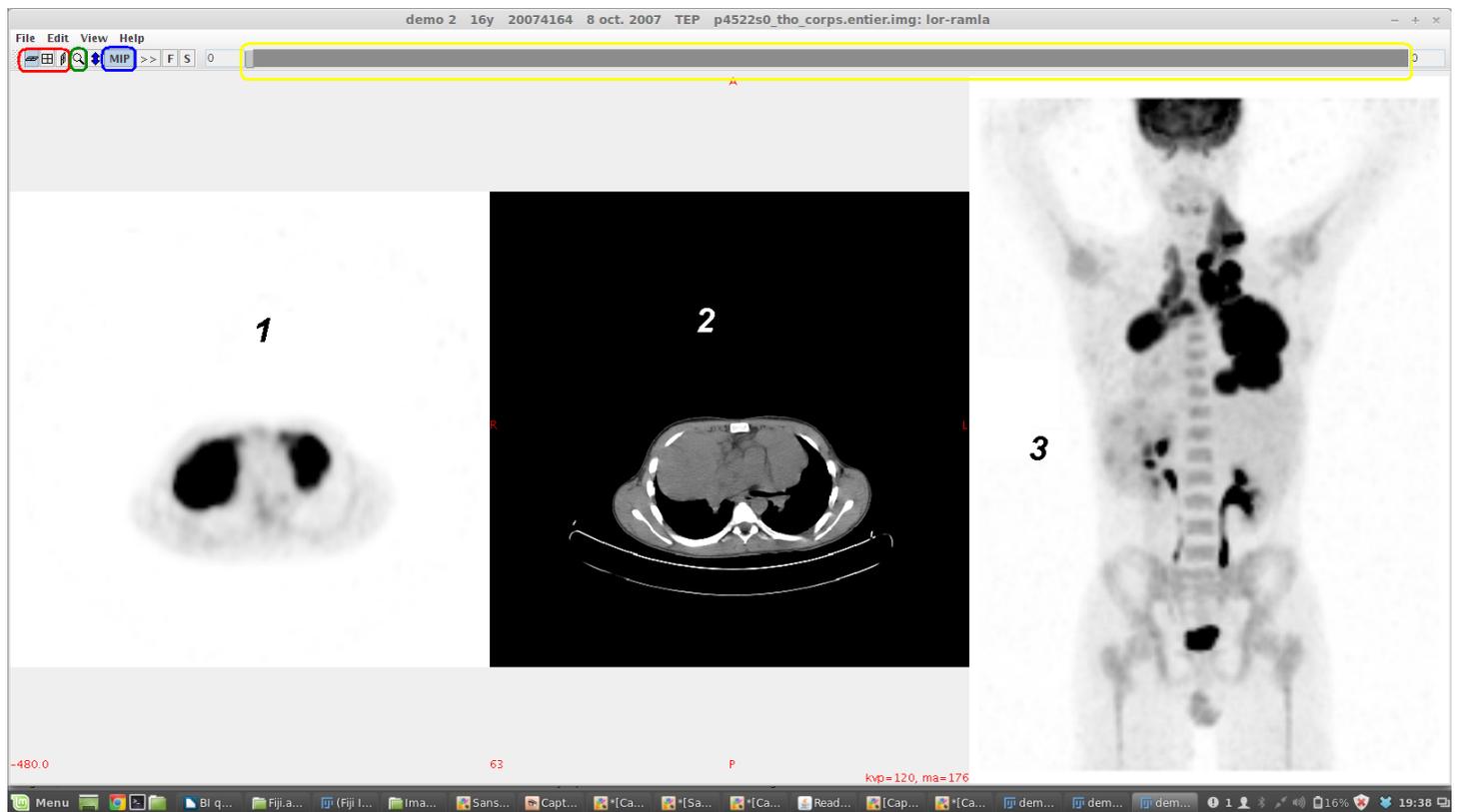


Buttons :
- Axial, coronal or sagital view axis (red)
- Zoom (green)
- Disable or Enable MIP (blue) ; if disabled PET-CT fusion will be shown
- Windowing (yellow) : you can change the center and the weight of the window through this bar

Area :
- 1 : PET slices. By right clicking you can change the look up table
- 2 : CT slices. By right clicking you can switch between pre-defined windowing
- 3 : MIP of PET-CT fusion (depending if MIP is displayed or not)

# Metabolic Tumor Volume

To calculate the Total Metabolic Tumor volume, in the PET-CT Viewer go to "edit" menu and "Brown Fat, ROIs"
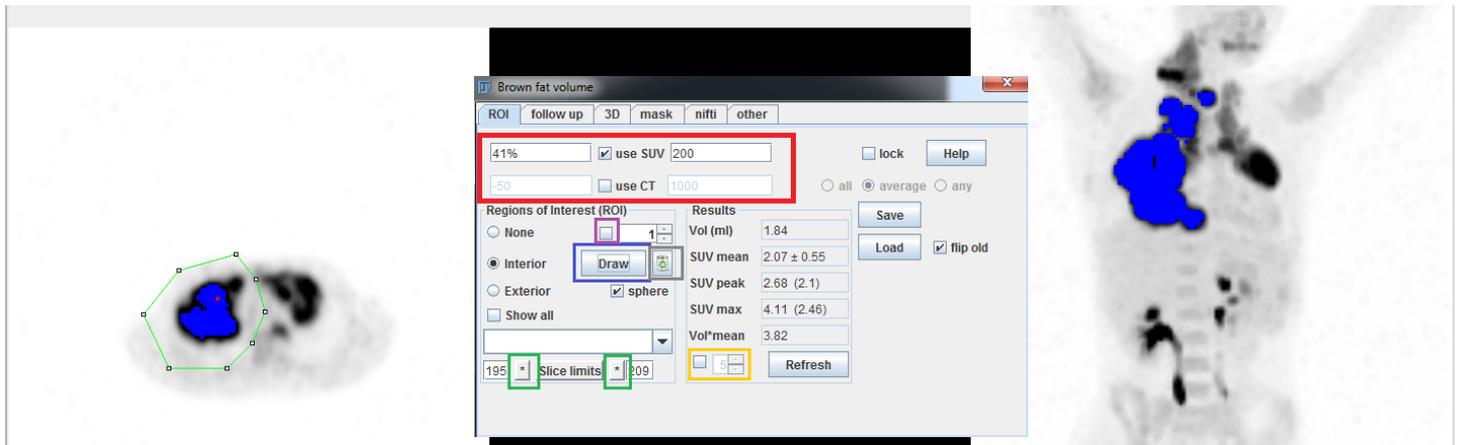


To set your calculation parameters use the 4 first white boxes (red) :
- You can set an SUV condition : The left box is for the lower limit and the right box is for the upper limit.
    - For TMTV, usually we don't need an upper limit so you can set it to a very high value (500) to be sure to include all high uptake voxels
    - In the left box you can use a fixed cut-off (for example : 2.5) or a SUVmax thresold (you just need to add % to do so, for example you can type 41% for 41% of SUVmax)
- You can also set a CT condition but it might be useless for TMTV calculation, if you don't need it just unselect "use CT"

- To Draw the ROI use the big button on the left bottom panel (blue), and click on the image to draw your ROI. Double click to close the ROI when drawing. Once your ROI shape is defined you have to expend in on other slices to get the third dimension.
You will notice two "*" buttons at the bottom (green), in the image go to the first slice you want to expend your ROI to and hit the first "*" than go to the last slice you want and  hit the other "*". Your VOI is defined.
If you click on the little box near the ROI number (purple) the display will automatically be updated to show the ROI position when you review your previous ROIs using up and down buttons.

-To erase a ROI, simply use the trash icon (gray)

- To visually control the calculated MTV, activate the checkbox on the bottom right (yellow) and increase the number in the box to show selected voxels in blue. If enabled, the MIP will also include the blue dots. Lastly, you can right click on the PET image and use "3-PET" to check your calculation in a 3 axis way

- The save button allows you to save all your results and ROI positions on a CSV file. You can load the saved ROIs using the load file (the generated CSV contains both results and ROI coordinates).
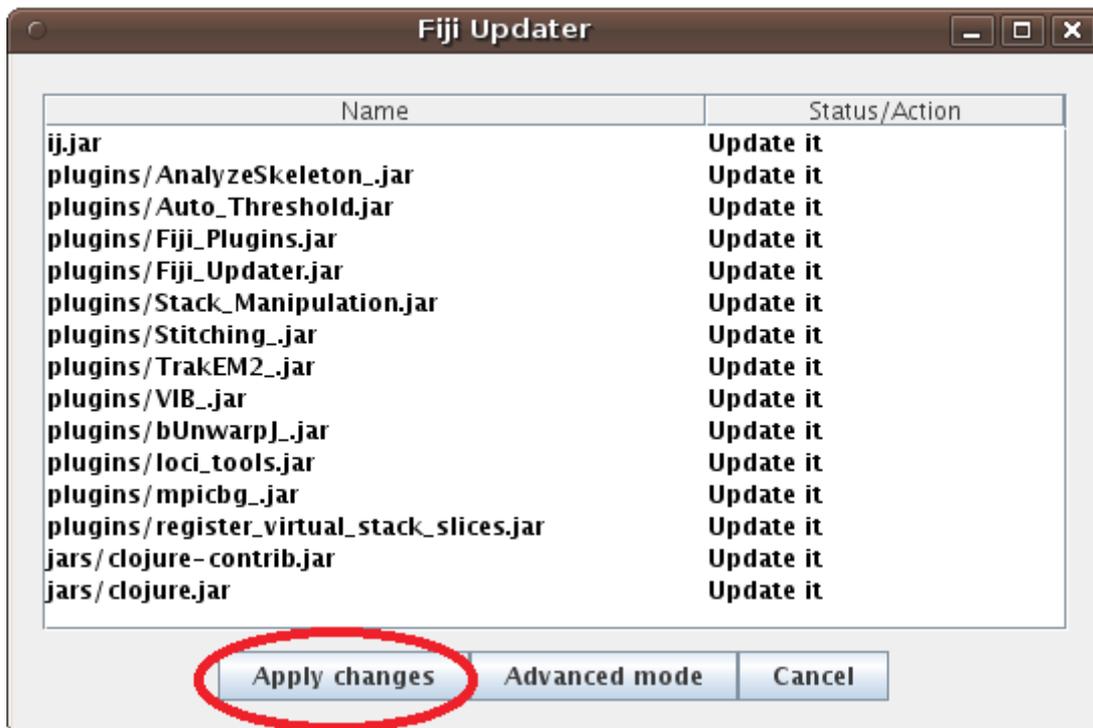
# Updates

Fiji automatically looks for update at startup (if your computer is connected to the Internet).

When an update is available, you will have an update request, simply Select on "Yes please" and click "OK"
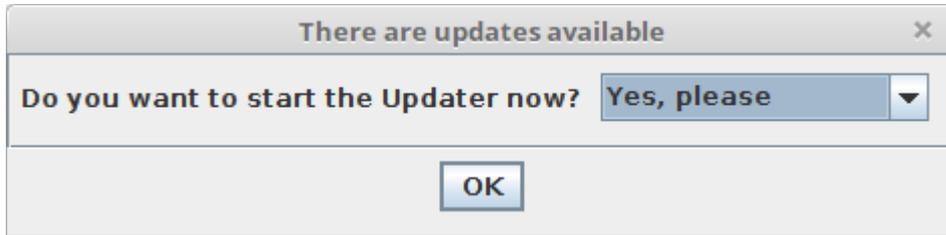


A second box will show all files that will be updated, simply confirm by clicking "Apply changes"



The download will start and you will be asked to restart Fiji. Close and restart Fiji, you will be up-to-date !

# Goodies : CSV Collector

As our software in mainly use for scientific purposes we made a software to automatically collect main quantification results stored across CSV file.
Rather than manually collecting your data, save all your CSV file in a folder.

The open the CSV collector in Fiji's menu Plugin>Nuclear Medicine> CSV Collector
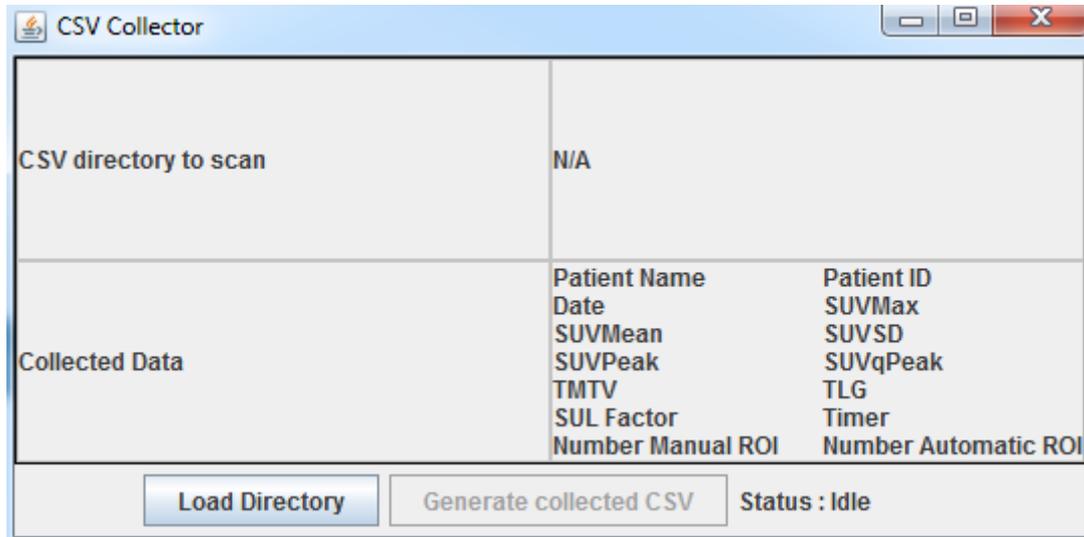


Click on "Load Directory" to define the folder where your CSVs are collected.
Then click "Generate Collected CSV" : All CSVs of this folder will be read and the main results (sum line of all ROIs) will be collected in a new CSV file (each patient in a new line each collected data in a separate column).