

Guidelines to identify and quantify Brain Microbleeds (BMBs) and mineral deposition (MD) in T2*-weighted images using Analyze 11.0

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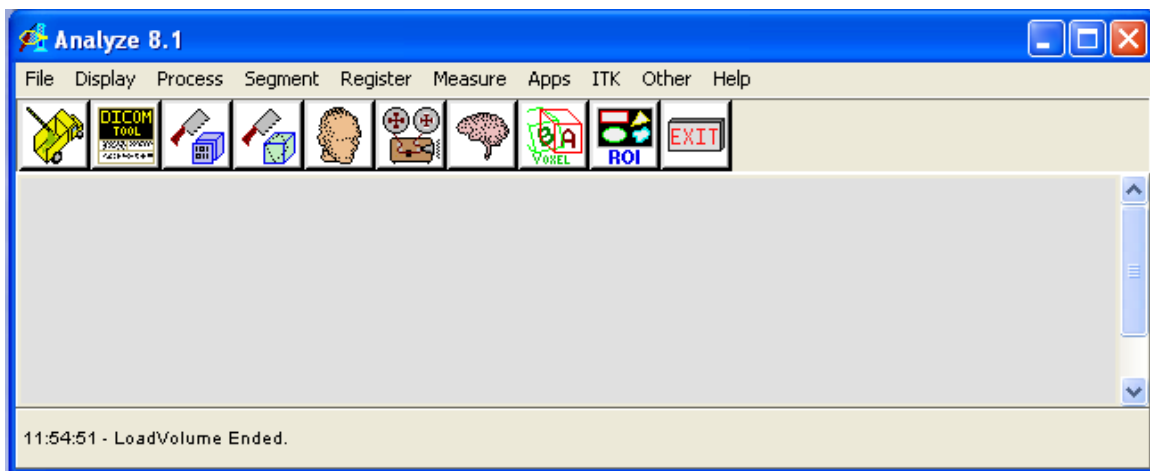
Tel. +44-131-465 9527

Created: 18.03.2009

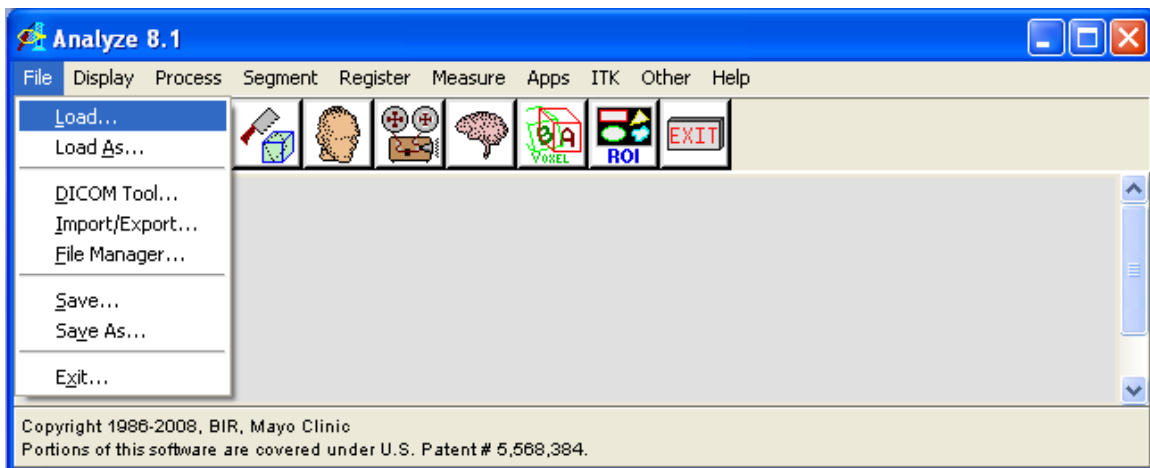
Updated: 18.03.2015

Loading files

1.- Open Analyze 11.0 doing a double click in the icon. The main window will appear. It looks similar as below (which actually corresponds to a former version: 8.1)



2.- Select **File | Load...** in the menu.



3.- Search for the T2*-weighted (gradient echo) file in Analyze format in the explorer's Load window that appear in the screen and click **Open**. The image volume selected will appear loaded and highlighted in the Analyze window.

Note: All processing menu options in Analyze need to have the images previously loaded and selected in the main window.

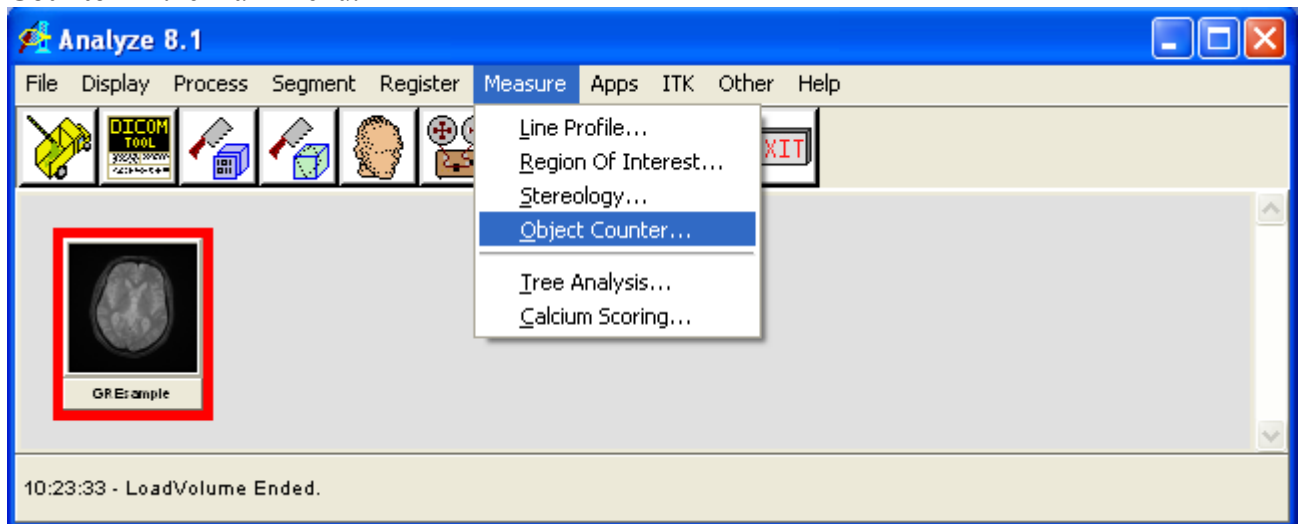
Defining Brain Microbleeds and Mineral Deposits

These guidelines consider brain microbleeds as small hypointense areas with less than 5 mm maximum diameter in the white matter, basal ganglia or at the cortico-subcortical junction on gradient echo T2*-weighted images (see: Cordonnier C, Salman RAS, Wardlaw J. Brain 2007; 130: 1988-2003, and Charidimou A, Krishnan A, Werring DJ, Jager HR. Neuroradiology 2013; 55: 655-674).

The mineral deposits are hypointense areas in gradient echo images that can be extensive or not, and are preferably localised in the basal ganglia, substantia nigra, brainstem, or in the cortex. These lately mentioned are known as meningeal siderosis. Also can be residuals of a former stroke.


Loading the volume in the Object Counter

1.- Once the image volume is selected showing a red frame, select **Measure | Object Counter** in the main menu.



The Object Counter module will open showing the image volume loaded. This module allows a user to count the number of objects that occur on each slice of a loaded data set. We will count the BMBs and MDs as defined in the section above.



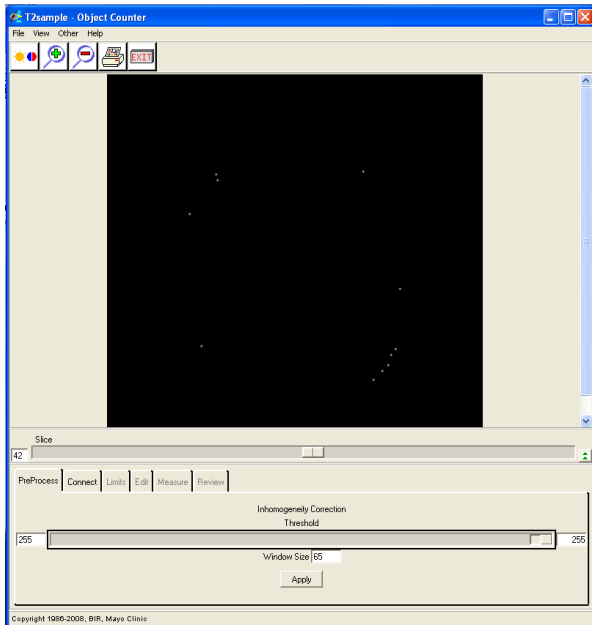
2.- Click on  button for increasing the size of the image and navigate through the volume using the slicer until you find the slice that shows BMBs or, if the volume contains areas with meningeal siderosis or other type of hemosiderin deposits, select the slice where the gray level to identify the areas selected is higher compared to the rest.

3.- Select the tab **PreProcess** in the lower half of the Object Counter window.

Pre-processing the image

This stage does the Inhomogeneity Correction to minimize the effect of intensity falloff near the edges of the images using a filter.

1.- Set the Threshold to maximum



2.- Click the **Apply** button

3.- Select the **Connect** tab

Preparing the settings for identifying BMBs and MD

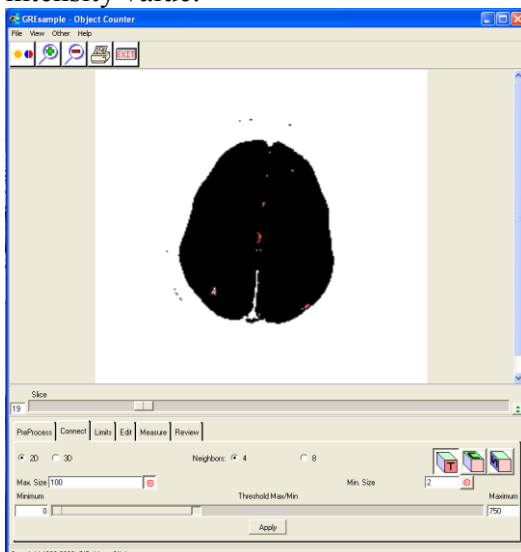
1.- In the Connect tab, select **2D**

2.- In **Neighbors**: select **4**

3.- Focus on the BMBs or MDs areas that you visually detected in the slice selected and move the threshold bar until they appear in the binary image.

The **Threshold Max/Min** slicer by default covers only the **hyperintense** areas. It is important to remember that here we are counting the **hypointense** areas.

Adjust the bar to cover only thresholds starting from 0 to less than half of the maximum intensity value.



4.- If the volume only has microbleeds: In **Max. Size** select **approximately 15** (15 pixels) and in **Min. Size** select **3** (3 pixels).

If the volume has hemosiderin deposits: Click the **Interactive Max Size** button and move the cursor onto the image. While holding down the left mouse button draw an ellipse that represents the size of the largest object (area) to be counted. If the *Ctrl* button is held down during the sizing process, the ellipse is forced to be a circle. For the minimum size, 3 pixels will be a good estimate.

5.- Click on the **Apply** button

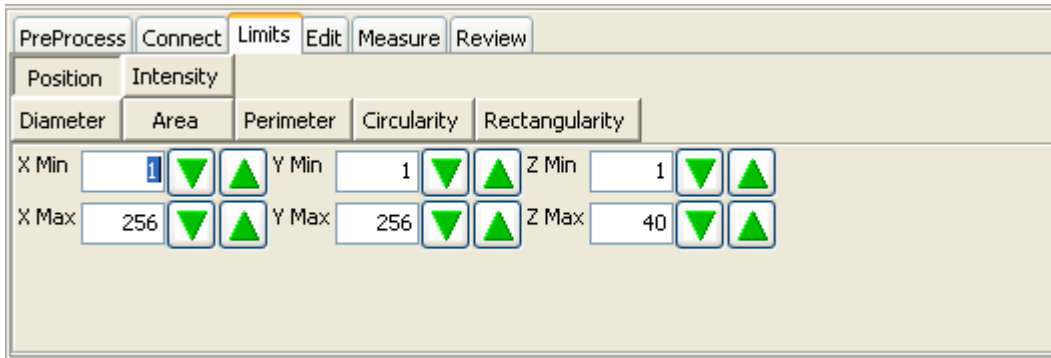
6.- If some of the hypointense areas that you visually determined that are BMBs or MDs do not appear selected, repeat from step 3 increasing the maximum threshold.



Moving the slice bar, all the hypointensities below the selected maximum threshold that have an area between 3 and 100 pixels (for the sample shown) can be seen highlighted and enumerated in all the slices throughout the volume, but all of them are not BMBs or MDs. It is necessary, now to remove those that are not. Limits can be set up pressing the tab **Limits** (see Object Counter tutorial in the Analyze help), but we use the default settings.

Limiting the number of slices for avoiding additional editing

Click on the tab **Limits**. A panel like the one represented below will appear. Clicking on the arrows that correspond to the Z Min and Z Max will limit the number of slices. Be sure to do this step before you edit the BMBs and MDs. Otherwise you will lose your edits.



Editing the BMBs and MDs

1.- Click on the tab **Edit**. 4 buttons appear. Clicking on each of them brings the functionality of each of them at the bottom



2.- The button  appears selected. Clicking on the false positives on each slice, it deletes them. If one is deleted by mistake, clicking over it will recover the selection.

If there are features considered MDs or BMBs that are not highlighted, press the button




and trace the boundary around the area. Zoom In and Out the image with  and



buttons respectively.



For oval tracings, use button .

It is advisable to have a reference window opened with the correspondent T1-weighted image to discern the mineralised areas, principally in the basal ganglia, from the areas where only hemosiderin is present. Other minerals, i.e. calcium, when associated to hemosiderin appear hypointense in T1-weighted images.

Obtaining the final report

1.- Select tab **Measure**

2.- Click on the parameters that will be included in the final report and press **Log Measurements** button. A window with the final report (summarised and/or detailed) like the one displayed below appears. Right-click when the mouse is over this window to save it.

Saving the Segmented Volume

1. Click on File > Save Segmented Volume
2. Select Analyze Workspace option + Name: Segmented
3. Save

In the Analyze Workspace:

1. Click on Segmented image
2. File > Save As
3. Change the format to: OBJMAP
4. Check directory location is correct
5. Save

Checking the Object Map

In the Analyze main workspace:



Select **Original** image and Click on the **ROI** button . Once the ROI window appears, in the menu, do:

1. File
2. Load Object Map
3. Select Segmented Map from previous step

In the ROI menu: click on View > Objects. Each microbleed or MD is assigned a different object by the previous tool. We need to combine them in one. For this, do the following: in the 'Objects' dialog:

1. Reassign Objects
2. Select Objects 2 – 10(or highest number) and change all to object 2
3. Rename Object 2 as 'Microbleeds' or 'MDs'

Edit the object map to include any missed microbleeds or MDs.

Remember to define the new object as microbleeds (or MDs) and make it part of the 'existing' object.

Save Binary > Select correct file > Save

***MUST SAVE NEW OBJECT MAP*:**

1. File > Save object map
2. Replace existing object map