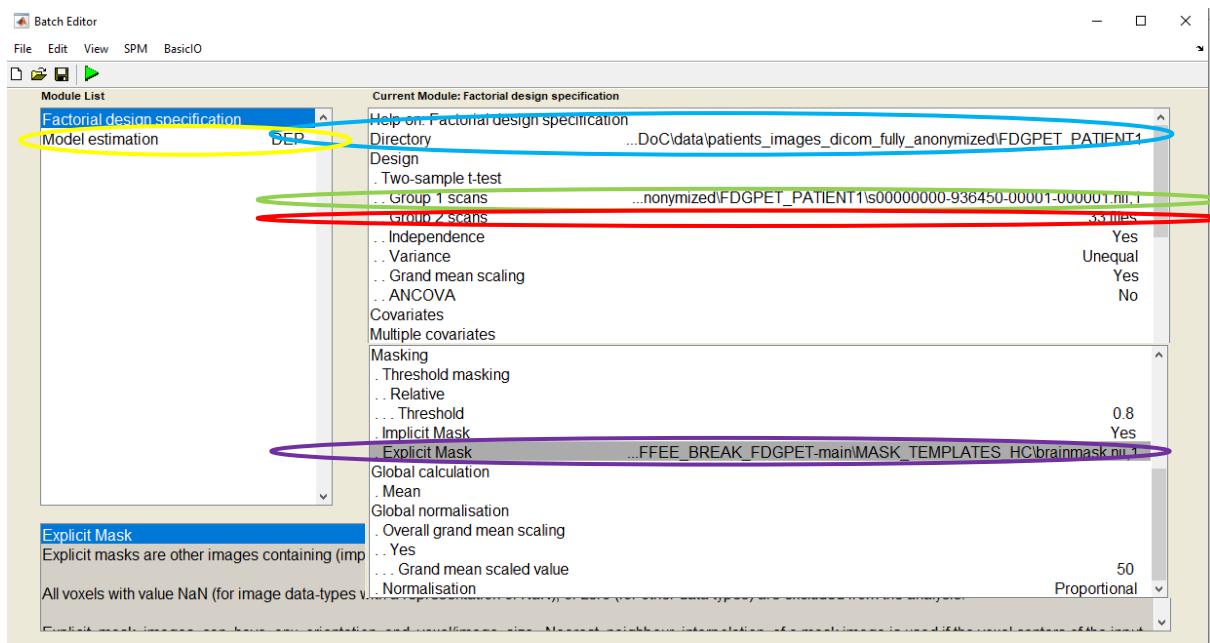


# SPM maps of relatively hypometabolism and relatively preserved metabolism based on FDG-PET images

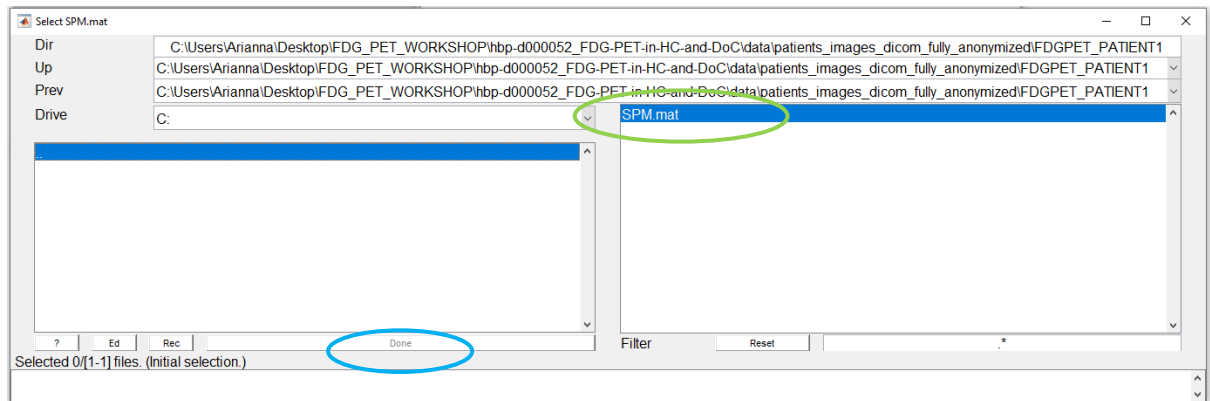
The software used in this procedure are Matlab and SPM 12 (make sure you know where the images and other batches are in the computer).

- 1) In the Menu window, click on “batch”. Open the “stat batch” (same procedure than before). Change the **directory** to the folder of the patient (same procedure than before). Change the **Group 1 scan** (use the **sws image** of your patient), and check that the **group 2** includes the sws image of the 33 healthy controls (path of your own computer). If needed, change the path of the explicit mask (**brain mask**, lower in the batch). Check also in the second module (left panel) that the model **estimation depends** on the first module (as in the “normalise & smooth” batch). Save the batch! Click on run.

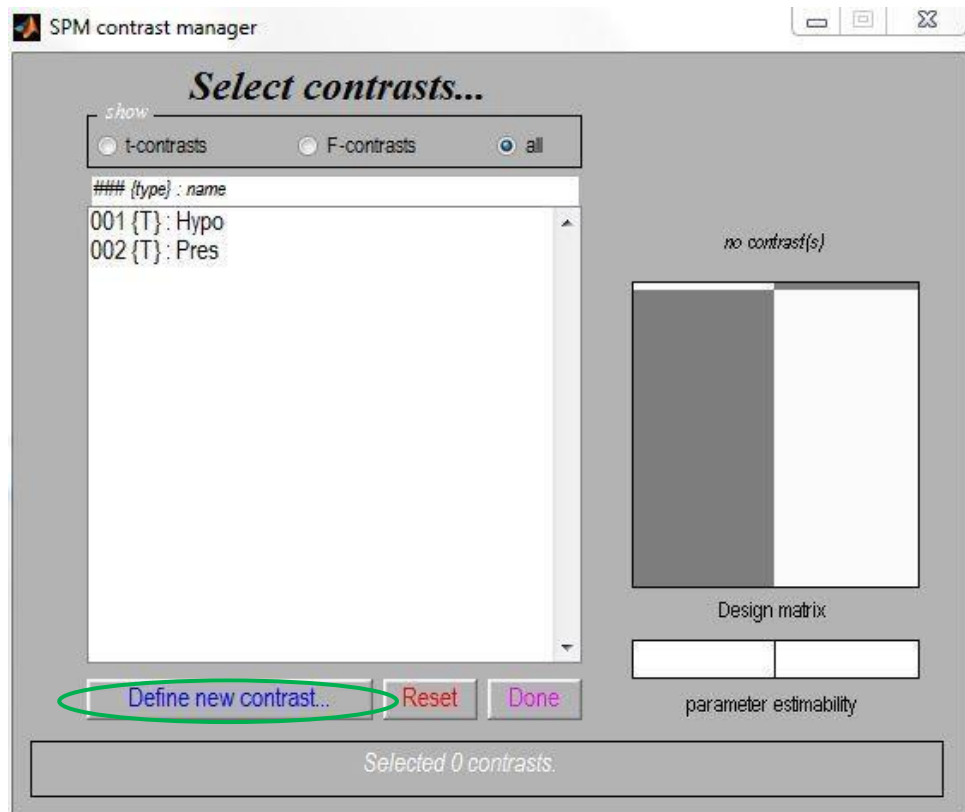


This tutorial was curated by Arianna Sala for the CGS's [18F]FDG-PET workshop, based on materials prepared by Sarah Wannez. Please contact [arianna.sala@uliege.be](mailto:arianna.sala@uliege.be) for questions and comments.

2) When Matlab has run, click on “Results” in the Menu window. Go as previously shown in the CTAC folder of your patient. Choose the SPM that was just created, it will make “done” available. Click on “done”.

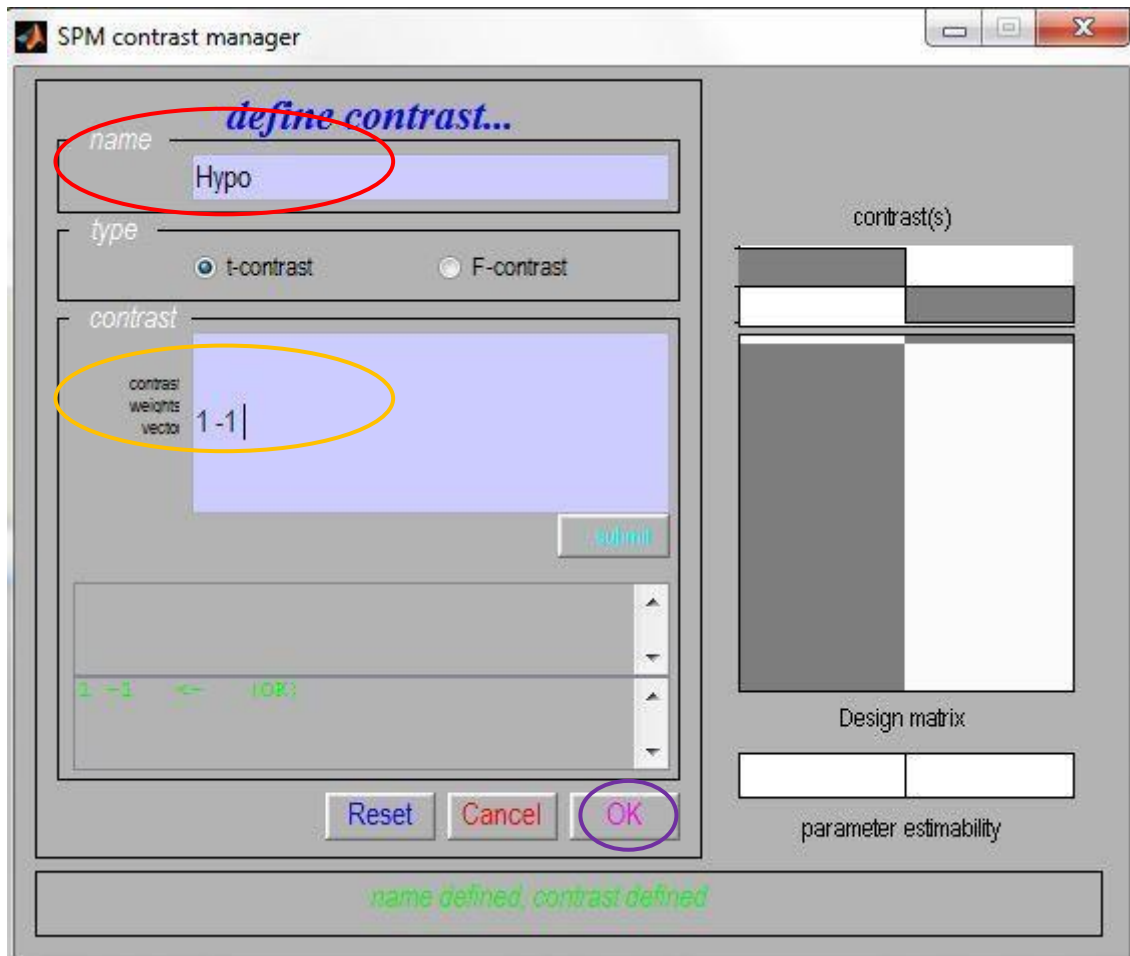


3) In the new window, specify the contrasts by clicking on “Define new contrast”.



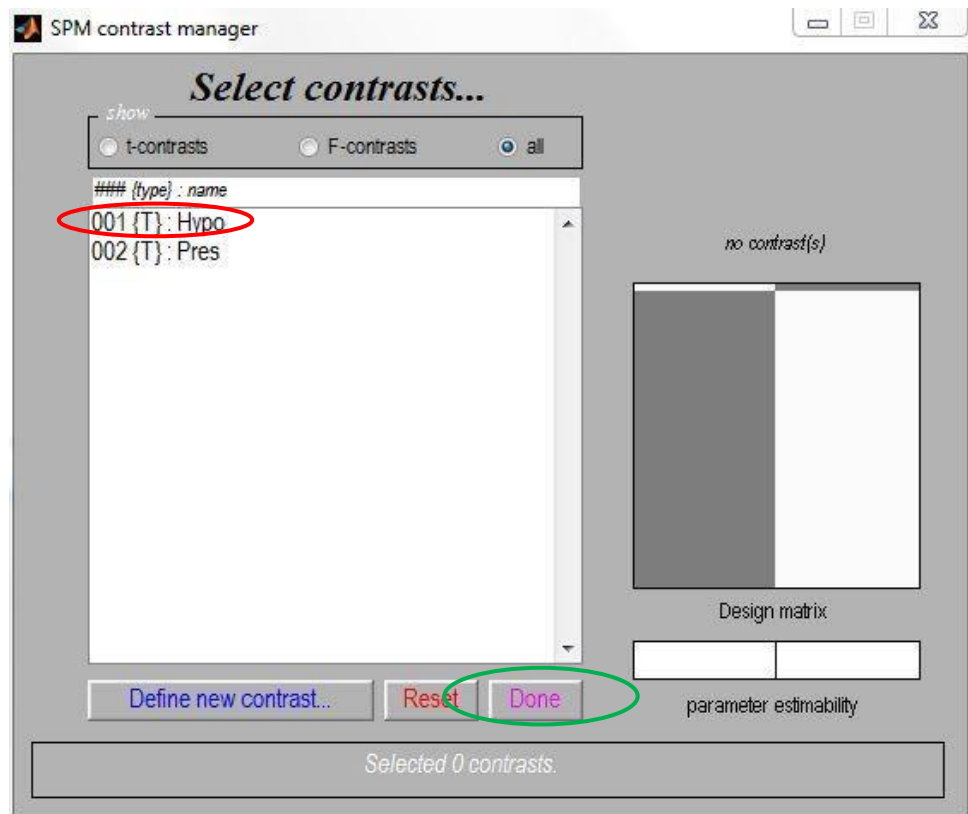
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4) Name the first one "HYPO" and specify "-1 1" (be careful to leave a space between both numbers), and then click on OK. Do the same for "PRES" with "1 -1" as a contrast

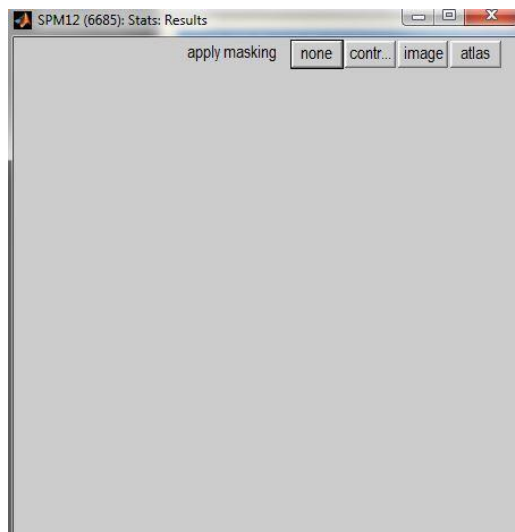


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5) When your two contrasts are prepared, click on "HYPO" and then "Done" to analyse the hypometabolic areas (what is less active than healthy controls)

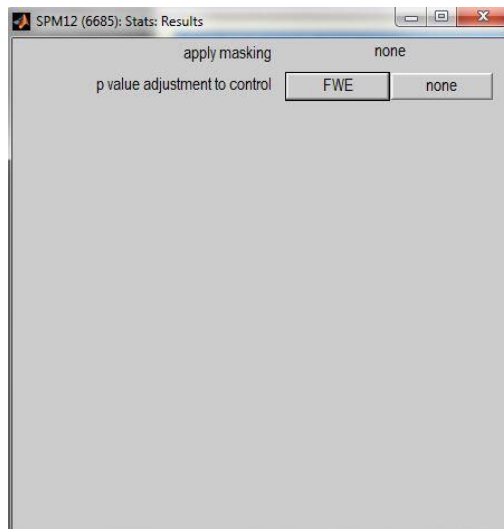


6) Choose none for the masking.

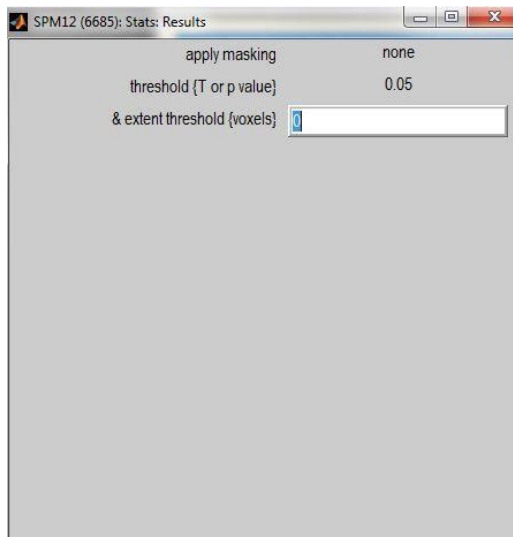


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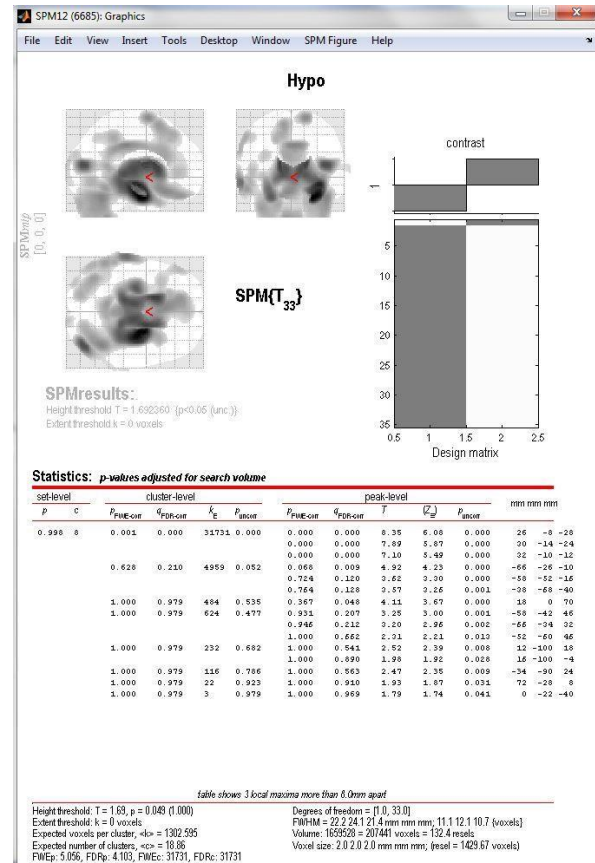
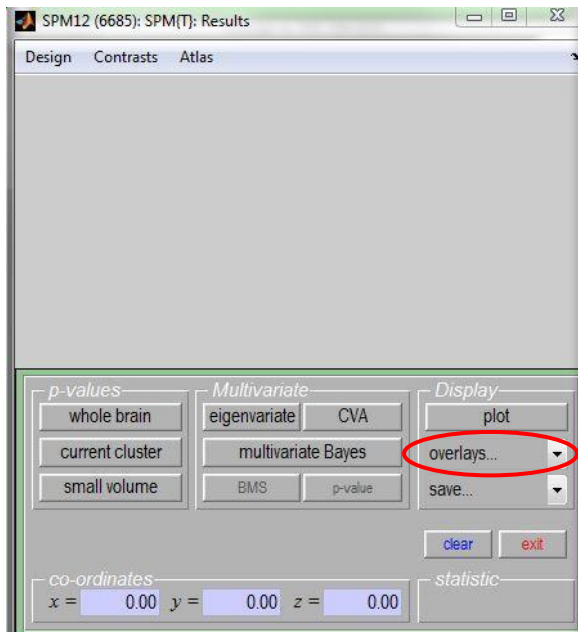
- 7) Choose none for the p adjustment. When the p adjustment ask for a value, enter 0.05 and then “enter”.



- 8) The extend threshold should be 0, then “enter”.

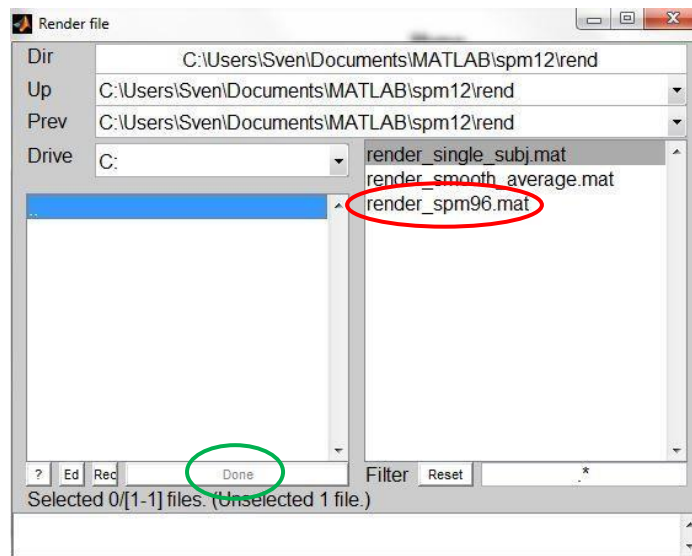


- 9) The results window opens, with the graphic results. To get the SPM figure, click on **“Overlays”** and then “render” (in the drop-down list).

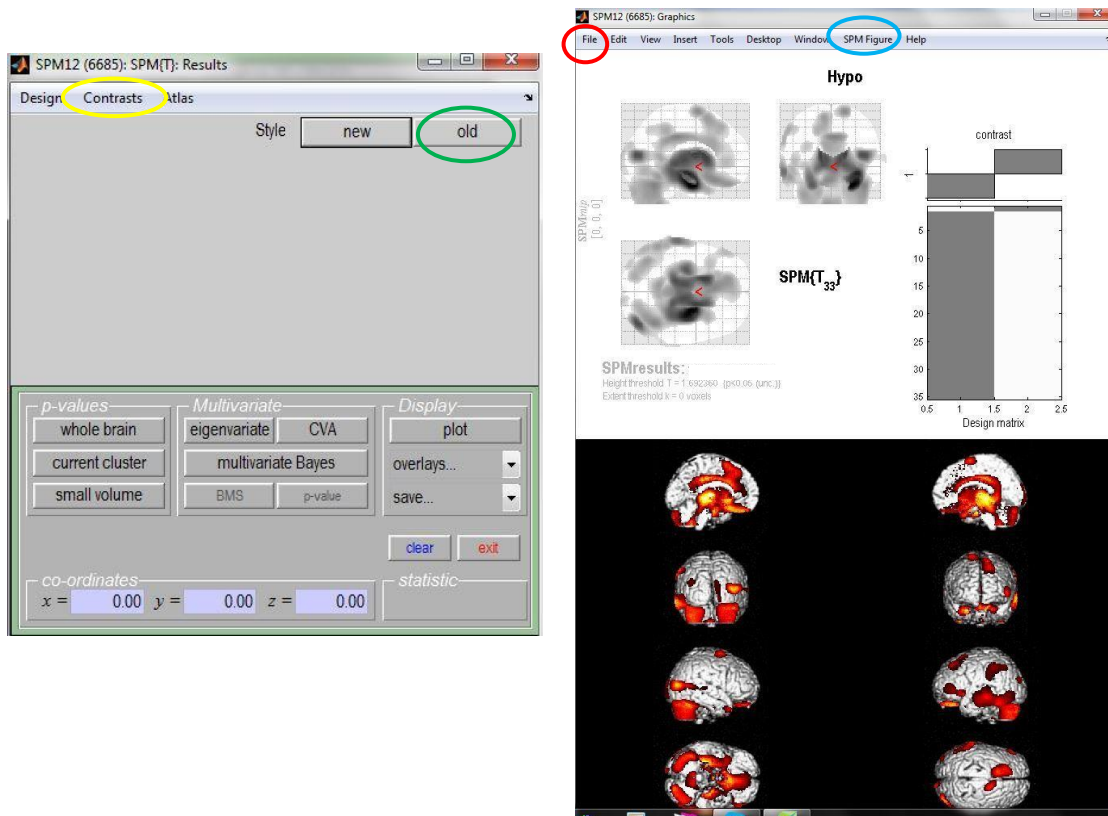


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10) Click on the "render\_spm96" file in the MATLAB\SPM12\rend folder (follow previously explained method to reach this folder). "Done" is then available: click on it.



11) Specify that you need the old style, and the SPM render will appear in the graph results (the new style does not provide median view of the brain but can also be OK if you do not need it).



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- 12) To change the color to blue, you can use "chgcOLOR" in the command window, or change it through "SPM figure – colours – colormap – gray cool" in the graph window.
- 13) Save the results in the graph window : file -> save as (be careful to save as JPG and not mat!! Otherwise not readable out of Matlab).
- 14) To do the preserved areas (as compared to controls), you can go to "contrasts" in the results window, and then click on "change contrast" and then select "pres". Then the procedure is the same (from point 9), except that you do not need to change the color (red is already good for preserved).