Searchlight analyses with The Decoding Toolbox.

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What?

- With these scripts you can do a searchlight analyses (both decoding as correlational) on your **own computer**, so no need to bother Nicky anymore or to try to find out yourself how the High Computer Cluster in Heverlee works (and trust me, that's an huge advantage for your mental health).

- The scripts are adapted for our specific use in the lab from a toolbox: The Decoding Toolbox (https://sites.google.com/site/tdtdecodingtoolbox/). So, if you use this scripts you **SHOULD REFERENCE** to the following article: http://journal.frontiersin.org/article/10.3389/fninf.2014.00088/full. Please do this, since the people who wrote this toolbox have invested couple of years in making it fast and efficient. And it is only fair to credit the people of whom you are using scripts.

- If you have any questions related to these scripts, you can contact me, but normally with this quick tutorial and the vastly commented scripts of the decoding toolbox (TDT), you should be able to get it working for you.

- Run the scripts in the following order:
  - (1) `SLA_analyses.m;`
  - (2) `combine_pairwise_comparisons.m;`
  - (3) `smooth_and_2nd_level.m`

Step 1. Prepare everything for SLA

- There are different variables that you should define before you can run the SLA. This is because I am not in your head and do not know what you want to do, how your directories look like, how your data is made, etc. There is only so much that I can automate. But I promise, I kept the amount of variables for you to adjust to a minimum. To get your script working correctly, read the instructions below and the comments in the script.

- Open `SLA_analyses.m`:
  - Locate the section "Variables for you to adjust" (normally the first section after the opening comments).
  - Give the pathways to your directories:
    - `dirs.ScriptDir`: the folder containing the folders "LBP Scripts" and "TDT Toolbox"
    - `dirs.DataDir`: the folder containing the folders of every subject with the beta images. So if you open this Data Folder, you should directly see the subject folders!
    - `dirs.ResultDir`: the folder where you want to write your SLA results to. If this folder does not exist yet, it will be made for you.
  - Select the searchlight variables:
    - `SLAvars.Analysis`: choose 'correlation' or 'decoding' (exactly this formulation)
    - `SLAvars.Radius_Unit`: choose 'voxels' or 'mm' (exactly this formulation)
    - `SLAvars.Radius_Size`: choose how many voxels or how many mm you want to include surrounding the center voxel
    - `SLAvars.Mask_Use`: choose whether you want to use the 'Grey Matter' mask or the 'Whole Brain' (exactly this formulation)

- Once you run the script, the following things are asked of you with means of GUI's:
  - *Select all the subjects you which to include in SLA*: Your data-folder may contain certain subjects or folders you wish not to include in your SLA, so with this GUI you can select all **the subjects** you **wish to include** (try the buttons ctrl and shift to help you select).

  - *Select the SPM model you wish to do the SLA on*: it might be the case that within your subject folder you have different models, such as a localizer, different experimental runs, … With this GUI you can select **which model** you want to do the SLA on. If you have not any different folders with the different models in a subject folder, this GUI will not be executed.

  - *Select the pairwise comparisons*: just as with a regular MVPA you correlate or decode each time two conditions. Select **which pairwise comparisons you wish to do**.
    - You can opt to load a previously made collection of pairwise comparisons (if it exists).
    - If you want to make a new one, you have two options:
      - All pairwise comparisons: select the conditions for which you want all the pairwise comparisons. For correlation searchlight, correlation within a condition (aka the diagonal) is also included.
      - Select out which pairwise comparisons: this is done couple per couple. So, for the first pairwise comparison, select the first condition, then select the second condition; and then indicate if you wish to include another pairwise comparison. Keep doing this until you included all pairwise comparisons that you want to do.

- Below the different things done in the `SLA_analyses.m` script are quickly explained. This way you know in general lines what is being done when you run the script.

A. Do preparations for the SLA

- This script works with couple of GUI's so that it is easier for you to select what you want to do on what (model) and who (which subjects).

- In `do_SLA_preps.m` the following things are done to make the general script working:
    - Check if the directories are all ending with a file separator.
    - The scriptdir is added to the pathway of matlab
    - Make the resultsdir if it does not exist yet
    - Load in default parameters for the SLA and set the type of analyses 'correlational' or 'decoding'
    - Get subject ID's
    - Get the model on which you want to do the SLA
    - Select which pairwise comparisons you want to run during the SLA: either load them from a previously made pairwise comparisons mat-file or make them new. They are saved by a name that you choose.

B. Coregister Grey Matter Mask to your beta-dimension.

- To reduce the computation time of the searchlight analyses (SLA), the SLA are done on only grey matter. If have included the easy option in the scripts to do it on the whole volume, but bear in mind that computation time will increase by factor 4. Also, I have compared SLA results from whole volume and only grey matter, and they do not differ. So, save yourself some time and run the SLA on only grey matter.

- How is the grey matter mask made? It is a nifti-image of the grey matter mask from the WFU PickAtlas toolbox (http://fmri.wfubmc.edu/software/pickatlas). Again, please also refer to this toolbox if you do the SLA on grey matter. References are mentioned on the site.

- Since the mask is a standard mask, the volume does not match the volume of your beta-images. To solve this, the script `coregister_mask_beta.m` has been made. This script runs for SPM8 or SPM12. It will automatically detect which version you have installed on your computer, so no need to worry about that.

C. Run the SLA

- In the `run_SLA.m` script, a searchlight is done for every subject, and every pairwise comparison and saved to the result directory.

Step 2. Do the SLA

- Now that you have adjusted everything you need to adjust in `SLA_analyses.m` and you understand what is happening there, you can press the "run" button for the `SLA.analyses.m` script. And now the waiting game has started…

Step 3. Do your thing with the pairwise comparisons

- With the SLA_analyses you have one volume image per pairwise comparison. However, that is not always what you want in the end:
  - For example, I have four Arabic digits that I do a pairwise comparison on. For example, symbol 2 versus symbol 4; symbol 2 vs symbol 6; etc. In that way I end up with six pairwise comparisons per subject. I would like to average across those six pairwise comparisons and end up with one volume image per subject.
  - Another example, for correlation searchlight you might want to not only average across certain conditions, but also subtract the diagonal. Or even, you might want to correlate your correlation matrix per subject with certain models.

- The script `combine_pairwise_comparisons.m` will help you to do whatever you want with the pairwise comparisons coming from the SLA. Below, I explain what you need to adjust in the script or what you need to do while running the script.

- Open `combine_pairwise_comparisons.m` script:
  - Locate the section "Variables for you to adjust" (normally the first section after the opening comments).
  - Give the pathways to your directories:
    - `dirs.ScriptDir`: the folder containing the folders "LBP Scripts" and "TDT Toolbox"
    - `dirs.SLAResultDir`: the folder where you have written all the SLA results to. If you open this folder, you should see a folder per subject. This is the pathway you need to refer to for this variable.
    - `dirs.MyThingResultDir`: The directory where you want to write the results to from this script.
  - Indicate which analyses you have done:
    - `SLAvars.Analysis`: choose 'correlation' or 'decoding' (exactly this formulation)

- Below, I'll discuss how you can make the measures you wish to get out of the SLA. It depends on what type of SLA you have done: decoding or correlation.

- After you have selected and made everything you wish to do on the SLA results, you can save "your thing" to the `dirs.MyThingResultDir` directory, so that you don't have to make it again. So, before you can make any new measures, you will be asked if you want to load a previous "measures" file. If yes, you can navigate through a GUI to the file and also choose to add an extra measure or not.

A. Prepare your measures

This is the script `combine_pc_prep.m`.

For decoding SLA

- When you have done decoding, there are two possibilities added in the scripts:
  - either you wish to average across all pairwise comparisons that you have done in the SLA;
  - or you wish to make couple of "averages" yourself, for example an average across 6 conditions ("symbols" or "faces") and an average across 6 other conditions ("dots" or "objects").
  - or you want to do both…

- If you have selected decoding for `SLAvars.Analysis`, then you'll get a GUI where you can choose between "I wish to select out which pairwise comparisons should be averaged" or "Average across all pairwise comparisons". Select one or both options.

- When you have opted for "*I wish to select out which pairwise comparisons should be averaged*", then a sequence of several boxes will help you to make one average at a time. For every average you have to give in a name (for example "faces" or "objects"). After the average has been added, you can say whether or not you wish to include another average. Once you have finished, you'll get a message box showing you all the averages you have included.

- When you have opted for "*average across all pairwise comparisons*", you don't have to do anything anymore. The average will be automatically included, and if successful included you'll get a message.

- When you have selected both options, you'll first be making your own averages and then the average across all pairwise comparisons will be created.

For correlation SLA
- If you have done correlation SLA, I have included three possible things you could do with the results coming out of the SLA:
    - Subtract all the non-diagonal pairwise comparisons from all diagonal pairwise comparisons;
    - Make a couple of 'diagonal minus non-diagonal' yourself, for example all same faces minus all different faces; all same objects minus different objects; etc.
    - Do a RSA: correlate your correlation matrix with a model or couple of models.

- If you have selected correlation for `SLAvars.Analysis`, then you'll get a GUI where you can choose between "Subtract all non-diagonal from all diagonal" , "Subtract a couple non-diagonal from diagonal". Select one or both options, or "Calculate the correlation with a model (RSA)". You can select one, two or three options. If you have selected two or three options, the sequence in which they will be done is the sequence that is mentioned in this paragraph.

- When you have opted for "*Subtract all non-diagonal from all diagonal*", you don't have to do anything anymore. The measure will be automatically included, and if successful included you'll get a message.

- If you have chosen for "*Subtract a couple non-diagonal from diagonal*", a GUI will pop up which will ask you first to select which diagonal comparison you wish to average across (f.e. select all pairwise comparisons between the same faces). Second, you will be asked to select all non-diagonal pairwise comparisons of which you want to subtract this average diagonal comparison (f.e. select all pairwise comparisons between different faces). Third, give a name to this measure. Finally, indicate whether or not you wish to include another comparison between certain diagonal and certain non-diagonal conditions. Once you have finished, you'll get a window showing you all the measures you have included.

- When you selected "*Calculate the correlation with a model (RSA)*", you'll get a message saying that in the next window you have to select the mat-file that contains **all** the models with which you want to do the analysis. When you'll proceed you'll get a GUI where you can navigate to that mat-file. The **models-mat file should contain one variable "models"** with 3 dimensions (f.e. if you have 8 conditions and 4 models, it should be 8 x 8 x 4; so four 8 x 8 matrices). You will also have to say whether you want to work with dissimilarities or similarities. And through a GUI indicate the sequence of your conditions: what column in the model matrix refers to what condition. For every condition a window will pop up and you will have to give in the number of the column in the model matrix that refers to this condition.

- Remark. You will also get the question whether or not you wish to transform the correlations to a Fisher correlation or not.

B. Analyze the SLA results

- This is the second step in the script `combine_pairwise_comparisons.m` where the measures that you have created in the former step, will be calculated and saved per subject to an image file.

- For this step you do not have to do anything. This will run without any interference from you when you run the `combine_pairwise_comparisons.m` script.

Step 4. Smooth images and do second-level

- I know, I know, these are unnecessary scripts because you can "click" yourself in SPM (a monkey could do it). But I am a strong believer in avoiding any possible click in SPM, which reduces many frustrations on my side. So, if you want to be lazy like me, you can just run the script `smooth_and_2nd_level.m` and the smoothing and second level analyses will be done for you. Of course, you'll need to give me a bit of information so that the scripts run optimally. The variables that you need to adjust are explained below.

- What to do, what to do, to be lazy:
  - Open the `smooth_and_2nd_level.m` script
  - Adjust the dir variable:
    - `dirs.ScriptDir`: the folder containing the folders "LBP Scripts" and "TDT Toolbox"
    - `dirs.MyThingResultDir`: a folder containing all the subjects images files of one certain measure that you have calculated.
    - `dirs.Results2ndLevel`: The directory where you want to write the results to
  - Smoothing:
    - Give in the amount of smoothing that you would like to have.

- That's it. Run the batch.

- **Remark**. If you do "check results", you have to overlay the results with the grey matter mask.