Portfolio assignment 1: Regression

Experimental methods II - 2019; Mikkel Wallentin, Isa Lykke Hansen

February 1, 2019

##Sleep deprivation excercise In this excercise we are going to look at response time as a function of days of sleep deprivation (see details below).

##Deadline February 12, 2019.

##Reporting: Use r_markdown in RStudio for your report. Submit report as a single pdf-file. Include commented code and figures all the way from data import.

Mark the beginning of each answer to a question with its relevant number/letter.

Students who worked with their study group in class may submit the same assignment report. Make sure to add your group number and note all the names of the people who contributed to the assignment in the beginning of the report.

Submit report to Blackboard.

##Data Find the data entitled "sleepstudy.csv" in Blackboard.

```
##load data, e.g.
#setwd("~/your_data_folder/")
#sleepstudy<-read.csv("sleepstudy.csv")
#str(sleepstudy)
```

##Tasks ####1. Plot the data: 1.a: Get the data from one participant, e.g. using subset(). Make a linear regression for reaction time as a function of days of sleep deprivation, e.g. using lm(). Report the F-statistics.

1.b: How many degrees of freedom does the relevant F-distribution have?

1.c: At which F-value does a regression with this distribution become statistically significant ($p<0.05$)?

1.d: Make a plot of the F-distribution.

####2. For all participant in the experiment: 2.a: Find the coefficients (slope and intercept) for the regression for reaction time as a function of days of sleep deprivation (a hint for the solution: use group_by() in tidyverse or this function here: https://stat.ethz.ch/R-manual/R-devel/library/nlme/html/lmList.html)

2.b: Combine both scatter plot and regression line in the same figure. You may also include all participants in one plot.

2.c: Collect and report the inferential statistics for each participant in a table using t-statistics, including t-value, df and p-value.

2.d: How many individual participants display a statistically significant effect of sleep deprivation (p-values uncorrected for mulitple comparisons)?

####3. Across participants: 3.a: Use the slopes you found for each participant in exercise 2 as a new dataset. Test the hypothesis that the slopes are larger than zero against the null-hypothesis that the slopes are zero (i.e. no differences in response time exist as a function of time).

3.b: Justify your use of test statistics.

3.c: Report inferential statistics.

3.d: Make a plot with the mean reaction time and standard errror bars for each day across participants and plot the averaged regression line in the same figure.

####Voluntory bonus task Add 10% white/uniform noise to the Reaction data. What happens to the single participant coefficients statistics and to the group effects?

##Study Details

The data are from a study by Belenky et al. (2003), for the sleep-deprived group and for the first 10 days of the study, up to the recovery period.

##Reference Gregory Belenky, Nancy J. Wesensten, David R. Thorne, Maria L. Thomas, Helen C. Sing, Daniel P. Redmond, Michael B. Russo and Thomas J. Balkin (2003) Patterns of performance degradation and restoration during sleep restriction and subsequent recovery: a sleep dose-response study. Journal of Sleep Research 12, 1???12.

##Study abstract Daytime performance changes were examined during chronic sleep restriction or augmentation and following subsequent recovery sleep. Sixty-six normal volunteers spent either 3 (n = 18), 5 (n= 16), 7 (n = 16), or 9 h (n = 16) daily time in bed (TIB) for 7 days (restriction/augmentation) followed by 3 days with 8 h daily TIB (recovery). In the 3-h group, speed (mean and fastest 10% of responses) on the psychomotor vigilance task (PVT) declined, and PVT lapses (reaction times greater than 500 ms) increased steadily across the 7 days of sleep restriction. In the 7- and 5-h groups speed initially declined, then appeared to stabilize at a reduced level; lapses were increased only in the 5-h group. In the 9-h group, speed and lapses remained at baseline levels. During recovery, PVT speed in the 7- and 5-h groups (and lapses in the 5-h group) remained at the stable, but reduced levels seen during the last days of the experimental phase, with no evidence of recovery. Speed and lapses in the 3-h group recovered rapidly following the first night of recovery sleep; however, recovery was incomplete with speed and lapses stabilizing at a level comparable with the 7- and 5-h groups. Performance in the 9-h group remained at baseline levels during the recovery phase. These results suggest that the brain adapts to chronic sleep restriction. In mild to moderate sleep restriction this adaptation is sufficient to stabilize performance, although at a reduced level. These adaptive changes are hypothesized to restrict brain operational capacity and to persist for several days after normal sleep duration is restored, delaying recovery.

Portfolio assignment 2: Vectors and matrices

Experimental methods II - 2019; Mikkel Wallentin, Isa Lykke Hansen

February 9, 2019

Matrix excercise

In this excercise we are going to look at response time as a function of days of sleep deprivation (see details below).

Deadline

February 20, 2019.

Reporting:

Use r_markdown in RStudio for your report. Submit report as a single pdf-file. Include commented code and figures all the way from data import.

Mark the beginning of each answer to a question with its relevant number/letter.

Students who worked with their study group in class may submit the same assignment report. Make sure to note all the names of people who contributed to the assignment in the beginning of the report.

Submit report to Blackboard.

Tasks

1. Linear regression

Participant 372 from the sleepstudy has the following data:

```
Reaction372<-c(269.41, 273.47, 297.60, 310.63, 287.17, 329.61, 334.48, 343.22, 369.14, 364.12)
Days372<-c(0,1,2,3,4,5,6,7,8,9)
```

1.a: Make a constant vector of the same length as the data, consisting of ones.

1.b: Report the inner product (aka dot product) of the days vector and the constant vector.

1.c: What does the dot product say about the possibility of finding an optimal linear regression?

1.d: Create a 10x2 matrix called X with the days vector and constant vector as columns and use the least squares method manually to find the optimal coefficients (i.e. slope and intercept) to reaction time.

1.e: Check result using lm(). Use the formula lm(Reaction372~0+X) - the zero removes the default constant.

1.f: Subtract the mean of Days372 from the Days372 vector. Replace the days vector with the new vector in X and redo the linnear regression. Did the coefficients change? (we will return to why this happened in a later class, but if you are curious, you can check this website out: https://www.theanalysisfactor.com/center-on-the-mean/)

1.g: Make a scatter plot with the mean-centered days covariate against response time and add the best fitted line.

2. Images and matrices

Load the data using something like:

```
#library(jpeg)
##Load data
#matrix<-readJPEG('portfolio_assignment2_matrices_data.jpg', native = FALSE)
```

2.a: report how many rows and how many columns the matrix has. What are the maximun, minimum and mean pixel values?

2.b: Make an image of the loaded matrix. Be sure to rotate the image into the correct orientation. The functions needed are found the in lecture slides. Furthermore, grey scale the picture with gray(1:100/100) - this will color values near 0 black/dark and values near 1 white/light.

2.c: Draw an image with the same dimensions as that from 2.b. But this image should be completely black (hint: use zeros).

2.d: Draw a white hat on the image from 2.b (hint: use ones).

2.e: Make an image which has the same dimensions as 2.b., and which only contains the parts which was hidden behind the hat in 2.d. The rest should be black.

3. Brains and matrices

Load the brain data using something like:

```
#library(jpeg)
##Load data
#brain<-readJPEG('portfolio_assignment2_matrices_data2.jpg', native = FALSE)
```

3.a: Make an image of the brain.

3.b: 3.b: We will attempt to find the interesting areas of this brain image, e.g. only areas with gray matter. To do this we will create two masks, one that filters all darker areas away, and one that filters the white matter away. The masks will work by having zeros at the areas we want to fliter away, and ones at the interesting areas. Thus, the mask will have the intended effect if we do element-wise mutiplication it with the brain matrix. Start by making an image which is white (have ones) where the pixel values of the brain image are larger than the mean value of the whole image. Let the image be black (have zeros) everywhere else. Call this matrix mask1.

3.c: Make an image which is white where the pixel values of the brain image are smaller than 2.5 times the mean value of the whole image. Call this matrix mask2

3.d: Convert mask1 and mask2 into one mask with ones where the two masks overlap and zeros everywhere else. What type mathematical procedure can be used to produce this?

3.e. Use the combined mask on the brain image to give you an image with only the image values where the mask has ones, and zeros everywhere else. Did we successfully limit our image to only contain gray matter?

3.e: Count the number of pixels in the combined mask.

4. Two equations with two unknowns

Two linear equations with two unknowns can be solved using matrix inversion. For example, see here: https://www.mathsisfun.com/algebra/matrix-inverse.html

4.a: In the friday bar, men were three times as likely as women to buy beer. A total of 116 beers were sold. Women were twice as likely as men to buy wine. 92 glasses of wine were sold. How many men and women attended the Friday bar?

Portfolio assignment 3: fMRI Regression

Mikkel Wallentin, Isa Lykke Hansen

15 februar 2019

fMRI single voxel data excercise

In this excercise we are going to look at data from an unpublished fMRI experiment. 400 whole-brain EPI images were acquired for each participant, but in this assignment, we will analyse a time-series from a single voxel in auditory cortex (transverse temporal gyrus, MNI coordinate: [-46,-20,6], with all time-points converted into a vector). A total of 37 participants were scanned. They listened to two types of stories (fiction and factual). A model of the hemodynamic response to the different story types are included in a separate file. The task is to perform a regresion with these two different independent variables using different models and also adding an additional covariate.

Deadline

February 27, 2019.

Data

Load data and design as time-series:

```
##data
#fmri<-as.matrix(read.csv("aud_fmri_data37.csv", header=FALSE))
##making it a time-series
#fmri2<-ts(fmri)
##design
#fmrides<-as.matrix(read.csv("aud_fmri_design.csv", header=FALSE))
##making it a time-series
#fmrides2<-ts(fmrides)
```

Tasks

Initial figures

1. Make two figures:

1.a. A figure with lineplots of the data from all participants as a function of time in one figure. Note how much the baseline signal can vary between participants.

1.b. A figure lineplots with the model covariates.

Investigating model

2. How many stories did the participants listen to in each condition?

3.a. Are the two model covariates correlated?

3.b. Have the covariates been mean-centered?

4. Please report the percentage of shared variance in the two covariates.

Analyses

Single participant:

5. Pick one participant's data set.

Conduct 6 analyses using lm():

5.a. Fit the model as it is, including intercept.

5.b. Fit the model as it is, excluding intercept.

5.c. Fit only the 1st covariate as a model.

5.d. Fit only the 2nd covariate as a model.

The residuals represent the variance left when fitting a model. They are thus data that have been "cleaned" from the variance explained by the model. We can use those "cleaned" data to fit another model on. This is similar to using a type III sum of squares approach to your statistics.

5.e. Fit the 2nd covariate to the residuals from analysis 5.c., the 1st covariate only analysis

5.f. Fit the 1st covariate to the resistuals from 5.d., the 2nd covariate only analysis

5.g. Does the order in which the predictor variables are fitted to the data matter for the estimates? If it does, what can explain this?

Group level analyses

6. Fit the full model to each of the 37 participants' data and extract the coefficients for each participant. (hint: the full participant data frame can be set as outcome. Alternatively, you can change the data structure and use lmList from assignement 1).

6.a. Test the two individual hypotheses that the set of coefficient from each covariate is different from zero across the whole group (similar to assignment 1).

Make a contrast that investigates the difference between the two covariates, i.e. the two types of stories (hint: subtraction).

6.b. Test the hypothesis that the contrast is different from zero across participants.

6.c. Make a bar diagram including the mean effect of the two coefficents and the contrast, including error bars (indicating standard error of mean).

Adding a covariate

7.a. For each partipant, add a covariate that models the effect of time (hint: 1:400).

7.a. Does that improve the group results in term of higher t-values?

8. Make a bar diagram like the above, but display effects as percent signal change (hint: percent signal change is slope divided by intercept).

Reporting:

Use r_markdown in RStudio for your report. Submit report as a single pdf-file. Include commented code and figures all the way from data import.

Submit report to Blackboard.

Details

These fMRI data are from an unpublished experiment conducted in Aarhus at CFIN. 37 participants listened to two different kinds of stories of different length. The onsets and durations for each kind is modelled in the two design variables that take into account the hemodynamic response function. 400 fMRI volumes were acquired with at repetition time of 3.5 seconds.The data from each participants were gathered from the voxel with the MNI coordinates: [-46,-20,6] in the proximity of the left primary auditory cortex.

Portfolio assignment4 fMRI Preprocessing

Mikkel Wallentin, Isa Lykke Hansen

25 february 2019

fMRI preprocessing excercise

In this exercise we are going to prepare fMRI data for analysis and look at some of the output. The data is the same dataset as last week, although this week we will be looking at all the fMRI data from one participant (participant 1).

Deadline

March 6, 2019.

Data

The data can be found in a zip-file at blackboard entitled "fMRI_data_raw.zip". Note that this file contains 400 functional images (called f...nii) and 1 structural anatomical image (called s...nii).

Save the structural data to a separate file.

Tasks

1. Intitial alignment of data to standard stereotachtic space (MNI-space)

Attempt to position the anterior commissure in [0,0,0] of the first functional image using the Display function in SPM (See Gazzaniga p. 133 or thehumanbrain.info for location of Anterior Commisure).

1.a. How much does it have to be moved (indicate 3 translations and 3 rotations)?

Apply transformation to all functional images.

Align the anterior commisure of the structural image to [0,0,0].

1.b. How much does that have to be moved?

2. Preprocessing of fMRI data

Follow the example in the SPM12 manual chapter 30. Apply the same preprocessing procedure to the current data. This means:

2.a. realignment,

2.b. coregistration of function and structural data (hint: use "dependency" to point to the mean functional image),

2.c. segmentation of structural data (again, use dependency to point the coregistered structural image),

2.d. normalization using the forward deformation field from segmentation (hint: dependency and NB: No need to change voxel size), and

2.e. smoothing (choose dependency and output from normalization) using a [8,8,8] mm FWHM gaussian kernel.

2.f. Save and report output from the graphics window for each step using the SPM figure menu. Use the "check reg." button to show an example of a smoothed image (sws..nii) and save that as well.

3. Realignment parameters

SPM produces a file with the realignment parameters, i.e. the calcultated participant movement and rotation per time point (called "rp...txt", saved together with the functional data).

Import the realignment parameters into R.

3.a. Make a lineplot of the realignment parameters in R.

3.b. How far has the participant moved for each dimension during the experiment (Hint: use "apply()" to run a function across columns)?

3.c. Are any of the realignment parameters significantly correlated with the fMRI model (same model as used in exercise 3)?

Remove linear effects of time from the realignment parameters (hint: 1:400, fit a line and use residuals).

3.d. Make a lineplot of the realignment parameters with time removed.

3.e. Make a lineplot including only the first realignment parameter before and after removal.

3.f. Are the realignment parameters (corrected for effects of time) now correlated with the fMRI model?

Reporting:

Use r_markdown in RStudio for the part of the report conducted in R. Collect figures and report and submit as a single pdf-file.

Submit report to Blackboard.

Portfolio assignment 05: Model specification

Experimental methods II - 2019; Mikkel Wallentin, Isa Lykke Hansen

March 5, 2019

fMRI design matrix excercise

In this exercise, we will make a model for the analysis of the data that we preprocessed in exercise 4. The model is specified by onsets for the different stories and by their duration. During the experiment, the participant also rated each story for emotional content. We will add the onsets for ratings as well. We will also add a covariate to each story condition with the ratings obtained.

Deadline

March 20, 2019.

Details:

TR=3.5

Number of scans: 400

Onsets for "story1" in seconds: [3 117 203 278 375 442 513 616 723 807 910 1003 1093 1186 1282]

Onsets for "story2" in seconds: [50 157 242 326 414 471 555 670 768 873 944 1054 1149 1242 1316]

Onsets for "ratings" in seconds: [39 106 146 191 231 267 315 364 403 431 460 502 544 605 659 711 757 796 862 899 933 992 1042 1082 1138 1175 1231 1271 1305 1348]

Durations for "story1" in seconds: [35 27 27 36 26 16 29 42 33 54 22 38 43 43 21]

Durations for "story2" in seconds: [55 33 23 37 16 30 48 40 26 24 46 27 25 27 30]

Durations for "ratings" in seconds: 10.

Rating values for "story1": [7 4 4 5 3 1 6 2 1 4 2 3 2 4 1]

Rating values for "story2": [8 2 3 2 5 7 7 3 3 2 3 3 2 4 3]

Tasks

1. Checking input using R

Test the following hypotheses:

1.a. There was a signifiant difference between the durations of the two story types.

1.b. There was a significant difference between the ratings of the two story types.

2. Create the model in SPM.

Create a model with three different conditions: “story1”“,”story2"" and “rating” using details above and the description in the SPM12 manual p. 229, but use “seconds” as timing rather than “scans”. Remember to save the batch file with the details of the model. You will need it later. It is also a good idea to have the model and its output in a different folder than the data.

If you created a batch for the preprocessing assignment, you can also add the model to that batch. This will enable you to use dependency for selecting the smoothed images. But it will also cause the script to run the whole preprocessing every time you run the model, which may take some time.

2.a. Make a screenshot and report the design matrix figure generated by SPM. How many columns does it have? What do the different columns represent?

3. Checking the model

Explore the design matrix using the “review” function (see p. 229-331 in the manual).

3.a Report periodogram plots of the Frequency domain for the three conditions.

3.b.Eye-balling task: What are the most predominant frequencies for the three condition, as seen from these plots?

4. Adding covariates

Under “Conditions” in the “fMRI model specification”, add the rating values as “Parametric Modulations” (i.e. covariates) for each of the story types. Choose 1st order “Polynomial Expansion” (this simply means that you are modelling linear effects of the covariate).

4.a. Make a screenshot and report the new design matrix figure. How many columns does it now have? Which columns model the rating effects?

A parametric modulation in SPM is basically an interaction between the modeled response and the mean centred covariate (i.e. where the mean has been subtracted).

4.b. Interpretation task: Why is it important to subtract the mean?

Under “Multiple regressors” in the “fMRI model specification”, add the motion parameters from the realignment procedure (simply attach the rp_....txt file produced by the realignment procedure).

4.c. Make a screenshot and report the new design matrix figure. How many columns does it now have? Which columns are modeling the motion?

5. Checking the new model

Explore the design matrix using the “review” function (see p. 229 in the manual).

5.a. Report plots of the Frequency domain for the three conditions.

5.b.Eye-balling task: What are the most predominant frequencies for the covariates, as seen from these plots?

The lowest frequencies in the design are filtered out using a “high pass” filter in the analysis. This is the part of the spectrum marked by gray in the frequency/density plot. Does this filter seem to affect the covariates?

5.c. The high-pass filter consists of low-frequency cosine-waves, which together can model any fluctuation below the specified frequency. Plot and report figures of the high-pass filter using these two lines in MatLab (you need to have loaded the SPM.mat file):

figure, imagesc(SPM.xX.K.X0)

figure, plot(SPM.xX.K.X0)

5.d. How many cosine waves are in this specific high-pass filter?

5.e. Make a hypothetical slow wave signal by creating a vector in Matlab (e.g. a=[2,1,4] for a row vector or a=[3;2;4] for a column vector) with the same length as the number of waves as in the high-pass filter. Multiply the vector with the filter (using "*") and plot the result (figure, plot(my_result_vector). Remember the matrix multiplication rules in order to figure out if the vector should be rows or columns. The plotted vector should have the same length as the number of fMRI images. Report the plot.

5.f. Eyeballing the bottomless pit of despair: Explore "design orthogonality" (in the "review" function). Dark colors in the design "orthonogality matrix" (include it in report) indicate that different covariates are correlated. Which covariates are most correlated in the current design?

5.g. Plot and report the hemodynamic response function (HRF) using this call in Matlab (you need to have loaded the SPM.mat file):

figure, plot(SPM.xBF.dt:SPM.xBF.dt:SPM.xBF.length,SPM.xBF.bf)

6. Voluntary extra task

A more flexible model of the hemodynamic response function can be obtained using the derivatives of the hemodynamic response function (i.e. the function plotted in 5.g) . In the model the "time"" and "dispersion" derivatives can be added under "Basis Functions".

6.a. Inspect the design matrix and see what it does to the model when these are added.

Again, the response functions used in making the design can be plotted using:

figure, plot(SPM.xBF.dt:SPM.xBF.dt:SPM.xBF.length,SPM.xBF.bf)

The flexibility arises due to a linear combination of the three model functions. This can model BOLD responses that differ somewhat in shape from the standard.

6.b. Try changing and reporting the values in the contrast matrix below (looking like this: [1,1,1]) and see what it does to the response function.

figure, plot(SPM.xBF.dt:SPM.xBF.dt:SPM.xBF.length,SPM.xBF.bf*[1;1;1])

Reporting:

Collect material and submit as a single pdf-file to Blackboard.

Portfolio_assignment6_model_estimation

Mikkel Wallentin, Isa Lykke Hansen

13 March 2019

fMRI model estimation excercise

In this exercise, we will estimate the model of the data that we designed in exercise 4.This means that we get the results and report them, if there are any. You do not need R for this excercise.

Deadline

March 27, 2019.

Details:

Model estimation (SPM manual p. 229)

If you have made the model from excercise 4, you should have a file called "SPM.mat" saved in your model directory.

Choose "estimate" in the SPM menu (or add it to your batch). Choose "Specify" under the "Select SPM.mat"-menu and locate your design file.

Save the job as estimate.mat and press the Run button.

Making contrasts (SPM manual p. 229)

After estimation: - Press "Results" - Select the SPM.mat file. This will invoke the contrast manager

T-contrasts

To see the effect of a specific condition we need to to turn all the other conditions "off", we do this by making a vector of 1s and 0s which will tell SPM which conditions we are interested in.

The contrast manager displays the design matrix (surfable) in the right panel and lists specified contrasts in the left panel. Either "t-contrast" or "F-contrast" can be selected. To examine statistical results for condition effects: - Select "Define new contrast" For each condition specify a positive t-contrast by making a vector with a 1 for the condition and 0s for all other (see also Flandin & Novak p. 70), e.g.

pos_story1: [1 0 0 0 0 0 0 0 0 0 0]

pos_story1rating: [0 1 0 0 0 0 0 0 0 0 0]

pos_story2: [0 0 1 0 0 0 0 0 0 0 0]

pos_story2rating: [0 0 0 1 0 0 0 0 0 0 0]

pos_rating: [0 0 0 0 1 0 0 0 0 0 0]

Do the same with negative effects (i.e. use -1 instead of 1). This will find voxels that have a negative BOLD response.

Make t-contrasts by subtracting conditions: [story1-story2] and [story2-story1] using +1 and -1, both for main effect and rating effect. This will find areas that differ in their response to the two conditions.

F-constrast

In order to investigate whether anything in the data is explained by the 6 motion parameters, make an F-contrast. If you model contains two story conditions, one response condition and two rating covariates, this can be done by creating a contrast matrix using the following formula:

[zeros(6,5) eye(6)]

Note: Since here, we are only interested in the effect of the realignment parameters, we want to "turn off"" the other covariates. We therefore set them to zero using zeros(6,5) which gives a square matrix of zeroes (if you have more than five non-realigment parameters you need to change the last number). eye(6) makes an identity matrix identifies the six realigment parameters, so our analysis will show if and where they explain any variance in the data.

Results

For each contrast, see if there are any significant results when correcting for multiple comparisons using family-wise error correction (FWE) for multiple comparisons (see Flandin and Novak p. 71). If you find nothing using the correction, try using an uncorrected threshold ($p<0.001$). Although this threshold is strictly speaking not statistically significant, it is often used anyway.

Displaying results

Under "display" use "overlays" and "sections" to choose image as background for activations. Choose either normalised structural image for participant or canonical image (found in the /SPM12/canonical folder under "single_subj_t1.nii")

Things to report:

1. Report the output coordinate table for each of the 14 contrasts, both significant and non-significant (e.g. using the "save figure" function in the "SPM Figure" menu).
2. For significant constrast, include a nice overlayed image, displaying the most significant effect.
3. How many voxels are included in your analysis? Recall that a p-value reflects the probability of finding a specific effect, given that the null hypothesis is true. If all voxels were independent, how many voxels would then on average appear to be activated by chance in this analysis if using an uncorrected threshold of $p<0.001$?

Reporting:

Collect material and submit as a single file (pdf) to Blackboard.

Portfolio Assignment 7 mixed effects

Mikkel Wallentin, Isa Lykke Hansen

27 March 2019

Deadline

April 3 2019.

A. Emotional faces experiment (response times)

This experiment was conducted during the fMRI laboratory days in 2016 and 2017. Participants responded to images of faces with button presses. The design was a 2x2x2 mixed effects experiment (color x emotion x frequency).

Stimuli

Participants viewed 4 different stimuli:

blue neutral face

blue fearful face

yellow neutral face

yellow fearful face

Participants viewed a total of 96 stimuli, each displayed for 700 ms, with a mean interstimulus interval of 4100 ms.

Frequency manipulation

Participants were, without being told, divided into two "frequency" groups:

Group 1 recieved the blue/yellow stimuli in a 2:1 proportion (64:32)

Group 2 recieved the blue/yellow stimuli in a 1:2 proportion (32:64)

Both groups recieved the fearful and neutral faces at the same proportion (48:48)

###Responses

Participants responded to the colour of the stimuli:

blue face -> index finger response

yellow face -> middle finger response

Hypotheses

The experiment had the following behavioral hypotheses:

H1: The index finger (blue) trials will lead to a shorter response time than middle finger (yellow) trials.

H2: Fearful faces will yield a shorter response time than neutral.

H3: Infrequent stimuli will yield longer responses time than frequent. This should surface as an interaction between color and frequency group.

Assignment A Tasks:

1. Understanding the experiment

1.a.Comprehension question. Please explain which factor was between-participants and which were within-participants and why.

1.b. What was the age range of the participants?

1. Data exploring and preparation

Find the data on blackboard. Load the data using somehting like the following code:

```
face_exp_2016<- read.csv("~/Dropbox/fmri_data/face_exp_2016/face_exp_data_all_160310.csv", sep=";")
face_exp_2017<- read.csv("~/Dropbox/fmri_data/face_exp_2017/face_exp_data/face_exp_all_logs_2017.csv", s
#Binding the two datasets together
face_exp<-rbind(face_exp_2016,face_exp_2017)
#conditions are coded in the "cond_blue", "cond_emo" and "freq" variables
```

Make sure that factorial variables are coded as factors using the as.factor() function.

2.a: make a box-plot of the data with RT on the y-axis and emotional condition on the x-axis. Make a box-plot for each of the color conditions by using "fill". Use facet_wrap() to make two seperate graphs for each frequency group. Give the boxes colors that mathces the stimuli, eg. use " + scale_fill_manual(values=c("yellow","blue","yellow","blue","yellow","blue","yellow","blue"))" .

2.b: Comprehension question. Explain why this plot shows that there is something wrong with the data.

2.c.: Make a subset of the data, including only correct responses.

2.d.: Make another boxplot similar to that in 2.a. Did it solve the observed problem?

2.e.: Use the by() function and stat.desc (in library(pastecs)) to get descriptive measures for the different conditions (e.g. see Field's book chapter 5.5.3.2.). Try to investigate the three hypotheses based on the descriptive statistics - would you expect any of the statistical analyses to be significant based on the descriptive stats?

2.f.: Explore if the RT data is normally distributed using a qq-plot (e.g. qqnorm()).

2.g.: log-transform the RT data.

2.h.: Use a qq-plot to explore if the transformed data appear more normal than the untransformed.

2.i.: Make a plot that explores the response times for participants, individually, using a box-plot. Does anybody stick out as unusual?

3. Data analysis

3.a Make mixed effects model where you predict reaction time using the three factors as fixed effects, and include random intercepts for each participant (use "ID" from the log). Include 2-way and 3-way interactions as well. To do this use lme() from the "nlme" package, and use maximum-likelihood as estimation method(method = "ML").

3.b.: Report the t-statistics using summary().

3.c.: Report the F-statistics using anova() and type='sequential', which gives you type='I' analysis.

3.d.: Report the F-statistics using anova() and type='marginal'. Why might there be differences between results from 3.c and 3.d?

3.e.: Make a new model including a random slope from trial number ('no' in the log-file). Repeat 3.b. What does the inclusion of such a random slope model? Did it change the results?

3.f.: Make a model comparison of model 3.a and 3.e using anova(). Did the inclusion of a random slope significantly improve the model?

3.g.: Response times are correlated in time which goes against the assumption of independence. It might therefore be an idea to model this by including a so-called auto-regressive component in the model (e.g. this is default in SPM analyses of fMRI-data). In lme(), this is done by adding the following to the model specification: "cor=corAR1(,form=~1|ID)". Make a new model comparison. Does that have an effect?

4. Results and interpretion.

4.a.: Comprehension question. If you were to report these results, which model would you use and why? Below are some ideas that you may want to consider:

Rule number 1: Report the first model you did.

Rule number 2: Report the most sensible model.

Rule number 3: Report the simplest model.

Rule number 4: Report the most extensive and complete model.

4.b.: Throughout part 3 of this exercise we made several models to choose from What is the problem of this strategy? (This is analogous to the motivation for using family-wise-error corrected p-values in the SPM analysis)

4.c. Write a few lines, briefly stating the results of the experiment in relation to the hypotheses, using the model you dicided upon in 4.a..

B. Tryptophan depletion study analysis

In this task you are going to analyze the data from a tryptohan depletion experiment. Students from the 2018 year in Cognitive Science at Aarhus University took part in a voluntary experiment where they were given a small portion (47 gram) of amino acids and ate that in stead of breakfast. Half of the portions also contained 3 gram of tryptophan, an amino acid needed for serotonin production.

Dependent variable

Participants monitored their mood on a visual analog scale (VAS) with scores from 0 (your worst mood) to 100 (your best mood).

Hypothesis 1

Being depleted of tryptophan is hypothesised to lead to alterations of mood.

Groups

Particiants were free to choose not to take part, and the study thus consisted of three groups: - Tryptophan depleted - Tryptophan loaded - Controls

Repeated measure

Mood rating was conducted at three time points:

- 6.55 (just before eating the amino acids)
- 7.05 (just after eating the amino acids)
- 12.00 (five hourse after eating the amino acids)

Hypotheses 2 and 3

In addition to the tryptophan depletion effect, mood was hypothesised to be altered by

Hypothesis 2: forcing yourself to eat a nasty powder at 7.00, or

Hypothesis 3: becoming hungry at 12.00.

Participants

Participants were given a participant number in the amino acid bag. This was to be used when reporting mood. 50 participants responded to the questionnaires. However, not everybody rated at all time-points and/or using consistent numbers. 43 participants were thus part of the final dataset, which was turned into long format.

5. Interpretation task

5.a. Find the data on Blackboard, load it and report figure and analysis using the code below.

5.b. Report and discuss the findings. What do they mean? How do they relate to the hypotheses?

```
#Load data
trypt_long<-read.csv(file='trypt_long.csv',header=TRUE,sep=",")
trypt_long$ID<-as.factor(trypt_long$ID)
trypt_long$time<-as.factor(trypt_long$time)

#use ggline to make nice line plot. Install ggpubr, if you haven't got it
library(ggpubr)
ggline(trypt_long, x = "time", y = "mood",col='Group',
       add = c("mean_se", "dodge"), palette = "jco")

library(lmerTest)
#Relevel to make the reference group "loaded"
trypt_long$Group<-relevel(trypt_long$Group,'loaded')
#Relevel to make the reference time "7.05"
```

```r
trypt_long$time<-relevel(trypt_long$time,'7.05')
#Make mixed effects model with Group and time as fixed effects and ID as random effect
trypt_model<-lmerTest::lmer(mood~Group*time+(1|ID), data = trypt_long)

#Get summary statistics
trypt_res<-summary(trypt_model)

#Apply Bonferroni correction for multiple comparisons to p-values (9 tests)
# and round a bit (5 decimals)
trypt_res$coefficients2<-matrix(round(c(trypt_res$coefficients,trypt_res$coefficients[,5]*9),
                                      digits=5),ncol=6)

#Add names to the new results matrix
colnames(trypt_res$coefficients2)<-c(colnames(trypt_res$coefficients),'p(bonf)')
rownames(trypt_res$coefficients2)<-c(rownames(trypt_res$coefficients))

#Show us what you've got
trypt_res$coefficients2

#Use library(emmeans) to get more comprehensible pairwise interactions (uncorrected for multiple compar
library(emmeans)
lsm = emmeans(trypt_model, ~Group*time)
contrast(lsm, interaction = "pairwise")
```

Handing in the assignment

Use r_markdown in RStudio for your report. Submit report as a single pdf file. Include commented code and figures all the way from data import.

Submit report to Blackboard.

Portfolio assignment8 EEG Stop-Signal-NoGo exp

Andreas Højlund (hojlund@cfin.au.dk)

April 10 2019

Stop-Signal-NoGo

This experiment was an EEG experiment with 3 levels

Deadline

April 30 2019

Stimuli

Participants listened to two different sounds:

"Go"-sound: piano note E (aka. "high note"), 100 ms, 20 ms rise and fall

"Stop"-/"NoGo"-sound: piano note C from the octave below E (i.e., 17 semitones lower than E, aka. "low note"), 100 ms, 20 ms rise and fall

Generally, participants were given max 1500 ms to respond (from the onset of the "Go"-sound). If no response, then a random waiting interval between 0-1000 ms; and if they responded, this waiting interval was varied randomly between 1000-2000.

For "Stop"-trials, ISI (inter-stimulus-interval, aka. "silent gap") = 100 ms at the outset, which then changed in steps of ±25 ms (first three steps were 200 ms, 100 ms, and 50 ms) depending on whether the participant correctly withheld his/her response (increased) or made a commission error (decreased). This adaptive approach ensured approximately 50% correct responses (i.e., no response) and 50% incorrect responses (i.e., pressing "space").

Number of stimuli

100 "Stop"-trials (approx. 50% hit/miss, i.e. 50 each)
50 "NoGo"-trials
~375 "Go"-trials (because of range from 0-5 "Go"-trials for each "Stop"-/"NoGo"-trial)

Hence, ~3.75:1 (~375:100) proportion of "Go"- vs. "Stop"-trials
and ~7.5:1 (~375:50) proportion of "Go"- vs. "NoGo"-trials

Responses/instructions

Participants were instructed to press "space" to the "Go"-sounds as fast as possible, but, crucially, NOT to respond if they heard the "Stop"-/"NoGo"-sound. Participants were furthermore informed that the "Stop"-/"NoGo"-sounds would occur either immediately after the "Go"-sounds or by themselves, and the participants were instructed to refrain from pressing "space" in both situations.

EEG details

Sampling rate = 1000 Hz
Analog high-pass-filter = 0.1 Hz
Number of channels = 32
Original reference = FCz
EOG channels = HEOG (chan. 28) and VEOG (chan. 32), ref. = FCz

Headerfile = 'Group[number].vhdr' (this is the inputfile for SPM)
Markerfile = 'Group[number].vmrk'
Datafile = 'Group[number].eeg'

NB! Changing filenames of the raw files is NOT straightforward (i.e., you have to also fix them inside '*.vhdr' and '*.vmrk', which are just plain text files, and then save these files in their original format (i.e., with their '.vhdr' and '.vmrk' suffixes)).

Trigger values:
Go = 'S 10'
Stop = 'S 11'
NoGo = 'S 12'
Go-Stop = 'S 20'
Response = 'S 1'

Tasks

File system setup

0. Setup your file system so that you have a "base path" in which you create the folders 'raw' (put ALL .vhdr, .vmrk, and .eeg files here), 'scratch' (destination for all your analyses), 'scripts' (save your batch file(s) here as well as code_snippets.m), and optionally also create 'results', 'stats', and 'figures' folders.

Preprocessing

1. Make a **batch** including the following modules:
   (Start out by setting everything up and testing it on your group's own dataset, then you can apply the code snippet below and run it on all the participants)
   i. **Conversion** (use default values; when looping over participants later on, "File Name" should be left empty [Edit > Clear Value])
   ii. **Montage** (use the 'avg_reref.mat' file available on Blackboard; "Keep other channels" > 'Yes' – we want to keep our two EOG-channels)
   iii. **Filter** (Highpass; 0.1 Hz – it says "Cutoff(s)", but the parenthesis refers to "optionally plural", not "= seconds"; should be specified in Hz)
   iv. [Optional] **Downsampling** (250 Hz), reducing data (every 4th sample)
   v. [Optional] **Filter** (Lowpass: 45 Hz (for you to play with and see how it affects your data)) - NB! Leave the option of a Filter in this particular spot in the batch, then edit the cutoff as you like
   vi. **Epoching** ("How to define trials" > 'Define trial'):

a. Time window > [-100 800]
b. Trial definitions:
   - Make 5 trials using the earlier specified trigger values
   - You decide the Condition labels (but for scripting purposes [evident later], consider sticking to my labels above)
   - Event type > 'Stimulus'
   - NB! Take notice of the order in which you create your trials ;)
c. Event padding > 0.4 (in seconds; this allows us to use the responses up to 1000 ms after sound onset if we later want to sort the trials based on correct responses, etc.)

vii. **Artefact detection** (use default settings, specify "Threshold channels" > 150); we simply flag as bad all 1 sec segments where the amplitude exceeds 150 μV (think back to what the eye blinks looked like)
viii. **Averaging** ("Robust" > 3; "Compute weights by condition" > 'Yes'; "Save weights" > 'No' – we don't normally save these weights, but if you want to know more about how this 'robust averaging procedure' actually works, you can input 'Yes' and inspect)
ix. **Filter** (Lowpass: 45 Hz (or whatever you used in your previous lowpass-step) – SPM advices you to re-apply your lowpass-filter after robust averaging as this procedure may induce high-frequency artefacts (mainly around the edges of the epochs, which is due to the weighting procedure)
x. **Contrast over epochs** ("Weight by replications" > 'No'):
Make 8 contrasts, replicating the 5 trials you already created, and adding 3 new:
   a. Stop-sound minus Go-sound ('Stop-vs-Go')
   b. NoGo-sound minus Go-sound ('Nogo-vs-Go')
   c. Stop-sound minus NoGo-sound ('Stop-vs-NoGo')
   If you use these exact labels (and order), you can easily average your data with those from last year's class
xi. **Convert2Images** ("Mode" > 'scalp x time'; "Select channels by type" > 'EEG' (don't forget to delete the default "All" value); default values otherwise -later on, you may consider also setting "Time window" to e.g. [0 400] in order to narrow down/focus your statistical analysis a bit)
xii. **Smooth** ("FHWM" > [20 20 20] (mm mm ms); "Implicit masking" > 'Yes' – this excludes the areas outside the scalp from the analysis)

Group analysis

2. "Use" the following code snippet to get your batch to run on all 12 participants (NB! Don't use the actual text from below – get the "code_snippets.m" from Blackboard):

```
%% Setting up the batch to run across a loop of subjects (step 2) - EXECUTE ME, PLZ

tic % checking how long it takes to run the batch on all subjects

% initialize the spm_jobman
spm_jobman('initcfg');

% load the relevant batch into the workspace (specified earlier)
load(batchPath)
```

```
% set the path for where to save your processed files, and cd there
savePath = fullfile(filePath, extScratch);
cd(savePath)

% create input structure
g = 1:12; % group numbers

for i = 1:length(g)
    inputs = cell(1,1); % this clears the inputs-structure on every interation
    inputs{1} = fullfile(filePath, extRaw, sprintf('Group%d.vhdr', g(i))); % exact path and
filename of each datafile to be processed
    spm_jobman('serial', matlabbatch, '', inputs); % spm_jobman will then run your batch on
your 12 selected files
end

toc % checking how long it takes to run the batch on all subjects
```

Grand-average (aka. group average) for plotting curvy ERPs

3. Make a batch with the following 2 modules (can also be run via one of the cells in the "extra_snippets.m" from Blackboard) – make sure you have downloaded last year's preprocessed data, as well:
    i. **Grandmean:**
        a. "File names" > input all 24 preprocessed datasets (hint: use the prefixes to identify the relevant .mat-files)
        b. "Output filename" > give your grandmean a funky name, or not
        c. "Weighted average?" > "No"
    ii. **Filter** (Lowpass: 30 Hz – for visualization purposes)

Stats (NB! Andreas will spend 10 mins introducing stats on Wed)

4. Make a batch with the following 3 modules:
    i. **Factorial design specification**:
        a. "Directory" > specify where to save your design matrix (I suggest '…/stats/{name_of_contrast}' [e.g. 'Stop-vs-NoGo'; NB! You need to create this subfolder])
        b. "Design" > "One-sample t-test" > "Scans" > input the relevant contrast-image from each group (both from this year and last year) – we will focus on the 'Stop-vs-NoGo'-contrast for now [hint: these will be in separate folders for each group, and don't forget: last step was to smooth the images]
    ii. **Model estimation** (defaults)
    iii. **Contrast manager** ("Contrast Sessions"):
        a. T-contrast > "Name" > 'diff-t'; "Weights vector" > 1
        b. T-contrast > "Name" > 'diff-t-neg'; "Weights vector" > -1
        c. F-contrast > "Name" > 'diff-f'; "Weights vector" > 1
    iv. **"Delete existing contrasts"** > 'Yes'
    v. After you've run your batch, click on "Results" in the GUI in order to inspect your effects:
        a. Select your contrast (e.g., 'diff-t'); "apply masking" > 'none'; "p value" > 'none' (or 'FWE'); "threshold" > 0.001 (or 0.05); "extent" > 50 (or 200); "Data Type: …" > 'Scalp-Time'

[See the end of this assignment on how to report your answers]

START Voluntary extra tasks

Successful and unsuccessful Stop-responses

5. Make an identical batch to your previous batch, only this should start with the module called **Artefact detection** (and the input should be left blank)
    i. Only change to this batch should be in the **Contrast over epochs** module where you will now specify 9 contrasts:
        a. replicate the 5 conditions you already created
        b. add 1 new condition: the StopError condition (see the relevant code snippet below for how this condition was created)
        c. add 3 actual contrasts:
            - Stop minus StopError ('Stop-vs-StopError')
            - Stop minus Go ('Stop-vs-Go')
            - StopError minus Go ('StopError-vs-Go')
6. Now **copy** all your epoched files into a subfolder called "success" (hint: use the prefixes to identify the epoched files)
7. Use the code snippet for 'Splitting into successful and unsuccessful Stop-trials in extra_snippets.m:

```
%% Splitting into successful and unsuccessful Stop-trials (NB! EXTRA STEP) - I DARE YOU!

extScratch = 'scratch/success'; % have you created a subfolder in your scratch-folder?
if ~exist(extScratch, 'dir')
    mkdir(fullfile(filePath, extScratch)); % if no scratch folder, create one
end

batchPath = fullfile(filePath, 'scripts/batch_stop_nogo_artefact_succ.mat'); % where have
you saved your new batch and under what name?

% initialize the spm_jobman
spm_jobman('initcfg');

% set the path for where to save your processed files (which should be different from our
base-scratch-folder), and cd there
savePath = fullfile(filePath, extScratch);
cd(savePath)

% create input structure
g = 1:12; % group numbers

for i = 1:length(g)
    loadPrefix = 'efdfMspmeeg'; % specify the prefix for the epoched files
    D = spm_eeg_load(fullfile(filePath, extScratch, sprintf('%s_Group%d.mat', loadPrefix,
g(i)))); % loading the already epoched file
    listConds = conditions(D)'; % list of all the epoched trials
    idxGoStop = strmatch('Go-Stop', listConds); % trial-indices of all the Go-Stop-trials
    idxStop = strmatch('Stop', listConds); % trial-indices of all the Stop-trials
    idxStopAll = idxStop; % creating a copy of our idxStop-list
    idxStop(idxStop==ntrials(D)) = []; % in case the very last trial is a Stop-trial, we
have to discard it for now (because we use "+1" in the next line to identify "Response"s)
    idxGoStopError = strmatch('Response', listConds(idxGoStop+1)); % identifying all trials
where there's a response right after the Go-Stop sound (aka. a pseudo-error)
    idxStopError = strmatch('Response', listConds(idxStop+1)); % identifying all trials
where there's a response right after the Go-Stop sound (aka. an error)
    D = conditions(D, idxStop(idxStopError), 'StopError'); % renaming all Stop trials where
there was a response AFTER the stop-signal
    D = conditions(D, idxGoStop(idxGoStopError), 'Go-StopError'); % renaming all Go-Stop
trials where there was a response BEFORE the stop-signal
    D = conditions(D, idxGoStop(idxGoStopError)+2, 'Stop-PreError'); % renaming all Stop
trials where there was a response BEFORE the stop-signal
    save(D);

    load(batchPath)
    inputs = cell(1,1); % this clears the inputs-structure on every interation
    inputs{1} = fullfile(filePath, extScratch, fname(D)); % exact path and filename of each
datafile to be processed
    spm_jobman('serial', matlabbatch, '', inputs); % spm_jobman will then run your batch on
your 12 selected files
end
```

8. Next, re-use the grandmean-batch from above (or run it from the extra_snippets.m)

only change which files you input, or change the scripts as below:

from

```
extScratch = 'scratch'; % have you created a scratch-folder?
% extScratch = 'scratch/success'; % in which scratch-folder are your grand-mean inputs?
```

to

```
% extScratch = 'scratch'; % have you created a scratch-folder?
extScratch = 'scratch/success'; % in which scratch-folder are your grand-mean inputs?
```

Stats

9. Input the images from the newly defined Stop-vs-StopError difference wave to your stats-batch (or use the following code snippet (from extra_snippets.m on Blackboard) in order to run your stats-batch - you can also run your stats-batch on any of the other contrasts that we've defined earlier)

```
%% STATS

% initialize the spm_jobman
spm_jobman('initcfg');

% load the relevant batch into the workspace
batchPath = fullfile(filePath, 'scripts/batch_stop_nogo_stats.mat');
load(batchPath)

% conditions
% conds = {'Stop-vs-Go', 'NoGo-vs-Go', 'Stop-vs-NoGo'}; % HAVE YOU NAMED YOUR CONTRASTS
EXACTLY AS I HAVE? OTHERWISE, ADJUST THESE STRINGS
conds = {'Stop-vs-StopError'}; % HAVE YOU NAMED YOUR CONTRASTS EXACTLY AS I HAVE? OTHERWISE,
ADJUST THIS/THESE STRING(S)

for i = 1:length(conds)
    savePath = fullfile(filePath, extStats, conds{i});
    if ~exist(savePath, 'dir')
        mkdir(savePath)
    end
    inputs{1} = cellstr(savePath);
    [inputs{2}, ~] = spm_select('ExtFPListRec', fullfile(filePath, extScratch),
sprintf('(^scondition_%s.nii)', conds{i}));
    inputs{2} = cellstr(inputs{2});

    spm_jobman('serial', matlabbatch, '', inputs{:});
end
```

   i. Again, click on "Results" in the GUI in order to inspect your effects:
      a. Select your contrast (e.g., 'diff-t'); "apply masking" > 'none'; "p value" > 'none' (or 'FWE'); "threshold" > 0.001 (or 0.05); "extent" > 50 (or 200); "Data Type: …" > 'Scalp-Time'

END Voluntary extra tasks

Reporting

I. Create and save a plot of your group's participant's ERPs to the Go-, Stop-, and NoGo-sounds from channel Fz (I suggest using Display… > M/EEG in the GUI, and when you have the figure open: File > Save As…, and then choose the pdf-option).

II. Do the same for the lowpass-filtered group-average, and create and save a plot of the three difference waves (aka. "contrasts") at Cz.

III. Report the stats output coordinate table (including the graphics) of your preferred contrast (default: Stop-vs-NoGo and diff-t).

IV. Voluntary: Save a plot for the Stop and StopError conditions incl. their difference wave (Stop-vs-StopError) at Cz for the lowpass-filtered group-average of the successful/unsuccessful data

V. Collect all material and submit as a single file (pdf or html) to Blackboard.

Portfolio assignment9 fMRI face experiment

Mikkel Wallentin, Isa Lykke Hansen

10 April 2019

Emotional faces

This experiment was a 2x2x2 fMRI experiment.

Deadline

May 16, 2019.

Stimuli

Participants viewed 4 different stimuli:

blue neutral face

blue fearful face

yellow neutral face

yellow fearful face

Number of stimuli

Participants viewed a total of 96 stimuli, displayed for 700 ms.

Frequency manipulation

Participants were divided into two groups:

Group 1 recieved the blue/yellow stimuli in a 2:1 proportion (64:32)

Group 2 recieved the blue/yellow stimuli in a 1:2 proportion (32:64)

Responses

Participants responded to the colour of the stimuli:

blue face -> index finger response

yellow face -> middle finger response

Participants

23 students participated during the 2016 and 2017 fMRI lab workshop. Two participants were scanned twice. For this exercise, we will treat these extra scans as additional participants, yielding a total of 25 scans.

Log data are placed in two files, one for 2016 and one for 2017 (see below) fMRI data are placed in separate folders. All data can be found on Blackboard in a zip-file.

fMRI details

240 fMRI volumes 39 slices per volume TR: 2 s Time specification: seconds

Data

Data can be found here: https://www.dropbox.com/sh/bpea3v125s6i9ph/AAD4ZkEcYWmBeGZQA0HcJnTza?dl=0

The same data as a single zip-file (4 GB) can be found here: https://www.dropbox.com/s/d40t09qbwx1qxf5/face_exp_fmri_data.zip?dl=0

Hypotheses (fMRI)

The experiment had the following brain related hypotheses:

H1: An activation is expected in the Ocipital Face Area (OFA) and Fusiform Face Area (OFA) across all stimuli. Coordinates for OFA and FFA can be found here: http://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.701.1669&rep=rep1&type=pdf (table 1)

H2: Fearful faces will yield a greater response than neutral images. This is hypothesised to originate in emotional regions, e.g. the amygdalae, but may also lead to a modulation of visual areas, e.g. OFA and FFA.

H3: The index finger (blue) trials will lead to a smaller BOLD response in the motor cortex than middle finger (yellow) trials, due to the hand being more adapted to using the index finger.

H4: Infrequent stimuli will yield stronger BOLD response than frequent in brain areas relevant for perception of faces and motor responses.

Tasks

1. Preprocessing and modeling of individual participants

The preprocessing and modeling of individual participants will be conducted using the supplied matlab script entitled: “face_SPM_batch_loop.m” (recall: in Matlab: .m-files are functions and scripts, .mat-files contain variables).

Investigate the batch loop script that your nice teacher has supplied and add the missing information: A directory where you have placed all the data and where all the outputs will be saved.

Check that everything is there: - Raw data, i.e. dicom (.dcm) files for both functional (fMRI) and anatomical images. - Paradigm files with information on conditions and onsets, one for each participant. - SPM batch file: ‘face_SPM_batch.mat’. It will run both the preprocessing and the analysis.

Check that the batch file contains: - Dicom (functional images) -> .nii conversion - Dicom (structural images) -> .nii conversion - Realignment (estimate and reslice (mean image only)) - Coregistration (estimate.

Reference image: mean image, source: structural image) - Segmentation (Deformation Fields: Forward; You will also need to update the path to the TPM.nii files to your local path. Note that you are updating the same 4D TPM.nii file 6 times, but with different indices, e.g. '. . . /TPM.nii,1', '. . . /TPM.nii,2', etc.) - Normalization (write: realigned functional images) - Normalization (write: coregistered structural image) - smoothing (8 mm FWHM) - fMRI model specification (paradigm files with onsets are supplied in a .mat file for each participant, and also including participant movement parameters in the model) - model estimation - contrast specification (7 contrasts)

Check that the batch file has the following "open" spots, marked by an "X": - Dicom import(1): DICOM files and Output directory - Dicom import(2): DICOM files and Output directory - Named File Selector: File Set - fMRI model specification: Directory

Check that the batch loop script provides these six missing pieces of info for each participant at the bottom of the loop.

1.a. Order of conditions

Open one of the paradigm files in Matlab. The variable "names" indicates the order of conditions in the design specification.

Report the order of conditions.

1.b. Comprehension question

What will the seven contrasts provided in the contrast specification test for? Add a bit of prose to the hypotheses that each contrast could test.

1.c. Run the preprocessing and participant analyses using the loop

Run the batch loop script.

BE AWARE: THIS STEP TAKES TIME AND REQUIRES DISC SPACE (2-5 hours on a laptop, ~25 GB).

The script monitors the time taken to analyse all participants. You can shorten the processing time by dividing participants up into groups and running each on a different computer. You will then need to change the "parnums" variable in the loop script to only run a subset of participants. Report the collected time it took to analyse all participants.

1.d. Checking preprocessing

Check if the preprocesing went well, by loading an unsmoothed, normalized image from each participant (files called "wfSubject..nii") into "check reg" together with a standardized image of the brain (look in the "canonical" folder in SPM). You can include up to 24 images at the same time. Include screnshots of these images in your report with a short written evaluation of any concerns related to data from particular participants.

During scanning of one participant, the scan seems not to have covered the whole brain. Which participant is this? Only brain areas present in all participants can be analysed. What are the pros and cons of keeping this participant in the dataset, given the hypotheses? What would you choose?

2. Investigating analysis of a single participant

2.a. Investigate the design matrix

Investigate the design matrix of a single participant using the "Review" function in SPM12 (select a SPM.mat file from a participant). Put a figure of the design matrix in the report.

In this particular participant, which stimulus colour was the more frequent, judging from the design matrix?

How many, if any incorrect responses did the participant have?

Why is it usually a good idea to discard or separately model incorrect responses?

2.b. Investigate the results

Investigate the results of the different contrasts. Choose one participant and report results at $p<0.001$ uncorrected for multiple comparisons with a nice overlay.

Briefly explain if you find signs to support the hypotheses.

3. Group analyses

Make a new folder called "2nd level analyses". In this folder, make a folder for each of the analyes below.

3.a. All positive condition

Take the contrast images for the "all positive" contrast. Use them to conduct a one-sample t-test (see ch.32.3 in the SPM12 manual for an example of how to do this), testing if any regions were consistently activated when seeing a face in general.

Which contrast would you use on this analysis in order to find positive effects?

Report data (image and coordinates) at $P<0.05$ FWE-corrected for multiple comparisons.

If significant, include a nice overlayed image, displaying the most significant/interesting effects.

Write a few sentence, interpreting the findings in relation to the hypotheses.

If there are results in areas not related to the hypotheses, can these then be explained by the way the study was designed?

3.b. Effect of emotion

Take the contrast images for each participant for the Fearful-Neutral condition. Use them to conduct a one-sample t-test, testing if any region (OFA and FFA in particular) consistently has more activation for the fearful than the neutral faces across participants.

Report data (image and coordinates) at $P<0.001$ uncorrected or $P<0.05$ FWE-corrected.

If significant, include a nice overlayed image, displaying the most significant/interesting effects.

Write a few sentence, interpreting the findings.

3.c. effect of color

Take the contrast images for each participant for the yellow-blue condition. Use them to conduct a one-sample t-test, testing for H3.

Report data (image and coordinates) at $P<0.001$ uncorrected or $P<0.05$ FWE-corrected.

If significant, include a nice overlayed image, displaying the most significant/interesting effects.

Write a few sentence, interpreting the findings.

3.d. Frequency group x colour interaction

For each participant, find out which colour was the infrequent (e.g. see number of onsets in paradigm files, e.g. using the provided script "face_exp_which_freq_group.m"). If "Blue"" was the frequent trial, take the "yellow>blue" contrast (i.e. infrequent-frequent) If "Yellow"" was the frequent trial, take the "blue>yellow" contrast (i.e. again infrequent-frequent) Collect these and conduct a one-sample t-test, testing if any region (OFA, FFA and motor cortex in particular) has more activation for infrequent stimuli compared to frequent (this is equivalent to a mixed-effects 2-way (Frequency group x colour) interaction).

Report data (image and coordinates) at $P<0.001$ uncorrected or $P<0.05$ FWE-corrected.

If significant, include a nice overlayed image, displaying the most significant/interesting effects.

Write a few sentence, interpreting the findings.

Voluntary extra tasks

You may also test the other possible contrasts at the group level, by making one-sample t-tests as explained above.

How would you do a 2-way (emotion x colour) interaction?

How would you do a 3-way (emotion x colour x frequency group) interaction?

Reporting:

Report the output coordinate table for both significant and non-significant contrasts (I suggest using the save function in the "SPM Figure" menu).

Collect material and submit as a single pdf-file to Blackboard.

Portfolio assignment 10: Principal Component Analysis and Factor analysis

Mikkel Wallentin, Isa Lykke Hansen

14 May 2019

Real World Immitating Task

You are working in a head-hunting agency. Your job is to filter candidates for a top position in a large corporation. During the interviews, the 105 candidates have been subjected to an empathy questionnaire.

1) People at your agency disagree on how many interesting components/factors are present in the test, so they ask you, the factor analysis expert, to determine this. Please add your argument for the number you end on.
2) In order to short-list candidates for the position, your job is to find the highest and lowest scoring candidate on each factor.
3) Your boss asks you what you think of his new empathy test (The physical empathy test). Does it really measure anything that the old scales cannot capture?
4) You also want to impress your boss with a couple of illustrative plots.

Deadline

May 22 2019.

Details about the questionnaire:

Participants were given 73 questions in pseudorandom order.

Three questionnaires were used:

The Balanced Emotional Empathy Scale (BEES)

30 questions were from the "Balanced Emotional Empathy Scale" (BEES)

Ref. Mehrabian, A. (1997). Relations among personality scales of aggression, violence, and empathy: Validational evidence bearing on the risk of eruptive violence scale. Aggressive Behavior, 23(6).

Here are the questions: 1. I very much enjoy and feel uplifted by happy endings.

2. I cannot feel much sorrow for those who are responsible for their own misery.
3. I am moved deeply when I observe strangers who are struggling to survive.
4. I hardly ever cry when watching a very sad movie.
5. I can almost feel the pain of elderly people who are weak and must struggle to move about.
6. I cannot relate to the crying and sniffling at weddings.
7. It would be extremely painful for me to have to convey very bad news to another.

8. I cannot easily empathize with the hopes and aspirations of strangers.
9. I don't get caught up easily in the emotions generated by a crowd.
10. Unhappy movie endings haunt me for hours afterward.
11. It pains me to see young people in wheelchairs.
12. It is very exciting for me to watch children open presents.
13. Helpless old people don't have much of an emotional effect on me.
14. The sadness of a close one easily rubs off on me.
15. I don't get overly involved with friends' problems.
16. It is difficult for me to experience strongly the feelings of characters in a book or movie.
17. It upsets me to see someone being mistreated.
18. I easily get carried away by the lyrics of love songs.
19. I am not affected easily by the strong emotions of people around me.
20. I have difficulty knowing what babies and children feel.
21. It really hurts me to watch someone who is suffering from a terminal illness.
22. A crying child does not necessarily get my attention.
23. Another's happiness can be very uplifting for me.
24. I have difficulty feeling and reacting to the emotional expressions of foreigners.
25. I get a strong urge to help when I see someone in distress.
26. I am rarely moved to tears while reading a book or watching a movie.
27. I have little sympathy for people who cause their own serious illnesses (e.g., heart disease, diabetes, lung cancer).
28. I would not watch an execution.
29. I easily get excited when those around me are lively and happy.
30. The unhappiness or distress of a stranger are not especially moving for me.

####The Interpersonal Reactivity Index (IRI) 28 questions were from the "Interpersonal Reactivity Index" (IRI)

Reference: Davis, M. (1980). A multidimensional approach to individual differences in empathy. JSAS Catalog of Selected Documents in Psychology, 10(4), 85.

The test supposedly taps into four factors underlying empathy, each tested with 7 questions:

A) "Fantasy" taps respondents' tendencies to transpose themselves imaginatively into the feelings and actions of fictitious characters in books, movies, and plays

B) "Empathic Concern" assesses "other-oriented" feelings of sympathy and concern for unfortunate others

C) "Perspective Taking" the tendency to spontaneously adopt the psychological point of view of others

D) "Personal Distress" measures "self-oriented" feelings of personal anxiety and unease in tense interpersonal settings

The questions can be found here: http://fetzer.org/sites/default/files/images/stories/pdf/selfmeasures/EMPATHY-InterpersonalReactivityIndex.pdf

The Physical Empathy Test. (PEST)

15 questions were from a home-made test constructed to tap into less abstract and more immediate "affective empathy" using no references to mental life or psychological conflict.

The questions were in Danish, but were of the sort:

1e) I can feel it in my body if I think of a bicycle crash where the head hits a sign post.

2e) I am NOT affected by the thought of somebody reaching into a crack where a venomous snake is hidden.

3e) The thought of a broken leg where the bone is sticking out does not affect me???

For Danish readers:

1) Jeg kan m??rke det i kroppen, hvis jeg t??nker p?? et cykelstyrt, hvor hovedet rammer et skilt.
2) Jeg p??virkes IKKE af tanken om en person, der stikker h??nden ned i en spr??kke, hvor en giftslange har gemt sig.
3) Tanken om et br??kket ben, hvor knoglen stikker ud af k??det, p??virker mig ikke.
4) Tanken om en person, der falder og hamrer t??nderne ned i kantstenen kan n??rmest m??rkes i mine egne t??nder.
5) Ideen om at se et stort bet??ndt s??r p?? maven af et barn giver mig ingen s??rlige f??lelser.
6) Jeg f??r et sug i maven ved tanken om at v??re i et passagerfly, der styrter ned.
7) Tanken om at overv??re en dreng blive sparket, mens han ligger ned, giver mig ingen fysisk ubehag.
8) Det er fysisk ubehageligt at t??nke p?? en kvinde, der kommer til at stikke h??nden ned i en grenkv??rn.
9) Jeg f??r ikke nogen s??rlige kropslige fornemmelser af at t??nke p?? et menneske, der kaster blod op.
10) Jeg kan f??le den panik, som en sv??mmer, der ser en stor haj n??rme sig, m?? f??le.
11) Tanken om at se en person styrte ned fra et h??jhus har ingen fysisk effekt p?? mig.
12) Tanken om at se en person f?? en t??negl revet af med en tang f??r mig n??rmest til at krumme t??er selv.
13) Jeg har ingen fysisk reaktion p?? tanken om at se et menneske f?? spr??jtet syre i ??jnene.
14) Det giver mig fysisk ubehag at t??nke p?? en amputation af et s??ret ben med koldbrand.
15) Det giver mig myrekryb at forestille mig en person sp??rret inde i et br??ndende hus.

Responses

For all questions, participants responded on a scale from -4 (very strongly disagree) to 4 (very strongly agree).

Some of the questions were negatively phrased, e.g. "I hardly ever cry when I see a sad film." However, for these questions "Very strongly disagree" is given the score 4. I.e. more empathic is always rated higher.

Data

Data can be found at Blackboard. Filename: 'emp_all_all.csv'

Data order

In the data file, the data is ordered as follows: 1-30 BEES, 31-37: IRI-Fantasy, 38-44: IRI-Concern, 45-51: IRI-Perspective taking, 52-58: IRI-distress, 59-73: PEST.

rows= participants columns=questions

Reporting

Submit report as a single file (pdf or html). Include commented code and figures all the way from data import.

Submit report to Blackboard.