EEGLab EMG_fMRI Manual

Based on:

-Day of the Scan
  by Robin Huizing
-Guide to Artifact Cleaning of the EMG
  by Johan van der Meer

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Contents

Scanning Procedure

Before the scan

- Prepare the EMG and bring your laptop.
- Test EMG and batteries
- Check the fMRI room (beamer, mirror, screen)

Attach the EMG wires and check the signal. Replace the wires if the signal is not good enough.

After the scan

All the original data must be copied to the local network in the following directory and subfolders. For each new patient you have to create multiple files and a directory, take e.g. patient 6666 and study Tremor.

Create directories:

- x:\onderzoek\fMRI\Tremor\ruw\6666
- x:\onderzoek\fMRI\Tremor\ruw\6666\parrec
- x:\onderzoek\fMRI\Tremor\ruw\6666\trc

Create files in the directory x:\onderzoek\fMRI\Tremor\ruw\6666:

- channels.txt
- files.txt
- notes.txt

The last thing to do is to copy the data from the MRI computer and EMG computer:

- MRI computer → parrec files → in x:\onderzoek\fMRI\Tremor\ruw\6666\parrec
- EMG computer → trc files   → in x:\onderzoek\fMRI\Tremor\ruw\6666\trc

In x:\onderzoek\fMRI\Tremor\ruw there are examples of what the channels.txt, the notes.txt and the files.txt must look like. Below are some screenshots of the files.:
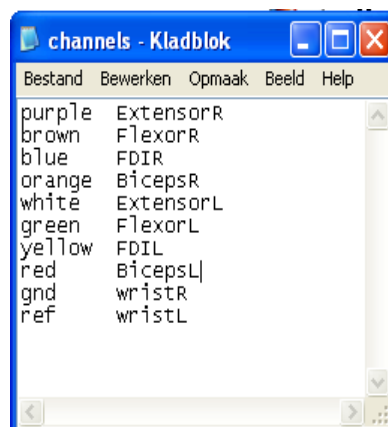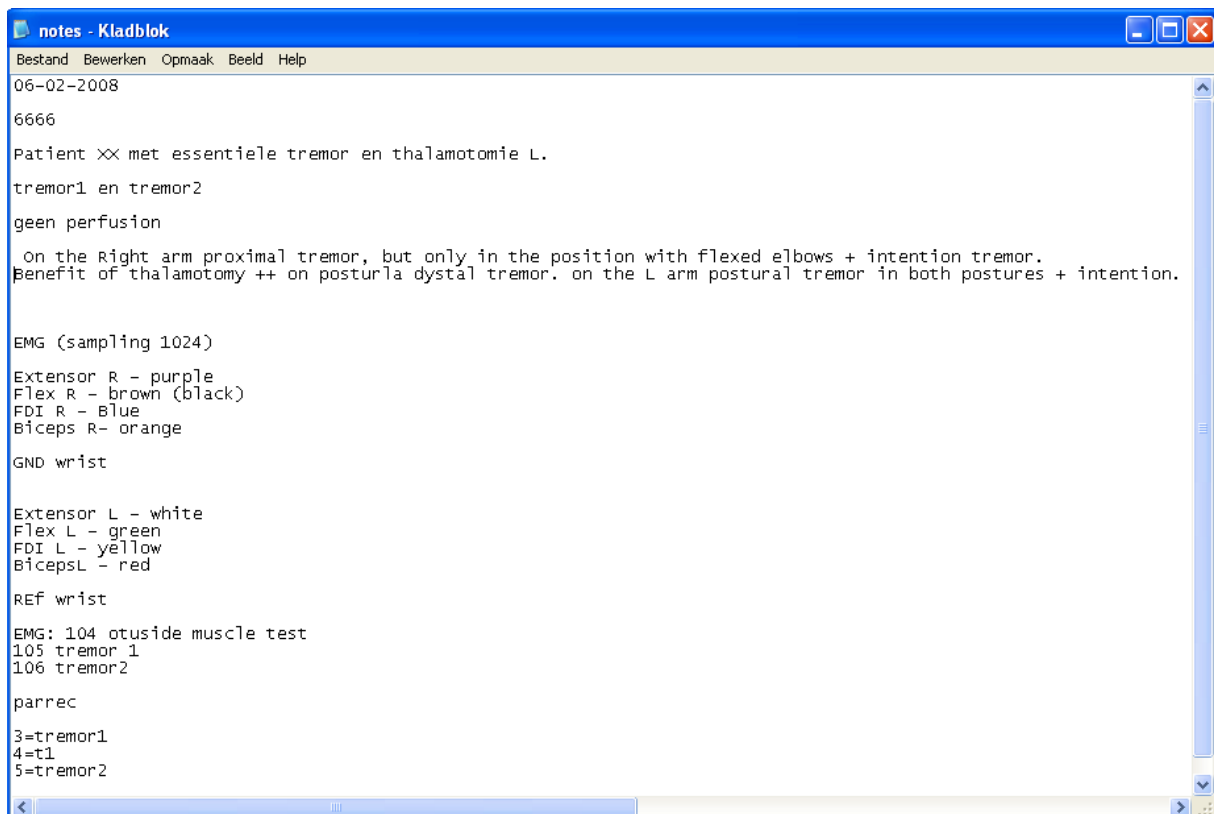

Figure 1: Example of notes.txt

Figure 2: Example of files.txt

In the files window:

```
files - Kladblok
Bestand  Bewerken  Opmaak  Beeld  Help

REC          6666    tremor1      DBIEX_3_1.REC      EEG_105.TRC    tremor1
REC          6666    tremor2      DBIEX_5_1.REC      EEG_106.TRC    tremor2
t1           6666    T1           DBIEX_4_1.REC      xx             xx
dti          6666    DTI          DBIEX_6_1.REC      xx             xx


emgprescan   6666    outsidetest  xx                 EEG_104.TRC    xx
```


Figure 3: Example of notes.txt

```
notes - Kladblok
Bestand  Bewerken  Opmaak  Beeld  Help

06-02-2008

6666

Patient XX met essentiele tremor en thalamotomie L.

tremor1 en tremor2

geen perfusion

 On the Right arm proximal tremor, but only in the position with flexed elbows + intention tremor.
Benefit of thalamotomy ++ on posturla dystal tremor. on the L arm postural tremor in both postures + intention.


EMG (sampling 1024)

Extensor R - purple
Flex R - brown (black)
FDI R - Blue
Biceps R- orange

GND wrist


Extensor L - white
Flex L - green
FDI L - yellow
BicepsL - red

REf wrist

EMG: 104 otuside muscle test
105 tremor 1
106 tremor2

parrec

3=tremor1
4=t1
5=tremor2
```

Conversion of raw files

Before the data can be processed in Matlab the raw files must be converted. This can be done directly after the scanning procedure or on another day.

Cygwin: Transformation of parrec files (MRI)

The first step is to transform the parrec files in to 4D.img and 4D.hdr files. This will be done in cygwin. Start cygwin and in the command line type the following:

- cd /cygdrive/x/Onderzoek/fMRI/Tremor/ruw/
- /cygdrive/x/ICT/Software/mltoolboxes/emgfmri/conversion/fmri/prep.sh Tremor 6666

Where 'Tremor' is the desired study and '6666' is the desired patient number. The first command will change the working directory of cygwin to x:\Onderzoek\fMRI\Tremor\ruw\ which is needed for the second command. That will call a script: prep.sh, with the parameters 'Tremor' and '6666', and then starts converting the parrec files of patient 6666 of the study 'Tremor'. The name of the protocols and study are capital sensitive! This procedure will take approximately 1 hour.

EEGLab plugin EMG_fMRI in Matlab

The EMG data will be transformed in Matlab using a graphical user interface. To start this procedure double click the shortcut 'start EMG fMRI'. This will open and configure Matlab with the settings that are needed. At last EEGLab will be opened.
Then load a random dataset into EEGLab, that will toggle the tools menu into clickable. To load a dataset into EEGLab execute the following:

- In EEGLab
- Click on the menu 'File
- Click on 'Load existing dataset'

It is allowed to load a patient's EMG data in EEGLab.

The following steps are necessary for all that follows! If Matlab is closed and restarted again, this step needs to be done! So keep in mind that every time you are going to work with the EMG_fMRI plugin execute the following:

- In EEGLab
- Click on the menu 'tools'
- Click on the submenu 'EMG_fMRI analysis'
- Click on 'Start Analysis'

A new popup window will occur. In this screen the study (Tremor) and the patient (6666) must be filled out and the study directory must be chosen (x:\Onderzoek\fMRI\Tremor). Furthermore the protocols must be filled out, e.g. tremor1 & tremor2. Not all places for protocols have to be filled out.

Transformation of trc and Log files and fMRI preprocessing

Make sure the previous step 'Start Preprocessing' has been done! Then the following steps will transform trc files to emg.mat files in all the folders and create two extra files inside the EMG folder (only if an emg measurement outside the scanner was done):

- In EEGLab
- Click on the menu 'tools'
- Click on the submenu 'EMG_fMRI analysis'
- Click on 'Preprocessing Data'

The pop up that will appear has three preprocessing options and one close button.

- Preprocess EMG Data → starts batch_emg_to_mat → transforms trc into emg.mat files
- Preprocess Log Data → starts batch_log_to_mat → transforms log files to block.mat and event.mat (if there are no log files, this script still has to be run for creating block.mat).
- Preprocess fMRI Data → starts SPM5 and batch_fmri_preprocessing → this will execute a bunch of correction methods in SPM. (If you choose this option, eeglab will be closed and preprocessing of the fMRI data will be done in SPM fMRI. After SPM fMRI is done you need to restart EEGLab with the following command in Matlab: "eeglab redraw".(The command window is the place where you can execute commands.)
  These steps require time to complete:
  - Slice timing correction
  - Reorienting image
  - Coregistration
  - Normalize
  - Smoothing

The preprocessing of EMG data will take approximately 10 minutes, the preprocessing of log data will take less then 20 seconds and preprocessing of fMRI data will take approximately 90 to 120 minutes

Artifact Cleaning of the EMG

The EMG signal is full of artifacts which basically consists of two major components:

- From moving wires in the 3Tesla field. The greater the velocity of the wires, the bigger the artifact. This one is the easiest to remove by simply using a filter.
- From the EPI sequence used by the scanner to record images. This artifact originates from the fast-changing 10 mTesla field. Although it is a relatively small field, the artifact is huge, because of the fast changes. This artifact consists of two types:
  - Volume artifact, once in every TR (e.g. 2.9 secs)
  - Slice artifact, once every slice (~60msec)

Correction procedure

The data will be corrected in EEGLab, using the EMG_fMRI Analysis plugin. This plugin uses EEGLab functions and the FMRIB plugin developed by the University of Oxford Centre. It also uses some Matlab scripts created by Johan van der Meer.

- In EEGLab
- Click on the menu 'tools'
- Click on the submenu 'EMG_fMRI Analysis'
- Click on 'Filtering of the Artifact'

The popup that will appear has two choices, standard and advanced. These will be described below.

The Standard method

If the standard method is selected and OK is pressed, a new screen will appear which displays the last used profile. There is a button to load another profile and one to view the current profile settings. The profile settings button displays another popup window in which the values can be verified and if necessary adjusted.

The Advanced method

Using the advanced method most steps can be manually executed and values can be manually assigned. The EMG data is processed per protocol, five new buttons will appear if you choose to use the advanced method. When the results are good enough there is a button to save the used settings as a new profile. This profile then can be used in the standard method. With the inspect data button two plots will show up. One plot showing the power spectrum and one plot showing the EMG data. There is also a save button which saves the EMG data into the ../protocol/emg directory (e.g. ../tremor1/emg/). The filename will be: emg_oude_methode_year.month.day.time. Or for the new artifact cleaning method: emg_nieuwe_methode_year.month.day.time

As you can see in the advanced method there are two options for preprocessing of EMG data representing by two bullets. In the panel method, there is a bullet 'new' and a bullet 'other'. The new one has one button 'execute' which will execute emg_corr. This is the script J.N. van der Meer has made to remove the artifacts. This script will run automatically. Below the other method, the old one which is the FASTR (fMRI artifact slice template removal) , will be described:

1. Choose Channel: will make the data bipolar using emg_make_bipolar. After this, a plot will be displayed with the bipolar EMG data. Then a popup will be displayed where a channel can be chosen. Look at the channels and choose the one with the greatest artifact and click on

the bullet consistent with the channel and press OK. This channel will be used for the placing of the slice triggers. To have a good view fill in a value of 20000 and go to e.g. slice 80.

2. Add Slice-triggers: runs the emg_add_slicetriggers script which add slice triggers to the data.
3. Apply Highpass filter: will apply a highpass filter on the data with the desired cutoff frequency. The standard values is 25.
4. Remove slice artifact: will start FMRIB Tools → FASTR. This will remove slice artifacts. The standard values are 0, 10, 10 and 0.07. Use dots, not commas! This will take ~10 min.
5. Remove volume artifact: will start FMRIB Tools → FASTR. This will remove volume artifacts. The standard values are 0, 10, 10 and 0.03. Use dots not commas! This will take ~10 min.
6. Apply freq. bandpass filter: runs emg_filter_bandpass. The standard values are 20 and 250.
7. Optional lowpass filter: is not needed, and does not have standard values.

Now it is done and the data can be inspected, if it is OK, save the data using the save data button and do not forget to save your profile if you want to use the settings again.

UT Method

In 2009 students of the Universiteit Twente were asked to write a new block design used in SPM. This block design is not based on the protocol information, but on EMG measurements. So it respresents the real activity of the patiënt. See also "Bepaling van de doelstructuur voor plaatsing van diepe hersenelektroden bij essentiële tremor met gecombineerde EMG-fMRI techniek" written by:

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The make a block design based on the EMG, in EEGLab do the following:

- In EEGLab
- Click on the menu 'tools'
- Click on the submenu 'EMG_fMRI Analysis'
- Click on 'Make Block EMG, (only for tremor1)'

A window will pop up with three options:

- Make Block EMG
- Delete Rest
- Make regressor

Make Block EMG
- Choose the filtered EMG data
- Determine the threshold so that the activation of the muscles is included
- Repeat the previous step 7 times (8 muscles). The thresholds will be saved in a directory
- Choose a right muscle (1-4) and a left one (5-8) in which you can recognize the tasks best. The model will be saved as 'block_emg.mat' in the map 'regressor'.
- After you have done this, you have two options: close all windows by hand or close all windows including EEGLab. You can restart EEGLab by the following command in the command window: eeglab redraw

Delete Rest
The rest period can also be deleted in the block model by pressing the delete rest button. Two new block models will be saved in the folder regressors: block_EMG_without_rest.mat (if that one is made) and block_without_rest.mat.

Make the regressors

If you like to make the blockdesign based on the artifact free EMG data, you will have to do the following:

- In EEGLab
- Click on the menu 'tools'
- Click on the submenu 'EMG_fMRI Analysis'
- Click on 'Make Regressors'

This step is optional, and can only be used for the protocol 'tremor1' of the study 'Tremor'.

After this a popup window will appear in which you can enter values for a frequency band filter. If you choose 1-250 Hz the whole EMG is used for the regressor, if you choose e.g. 3-7 Hz only the EMG with frequencies around the tremor frequency will be used as regressor (for essential tremor). Standard is 3-7 Hz. In the popup window also 5 buttons are visible, which represents the protocol which you entered at the first step of the EMG-fMRI tool. If you press a button a new popup window will appear in which you can select the EMG data This EMG will be used for the regressor and the bandpass filter of the previous step will be applied to this EMG. After that the EMG is loaded in Matlab (duration: $\pm$ 1 minute) and the bandpass filter is applied, a new window will popup. In this window you can select the muscles you like to use for your new regressor by clicking on the checkboxes. You can also inspect the EMG-data with the inspect button. You can only select two muscles, but for one model you mostly need one muscle . What you will see in this window is a picture of the values of the regressors in the freqreg matrix, that is the matrix after the bandpass filter. So if you had chosen 3-7 Hz, you see a the EMG in the tremor area. You can view the different muscles by clicking on the next and previous buttons. After selecting the muscles, you press the 'Ready & Make regressors' button. Then you will be asked to select a .mat file to orthogonalize with, this can be the block_emg.mat (created with the UT method), but also the block.mat (the other one). You can find these files in the regressor directory. Then the new EMG regressors will be made and three windows will popup.

- a blockmodel
- an orthoganalized version of the EMG and the EMG power
- (and a new chipped model)

After the last window appeared you can inspect the data and close the windows. After that you can process the other protocols.

The following regressors will be made:

- frequency regressor: The EMG regressor with the bandpassfilter (e.g. 3-7 Hz)
- orthogonalized frequency regressor;
- orthogonalized regressor; The above regressor orthogonalized with the normal model (block or block_emg), and divided by it's standard deviation
- convolved frequency regressor; The above regressor with
- convolved orthoganalized frequency regressor; The above one with
- convolved orthogonalized regressor
  Is the convolved orthogonalalized frequency regressor divided tot task

Orthogonalizing will be done with the selected Block model: block.mat or block_emg.mat. The 'frequency regressor' means that this is the EMG with the bandpass filter. Convolving is done with the canonical Hemodynamic Response Function.

Make the model for SPM

After you made the new regressors for the protocols which you have processed in the previous step, you can make a model for SPM fMRI per protocol, e.g. for tremor1 or tremor2. This step is only needed when you want to a model with several regressors, e.g. a model that contains the 'normal EMG-regressor' but also the movementparameters. To make the new model for SPM you will have to do the following:

- In EEGLab
- Click on the menu 'tools'
- Click on the submenu 'EMG_fMRI Analysis'
- Click on 'Select Model'

After that, a window will popup which allow you to select a protocol. After selecting the protocol, a new window will popup in which you can select the regressors you want to use for the model. You can look for regressors which show tremor. Optional you can select the rp_a4D (realignment) parameters. When the parameters are 'high' (above 0.5) but not block like you can select them, but if they are low it is not needed. When they are 'low' and 'block like' you can select them, but if they are 'high' and block like you have a problem. There is some discussion about what to do then. (if you are not sure if they are block like, you can also try and make 2 models, one with and one without the movement parameters and compare the design orthogonalities. If they are mostly independent of task, you can choose for the model with the parameters)

After you 've selected the regressors, the new model will be made if you press the 'Make model' button. A dialog will ask you for a filename and it is also possible to change the folder, but the default folder is recommended to use.

Analysis

Model Making: model of the block design

The following steps will be done manually in SPM and will quit EEGLab.

- In EEGLab
- Click on the menu 'tools'
- Click on the submenu 'Start SPM fMRI'
- A confirmation popup will occur, click OK.

The first thing to do now is to create two directories in \pp\6666\protocol\ (protocol is e.g. tremor1). Create a results folder:

- x:\onderzoek\fMRI\Tremor\pp\6666\tremor1\results

Create a subfolder with the name of your model in the results folder:

- x:\onderzoek\fMRI\Tremor\pp\6666\tremor1\results*name of your model*

In SPM do the following:

- ➔ specify first level
- ➔ fMRI model specification
- ➔ directory
    - o specify files: …\pp\6666\tremor1\results*name of your model*
- ➔ timing parameters
    - o units for design = seconds
    - o interscan interval = 2.8889
    - o microtime resolution = 16
    - o microtime onset = 1 (this depends on the slice timing)
- ➔ data and design
- ➔ new subject\session
    - o scans
        - ▪ specify files (which files must be analysed)
            - • \pp\6666\tremor1\fmri\swa4D (wrapped)
            - • Or \pp\6666\tremor1\fmri\sra4D (not-wrapped)
        - ▪ If you type sra.* (ore swa) and in the place beneath 1:1000 you are sure you can select all sra-files. For selecting you can use Control A.
- ➔ Multiple conditions
    - o Specify file = x:\Onderzoek\fMRI\Tremor\pp\6666\tremor1\regressor\block.mat
        - ▪ or block_emg.mat, block_emg_without_rest.mat or block_without_rest.mat (this are the regressors made with the UT method, or the other method)
- ➔ Multiple regressors

- o Specify file = x:\Onderzoek\fMRI\Tremor\pp\6666\tremor1\regressor*name of the model you've made. This is for example the convolved orthogonolized frequency regressor of the Extensor Left together with the movement parameters.*
- ➔ Save as Job.mat (in the pp\6666\tremor1\results*name of your model)*
- ➔ Run
  - o This will get the SPM.mat file, to check the file
    - ▪ Review
    - ▪ Select spm.mat
    - ▪ Click design
    - ▪ Design matrix and/or Design orthogonality
- ➔ Estimate
  - o This takes approximately 10 min.
  - o Model estimation
    - ▪ Specify files = x:\Onderzoek\fMRI\Tremor\pp\6666\tremor1*name of your model*\SPM.mat
  - o Method = classical
  - o Run

Contrasts

To look at the activation of the brain at different conditions, use contrasts in SPM:

- ➔ Results
  - o Select SPM.mat in the directory:
    - ▪ X:\Onderzoek\fMRI\Tremor\pp\6666\tremor1*name of your model*\SPM.mat
  - o Define the contrasts you are interested in
    - ▪ Mask with other contrasts = 'NO'
    - ▪ Name of your contrast
    - ▪ None
    - ▪ Threshold = 0.001
    - ▪ Extend threshold = 0
      - • Overlays
        - o Sections = select the t1 (you can find this in pp/*patient's number*
      - • Goto global maxima (ore another place you're interested in)
  - o You can save figures as e.g. jpg-pictures.