

BrainVoyager QX™ analysis - Predictor Tool Manual

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About the program:

BVA-PT is developed as an adaptation of a utility that the author wrote when he was working on fMRI data with BrainVoyager QX™¹. It provides easy to use processing of .rtc and .sdm files, which contain predictors (regressors) for general linear model (GLM) analyses with BrainVoyager QX™. In case of problems, suggestions or any comments on the program or the documentation, please contact HelperTools@gmail.com.

If you encounter a problem, please try to give as many details on how the problem occurred: what were you doing, which file was processed and were there any other factors that may have affected the program's performance. If you use the program, please cite it as "(BVA-Predictor Tool, J.M. Born, Maastricht, The Netherlands)". Additionally, creating and maintaining this software is a time consuming business, therefore if you use this tool, please consider donating any amount of money to the author (Paypal: HelperTools@gmail.com), just remember how helpful it has been to you and how much time it has hopefully saved you.

2. Functions:

2.1 Adding 'dummy'-coded predictors:

When comparing multiple measurements in multiple conditions, it may be required to add empty i.e. 'dummy'-coded predictors to the design matrix of a GLM. For example if your test subjects are measured in two conditions, you have consequently multiple subjects (that you need to group by subject) and multiple conditions that you want to compare. It then becomes necessary to split up the data similar to the example shown below:

	Predictors Group A Pred1, Pred2, ...	Predictors Group B Pred1, Pred2, ...
(Multiple sets) condition A	Real predictors	Dummy coded predictors
(Multiple sets) condition B	Dummy coded predictors	Real predictors

The above implies, that you need to add an identifier to your predictors, which corresponds to your groups. In this example that would be "Group A" and "Group B" for the predictors for condition A and condition B, respectively. By doing so, all different measurements contain the same number of predictors and those have the same labels, allowing GLM analysis.

BVA-PT allows you to easily add additional groups of dummy-coded predictors where the predictors that are present in the original file are used as template for the dummy coded set. The group-identifier is added to yield predictors Group A_Pred1, GroupA_Pred2, ... and Group B_Pred1, Group B_Pred2, ... in case of the

¹ BrainVoyager™ is a product of Brain Innovation B.V., Maastricht, the Netherlands

example above.

2.2 Linear trend removal and z-transformation of 3D-motion correction parameters:

In BrainVoyager™, motion that occurs during the test is usually corrected in the preprocessing of the functional MRI data. In some cases it may still be helpful to include the motion-estimates (output from the motion-correction) in the GLM. When doing so, these predictors may be improved by removal of any linear trends and de-meaning, which ensures that the predictor can be fitted more closely to the data (from which linear trends were also removed). To standardize the scaling of the predictors, a z-transformation may be applied as well, which scales the data according to its own variation.

2.2.1 High pass filter

The motion estimates that BrainVoyager produces contain both low and high frequency components. Although the motion is corrected for in the data preprocessing, it is possible that residual signal changes might be present. Especially fast movements may induce fast fluctuations in the data. Using a high pass filter, it is possible to obtain this high frequency noise only for the GLM. When briefly tested, the best results were obtained when a filter width of 5-8 cycles in time course were used.

2.2.2 Low pass filter

Low frequencies consist of slow position shifts of the subject in the scanner, which should be effectively removed by BrainVoyager's 3D-motion correction functions. If you would rather use a predictor that contains these low frequency drifts you may use a low pass filter.

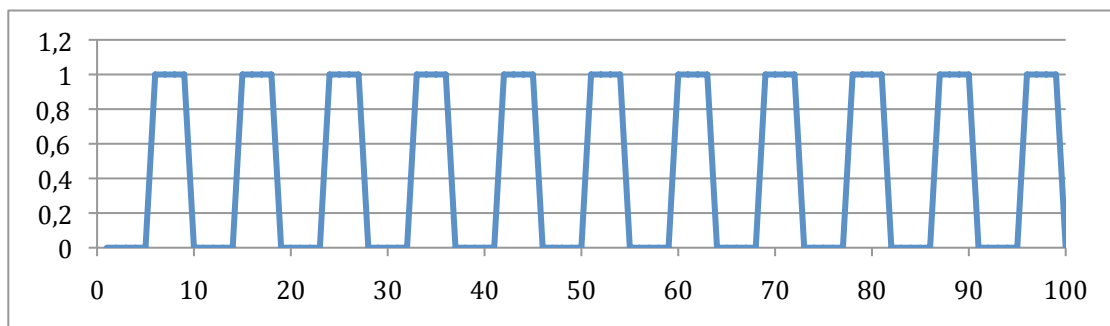


Figure 2.1: Eleven simple box car experiment predictors as might be seen in a given experiment

2.3 Adding predictors for habituation / diminished returns

When testing our subjects in the scanner, there are multiple reasons why the stimulus related signal that we measure would decrease over time: Firstly, the most straightforward effect is fatigue. A subject performing the paradigm after just entering the scanner will usually be more alert than a subject who has been performing tests for many minutes. Secondly, in event related paradigms, and probably most pronounced in fast event related designs, subject will get used to

the stimuli and the procedure and loose attention. These effects are known in statistics as the law of diminishing returns. Although it is best to avoid the effects

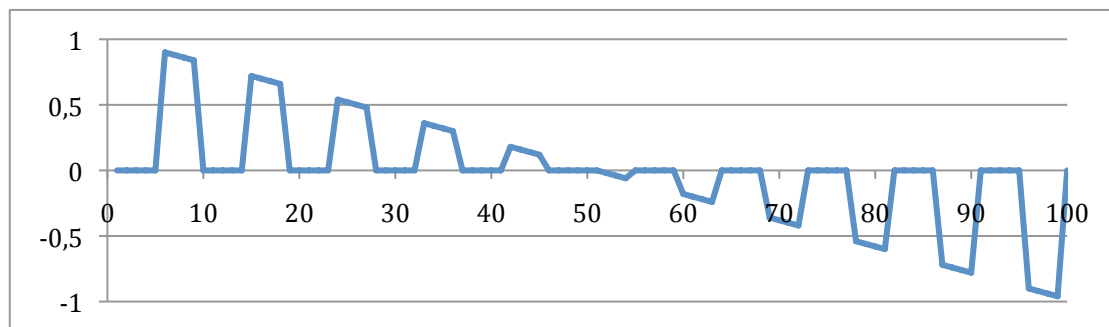


Figure 2.2: Model of linear decrease of fMRI signal return. Note that the habituation predictors are comparable to the original predictors in terms of their timing, however, the habituation predictors decrease from positive value to negative value at the end of the time course.

described altogether, this is not possible, since the first loss of attention may already be present after a few minutes.

To give an example, think of an experiment that is modeled with simple box car

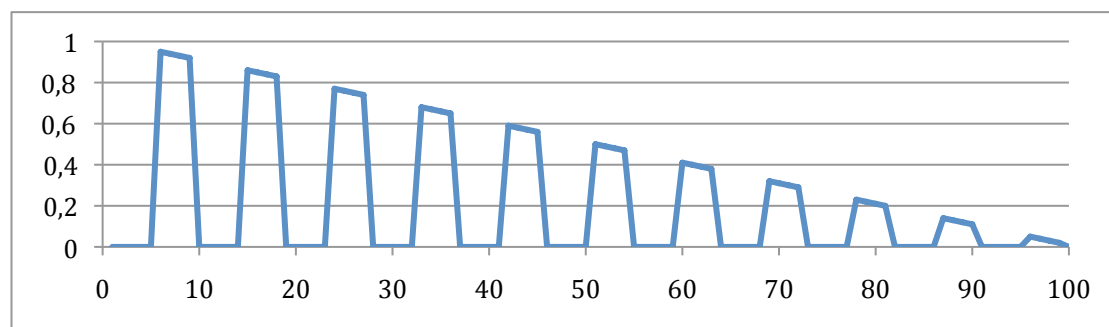


Figure 2.3: Both predictors added together, both with a beta value of 0.5. The resulting model predicts full signal at the start of the test and no signal at the end of the session.

predictors (Figure 2.1). During the experiment we presume that there is some habituation that, in this case is modeled as a linear process (Figure 2.2).

The GLM that includes the original predictors and the habituation predictors scales both predictors to the best fit with the actual data. In figure 2.3 an example is shown in which the predictors are added equally (both with a beta value of 0.5).

To model the decreasing signal due to habituation predictors can be included, which model the stimuli as a decreasing predictor. Scaled to best fit and added to the standard predictors using the standard GLM, these predictors can often significantly improve the model.

2.3.1 Linear habituation model

The linear habituation model uses a continuously decreasing adaptation of the stimulus predictor. Leading to a predictor that linearly decreases from +stimulus

at the start of the time course and –stimulus at the end of the time course. This is shown in the given example (Figures 2.1-3).

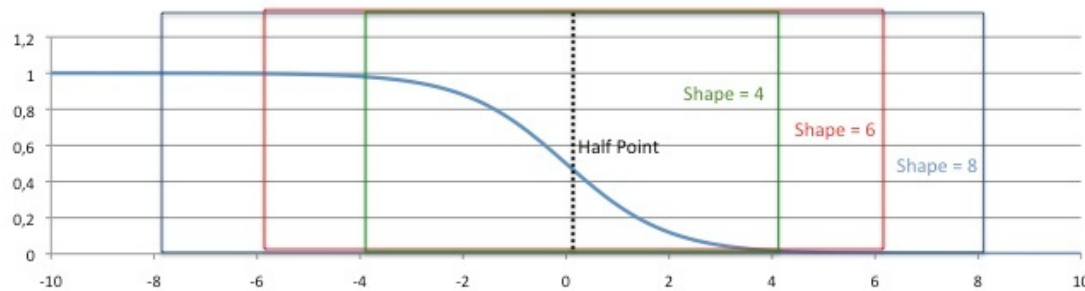


Figure 2.4: The sigmoidal curve with its definition. Half point indicates the point at which the sigmoidal curve reaches half the original value. The part of the curve that is used, is defined by the shape setting.

2.3.2 Sigmoidal habituation model

In many cases, it may be more suitable to predict habituation as a non linear function. The sigmoid function can be used to model multiple biological systems. Therefore, this function is included as option. The sigmoidal curve is defined by two numbers in BVA-PT (Figure 2.4).

The sigmoidal curve is defined as reaching full shape with x-values ranging from -6 to +6 in standard space. If the shape is chosen as “6” in BVA-PT, the time course is fitted to this standard window. By choosing larger or smaller number for its shape, the time course is scaled accordingly, leading to a different slope. The half point of the sigma curve can be shifted within the time course, to fine tune the volume or time where the habituation is half way.

2.3.3 (Simple) non-linear habituation model

The third model that can be chosen to model the habituation, is the simple non-linear model, which is defined by only one number, the power (p) to which the expression is raised. The function is defined as

$$y = 1 - \left(\frac{x-1}{n-1} \right)^p$$

in which x is the current point in the time course, and n is the total number of points in time course. This function is up-scaled to range from 1 to -1. The chosen p has to be a value >0. Additionally, this function can be chosen as mirrored along the line y=x.

2.4 Analyze the predictors with GLM / correlations

When modeling any signal by means of GLM, it is important to ensure that the given predictors are orthogonal, i.e. not correlated, since the beta values cannot be determined unambiguously if multiple predictors can explain the same part of the given signal. In Brainvoyager QX, correlated predictors will therefore lead to a singularity warning, indicating that the predictors are sub-optimal to create a good model. To determine how orthogonal the predictors are, BVA-PT includes a predictor analysis functionality. The analysis consists of two parts. In the first

place, simple correlations are calculated between pairs of all predictors. From this analysis, graphical and numerical displays are shown. Furthermore, a GLM analysis is performed, in which each predictor is modeled by with all other predictors. Thereby it is possible to determine whether two predictors are strongly correlated and whether predictors potentially might be excluded because they can be predicted by the weighted sum of the other remaining predictors.

3. Using the program

The main screen of the program is a simple window, showing buttons for all the procedures that can be performed (Figure 3.1). The only exceptions are the about box and manual check for updates which can be invoked using the “Help” menu. The about box can also be invoked using the keyboard shortcut command -“A” on Mac, and ctrl-A on windows and linux.

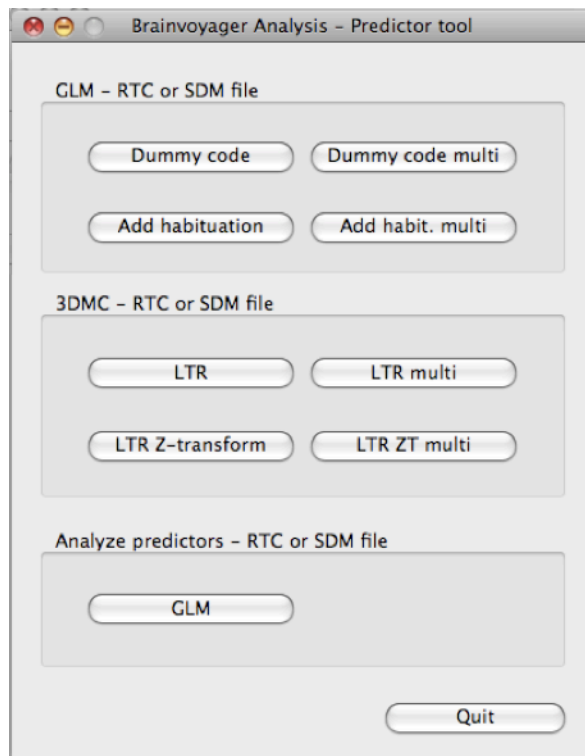


Figure 3.1: the main screen of BVA-HT. Each given procedure is represented here with its own button. Abbreviations used are “LTR” = “linear trend removal”, “ZT” = “Z-transform” and “habit.” = “habituation”. The term “multi” stands for “multiple files”.

3.1.1 Adding dummy coded predictors to a single file

Click on the button Dummy code and open the desired file. If your file is readable, you should see a dialog similar to figure 3.1.1. The contents of the RTC file are shown in the left part of the window, above which the file name is shown. In the “group” field there will be only one group present, which is called “Group1” by default. This group represents all the predictors that are present in the chosen file and which should be shown in the “Items” box. In figure 3.1.1, a 3D motion correction file was opened, therefore the six translation and rotation parameters are shown. If you were to save the file now by clicking on the “Go!”, the created file would be only different from the original file in having “Group1_” added to every predictor name. In the right part of the window, there is the “Identifier” (ID) field.

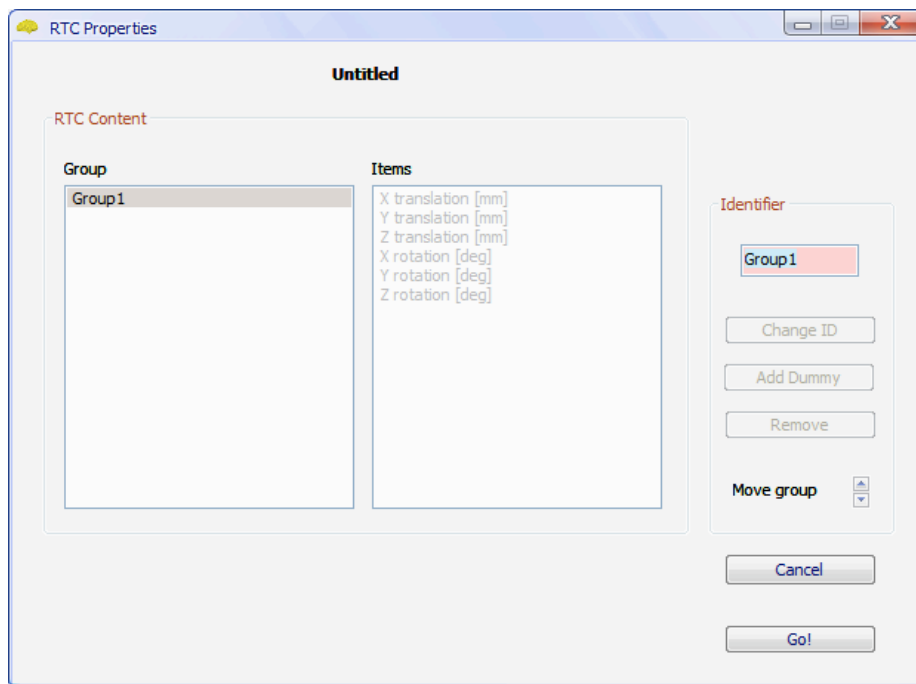


Figure 3.1.1 The “Dummy code” dialog. A red background in this field indicates that the selected group is the group that is contained in the predictor file. This group can only be renamed but not removed. To rename the group, simply change the text in the ID field and click “change ID”. Groups (that will contain dummy predictors) can be similarly created by clicking “Add Dummy” instead (Figure 3.1.2).

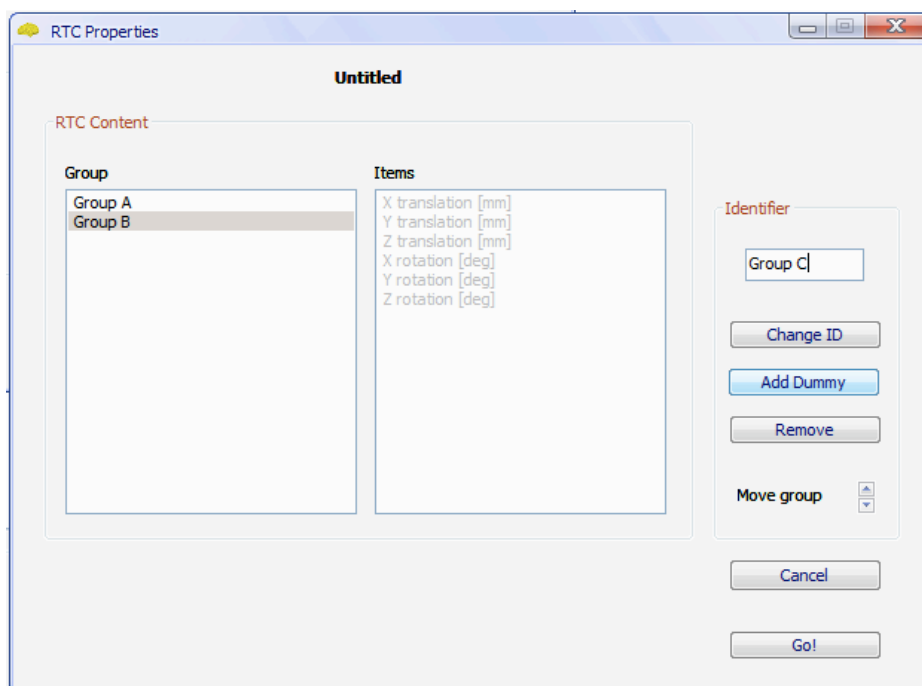


Figure 3.1.2 Adding and renaming groups. To create the correctly dummy coded file, you may need to change the order of the groups. This is easily done with the “Move group” arrows. When creating multiple dummy coded files, as described under 2.1, make sure to name the groups correctly and always use the same order of groups. When done with the settings, simply click go, then choose a location/filename to save the new file in the next window.

3.1.2 Adding dummy coded predictors to multiple files

To dummy code multiple files, click on “Dummy code multi” in the main program window. This will open the dialog shown in Figure 3.1.3.

The “multi” dialog is in essence the same as the “Dummy code” single file dialog. However, there are a few extra settings that can be changed in the dialog.

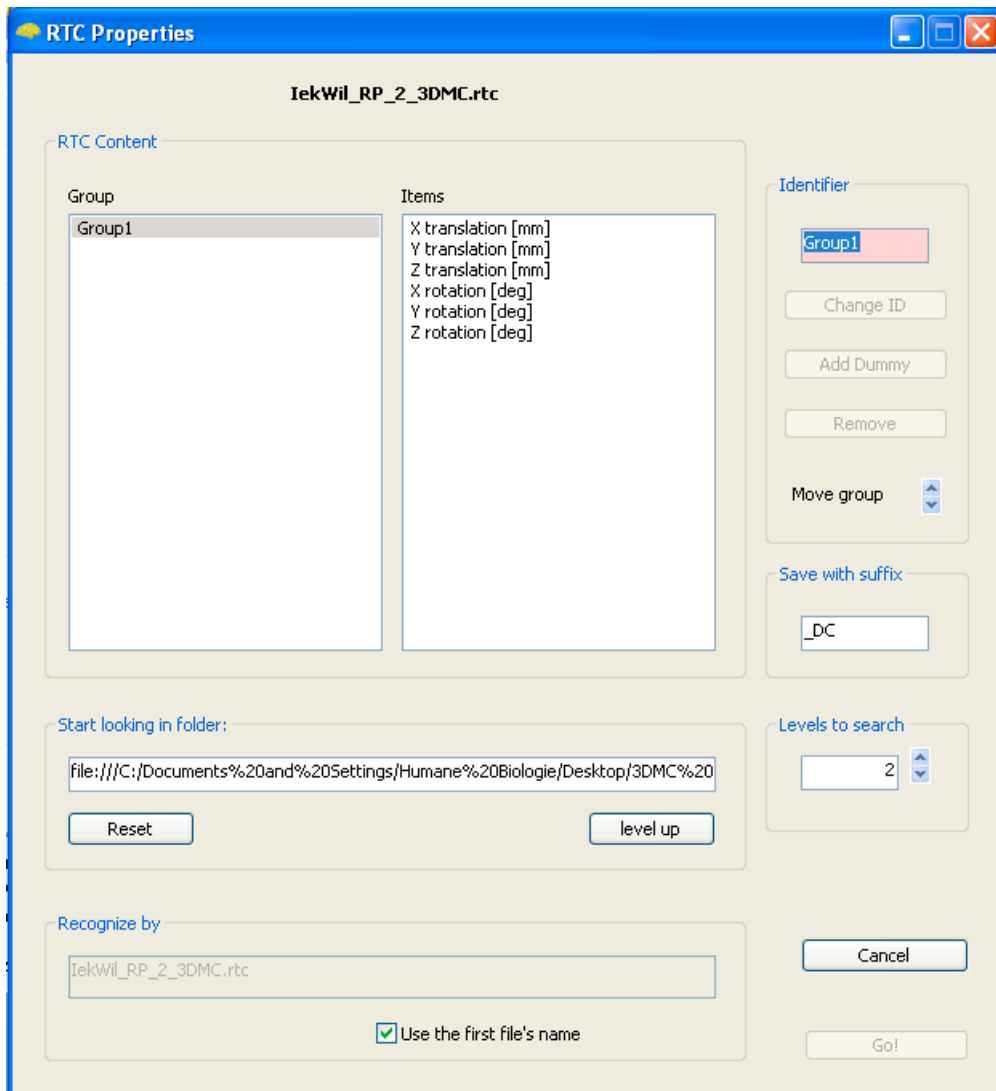


Figure 2.1.3: The “Dummy code multi” dialog.

- The text-field ‘Start looking in folder:’ shows the folder where the program starts searching for files.
- BVA-PT will search for files in up to 10 levels, i.e. within the folder that you specify, within all folders that it contains, the subfolders contained therein and so forth. You may press the button ‘level up’ to go up one level in your directory. The ‘reset’ button will reset the path to the folder that contains the file you opened originally. You cannot enter a path directly into this field.
- Note: please realize that searching through many folder levels can result in long waiting times, since you may end up searching most or all files on the whole computer.

- The 'Recognize by' field allows you to specify a pattern in the filename that the program uses to recognize files it should include.
- NOTE: be aware that ambiguous patterns may lead to strange results, i.e. if you were to specify '3' as a pattern, any file that contains the number '3' will be probed and potentially included.
- You can specify your own suffix for the treated data. Standard is a suffix '_DC'.

WARNING: Any multi dialog will create the resulting files according to the scheme OriginalFilename_SuffixThatWasSpecified.rtc. The new file will be written to the directory that contains the original file. NO CHECK IS PERFORMED TO DETERMINE IF A FILE WITH THIS EXACT FILENAME IS ALREADY PRESENT! If you do not use the suggested standard naming scheme, make sure that you specify a naming scheme that is unique. Otherwise, the newly created files may accidentally overwrite preexisting data!

3.2.1 Linear trend removal & de-meaning of 3D motion correction

parameters

To perform this action, simply click on the button "LTR" and choose a RTC/SDM file containing motion correction estimates (typically those files are named ...3DMC.rtc or .sdm). After the processing is done, you will be prompted to specify an output location for the de-trended/de-meant file. The original file name with the addition "_L" is suggested as the new file name, however, you may choose any desired filename. You will be asked to specify if you want to use a filter, either high pass or low pass (see 3.2.3).

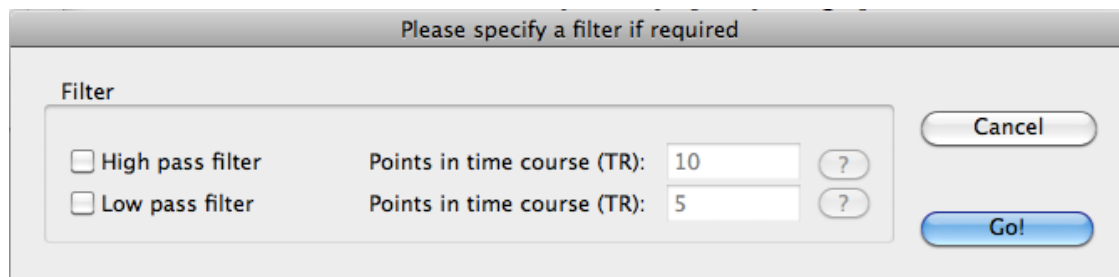
3.2.2 LTR, de-meaning & z-transformation of 3D motion correction

parameters

This function is used by clicking LTR Z-transformation. Essentially the option does the exact same thing as 3.3, except that a z-transformation is performed before the de-meaning step. Consequently, the standard suggested file name has the addition "LTRZT". You will be asked to specify if you want to use a filter, either high pass, low pass or both (see 3.2.3).

3.2.3 Filtering the data

If you want to filter the motion correction estimates, you may specify a high pass filter or a low pass filter. If there is reason to use both, this is possible. However, the settings used will be of major importance, since it is quite possible to filter out all the signal. Generally, you would want a high pass filter to obtain the fast movements, rather than the slow motion that may correlate more closely with the actual BOLD signal. To view the filter settings in cycles in time course or frequency in Hz, click on the '?' button next to the filter settings (Figure 3.2.3 and 3.2.4), which will open the filter specifications (Figure 3.2.5).



3.2.3 The filter dialog. Simply indicate which filter you want to apply, and specify the filter's window

3.2.4 LTR, de-meaning with or without z-transformation on multiple files

To easily process whole datasets at once, you may choose to perform LTR and de-meaning, with or without z-transformation on multiple files. Click on the button “LTR-multi” or “LTR ZT-Multi”. You will be prompted to choose a 3D motion correction file. After you select such a file, you will be asked to specify the task with the window in Figure 3.2.4:

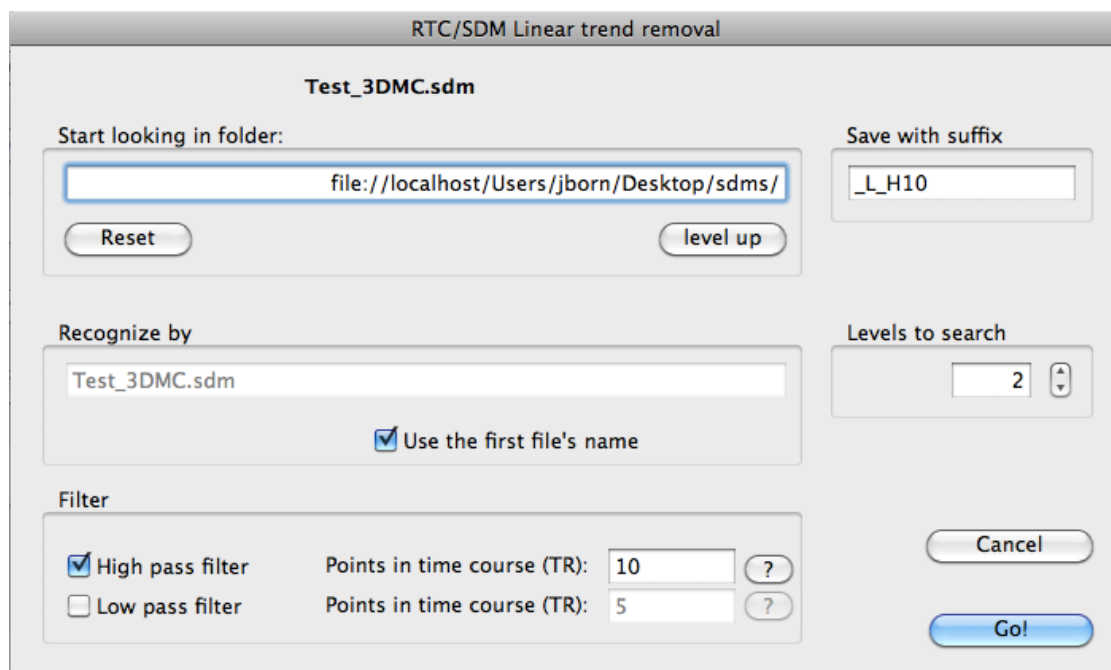


Figure 3.2.4 The “Linear trend removal multi” dialog.

- You can specify your own suffix for the treated data. Standard is a suffix ‘_L’ for LTR and de-meaning and ‘_LZ’ for data that has been additionally z-transformed.
- If you want to filter the motion correction estimates, you may specify a high pass filter, a low pass filter or both. If there is reason to use both, this is possible. However, the settings used will be of major importance, since it is quite possible to filter out all signal. Generally, you will want a high pass

The image shows a software dialog box titled 'Specify filter'. It is divided into two main sections. The top section, 'Scan settings', contains two input fields: 'TR' with the value '2' and 'Volumes' with the value '988'. The bottom section, 'Filter settings', contains three input fields: 'Frequency' with the value '0.025', 'Cycles' with the value '49.400', and 'Points in Time course' with the value '10' and small up/down arrow buttons. A 'Done' button is located at the bottom center of the dialog.

3.2.5 The specify filter dialog. Review the filter settings in terms of cycles and frequency. Adjust the filter by adjusting points in time course and review the changes The filter dialog.

filter to obtain the fast movements, rather than the slow motion that may correlate more closely with the actual BOLD signal.

- The standard suffix for the filters are '_H' or '_L' followed by the filter width, for high pass filter or low pass filter, respectively.
- The text-field 'Start looking in folder:' shows the folder where the program starts

searching for files.

- BVA-PT will search for files in up to 10 levels, i.e. within the folder that you specify, within all folders that it contains, the subfolders contained therein and so forth. You may press the button 'level up' to go up one level in your directory. The 'reset' button will reset the path to the folder that contains the file you opened originally. You cannot enter a path directly into this field.
- NOTE: please realize that searching through many folder levels can result in long waiting times, since you may end up searching most or all files on the whole computer.
- The 'Recognize by' field allows you to specify a pattern in the filename that the program uses to recognize files it should include.
- NOTE: be aware that ambiguous patterns may lead to strange results, i.e. if you were to specify '3' as a pattern, any file that contains the number '3' will be probed and potentially included.

After you complete the entries in the dialog, simply click 'Go!'. The program will show a progress window to indicate the status of the conversions.

WARNING: Any multi dialog will create the resulting files according to the scheme OriginalFilename_SuffixThatWasSpecified.rtc. The new file will be written to the directory that contains the original file. NO CHECK IS PERFORMED TO DETERMINE IF A FILE WITH THIS EXACT FILENAME IS ALREADY PRESENT! If you do not use the suggested standard naming scheme, make sure that you specify a naming scheme that is unique. Otherwise, the newly created files may accidentally overwrite preexisting data!

3.3 Adding habituation predictors

3.3.1 Single file

To add habituation predictors to a single file, click on “Add habituation”. After selecting the appropriate file, the screen shown in Figure 3.3.1 is shown. In this dialog simply specify which predictors you want to model for habituation, and

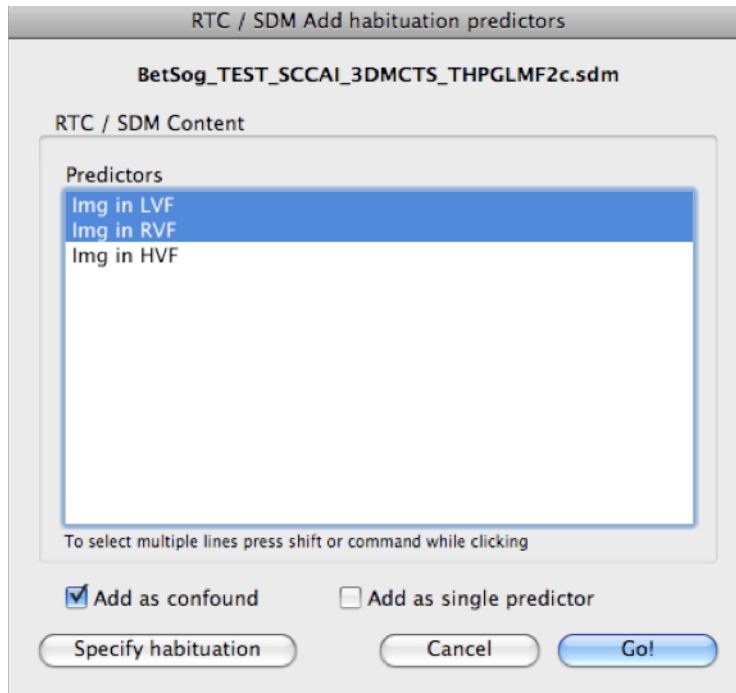


Figure 3.3.1 The add habituation predictors dialog. In this window, select the predictors that you want to have modeled as habituation related predictors, choose whether you want them to be included as confounds (SDM files only). If you check “add as single predictor”, all selected predictors will be modeled and merged into one new predictor. Otherwise, one habituation model is made per original predictor.

choose whether you want them to be added as a single predictor, or one habituation predictor per included original predictor. If you are using SDM files you can choose to add the habituation predictors as a normal predictor as opposed to the default of adding it as a confound. Generally, however, it seems a more plausible option to add it as confound. To specify the shape of the habituation that will be assumed for the model, use the ‘specify habituation’ button. There are 3 models available in the ‘specify habituation dialog’ (Figure 3.3.2).

3.3.2 Multiple files

The multi dialog (Figure 3.3.3) is similar to the single dialog, except for the options that are associated with the searching of multiple files.

- You can specify your own suffix for the treated data. Standard is the suffix ‘_HP’
- The text-field ‘Start looking in folder:’ shows the folder where the program starts searching for files.

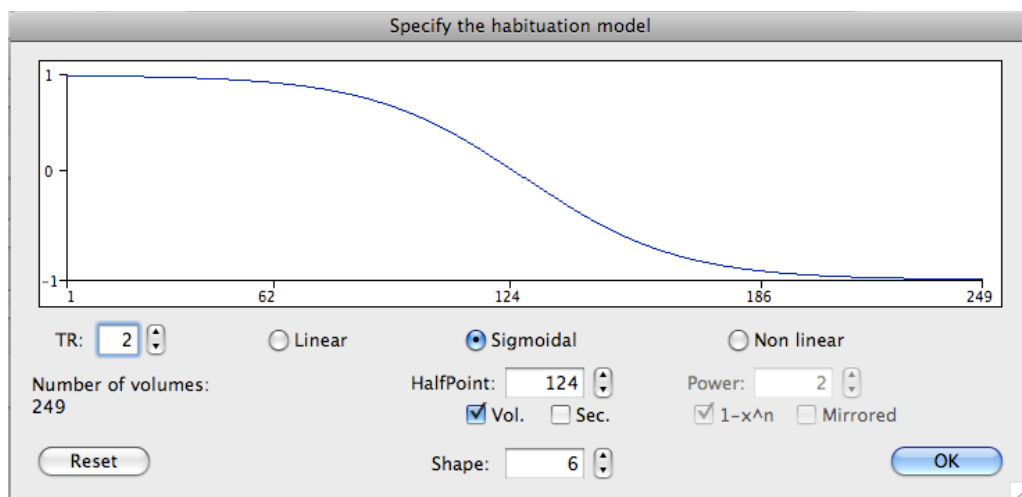


Figure 3.3.2 The specify habituation dialog. In this dialog you can specify the shape of the habituation effect using the method of your choice. Generally it is possible to directly enter numbers into the fields, however, make sure that the graph shows a plausible curve after you did. The 'Reset' button restores the default settings (HalfPoint = Number of volumes/2 = Duration/2, Shape =6, power =2). The TR setting is necessary only to convert between volumes and seconds for the sigmoidal model

- BVA-PT will search for files in up to 10 levels, i.e. within the folder that you specify, within all folders that it contains, the subfolders contained therein and so forth. You may press the button 'level up' to go up one level in your directory. The 'reset' button will reset the path to the folder that contains the file you opened originally. You cannot enter a path directly into this field.
- NOTE: please realize that searching through many folder levels can result in long waiting times, since you may end up searching most or all files on the whole computer.
- The 'Recognize by' field allows you to specify a pattern in the filename that the program uses to recognize files it should include.

NOTE: be aware that ambiguous patterns may lead to strange results, i.e. if you were to specify '3' as a pattern, any file that contains the number '3' will be probed and potentially included.

WARNING: Any multi dialog will create the resulting files according to the scheme OriginalFilename_SuffixThatWasSpecified.rtc. The new file will be written to the directory that contains the original file. NO CHECK IS PERFORMED TO DETERMINE IF A FILE WITH THIS EXACT FILENAME IS ALREADY PRESENT! If you do not use the suggested standard naming scheme, make sure that you specify a naming scheme that is unique. Otherwise, the newly created files may accidentally overwrite preexisting data!

RTC / SDM add habituation predictors

BetSog_TEST_SCCAI_3DMCTS_THPGLMF2c.sdm

RTC Content

Predictors

Img in LVF
 Img in RVF
 Img in HVF

To select multiple lines press shift or command while clicking

Save with suffix

_HP

☒ Add as confound
☐ Add as single predictor

Specify habituation

Start looking in folder:

sussen/MBIC_fMRIWorkshop2008/GSG_Exercise%20copy/data/

Reset

level up

Levels to search

2

Recognize by

BetSog_TEST_SCCAI_3DMCTS_THPGLMF2c.sdm

☒ Use the first file's name

Cancel

Go!

Figure 3.3.3 The add habituation predictors multi dialog. In this window, select the predictors that you want to have modeled as habituation related predictors, choose whether you want them to be included as confounds (SDM files only). If you check "add as single predictor", all selected predictors will be modeled and merged into one new predictor. Otherwise, one habituation model is made per original predictor.

3.4 Analyze the predictors with GLM / correlations

Open the file you want to analyze by clicking on the button 'GLM' or via the menu. The file is analyzed and the analysis report is shown (Figure 3.4.1 and 3.4.2).

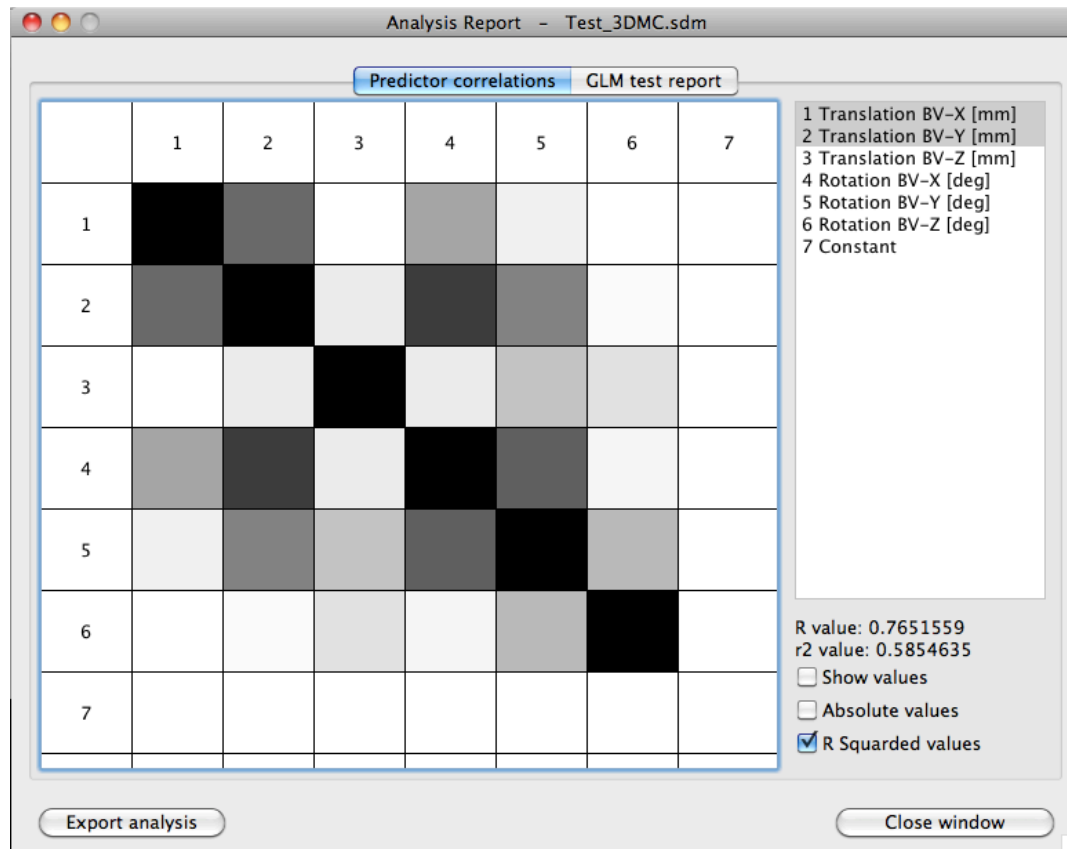


Figure 3.4.1 The analysis report window – predictor correlations tab. On this tab, you find a simple graphical representation of the correlation matrix. Every predictor is shown correlating with every other. Starting with this version of BVA-PT, R^2 values are selected by default, because these values represent the explained variance, which is most informative. Also absolute values $|R|$ can be shown, i.e. black is a correlation of both 1 and -1, while zero is represented by white and if nothing is selected, white represents -1 black 1. Additionally you can check the 'show values' box to show values instead of colors in the graph. When moving the mouse over the matrix, the R value of the correlation over which the mouse is located is shown, and the

In the given example here, the analysis can be described as such: Looking at the analysis shown in figure 3.4.1, it is probably best to avoid anything that looks like dark gray or black. If all correlations show white, the given model is best (= completely orthogonal). From figure 3.4.1 can be determine that in this example predictor 2 (BV-Y) has the strongest correlations with other predictors, so this may be a good candidate to exclude from the model to improve orthogonality of the design.

Another way to determine one or multiple predictors that should be excluded, is the GLM analysis shown in figure 3.4.2: this analysis determines how well a given predictor can be modeled by all the other predictors in the set. The analysis

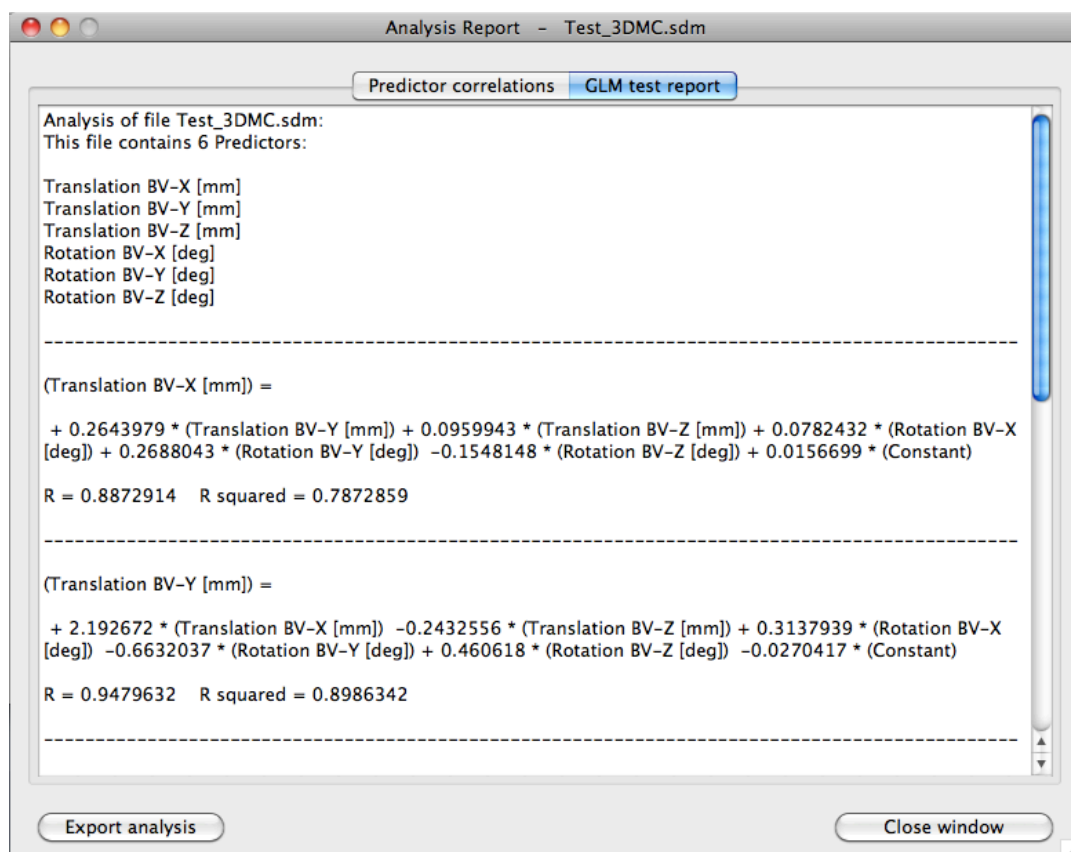


Figure 3.4.2 The analysis report window – GLM test report tab. On this tab, you find an extensive GLM report of your design matrix. Via GLM, it is attempted to model each predictor with the weighted sum of the other predictors. The fit of the model is given as R value. Additionally, the report states if predictors were excluded because they were either empty, or a constant. Export analysis creates a text file, containing the matrix values and the GLM report (Figure 3.4.2)

itself is comparable with what Brainvoyager does when fitting predictors to the data. The difference is that the 'data' in BVA-PT onto which the other predictors are fitted, is actually one of the predictors. This might be explained in another way: given a set of predictors called a, b, c and d we would like to know if predictor a is needed, or in other words: if the remaining predictors (b, c and d) are scaled (= beta weights), do they together actually contain a? Or in math terms: to what extent is the formula "a = beta1*b + beta2*c + beta*d" true?

It is hard to specifically define the cut off point to include or excluded predictors. If one of the predictors on the GLM tab can be explained by the scaled other predictors in your model, to reach an R^2 of ~ 0.8 or higher (explained variance of $>80\%$), it is worth considering to remove this predictor. Unfortunately, this is no exact science: testing of different models may be the best way to determine the costs and benefits of a predictor; however, if Brainvoyager QX issues a singularity warning it may be best to remove one or more relatively strongly correlated predictors.

3.5 Additional notes on BVA-PT

BVA-PT 1.5 is the first version to write programmed settings to a preference file under windows and linux. So far, only a few settings, such as the last visited paths for saving/opening are recorded.

BVA-PT 1.5 includes an automatic check for updates function, which is set to check for updates once a week. No information at all is recorded concerning these checks, and to keep up to date with any bug fixes and new features, this function is intended to guarantee that. One of the next minor updates of the program will include extensive preferences support, which will also included options for the automatic update check.

If you run into any problem, or if you have suggestions or wishes for functions to include in the program, please feel free to mail to HelperTools@gmail.com with your comments.