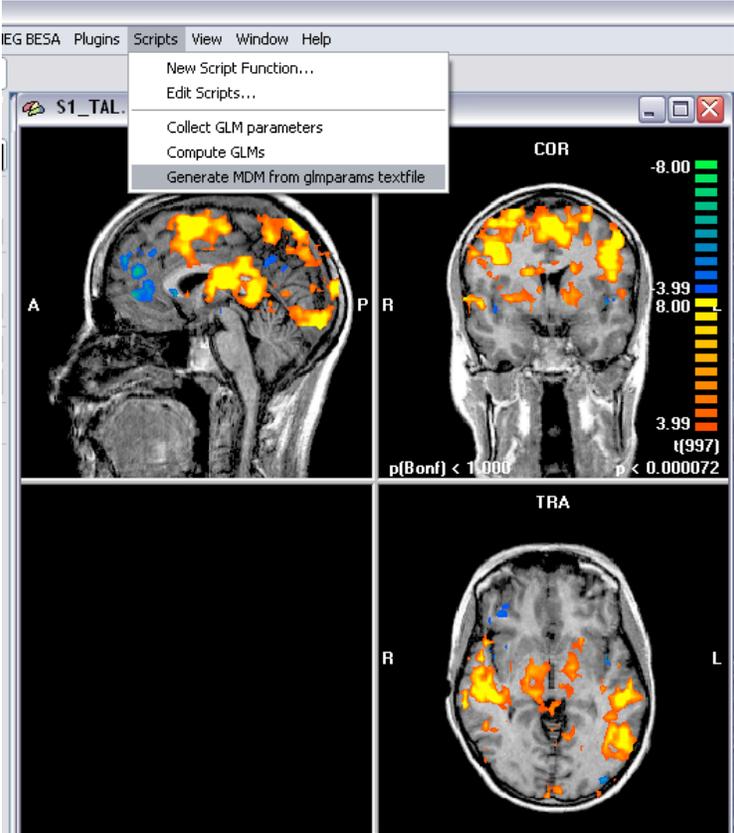


Batch processing of GLMs



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Introduction

The BatchProcessingStatistics_v01_bvqx18.qsa script project for BrainVoyager QX is created to facilitate the computation of GLM files. The script project is based on text files with filenames and/or parameters.

The functions can be started via the BrainVoyager QX 'Scripts' menu. The functions can be used directly, without modification of the scripts in the script project. The GLM files will be written to the same directory as the source files, with the name of the functional file and the design matrix file (*.rtc).

Currently, the script project has three functions. The first two functions are meant to facilitate batch processing of single subject GLMs. The third function is a bonus as it generates an multi-study (*.mdm) file based on the file "glmparams.txt" resulting from the first function.

Note for version 0.1

Please note that this is the very first version of the project. So not all GLM possibilities are yet implemented in the script project. Please check the results carefully. All appropriate disclaimers apply.

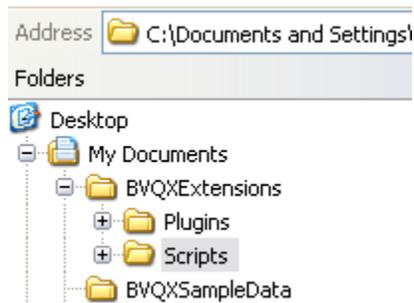
*Hester Breman, Brain Innovation B.V.
June 2007*

Installing the project

To use the functions described above, two simple steps need to be taken. At first, ensure the proper location of the script project. Secondly, load the script project as current script project in BrainVoyager QX.

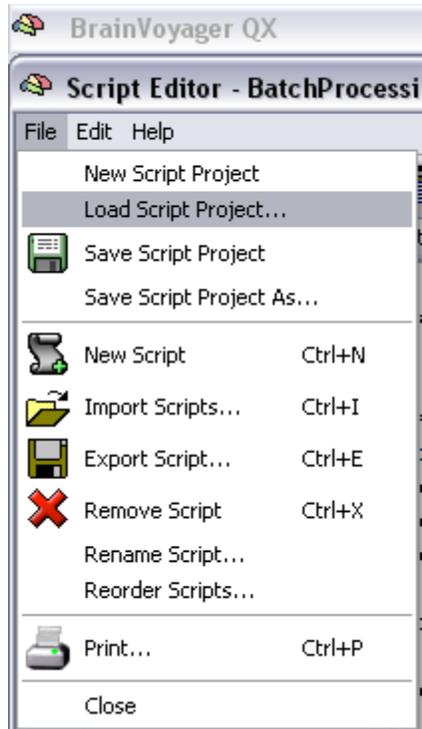
1. Location of the script project

The script project 'BatchProcessingStatistics_v01_bvqx18.qsa' should be located in the folder /(My) Documents/BVQXExtensions/Scripts/.



2. Setting the project as current in BrainVoyager QX

To load the script project, open the script editor via the BrainVoyager QX 'Scripts...' menu. Select the 'Edit scripts...' option. The script editor will open. On the Mac, the editor screen is sometimes behind the main BrainVoyager window, but it should be visible in the dock. Then, load the script project via the script editor menu 'File'. Select the 'Load script project' function.



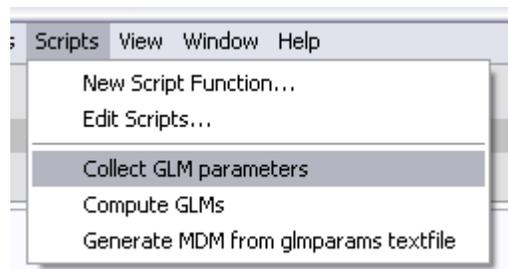
Click the 'Save' icon (floppy disk) or use the 'Save Script Project' function. Close the script editor. The functions should now be visible in the Scripts menu of the BrainVoyager QX main menu.

Use of the functions

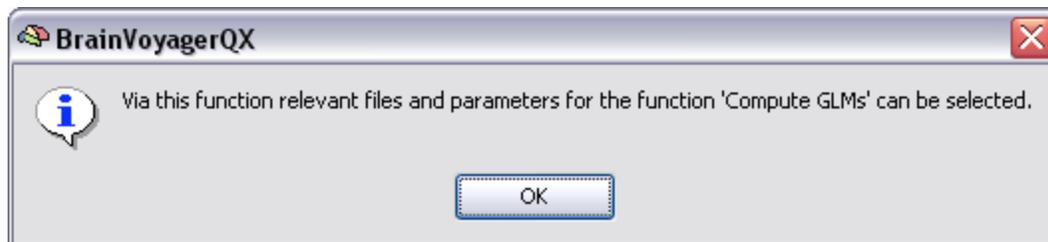
The functions do not need to be modified, since the parameters are entered interactively via the function “Collect GLM parameters”. Since the parameters are written to a text file, the GLMs can be computed at any convenient time, by loading the “glmparams.txt” file and activating the function “Compute GLMs” in the Scripts menu.

Collecting parameters for the GLMs

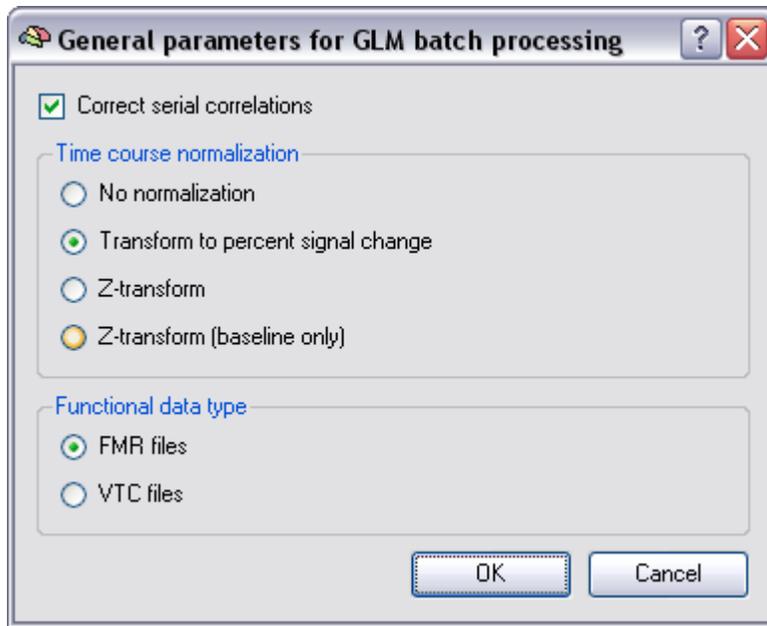
To write the parameters for the GLM batch process to a text file, select the function “Collect GLM parameters” in the ‘Scripts’ menu option of the BrainVoyager QX main window.



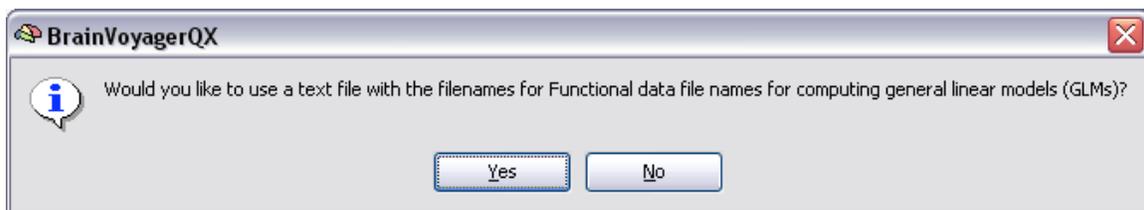
A message box announces the purpose of the function:



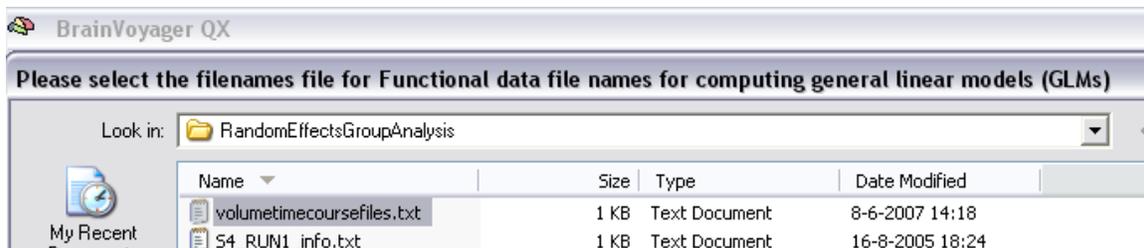
Then, select time course normalization, the type of files and whether to correct for serial correlations or not:



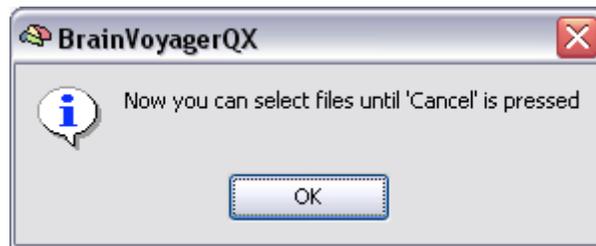
For a short explanation of the options, please see the 'GLM Options' background information. Next, the functional data files can be selected, which are either *.fmr files or *.vtc files:



For each batch of files, one can select the text file that was a result from a previous batch (see 'volumetimecoursefiles.txt' in the figure below).



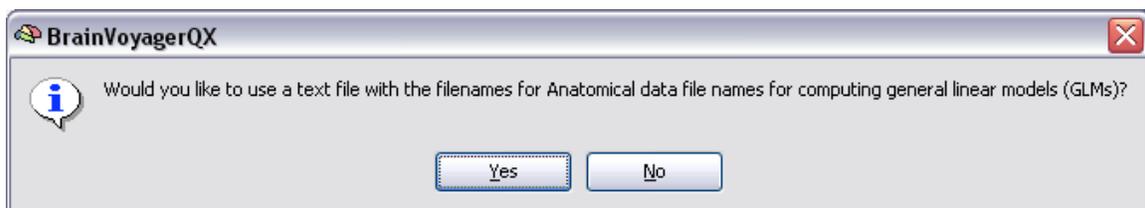
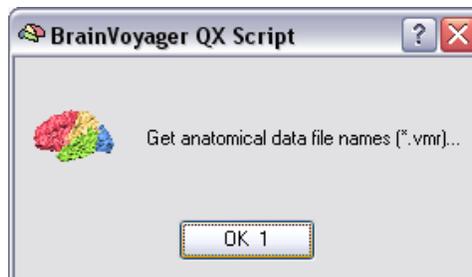
It is also possible to select the files one by one:



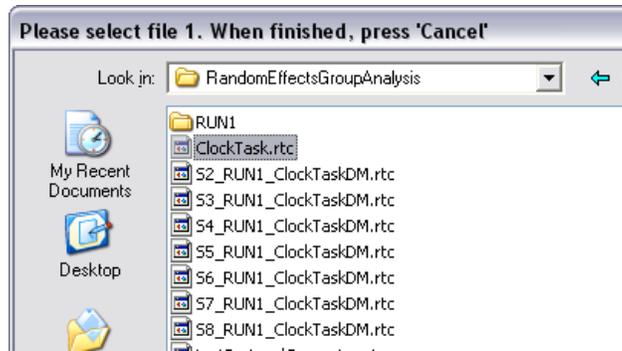
To stop selecting, simply press 'Cancel' in the file dialog. Then, the design matrix filenames can be selected:



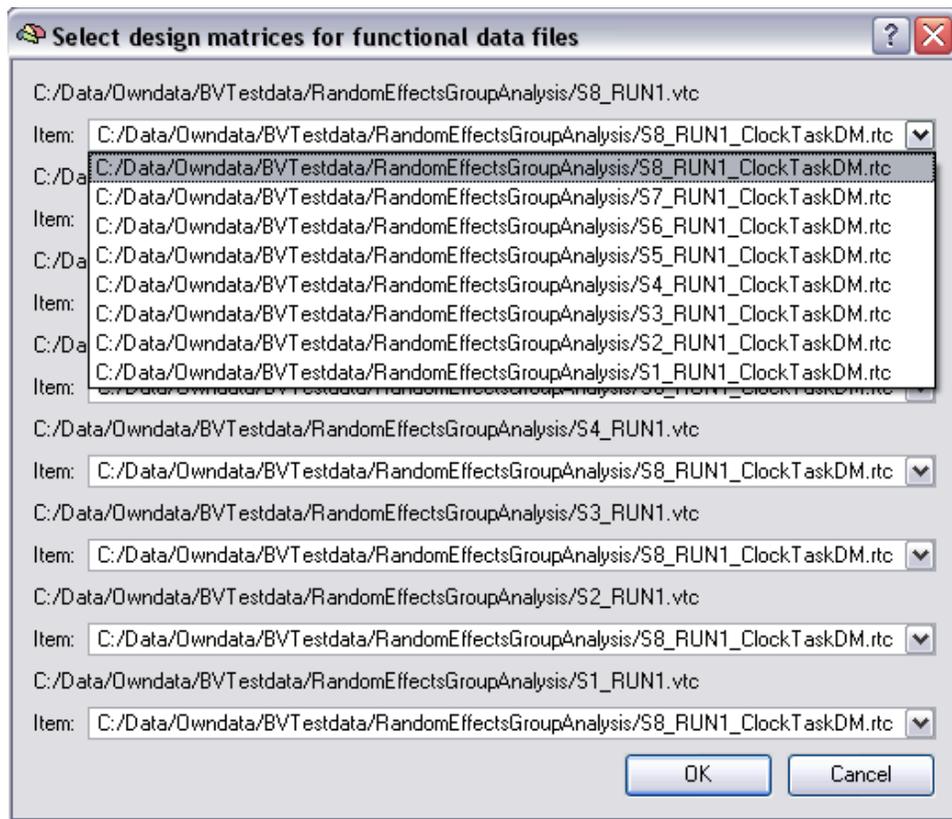
In case volume time course files (*.vtc) files are chosen as functional data, also anatomical files need to be collected. Actually, only one anatomical file should suffice.



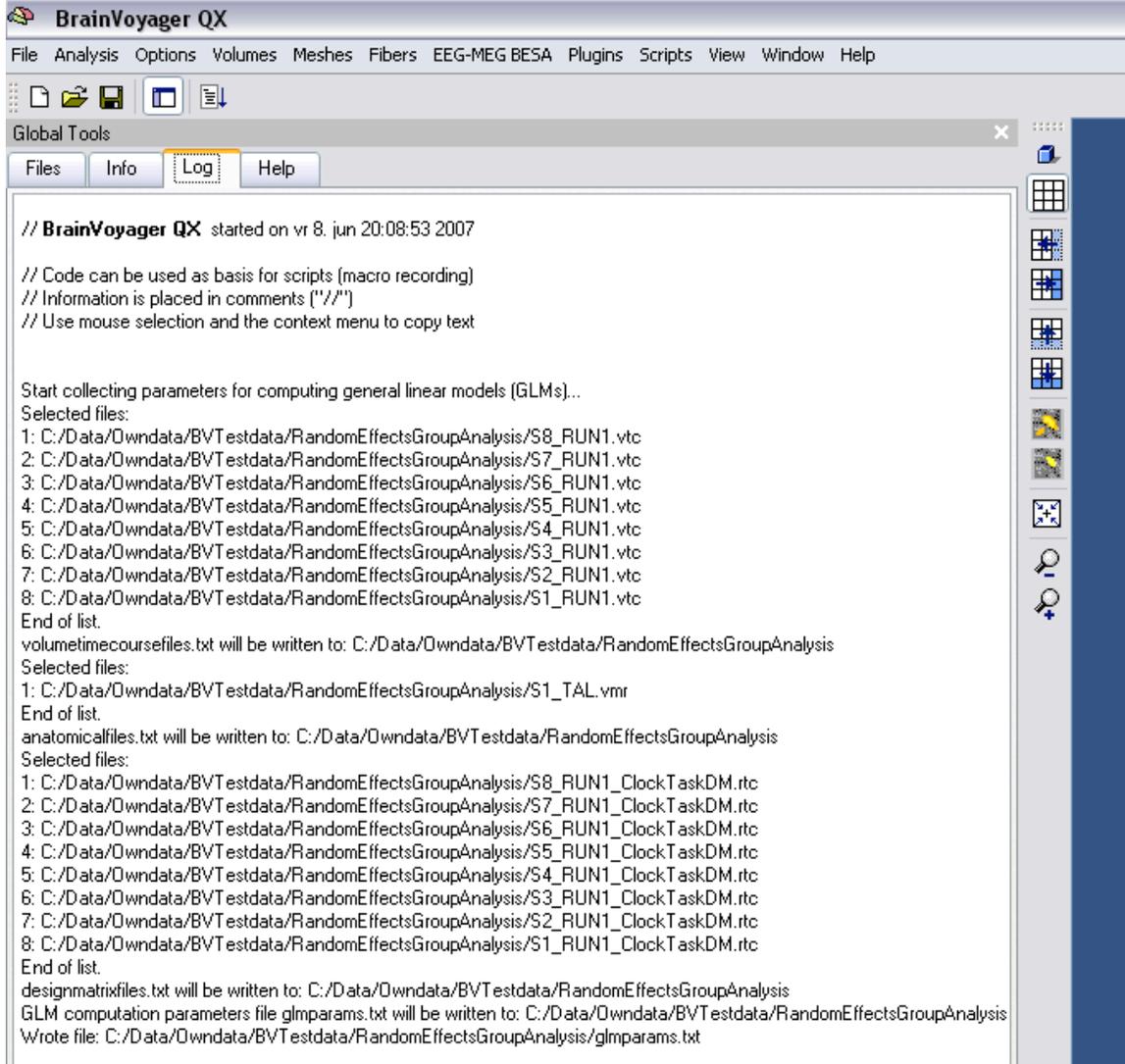
If 'No' is selected, the file dialog will appear until 'Cancel' is pressed:



When all functional data and design matrices are collected, a dialog appears. For each functional file a drop-down box is provided, from where the appropriate design matrix file can be selected.

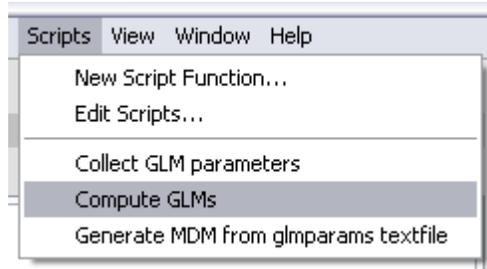


The results are not only written to the text file “glmparams.txt” but also to the BrainVoyager QX Log tab:

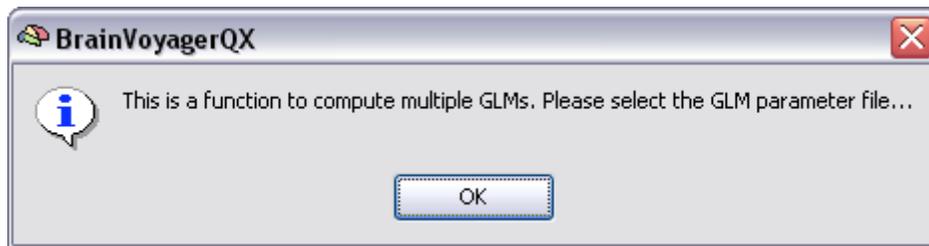


Computing the general linear models

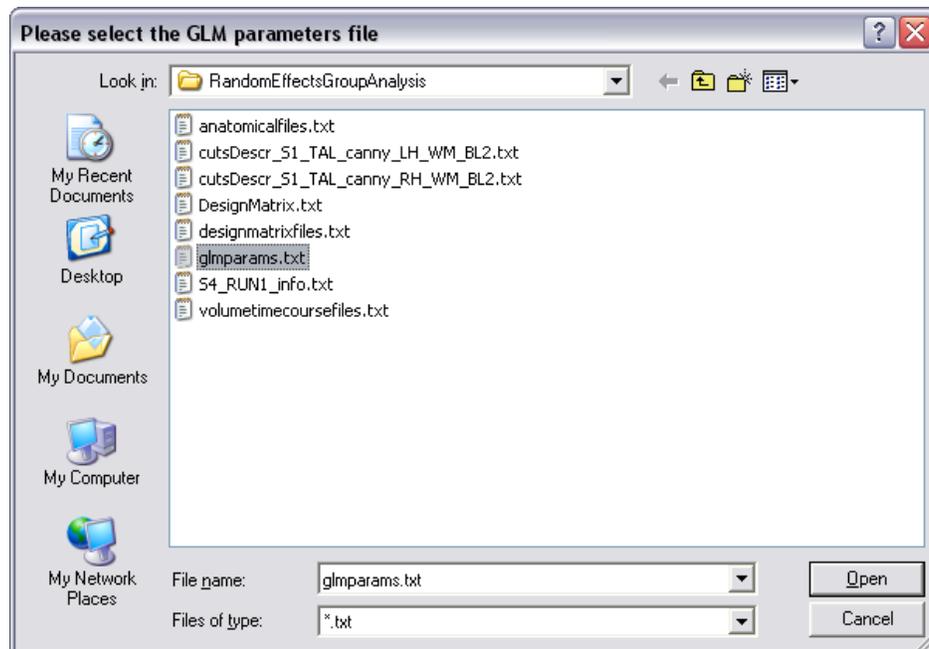
To compute the GLMs after the “glmparams.txt” file has been generated via the function “Collect GLM parameters”, simply activate the “Compute GLMs” function in the ‘Scripts’ menu.



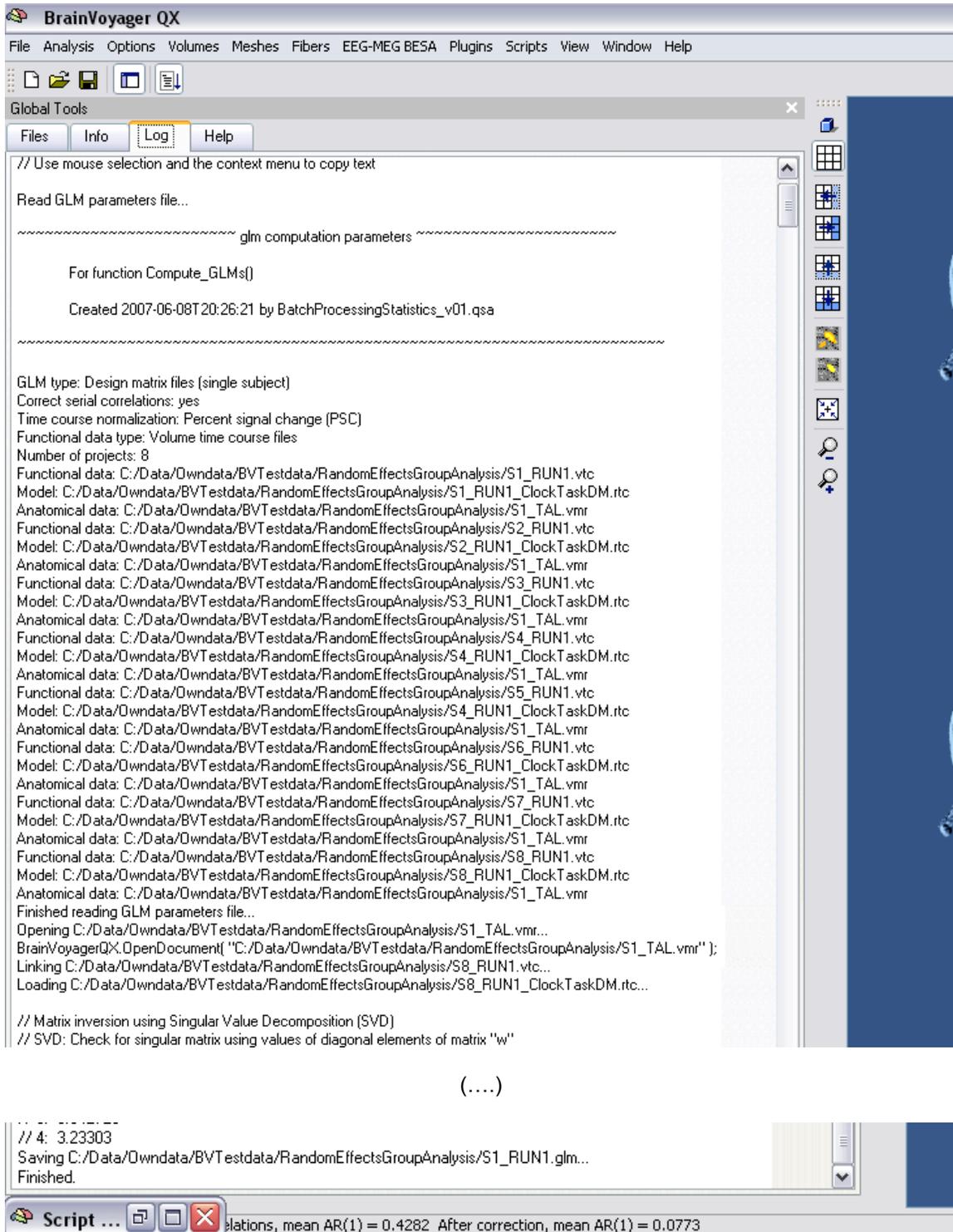
The only prerequisite is to load the “glmparams.txt” file:



When the file is selected...

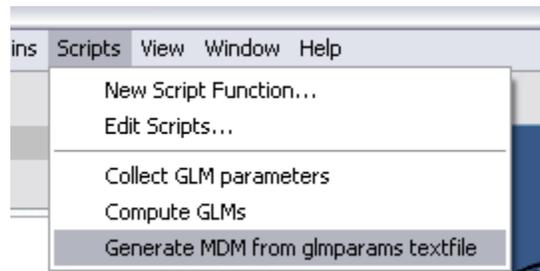


...the GLMs will be computed and a report appears in the BrainVoyager QX Log tab:

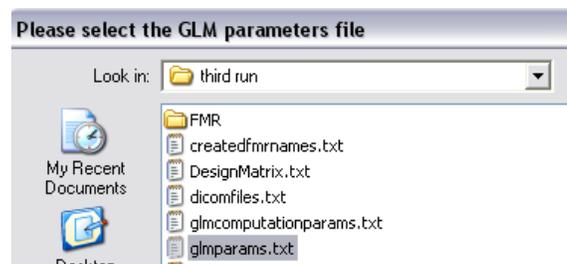


Generating a multi-study design matrix definition file from glmparams.txt

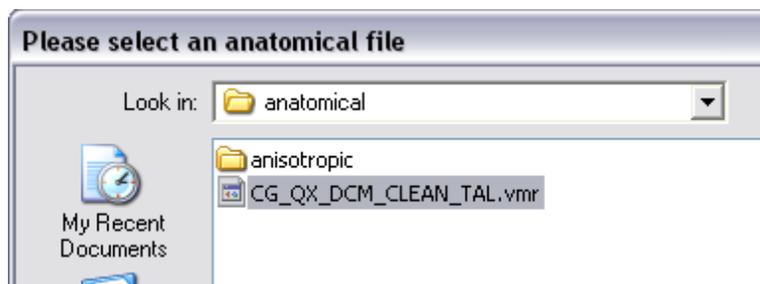
As a result of the function “Collect GLM parameters”, a text file with functional data files (*.fmr/*.stc or *.vtc) and design matrix files (*.rtc) is generated. This file can be used to generate a multi-study design matrix definition file (*.mdm). Activate the function “Generate MDM from glmparams textfile” via the BrainVoyager QX ‘Scripts’ menu:



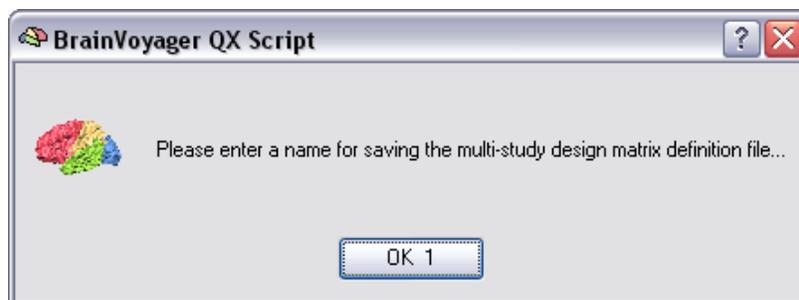
First, select the “glmparams.txt” file:

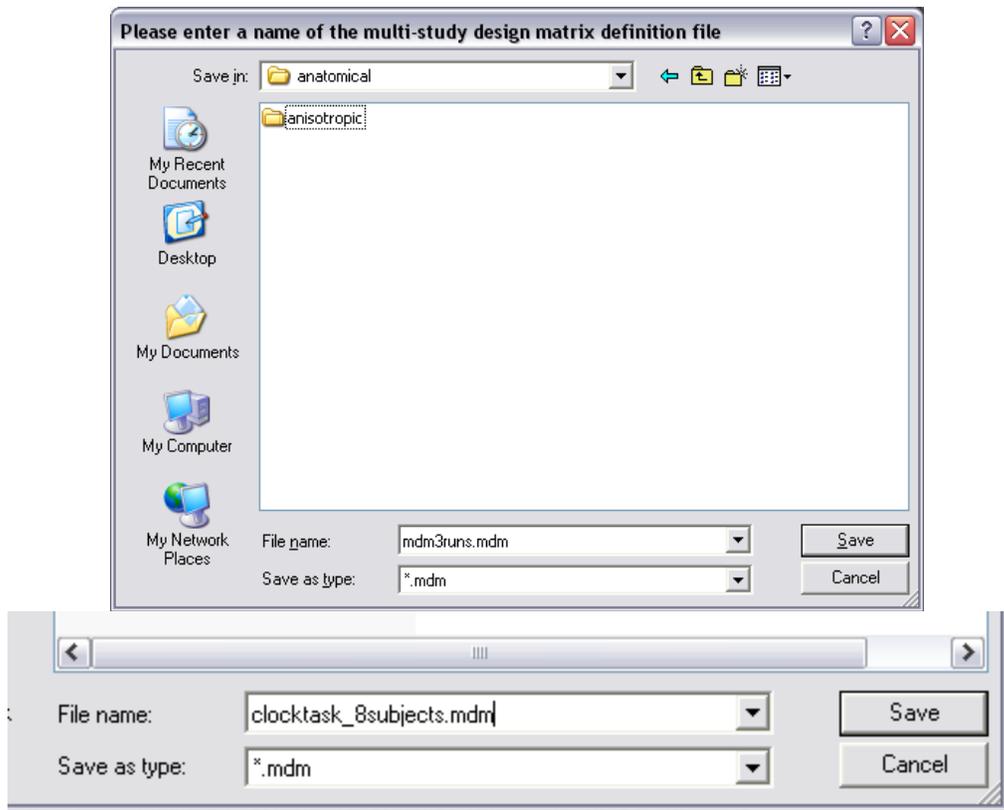


Then, select an anatomical file (*.vmr):

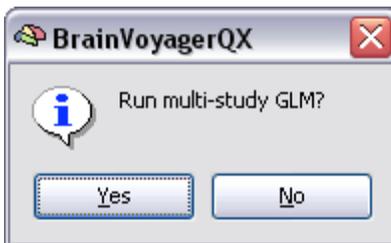


Then a name for the multi-study design matrix definition file can be provided:





It is possible to run the multi-study GLM immediately:



Results are displayed in the BrainVoyager QX Log tab:

```
Model: C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S8_RUN1_ClockTaskDM.rtc
Anatomical data: C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S1_TAL.vmr
BrainVoyagerGX: OpenDocument( "C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S1_TAL.vmr" );
Adding:
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S8_RUN1.vtc
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S8_RUN1_ClockTaskDM.rtc
Adding:
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S7_RUN1.vtc
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S7_RUN1_ClockTaskDM.rtc
Adding:
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S6_RUN1.vtc
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S6_RUN1_ClockTaskDM.rtc
Adding:
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S5_RUN1.vtc
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S4_RUN1_ClockTaskDM.rtc
Adding:
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S4_RUN1.vtc
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S4_RUN1_ClockTaskDM.rtc
Adding:
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S3_RUN1.vtc
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S3_RUN1_ClockTaskDM.rtc
Adding:
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S2_RUN1.vtc
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S2_RUN1_ClockTaskDM.rtc
Adding:
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S1_RUN1.vtc
C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/S1_RUN1_ClockTaskDM.rtc
Name for MDM file: C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/clocktask_8subjects.mdm

// Matrix inversion using Singular Value Decomposition (SVD)
// SVD: Check for singular matrix using values of diagonal elements of matrix "w"
// SVD: Matrix "w" - zero values indicate reduced dimensionality:
// 1: 0.00538499
// 2: 0.177565
// 3: 0.0349233
// 4: 0.0381324
// 5: 0.00793651
// 6: 0.00793651
// 7: 0.00793651
// 8: 0.00793651
// 9: 0.00793651
// 10: 0.00793651
// 11: 0.00793651
Saving C:/Data/Owndata/BVT estdata/RandomEffectsGroupAnalysis/clocktask_8subjects.glm...
Finished.
```

Background information

GLM Options

Predictor scaling

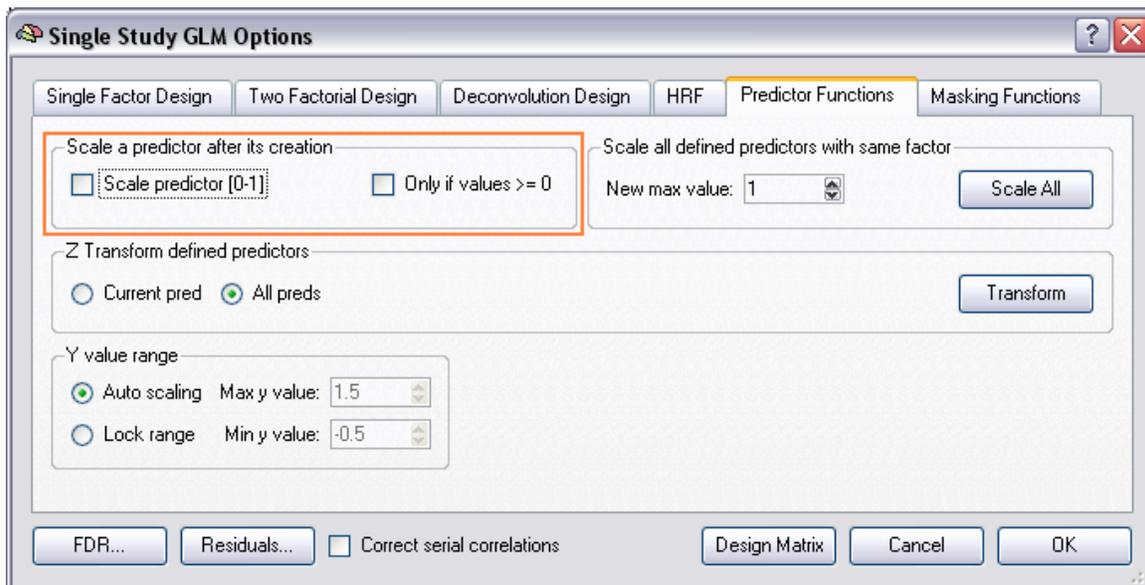
When predictors are defined over short time intervals, the resulting amplitude after application of the hemodynamic response function can be very low. In order to keep the predictors visible, they are now scaled appropriately as default in such a way, that the maximum value of the predictor is mapped to a value of "1.0". The identified scaling parameter for mapping the maximum value is also applied to any other value keeping relative amplitudes intact as without scaling. Automatic predictor scaling can be turned off using the "Scale predictor [0-1]" option in the "HRF and mask functions" of the "Single Study GLM Options" dialog.

Via scripting, the predictor scaling can be set via the property

```
doc.ScalePredictorValues("Linear Trend", 1.0, false);
```

The three parameters of the `ScalePredictorValues` (<parameter 1>, <parameter 2>, <parameter 3>) specify the following settings:

1. Name of predictor
2. Maximum value
3. Scale only when values are larger than zero

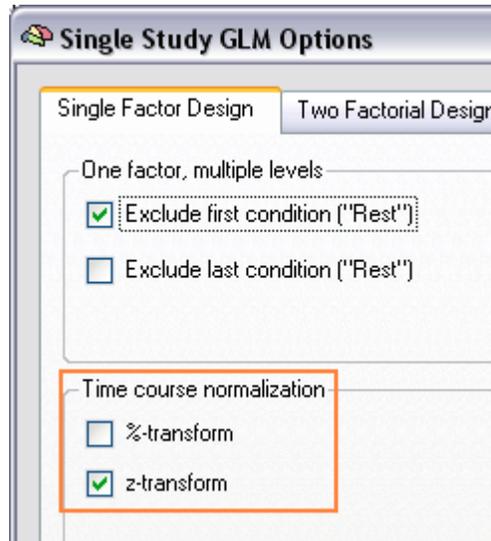


Baseline-Only z-Transformation

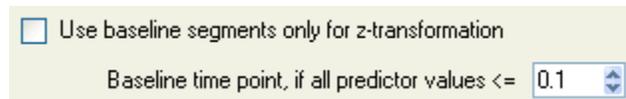
When running multi-study GLMs, it is often useful to perform a z-transformation for the voxel time courses from different runs. Such a transformation normalizes the mean of a study time course to zero and the variance to a value of one. This transformation equalizes the potential contribution of each study for explaining the overall variance of a signal time course. One disadvantage of z-normalization is that it diminishes real differences in the effect size of different runs from different subjects. To avoid this effect, a variant of z-normalization is available, which normalizes using

only those values constituting the base line condition. This results in a z normalization based solely on the noise variance and leads to effect estimations which are expressed relative to the noise variance. This alternative z-normalization approach is available both for multi-run GLMs (see "Multi-Run GLM Options" dialog) as well as for ROI GLMs (see "ROI GLM Specifications" dialog).

Via scripting, the z-transformation can be set via the document property [ZTransformStudies](#).



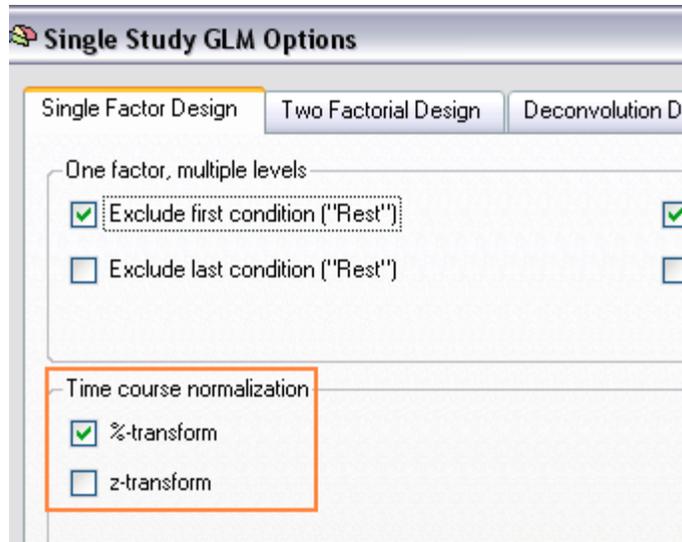
For multi-subject studies the [ZTransformStudiesBaselineOnly](#) is available.



Percent Signal Change Time Course Normalization

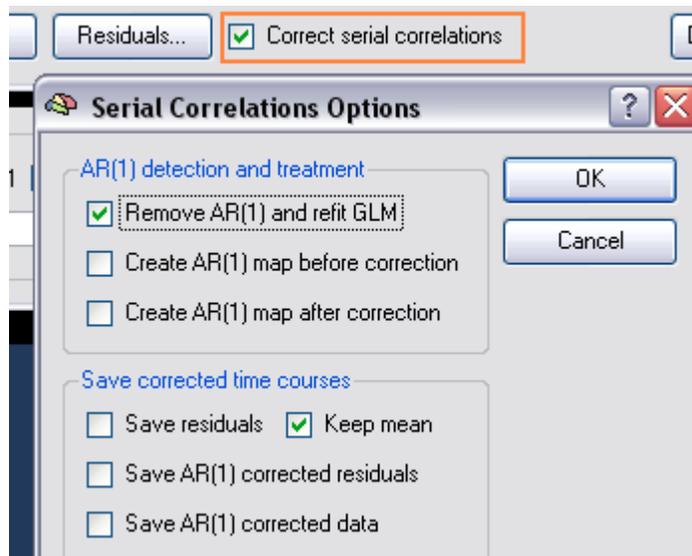
This new option allows to normalize a voxel's or ROI's time course in such a way that the mean signal value will be transformed to a value of 100 and the individual values will be fluctuating around that mean as percent signal deviations. If, for example, the original mean of a time course is 600 and an individual value is 612, the resulting value will be 102. This normalization approach appears to be well suited to integrate fMRI data from different subjects in a multi-subject GLM because it retains better individual effect size differences across subjects than z-Normalization. Percent Signal Change normalization is therefore now the default normalization option for the new RFX GLM, but can be also chosen for the standard multi-study GLM as well as for multi-study ROI analyses. If turned on, percent signal change normalization is applied separately for each run referenced in multi-subject design matrix files.

Via scripting, the percent signal change time course normalization can be set via the document property [PSCTransformStudies](#).



Correction for autocorrelation in the residuals

Autocorrelation in the noise can be corrected via the property **CorrectForSerialCorrelations**. An AR(1) model is then applied to filter the fitted data.



Calculation of the baseline for the GLM

By Armin Heinecke

The way the baseline (and the corresponding percentual signal change) is estimated might differ (depending on your specification) between the statistic used (e.g. the GLM) and the visualisation in the event related averaging plot.

In the calculation of the GLM, the baseline is estimated from all the non-defined (non-predictors) periods in the timecourse. As an example, Excel computations below show the calculation of a linear regression for the timecourse of a specific region chosen in BrainVoyager (simple one-run, two predictor example, chosen from BrainVoyagers sample data).

The examples contain the data, model estimation and formulas as well as the output of BrainVoyagers ROI GLM. I chose standard regression formulas to make this a little more accessible although in BrainVoyager's GLM approach, matrix calculation is used.

You can see nicely that the estimation of parameters (beta weights), their standard errors and the resulting model estimation is nearly perfectly the same when comparing the different approaches.

On the other hand, the way the baseline can be defined is very specific in the event related averaging (avg) dialog.

You may select:

a) different time windows ("Average From: To:" field)

->Looking at this point, it is interesting how long the period for baseline estimation was and if the sampling possibly ranged into the other conditions defined (happens easy if an event-related design is used).

b) different methods ("epoch" based, "condition per file" based and "file" based) to sample the baseline for the avg plot.

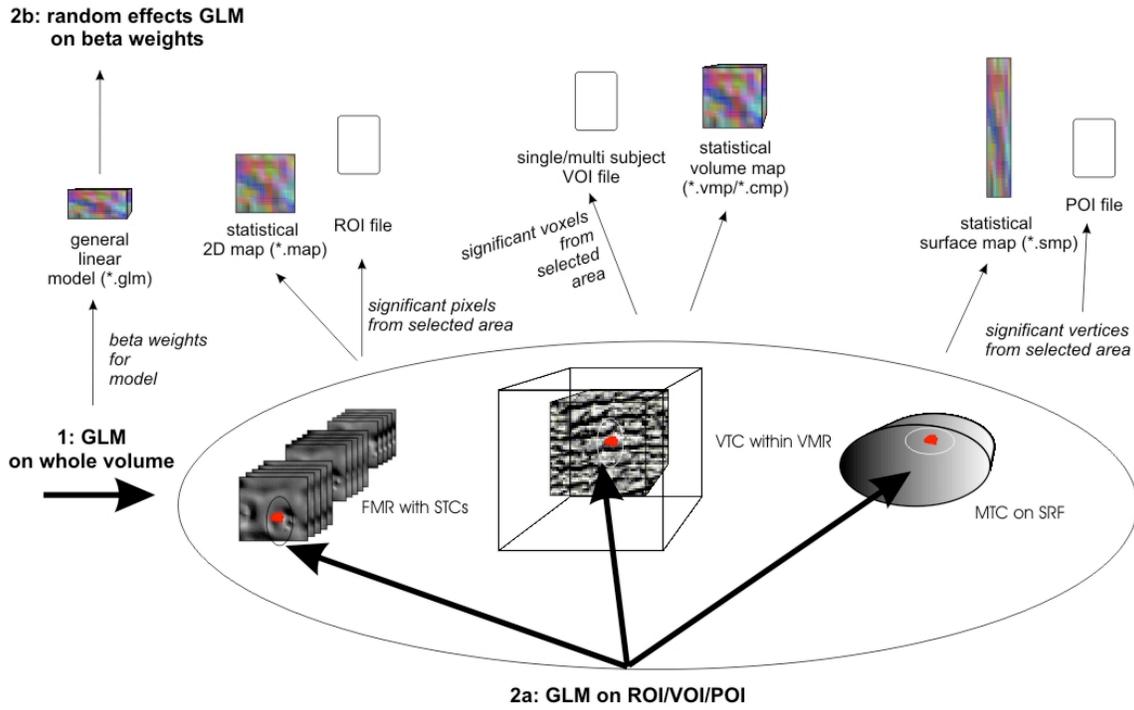
The main difference here is how specific the baseline values chosen are taken into account for the percent signal change calculation.

This may be performed specific for every instance (repetition of a condition), averaged within conditions or averaged for the whole run.

(For a more elaborate explanation, please contact Armin Heinecke via support [at brainvoyager.com](mailto:support@brainvoyager.com))

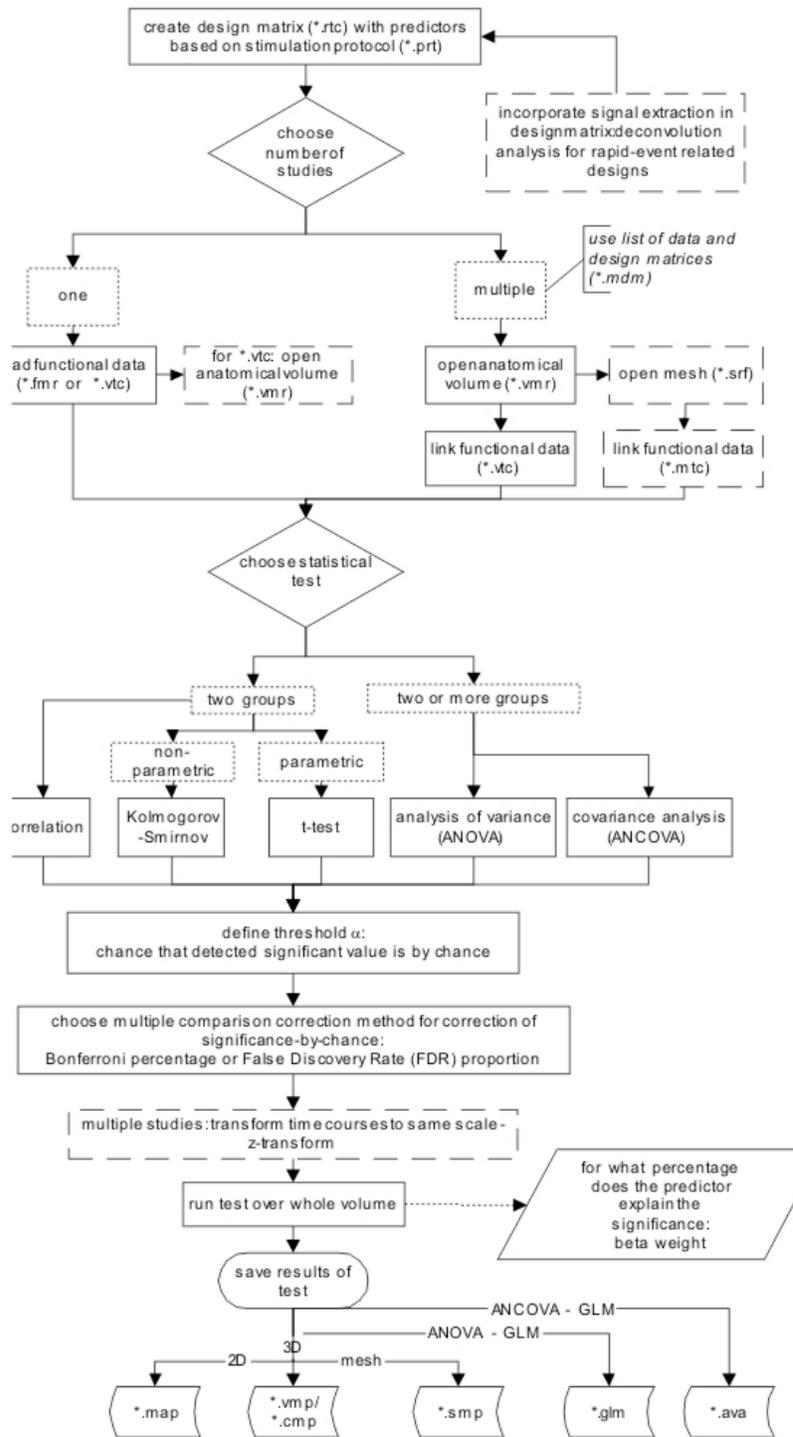
Figure of statistical files in BrainVoyager QX

Statistical maps in BrainVoyager
brain areas being activated during task performance



Flowcharts of statistical procedures in BrainVoyager QX

Standard hypothesis testing procedure



Options for hypothesis testing

