

Description of designmatrixgenerator v0.8.3

for BrainVoyager QX 2.8

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Introduction

This tool converts BrainVoyager stimulation protocols (*.prt) to design matrices (*.sdm), optionally including external confounds. The plugin requires a text file with protocol file names to be converted and functional data (*.vtc) for each protocol. During conversion, the confounds can be z-transformed.

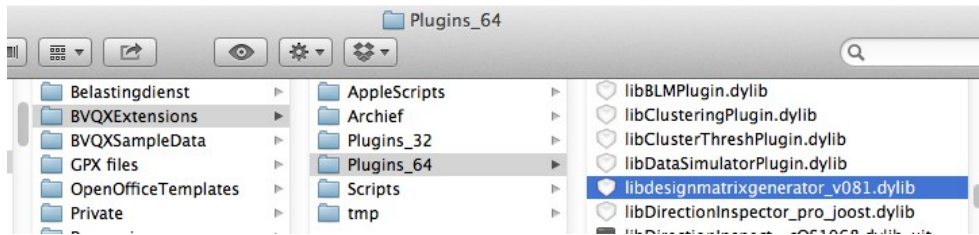
The plugin, manual and code can be downloaded from our support site at <http://support.brainvoyager.com/available-tools/49-available-plugins/361-designmatrixgenerator.html>.

For more plugins, see the plugins website at <http://www.BrainVoyager.com/> > Downloads > Plugins.

For more information about creating plugins for BrainVoyager QX, see the Developer's Guide that is installed in the folder /BrainVoyager QX/UserGuides/. In case of questions, please email support@brainvoyager.com.

Installation

Place the 'designmatrixgenerator_v083.dll' in //(My) documents/BVQXExtensions/Plugins_64/'. BrainVoyager QX will recognize this as a plugin and make its functions available via the 'Plugins' menu of BrainVoyager.



Use of the designmatrixgenerator

Creating the list with filenames

Converting one or multiple protocol files

The protocol file name(s) and optionally the motion estimates (*_3DMC.sdm/rtc), heart rate measurements (*.sdm/*.rtc) and respiration (*.sdm/*.rtc) are retrieved from a text file. This text file can be generated using a script or by manually writing the text file.

Generate text file using a script

There are two scripts, either the filenamecollector.js (for only *.prt, *.vtc and optionally *_3DMC) or filenamecollector_tbv_v02.js (for also adding heart rate and respiration files). The scripts can be downloaded from our support site at: <http://support.brainvoyager.com/available-tools/50-available-scripts/470-script-to-collect-text-file-names.html>

Generate text file manually

The text file should be in unformatted format (*.txt).
This text file has the following structure:

```
<number of PRT-VTC(-SDM) pairs/triples>
<prt name 1>
<vtc name 1>
(<*_3DMC.sdm name 1>)
(<*.sdm heart rate measurement name 1>)
(<*.sdm respiration measurement name 1>)
<prt name 2>
<vtc name 2>
(<*_3DMC.sdm name 2>)
(<*.sdm heart rate measurement name 2>)
(<*.sdm respiration measurement name 2>)
...
<prt name n>
<vtc name n>
(<*_3DMC.sdm name n>)
(<*.sdm heart rate measurement name n>)
(<*.sdm respiration measurement name n>)
```

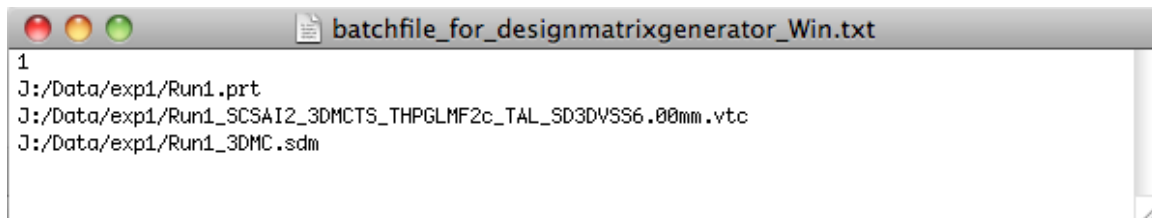
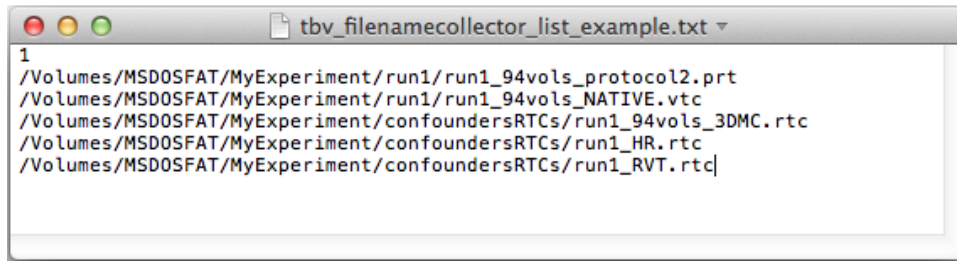


Figure: example file for Windows



```
1
/Volumes/MSDOSFAT/MyExperiment/run1/run1_94vols_protocol2.prt
/Volumes/MSDOSFAT/MyExperiment/run1/run1_94vols_NATIVE.vtc
/Volumes/MSDOSFAT/MyExperiment/confoundersRTCs/run1_94vols_3DMC.rtc
/Volumes/MSDOSFAT/MyExperiment/confoundersRTCs/run1_HR.rtc
/Volumes/MSDOSFAT/MyExperiment/confoundersRTCs/run1_RVT.rtc|
```

Figure: example file for Mac OS X

Requirements

Assumptions for designmatrixgenerator v0.8.3:

Expected order of files in script:

PRT
VTC
(3DMC)
(HR)
(RVT)

Requirements for filenames:

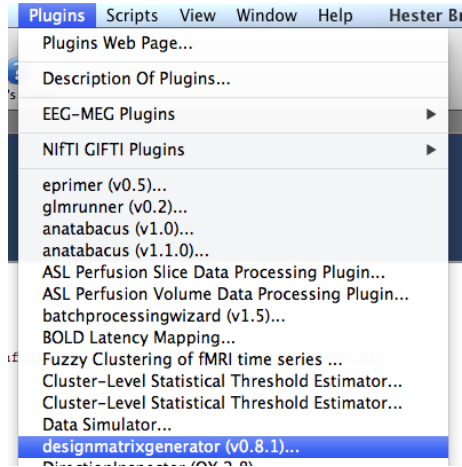
A stimulation protocol file should contain substring ".prt"
A volume time course file should contain substring ".vtc"
A motion estimates file should contain substring "_3DMC"
A heart rate measurement file should contain substring "_HR"
A respiratory measurement file should contain substring "_RVT"

Remarks

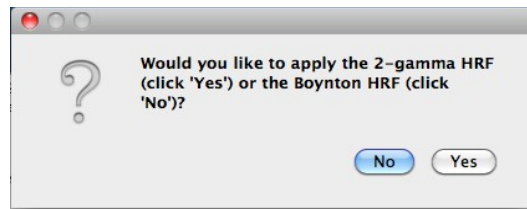
1. It is required that the *.prt file is in the same directory as the *.vtc file, for automatic linking of the protocol to the *.vtc.
2. The number of time points in the *.sdm will depend of the number of time points in the *.vtc file.
3. If the number of time points in the confound file is lower than the one in the design matrix, the conversion procedure is canceled.

Running the plugin

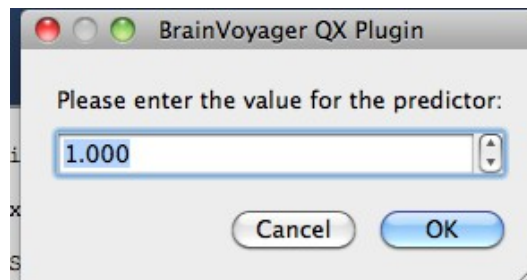
Before starting the conversion, load an anatomical file (*.vmr). Activate the plugin via the Plugins menu:



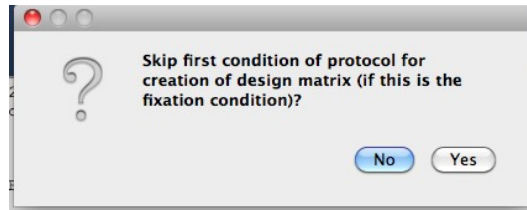
After the designmatrixgenerator has been selected, a question dialog will ask which hemodynamic response function (HRF) model should be used, either the 2-gamma model or the Boynton model:



For the 2-gamma HRF function, click 'Yes' else click 'No'. This value will be used for all files. Next, the plugin will ask for the predictor value, which is default 1.0 and will also be applied in all cases:



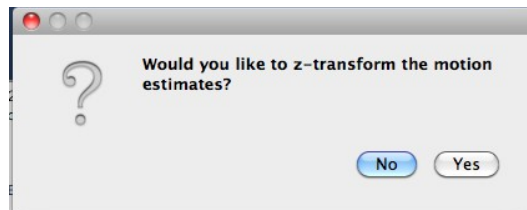
To exclude the "Fixation" condition from the protocol, click "Yes" when the dialog asks if this condition should be skipped:



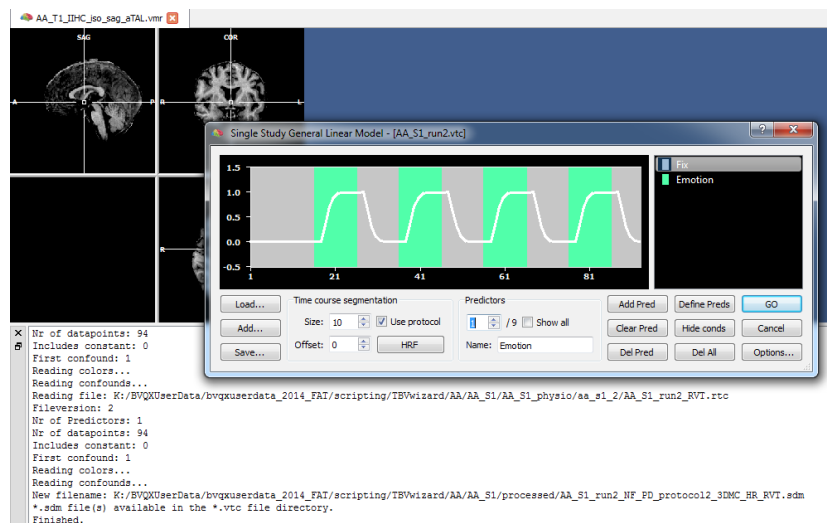
From designmatrixgenerator v0.7 it is possible to z-transform confounds. In that case, the z-score is calculated per column (predictor) in the following way:

$$z = \frac{x - \bar{x}}{\sigma_x}$$

where σ_x is $\sqrt{\frac{\sum(x - \bar{x})^2}{n}}$ and \bar{x} is the mean of the column.



The process can be observed via the BrainVoyager QX Log tab. The *.sdm file(s) can be found in the directory where the *.vtc is located. The name will contain the name of the *.vtc file and *.prt file, and the names of selected confounds ("_3DMC", "_HR", "_RVT") and indication of z-transformation, if this has been selected ("_z").



References

For information about the statistical procedures for fMRI data in BrainVoyager, please consult:

- the User's Guide:

<http://www.brainvoyager.com/bvqx/doc/UsersGuide/BrainVoyagerQXUsersGuide.html>

- the support site:

<http://support.brainvoyager.com/functional-analysis-statistics.html>

For Turbo-BrainVoyager (TBV) information, please see

- the TBV User's Guide:

<http://download.brainvoyager.com/tbv/TBVUsersGuide/TurboBrainVoyagerUsersGuide.html>

History

Changes in the code

v0.8.3 (20-11-14): Automated recognition of added confounds, from names in text file. Changed naming of resulting *.sdm names (SDM with motion estimates contains "_3DMC", SDM with heart rate contains "_HR" and SDM with respiratory contains "_RVT").

v0.8.2 (14-11-14): Filename of resulting *.sdm contains *.vtc and *.prt name. Number of confounds to be added can now be arbitrary (between zero and three: 0: no added confound 1-3: one or several of motion estimates (*.3dmc), heart rate and respiration files). Since BrainVoyager always states a constant is added in the *.sdm, the choice for users to leave it out has been removed.

v0.8.1 (22-10-14): Made it possible to also add confounds from external *.rtc files.

v0.8 (20-10-14): Added option to add three confounds from external *.sdm files.

v0.7: Added option to z-transform the motion estimates.

v0.6: This plugin gives the option to skip the first condition of the stimulation protocol, for example when this is a Fixation condition. Because the 'IsConstant' value in the header appears to be set to 1 automatically when generating a design matrix, an option to add the column (physically) is added to the plugin.

v0.5: This plugin now also includes the option to add of motion estimates (in *_3DMC.sdm file) as confounds. The text file to feed the designmatrixgenerator in case this option is used, should have the number of protocols at the top, followed by one line per protocol file (*.prt), vtc file (*.vtc) and motion estimates (*.3DMC.sdm) file:

v0.4 This plugin can be used to generate design matrix files (*.sdm) for a variable length of VTC files.

v0.2 (recompilation for Windows)

31-07-08: Replaced pow() by powf()

Changes in the manual

27-11-14: Adapted the manual for designmatrixgenerator v0.8.3.

14-11-14: Removed option about the constant in "Running the plugin". Added link to online TBV User's Guide.

22-10-14: Added the information about adding more confounds and references to the filenamecollector.js script.

11-09-14: New screenshots and adapted the procedure. Removed the CreateFileList references (code does not work in the current Qt Script Module).

06-03-09: Added code of CreateFileList_v02.qs

31-07-08: Added history section