

BROCCOLI

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**Software for Fast fMRI Analysis
on Many-Core CPUs and GPUs**

Anders Eklund

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Chapter 1

Introduction

1.1 Introduction

BROCCOLI is a software mainly created for analysis of functional magnetic resonance imaging (fMRI) data. The major advantage of BROCCOLI, compared to other software packages, is that it is much faster. The main reason for this is that BROCCOLI is written in OpenCL (Open Computing Language), making it possible to run the analysis in parallel on a large variety of hardware platforms (such as CPUs, Nvidia GPUs and AMD GPUs).

1.2 Downloading BROCCOLI

BROCCOLI is available as open source at <https://github.com/wanderine/BROCCOLI/>. For Linux and Mac computers, the following git command can be used to download BROCCOLI into the directory BROCCOLI.

```
git clone https://github.com/wanderine/BROCCOLI.git BROCCOLI
```

For Windows computers, see <https://windows.github.com/> or download BROCCOLI as a zip file from github.

1.3 Installing OpenCL

BROCCOLI requires that at least one OpenCL driver is installed. All hardware platforms (e.g. Intel, AMD and Nvidia) require a specific OpenCL driver. It is possible to install several OpenCL drivers on a single machine.

Intel drivers (runtime) are currently located at

<https://software.intel.com/en-us/articles/opencl-drivers> ,

and can for CentOS / Fedora / Redhat also be downloaded from

https://dl.dropboxusercontent.com/u/4494604/openc1_runtime_15.1_x64_5.0.0.57.tar

and for Ubuntu from

[https://dl.dropboxusercontent.com/u/4494604/
intel_code_builder_for_openc1_2015_ubuntu_5.0.0.43_x64.tgz](https://dl.dropboxusercontent.com/u/4494604/intel_code_builder_for_openc1_2015_ubuntu_5.0.0.43_x64.tgz)

AMD drivers can be found at <http://developer.amd.com/tools-and-sdks/openc1-zone/openc1-tools-sdks/amd-accelerated-parallel-processing-app-sdk/>

Nvidia drivers can be found at <http://www.nvidia.com/Download/index.aspx>.

Note that a driver for an Nvidia graphics cards includes an OpenCL driver.

On Ubuntu machines, an Nvidia driver can be installed using

```
sudo apt-get install nvidia-current
```

1.4 Checking the OpenCL drivers

To check the installation of the OpenCL driver(s) on Linux and Mac computers, the BROCCOLI bash function `GetOpenCLInfo` can be used (located in the directory `BROCCOLI/compiled/Bash/Linux/Release` and `BROCCOLI/compiled/Bash/Mac/Release`). It lists all the available devices for each OpenCL platform. The following output is from a computer with three OpenCL drivers (Intel, AMD, Nvidia) and one Intel CPU (with 32 GB of memory), one AMD graphics card (3 GB of memory) and one Nvidia graphics card (6 GB of memory). For each bash function, it is easy to select which platform and which device to use. Note that the Intel CPU can be used with the Intel platform or the AMD platform.

```
[andek@localhost]$ GetOpenCLInfo
```

```
Device info
```

```
-----  
Platform number: 0  
-----
```

```
Platform vendor: Intel(R) Corporation
```

```
Platform name: Intel(R) OpenCL
```

```
Platform extentions: cl_khr_fp64 cl_khr_icd cl_khr_global_int32_base_atomics  
cl_khr_global_int32_extended_atomics cl_khr_local_int32_base_atomics  
cl_khr_local_int32_extended_atomics cl_khr_byte_addressable_store
```



```
cl_intel_printf cl_ext_device_fission cl_intel_exec_by_local_thread
Platform profile: FULL_PROFILE
```

```
-----
Device number: 0
-----
```

```
Device vendor: Intel(R) Corporation
Device name:      Intel(R) Core(TM) i7-3770K CPU @ 3.50GHz
Hardware version: OpenCL 1.2 (Build 67279)
Software version: 1.2
OpenCL C version: OpenCL C 1.2
Device extensions: cl_khr_fp64 cl_khr_icd cl_khr_global_int32_base_atomics
cl_khr_global_int32_extended_atomics cl_khr_local_int32_base_atomics
cl_khr_local_int32_extended_atomics cl_khr_byte_addressable_store
cl_intel_printf cl_ext_device_fission cl_intel_exec_by_local_thread
Global memory size in MB: 32071
Global memory cache size in KB: 256
Local memory size in KB: 32
Constant memory size in KB: 128
Parallel compute units: 8
Clock frequency in MHz: 3500
Max number of threads per block: 1024
Max number of threads in each dimension: 1024 1024 1024
```

```
-----
Platform number: 1
-----
```

```
Platform vendor: Advanced Micro Devices, Inc.
Platform name: AMD Accelerated Parallel Processing
Platform extensions: cl_khr_icd cl_amd_event_callback cl_amd_offline_devices
Platform profile: FULL_PROFILE
```

```
-----
Device number: 0
-----
```

```
Device vendor: Advanced Micro Devices, Inc.
Device name: Tahiti
Hardware version: OpenCL 1.2 AMD-APP (1214.3)
Software version: 1214.3 (VM)
OpenCL C version: OpenCL C 1.2
Device extensions: cl_khr_fp64 cl_amd_fp64 cl_khr_global_int32_base_atomics
cl_khr_global_int32_extended_atomics cl_khr_local_int32_base_atomics
```

```

cl_khr_local_int32_extended_atomics cl_khr_int64_base_atomics
cl_khr_int64_extended_atomics cl_khr_3d_image_writes
cl_khr_byte_addressable_store cl_khr_gl_sharing cl_ext_atomic_counters_32
cl_amd_device_attribute_query cl_amd_vec3 cl_amd_printf
cl_amd_media_ops cl_amd_media_ops2 cl_amd_popcnt cl_khr_image2d_from_buffer
Global memory size in MB: 3035
Global memory cache size in KB: 16
Local memory size in KB: 32
Constant memory size in KB: 64
Parallel compute units: 32
Clock frequency in MHz: 1000
Max number of threads per block: 256
Max number of threads in each dimension: 256 256 256

```

```

-----
Device number: 1
-----

```

```

Device vendor: GenuineIntel
Device name: Intel(R) Core(TM) i7-3770K CPU @ 3.50GHz
Hardware version: OpenCL 1.2 AMD-APP (1214.3)
Software version: 1214.3 (sse2,avx)
OpenCL C version: OpenCL C 1.2
Device extensions: cl_khr_fp64 cl_amd_fp64 cl_khr_global_int32_base_atomics
cl_khr_global_int32_extended_atomics cl_khr_local_int32_base_atomics
cl_khr_local_int32_extended_atomics cl_khr_int64_base_atomics
cl_khr_int64_extended_atomics cl_khr_3d_image_writes
cl_khr_byte_addressable_store cl_khr_gl_sharing cl_ext_device_fission
cl_amd_device_attribute_query cl_amd_vec3 cl_amd_printf cl_amd_media_ops
cl_amd_media_ops2 cl_amd_popcnt
Global memory size in MB: 32071
Global memory cache size in KB: 32
Local memory size in KB: 32
Constant memory size in KB: 64
Parallel compute units: 8
Clock frequency in MHz: 1600
Max number of threads per block: 1024
Max number of threads in each dimension: 1024 1024 1024

```

```

-----
Platform number: 2
-----

```

```

Platform vendor: NVIDIA Corporation
Platform name: NVIDIA CUDA
Platform extensions: cl_khr_byte_addressable_store cl_khr_icd

```

```

cl_khr_gl_sharing cl_nv_compiler_options cl_nv_device_attribute_query
cl_nv_pragma_unroll
Platform profile: FULL_PROFILE
-----

-----
Device number: 0
-----

Device vendor: NVIDIA Corporation
Device name: GeForce GTX TITAN
Hardware version: OpenCL 1.1 CUDA
Software version: 331.67
OpenCL C version: OpenCL C 1.1
Device extensions: cl_khr_byte_addressable_store cl_khr_icd cl_khr_gl_sharing
cl_nv_compiler_options cl_nv_device_attribute_query cl_nv_pragma_unroll
cl_khr_global_int32_base_atomics cl_khr_global_int32_extended_atomics
cl_khr_local_int32_base_atomics cl_khr_local_int32_extended_atomics cl_khr_fp64
Global memory size in MB: 6143
Global memory cache size in KB: 224
Local memory size in KB: 48
Constant memory size in KB: 64
Parallel compute units: 14
Clock frequency in MHz: 875
Max number of threads per block: 1024
Max number of threads in each dimension: 1024 1024 64

```

1.5 Setting environment variables

Just like for FSL, it is necessary to set a Linux environment variable called BROCCOLI_DIR. The variable should contain the path of the BROCCOLI installation. Using bash, it can for example be set by

```
export BROCCOLI_DIR=/home/andek/BROCCOLI/
```

Note that the path should end with a "/" character. To make the change permanent, add the expression to your configuration file (e.g. /home/andek/.bash_profile).

It may also be a good idea to add the BROCCOLI path to your local PATH variable, such that the BROCCOLI functions can be called from any location, e.g. for Linux

```
export PATH=$PATH:/home/andek/BROCCOLI/compiled/Bash/Linux/Release
```

and for Mac

```
export PATH=$PATH:/Users/andek/BROCCOLI/compiled/Bash/Mac/Release
```

Some parts of BROCCOLI use the cBLAS library for matrix operations. It is therefore necessary to add the following definition (for Linux only)

```
export LD_LIBRARY_PATH=$LD_LIBRARY_PATH
:/home/andek/BROCCOLI/code/BROCCOLI_LIB/cBLASLinux
```

Some parts of BROCCOLI support OpenMP (open multi processing on the CPU), to speedup code not written in OpenCL. The number of OpenMP threads can, for example, be set using

```
export OMP_NUM_THREADS=4
```

to run 4 threads in parallel. If this variable is not defined, the default is to use a single CPU thread.

1.6 Selecting the OpenCL platform and device

As mentioned previously, it is easy to select which OpenCL platform and device to use for each BROCCOLI function (the default platform and device is 0). For each bash function, the option `-platform` sets the OpenCL platform to use, and the option `-device` sets the device to use. The first level analysis can, for example, be performed using platform 1 and device 1 by using the command

```
FirstLevelAnalysis fMRI.nii T1.nii BrainTemplate.nii ...
regressors.txt contrasts.txt -platform 1 -device 1
```

For the test computer used in the introduction, this means that the analysis runs on the Intel CPU using the AMD platform. By changing the device to 0, the AMD graphics card will instead be used.

1.7 Compiling the OpenCL kernel code

The files `kernelBayesian.cpp`, `kernelClusterize.cpp`, `kernelConvolution.cpp`, `kernelMisc.cpp`, `kernelRegistration.cpp`, `kernelStatistics1.cpp`, `kernelStatistics2.cpp` and `kernelWhitening.cpp` (in the directory `BROCCOLI/code/Kernels`) contain all the OpenCL code that runs on the selected device. The first time BROCCOLI uses a specific device, it has to compile all the OpenCL code to a form that can be used by the device. For this reason, the first function call will take more time. The compiled code will, however, be saved as binary files (for Linux and Mac computers in the `BROCCOLI/compiled/Kernels` directory), such that BROCCOLI can simply read the compiled code for all subsequent function calls. For our specific test computer, BROCCOLI will for example produce the following binary files for the Nvidia device

```
broccoli_lib_kernel_Nvidia_GeForceGTXITAN_Bayesian.bin
broccoli_lib_kernel_Nvidia_GeForceGTXITAN_Clusterize.bin
broccoli_lib_kernel_Nvidia_GeForceGTXITAN_Convolution.bin
broccoli_lib_kernel_Nvidia_GeForceGTXITAN_Misc.bin
broccoli_lib_kernel_Nvidia_GeForceGTXITAN_Registration.bin
broccoli_lib_kernel_Nvidia_GeForceGTXITAN_Statistics1.bin
broccoli_lib_kernel_Nvidia_GeForceGTXITAN_Statistics2.bin
broccoli_lib_kernel_Nvidia_GeForceGTXITAN_Whitening.bin
```

If compilation of a kernel file fails, some information will be given in the corresponding build info file (e.g. buildInfo_Nvidia_GeForceGTXITAN_Convolution.txt) in the directory BROCCOLI/compiled/Kernels.

1.8 Compiling the BROCCOLI library

BROCCOLI is written as a C++/OpenCL library, such that it can be linked to a number of softwares. Precompiled versions of the BROCCOLI library are located in BROCCOLI/compiled/BROCCOLI_LIB/Linux and in BROCCOLI/compiled/BROCCOLI_LIB/Mac . To compile the BROCCOLI library, it is necessary to first install an OpenCL SDK. For Intel, the OpenCL SDK (code builder) can be downloaded from

<https://software.intel.com/en-us/articles/opencl-drivers>

and for Linux (CentOS / Fedora / Redhat) also from

[https://dl.dropboxusercontent.com/u/4494604/
intel_code_builder_for_opengl_2015_5.0.0.62_x64.tar](https://dl.dropboxusercontent.com/u/4494604/intel_code_builder_for_opengl_2015_5.0.0.62_x64.tar)

and for Ubuntu the SDK and the driver is combined in one file

[https://dl.dropboxusercontent.com/u/4494604/
intel_code_builder_for_opengl_2015_ubuntu_5.0.0.43_x64.tgz](https://dl.dropboxusercontent.com/u/4494604/intel_code_builder_for_opengl_2015_ubuntu_5.0.0.43_x64.tgz)

To compile the BROCCOLI library on a Linux computer, the following command can be used from the directory BROCCOLI/code/BROCCOLI_LIB

```
./compile_broccoli_library.sh
```

Note that you may need to edit compile_broccoli_library.sh to point to a directory which contains opengl.h.

For Mac, the BROCCOLI library can be compiled by using a similar bash script

```
./compile_broccoli_library_mac.sh
```

In these scripts it is easy to change the compilation mode from release to debug.

On Windows computers, the BROCCOLI library can for example be compiled using Microsoft Visual Studio. Visual Studio project files are available in BROCCOLI/code/BROCCOLI_LIB.

1.9 Compiling the bash wrappers

It is possible to run BROCCOLI in a number of ways, for example from a Matlab terminal or from a Python terminal. The fMRI software packages FSL and AFNI can be launched from a Linux terminal, and BROCCOLI includes a bash wrapper for this purpose. Precompiled versions of the bash functions are located in BROCCOLI/compiled/Bash/Linux and in BROCCOLI/compiled/Bash/Mac .

The following bash script can be used to compile the bash wrappers (available in BROCCOLI/code/Bash_Wrapper)

```
./compile_wrappers.sh
```

Similarly, the following script can be used for Mac

```
./compile_wrappers_mac.sh
```

In these scripts it is easy to change the compilation mode from release to debug. Since BROCCOLI uses the NIfTI library to read NIfTI files, it may be necessary to first compile the NIfTI library, by running make in the directory BROCCOLI/code/Bash_Wrapper/nifticlib-2.0.0.

1.10 Required libraries

For Linux computers, it may be necessary to install some development libraries, to be able to compile the BROCCOLI library.

CentOS / Fedora / Redhat

```
yum -y install git
```

```
yum -y install libXp.x86_64
```

```
yum -y install libXpm.x86_64
```

```
yum -y install libXmu.x86_64
```

```
yum -y install gcc-c++
```

```
yum -y install zlib-devel
```

Ubuntu

```
sudo apt-get install git
```

```
sudo apt-get install zlib1g-dev
```

```
sudo apt-get install g++
```


Chapter 2

First level analysis

2.1 Introduction

BROCCOLI performs first level fMRI analysis using a single command. The analysis involves registering the anatomical volume to a brain template (using linear as well as non-linear registration), registering one fMRI volume to the anatomical volume, slice timing correction, motion correction, smoothing and statistical analysis. In contrast to other software packages, it is up to the user to decide which intermediate results to save. In its simplest form, a first level analysis can with the bash wrapper be performed as

```
FirstLevelAnalysis fMRI.nii T1_brain.nii BrainTemplate.nii ...  
    regressors.txt contrasts.txt
```

fMRI.nii is here the 4D fMRI data, T1_brain.nii is the skullstripped anatomical volume of the subject and BrainTemplate.nii is for example the MNI template in the FSL software (without skull). Currently it is necessary that all the NIfTI files are stored in the same orientation (e.g. RPI). The orientation can for example be checked with the AFNI function 3dinfo, and the orientation can be changed using the function 3dresample (e.g. 3dresample -orient RPI -input volume.nii -prefix volume_RPI.nii).

regressors.txt is a text file that contains the number of regressors to use, and the filename of each regressor. It can for example look like

```
NumRegressors 3
```

```
task1.txt  
task2.txt  
task3.txt
```

Each task file needs to include the number of events, the start time of each event, the length of each event and the value for the regressor of each event

(this format is very similar to the one used by the FSL software). A task file can for example look like

NumEvents 8

47.532543	2.517515	1
68.789386	2.950905	1
93.547212	2.934332	1
165.670213	3.584591	1
190.078151	1.817203	1
257.349564	2.584177	1
280.457018	1.367038	1
308.66593	2.084071	1

The regressors can also be raw, in the sense that you instead directly provide the value for each volume / time point in the fMRI data. A regressor file for an fMRI dataset with 8 volumes should then look like

0.3
0.5
1.0
1.0
1.0
2.0
3.1
2.2

where each row represents the value of the regressor for that volume. The number of rows must be equal to the number of volumes. It is also possible to give the whole design matrix as a single text file, it can for example look like

NumRegressors 2

0.5377	-0.1241
1.8339	1.4897
-2.2588	1.4090
0.8622	1.4172
0.3188	0.6715
-1.3077	-1.2075
-0.4336	0.7172
0.3426	1.6302

In all cases, BROCCOLI will automatically add detrending regressors and remove the mean of all the activity regressors.

contrasts.txt contains a list of all the contrasts for which BROCCOLI will calculate a volume with t-scores. An example is given by

```
NumRegressors 3
NumContrasts 9
```

```
1.0 0.0 0.0
0.0 1.0 0.0
0.0 0.0 1.0
1.0 -1.0 0.0
-1.0 1.0 0.0
1.0 0.0 -1.0
0.0 1.0 -1.0
-1.0 0.0 1.0
0.0 -1.0 1.0
```

The user only has to define the contrast values for the original activity regressors. BROCCOLI will automatically add additional zeros for nuisance regressors (motion, global mean) and temporal derivatives.

2.1.1 Several runs

If several runs are available for one subject, they can be analyzed together as

```
FirstLevelAnalysis -runs 3 run1.nii run2.nii run3.nii T1_volume.nii MNI_volume.nii
regressors_run1.txt regressors_run2.txt regressors_run3.txt contrasts.txt [options]
```

for a GLM, or as

```
FirstLevelAnalysis -runs 3 run1.nii run2.nii run3.nii
T1_volume.nii MNI_volume.nii -regressonly [options]
```

if only preprocessing and regression of nuisance variables (mean, trends, (motion), (global mean)) is desired.

If, for some reason, a subject did not do a specific task for one or several runs, this can be handled by using a dummy regressor, e.g.

```
NumRegressors 3
```

```
task1.txt
task2.txt
dummy.txt
```

where dummy.txt only contains

```
NumEvents 0
```

2.1.2 Checking the design matrix

To check if the design matrix looks correct, the options `-savedesignmatrix` and `-saveoriginaldesignmatrix` can be used. A text file will be generated with all the regressors (`-savedesignmatrix`), or only the task regressors (`-saveoriginaldesignmatrix`). If the AFNI software package is installed, these can for example be viewed as

```
1dplot fMRI_total_designmatrix.txt
```

or

```
1dplot fMRI_original_designmatrix.txt
```

2.2 OpenCL options

The following OpenCL options are available

- `-platform`

The OpenCL platform to use (default 0).

- `-device`

The OpenCL device to use (default 0).

2.3 Registration options

Several options can be used to control the image registration, see the chapter about image registration for further information.

2.4 Preprocessing options

The following preprocessing options are available

- `-noslicetimingcorrection`

Do not apply slice timing correction.

- `-nomotioncorrection`

Do not apply motion correction.

- -nosmoothing

Do not apply any smoothing.

- -slicepattern

Set the sampling pattern used during scanning

(overrides pattern provided in NIFTI file)

0 = sequential 1-N (bottom-up), 1 = sequential N-1 (top-down),

2 = interleaved 1-N, 3 = interleaved N-1

No slice timing correction is performed if pattern in

NIFTI file is unknown and no pattern is provided.

- -iterationsmc

Set the number of iterations used for the

motion correction (the default is 5).

- -smoothing

Set the amount of smoothing applied to

each fMRI volume (the default is 6 mm FWHM).

- -slicecustom

Provide a text file with the slice times,

one value per slice, in milli seconds (0 - TR).

- -slicecustomref

Provide a reference slice for the custom slice times,

between 0 and N-1, where N is the number of slices.

The default reference slice is N/2.

A text file with slice timing information can for example look like

```
0.0000
180.0000
362.5000
545.0000
727.5000
60.0000
242.5000
```

```

425.0000
605.0000
787.5000
120.0000
302.5000
485.0000
667.5000
  0.0000
180.0000
362.5000
545.0000
727.5000
  60.0000
242.5000
425.0000
605.0000
787.5000
120.0000
302.5000
485.0000
667.5000

```

which means that the first slice was collected at time 0, the second slice was collected after 180 milli seconds, the third slice was collected after 362.5 milli seconds, and so on.

2.5 Statistical options

The following statistical options are available

- -runs

Number of fMRI runs that will be concatenated and analyzed together, necessary to provide one design file per run. Separate detrending regressors will be added for each run. The number of task regressors will not change compared to a single run, meaning that the contrast vectors are the same as for a single run.

- -preprocessingonly

Only perform preprocessing, no GLM or regression is performed.

- -detrendingregressors

Set the number of detrending regressors (per run), 1 - 4. 1 means

a single regressor for the intercept, 2 means intercept + linear trends, 3 means intercept + linear trends + quadratic trends, 4 means intercept + linear trends + quadratic trends + cubic trends (the default is 4 detrending regressors).

- -betasonly

Only perform preprocessing and calculate beta values and contrasts, no t- or F-scores are calculated. Possible to use the options -regressmotion and -regressglobalmean.

- -regressonly

Only perform preprocessing and regress nuisance variables, no beta values or contrasts are calculated. Regressor and contrast files are not needed. Possible to use the options -regressmotion and -regressglobalmean.

- -rawregressors

Use raw regressors (FSL format, one line per volume/TR). These regressors will not be convolved with any hemodynamic response function.

- -rawdesignmatrix

Provide the design matrix in a single text file (FSL format, one regressor per column, one value per volume/TR). These regressors will not be convolved with any hemodynamic response function. It is still possible to use the options -regressmotion and -regressglobalmean.

- -regressmotion

Add the 6 estimated motion parameters (3 for translation and 3 for rotation) to the design matrix, to further suppress the effect of head motion. The contrast vectors are automatically extended with zeros for these additional regressors.

- -regressglobalmean

Include a regressor for the global mean in the design matrix. The contrast vectors are automatically extended with one zero for this additional regressor.

- -temporalderivatives

Add one additional regressor for each original regressor; the temporal derivative of each regressor. This makes it possible to adjust for

a small time difference between the original regressor and the time series in each voxel. The contrast vectors are automatically extended with zeros for these additional regressors. Not possible to use for `-rawdesignmatrix`.

- `-permute`

Run a permutation test after the conventional first level analysis. In each permutation, a random reshuffling of the fMRI volumes is performed to create a new set of null data. The statistical analysis is performed in each permutation, to empirically estimate the null distribution.

- `-inferencemode`

Set if voxel-wise or cluster-wise p-values should be calculated for the permutation test, 0 = voxel, 1 = cluster extent, 2 = cluster mass, 3 = threshold free cluster enhancement (TFCE) (default 1)

- `-cdt`

Cluster defining threshold for permutation based cluster inference (default 2.5).

- `-permutations`

Set the number of permutations (default 1,000)

- `-bayesian`

Run Bayesian first level analysis. Note that this option currently only works for 2 regressors. In each voxel, a Gibbs sampler is used to estimate the posterior probability of each contrast being larger than 0. This option cannot be combined with `-permute`.

- `-iterationsmcmc`

Set the number of MCMC iterations to be used (default 1,000).

2.6 Outputs

The first level analysis results in beta weights, contrast estimates, t-scores and p-values (if the option `-permute` is used). For an analysis with 2 regressors, a total of 6 regressors will be used (the 2 original regressors and 4 detrending regressors). The beta weights for these regressors will be saved in the brain template space as


```
fMRI_beta_regressor001_MNI.nii
fMRI_beta_regressor002_MNI.nii
fMRI_beta_regressor003_MNI.nii
fMRI_beta_regressor004_MNI.nii
fMRI_beta_regressor005_MNI.nii
fMRI_beta_regressor006_MNI.nii
```

For each contrast, BROCCOLI will also store the contrast of parameter estimate (COPE) and the corresponding t-scores, e.g.

```
fMRI_cope_contrast001_MNI.nii
fMRI_cope_contrast002_MNI.nii

fMRI_tscores_contrast001_MNI.nii
fMRI_tscores_contrast002_MNI.nii
```

2.7 Output options

The following output options are available

- -savetransformations

Save all affine transformation matrices (T1-MNI,EPI-T1,EPI-MNI). They can be used with the function TransformVolume (default no).

- -savet1interpolated

Save T1 volume after resampling to MNI voxel size and resizing to MNI size (default no).

- -savet1alignedlinear

Save T1 volume linearly aligned to the MNI volume (default no).

- -savet1alignednonlinear

Save T1 volume non-linearly aligned to the MNI volume (default no).

- -saveepialignedt1

Save EPI volume aligned to the T1 volume (default no).

- -saveepialignedmni

Save EPI volume aligned to the MNI volume (default no).

- -saveallaligned

Save all aligned volumes (T1 interpolated, T1-MNI linear, T1-MNI non-linear, EPI-T1, EPI-MNI) (default no).

- -saveepimask

Save EPI mask for fMRI data (default no).

- -savemnimask

Save mask for fMRI data, in MNI space (default no).

- -saveslicetimingcorrected

Save slice timing corrected fMRI volumes (default no).

- -savemotioncorrected

Save motion corrected fMRI volumes (default no).

- -savemotionparameters

Save motion parameters to a text file (default no).

- -savesmoothed

Save smoothed fMRI volumes (default no).

- -saveactivityepi

Save activity maps in EPI space
(in addition to MNI space, default no).

- -saveactivityt1

Save activity maps in T1 space
(in addition to MNI space, default no).

- -saveresiduals

Save residuals after GLM analysis (default no).

- -saveresidualsmni

Save residuals after GLM analysis, in MNI space (default no).

- -saveoriginaldesignmatrix

Save the original design matrix used (default no). This is the design matrix before convolving the regressors with the hemodynamic response function.

- -savedesignmatrix

Save the total design matrix used (default no). This is the total design matrix being used by BROCCOLI. It contains detrending regressors and motion regressors (if -regressmotion is used).

- -savearparameters

Save the estimated AR coefficients (default no).

- -savearparameterst1

Save the estimated AR coefficients, in T1 space (default no).

- -savearparametersmni

Save the estimated AR coefficients, in MNI space (default no).

- -saveallpreprocessed

Save all preprocessed fMRI data
(slice timing corrected, motion corrected, smoothed) (default no).

- -saveunwhitenedresults

Save all statistical results without voxel-wise whitening (default no).

- -saveall

Save everything (default no).

- -output

Set output filename prefix (default fMRI_).

2.8 Additional options

The following additional options are available

- -quiet

Don't print anything to the terminal (default false).

- -verbose

Print extra stuff (default false).

- -debug

Get additional debug information saved as nifti files (default no).
Warning: This will use a lot of extra memory!

2.9 Checking the registration

To check the registration between the anatomical volume and the brain template, set one volume as the underlay (e.g. T1_brain_aligned_linear.nii or T1_brain_aligned_nonlinear.nii) and one as the overlay (e.g. MNI152_T1_1mm_brain.nii.gz). To check the registration between the fMRI volume and the anatomical volume, set the interpolated anatomical volume (e.g. T1_brain_interpolated.nii) as the underlay and the aligned fMRI volume (e.g. fMRI_aligned_t1.nii) as the overlay.

Chapter 3

Registration

3.1 Introduction

BROCCOLI provides a separate function for image registration. Linear as well as non-linear registration is applied to the input volume. The function automatically resizes and rescales the input volume to match the reference volume. In its simplest form, a registration between two volumes can with the bash wrapper be performed as

```
RegisterTwoVolumes input_volume.nii reference_volume.nii
```

3.2 OpenCL options

The following OpenCL options are available

- -platform

The OpenCL platform to use (default 0).

- -device

The OpenCL device to use (default 0).

3.3 Registration options

The following registration options are available

- -iterationslinear

Number of iterations for the linear registration (default 10), 0 means that no linear registration is performed (the two volumes must then be of the same size).

- `-iterationsnonlinear`

Number of iterations for the non-linear registration (default 10), 0 means that no non-linear registration is performed.

- `-sigma`

Amount of Gaussian smoothing applied for regularization of the displacement field, defined as sigma of the Gaussian kernel (default 5.0).

- `-zcut`

Number of mm to cut from the bottom of the input volume, can be negative, useful if the head in the volume is placed very high or low (default 0).

3.4 Outputs

By default, the function saves the results as `input_volume_aligned_linear.nii` (the result after linear registration) and `input_volume_aligned_nonlinear.nii` (the result after non-linear registration). If `-savematrix` is used, the estimated affine transformation matrix will be saved as `input_volume_affinematrix.txt`.

3.5 Output options

The following output options are available

- `-savematrix`

Save the estimated affine transformation matrix to a textfile (default false). It can be used with the function `TransformVolume`.

- `-savefield`

Save the estimated non-linear displacement field to file (default false). This will generate `input_volume_displacement_x.nii`, `input_volume_displacement_y.nii.gz` and `input_volume_displacement_z.nii.gz`. They can be used with the function `TransformVolume`.

- `-saveinterpolated`

Save the input volume rescaled and resized to the size and resolution of the reference volume, before alignment (default false).

- -output

Set output filename prefix (default `input_volume_aligned_linear.nii` and `input_volume_aligned_nonlinear.nii`).

3.6 Additional options

The following additional options are available

- -mask

Mask to apply after linear and non-linear registration, to the aligned volume. The option can for example be used to do a skullstrip (default none).

- -maskoriginal

Mask to apply after linear registration. The option can for example be used to do a skullstrip. Returns the volume skullstripped and unregistered (but interpolated to the reference volume size) (default none).

- -quiet

Don't print anything to the terminal (default false).

- -verbose

Print extra stuff (default false).

- -debug

Get additional debug information saved as nifti files (default no).
Warning: This will use a lot of extra memory!

Chapter 4

Transformation

4.1 Introduction

BROCCOLI provides a separate function for transformation of volumes. In its simplest form, a non-linear transformation can with the bash wrapper be performed as

```
TransformVolume volume_to_transform.nii reference_volume.nii -field  
displacement_field_x.nii displacement_field_y.nii displacement_field_z.nii
```

where `reference_volume.nii` is the reference volume that was used for the registration, and `displacement_field_x.nii` `displacement_field_y.nii` `displacement_field_z.nii` are the non-linear deformation fields generated by `RegisterTwoVolumes`. For a linear transformation, the following command can be used

```
TransformVolume volume_to_transform.nii reference_volume.nii -matrix affinematrix.txt
```

where `affinematrix.txt` contains a 4 x 4 affine transformation matrix (generated manually or by `RegisterTwoVolumes`).

4.2 OpenCL options

The following OpenCL options are available

- `-platform`

The OpenCL platform to use (default 0).

- `-device`

The OpenCL device to use (default 0).

4.3 Transformation options

The following transformation options are available

- -matrix

Apply an affine transformation matrix (4 x 4) given in a text file.

- -scaling

Apply a scaling to each dimension. Using '-scaling 1' will return the volume to transform, interpolated to the size of the reference volume.

- -centering

Center the volume mass of a single volume or all volumes in a 4D dataset.

- -field

Apply an arbitrary deformation field provided in three separate nifti files. The deformation field needs to have the same size as the reference volume.

- -interpolation

The interpolation to use, 0 = nearest, 1 = trilinear (default 1). Nearest interpolation can for example be useful if you want to transform a mask with only integer values.

- -zcut

Number of mm to cut from the bottom of the input volume, can be negative (default 0). Should be the same as for the call to RegisterTwoVolumes.

4.4 Outputs

By default, the function saves the result as `volume_to_transform_warped.nii`.

4.5 Output options

The following output options are available

- -output

Set output filename (default `volume_to_transform_warped.nii`).

4.6 Additional options

The following additional options are available

- -quiet

Don't print anything to the terminal (default false).

Chapter 5

Motion correction

5.1 Introduction

BROCCOLI provides a separate function for motion correction. In its simplest form, motion correction can with the bash wrapper be performed as

```
MotionCorrection fMRI.nii
```

where fMRI.nii is a 4D fMRI dataset.

5.2 OpenCL options

The following OpenCL options are available

- -platform

The OpenCL platform to use (default 0).

- -device

The OpenCL device to use (default 0).

5.3 Motion correction options

The following motion correction options are available

- -referencevolume

Provide a reference volume to which all other volumes will be aligned to (default false). If a 4D dataset is provided, all volumes will be aligned to the first volume in this 4D dataset.

- -iterations

Number of iterations for the motion correction (default 5).

5.4 Outputs

By default, the function saves the results as `input_mc.nii`. The estimated motion parameters are saved as `input_motionparameters.1D`. They can for example be viewed using the AFNI function `1dplot` (`1dplot input_motionparameters.1D`).

5.5 Output options

The following output options are available

- -output

Set output filename (default `input_mc.nii`).

5.6 Additional options

The following additional options are available

- -quiet

Don't print anything to the terminal (default false).

- -verbose

Print extra stuff (default false).

- -debug

Get additional debug information saved as nifti files (default no).
Warning: This will use a lot of extra memory!

Chapter 6

Smoothing

6.1 Introduction

BROCCOLI provides a separate function for smoothing. In its simplest form, smoothing can with the bash wrapper be performed as

```
Smoothing fMRI.nii
```

where fMRI.nii is a 4D fMRI dataset.

6.2 OpenCL options

The following OpenCL options are available

- -platform

The OpenCL platform to use (default 0).

- -device

The OpenCL device to use (default 0).

6.3 Smoothing options

The following smoothing options are available

- -fwhm

Amount of smoothing to apply (in mm, default 6 mm).

- -mask

Perform smoothing inside mask (normalized convolution).

- -automask

Generate a mask and perform smoothing inside mask (normalized convolution).

6.4 Outputs

By default, the function saves the results as `input_sm.nii`. If -automask is selected, the generated mask will be saved as `input_mask.nii`.

6.5 Output options

The following output options are available

- -output

Set output filename (default `input_sm.nii`).

6.6 Additional options

The following additional options are available

- -quiet

Don't print anything to the terminal (default false).

- -verbose

Print extra stuff (default false).

Chapter 7

GLM

7.1 GLM

BROCCOLI provides a separate function for the general linear model (GLM).
A GLM can for a single subject be performed as

```
GLM volumes.nii -design design.txt -contrasts contrasts.txt -firstlevel
```

where volumes.nii is a 4D file containing all volumes from an experiment,
design.txt contains all the raw regressors and can for example be defined as

```
NumRegressors 2
```

```
1.0 0.0  
1.0 0.0  
1.0 0.0  
1.0 0.0  
1.0 0.0  
0.0 1.0  
0.0 1.0  
0.0 1.0  
0.0 1.0  
0.0 1.0
```

while the contrasts.txt file can be defined as

```
NumRegressors 2  
NumContrasts 2
```

```
1.0 -1.0  
-1.0 1.0
```

For a single subject, the GLM can also be performed as

```
GLM data.nii -designfiles regressors.txt -contrasts contrasts.txt -firstlevel
```

where regressors.txt can look like

```
NumRegressors 3
```

```
task1.txt
```

```
task2.txt
```

```
task3.txt
```

Each task file needs to include the number of events, the start time of each event, the length of each event and the value for the regressor of each event (this format is very similar to the one used by the FSL software). A task file can for example look like

```
NumEvents 8
```

47.532543	2.517515	1
68.789386	2.950905	1
93.547212	2.934332	1
165.670213	3.584591	1
190.078151	1.817203	1
257.349564	2.584177	1
280.457018	1.367038	1
308.66593	2.084071	1

For all first level analyses, BROCCOLI will automatically add detrending regressors and remove the mean of all the activity regressors.

7.1.1 Several runs

If several runs are available for one subject, they can be analyzed together as

```
GLM -runs 3 volumes1.nii volumes2.nii volumes3.nii -design design1.txt
design2.txt design3.txt -contrasts contrasts.txt -firstlevel [options]
```

or

```
GLM -runs 3 volumes1.nii volumes2.nii volumes3.nii -designfiles regressors1.txt
regressors2.txt regressors3.txt -contrasts contrasts.txt -firstlevel [options]
```

If, for some reason, a subject did not do a specific task for one or several runs, this can be handled by using a dummy regressor, e.g.

```
NumRegressors 3
```

```
task1.txt  
task2.txt  
dummy.txt
```

where dummy.txt only contains

```
NumEvents 0
```

7.1.2 Checking the design matrix

To check if the design matrix looks correct, the options `-savedesignmatrix` and `-saveoriginaldesignmatrix` can be used. A text file will be generated with all the regressors (`-savedesignmatrix`), or only the task regressors (`-saveoriginaldesignmatrix`). If the AFNI software package is installed, these can for example be viewed as

```
1dplot volumes_total_designmatrix.txt
```

or

```
1dplot volumes_original_designmatrix.txt
```

7.1.3 Group analysis

For a group analysis, a GLM can be performed as

```
GLM volumes.nii -design design.txt -contrasts contrasts.txt -secondlevel
```

where volumes.nii is a 4D file containing beta values from each subject.

7.2 OpenCL options

The following OpenCL options are available

- `-platform`

The OpenCL platform to use (default 0).

- `-device`

The OpenCL device to use (default 0).

7.3 GLM options

The following GLM options are available

- -design

The design matrix to use in the GLM.

- -designfiles

The regressors to use in the GLM, each line in the text file points to a task file.

- -contrasts

The contrast vector(s) to apply to the estimated beta values.

- -firstlevel

Do a GLM for a single subject.

- -secondlevel

Do a GLM for several subjects.

- -teststatistics

Test statistics to use, 0 = GLM t-test, 1 = GLM F-test (default 0).

- -betasonly

Only save the beta values (no t- or F-test), contrast file not needed (default no)

- -contrastonly

Only save the contrast values (default no)

- -betasandcontrastonly

Only save the beta values and the contrast values (default no)

- -mask

A mask that defines which voxels to analyze (default none).

7.4 Single subject options

The following single subject options are available

- -runs

Number of fMRI runs that will be concatenated and analyzed together, necessary to provide one design file per run. Separate detrending regressors will be added for each run. The number of task regressors will not change compared to a single run, meaning that the contrast vectors are the same as for a single run.

- -rawregressors

Use raw regressors (FSL format, one line per volume/TR). These regressors will not be convolved with any hemodynamic response function. Intended for -designfiles, not for -design.

- -detrendingregressors

Set the number of detrending regressors (per run), 1 - 4. 1 means a single regressor for the intercept, 2 means intercept + linear trends, 3 means intercept + linear trends + quadratic trends, 4 means intercept + linear trends + quadratic trends + cubic trends (the default is 4 detrending regressors).

- -temporalderivatives

Use temporal derivatives for the activity regressors (default no). The contrast vectors will automatically be extended with zeros for these additional regressors. Only possible for -designfiles, not for -design.

- -regressmotion

Provide a file with motion regressors to use in the design matrix (default no). The file can be generated by FirstLevelAnalysis or Motion-Correction. The contrast vectors will automatically be extended with zeros for these additional regressors.

- -regressglobalmean

Include global mean in design matrix (default no). The contrast vectors will automatically be extended with zeros for this additional regressor.

7.5 Outputs

By default, the GLM function saves each beta value as

```
volumes_beta_regressor001.nii ... volumes_beta_regressor00R.nii
```

for R regressors. For each contrast, BROCCOLI also saves the contrast of parameter estimate (COPE) and the corresponding t-scores, e.g.

```
volumes_cope_contrast001.nii - volumes_cope_contrast00C.nii
```

```
volumes_tscores_contrast001.nii - volumes_tscores_contrast00C.nii
```

7.6 Output options

The following output options are available

- -saveresiduals

Save the residuals (default no).

- -saveresidualvariance

Save the residual variance (default no).

- -savearparameters

Save the estimated AR coefficients (first level only, default no).

- -saveoriginaldesignmatrix

Save the original design matrix used (default no).

- -savedesignmatrix

Save the total design matrix used (default no).

- -output

Set output filename (default volumes_).

7.7 Additional options

The following additional options are available

- -quiet

Don't print anything to the terminal (default false).

- -verbose

Print extra stuff (default false).

Chapter 8

Permutation testing

8.1 Randomise

BROCCOLI provides a function for permutation testing at the group level, similar to the FSL function `randomise`. In its simplest form, a permutation test can with the bash wrapper be performed as

```
RandomiseGroupLevel volumes.nii -design design.mat -contrasts design.con
```

where `volumes.nii` is a 4D file with data from all subjects in the group(s). The `design.mat` file can for example be defined as

```
NumRegressors 2
NumSubjects 10
```

```
1.0 0.0
1.0 0.0
1.0 0.0
1.0 0.0
1.0 0.0
1.0 0.0
0.0 1.0
0.0 1.0
0.0 1.0
0.0 1.0
0.0 1.0
```

while the `design.con` file can be defined as

```
NumRegressors 2
NumContrasts 2
```

```
1.0 -1.0
-1.0 1.0
```

8.2 OpenCL options

The following OpenCL options are available

- -platform

The OpenCL platform to use (default 0).

- -device

The OpenCL device to use (default 0).

8.3 Permutation options

The following permutation options are available

- -design

The design matrix to apply in each permutation.

- -contrasts

The contrast vector(s) to apply to the estimated beta values.

- -groupmean

Test for group mean, using sign flipping
(design and contrast not needed).

- -mask

A mask that defines which voxels to permute (default none).

- -permutations

Number of permutations to use (default 5,000).

- -teststatistics

Test statistics to use, 0 = GLM t-test, 1 = GLM F-test (default 0).

- -inferencemode

Inference mode to use, 0 = voxel, 1 = cluster extent, 2 = cluster mass, 3 = threshold free cluster enhancement (TFCE) (default 1).

- -cdt

Cluster defining threshold for cluster inference (default 2.5).

- -significance

The significance level to calculate the threshold for (default 0.05).

- -permutationfile

Use a specific permutation file or sign flipping file (e.g. from FSL), provide the filename after the option.

8.4 Outputs

By default, the function saves the results as `volumes__perm_tvalues.nii` (t-scores for the unpermuted case) and `volumes__perm_pvalues.nii` (p-values from the permutation test).

8.5 Output options

The following output options are available

- -output

Set output filename (default `volumes__perm_tvalues.nii` and `volumes__perm_pvalues.nii`).

- -writepermutationvalues

Write all the permutation values to a text file, provide the filename after the option.

- -writepermutations

Write all the random permutations (or sign flips) to a text file, provide the filename after the option.

8.6 Additional options

The following additional options are available

- -quiet

Don't print anything to the terminal (default false).

- -verbose

Print extra stuff (default false).

Chapter 9

ICA

9.1 ICA

BROCCOLI provides a function for independent component analysis (ICA). In its simplest form, it can be used as

```
ICA volumes.nii
```

where volumes.nii is a 4D file with several volumes.

9.2 OpenCL options

The following OpenCL options are available

- -platform

The OpenCL platform to use (default 0).

- -device

The OpenCL device to use (default 0).

9.3 ICA options

The following ICA options are available

- -var

Proportion of variance to save before ICA (default 80 %).

- -mask

Provide a spatial mask (default false), otherwise a mask will automatically be created.

- -zscore

Z-score each time series before ICA (default false).

- -cpu

Use the CPU only (default false).

- -double

Use double precision for all calculations, instead of single precision floats (default false).

9.4 Outputs

By default, the function saves the independent components as `volumes_ica.nii`.

9.5 Output options

The following output options are available

- -output

Set output filename (default `volumes_ica.nii`).

9.6 Additional options

The following additional options are available

- -quiet

Don't print anything to the terminal (default false).

- -verbose

Print extra stuff (default false).

