

Neuroimaging Analysis Kit – NIAK – user's guide



<http://www.nitrc.org/projects/niak/>

Release 0.7 – June 2013

1 The fMRI preprocessing pipeline

- Overview of the pipeline
- Input files
- Pipeline options
- Quality control

2 The region growing pipeline

3 Connectome pipeline

4 Pipeline manager

5 Installation, contributions and further resources

What's NIAK ?

- The neuroimaging analysis kit (NIAK) is an opensource (MIT license) library of functions dedicated to process functional magnetic resonance images (fMRI) using Octave or Matlab(r).
- Currently NIAK supports Linux operating systems (Ubuntu recommended) and the MINC file format.
- Running NIAK on a dataset consists of editing a small Matlab/Octave script to describe where the data is located, where to store the outputs as well as the options of the processing tools.

What's NIAK ?

The current version of NIAK (0.6.5) features :

- Reader/writer of medical images, supporting MINC1 and MINC2 file formats.
- The pipeline system for Octave and Matlab (PSOM).
- A pipeline for T_1 image preprocessing.
- A pipeline for fMRI preprocessing.
- A pipeline for region growing and the generation of full brain parcelations & connectomes.

How to start the fMRI preprocessing pipeline ?

Running (or restarting) the pipeline in a matlab session is just one call to the following function :

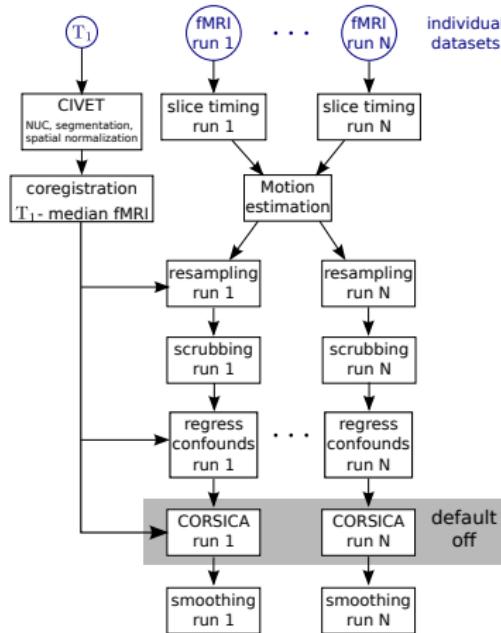
```
niak_pipeline_fmri_preprocess(files_in,opt)
```

- ① files_in is a structure describing how the dataset is organized.
- ② opt is a structure describing the options of the pipeline.

The list of the results and a detailed tutorial of the pipeline can be found at :

<http://www.nitrc.org/plugins/mwiki/index.php/niak:FmriPreprocessing>.

Overview of the pipeline



Simplified flowchart of the fMRI preprocessing pipeline for one subject.

Describing the dataset

An example of script to build the `files_in` structure for the small example dataset available to test NIAK :

```
%% Subject 1

% The structural scan
files_in.subject1.anat      = '/home/pbellec/demo_niak/anat_subject1.mnc';

% fMRI - motor condition
files_in.subject1.fmri.session1.motor = '/home/pbellec/demo_niak/func_motor_subject1.mnc';

% fMRI - rest
files_in.subject1.fmri.session1.rest  = '/home/pbellec/demo_niak/func_rest_subject1.mnc';

%% Subject 2

% The structural scan
files_in.subject2.anat      = '/home/pbellec/demo_niak/anat_subject2.mnc';

% fMRI - motor condition
files_in.subject2.fmri.session1.motor = '/home/pbellec/demo_niak/func_motor_subject2.mnc';

% fMRI - rest
files_in.subject2.fmri.session1.rest  = '/home/pbellec/demo_niak/func_rest_subject2.mnc';
```

General options I

Specifying the output directories of the pipeline

The field `opt.folder_out` is a string that specifies the folder where the results of the pipeline will be saved. The pipeline manager will create but can also delete files and subfolders in that location. Example :

```
opt.folder_out = '/database/data_demo/fmri_preprocess/';
```

General options II

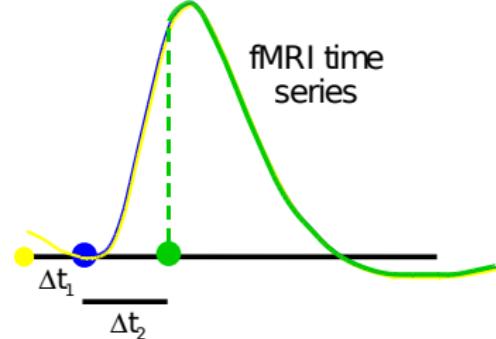
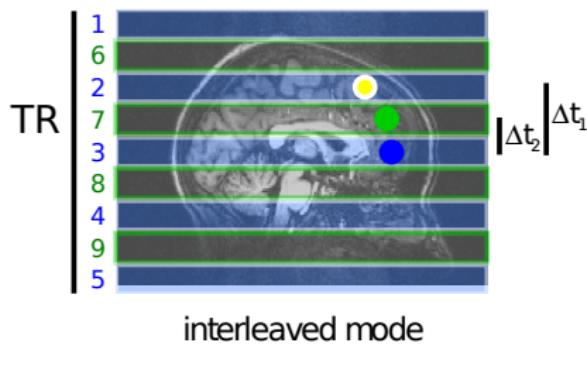
Size of outputs

The option `opt.size_output` can be used to adjust the quantity of intermediate results that are generated by the pipeline. Example :

```
opt.size_output = 'quality_control';
```

- ① '`quality_control`' : some outputs are generated at each step of the analysis for the purposes of quality control. Intermediate steps are deleted as soon as they are no longer necessary.
- ② '`all`' : all possible outputs are generated at each stage of the pipeline.

Slice timing correction I



→ temporal interpolation to a single reference time
for each volume (cubic spline interpolation)

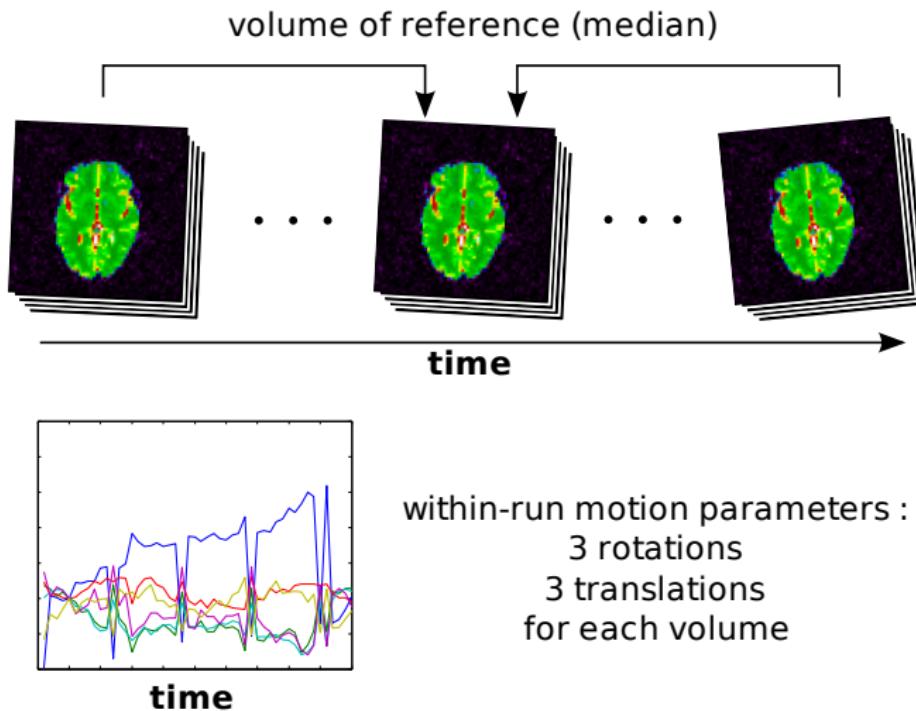
Courtesy of Dr M. Péligrini-Issac.

Slice timing correction II

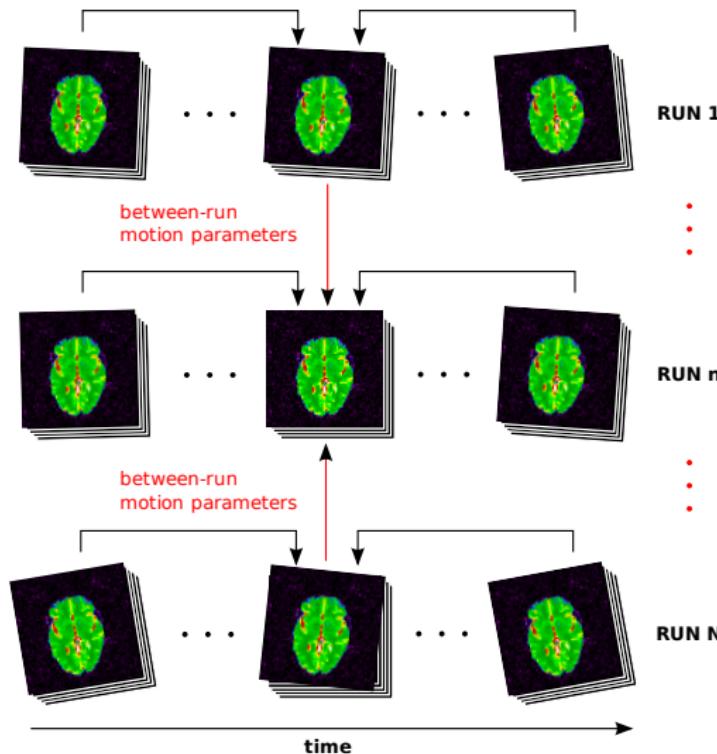
A complete list of options for this brick can be found in the help of `niak_brick_slice_timing`.

```
% Number of dummy scans to suppress.  
opt.slice_timing.suppress_vol = 0;  
  
% Slice timing order. Available options :  
% 'sequential ascending' , 'sequential descending',  
% 'interleaved ascending' , 'interleaved descending'  
opt.slice_timing.type_acquisition = 'interleaved ascending';  
  
% Scanner manufacturer.  
% Only the value 'Siemens' will actually have an impact  
opt.slice_timing.type_scanner      = 'Bruker';  
  
% The delay in TR ("blank" time between two volumes)  
opt.slice_timing.delay_in_tr      = 0;  
  
% Skip the slice timing (0: don't skip, 1 : skip)  
opt.slice_timing.flag_skip        = 0;
```

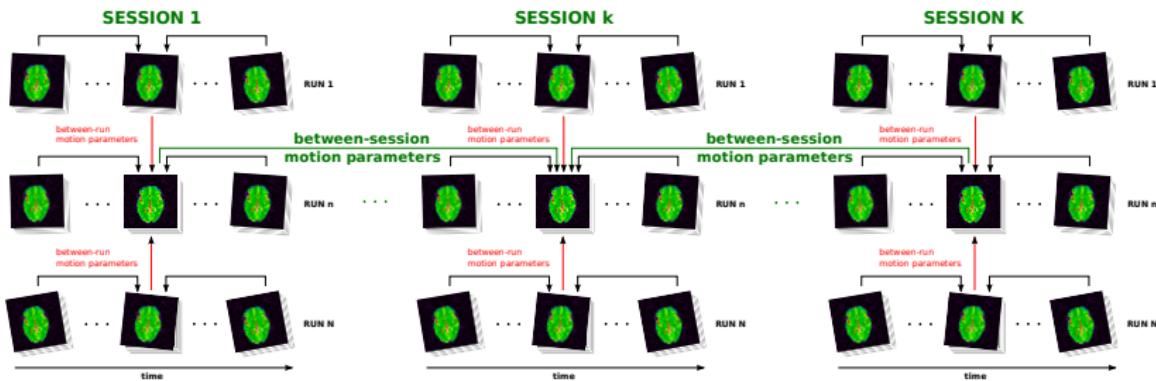
Motion estimation: within-run



Motion estimation: between-run / within-session



Motion estimation: between sessions



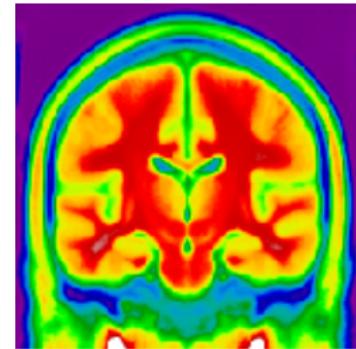
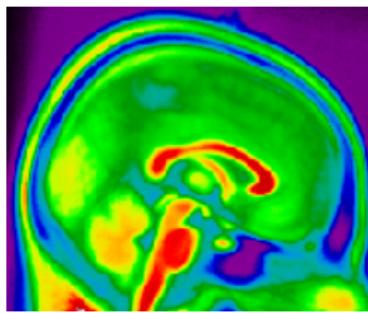
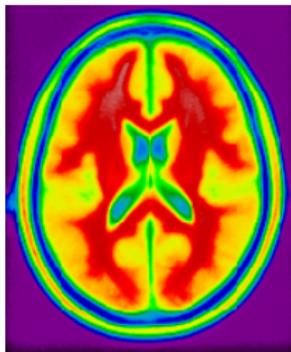
Estimation of between-run (between-session) rigid-body motion.

Motion estimation: parameters

A complete list of options for this brick can be found in the help of `niak_brick_motion_correction`. Example :

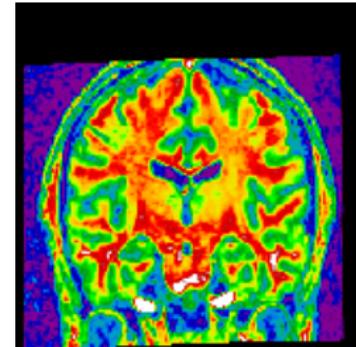
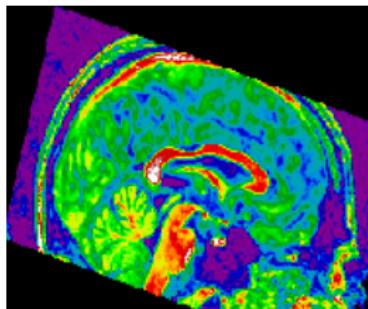
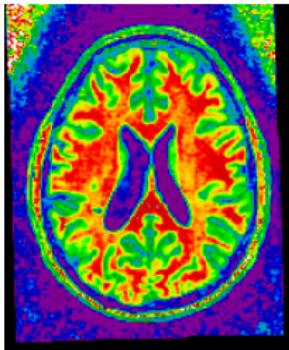
```
% The session that is used as a reference.  
% In general, use the session including the acquisition of the T1 scan.  
opt.motion_correction.session_ref = 'session1';
```

T_1 processing: linear template



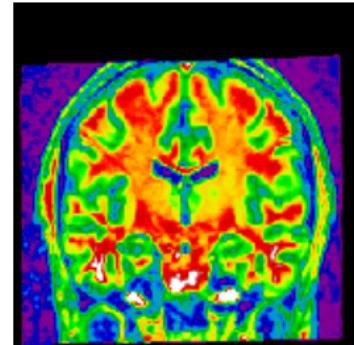
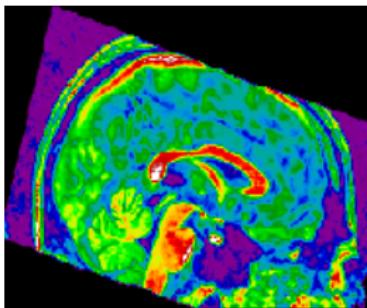
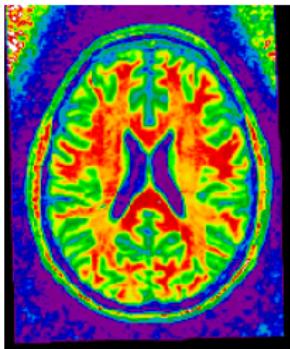
Linear ICBM template (average of 152 subjects)

T_1 processing: linear coregistration



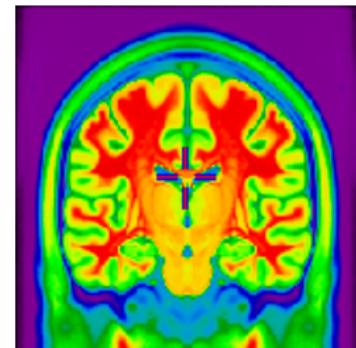
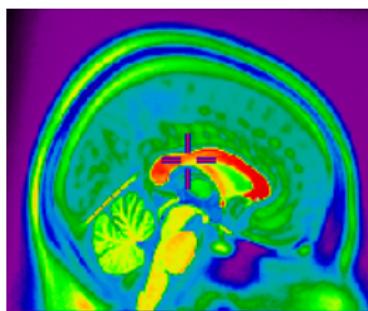
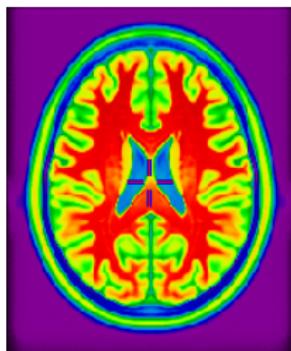
Individual structural scan (linear coregistration)

T_1 processing: non-linear coregistration



Individual structural scan (non-linear coregistration)

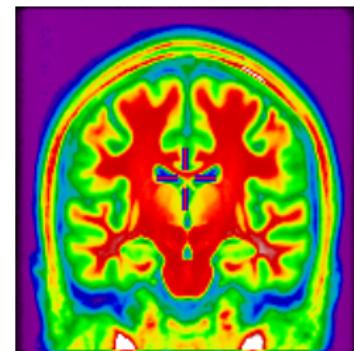
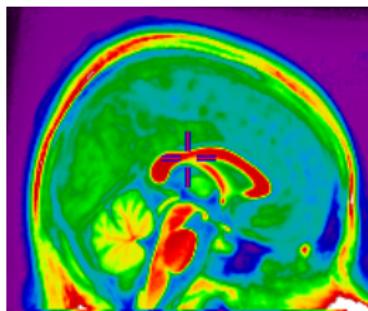
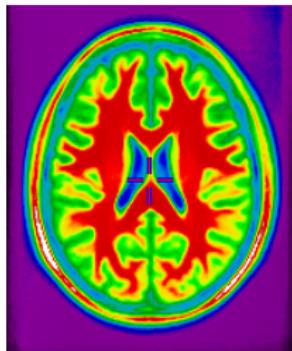
T₁ processing: nonlinear template



Symmetric non-linear ICBM template (average of 152 subjects)
release 2009a.

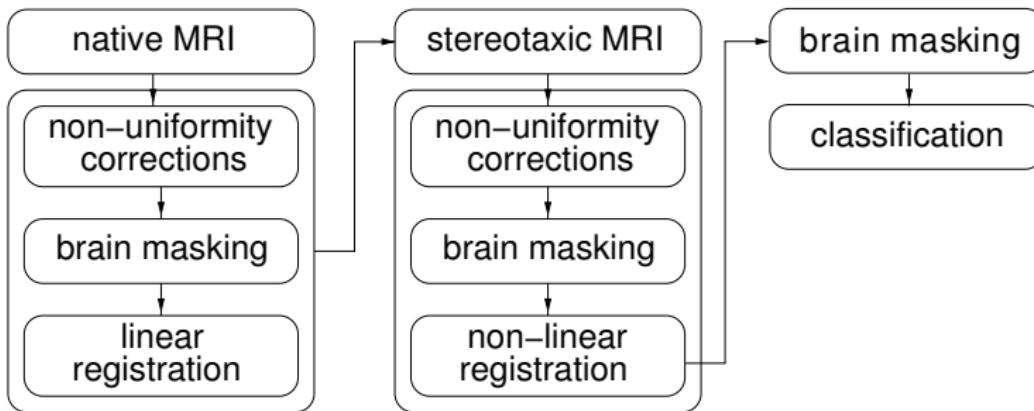
<http://www.bic.mni.mcgill.ca/ServicesAtlases/ICBM152NLin2009>

T₁ processing: group average



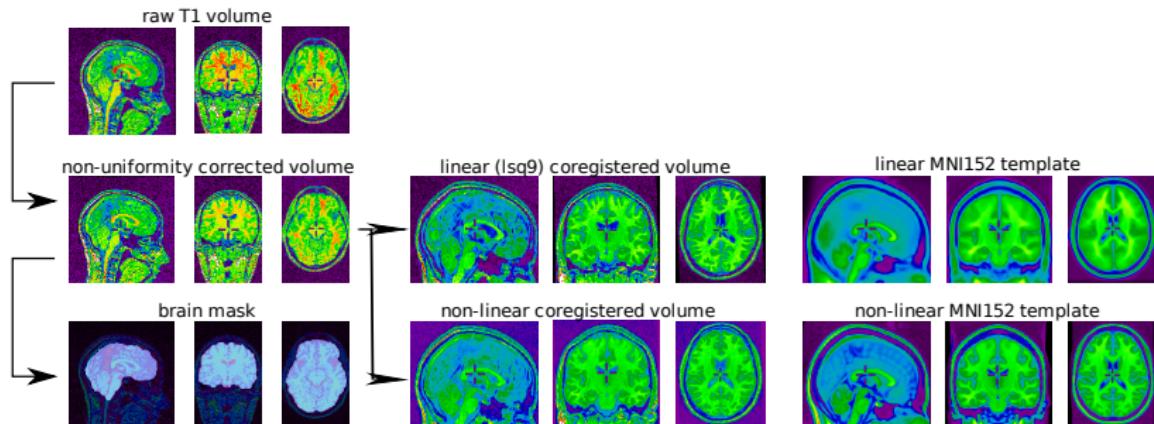
Average of 17 subjects (non-linear coregistration)

T₁ processing: Flowchart of the CIVET pipeline



Flowchart of the T₁ preprocessing.

T₁ processing: main outputs



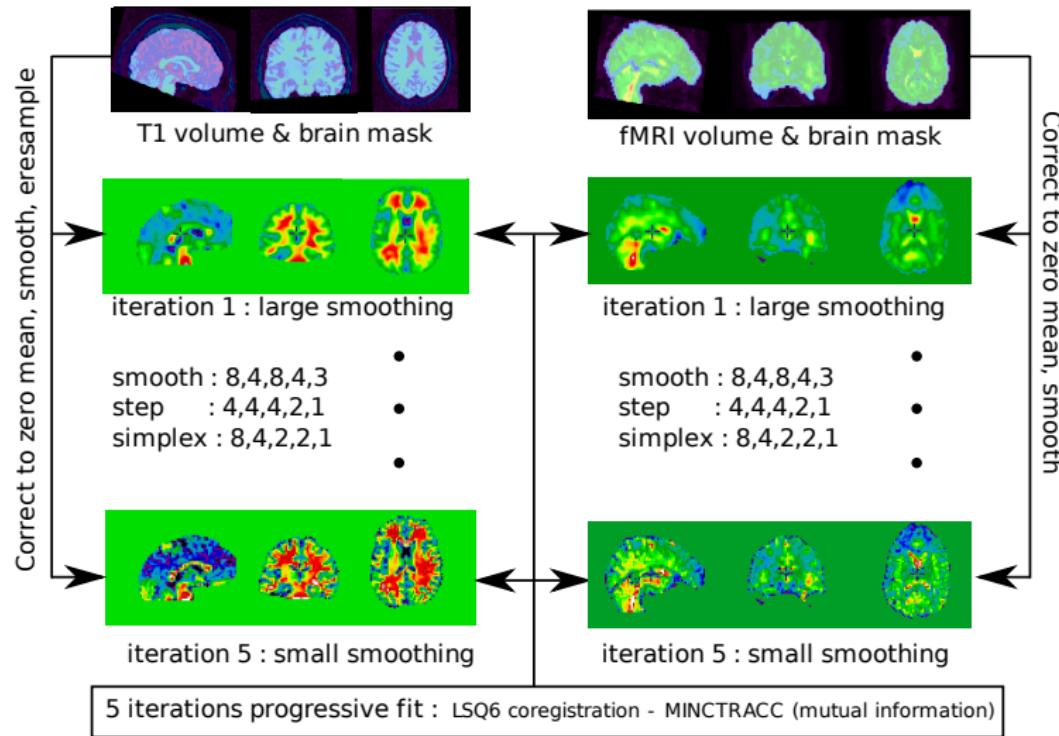
The main outputs of the T₁ processing pipeline.

T₁ processing: parameters

A complete list of options for this brick can be found in the help of `niak_brick_t1_preprocess`. Example :

```
% Parameter for non-uniformity correction.  
% Suggested values :  
% 200 for 1.5T images,  
% 50 for 3T images.  
  
opt.t1_preprocess.nu_correct.arg = '-distance 50';
```

Coregistration between the T₁ and fMRI volumes I



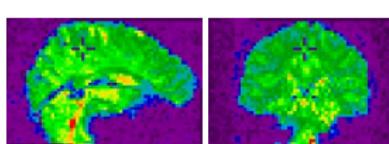
Coregistration between the T₁ and fMRI volumes II

A complete list of options for this brick can be found in the help of `niak_brick_anat2func`. Example :

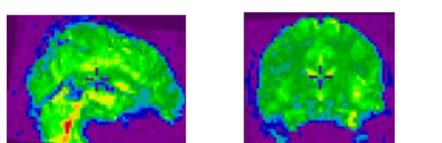
```
% An initial guess of the transform.  
% Possible values 'identity', 'center'.  
% 'identity' is self-explanatory.  
% The 'center' option usually does more harm than good.  
% Use it only if you have very big misrealignment between  
% the two images (say, > 2 cm).  
  
opt.anat2func.init = 'identity';
```

Spatial resampling I

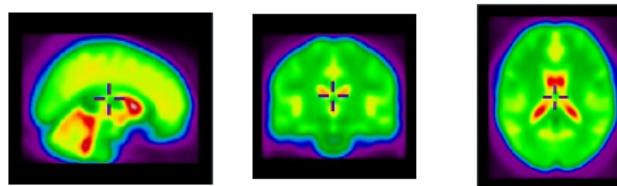
native functional space



stereotaxic space - individual volume - non-linear transform -



stereotaxic space - average of 40 subjects



The transformations to correct for rigid-body motion during the fMRI acquisition and the transformation to match the T₁ image and then (non-linearly) coregister into stereotaxic space are all combined, and a single step of spatial resampling is applied.



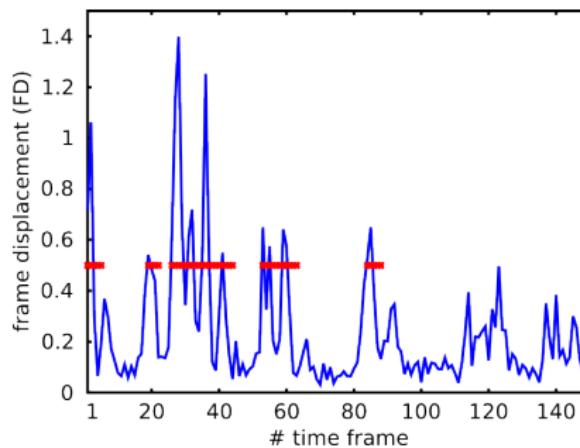
Spatial resampling II

A complete list of options for this step can be found in the help of `niak_brick_resample_vol`. Example :

Spatial resampling

```
% The resampling scheme.  
% The most accurate is 'sinc' but it is awfully slow  
opt.resample_vol.interpolation      = 'trilinear';  
  
% The voxel size to use in the stereotaxic space  
opt.resample_vol.voxel_size        = [3 3 3];  
  
% Skip resampling  
% (data will stay in native functional space  
% after slice timing/motion correction)  
% (0: don't skip, 1 : skip)  
opt.resample_vol.flag_skip        = 0;
```

Scrubbing: frame displacement

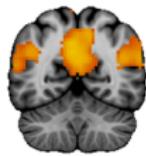


Frame displacement is the sum of absolute displacements in translation and rotation motion parameters. For each frame with excessive FD (here $FD > 0.5$), four frames are suppressed (the target one + one before + two after, marked with red stars on the figure). The original method was proposed by Power et al. Neuroimage 2012. Note that, unlike the original method, only FD is used in NIAK (and not DVARS).

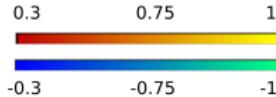
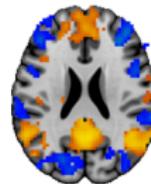
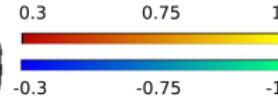
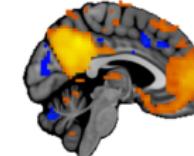
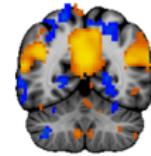
Scrubbing: example of impact on the DMN

Seed based analysis in the PCC Default mode

No scrubbing



Scrubbing 0.2



See Power et al. Neuroimage 2012 for more infos.

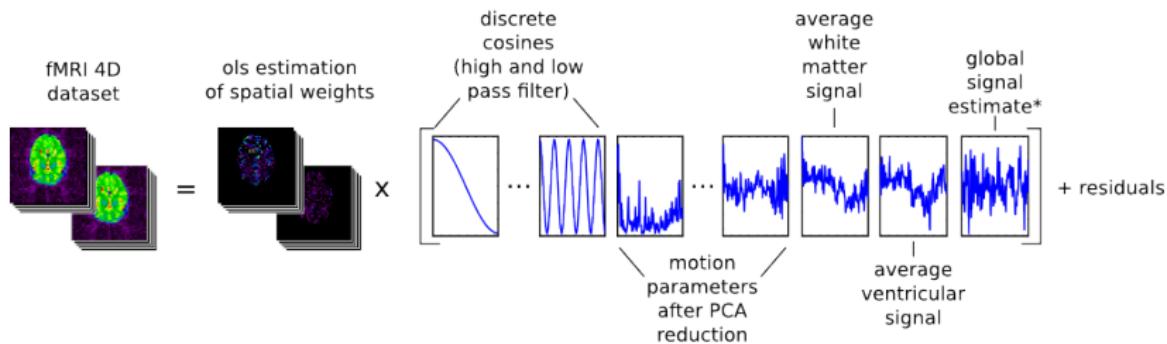
Scrubbing: parameters

The scrubbing is implemented as part of `niak_brick_regress_cofounds`. WARNING: the scrubbing is changing the temporal grid of the dataset. Most software will not handle these changes properly. If NIAK is used to preprocess a dataset before analysis in another software package such as FSL, **it is important to skip scrubbing**. Example of options:

```
% Turn on/off the scrubbing of time frames  
% with excessive motion  
%(true: apply / false : don't apply)  
opt.regress_cofounds.flag_scrubbing = true;  
  
% The threshold on frame displacement that is used to  
% determine frames with excessive motion  
opt.regress_cofounds.thre_fd = 0.5;
```

Regress confounds: model

Regression model for confounds in resting-state fMRI



* the global signal estimate is based on a PCA decomposition,
as described in Carbonell, Bellec and Shmuel, Brain connectivity 2012

Regress confounds: parameters

A complete list of options for this brick can be found in the help of `niak_brick_time_filter` and `niak_brick_regress_confound`s.

Example :

```
% Cut-off frequency for high-pass filtering (in Hz).
opt.time_filter.hp = 0.01;

% Cut-off frequency for low-pass filtering (in Hz).
opt.time_filter.lp = Inf;

% Turn on/off the regression of the average white matter signal
opt.regress_confound.flag_wm = true;

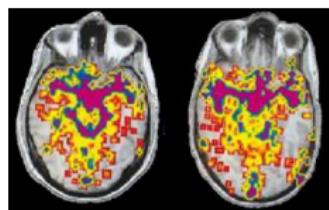
% Turn on/off the regression of the average of the ventricles
opt.regress_confound.flag_vent = true;

% Turn on/off the regression of the motion parameters
opt.regress_confound.flag_motion_params = true;

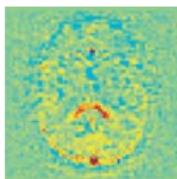
% Turn on/off the regression of the PCA-based estimation
% of the global signal
opt.regress_confound.flag_gsc = false;
```

CORSICA: sources of structured noise

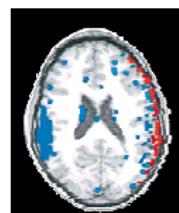
Many sources of space-time correlated noise fluctuations are corrupting fMRI time-series:



Cardiac fluctuations
Dagli et al. Neuroimage (1999)



Respiratory fluctuations
Raj et al. Phys. Med. Biol. (1999)

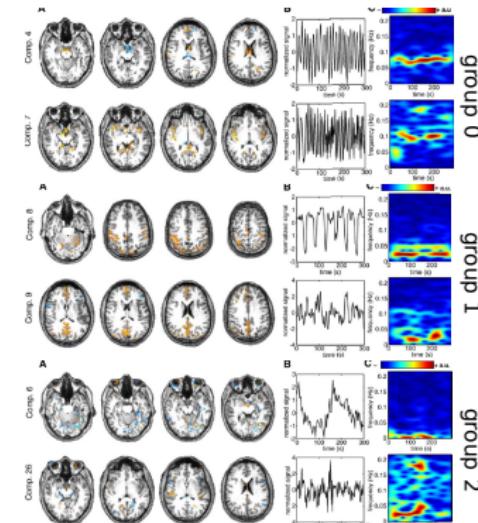
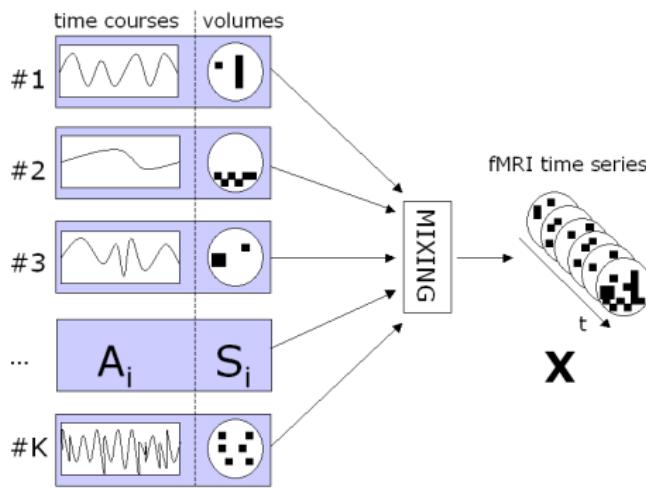


Residual motion
McKeown et al. HBM (1998)

1/f acquisition noise
space-time filtering
slice-timing correction
motion
motion correction

•
•
•

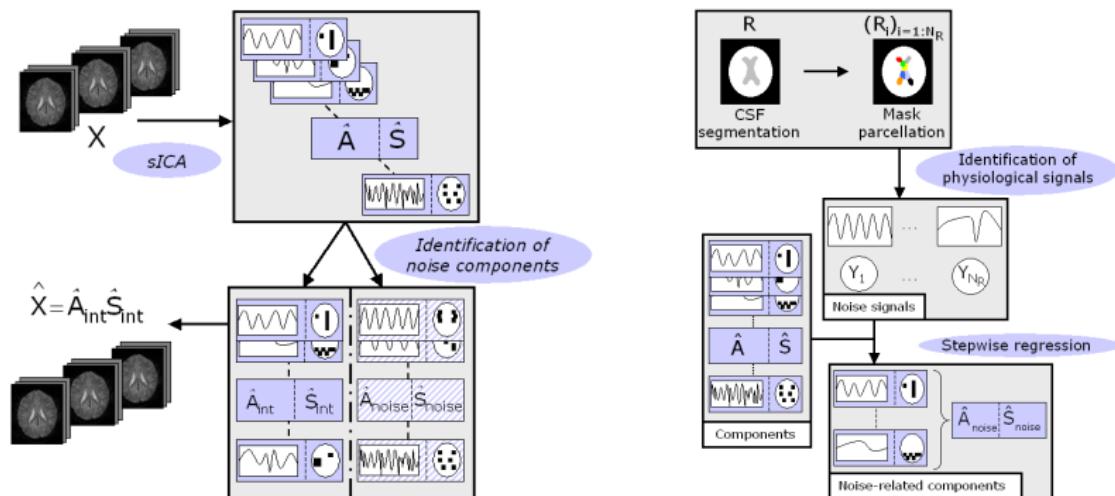
CORSICA: independent component analysis



spatially independent components analysis

Perlbarg et al. Magnetic Resonance Imaging, 2007, 25: 35-46.

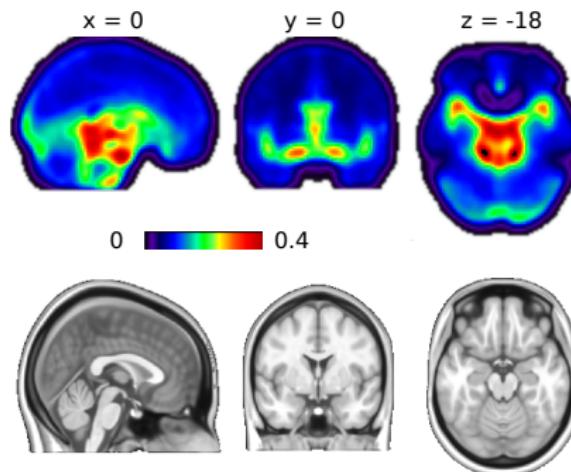
CORSICA: selection of “noise” components



Flowchart of the CORSICA algorithm for correcting structured noise in fMRI

Perlberg et al. Magnetic Resonance Imaging, 2007, 25: 35-46.

CORSICA: effect map



Relative variance of estimated structured noise using CORSICA. Average on 40 subjects, 5 tasks per subject.

P. Bellec, V. Perlberg and A. C. Evans, Magnetic Resonance Imaging, 2009, pp. 1382-1396..

CORSICA: parameters

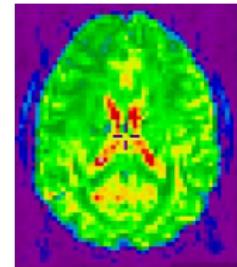
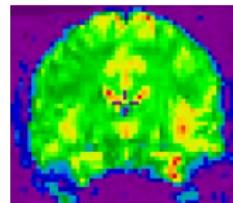
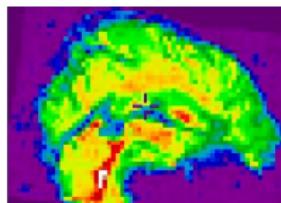
Although generally beneficial, the CORSICA selection is not stable enough to be used completely unsupervised. It is usually better to skip this step. A complete list of options for this brick can be found in the help of `niak_pipeline_corsica`. Example :

CORSICA

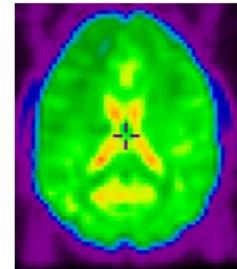
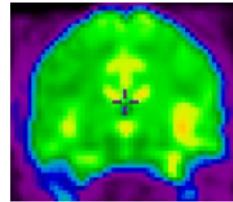
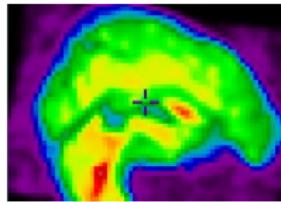
```
% Number of components estimated during the ICA.  
% 20 at a minimum, 60 was used in the validation of CORSICA.  
opt.corsica.sica.nb_comp = 60;  
  
% Threshold for selecting noise components.  
% 0.15 has been calibrated on a validation database.  
opt.corsica.threshold      = 0.15;  
  
% Skip CORSICA (0: don't skip, 1 : skip).  
opt.corsica.flag_skip      = 1;
```

Spatial smoothing I

native resolution



**smoothed image
isotropic Gaussian
kernel - 6 mm FWHM**



Spatial smoothing II

A complete list of options for this step can be found in the help of `niak_brick_smooth_vol`. Example :

Spatial smoothing

```
% Full-width at half maximum (FWHM) of the  
% Gaussian blurring kernel, in mm.  
opt.smooth_vol.fwhm      = 6;  
  
% Skip spatial smoothing (0: don't skip, 1 : skip)  
opt.smooth_vol.flag_skip = 0;
```

The fMRI preprocessing pipeline

Quality control

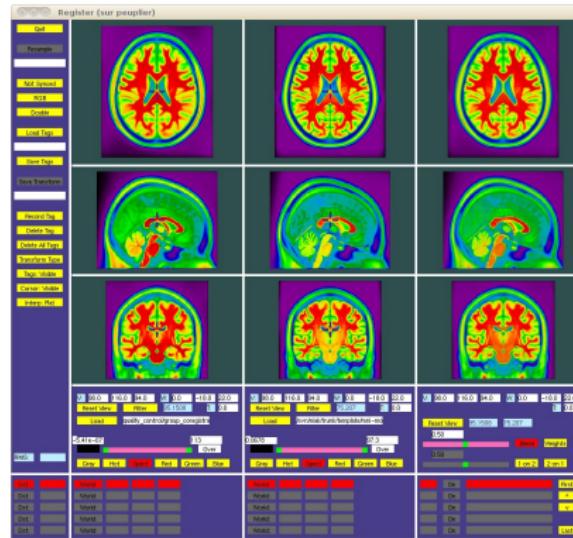
Structural group average vs template

Average T1 across all subjects in stereotaxic space (non-linear) :

FOLDER_OUT/quality_control/group_coregistration/anat_mean_average_stereonl.mnc.gz

T1 template = stereotaxic space (non-linear) :

PATH_NIAK/template/mni-models_icbm152-nl-2009-1.0/mni_icbm152_t1_tal_nlin_sym_09a.mnc.gz



The fMRI preprocessing pipeline

Quality control

Structural group average vs functional group average

Average T1 across all subjects in stereotaxic space (non-linear) :

FOLDER_OUT/quality_control/group_coregistration/anat_mean_average_stereonl.mnc.gz

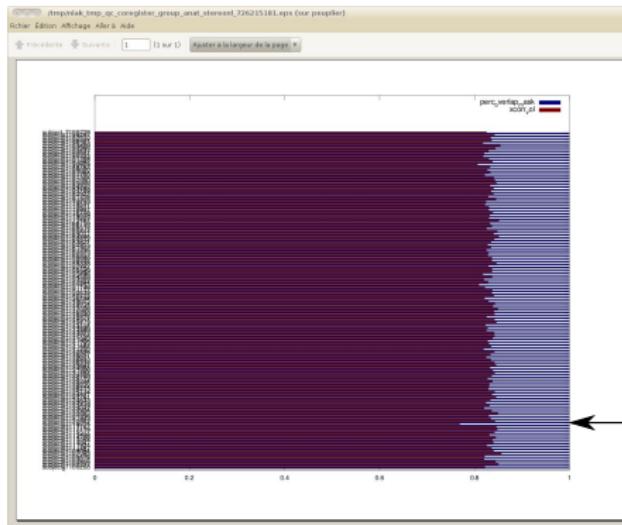
Average mean fMRI volume across all subjects in stereotaxic space (non-linear) :

FOLDER_OUT/quality_control/group_coregistration/func_mean_average_stereonl.mnc.gz



Quantitative metrics for coregistration (T1 and fMRI) I

```
T1    : FOLDER_OUT/quality_control/group_coregistration/anat_fig_qc_coregister_stereonl.pdf
fMRI : FOLDER_OUT/quality_control/group_coregistration/func_fig_qc_coregister_stereonl.pdf
blue  : percentage of overlap between individual brain masks and group brain mask (check FOV).
red   : spatial correlation of individual scans and the group average (Check coregistration).
```



Quantitative metrics for coregistration (T1 and fMRI) II

T1 : FOLDER_OUT/quality_control/group_coregistration/anat_tab_qc_coregister_stereonl.csv
fMRI : FOLDER_OUT/quality_control/group_coregistration/func_tab_qc_coregister_stereonl.csv
Same info as last slide, but in a CSV file (view with open office or excel).

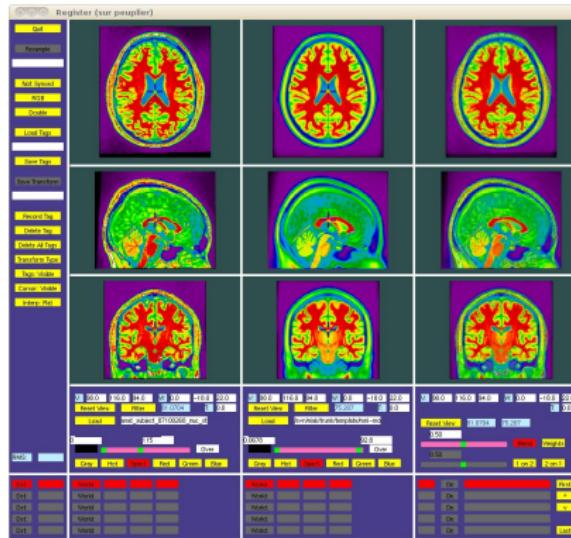
Individual coregistration : T1 vs template

Individual T1 in stereotaxic space (non-linear) :

FOLDER_OUT/anat/<SUBJECT>/anat_subject_<SUBJECT>.nuc-stereonl.mnc.gz

T1 template (non-linear) :

PATH_NIAK/template/mni-models_icbm152-nl-2009-1.0/mni_icbm152_t1_tal_nlin_sym_09a.mnc.gz



Individual coregistration : T1 vs fMRI

Individual T1 scan in native functional space :

FOLDER_OUT/anat/<SUBJECT>/anat_subject_<SUBJECT>_nuc_nativefun_hires.mnc.gz

Individual mean fMRI volume in native functional space :

FOLDER_OUT/anat/<SUBJECT>/func_subject_<SUBJECT>_mean_nativefunc.mnc.gz



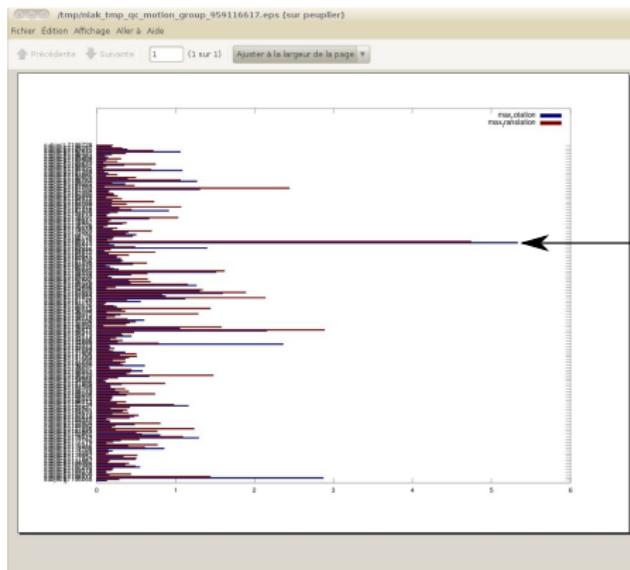
Group summary of maximal transition in motion

Bar plot in PDF : FOLDER_OUT/quality_control/group_motion/qc_motion_group.pdf

Table in CSV : FOLDER_OUT/quality_control/group_motion/qc_motion_group.csv

Blue : maximal transition in rotation (degree) for each subject.

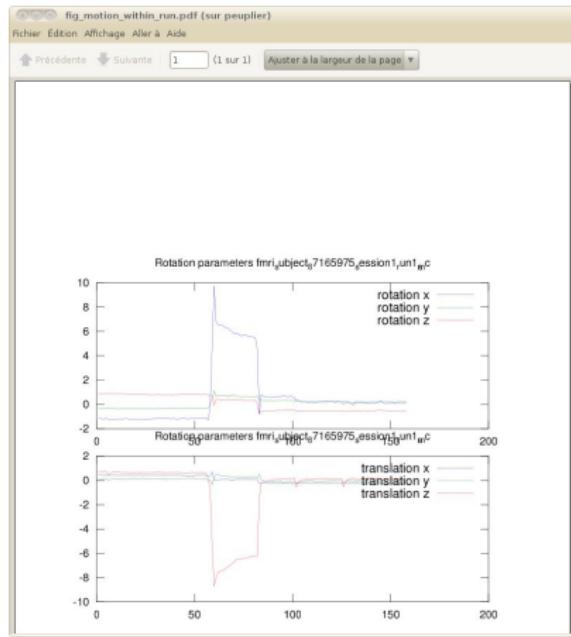
Red : maximal transition in translation (mm) for each subject.



**check the motion
parameters of this
subject (at least)**

Individual within-run motion parameters

Individual within-run motion parameters in PDF :
FOLDER_OUT/quality_control/<SUBJECT>/motion/fig_motion_within_run.pdf



Group summary of between-run motion correction

Bar plot in pdf :

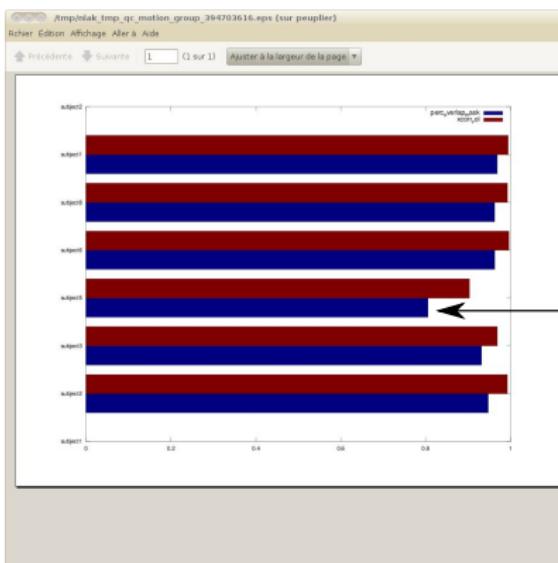
FOLDER_OUT/quality_control/group_motion/qc_coregister_between_runs_group.pdf

Table in CSV :

FOLDER_OUT/quality_control/group_motion/qc_coregister_between_runs_group.csv

blue : Min over all runs of the percentage of overlap between brain masks of individual runs and the individual brain mask for each subject.

red : Min over all runs of the spatial correlation of the mean volume of individual runs and the average of all runs for each subject (check coregistration).



check the between-run motion correction of this subject

Individual quality measure of between-run motion correction

Bar plot in pdf :

FOLDER_OUT/quality_control/group_motion/<subject>/motion/tab_coregister_motion.pdf

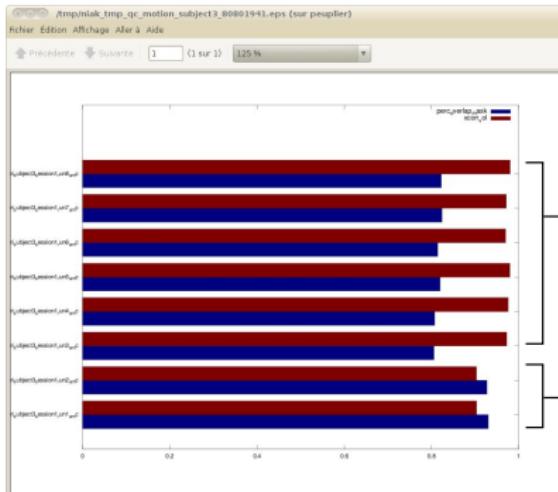
Table in CSV :

FOLDER_OUT/quality_control/group_motion/<subject>/motion/tab_coregister_motion.csv

blue (check FOV) :

percentage of overlap between brain masks of individual runs and the individual brain mask.
red (check coregistration) :

spatial correlation of the mean volume of individual runs and the average of all runs.



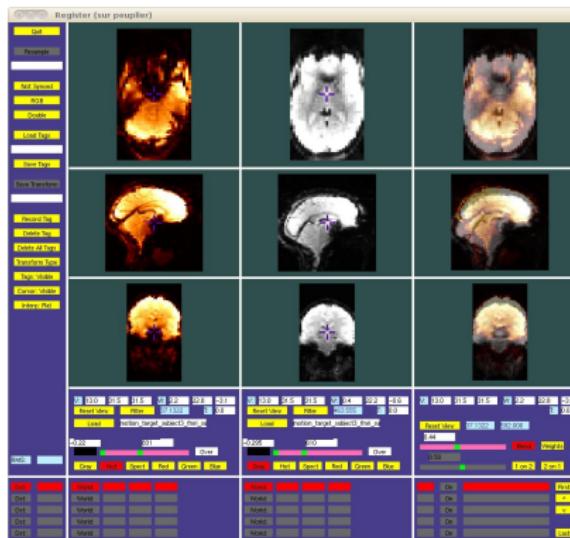
What happened
between runs 1&2
and runs 3-8 ?

Evaluation of the motion correction between runs

Back to the intermediate results ! Let's check the targets for motion correction of different runs, before motion correction :

Target of motion correction per subject & run :

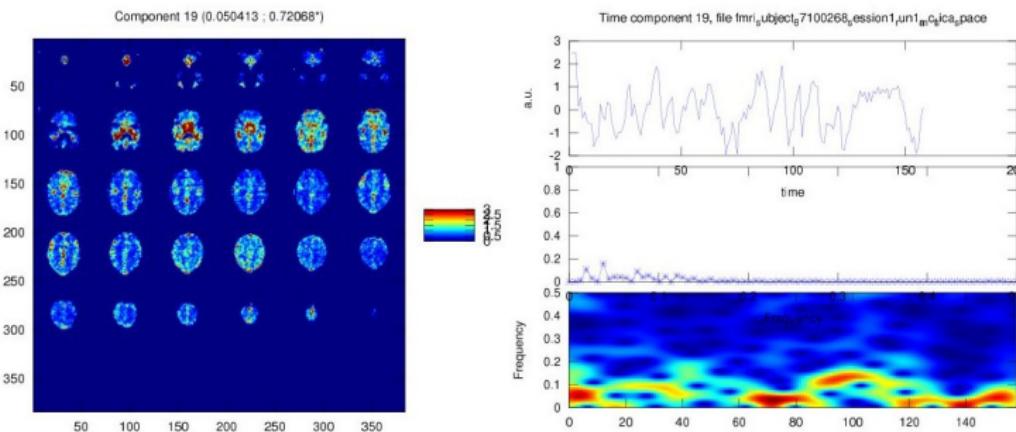
FOLDER_OUT/intermediate/<subject>/motion_correction/motion_target_<subject>_<session>_<run>.a.mnc.gz



Whoa ! That's a big between-run motion ! In this case, it seems that two subjects were mixed up when converting data from DICOM to MINC. A good thing we found out ...

Evaluation of the physiological noise correction (CORSICA)

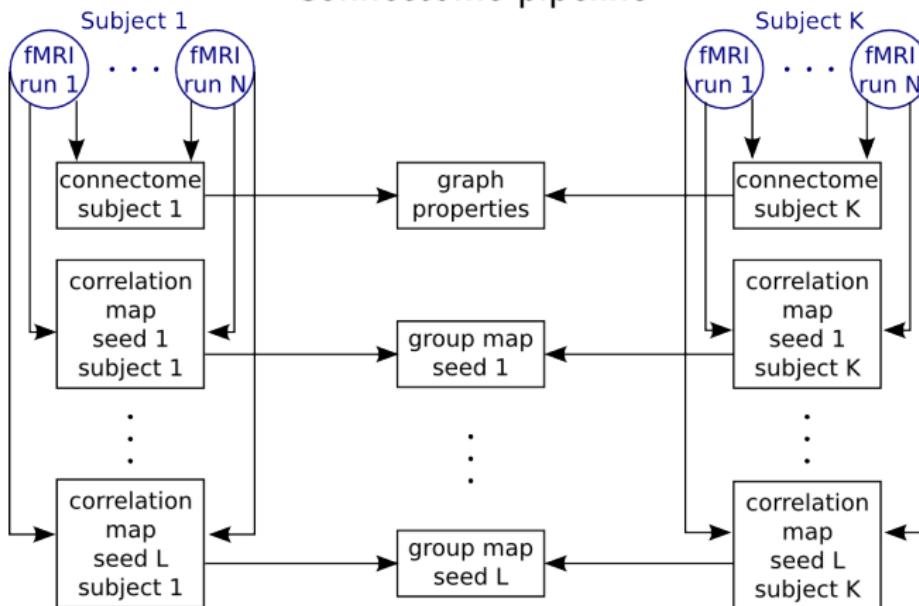
PDF summary of the analysis per subject and per run in FOLDER_OUT/quality_control/<subject>/corsica/fmri_<SUBJECT>_<SESSION>_<RUN>_a_mc_f_sica_space_qc_corsica.pdf



For each component, the spatial component is shown in “montage” style, and the time course is plotted along with the power spectrum and a time-frequency analysis. The selection score for CORSICA (ventricle mask, stem mask) is indicated. A star means that the component was identified as physiological noise.

Flowchart

Connectome pipeline



The networks and seeds input files have not been included for clarity.

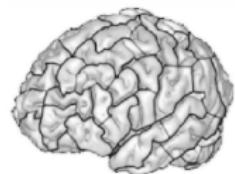
User template

Grab preprocessed data

```
1 opt_g.min_nb_vol = 100;  
2 opt_g.min_xcorr_func = 0.5;  
3 opt_g.type_files = 'glm_connectome';  
4 files_in.fmri = niak_grab_fmri_preprocess('/data/fmri_preprocess',opt_g).fmri;
```

- ➊ Set the minimum acceptable number of time frames that passed scrubbing.
- ➋ Minimum spatial correlation between the individual BOLD volume and a group average (QC tool on coregistration).
- ➌ Prepare the files to feed in the connectome pipeline
- ➍ Grab the files

Input files



files_in.networks



network label

files_in.seeds

A	B
1	roi_basc
2	PCC
3	dMPFC
4	aMPFC
5	dMPFC2
6	TPJ
7	PCUN
8	PHC
9	FUS

number of
the network

User template ... continued

Input file: brain parcellation

```
files_in.networks = '/home/pbellec svn/niak/template/roi_aal_3mm.mnc.gz';
```

Input file: seed regions (csv files)

```
files_in.seeds = '/home/toto/database/list_seeds.csv';
```

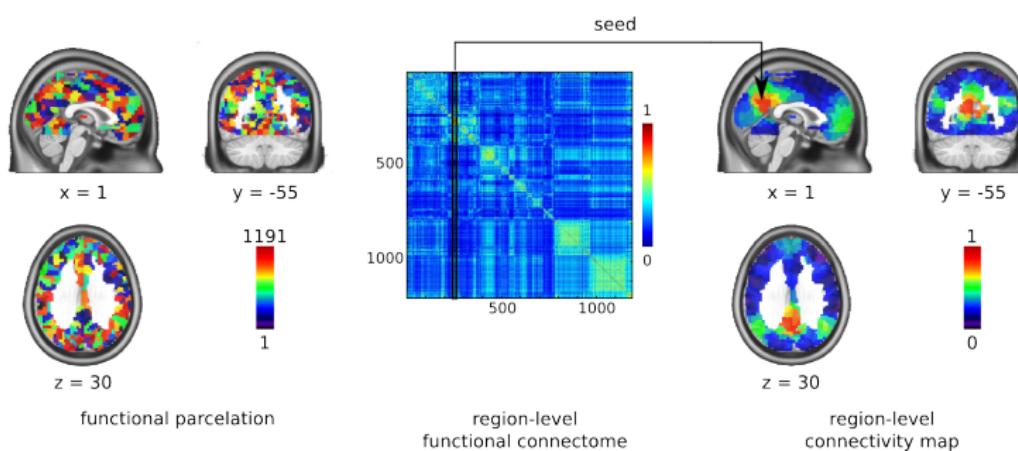
Options

```
opt.connectome.type = 'Z'; % The type of connectome.  
opt.connectome.thresh.type = 'sparsity_pos'; % how to binarize the connectome.  
opt.connectome.thresh.param = 0.2; % the cut-off on connectivity
```

Run the pipeline

```
pipeline = niak.pipeline_connectome(files_in,opt_pipe);
```

Output: individual connectomes



Saved in individual .mat files.

Output: graph properties

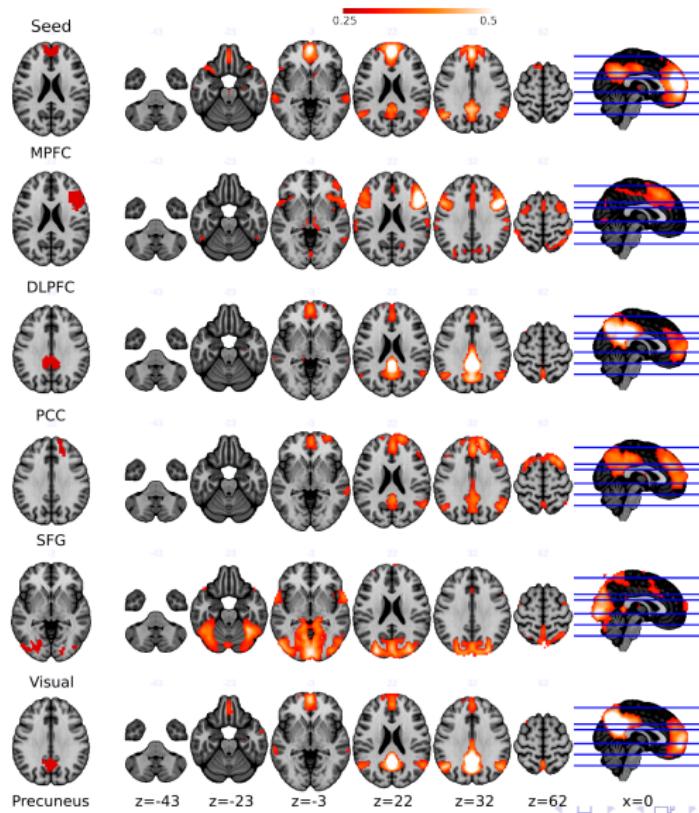
	A	B	C	D
1		Dcentrality_DLPFCI	Dcentrality_DMO	Dcentrality_FUS
2	session1_sub05676	-0.4180975675	0.1320308108	0.2420564864
3	session1_sub08224	0.7485541619	-0.1643167673	-0.5294651389
4	session1_sub08889	2.4971908638	-0.7043358847	-0.5442595472
5	session1_sub09607	1.0599716142	0.1382571671	0.1382571671
6	session1_sub14864	0.1862837144	0.6943302082	0.6943302082
7	session1_sub18604	1.1220449913	1.3059867931	1.8578121986
8	session1_sub22894	-0.5935012783	1.0648111169	1.0648111169
9	session1_sub27641	0.3672248004	0.2797903241	1.0667006108
10	session1_sub33259	1.1411152971	-0.4251213852	-0.089499239
11	session1_sub34482	1.3486391285	0.1226035571	1.1442998666
12	session1_sub36678	1.7417839427	0.3440560875	1.3117138334
13	session1_sub38579	-0.1304375846	0.3587033577	0.1956563769
14	session1_sub39529	1.1375060069	-0.8204961361	1.7901733879

• • •
graph metrics

-
- subjects
-

Graph properties are generated with the brain connectivity toolbox
<https://sites.google.com/site/bctnet/Home/functions>. See
Rubinov and Sporns, Neuroimage 2010.

Output: connectivity maps



The pipeline system for Octave and Matlab (PSOM)

The pipeline execution is powered by a generic manager called PSOM. PSOM has many interesting features :

- **Parallel computing** : If you have access to multiple cpus or computers, PSOM can run multiple jobs in parallel.
- **Job failures** : Job failures will not crash the pipeline. You will have access to the logs to fix the problem, and restarting the pipeline will reprocess the failed jobs only.
- **Pipeline update** : If for some reason you decide to restart the pipeline after changing some options, PSOM will examine the changes made to the pipeline and restart only the jobs that need to be reprocessed. You can also add some subjects and restart the pipeline, PSOM will process only these new subjects.

More info can be found in the paper Bellec et al. *Fontiers in Neuroinformatics*, 2012.

Example of execution history

Example of pipeline running history on the BIC cluster for the demo
NIAK dataset :

```
*****
The pipeline PIPE is now being processed.
Started on 25-Mar-2009 14:53:32
user: pbellec, host: zeus, system: unix
*****
25-Mar-2009 14:53:34 - The job anat_subject1 has been submitted to the queue (1 jobs in queue).
25-Mar-2009 14:53:35 - The job anat_subject2 has been submitted to the queue (2 jobs in queue).
25-Mar-2009 14:53:36 - The job motion_correction_subject1 has been submitted to the queue (3 jobs in queue).
25-Mar-2009 14:53:37 - The job motion_correction_subject2 has been submitted to the queue (4 jobs in queue).
.....
25-Mar-2009 15:05:49 - The job motion_correction_subject1 has been successfully completed (3 jobs in queue).
25-Mar-2009 15:05:50 - The job sica_subject1_run1 has been submitted to the queue (4 jobs in queue).
25-Mar-2009 15:05:51 - The job sica_subject1_run2 has been submitted to the queue (5 jobs in queue).
25-Mar-2009 15:06:41 - The job motion_correction_subject2 has been successfully completed (4 jobs in queue).
25-Mar-2009 15:06:51 - The job sica_subject2_run1 has been submitted to the queue (5 jobs in queue).
25-Mar-2009 15:06:52 - The job sica_subject2_run2 has been submitted to the queue (6 jobs in queue).
25-Mar-2009 15:08:07 - The job sica_subject1_run1 has been successfully completed (5 jobs in queue).
25-Mar-2009 15:09:04 - The job sica_subject2_run2 has been successfully completed (4 jobs in queue).
25-Mar-2009 15:09:19 - The job sica_subject1_run2 has been successfully completed (3 jobs in queue).
25-Mar-2009 15:09:31 - The job sica_subject2_run1 has been successfully completed (2 jobs in queue).
.....
(... Some history lines were omitted to fit everything on one slide ...)
*****
The processing of the pipeline was completed.
25-Mar-2009 16:05:46
*****
All jobs have been successfully completed.
```



Configuration of the pipeline manager

A complete list of options for this step can be found in the web tutorial :

<http://code.google.com/p/psom/wiki/ConfigurationPsom>.

The configuration can be set up by editing a configuration file.

PSOM

```
% Number of jobs that can run in parallel.  
% This is usually the number of cores.  
opt.psom.max_queued = 2;
```

Installation I

Downloading and installing the NIAK library

The latest stable version can be found here:

http://www.nitrc.org/frs/?group_id=411

Once the library has been decompressed, all you need to do is to start a Matlab or Octave session and add the NIAK path (with all its subfolders) to your search path, example :

```
path_niak = '/home/pbellec/public/niak/' ;  
P = genpath(path_niak) ;  
addpath(P) ;
```

Current requirements : Matlab 7+/Octave 3+ and Linux.

More detailed instructions can be found at :

<http://www.nitrc.org/plugins/mwiki/index.php/niak:Installation>

Installation II

Demo data

There is also a small demo dataset you can download in various formats at http://www.nitrc.org/frs/?group_id=411

The main functions available in NIAK have demonstrations (invoked by `niak_demo_`) that run on this data. You can either copy the demo data in the `/niak/data_demo/` folder (default location) or in an arbitrary folder that will need to be passed as an argument to the demo functions.

Minc tools

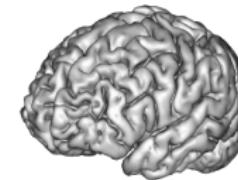
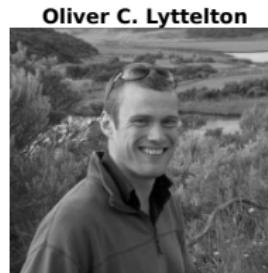
For most operations you will need to install a version of the MINC tools. The MINC tools are publicly available for LINUX and MAC OSX at <http://packages.bic.mni.mcgill.ca/>

Instructions for installation can be found at :

<http://en.wikibooks.org/wiki/MINC/Installation>

Who contributed to NIAK ? People

The kit was originally designed by Pierre Bellec in the lab of Alan C. Evans, Canada, 2008-10. The following people contribute to NIAK, either through code or ideas :



Felix Carbonell

Vladimir Fonov

Andrew Janke

Claude Lepage

Alan C. Evans

Who contributed to NIAK ? Institutions

The following institutions support the authors of NIAK. NITRC and Google Code are generously hosting the project.



McGill University



Montreal Neurological Institute



TAMPERE UNIVERSITY OF TECHNOLOGY



Who contributed to NIAK ? Software and testing

NIAK is including or depending on a number of software :

- ① The MINC tools that have been developed by members and collaborators of the MNI over the past 15 years.
- ② The linear model analysis is a port of the fMRIstat project developed by the late Keith Worsley, who will be sorely missed.
- ③ Some functions were based upon existing open-source software. See the NIAK website for a detailed list of contributions.

A lot of people have been involved in beta-testing the project and gave very precious feedback over the past two years. A non-exhaustive list includes Benjamin D'hont, Pr Christophe Grova's lab, Pr Jean Gotman's lab, Pr Alain Dhager's lab, Pr Pedro Rosa-Neto's lab and Sébastien Lavoie-Courchesne.

Useful links



- 1 The download page, with this pdf presentation, NIAK releases and the demo dataset

http://www.nitrc.org/frs/?group_id=411



- 2 The NIAK online user's guide

<http://www.nitrc.org/plugins/mwiki/index.php/niak:MainPage>



- 3 The NIAK project page and developer's guide

<http://code.google.com/p/niak/>



- 4 The PSOM project page

<http://code.google.com/p/psom/>

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