

Preprocessing of fMRI data

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pierre_bellec

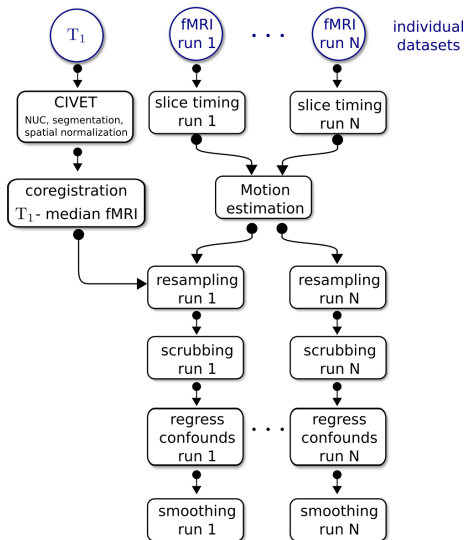


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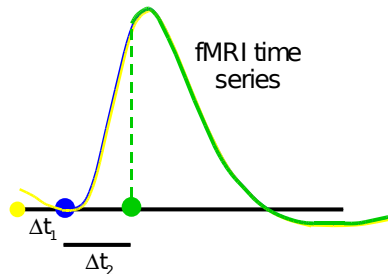
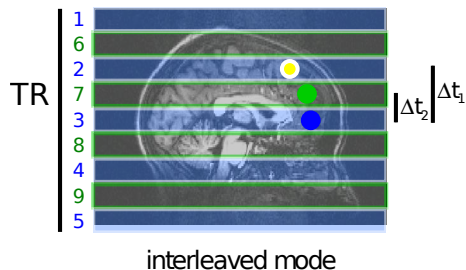
CRIUGM, DIRO, Udm



Flowchart of the NIAK fMRI preprocessing pipeline



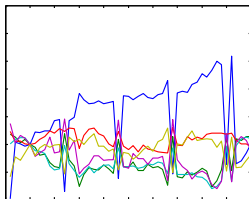
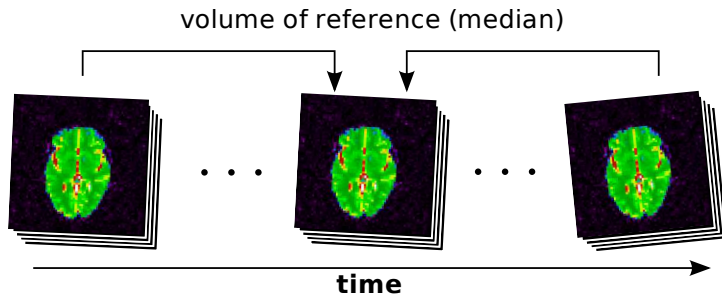
Slice timing correction



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

Courtesy of Dr M. Péligrini-Issac.

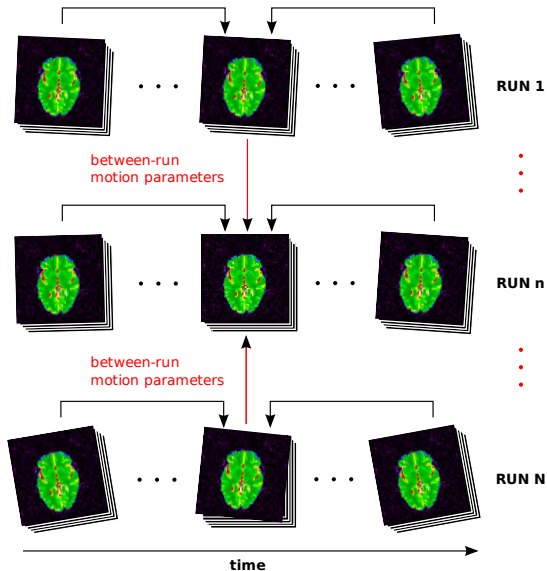
Motion estimation: within-run



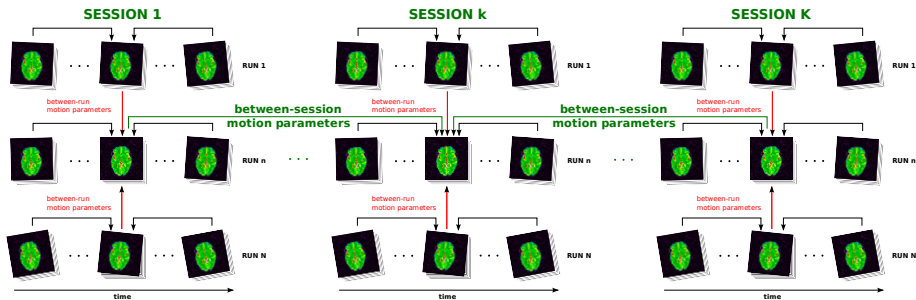
time

within-run motion parameters :
3 rotations
3 translations
for each volume

Motion estimation: between-run / within-session

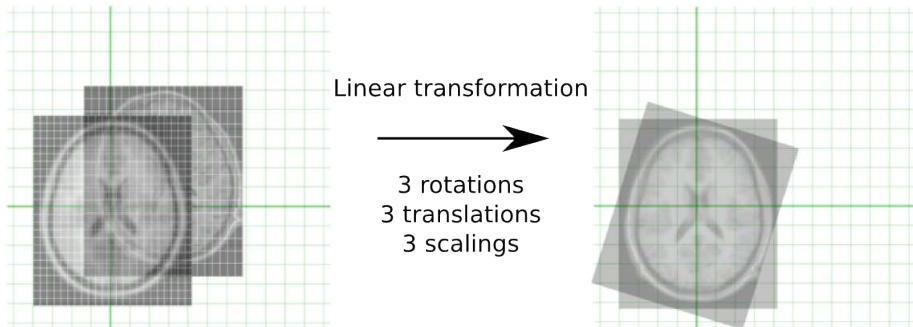


Motion estimation: between sessions



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

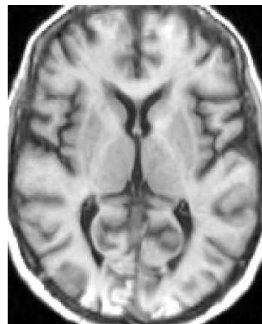
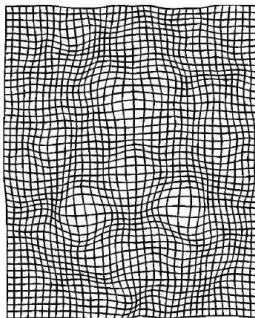
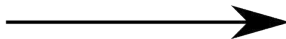
T_1 processing: linear coregistration



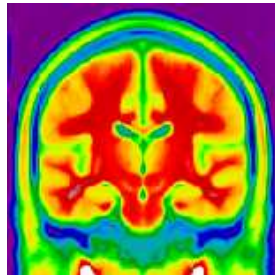
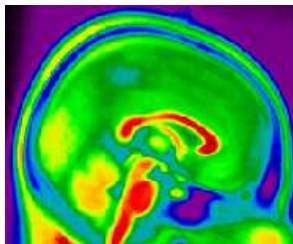
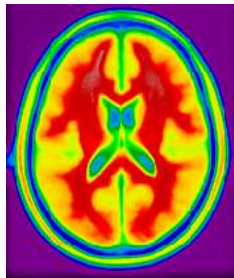
T_1 processing: non-linear coregistration



Non-linear (smooth)
transformation

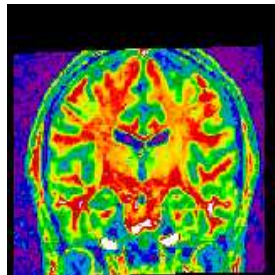
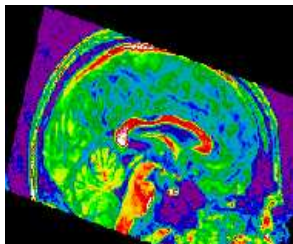
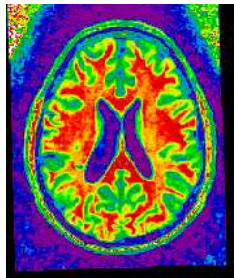


T_1 processing: linear template



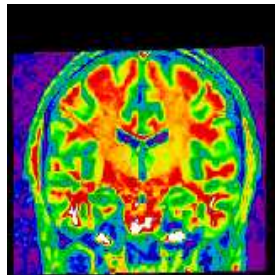
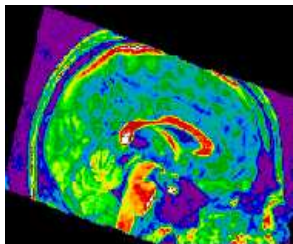
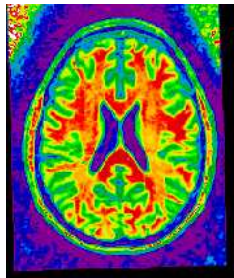
Linear ICBM template (average of 152 subjects)

T_1 processing: linear coregistration



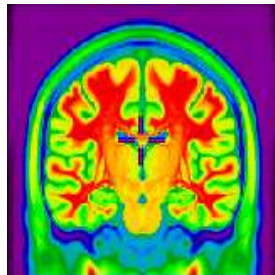
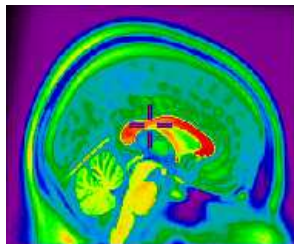
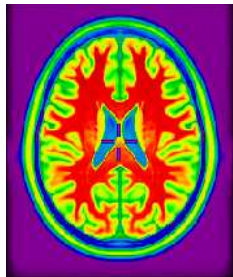
Individual structural scan (linear coregistration)

T_1 processing: non-linear coregistration



Individual structural scan (non-linear coregistration)

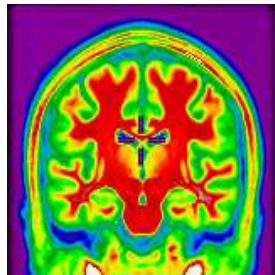
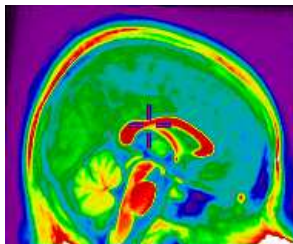
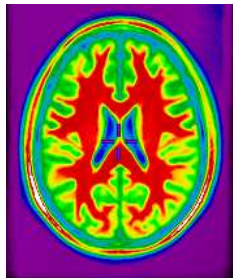
T_1 processing: nonlinear template



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

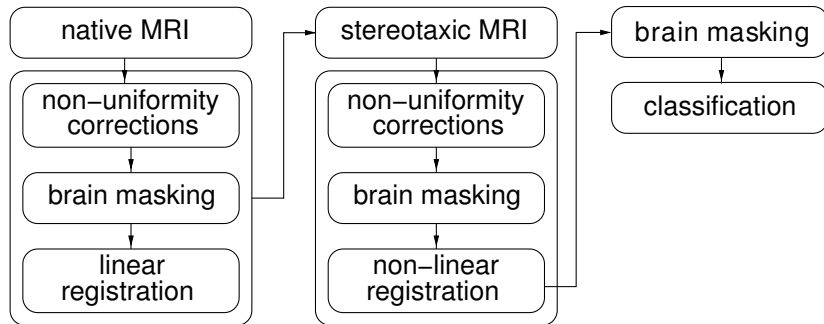
<http://www.bic.mni.mcgill.ca/ServicesAtlases/ICBM152NLin2009>

T_1 processing: group average



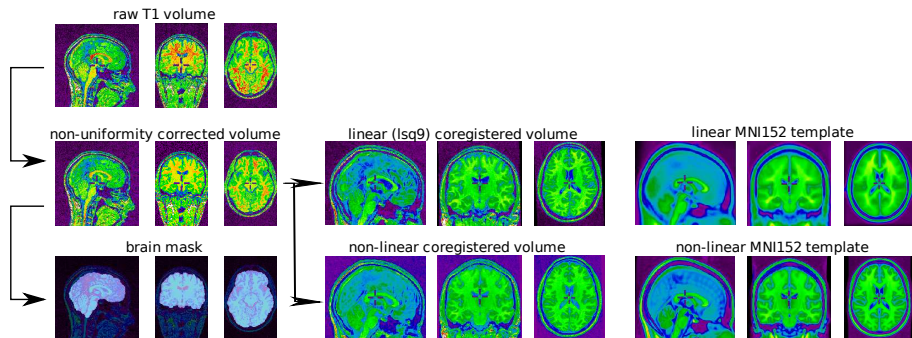
Average of 17 subjects (non-linear coregistration)

T₁ processing: Flowchart of the CIVET pipeline



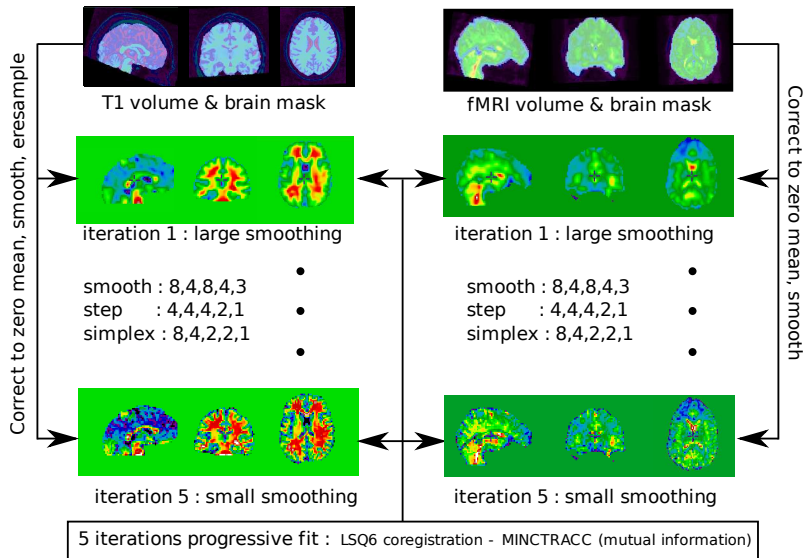
Flowchart of the T1 preprocessing.

T_1 processing: main outputs



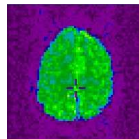
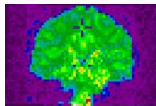
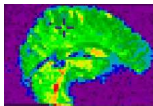
The main outputs of the T_1 processing pipeline.

Coregistration between the T_1 and fMRI volumes

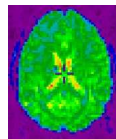
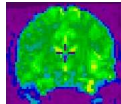
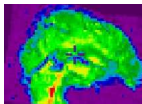


Spatial resampling

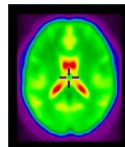
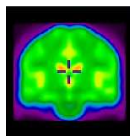
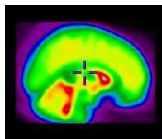
**native functional
space**



**stereotaxic space -
individual volume -
non-linear transform -**

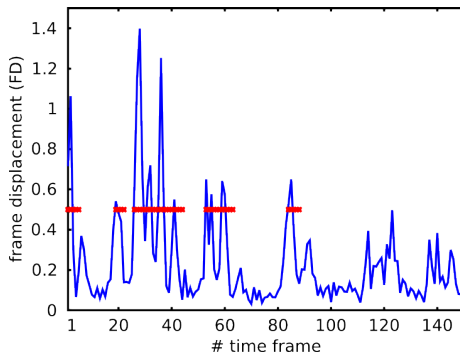


**stereotaxic space -
average of 40 subjects**



The transformations to correct for rigid-body motion during the fMRI acquisition and the transformation to match the T_1 image and then (non-linearly) coregister into stereotaxic space are all combined, and a single step of spatial resampling is applied.

Scrubbing: frame displacement

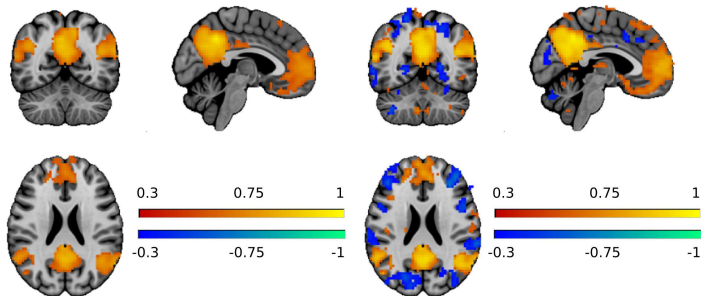


Frame displacement is the sum of absolute displacements in translation and rotation motion parameters. For each frame with excessive FD (here $FD > 0.5$), four frames are suppressed (the target one + one before + two after, marked with red stars on the figure). The original method was proposed by Power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

Seed based analysis in the PCC Default mode

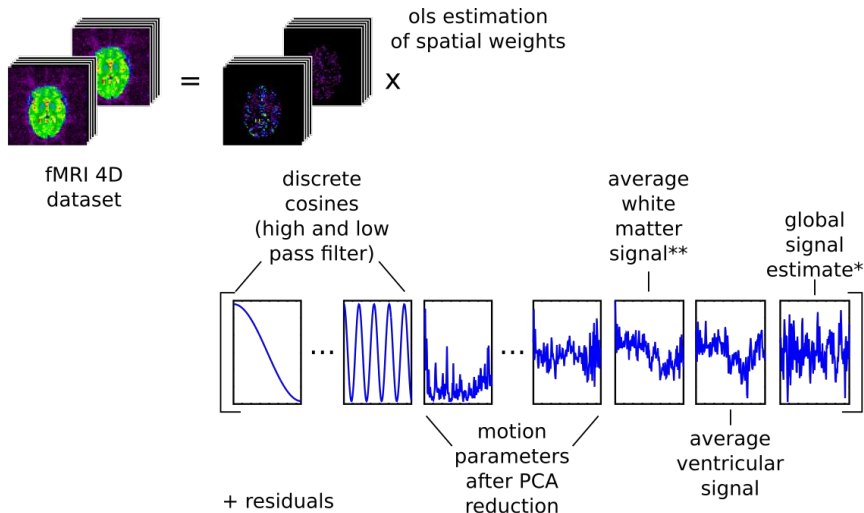
No scrubbing

Scrubbing 0.2



See Power et al. Neuroimage 2012&2014 for more info.

Regress confounds: model

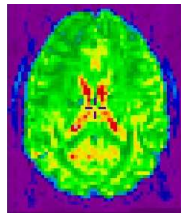
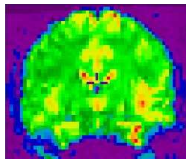
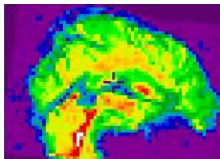


* the global signal estimate is based on a PCA decomposition (Carbonell et al., Brain connectivity 2012).

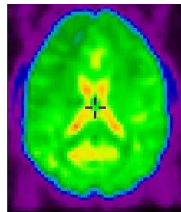
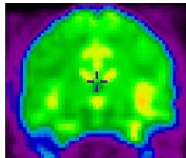
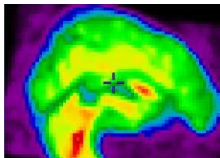
** can be replaced by a PCA reduction, aka anat COMPCOR (Chai et al., NeuroImage 2012).

Spatial smoothing

native resolution



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



Interactive report

Reports can be consulted offline or online. Live demo at https://simexp.github.io/qc_cobre/.



Guidelines for quality control of brain registration

Simplified guidelines for quality control as well as a collection of images to rate are available on zooniverse <https://www.zooniverse.org/projects/simexp/brain-match/classify>:

<https://www.zooniverse.org/projects/simexp/brain-match/classify>



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