Preprocessing of fMRI data

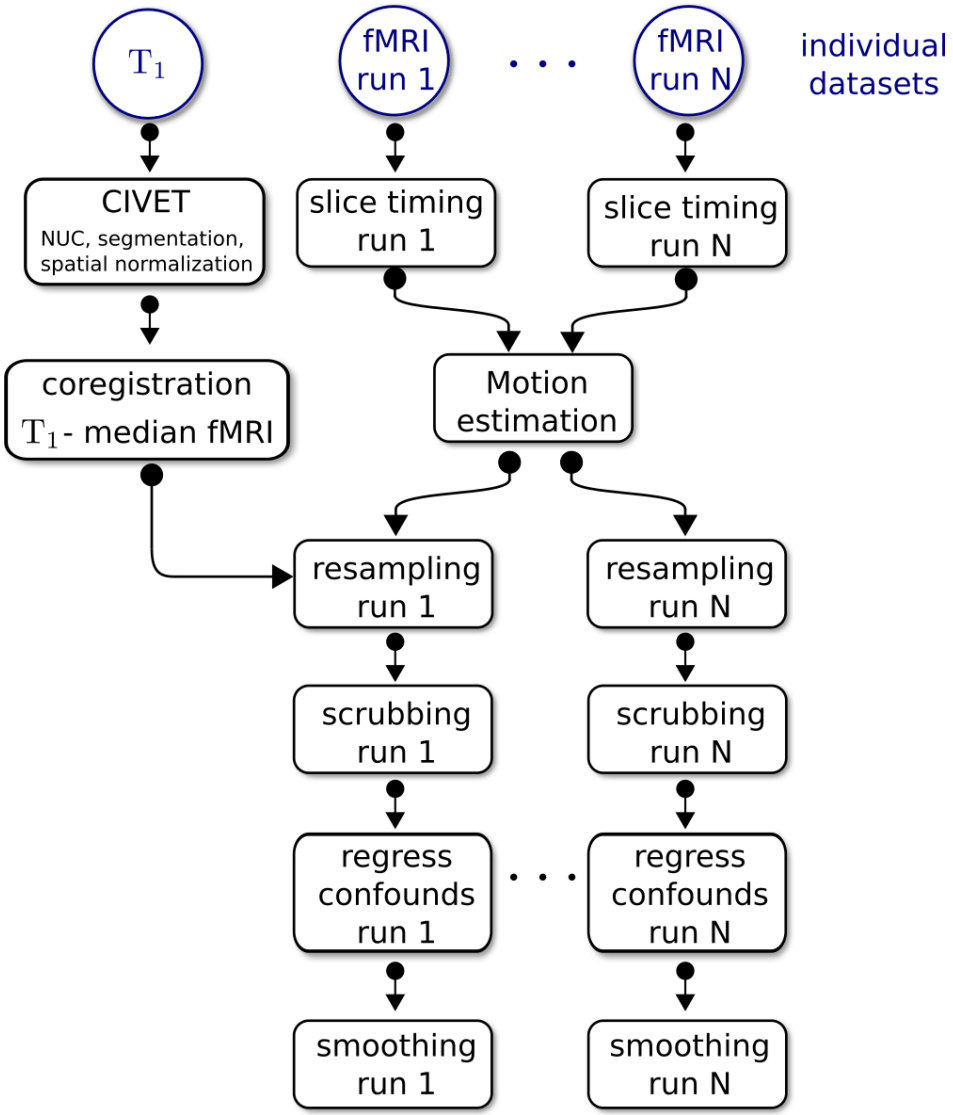
Pierre Bellec


pierre.bellec@criugm.qc.ca

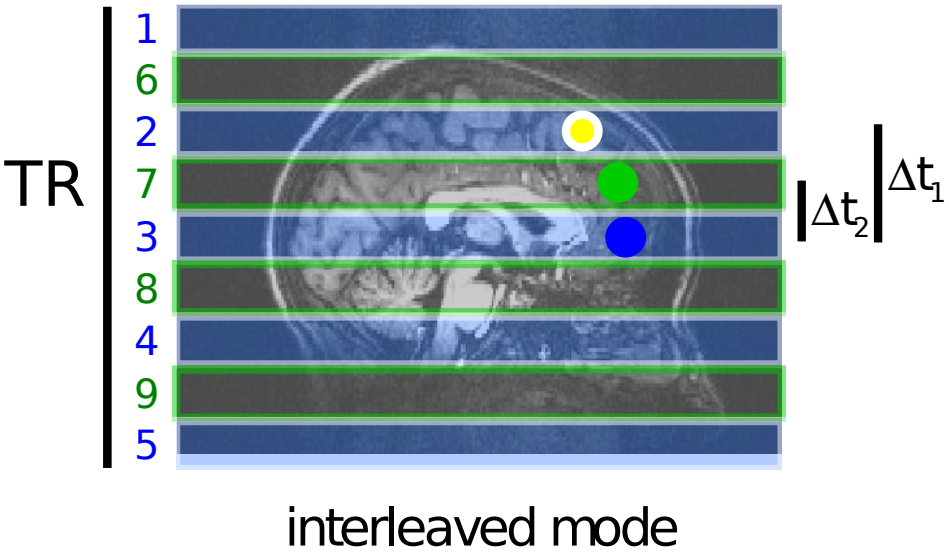

pierre_bellec 
pierre.bellec

CRIUGM, DIRO, UdM

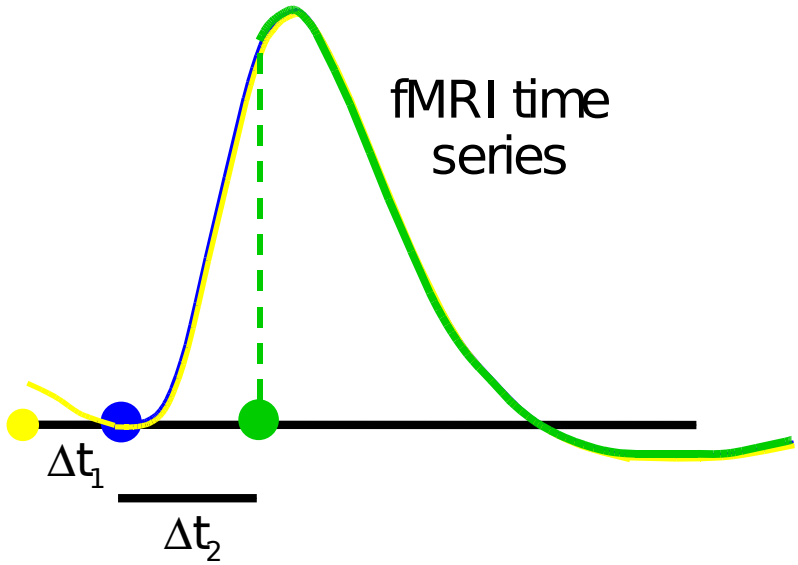
Flowchart of the NIAK fMRI preprocessing pipeline



Slice timing correction



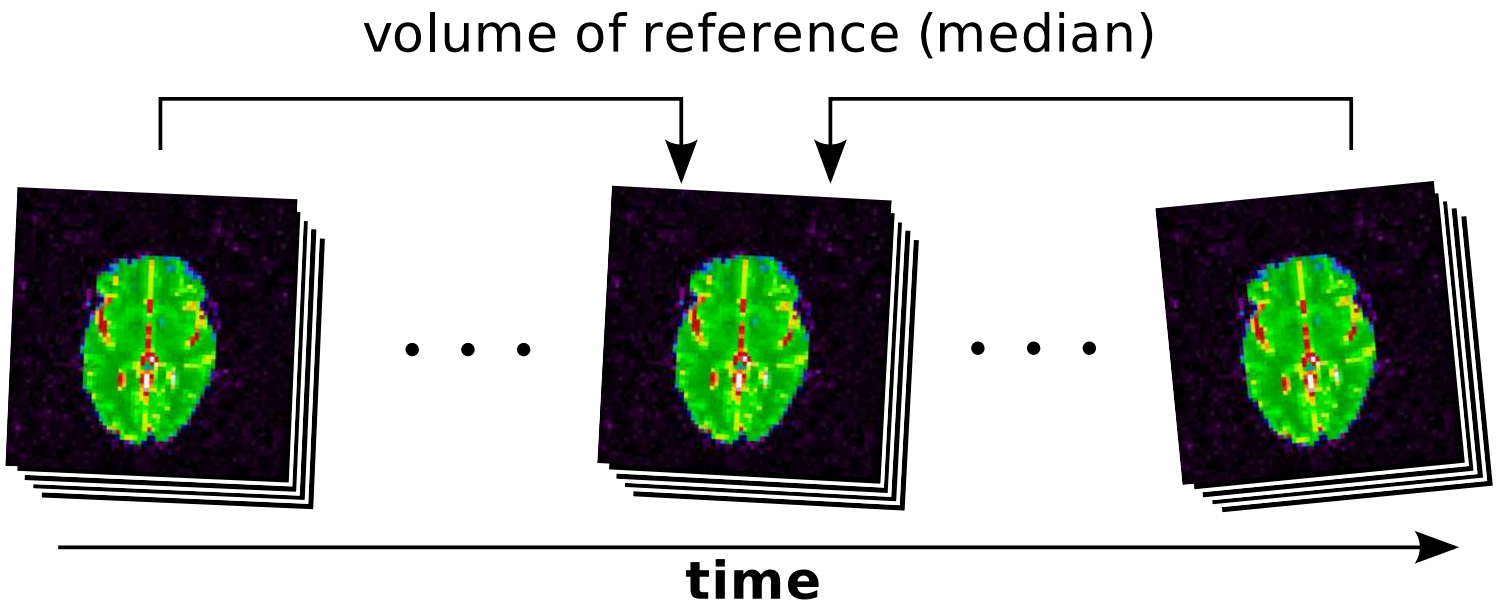
interleaved mode

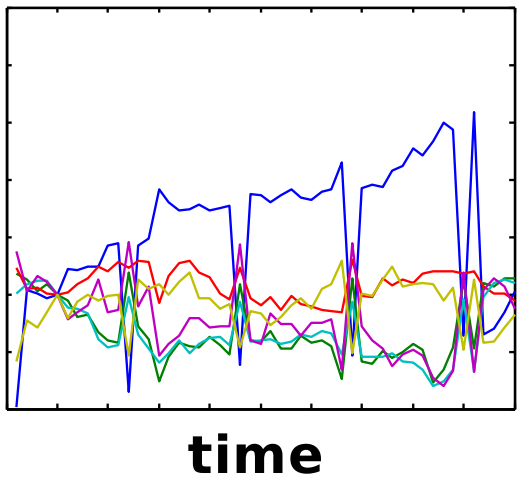


→ temporal interpolation to a single reference time for each volume (cubic spline interpolation)

Courtesy of Dr M. Pélégrini-Issac.

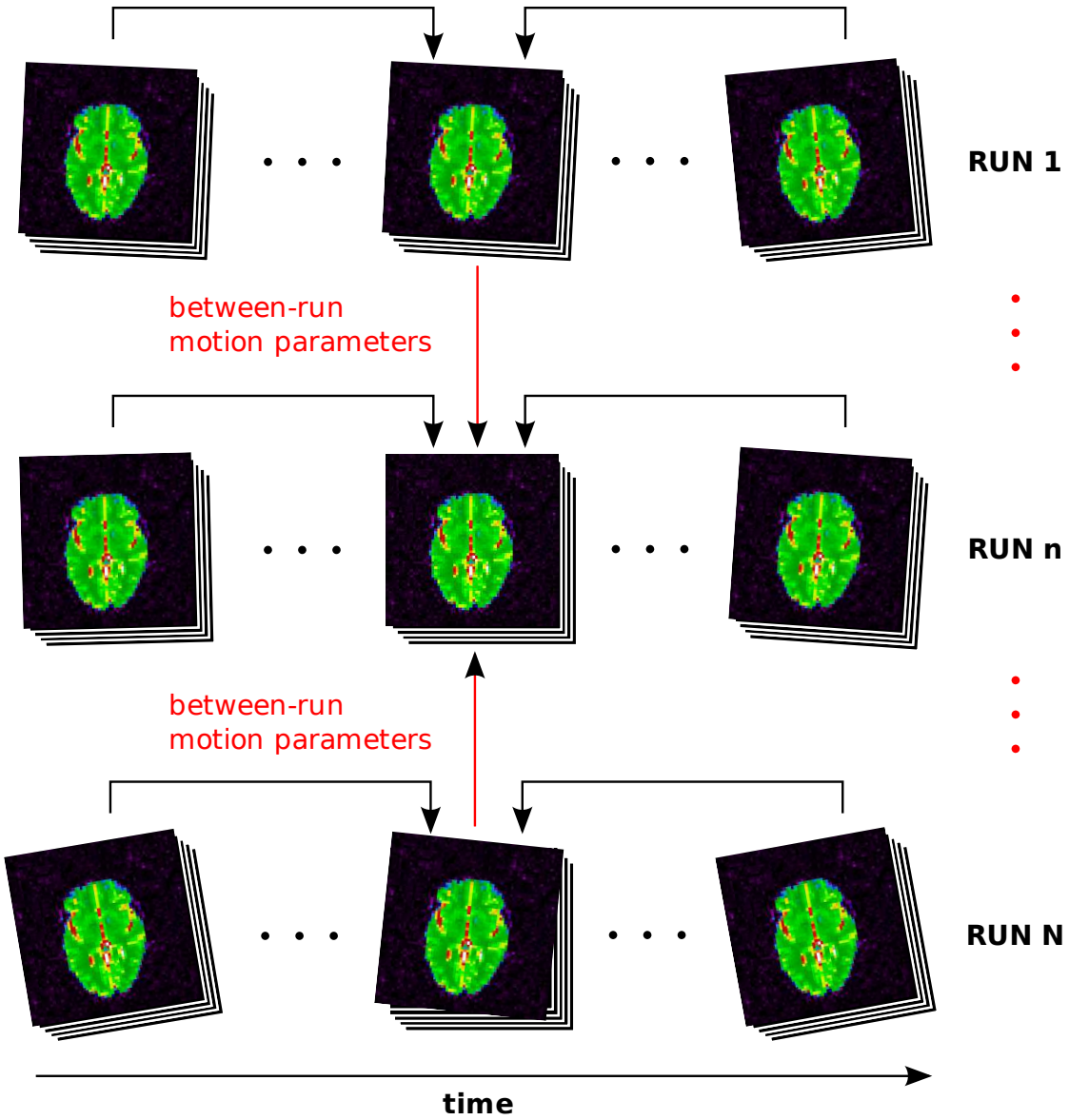
Motion estimation: within-run



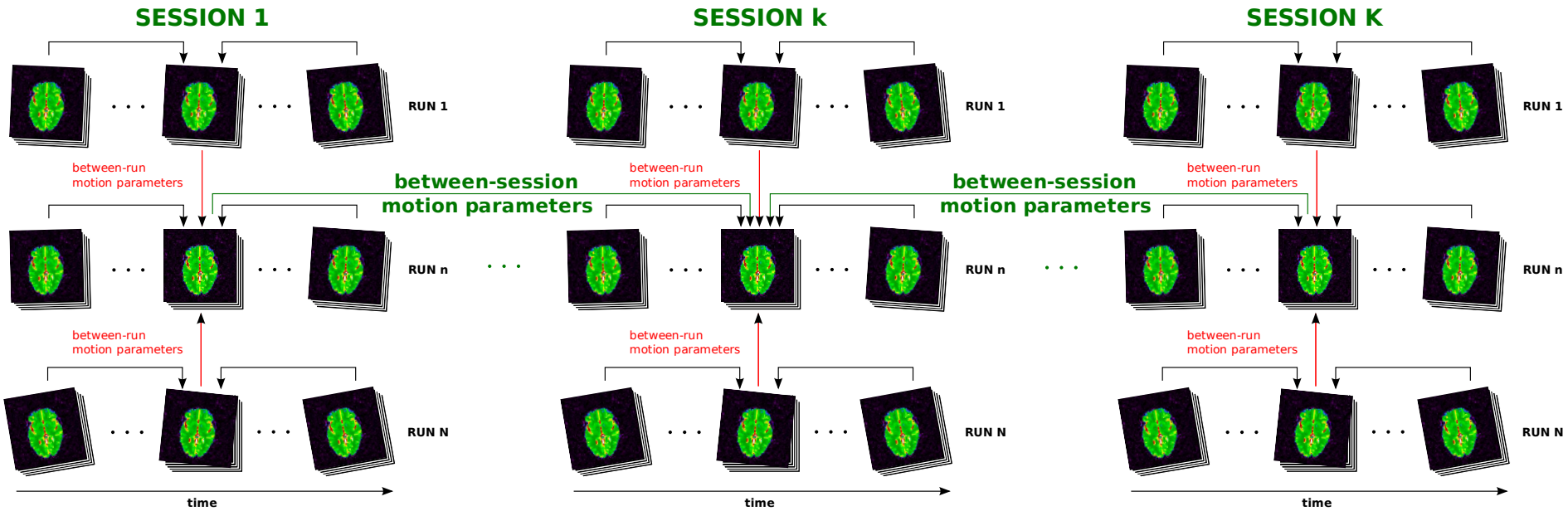


within-run motion parameters :
3 rotations
3 translations
for each volume

Motion estimation: between-run / within-session

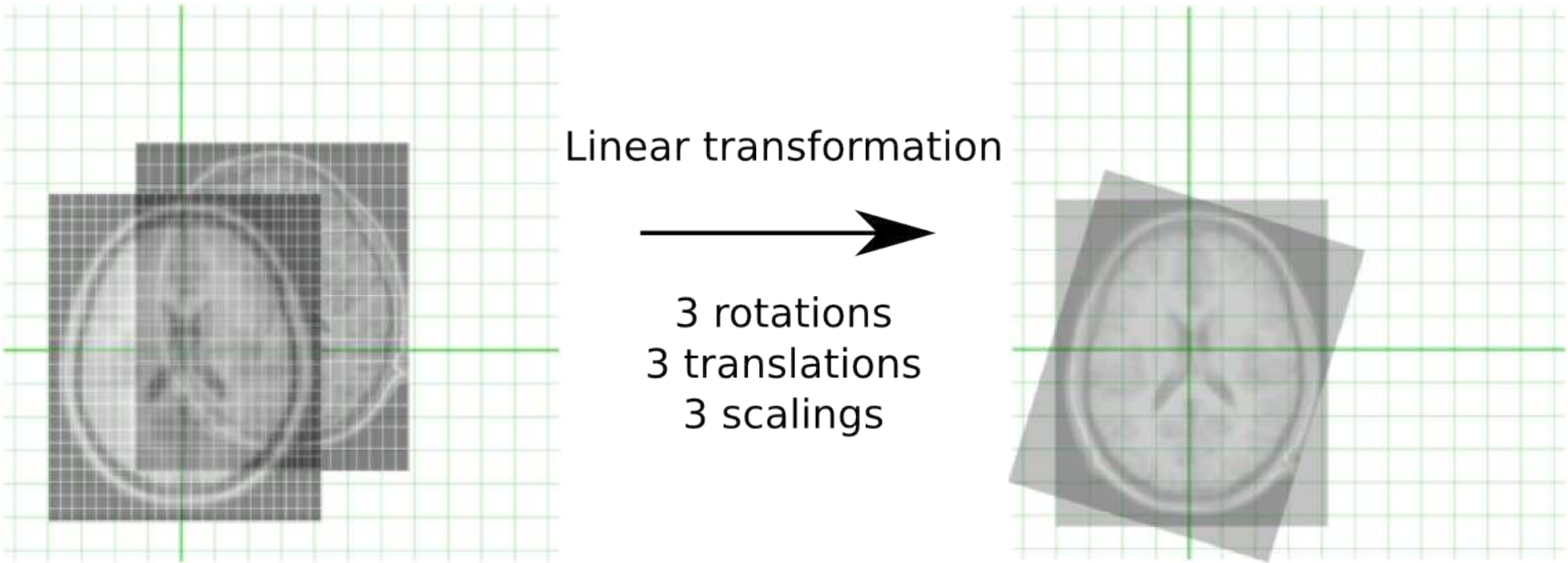


Motion estimation: between sessions

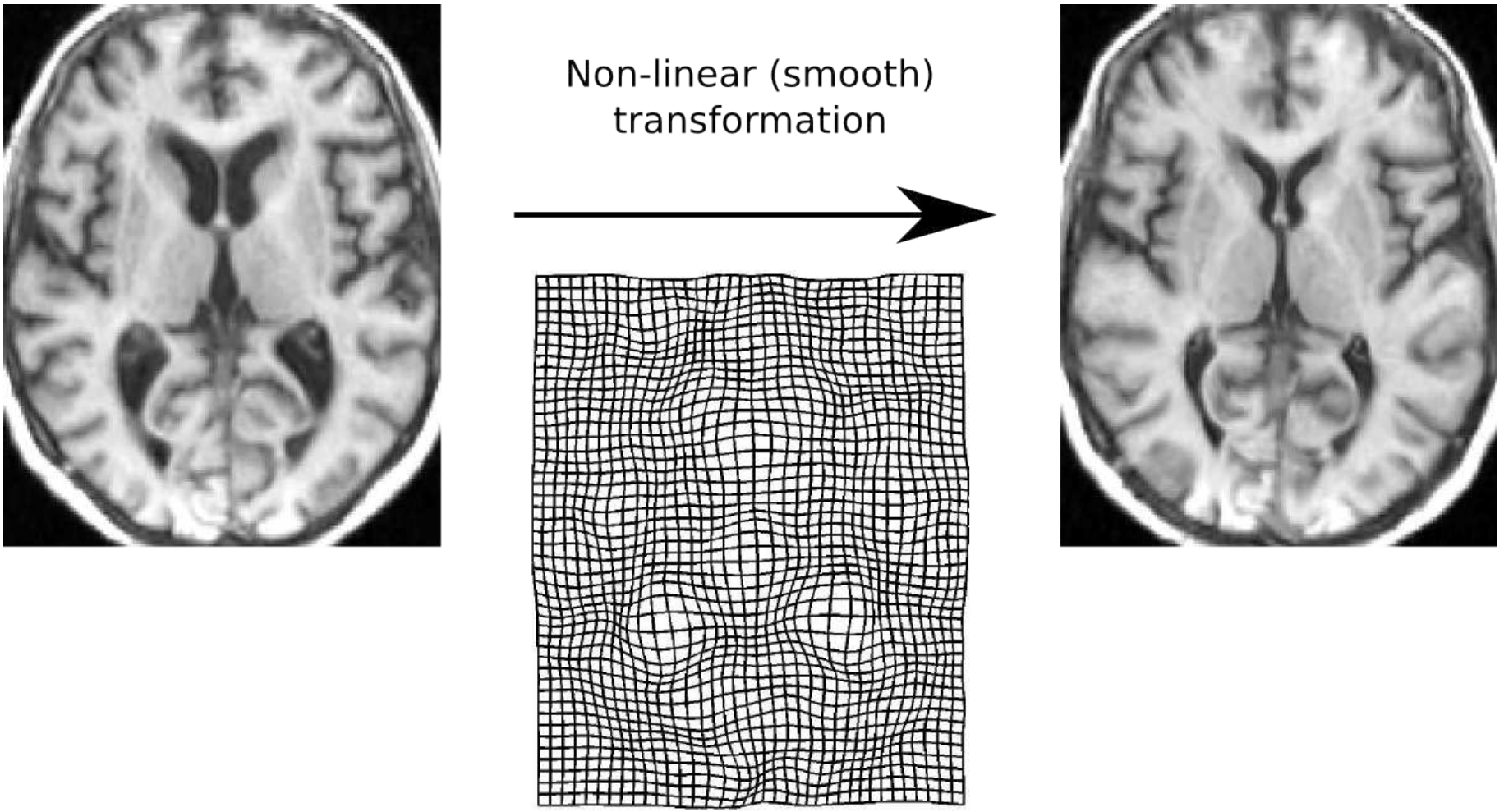


Estimation of between-run (between-session) rigid-body motion.

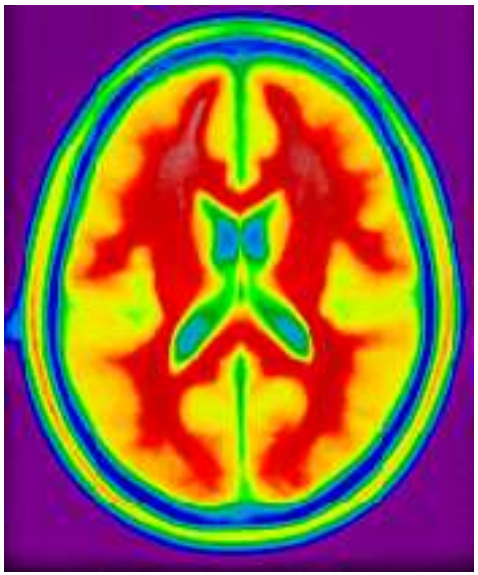
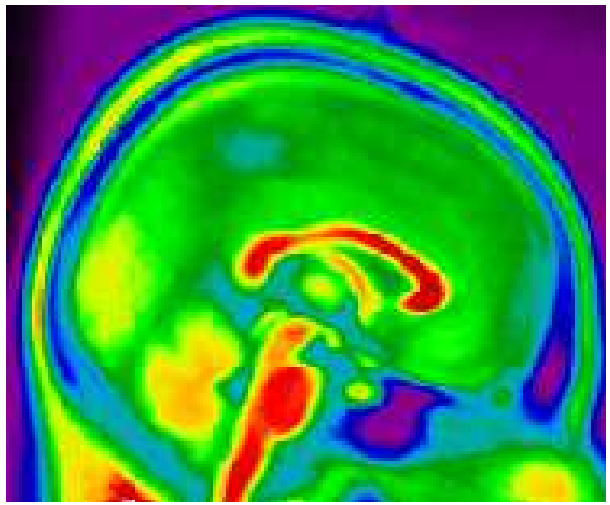
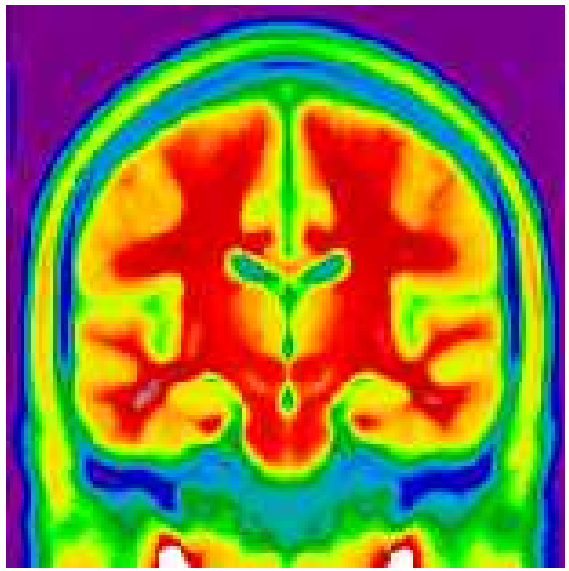
T_1 processing: linear coregistration



T_1 processing: non-linear coregistration

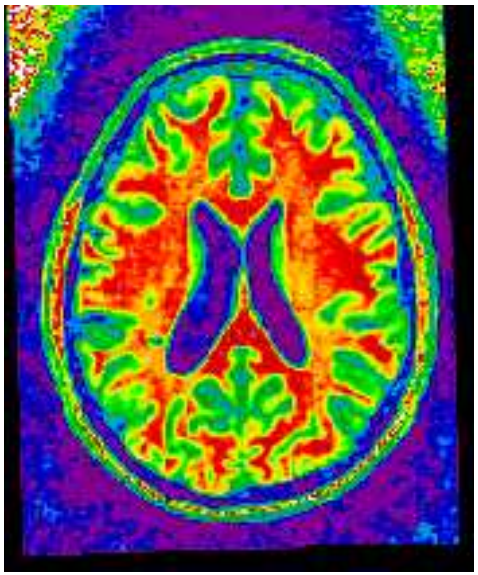
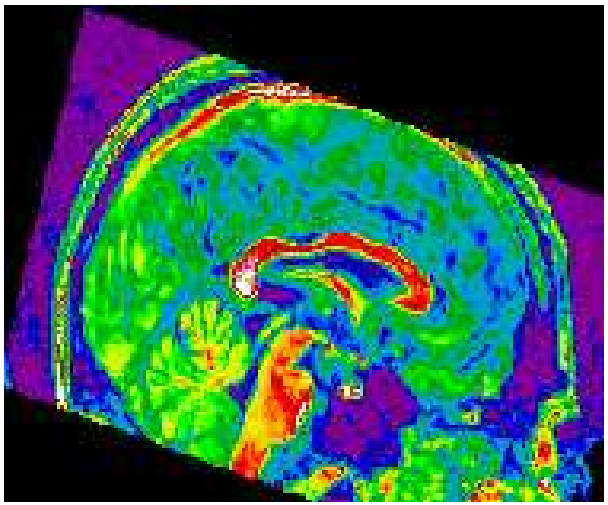
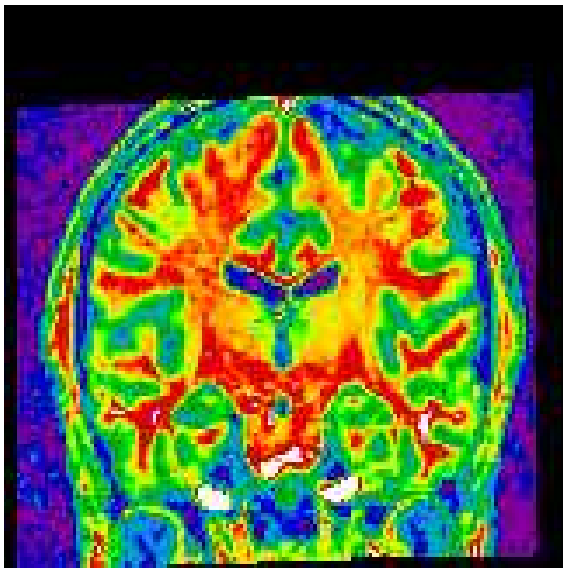


T_1 processing: linear template

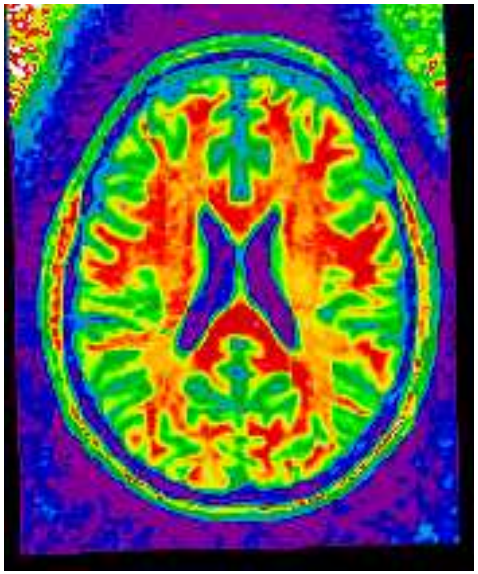
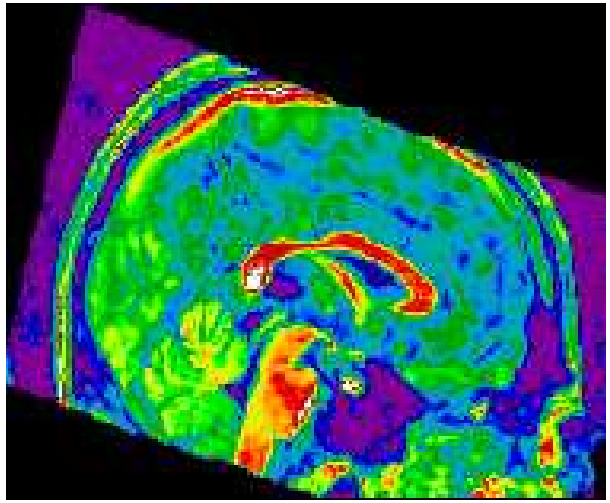
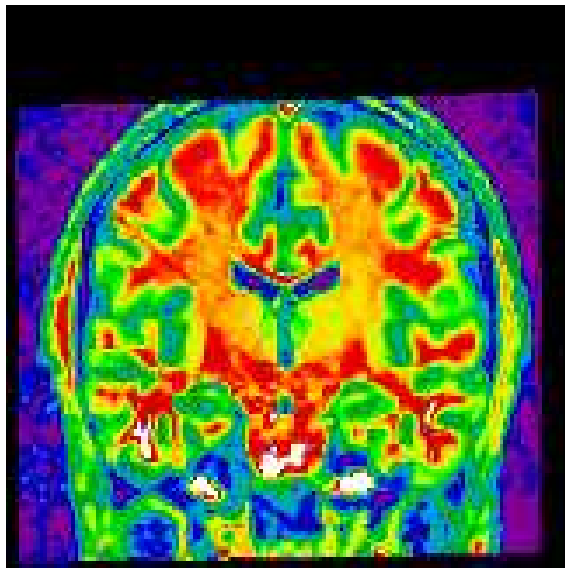
Linear ICBM template (average of 152 subjects)

T_1 processing: linear coregistration

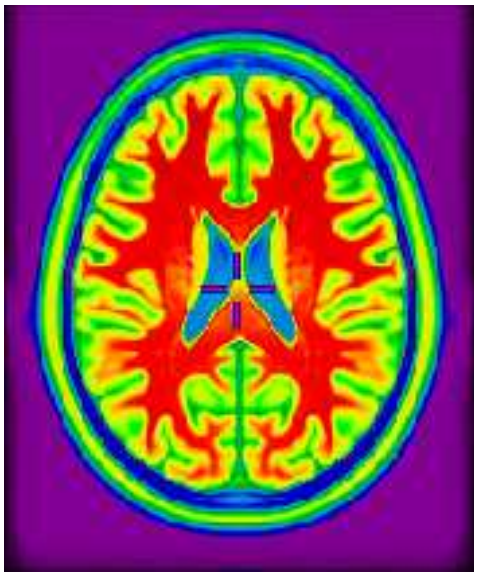
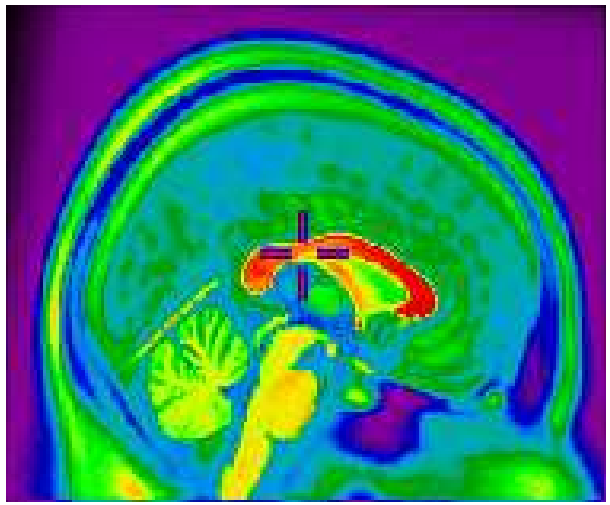
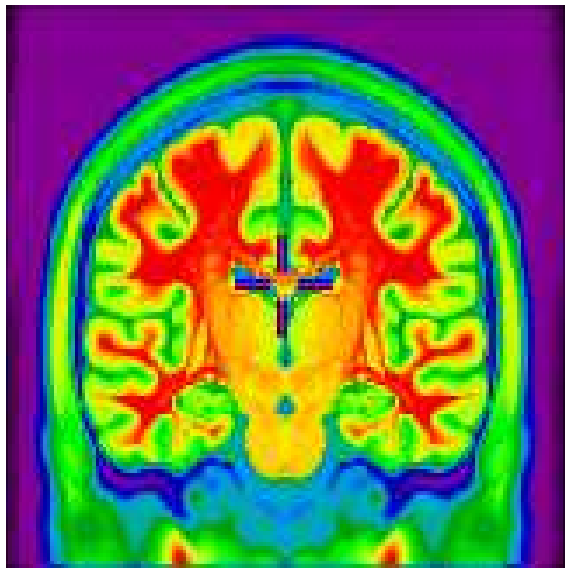
Individual structural scan (linear coregistration)

T_1 processing: non-linear coregistration

Individual structural scan (non-linear coregistration)

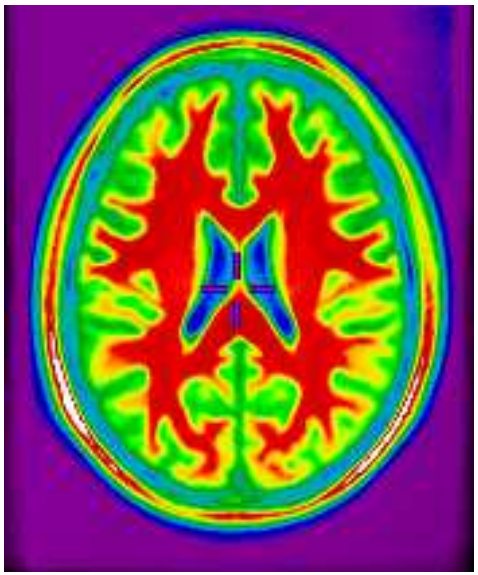
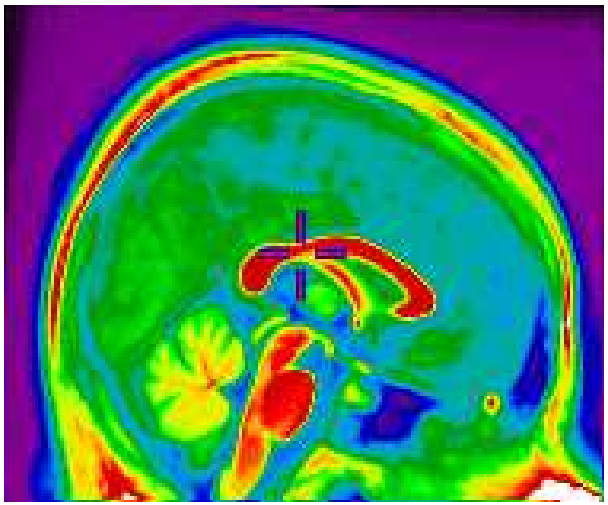
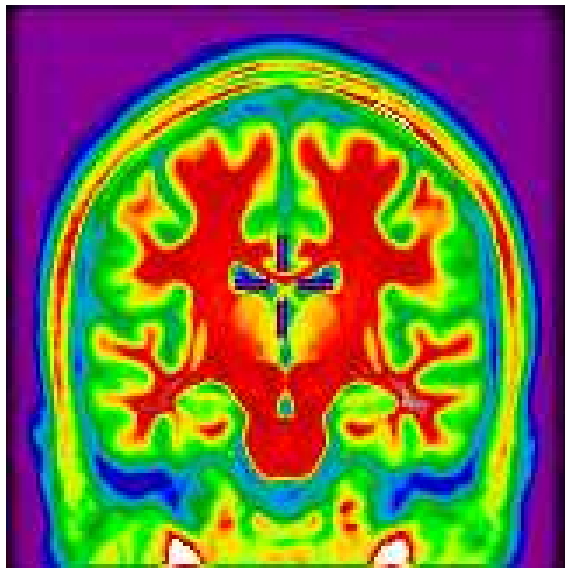
T_1 processing: nonlinear template

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

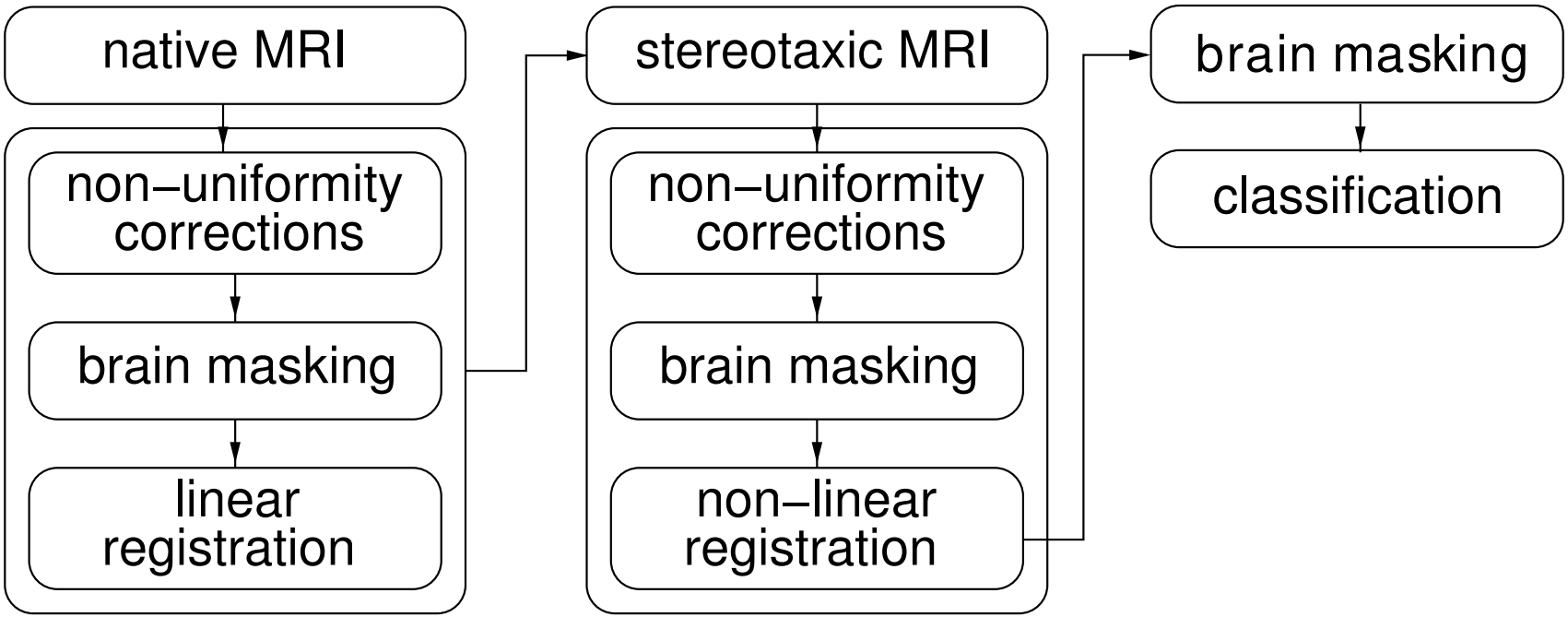
`http://www.bic.mni.mcgill.ca/ServicesAtlases/ICBM152NLin2009`

T_1 processing: group average

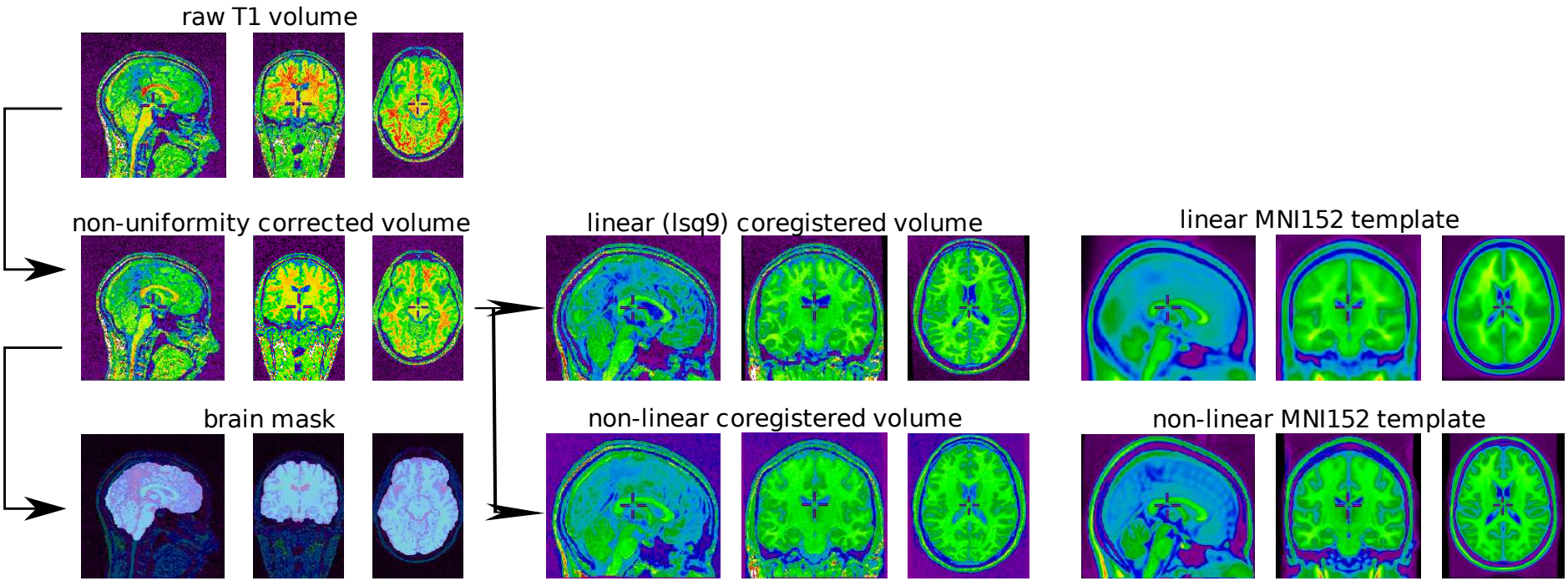
Average of 17 subjects (non-linear coregistration)

T_1 processing: Flowchart of the CIVET pipeline



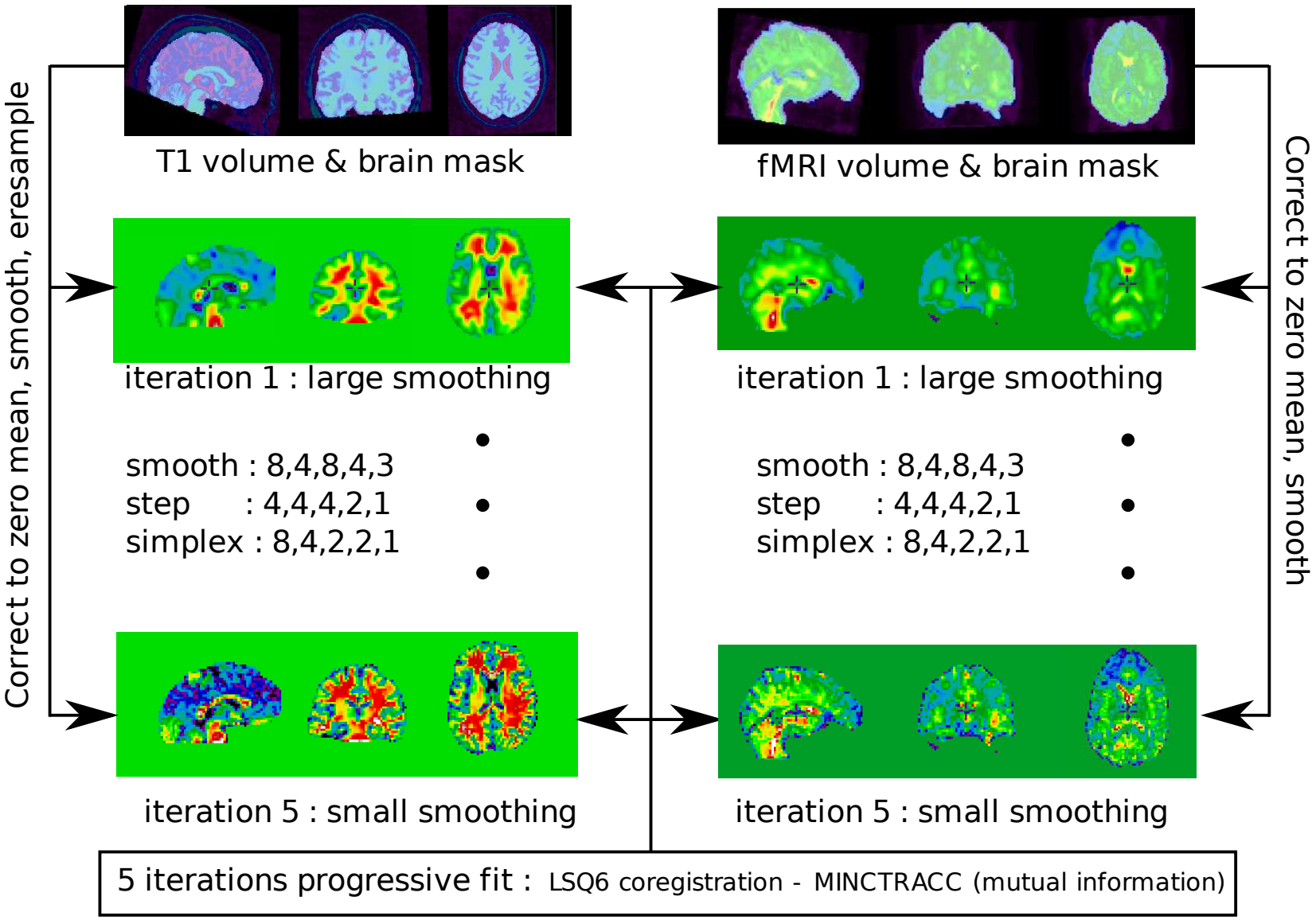
Flowchart of the T1 preprocessing.

T_1 processing: main outputs



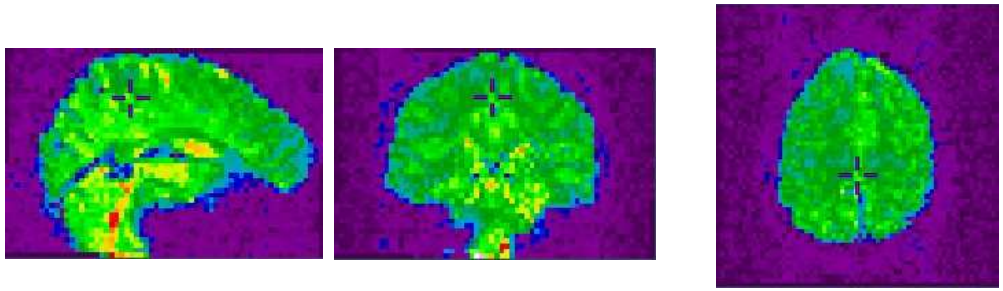
The main outputs of the T_1 processing pipeline.

Coregistration between the T_1 and fMRI volumes

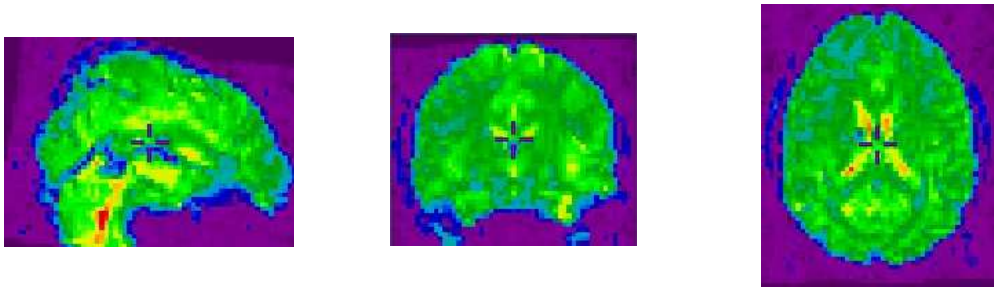


Spatial resampling

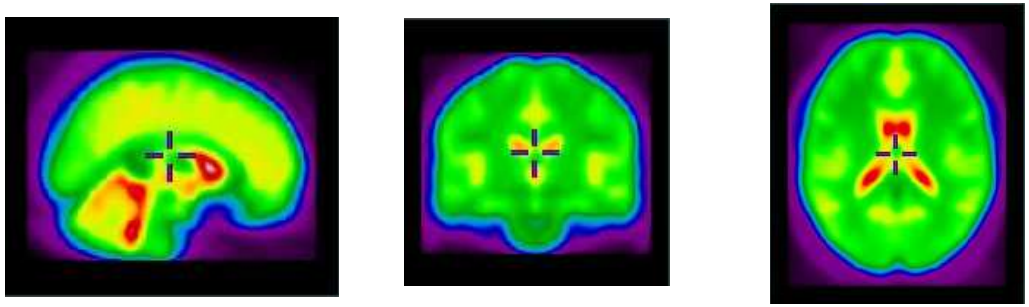
native functional space



stereotaxic space - individual volume - non-linear transform -

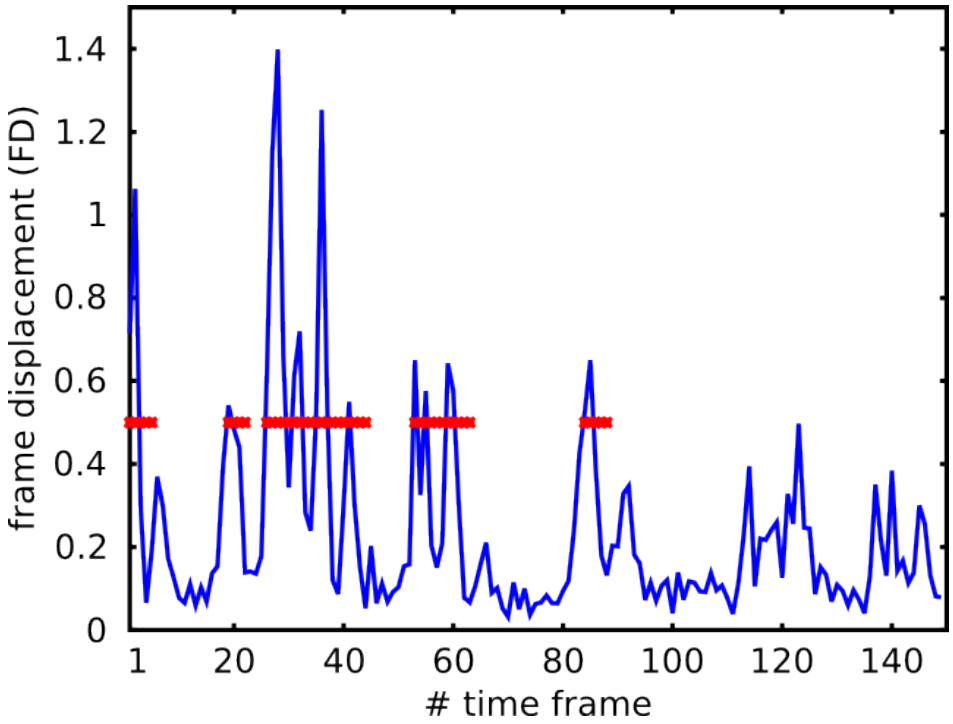


stereotaxic space - average of 40 subjects



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



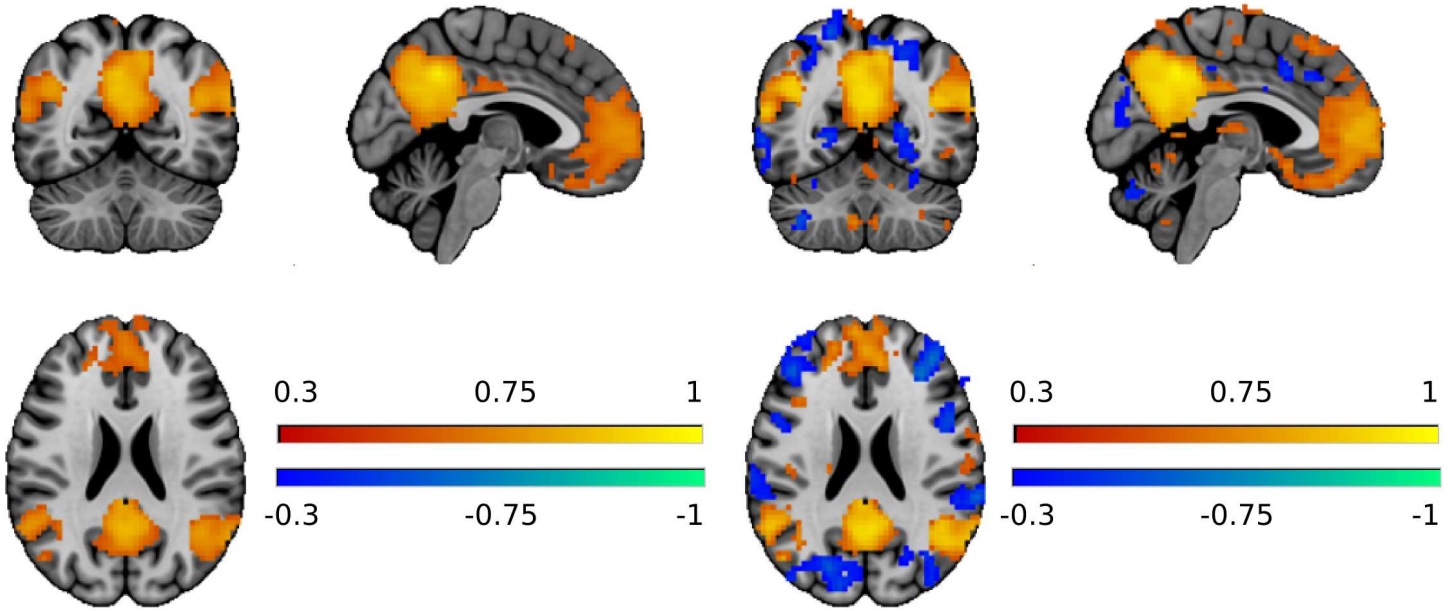
Frame displacement is the sum of absolute displacements in translation and rotation motion parameters. For each frame with excessive FD (here FD$>$ 0.5), four frames are suppressed (the target one + one before + two after, marked with red stars on the figure). The original method was proposed by Power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

Scrubbing: example of impact on the DMN

Seed based analysis in the PCC
Default mode

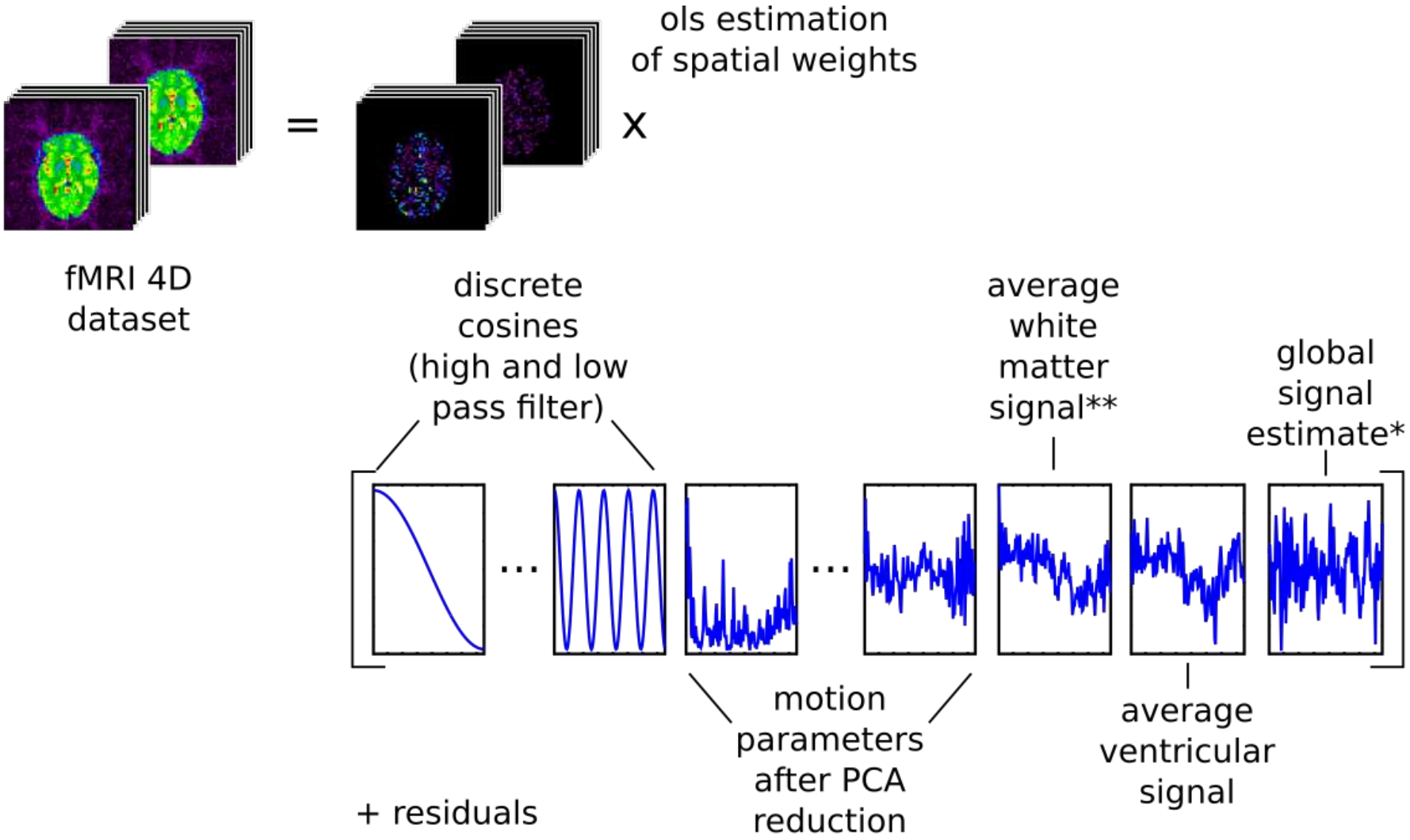
No scrubbing

Scrubbing 0.2



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

Regress confounds: model

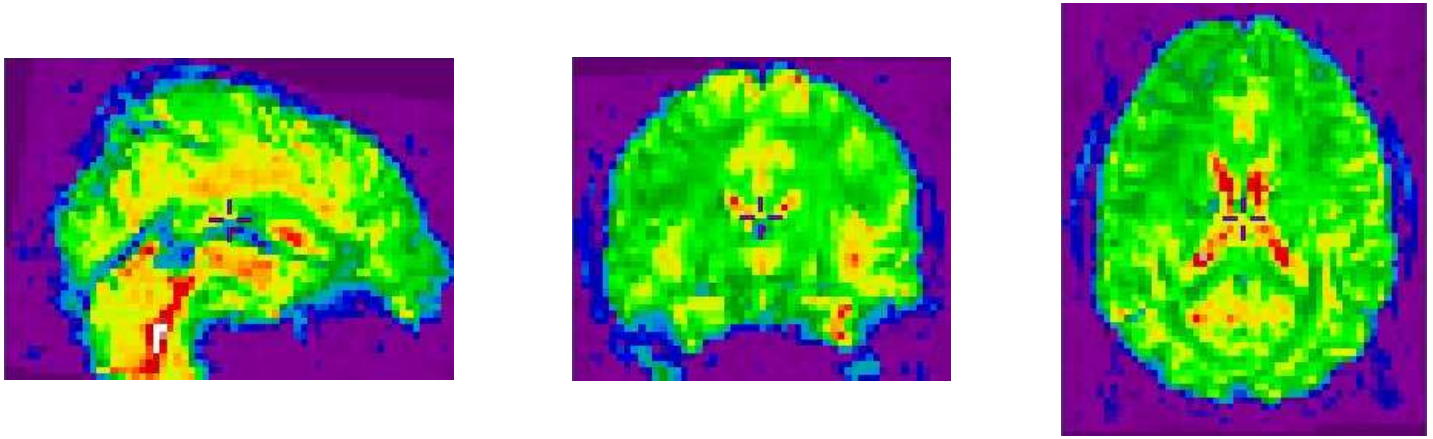


* the global signal estimate is based on a PCA decomposition (Carbonell et al., Brain connectivity 2012).

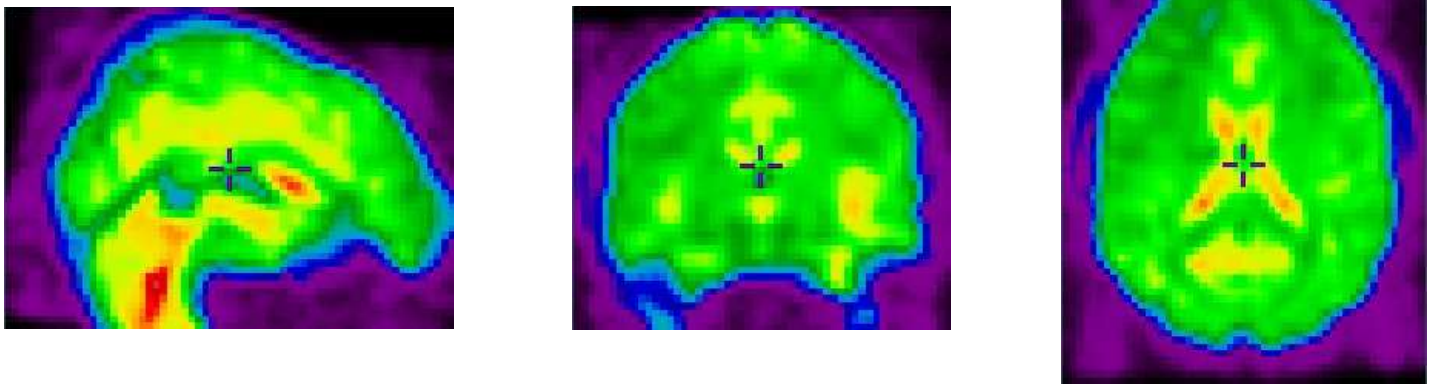
** can be replaced by a PCA reduction, aka anat COMPCOR (Chai et al., NeuroImage 2012).

Spatial smoothing

native resolution

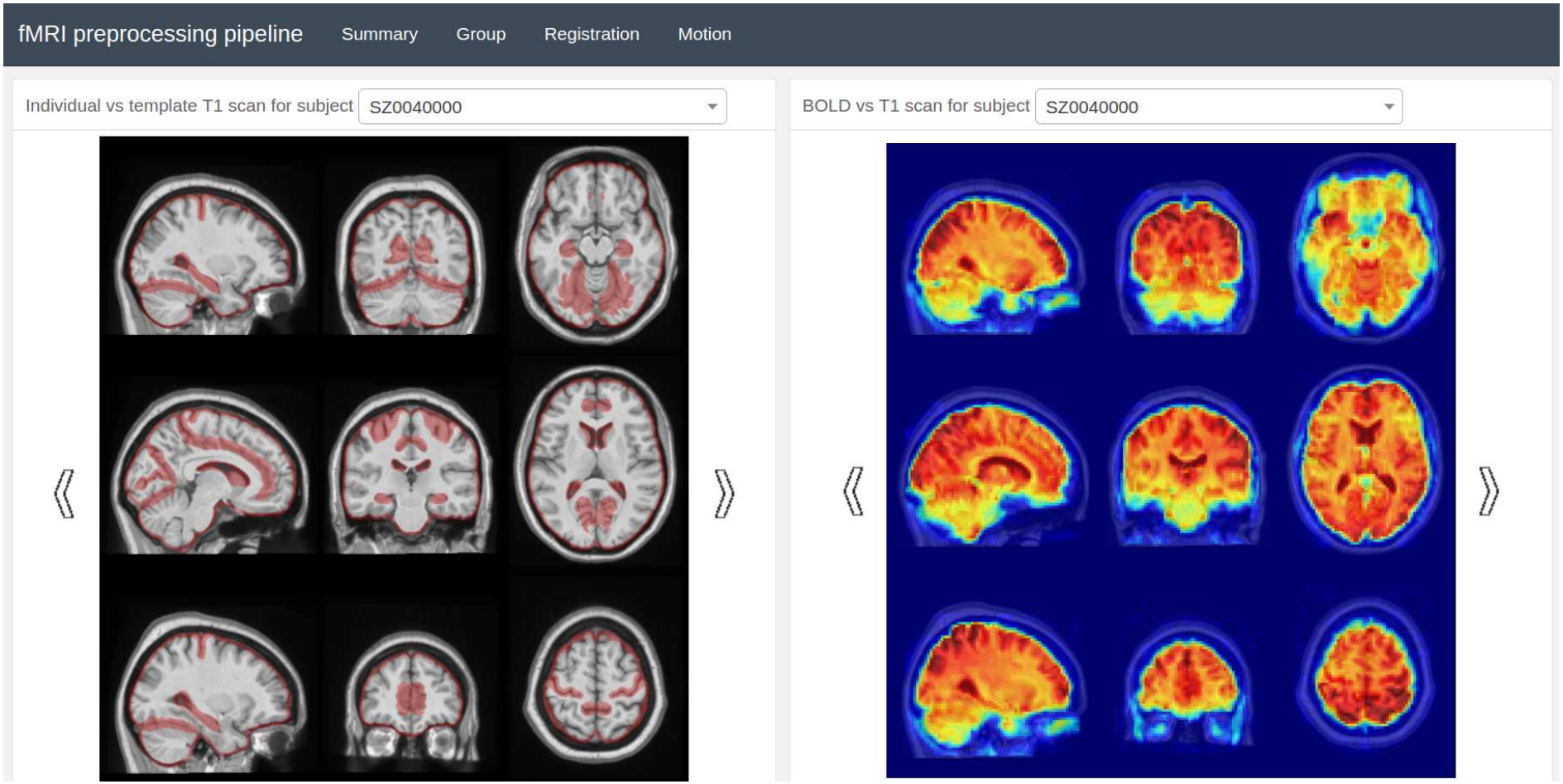


smoothed image isotropice Gaussian kernel - 6 mm FWHM



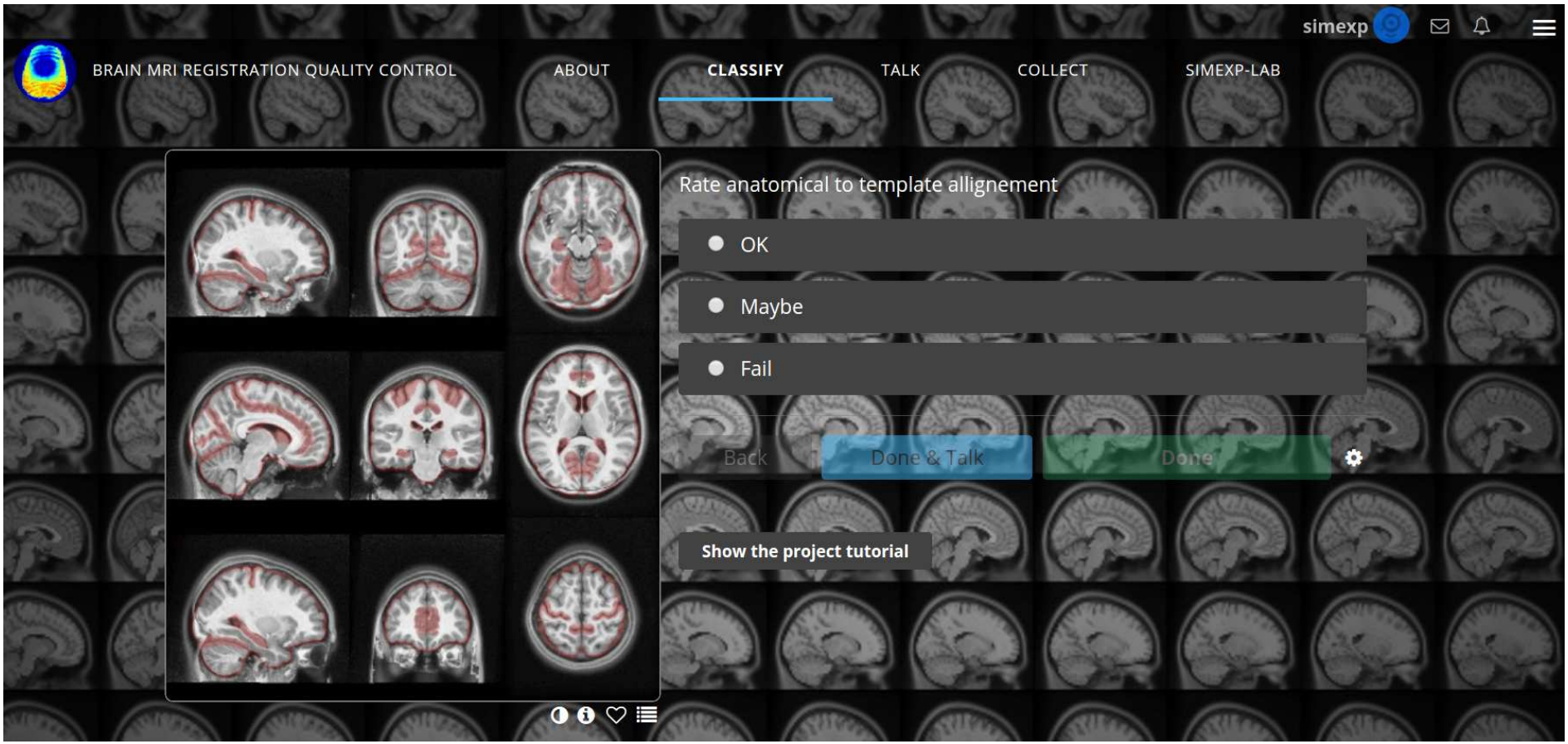
Interactive report

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



Guidelines for quality control of brain registration

Simplified guildelines 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`



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