

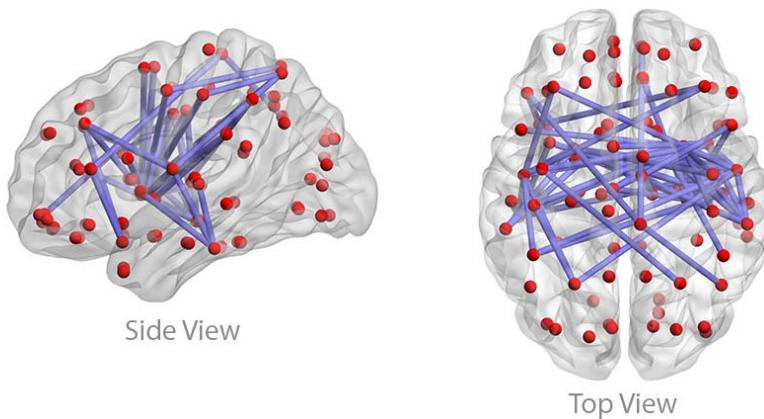
Functional MRI

Dr. Peter Van Schuerbeek

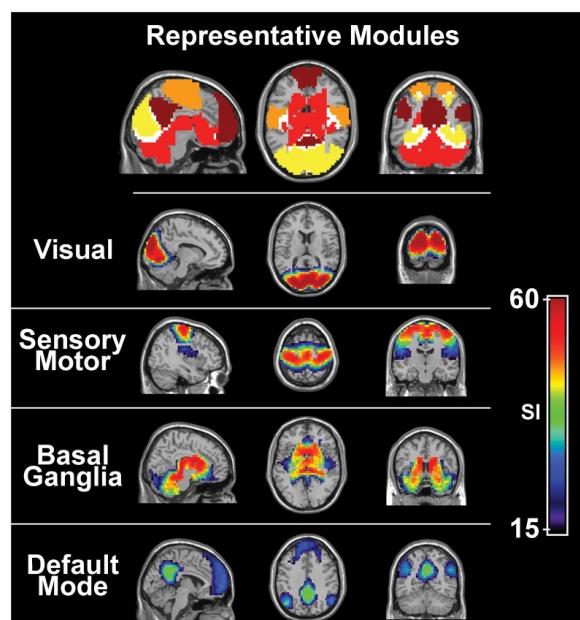
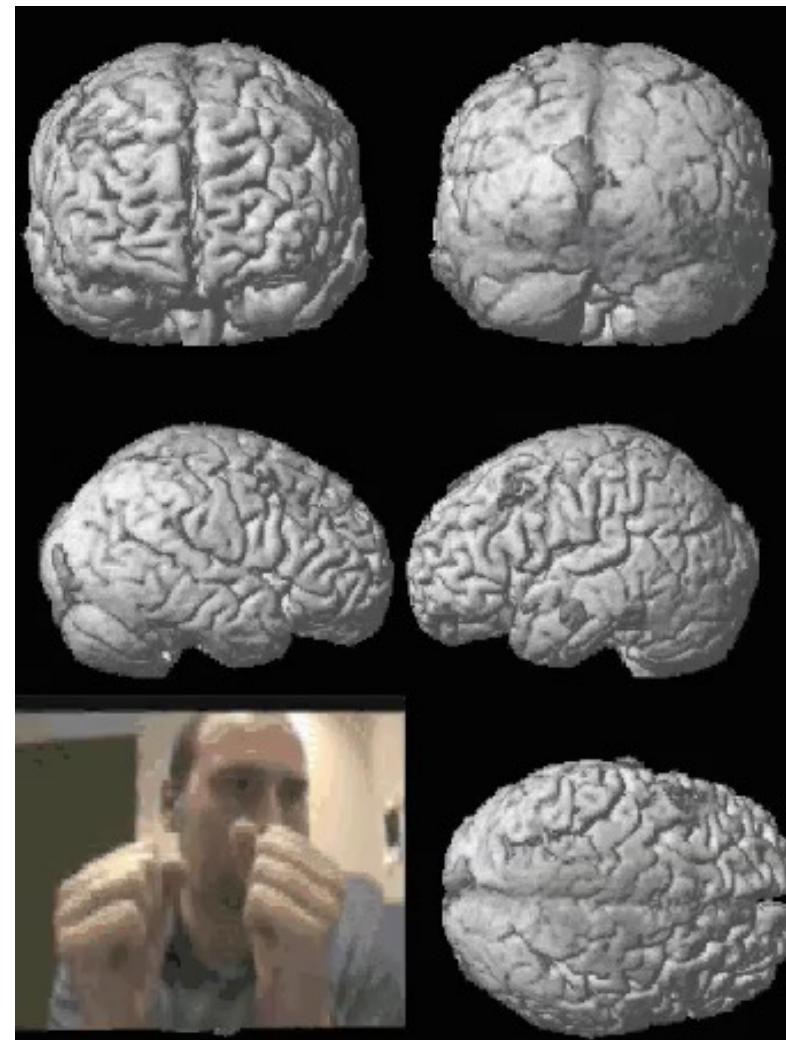
Introduction



Functional connectivity



Task based fMRI



Resting state fMRI

Short introduction to MRI

Interesting sides about the physics of MRI:

[.mri-q.com](http://mri-q.com)

[.mri-physics.net](http://mri-physics.net)

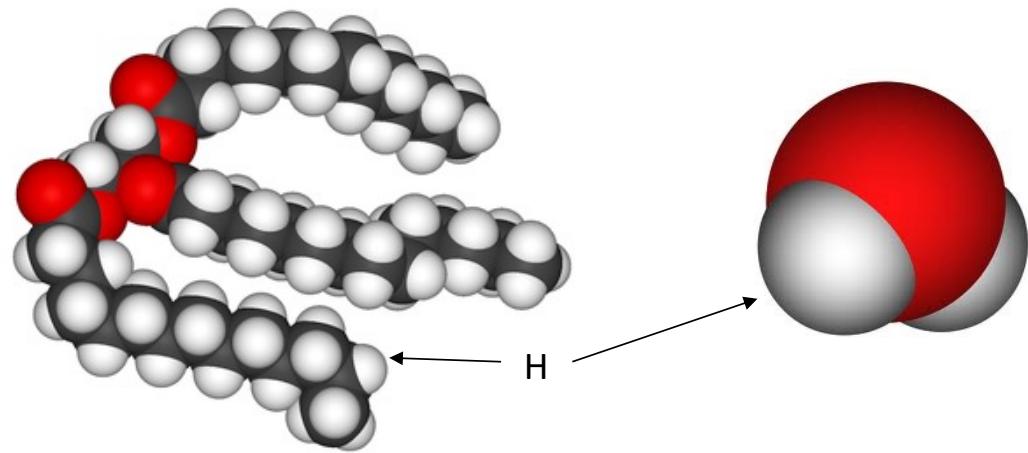
[.cis.rit.edu/htbooks/mri/](http://cis.rit.edu/htbooks/mri/)

[.www.mritutor.org](http://www.mritutor.org)

[.revisemri.com](http://revisemri.com)

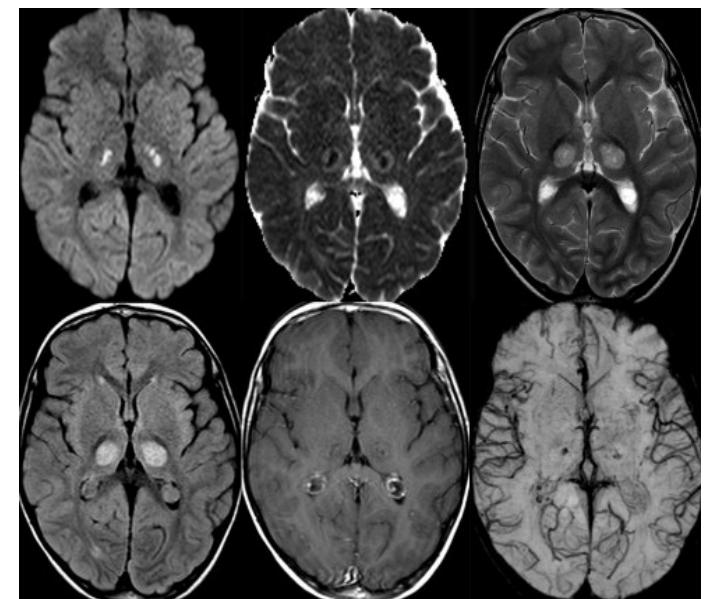
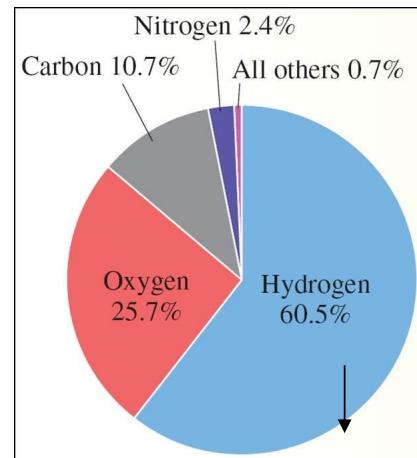
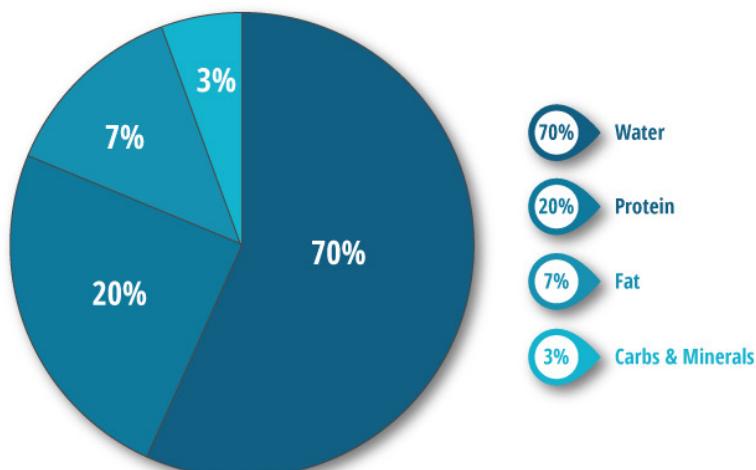
[.https://radiopaedia.org](https://radiopaedia.org)

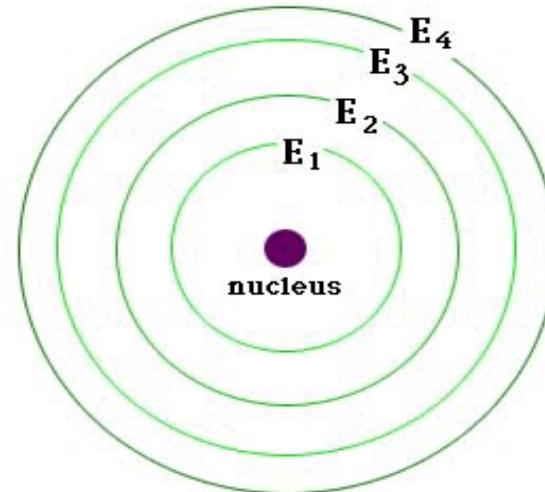
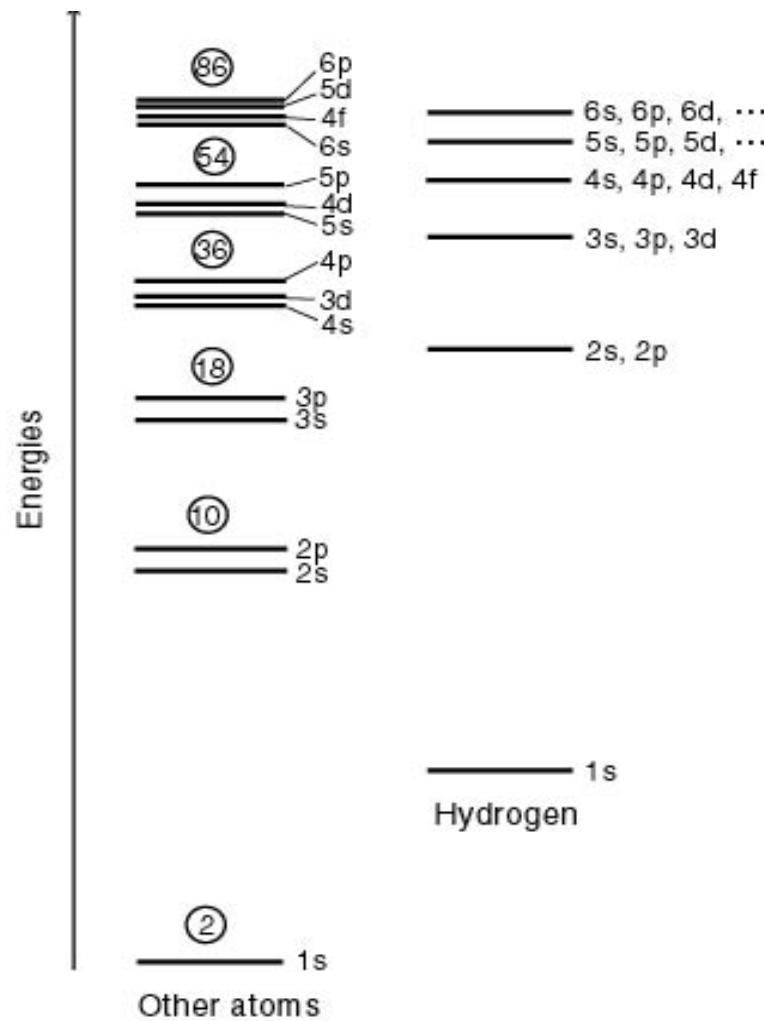
[.https://www.imaios.com/en/e-Courses/e-MRI](https://www.imaios.com/en/e-Courses/e-MRI)



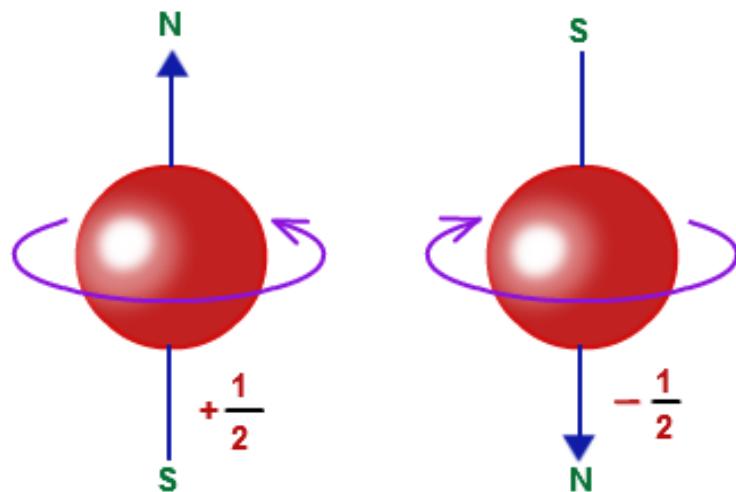
Soft tissues
Fluids
Fat
 ↓
Contains H_2O or $\text{CH}_3(\text{CH}_2)_n\ldots\text{CO}_2\text{H}$

HUMAN BODY COMPOSITION





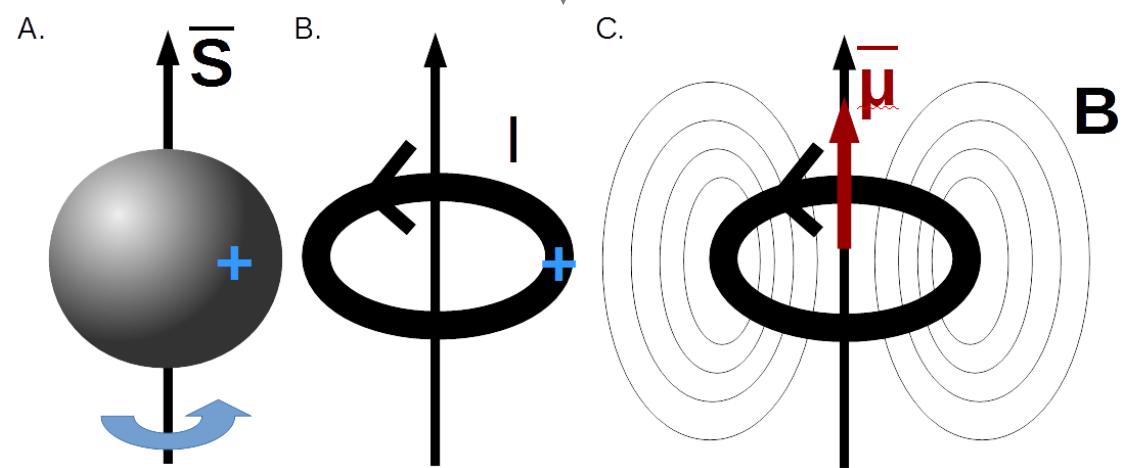
| Principal quantum number n | Azimuthal (orbital) quantum number l | Magnetic quantum number m_l | Spin quantum number m_s | Number of electrons |
|--------------------------------------|--|--|--|---------------------|
| 1 | 0 (s) | 0 | -1/2 +1/2 | 2 |
| 2 | 0 (s) | 0 | -1/2 +1/2 | 2 |
| | 1 (p) | -1 0 1 | -1/2 +1/2 | 6 |
| 3 | 0 (s) | 0 | -1/2 +1/2 | 2 |
| | 1 (p) | -1 0 1 | -1/2 +1/2 | 6 |
| | 2 (d) | -2 1 0 1 2 | -1/2 +1/2 | 10 |
| ... | ... | ... | ... | ... |



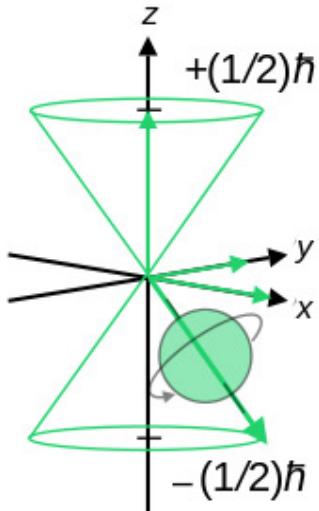
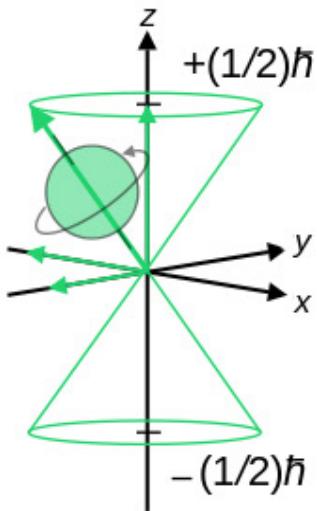
The spin angular momentum

The magnetic moment

$$\vec{\mu} = \gamma \cdot \vec{S}$$



Spin angular momentum (spin-1/2 particles)

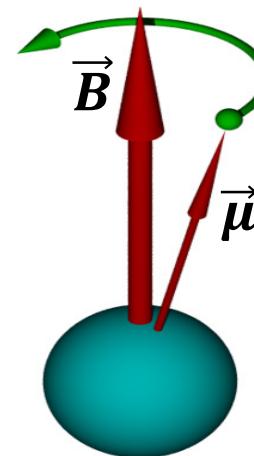


$$|\uparrow\rangle \equiv \left| +\frac{1}{2} \right\rangle$$

spin-up

$$|\downarrow\rangle \equiv \left| -\frac{1}{2} \right\rangle$$

spin-down



$$\vec{\Gamma} = \vec{\mu} \times \vec{B}$$

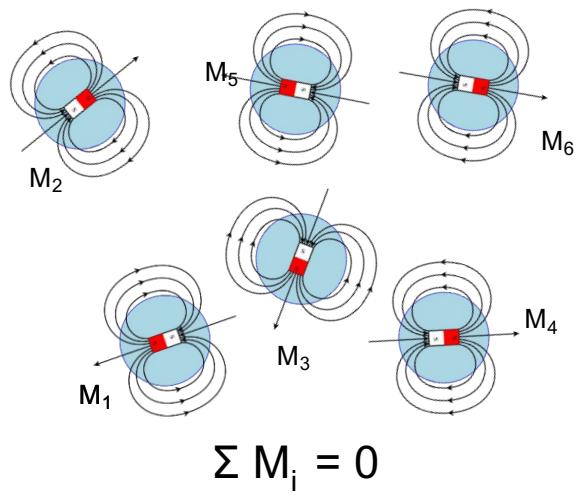
$$\tau = \frac{dS}{dt} = \mu \cdot B \cdot \sin \varphi$$

Precession of μ around B

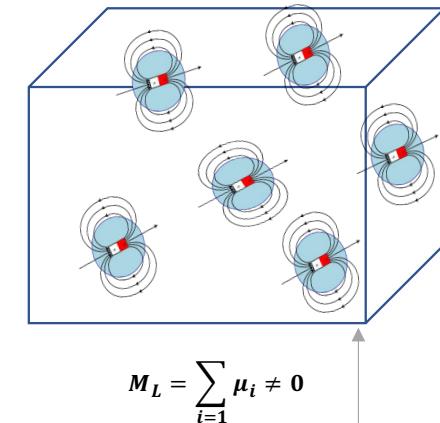
The Larmor frequency: $\omega_L = \gamma \cdot B$

Generating a MRI signal step 1: the homogeneous magnetic field B_0

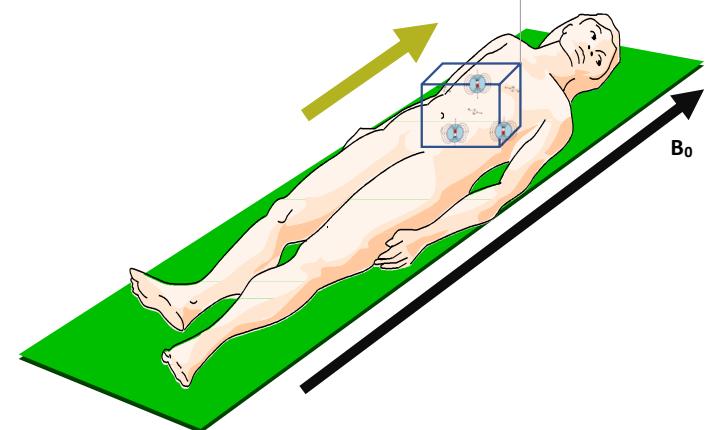
Without magnetic field:



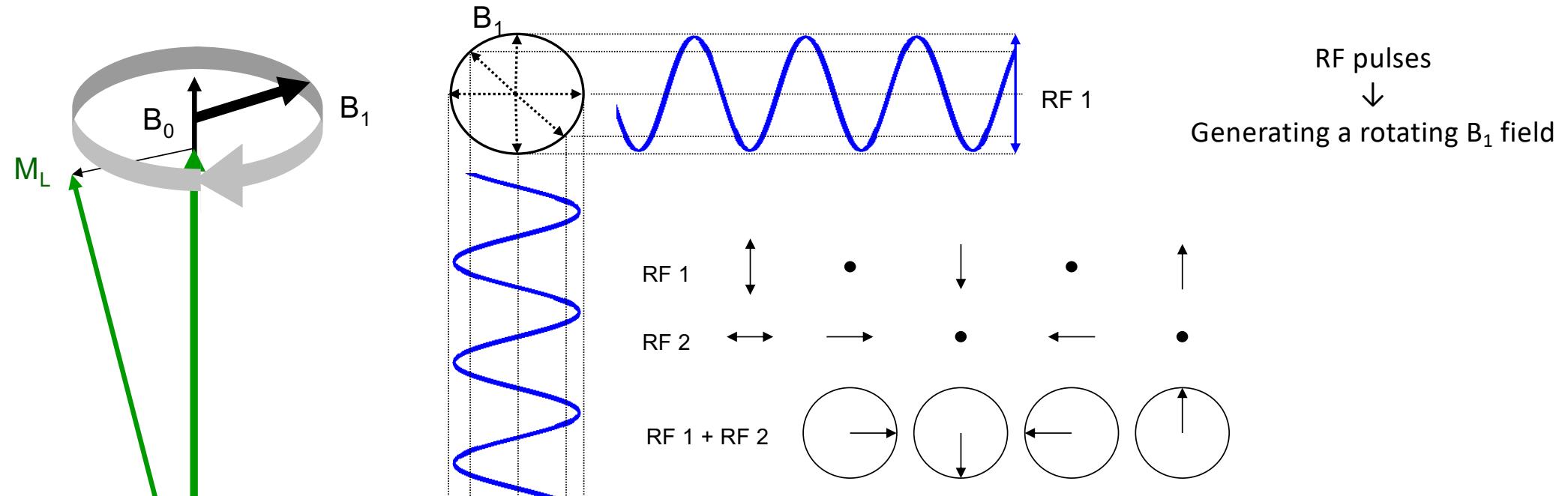
With magnetic field



**Resulting net longitudinal magnetization (M_L)
parallel to the field B_0**



Generating a MRI signal step 2: applying a RF pulse

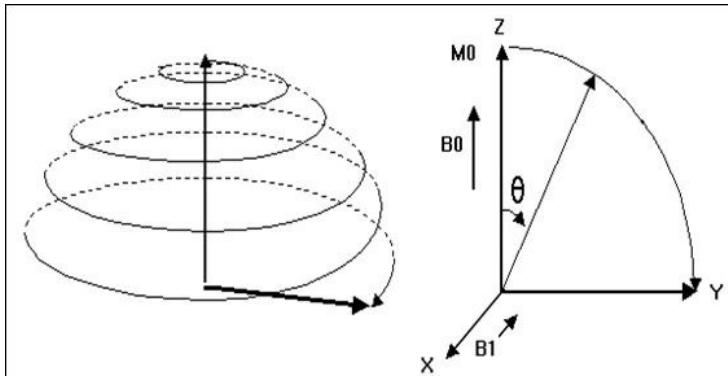


Precession of M_L at the Larmor frequency

$$\omega = \gamma \cdot B_0$$

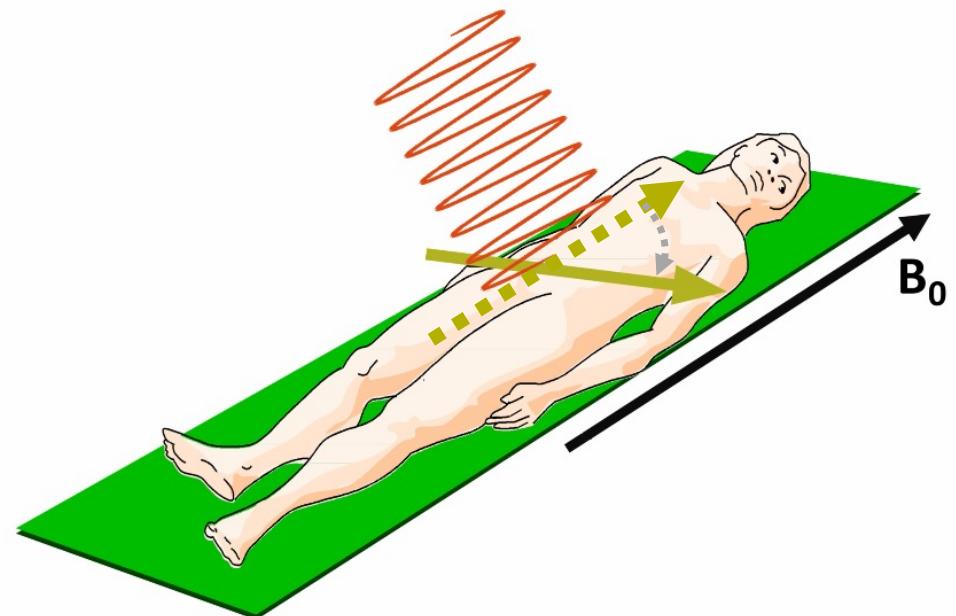
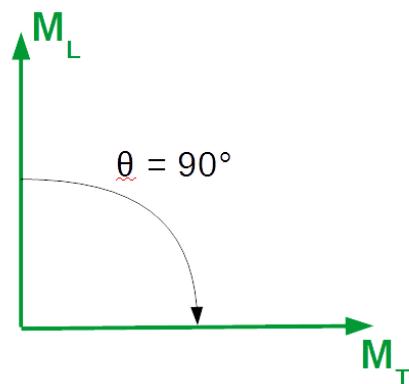
Generating a MRI signal step 2: applying a RF pulse

If $\omega_{RF} = \omega_L$ (resonance condition)

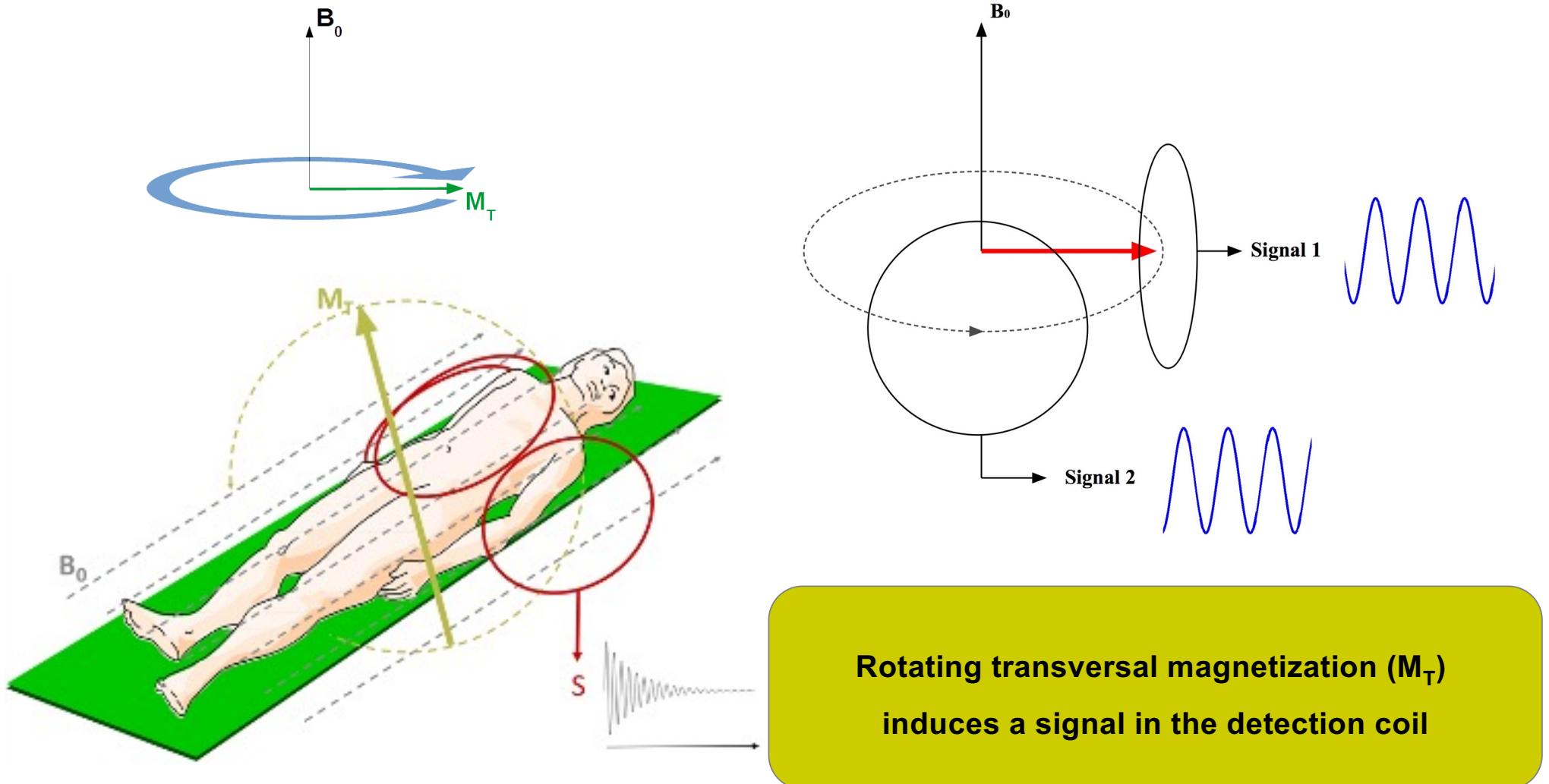


Longitudinal magnetization (M_L) flipped into transversal magnetization (M_T)

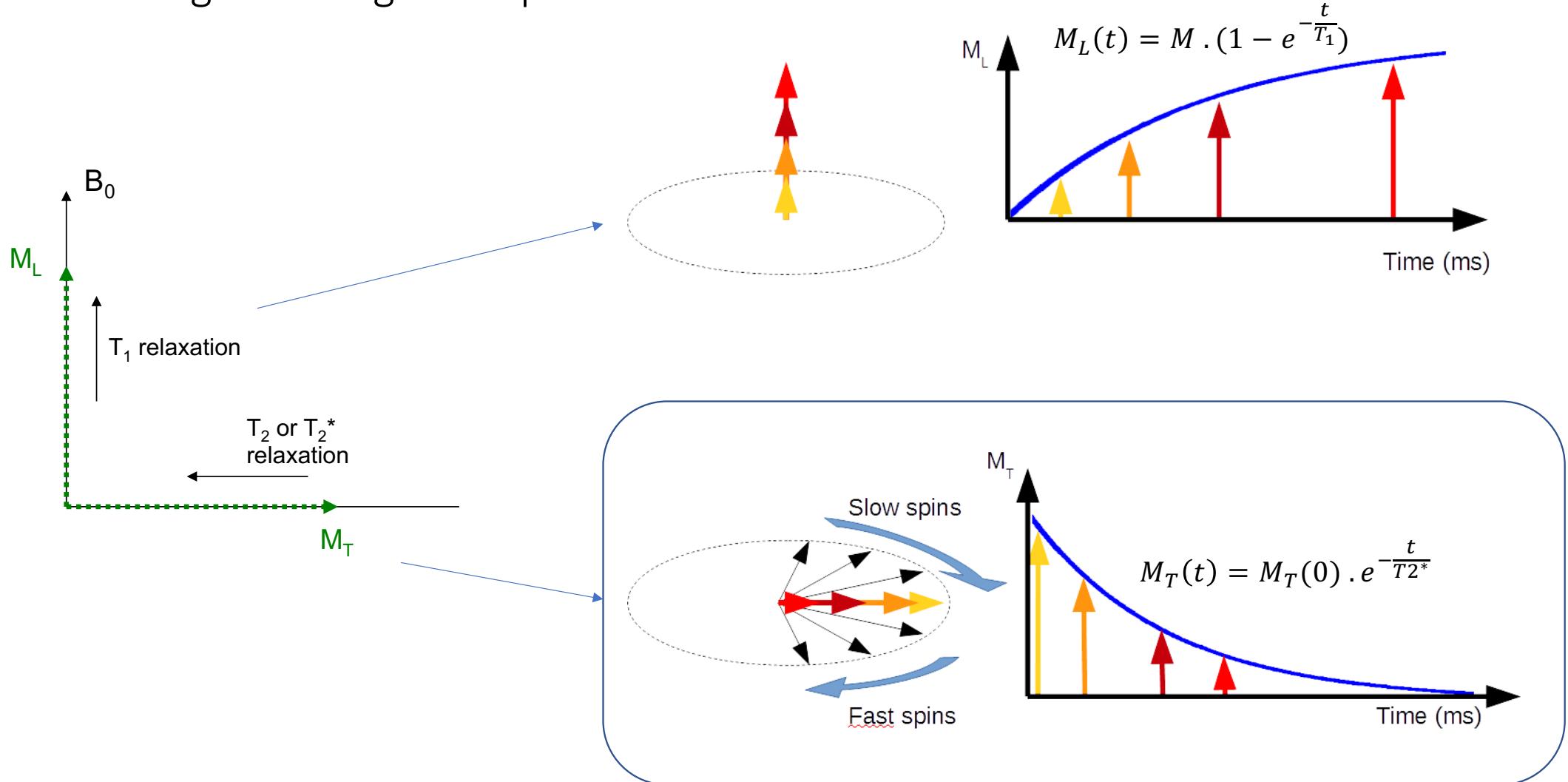
$$\omega_L = \gamma \cdot B_0$$



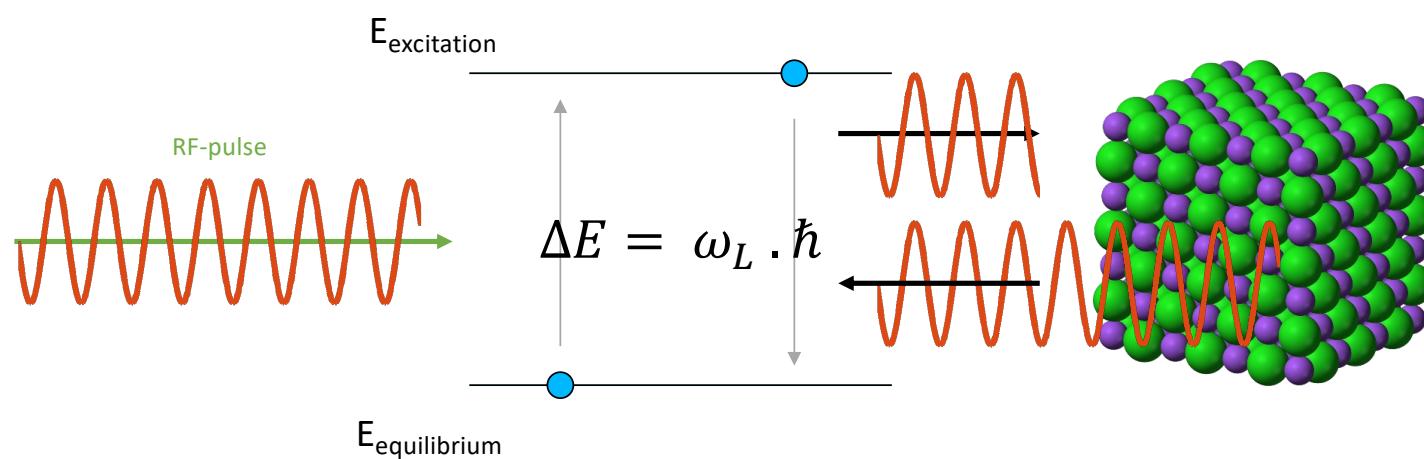
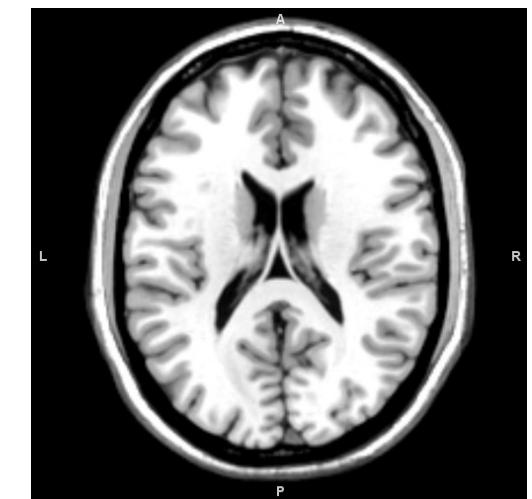
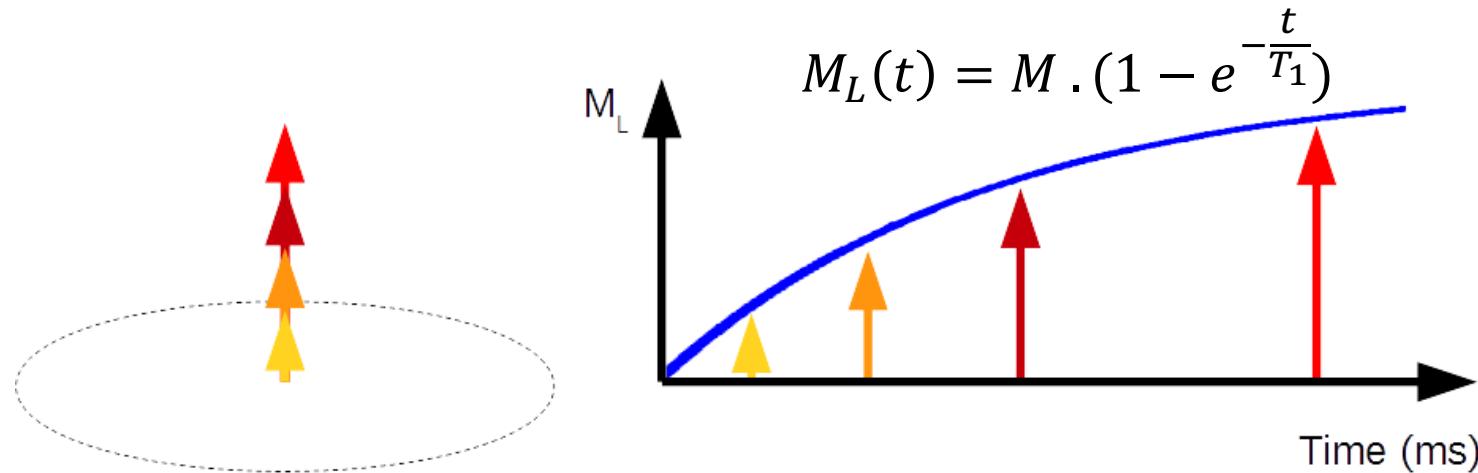
Generating a MRI signal step 3: induction of an MRI signal



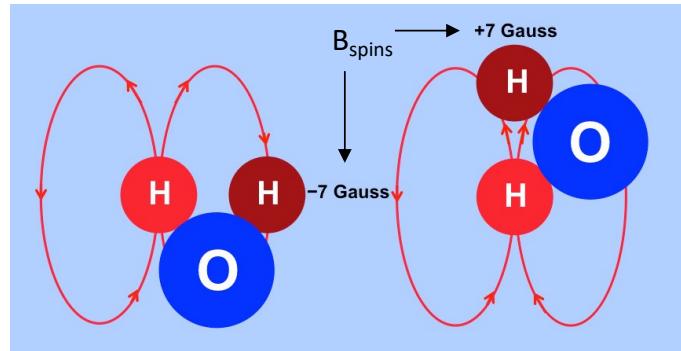
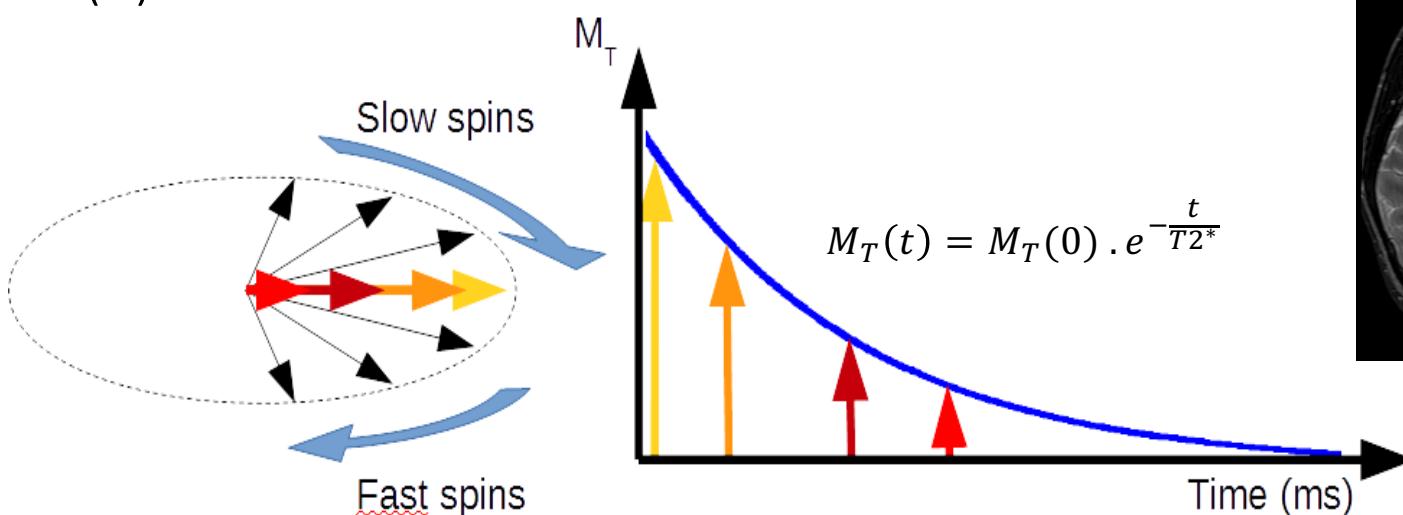
Generating a MRI signal step 4: relaxation



T1 relaxation



T2(*) relaxation



$$\omega_L = \gamma \cdot (B_0 + B_{spins} + \Delta B)$$

$\frac{1}{T2^*} = \frac{1}{T2} + \gamma \cdot \Delta B$

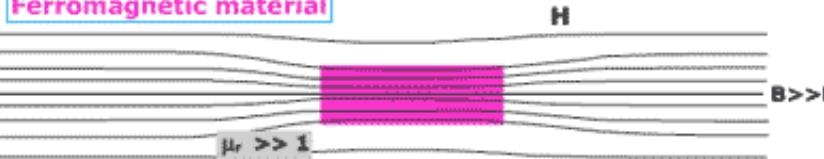
Diamagnetic material



Paramagnetic material



Ferromagnetic material



Example:

- diamagnetism: human tissues
- Paramagnetism: air
- Ferromagnetism: iron objects

Magnetic **susceptibility** (χ) = a measure of how much a material will become magnetized in an applied magnetic field.

Permeability ($\mu_r = (1 + \chi)$) = the measure of magnetization that a material obtains in response to an applied magnetic field.
(μ_r the relative permeability of a tissue, μ_0 the permeability of free space)

The magnetic induction (B) is linked to the magnetic field strength (H) by
 $B = \mu_r \cdot H = \mu_0(1 + \chi)H$

In diamagnetic and paramagnetic materials: $\mu_r \approx 1$



No distortion of the magnetic field $\rightarrow \Delta B = 0 \rightarrow T_2^* = T_2$

In ferromagnetic materials: $\mu_r \gg 1$

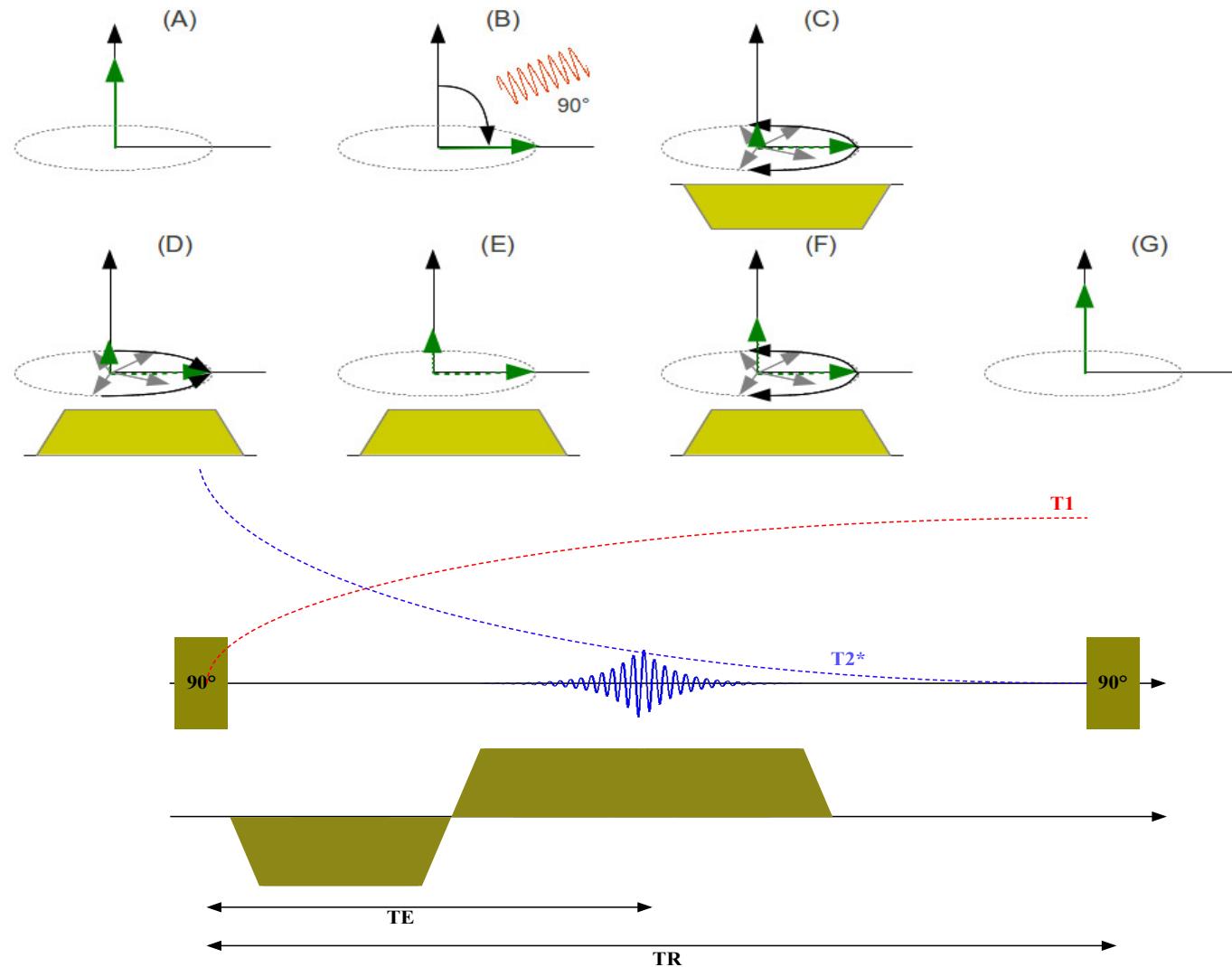


Strong distortion of the magnetic field $\rightarrow \Delta B > 0 \rightarrow T_2^* < T_2$

If the local field inhomogeneity increases

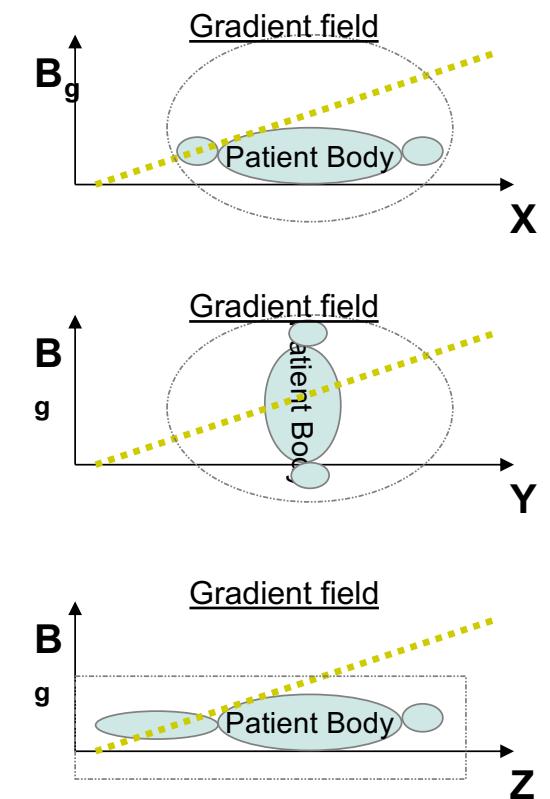
- a. $T2^*$ will increase
- b. $T2^*$ will decrease
- c. $T2^*$ will not be affected

Gradient echo

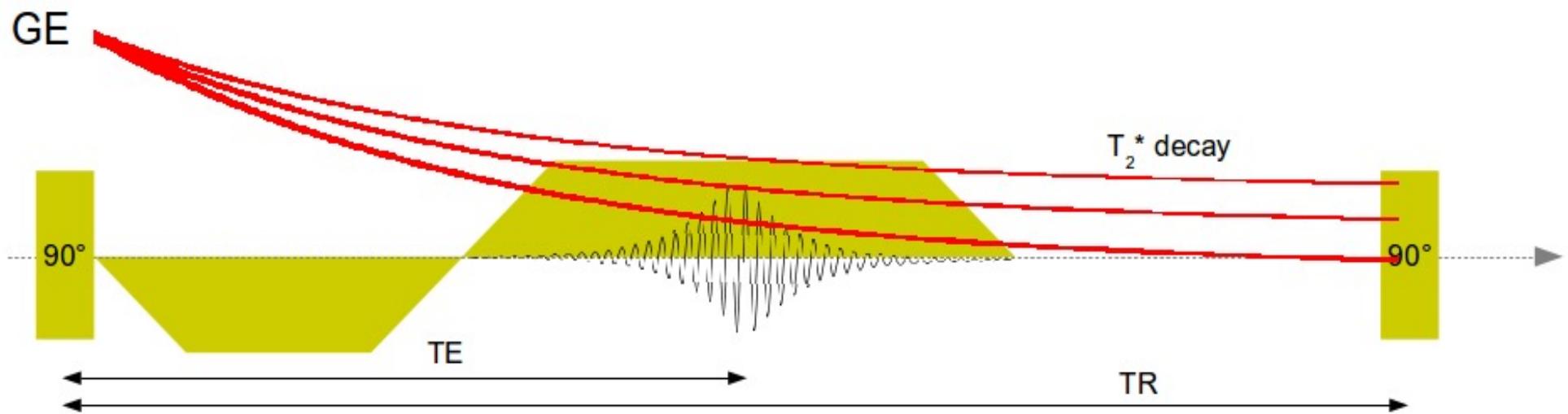


$$\text{Off: } \mathbf{B}(x,y,z,t) = \mathbf{B}_0$$

$$\text{On: } \mathbf{B}(x,y,z,t) = \mathbf{B}_0 + \mathbf{B}_G(x,y,z,t)$$



T2* contrast



Longer T2* relaxation → Larger signals → Brighter image contrast

Shorter T2* relaxation → smaller signals → Darker image contrast

An increase in T2* will result in a loss of image contrast

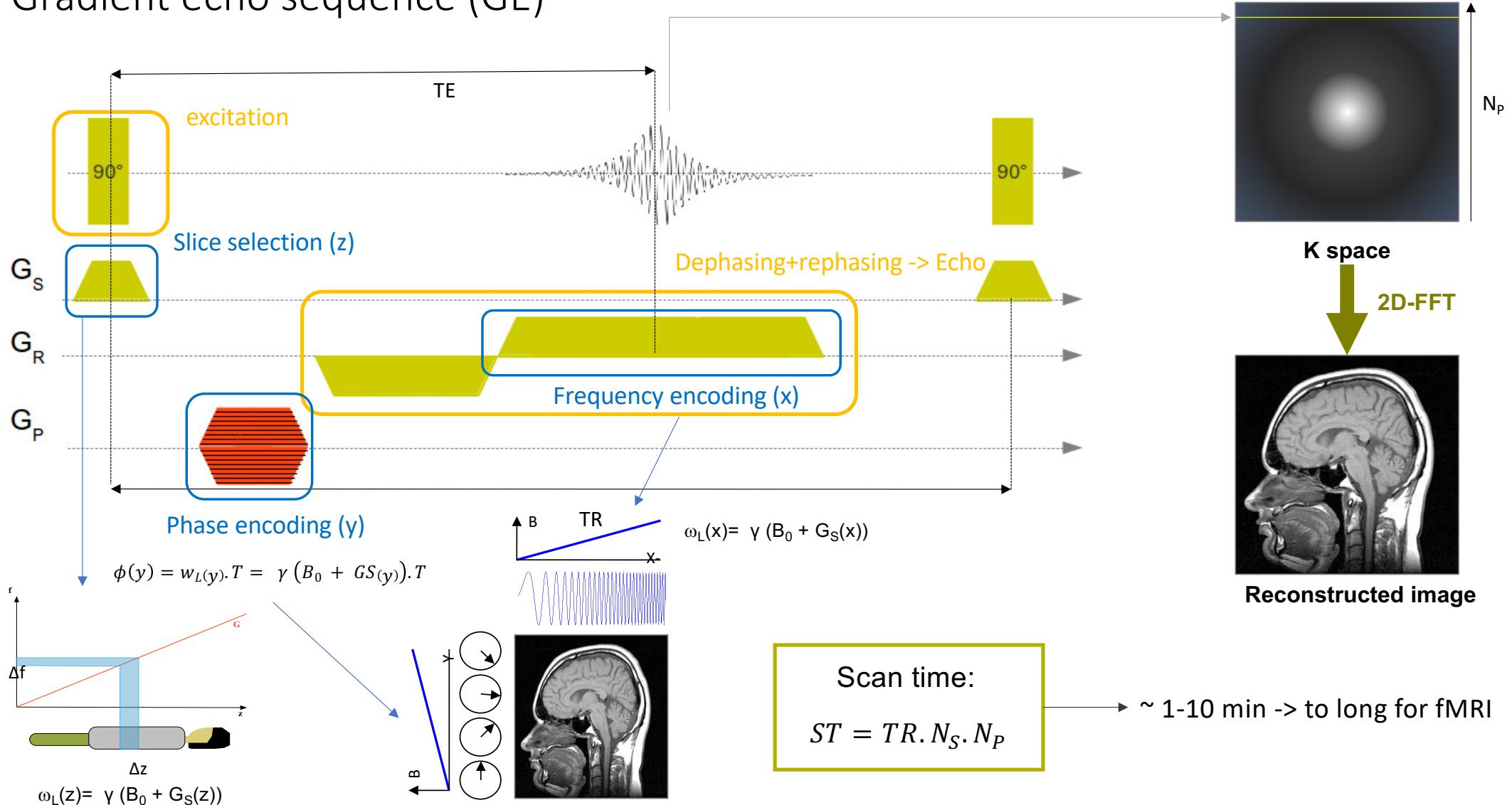
Ferromagnetic screw
↓
susceptibility effect



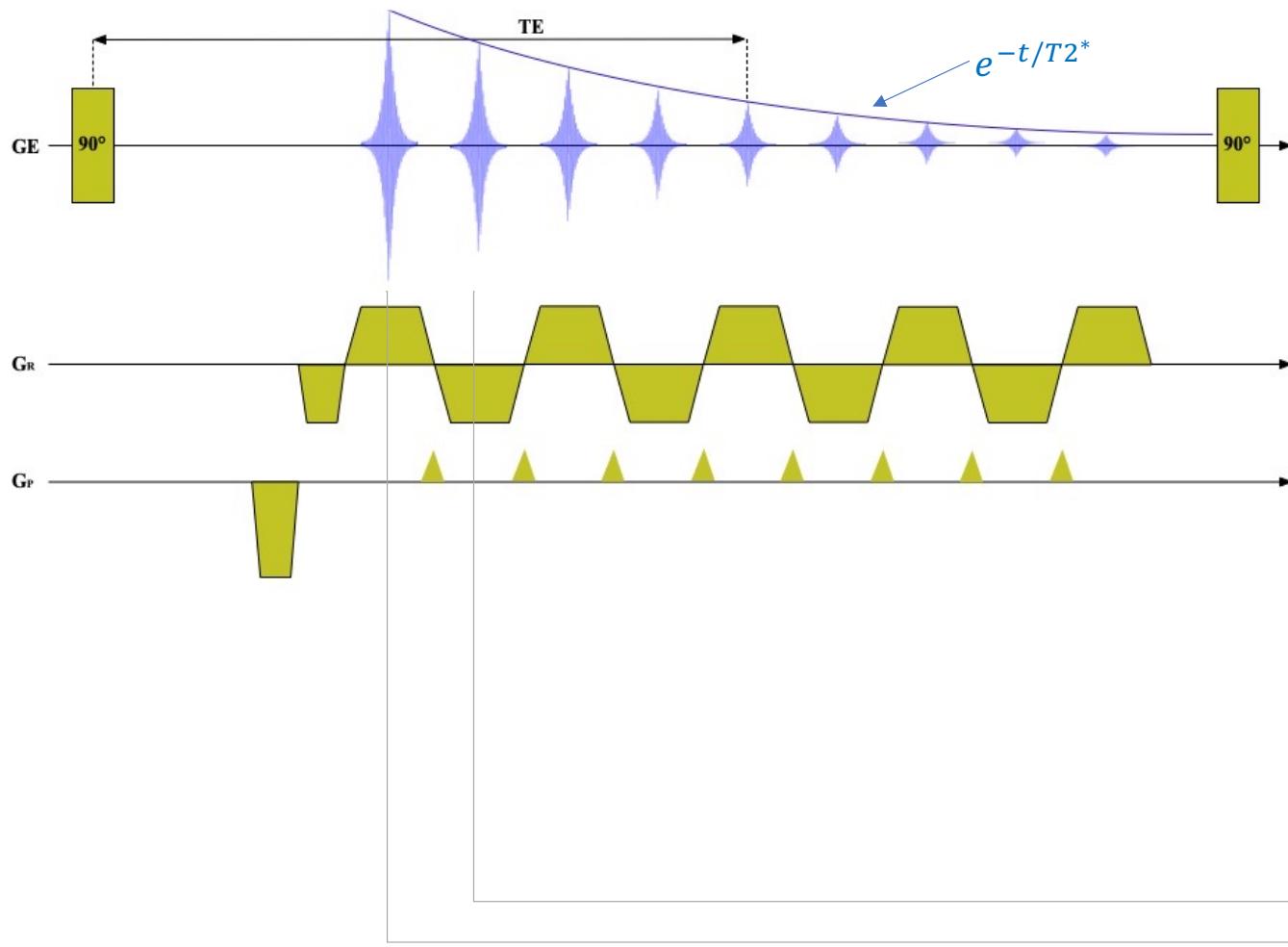
If the local field inhomogeneity increases

- a. The image contrast will increase
- b. The image contrast will decrease
- c. The image will not be affected

Gradient echo sequence (GE)

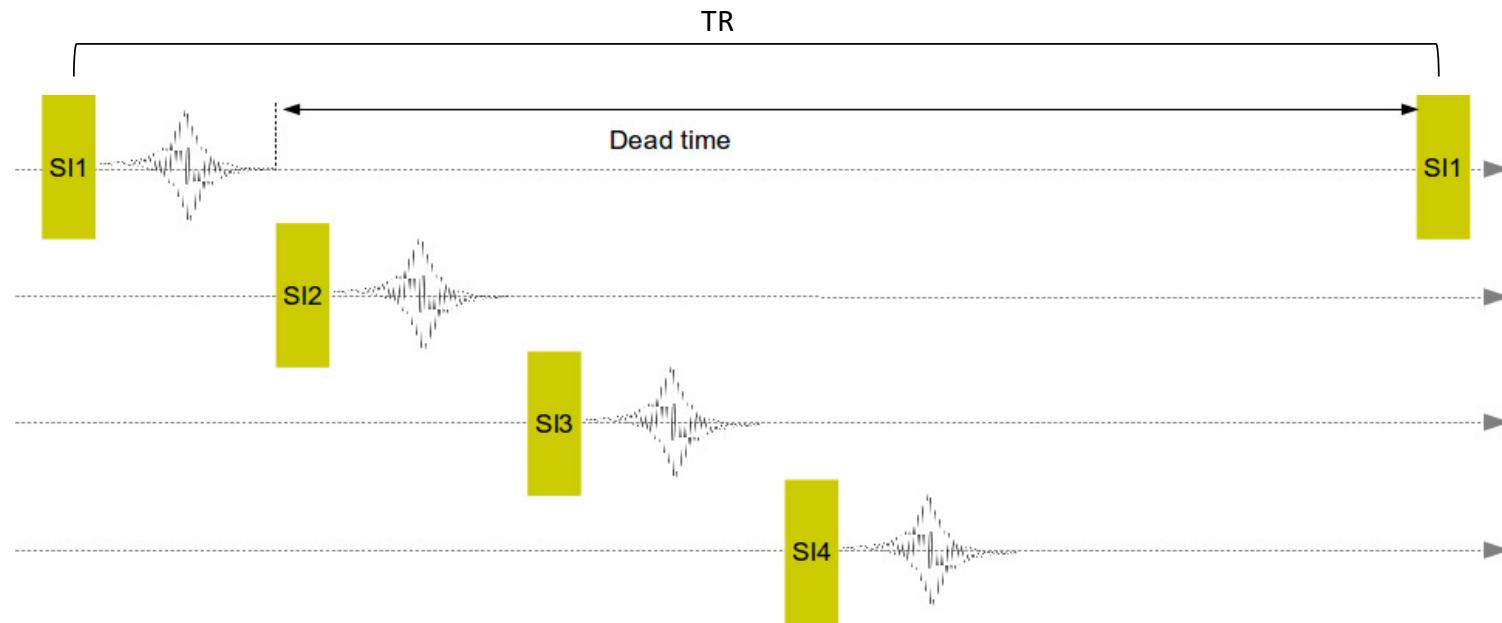


GE-EPI: Echo Planar Imaging



$$ST = TR \cdot NS$$

Multi slice imaging

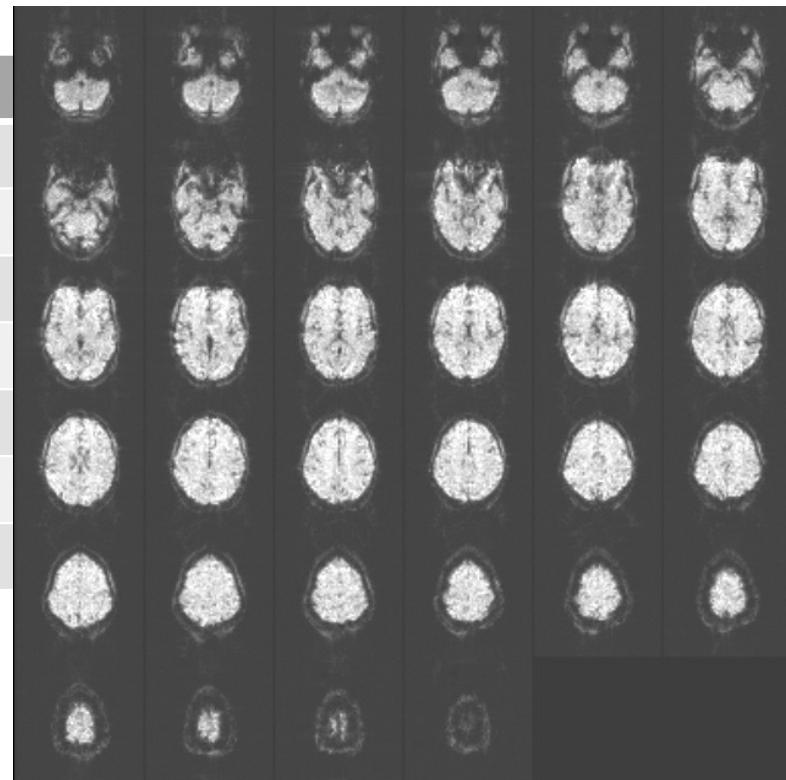


$$ST = TR$$

→ $\sim 1500 - 3000$ ms

Example of fMRI GE-EPI settings

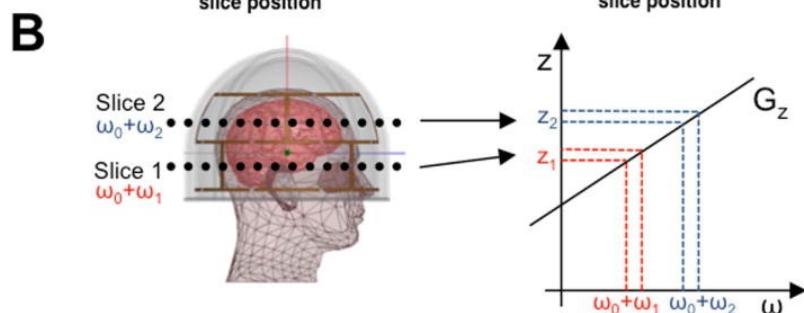
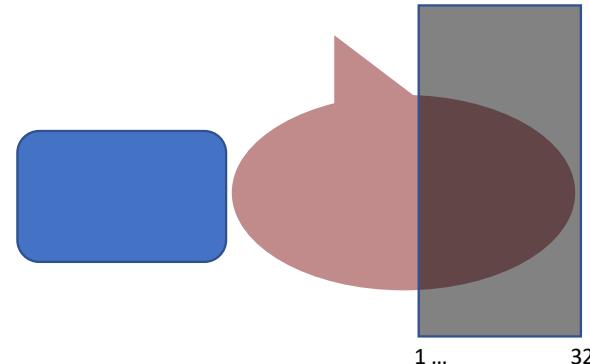
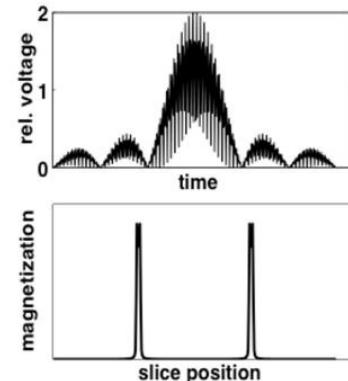
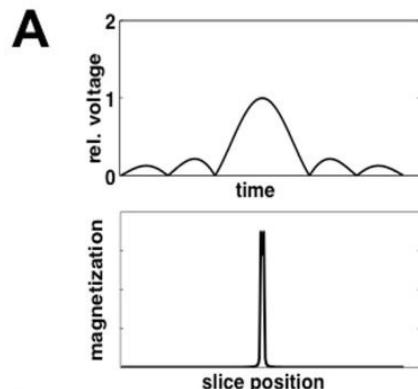
| | |
|------------------|---------------------------|
| TR | 2000 ms |
| TE | 30 ms |
| Number of slices | 36 |
| Slice thickness | 3 mm |
| Slice gap | 0 mm |
| FOV | 240 x 240 mm ² |
| Scan matrix | 80 x 80 |
| EPI factor | 80 |



Scan time: 2s

Scan resolution: 3 x 3 x 3 mm³

Simultaneous Multi-Slice (SMS) / MultiBand/ HyperBand



Without SMS: 1, 3, 5... 31, 2, 4, ... 32 (interleaved order)



32 individual slices to measure

With SMS: (1, 5, 9, ... 29), (3, 7, 11,...31), (2, 6, 10,...30), (4, 8, 12,...32)



Only 4 slice packages with 8 slices each to measure

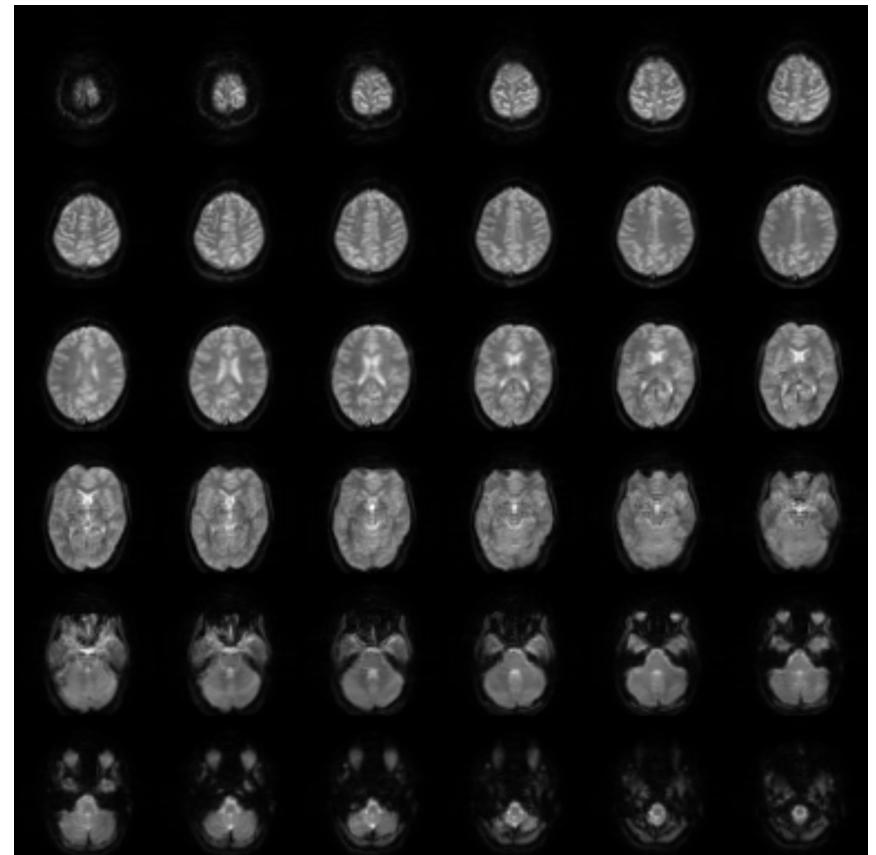
$$RF(t) = A(t) \cdot \sum_N e^{i \cdot \omega_n \cdot t + \varphi_n}$$

Current HCP fMRI scan protocol

| | |
|------------------|---------------------------|
| TR | 720 ms |
| TE | 33 ms |
| Flip angle | 52 deg |
| Number of slices | 72 |
| Slice thickness | 2 mm |
| Slice gap | 0 mm |
| FOV | 208 x 180 mm ² |
| Scan matrix | 104 x 90 (2x2 mm) |
| EPI factor | 90 |
| HyperBand factor | 8 |

Temporal resolution = 720 ms

Spatial resolution is 2 mm isotropic

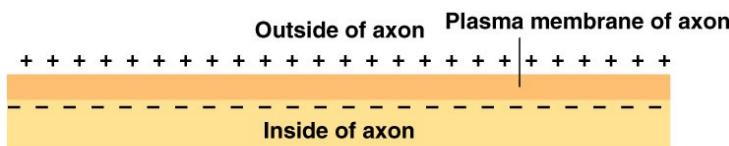


The hemodynamic response

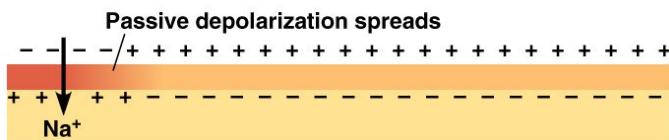
Equilibrium state:
(rest)

Disturbance of the
equilibrium state:
(activation)

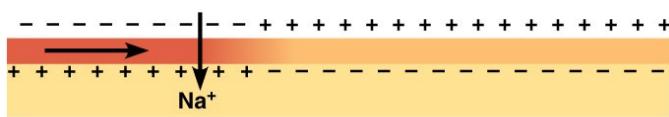
Active repolarization:
(going back to rest)



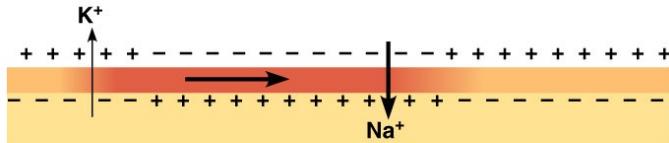
- ① At the start, the membrane is completely polarized.



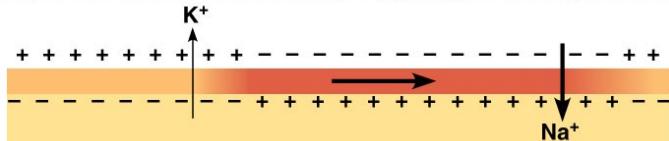
- ② When an action potential is initiated, a region of the membrane depolarizes. As a result, the adjacent regions become depolarized.



- ③ When the adjacent region is depolarized to its threshold, an action potential starts there.



- ④ Repolarization occurs due to the outward flow of K⁺ ions. The depolarization spreads forward, triggering an action potential.



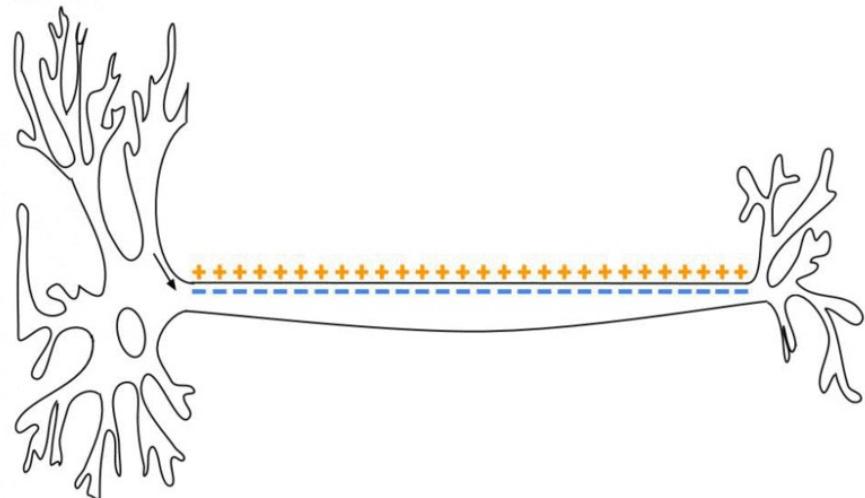
- ⑤ Depolarization spreads forward, repeating the process.

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Neural processing



processing and exchanging electric signals
between neurons



MakeAGIF.com

Neural activation -> chain of events from the neural to the vascular level (= neurovascular coupling)

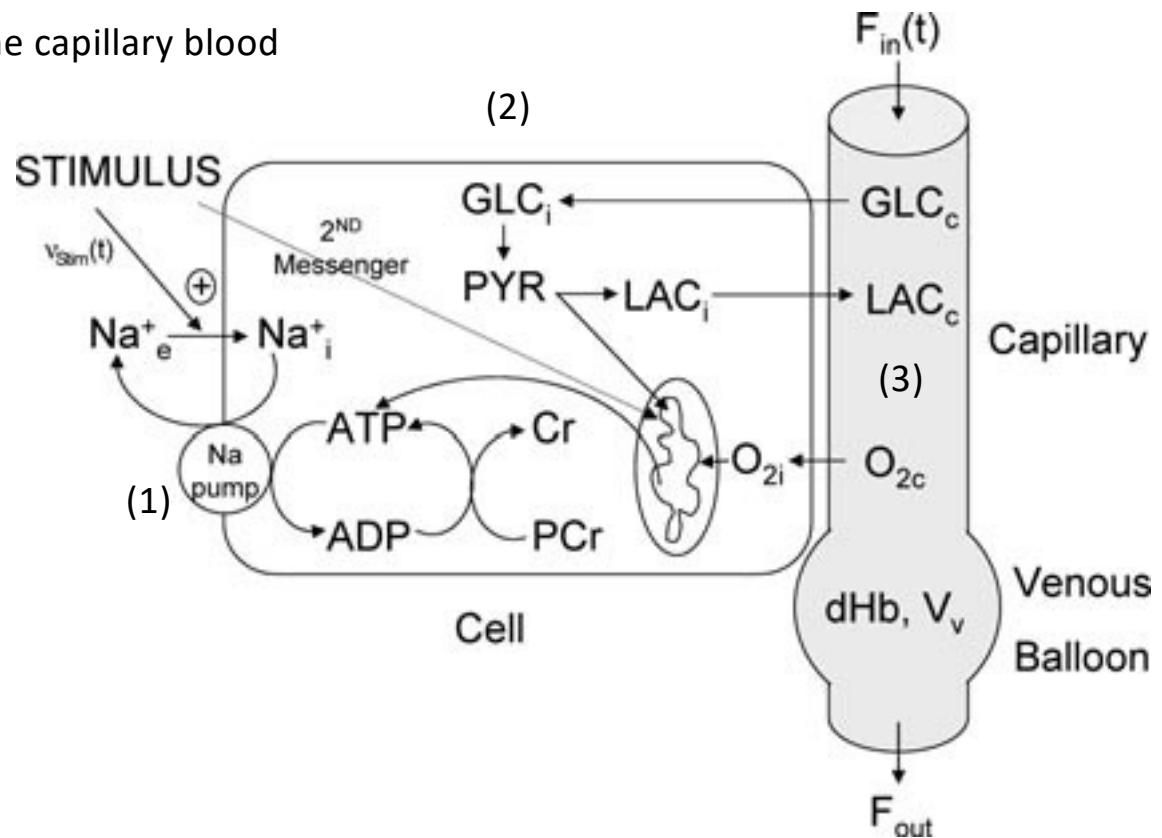
(1) Repolarization of the cell membrane requires energy

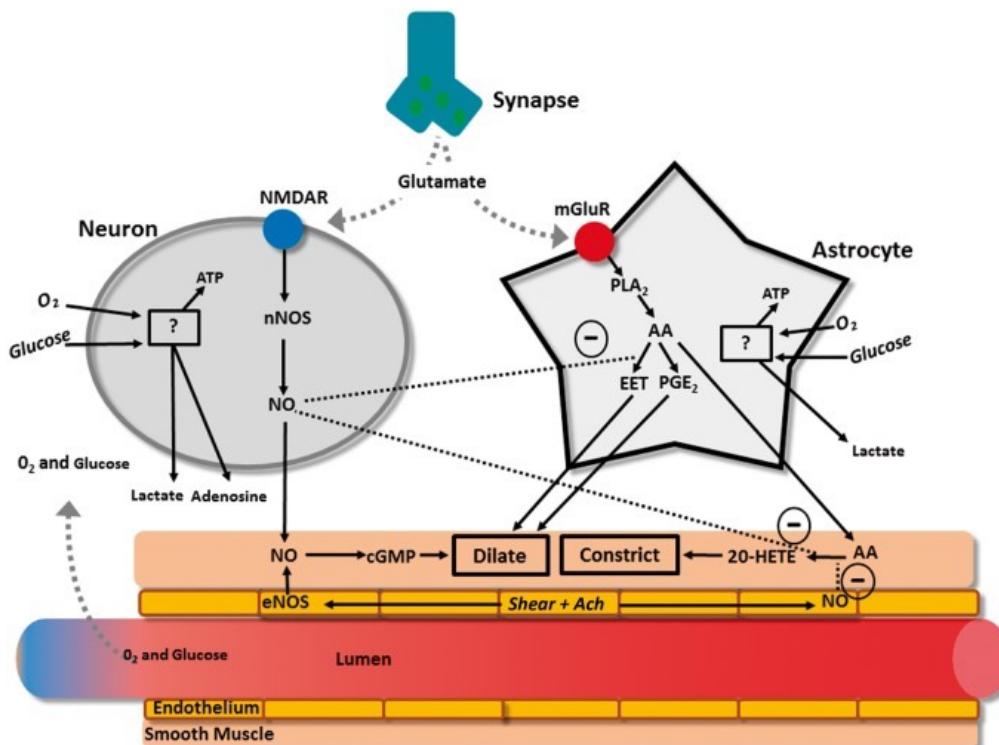


(2) Increased energy production in the neuron requires glucose (GLC) and oxygen (O_2)



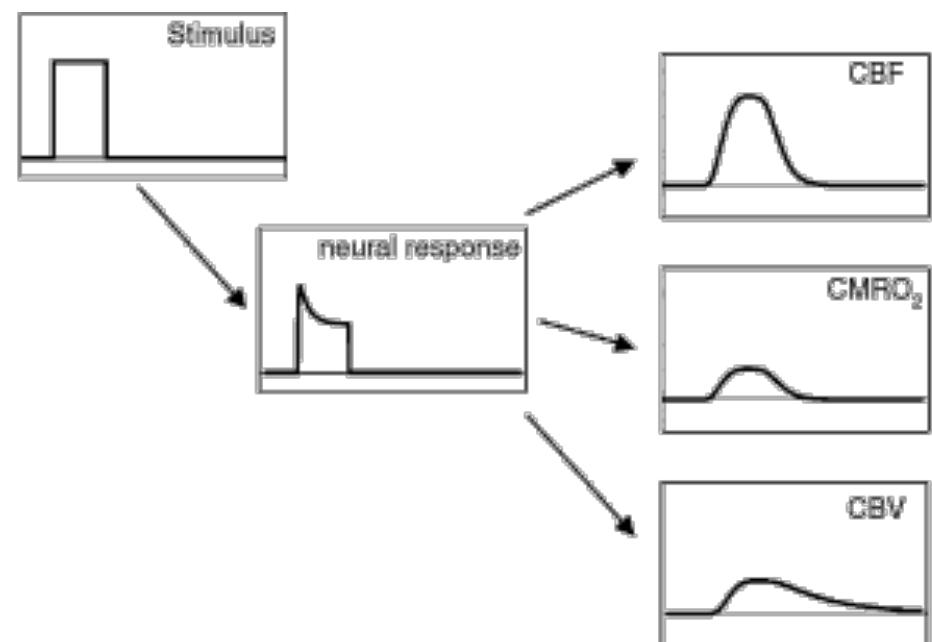
(3) Increased extraction of glucose and oxygen from the capillary blood



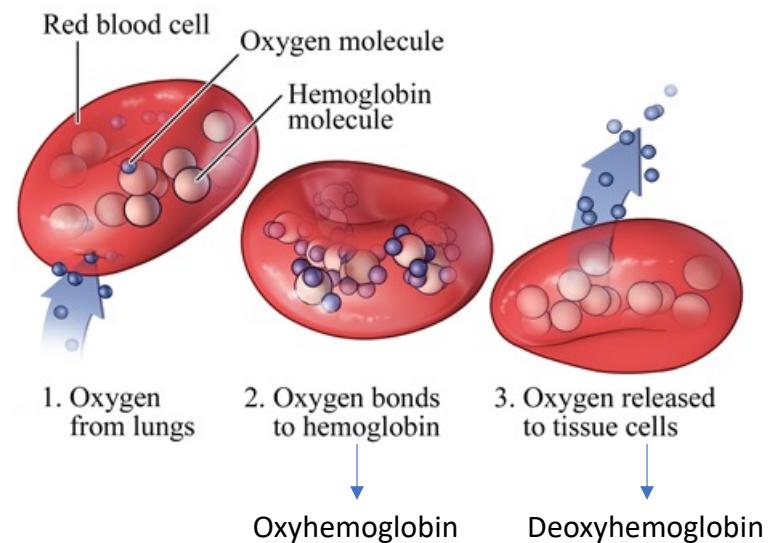
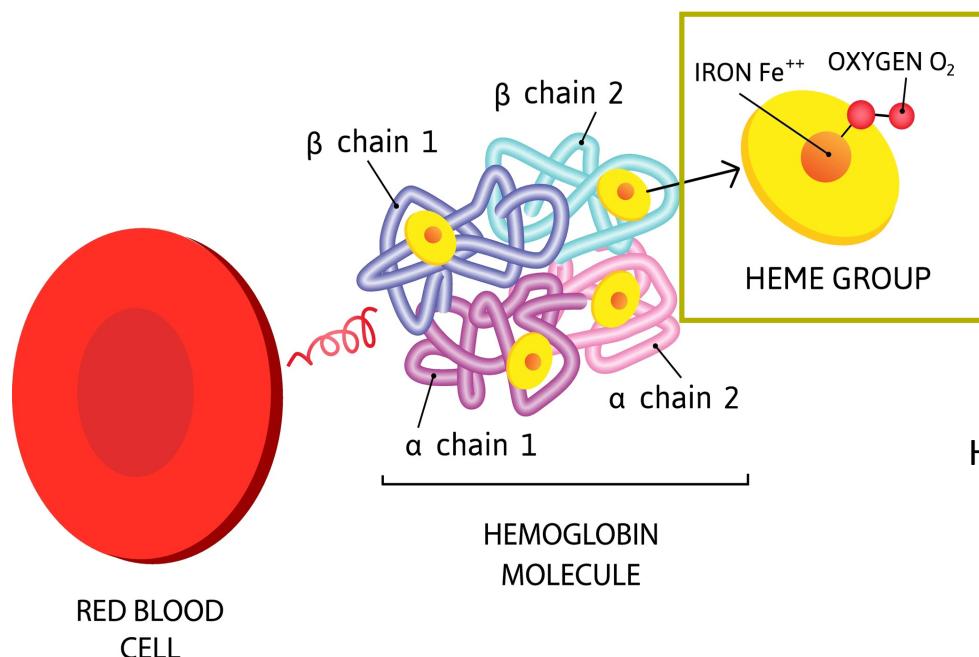


Neurovascular coupling:

- Due to the increased use of oxygen = increased CMRO₂
- Local dilatation of capillaries
 - Increased blood volume (CBV)
 - Increased blood flow (CBF)



Oxygen in the blood is transported by the hemoglobin molecule in the red blood cells

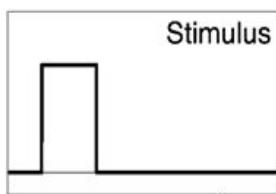


Hemoglobin = 4 chains with a heme group containing Fe^{++}

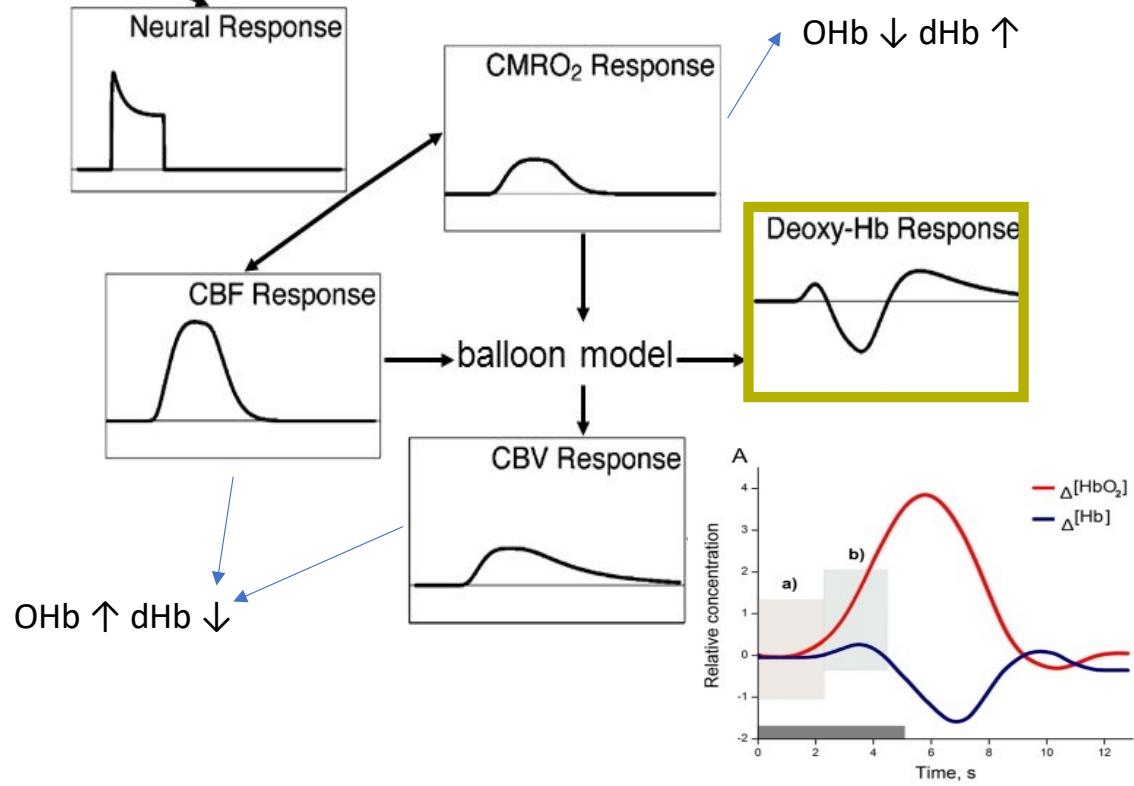


Deoxyhemoglobin (no oxygen bound to Fe) $\rightarrow \text{Fe}^{++}$

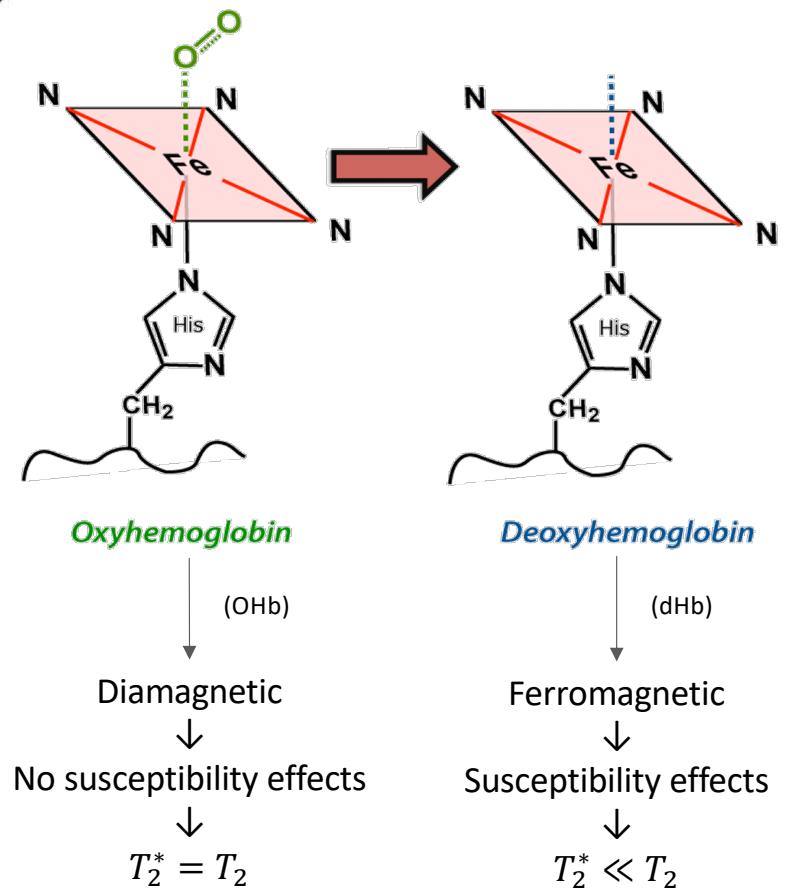
Oxyhemoglobin (oxygen bound to Fe) $\rightarrow \text{FeO}_2$

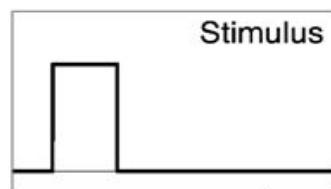


Haemodynamic Response

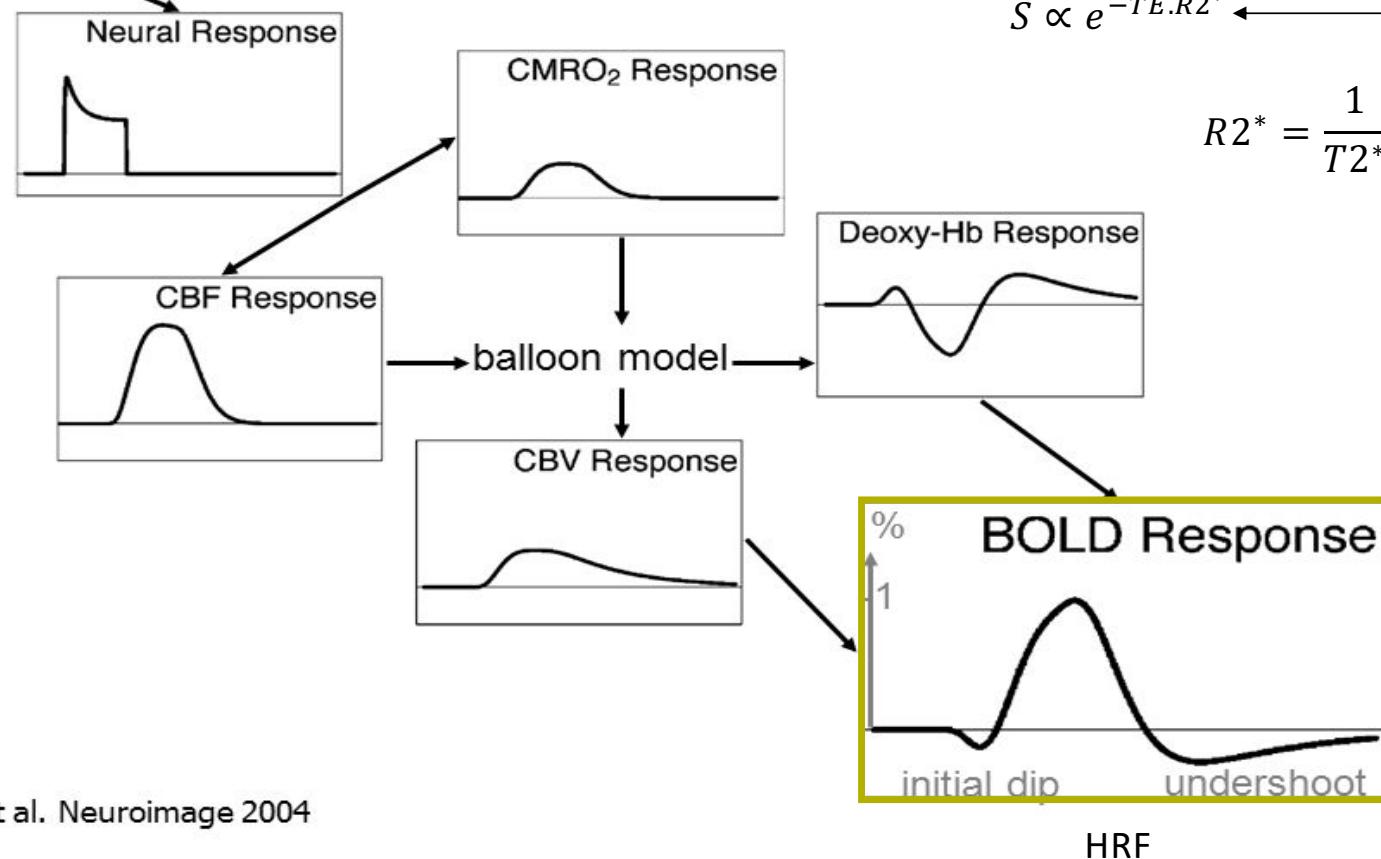


Buxton R et al. Neuroimage 2004





Haemodynamic Response



$$S \propto e^{-TE.R2^*}$$

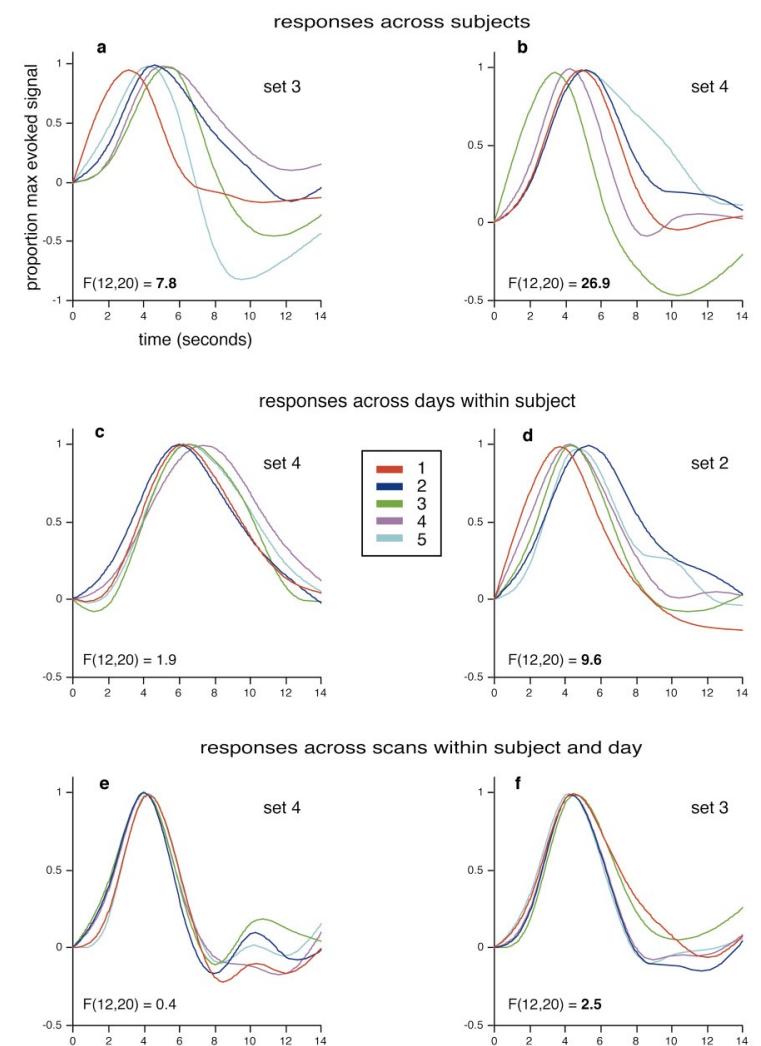
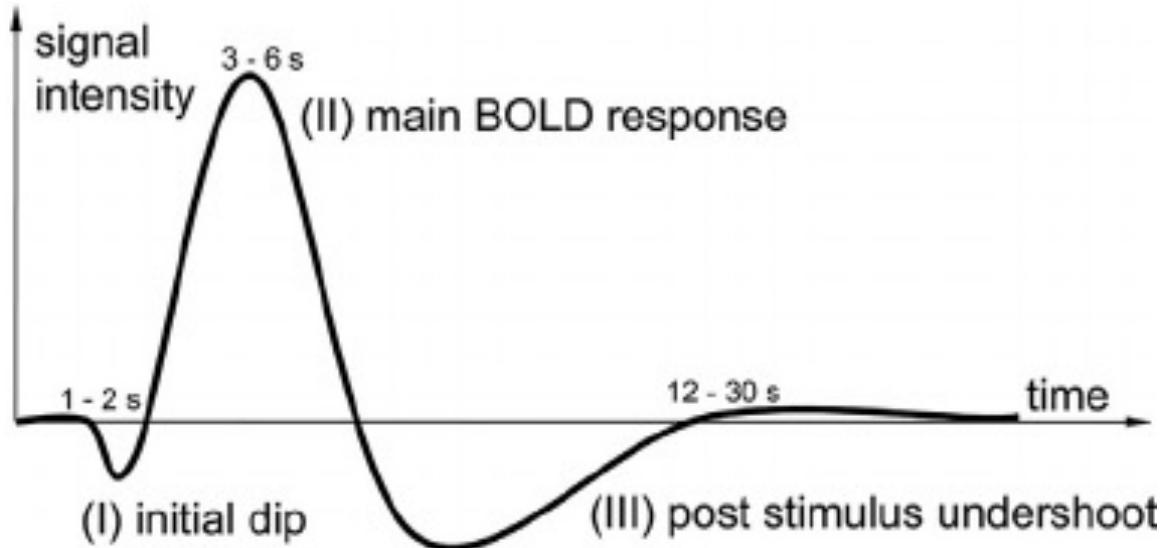
$$R2^* = \frac{1}{T2^*} = r_2^* \cdot \left[\frac{O\text{Hb}}{d\text{Hb}} \right]$$

$$\begin{cases} \frac{O\text{Hb}}{d\text{Hb}} \uparrow \rightarrow T2^* \uparrow \rightarrow S \uparrow \\ \frac{O\text{Hb}}{d\text{Hb}} \downarrow \rightarrow T2^* \downarrow \rightarrow S \downarrow \end{cases}$$

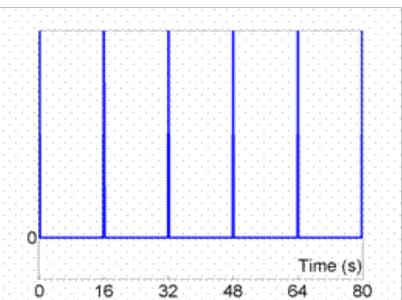
BOLD

||

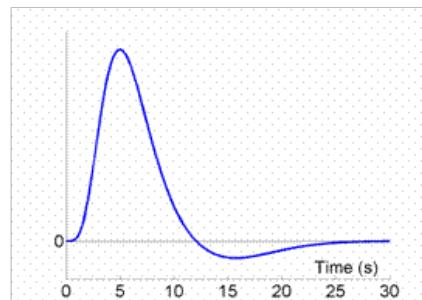
Blood Oxygen Level Depended
contrast



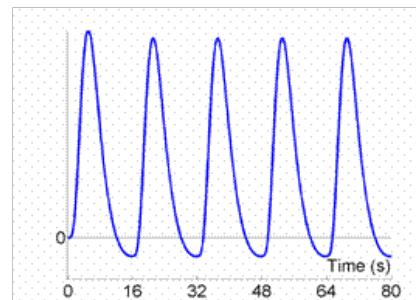
Stimulus (“Neural”)



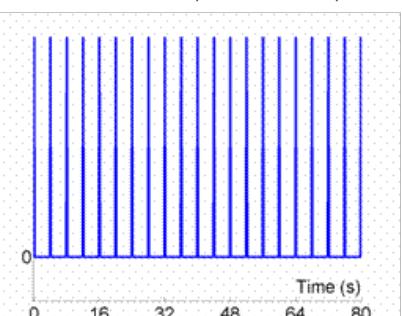
IR



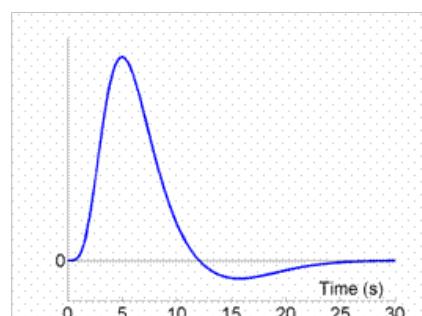
Predicted fMRI Data



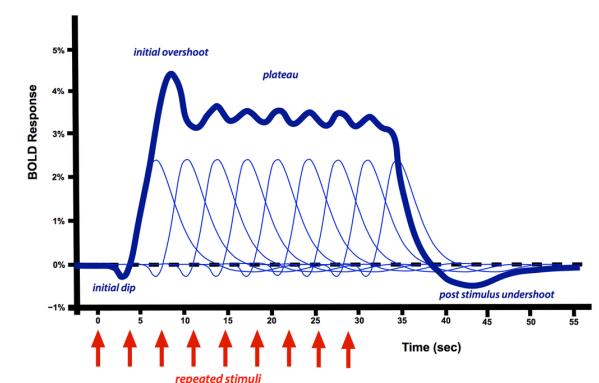
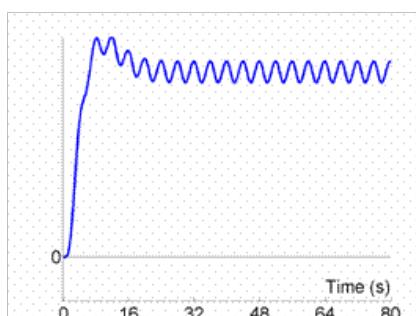
Stimulus (“Neural”)



IR



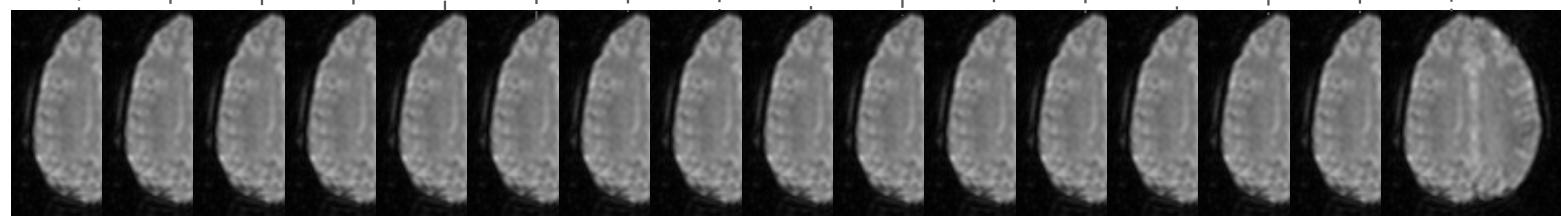
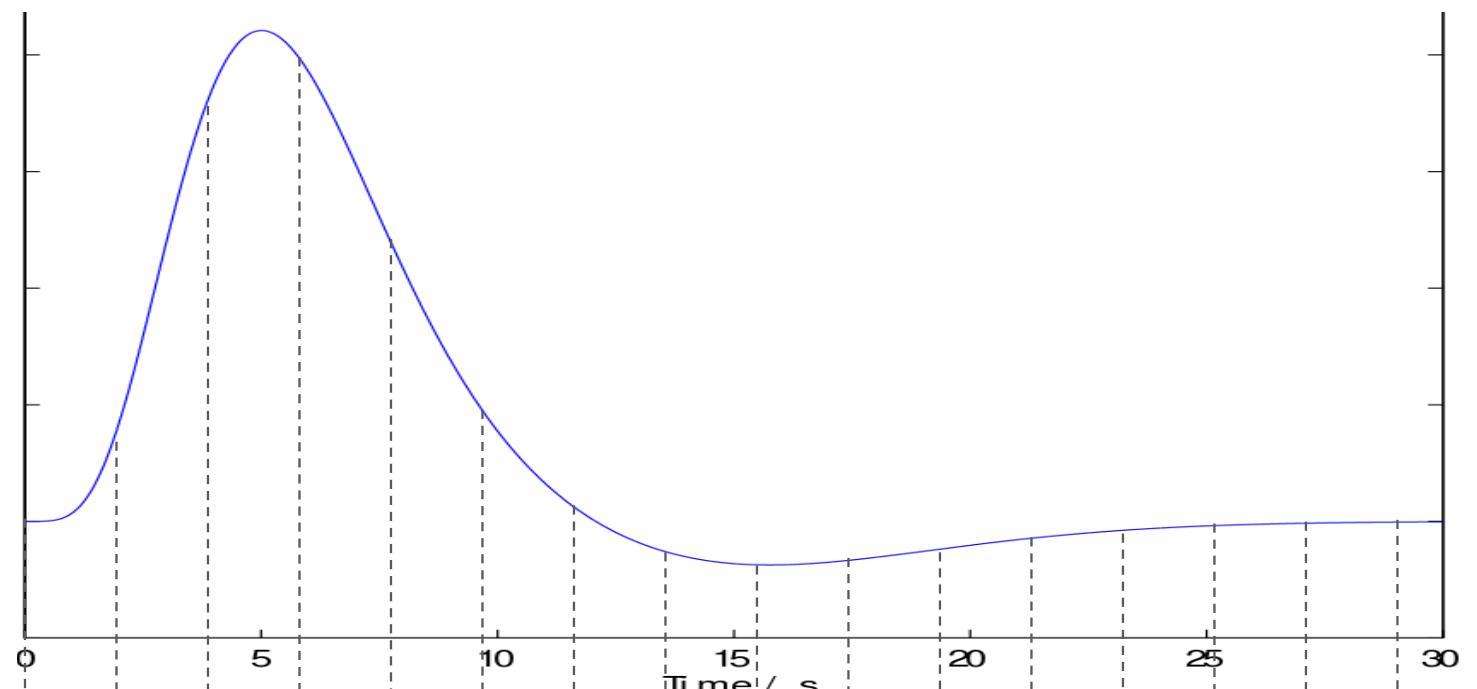
Predicted fMRI Data



When neurons are constantly activated (constant neural activity)

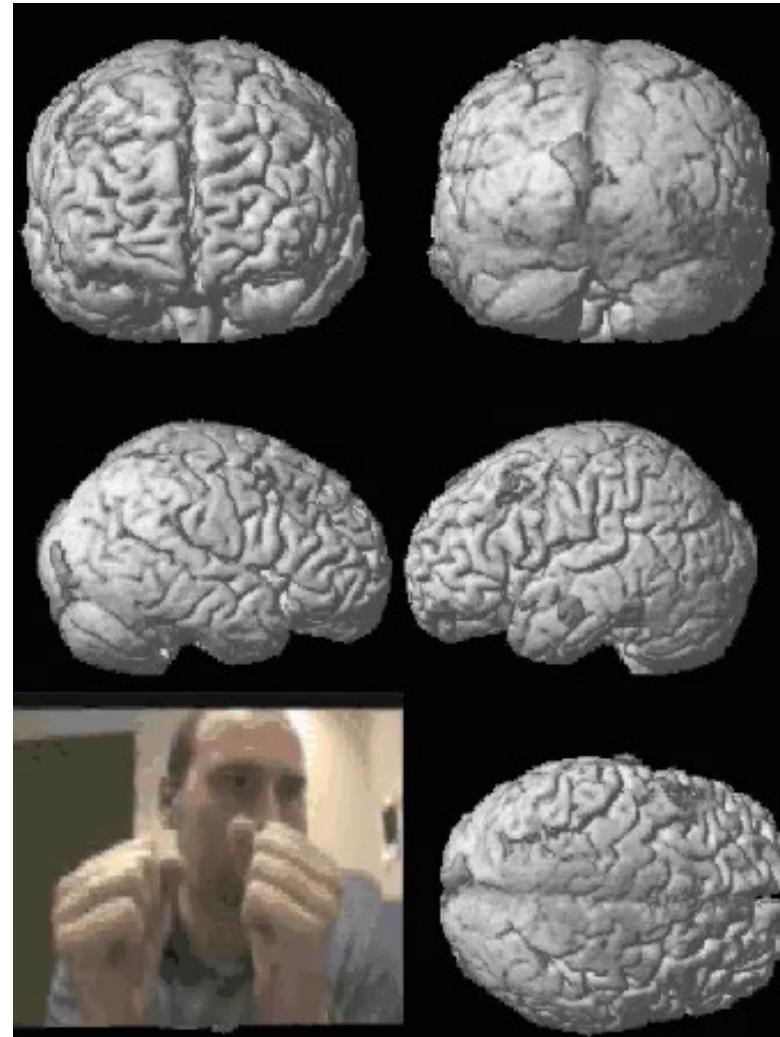
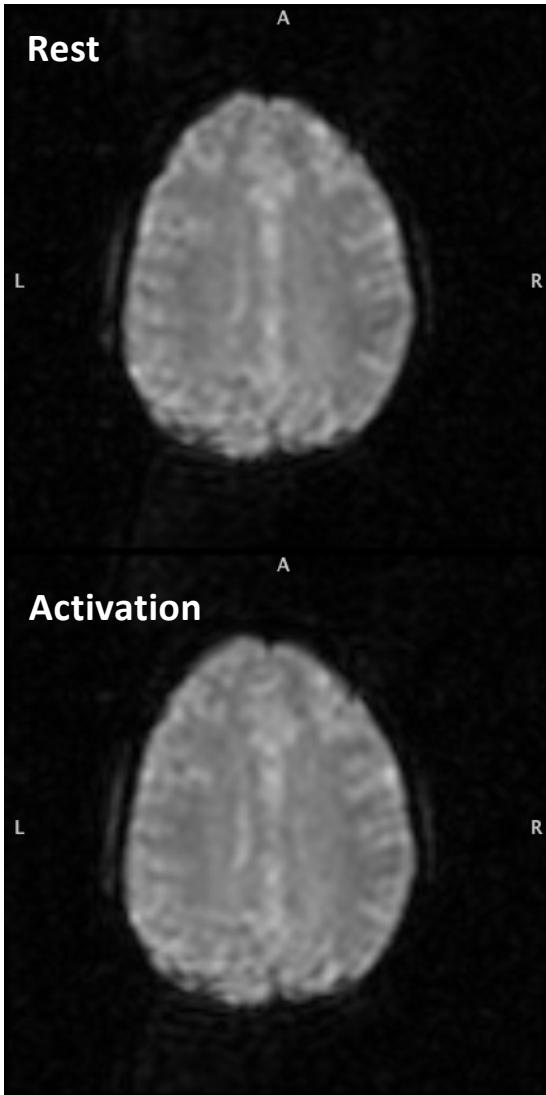
- a. The image contrast will increase
- b. The image contrast will decrease
- c. The image will remain constant

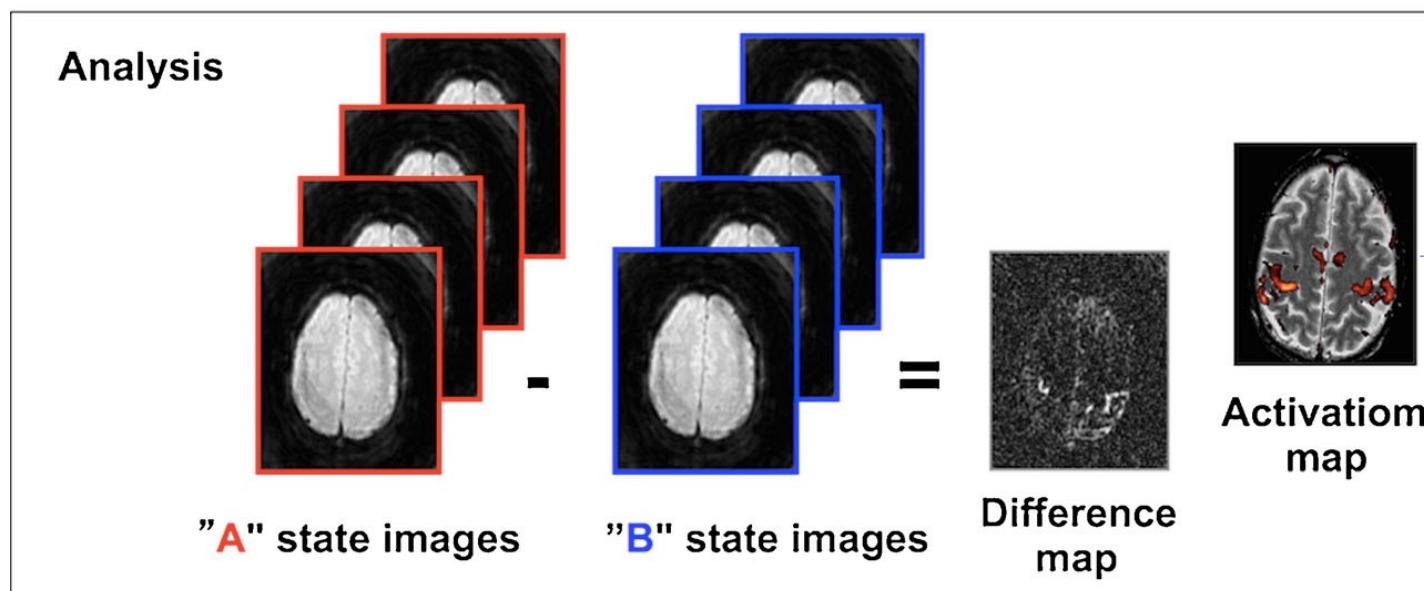
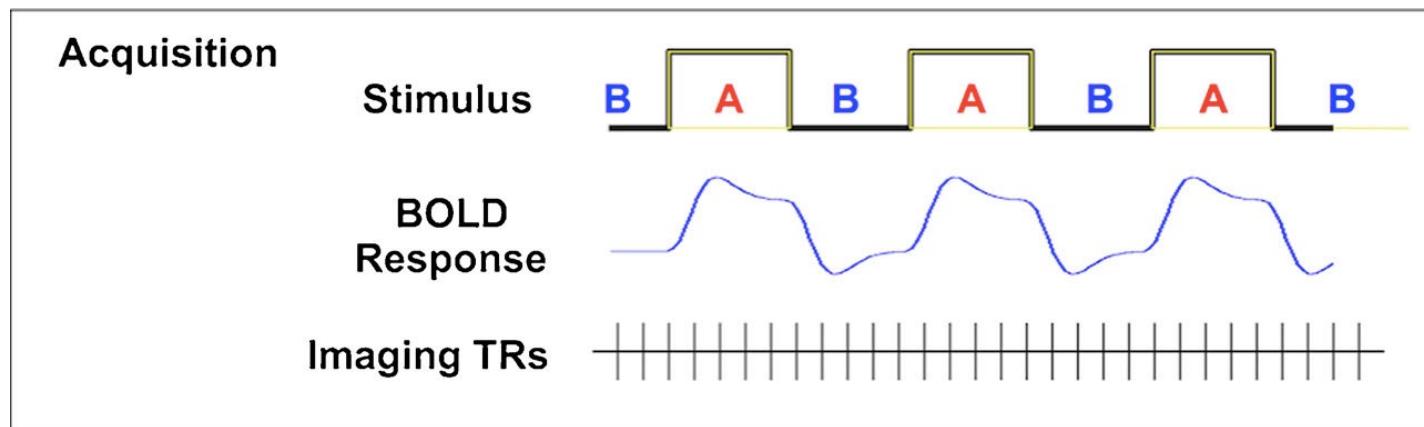
fMRI scan techniques



$$\Delta t = 0.5-3\text{s}$$

Statistical problem





T-test:

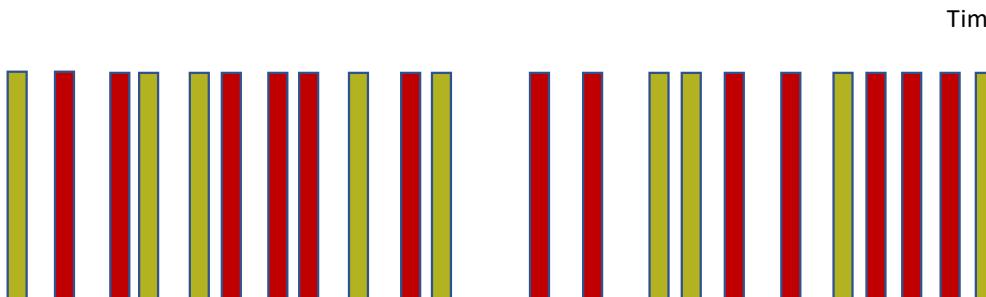
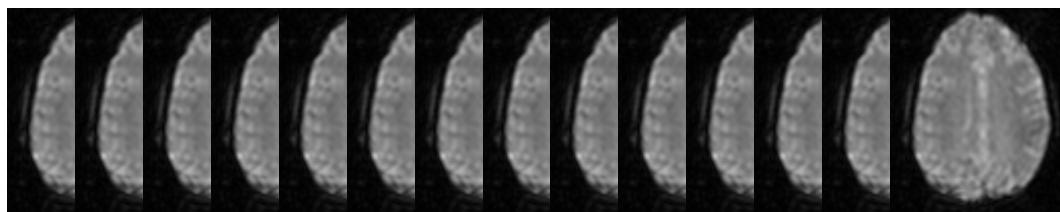
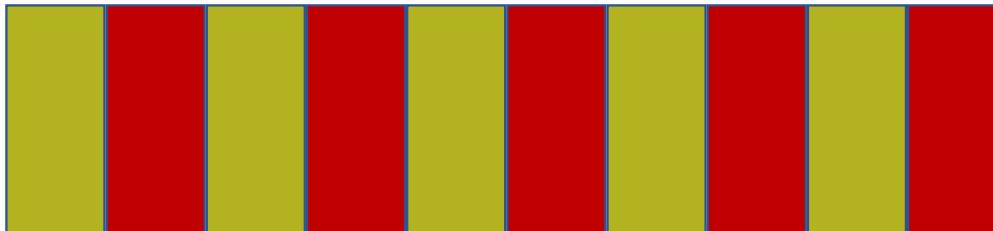
$H_0: \text{mean}(A) = \text{mean}(B)$

$H_1: \text{mean}(A) \neq \text{mean}(B)$

Task paradigm

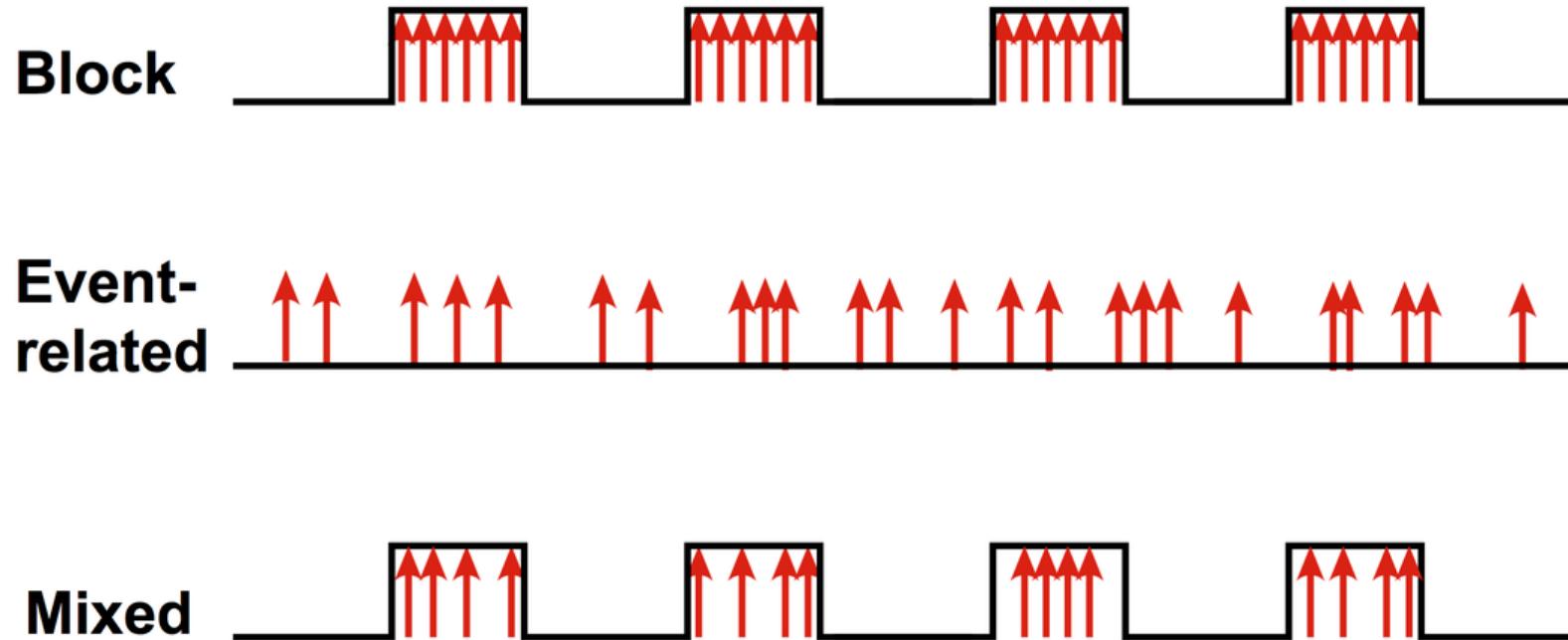
Task paradigm

Block design: sequence of task blocks



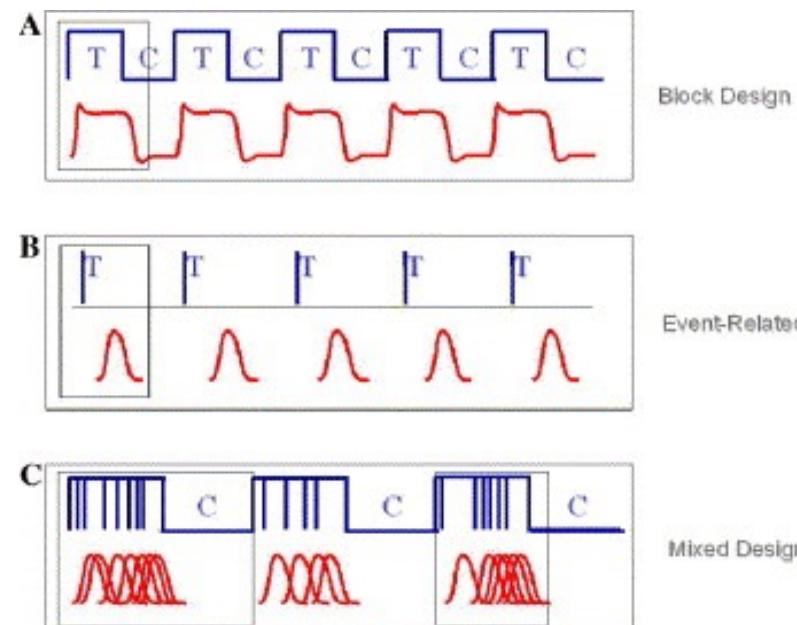
Event related design: sequence of random individual events

Paradigm design

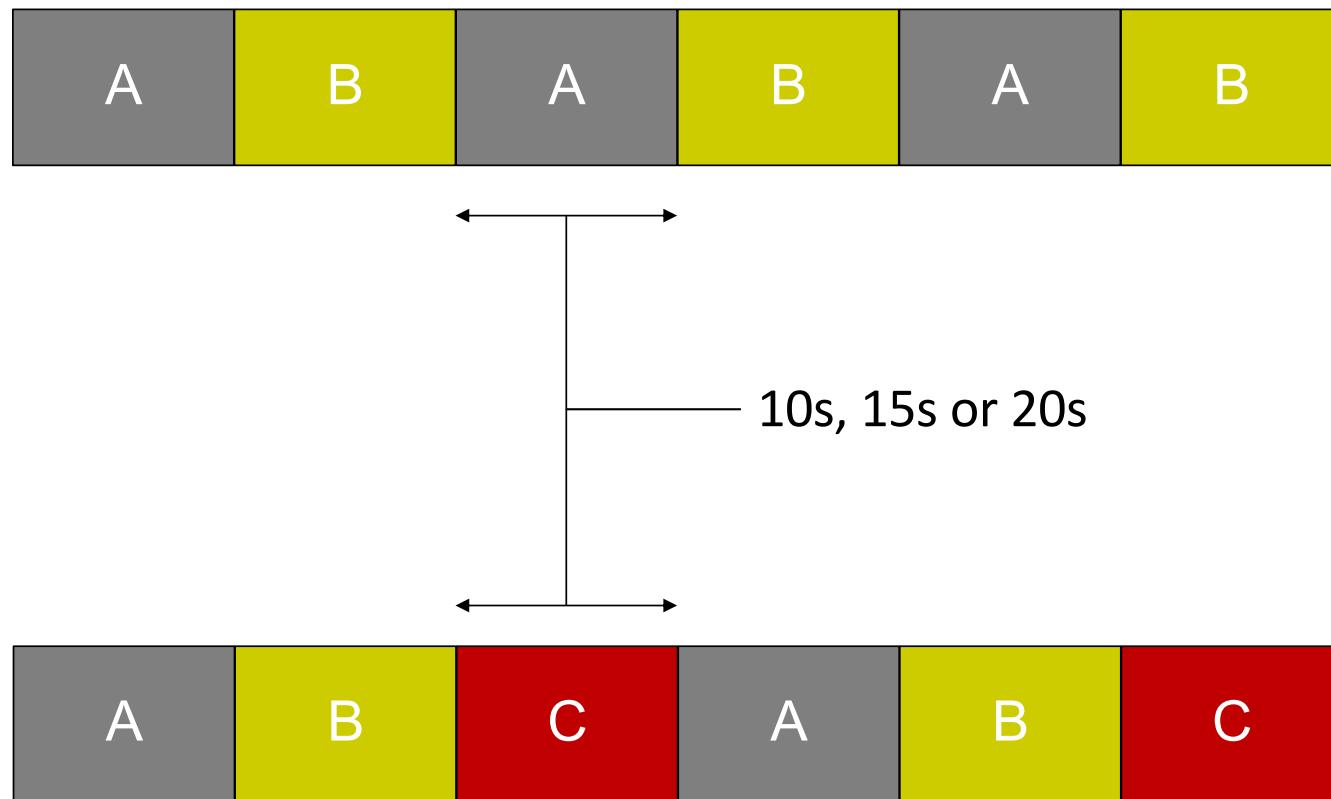


Comparison between paradigm designs

| | Block | Event-related | Mixed |
|-----------------------|-------|---------------|--------|
| Detection power | High | Low | High |
| Estimation efficiency | Low | High | High |
| Predictability | High | Low | Medium |
| SNR | High | Low | Medium |



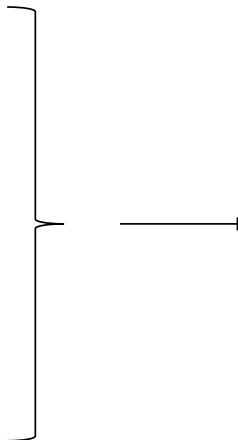
Optimal block design



Optimal event-related design

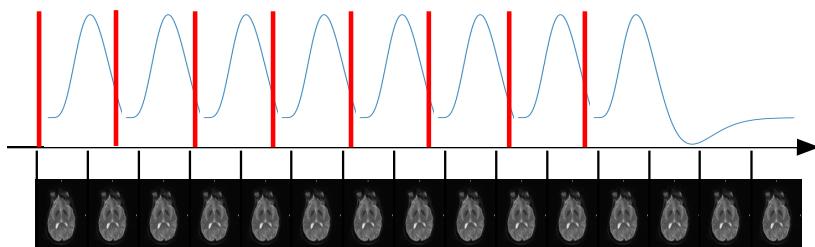
Parameters to optimize

- Total scan duration
- Number of trials per condition
- Trial order
- Inter-stimulus interval (ISI) + jittering

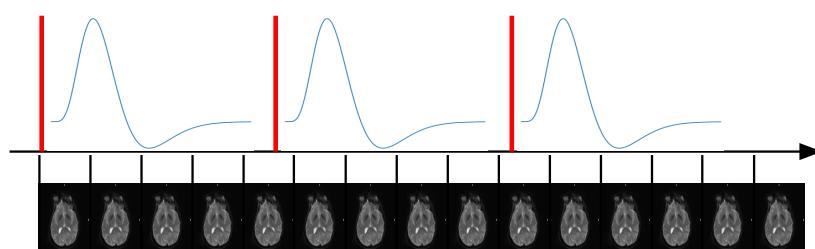


To optimize for

- Detectability
- Efficiency
- Predictability



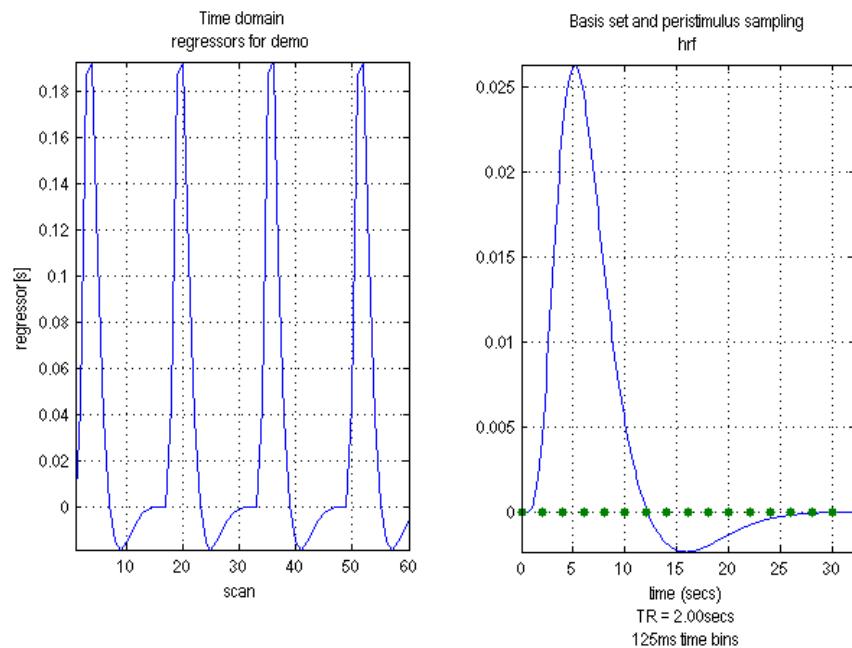
High detectability + low efficiency



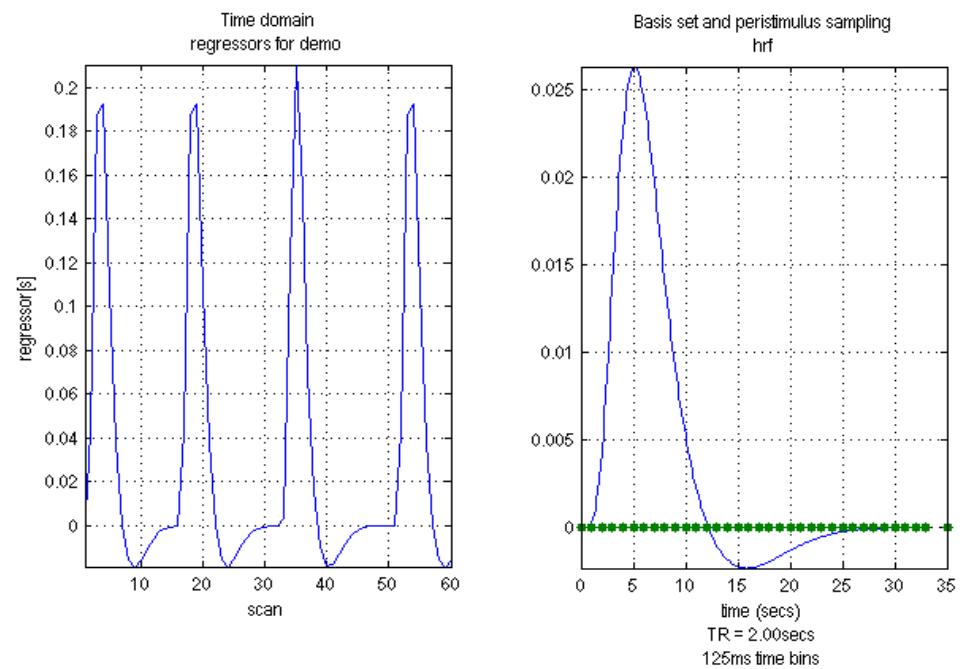
Low detectability + high efficiency

Jitter

Without jittering, TR=2s, ISI=32s



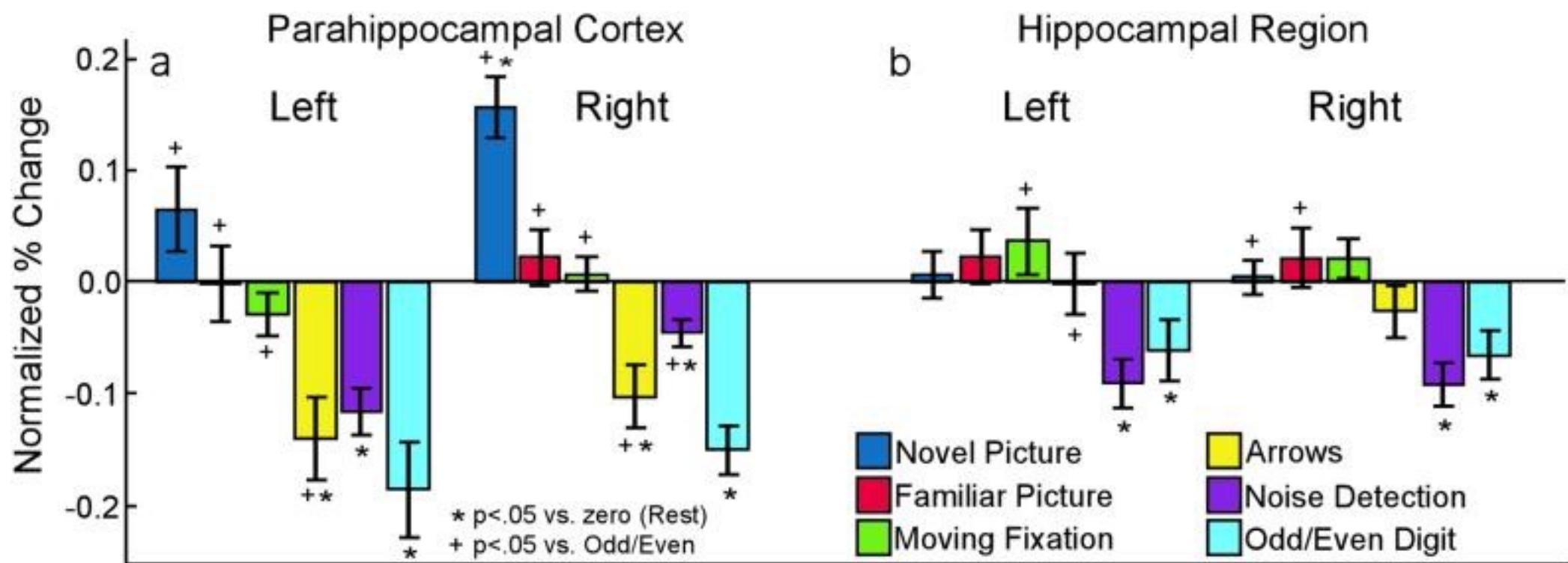
With jittering, TR=2s, Mean ISI=32s±7s



General rules of thumb for event-related designs

- Scan as long as possible
- Keep the subjects busy
- Do not contrast trials far apart in time
- Randomize trial order (and ISI)
- Log what happens and when during the fMRI scan

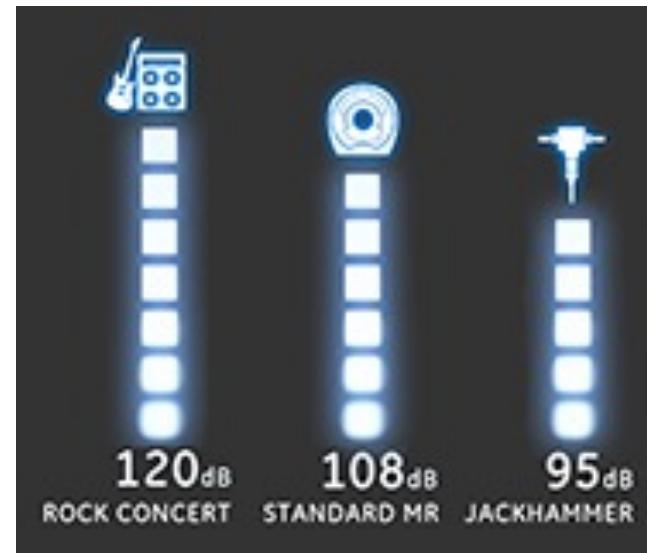
REST is never REST



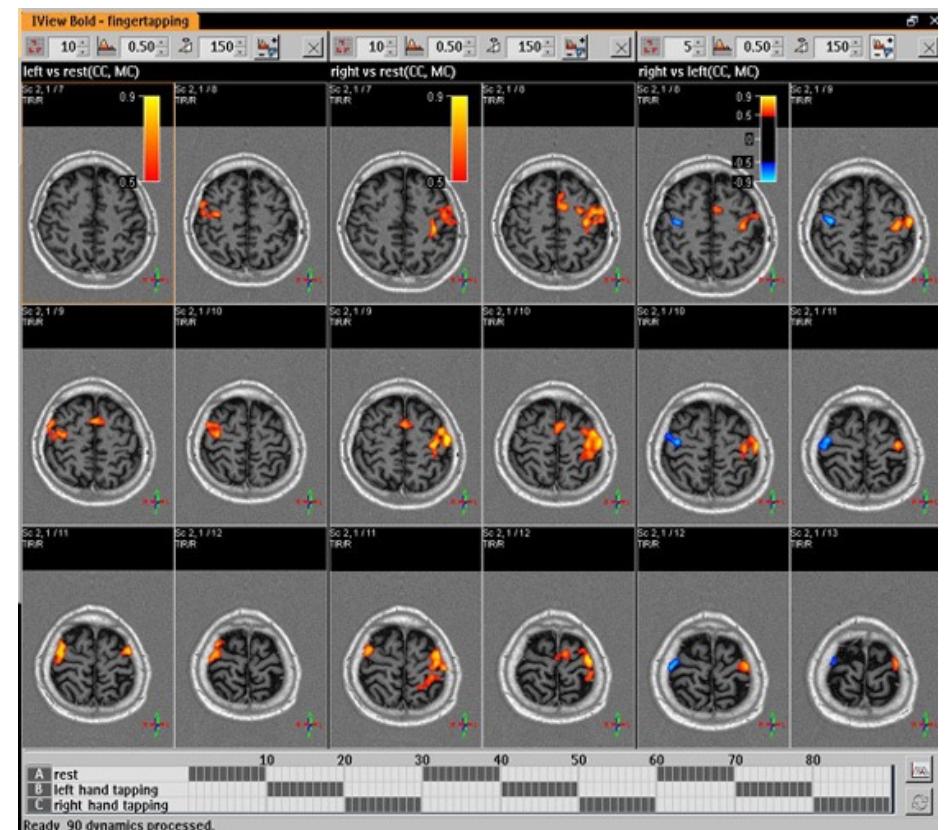
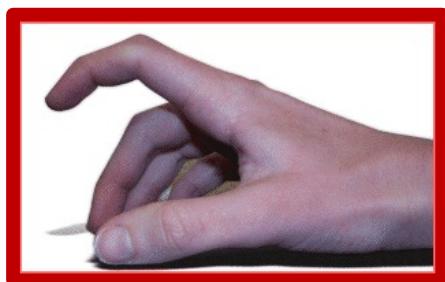
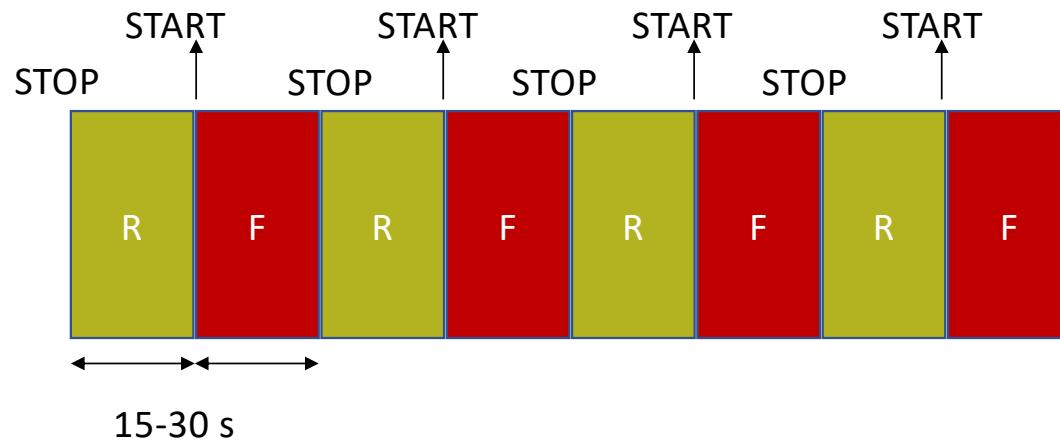
The power of an fMRI study depends on

- a. The difference between the active and rest task conditions
- b. The number of trials (events)
- c. The duration of the trials (events)
- d. The total length of the experiment
- e. The TR of the fMRI scan

Examples of fMRI paradigms



Example 1: finger tapping -> motor cortex



Stathopoulos et al. Preoperative functional MRI of motor and sensory cortices: how imaging can save vital functions.
Review Article - Imaging in Medicine (2012) Volume 4, Issue 1

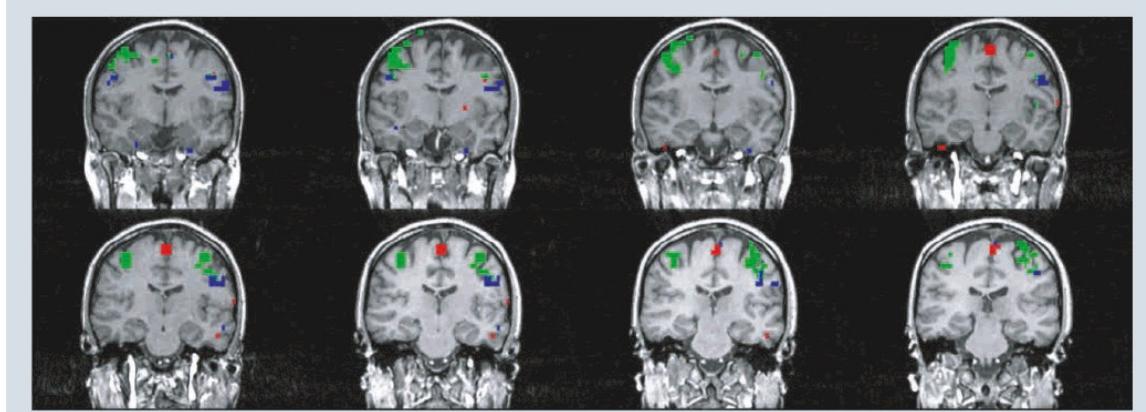


Figure 2. Localization of the different parts of the motor gyrus using functional MRI. The location of the foot homunculus is seen in red, the hand in green and face/tongue in blue, respectively.

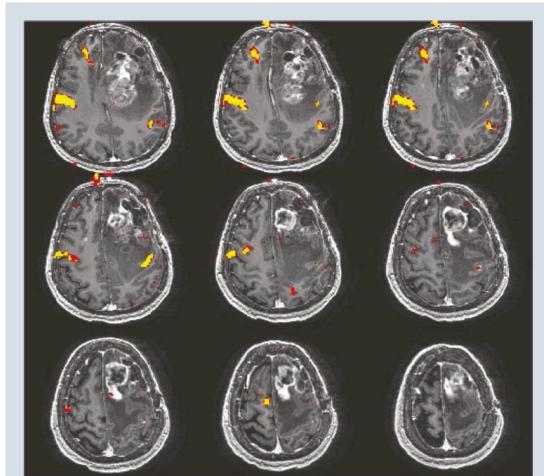


Figure 4. Left frontal glioblastoma. Notwithstanding the presence of motion artifact, prior surgery and abnormal tumor neovasculation the location of the ipsilateral motor gyrus is clearly depicted by functional MRI. The signal activation outside the brain is probably caused by motion artifact.

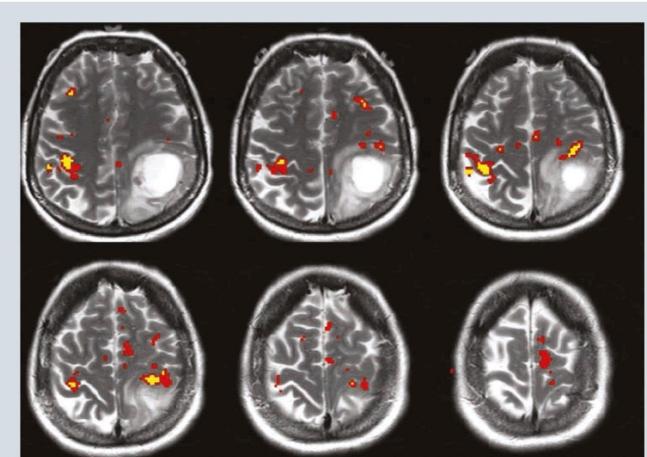


Figure 3. Patient with a left parietal glioblastoma. The patient's motor function was significantly compromised, which precluded the use of an active motor paradigm. Nevertheless, the location of the precentral (motor) gyrus could be deduced using a passive sensory functional MRI paradigm, which did not include any activity by the patient.

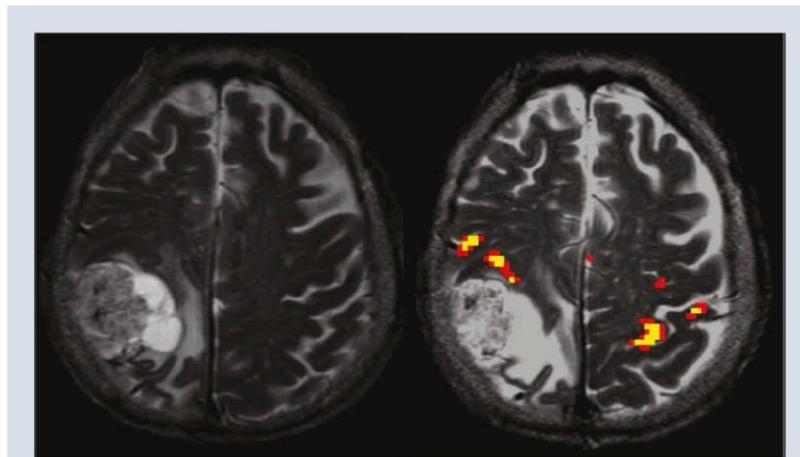
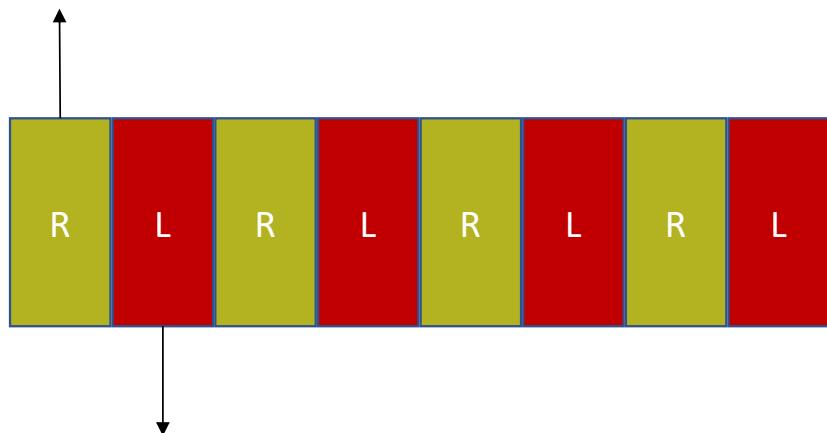


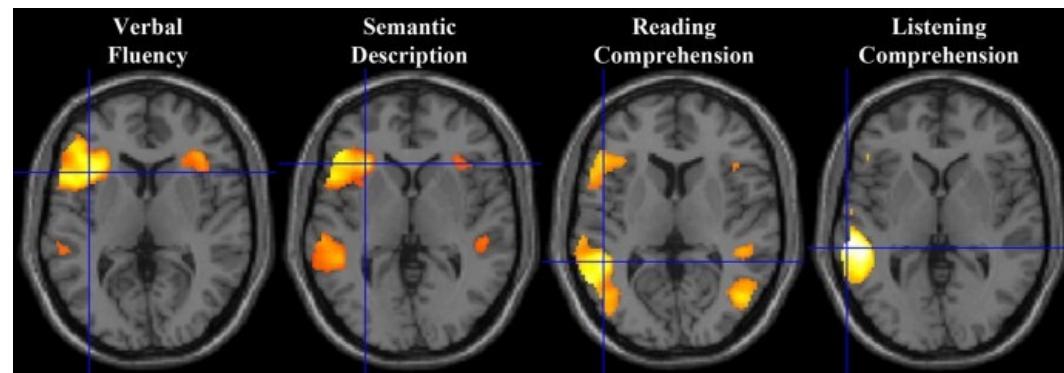
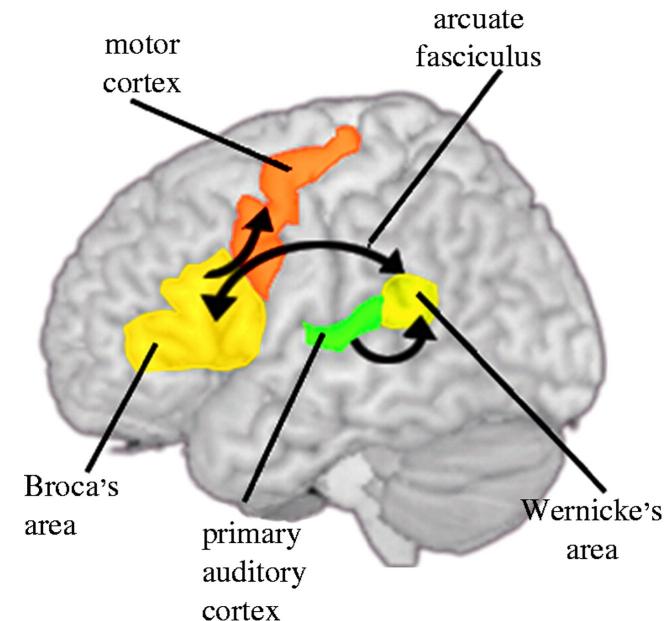
Figure 1. Glioblastoma of the right parietal lobe. The large tumor displaces the normal anatomy, making identification of the precentral (motor) gyrus difficult or impossible. Functional MRI clearly identifies the motor gyrus (yellow and red dots) and the relationship to the tumor.

Example 2: Language -> Broca and Wernicke areas

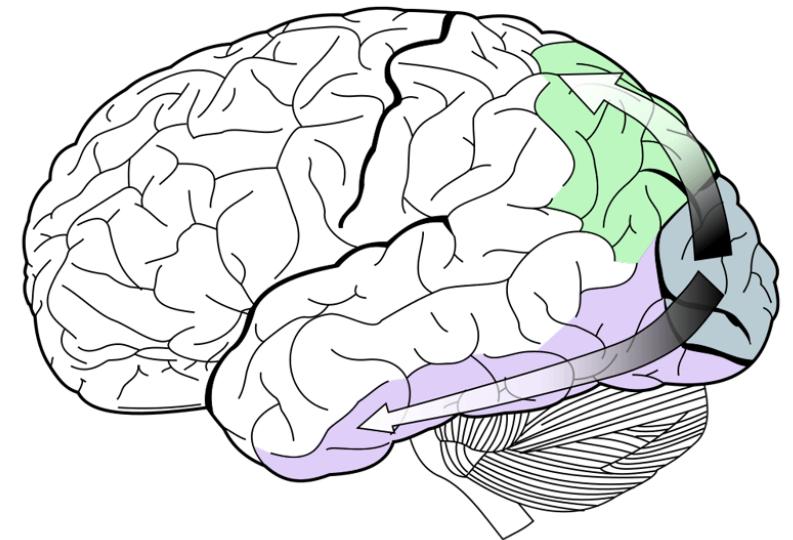
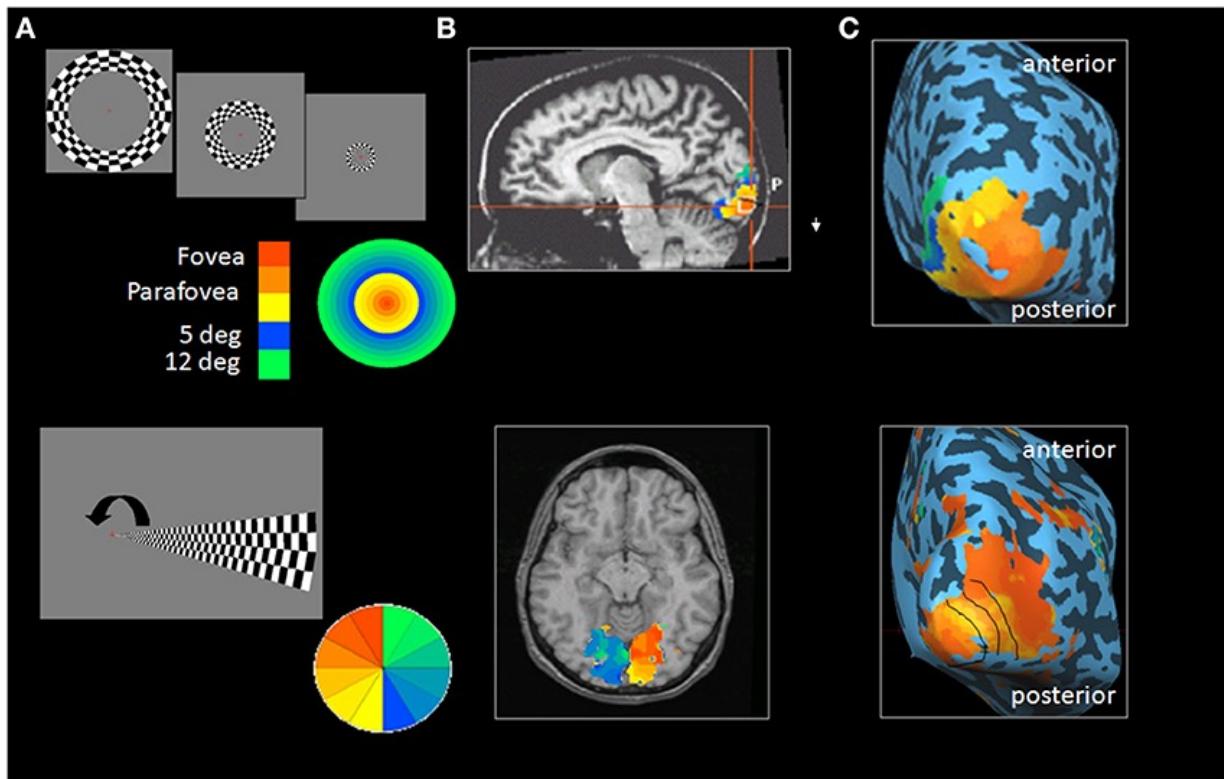
- Rest
- Non-existing words



- Categories -> instruction: "Sports"
- Sentences -> instruction: "Tool used for writing"
- Words -> instruction: "Ball"

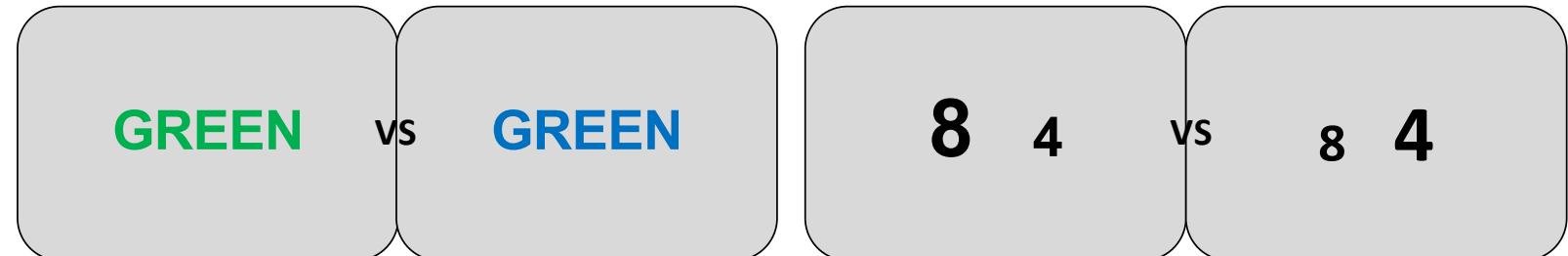


Example 3: The visual cortex

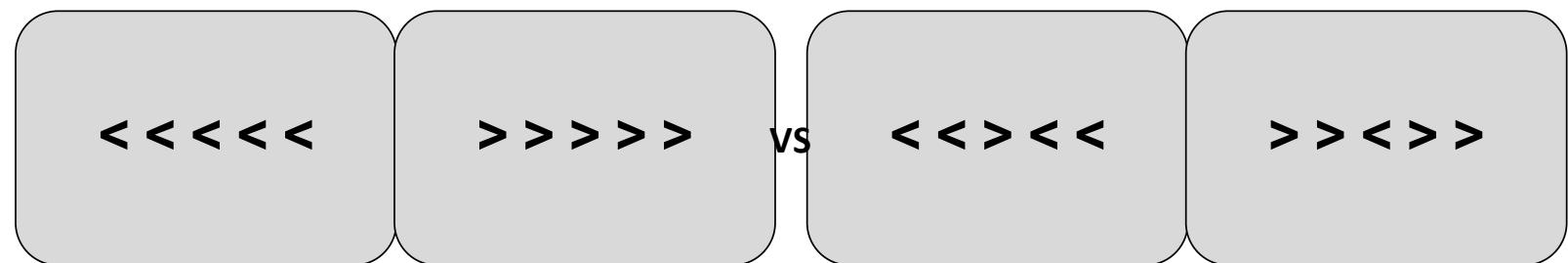


Examples of cognitive tasks

STROOP tasks



FLANKER task



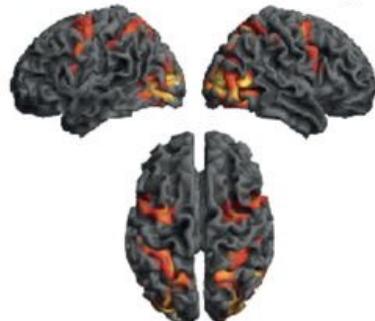
Discriminate
emotional
expressions



Examples of cognitive tasks

A. Working memory

Working memory
Left Right



Control



0 10

0 10

B. Switching

Switch



Stay



0 15

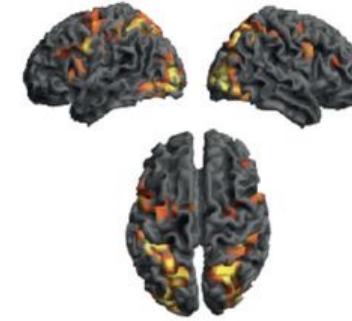
0 10

C. Planning

Tower of London



Control



0 11

0 11

D. Inhibition

Incongruent



Congruent



0 10

0 10

fMRI processing tutorial:

Audiovisual Valence Congruence

Task paradigm: Audiovisual Valence Congruence

What you see has the same valence (emotion) as what you hear (congruent)

Versus

What you see has the opposite valence (emotion) as what you hear (incongruent)
for positive versus negative stimuli



2x2 design: (congruent - incongruent) x (positive - negative)

Visual stimuli (video) + Auditory stimuli (music)

Stimulation as individual events (3s long)

4 conditions:

1. Visual positive + Auditory positive
2. Visual positive + Auditory Negative
3. Visual negative + Auditory positive
4. Visual negative + Auditory negative

Congruent trials

Incongruent trials

12 trials / run / condition -> 48 trials / run

8 catch trials (no stimulus, but responses recorded -> attention test)

20 subjects (all healthy adult volunteers)



Positive valence

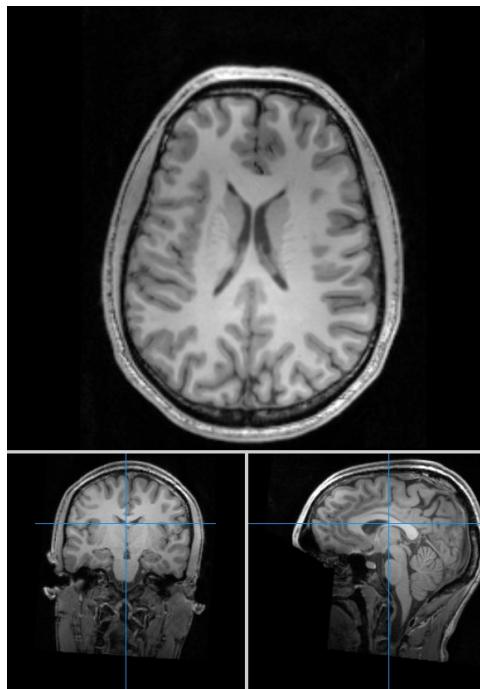


Negative valence

Scan protocol (Siemens 3T)

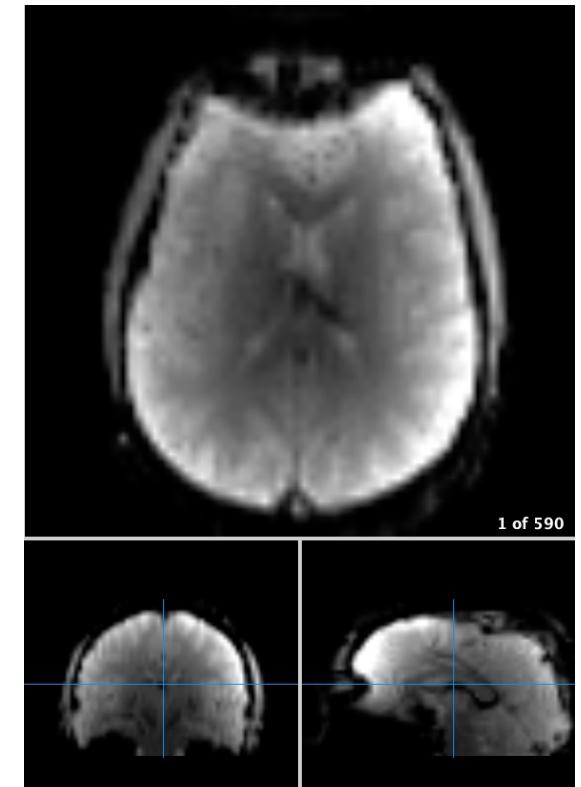
T1 weighted anatomical scan

- 3D TGE (MPRAGE) (sagittal slices)
- Scan volume: 192 x 256 x 256 mm
- Matrix: 192 x 256 x 256
- Voxel dimensions: 1 x 1 x 1 mm



fMRI scan

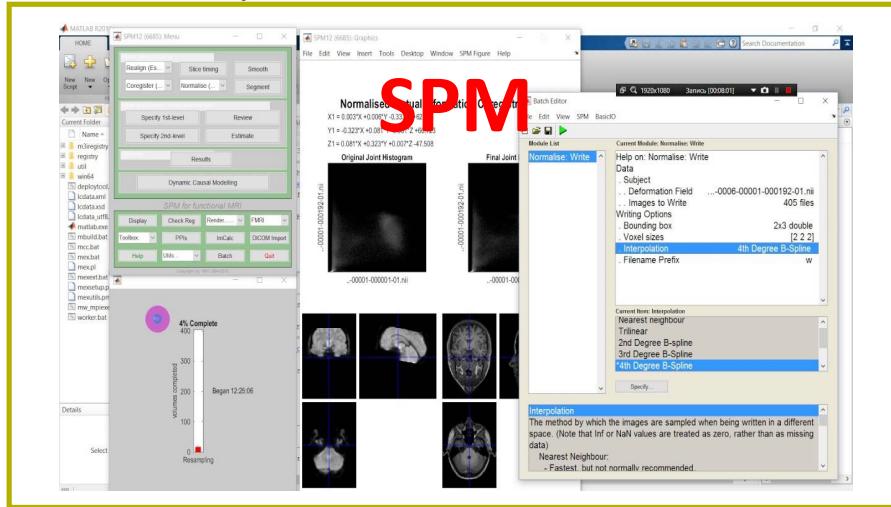
- GE-EPI (axial slices)
- Scan volume: 202 x 256 x 256 mm
- Matrix: 70 x 70 x 40
- Voxel dimensions: 3 x 3 x 3 mm
- Temporal resolution: 1s
- 590 dynamics
- HyperBand: 4



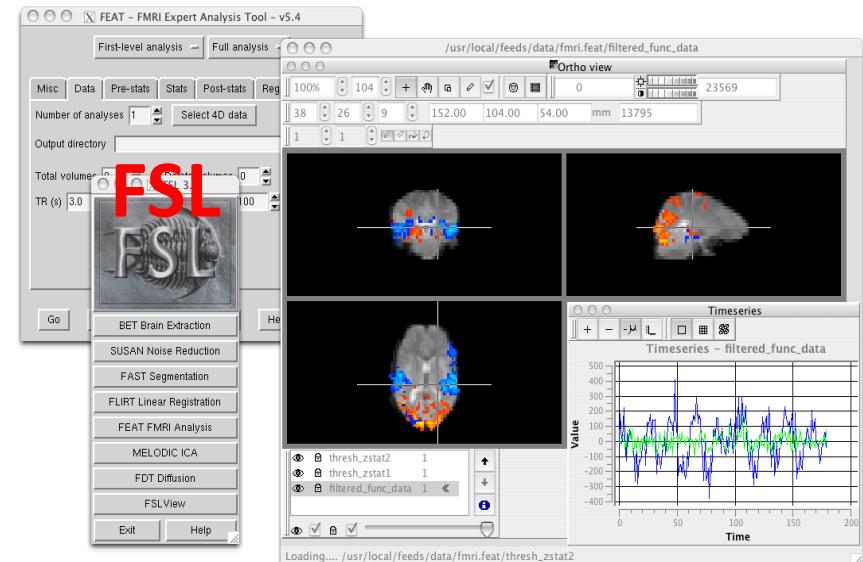
Fieldmap scan

- 2x GE-EPI (axial slices)
- Scan volume: 202 x 256 x 256 mm
- Matrix: 70 x 70 x 40
- Voxel dimensions: 3 x 3 x 3 mm
- HyperBand: 4
- Phase encoding direction scan 1: AP
- Phase encoding direction scan 2: PA

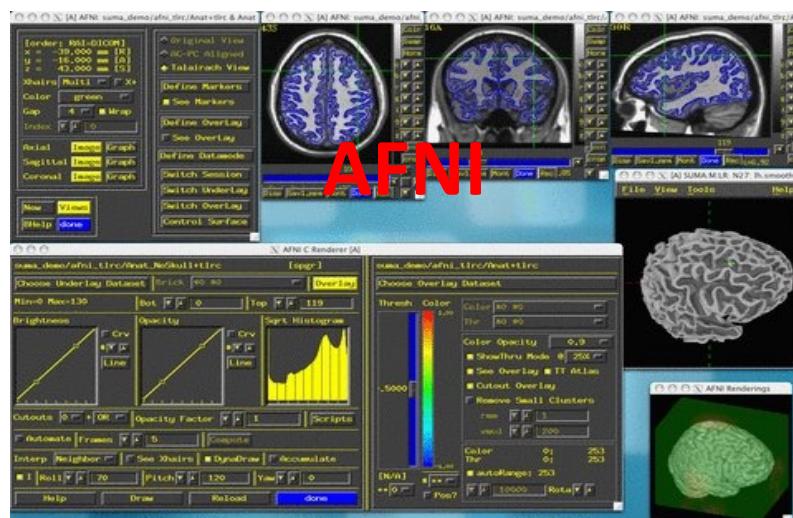
fMRI analysis software



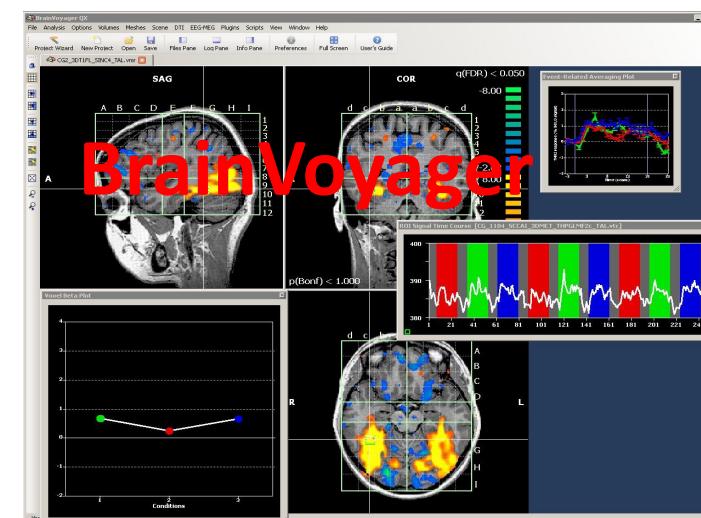
SPM



FSL

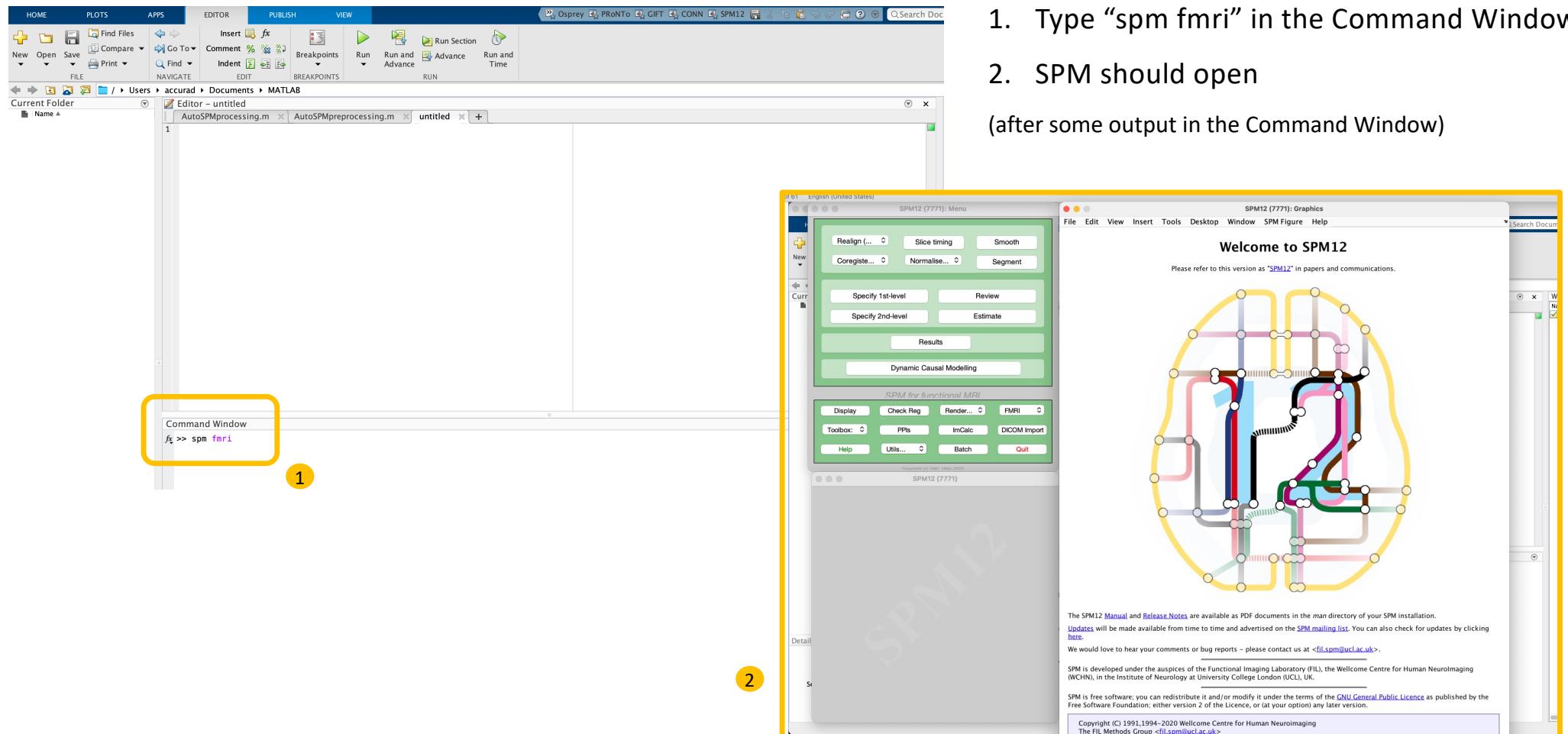


AFNI



BrainVoyager

Starting SPM12

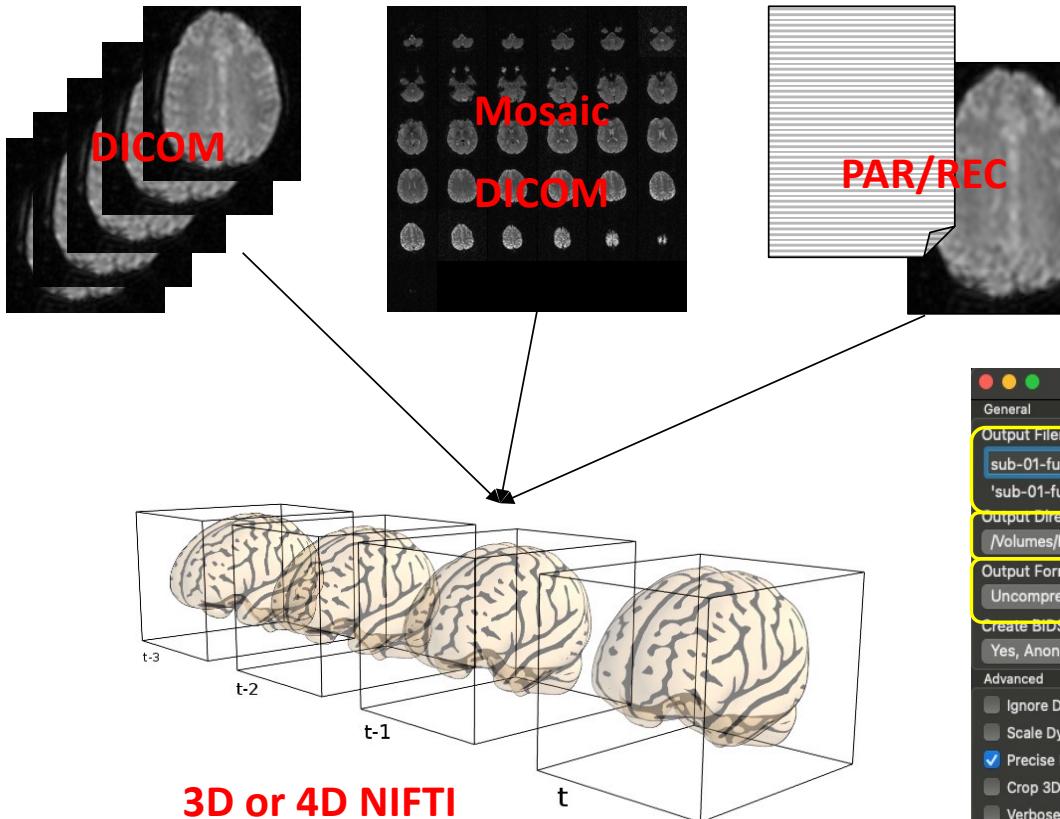


In Matlab

1. Type "spm fmri" in the Command Window
2. SPM should open
(after some output in the Command Window)

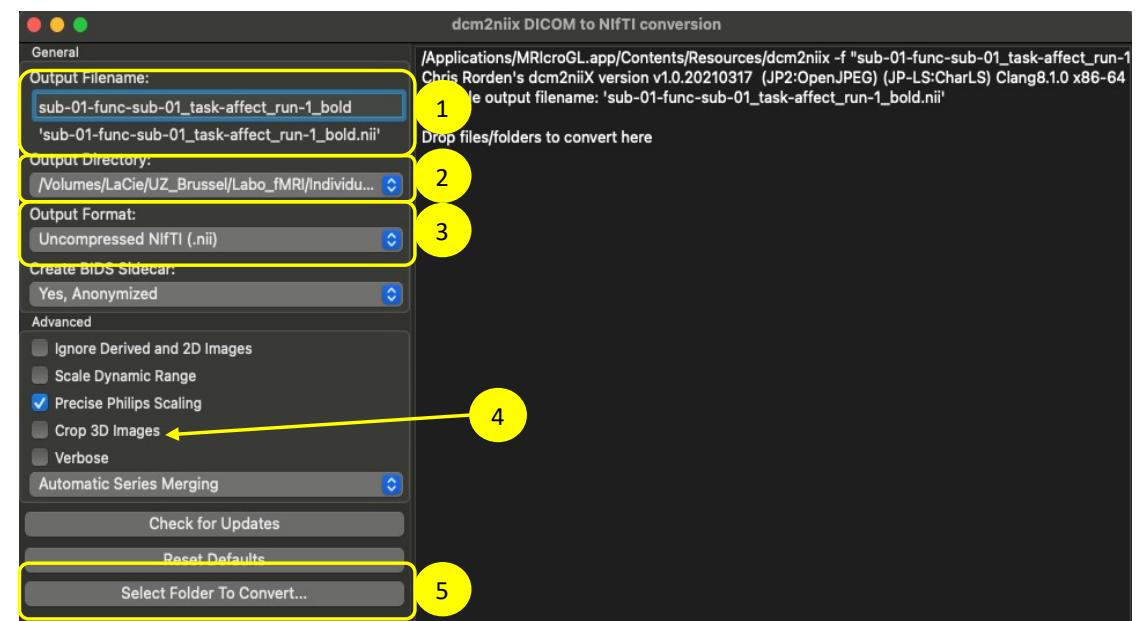
Preparing the fMRI data

Converting data into NIFTI format

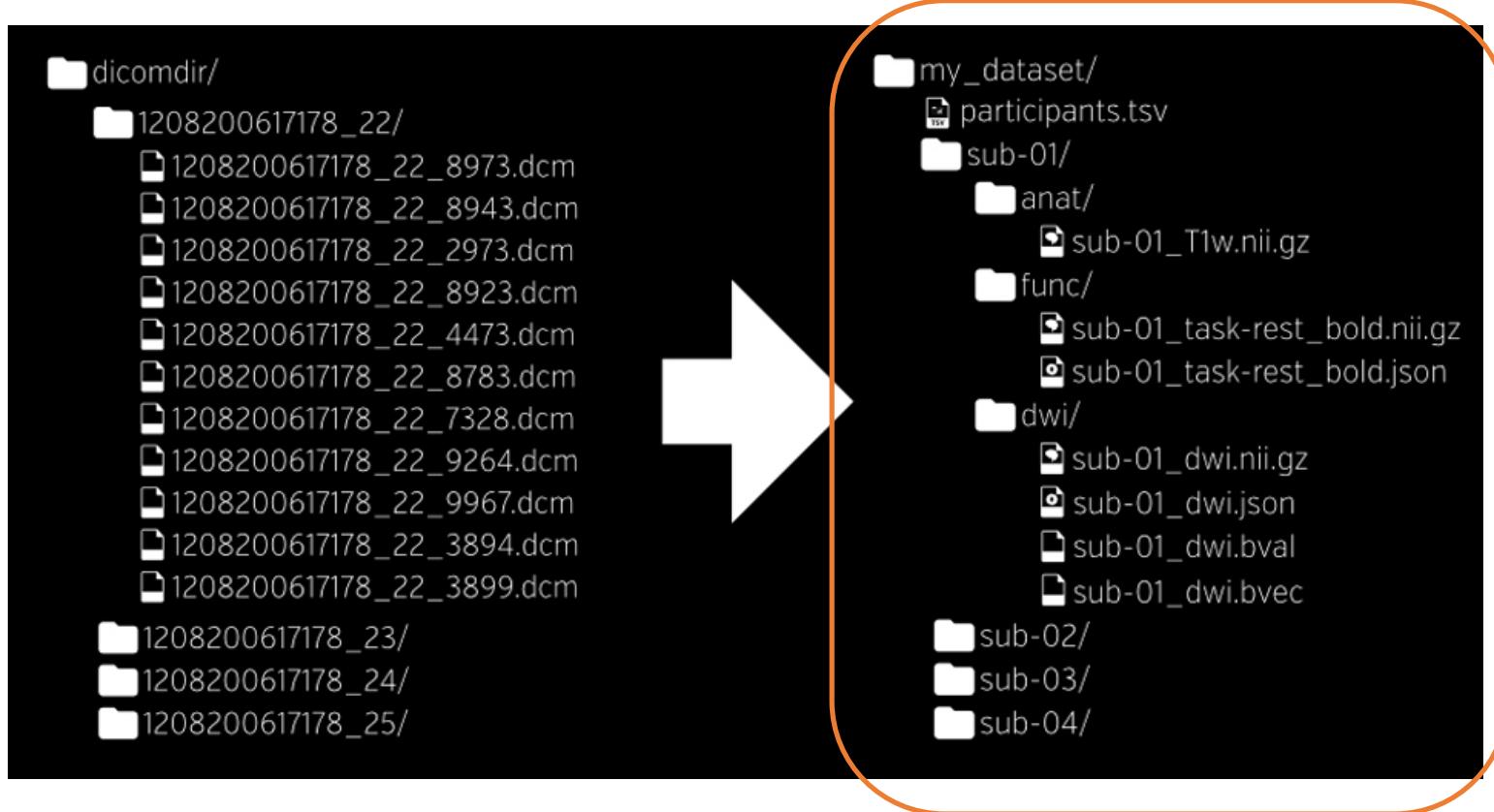


Using dcm2nix in MRIcroGL:

1. Set the output filename
2. Select the output data directory
3. Select Uncompressed NIFTI (.nii)
4. For the 3D T1 scan: Select 'Crop 3D Image'
5. Select the dicom data folder

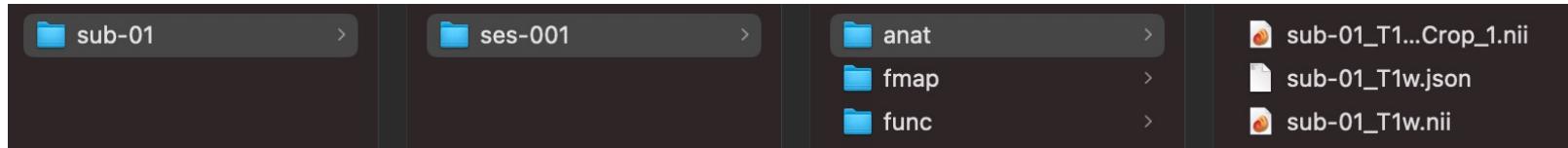


Organize data according to the BIDS standard



The individual data for subject 1

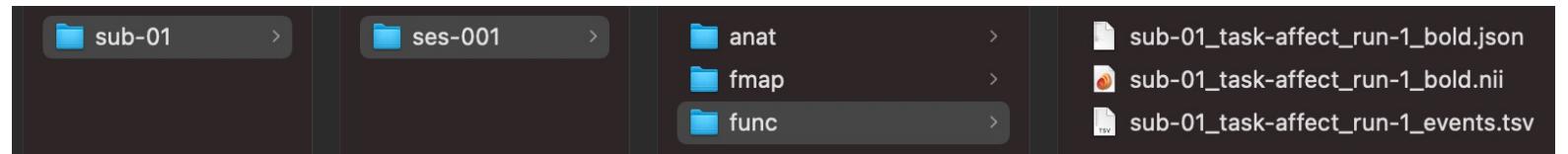
T1 weighted anatomical scan



Fieldmap scans



fMRI scan



.json file = text file with the fMRI scan parameters

.nii file = the actual image data

Events.tsv file = text file with the onsets and duration of the task conditions

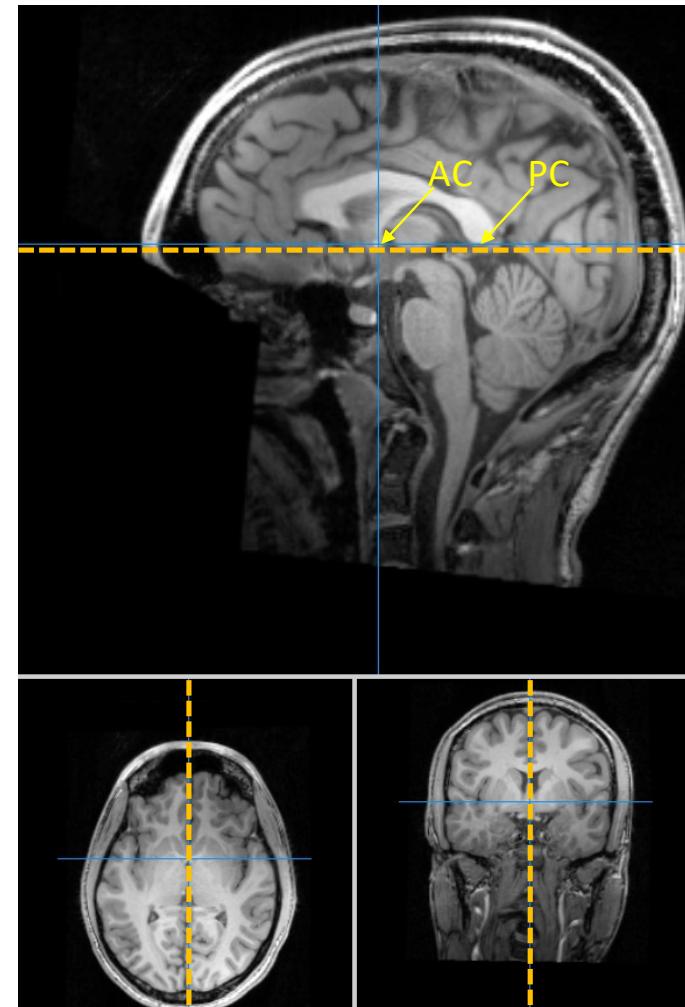
Preprocessing the data

Step 1: setting the image origin and orientation

To improve the image registration, segmentation and normalization steps, all scans should be set with the origin in the anterior commissure (AC) and oriented to put the head straight in all orientations.

Reference axes:

1. AC-PC line
2. Space between the left and rights hemispheres



Step 1: setting the image origin and orientation

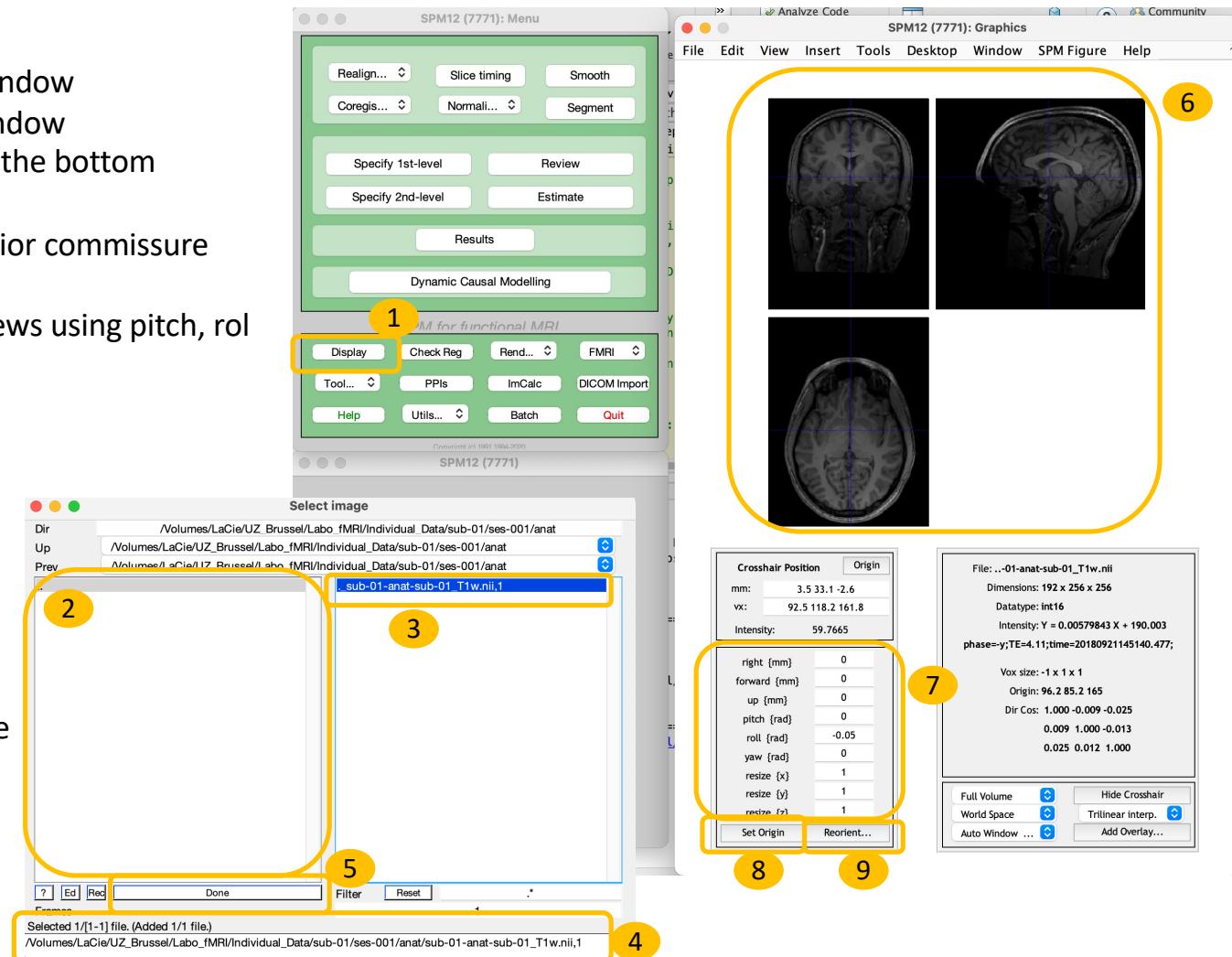
1. In SPM Menu: click "Display"
2. In Select Image: go to the data folder in the left window
3. In Select Image: select the nifty file in the right window
4. In Select Image: the selected file should appear at the bottom
5. In Select Image: click "Done"
6. In Graphics Window: set the crosshair at the anterior commissure (AC)
7. In Graphics Window: set the head straight in all views using pitch, roll and yaw

(Step 7 and 8 are done interactively)

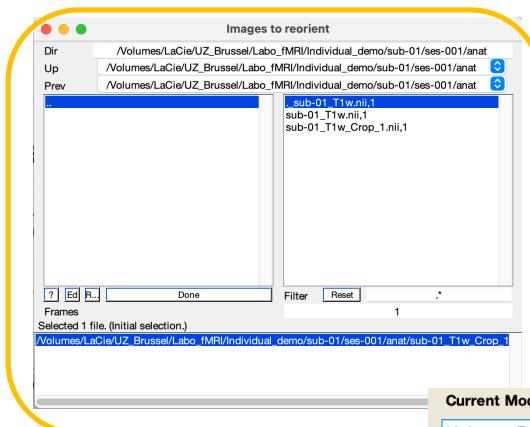
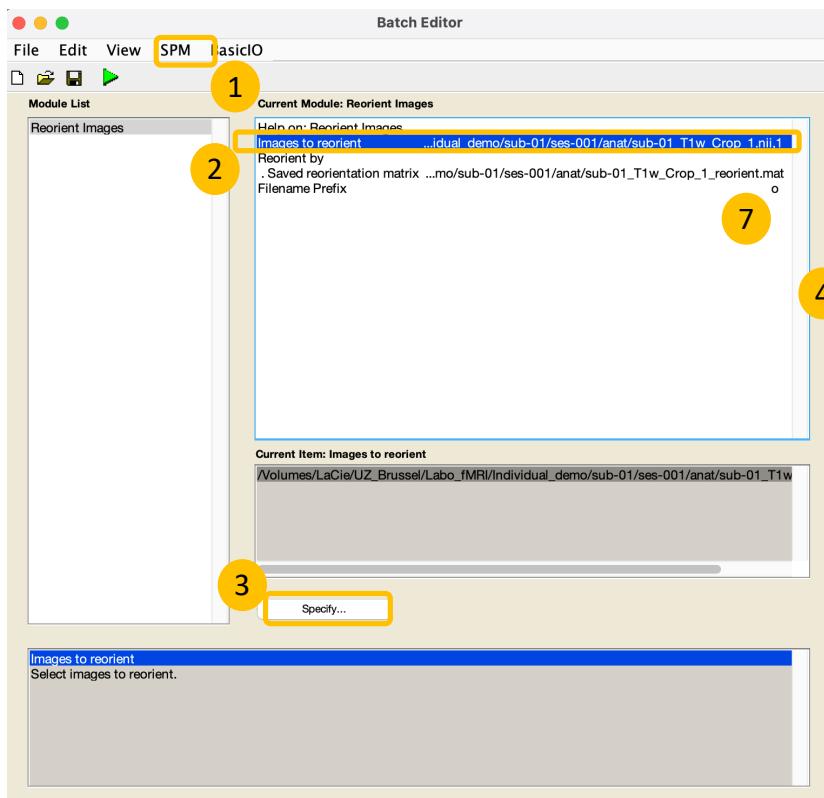
If the crosshair is at the AC and all orientations are ok:

8. In Graphics Window: click "Set Origin"
9. In Graphic Window: click "Reorient"
10. In Image(s) to reorient: deselect all files and click "Done"
8. In Save Matrix: click "Yes" and save the reorient.mat files inn the folder of the nifty file

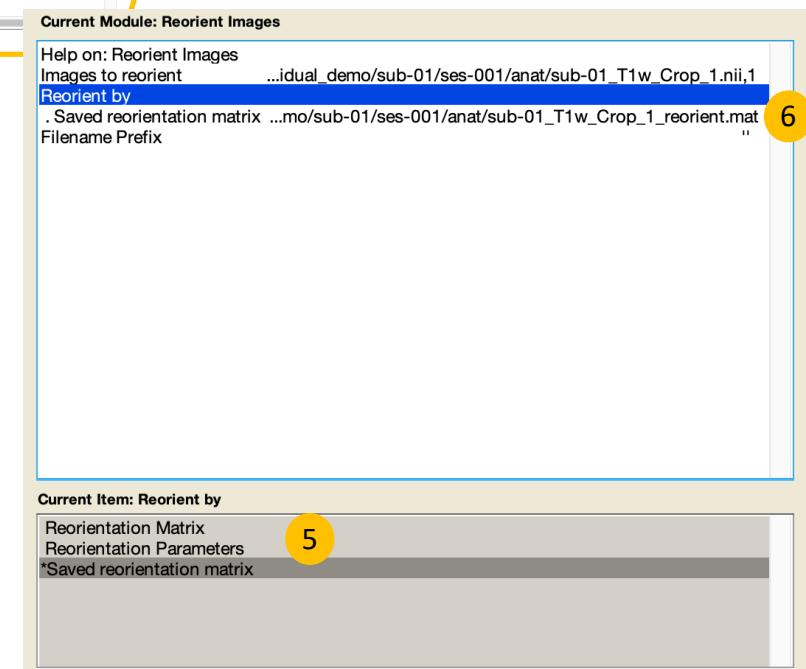
This step should be done separately for the anatomical scan, the fieldmap scans and the fMRI scan



Step 1: setting the image origin and orientation for the 3D T1 scan



Open the Batch Editor

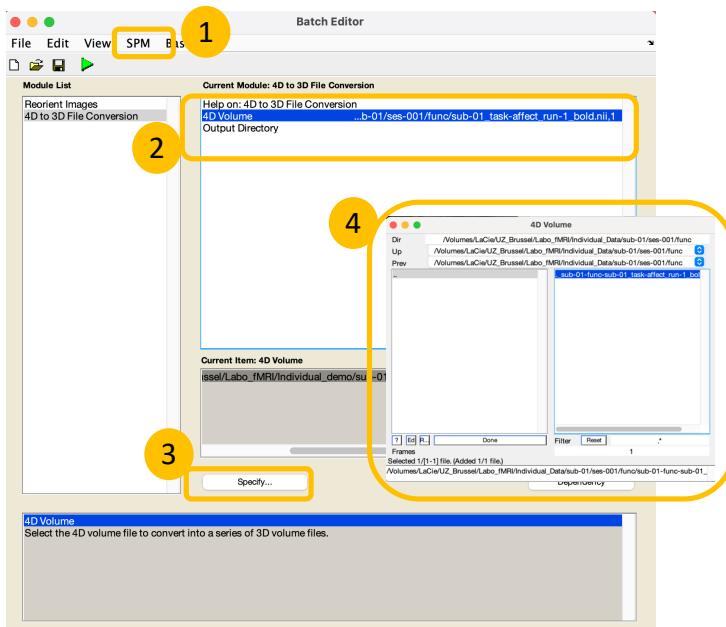


1. In the top Menus: select SPM -> Util -> Reorient Images
2. Select Images to reorient
3. Click "Specify..."
4. In the data selection window: select the anatomical scan (advisable the cropped version)
5. Reorient by: select 'Saved reorientation matrix'
6. Saved reorientation matrix: select the reorient.mat file for the anatomical scan

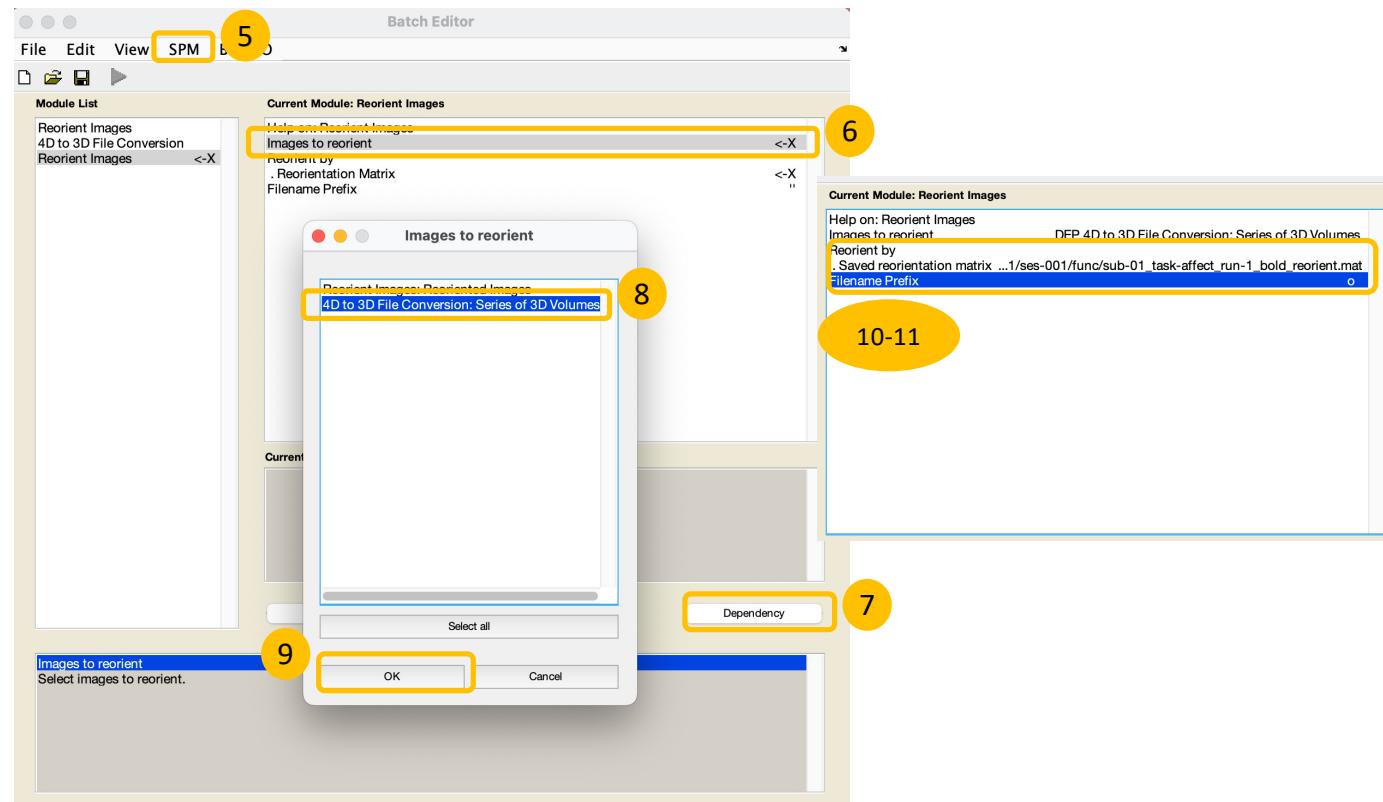
7. Optionally:
The orientation of the data will only change the orientation information in the header of the nifty file. Consequently, repeating the data processing multiple times can lead to wrong results. To overcome the overwriting of the original nifty file, and Filename Prefix for the reoriented data can be specified.

Step 1: setting the image origin and orientation for the func and fmap scans

4D to 3D conversion

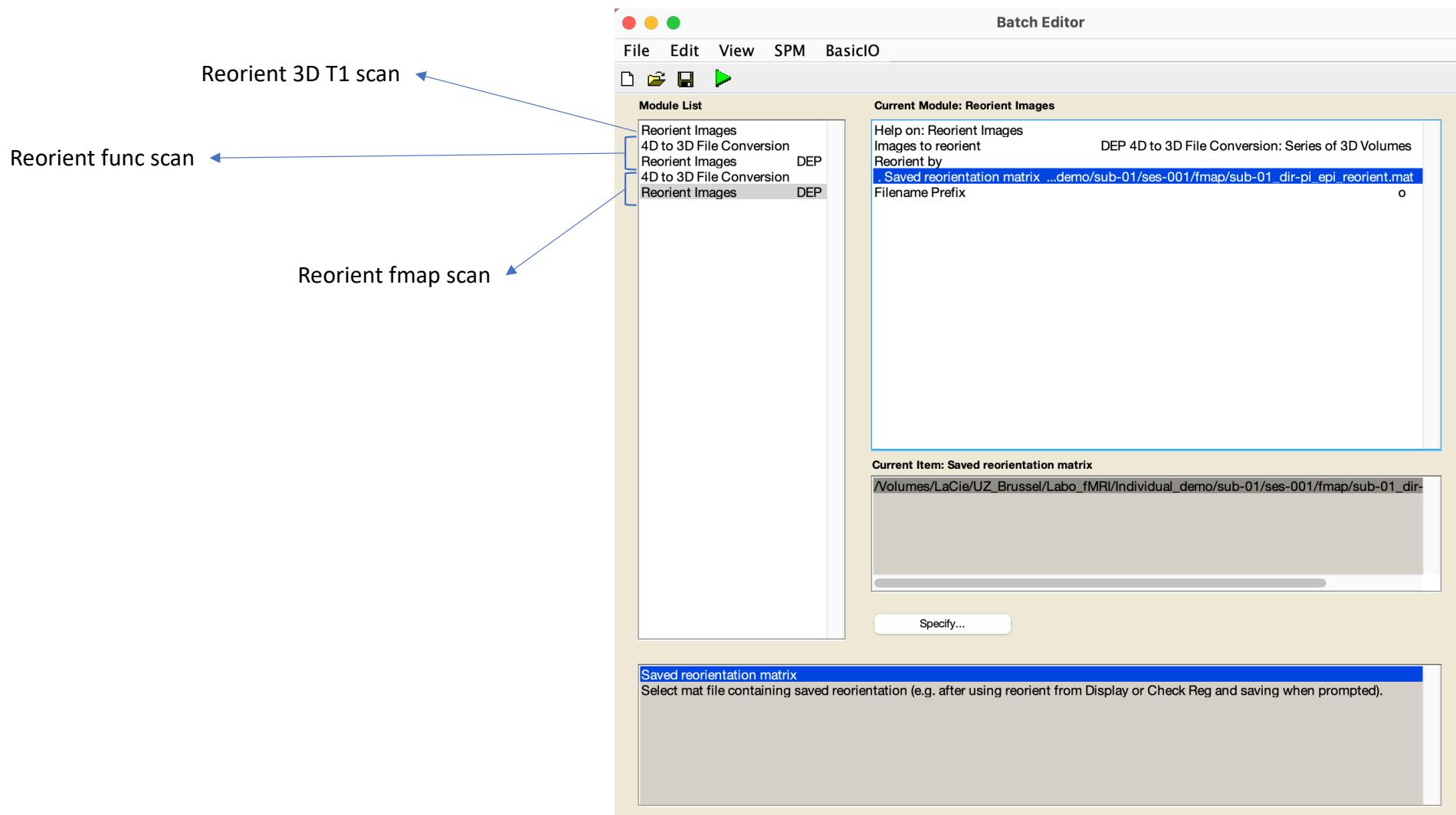


1. In the top Menus: select SPM -> Util -> 4D to 3D File Conversion
2. Select “4D Volume”
3. Click “Specify”
4. In the data selection window: select the fMRI scan

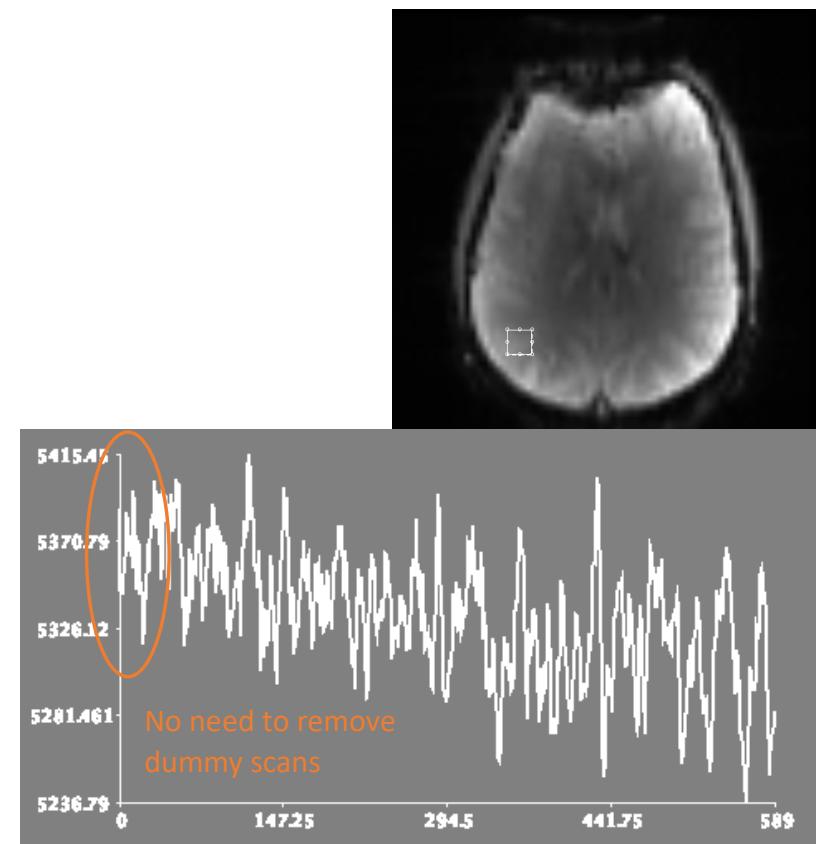
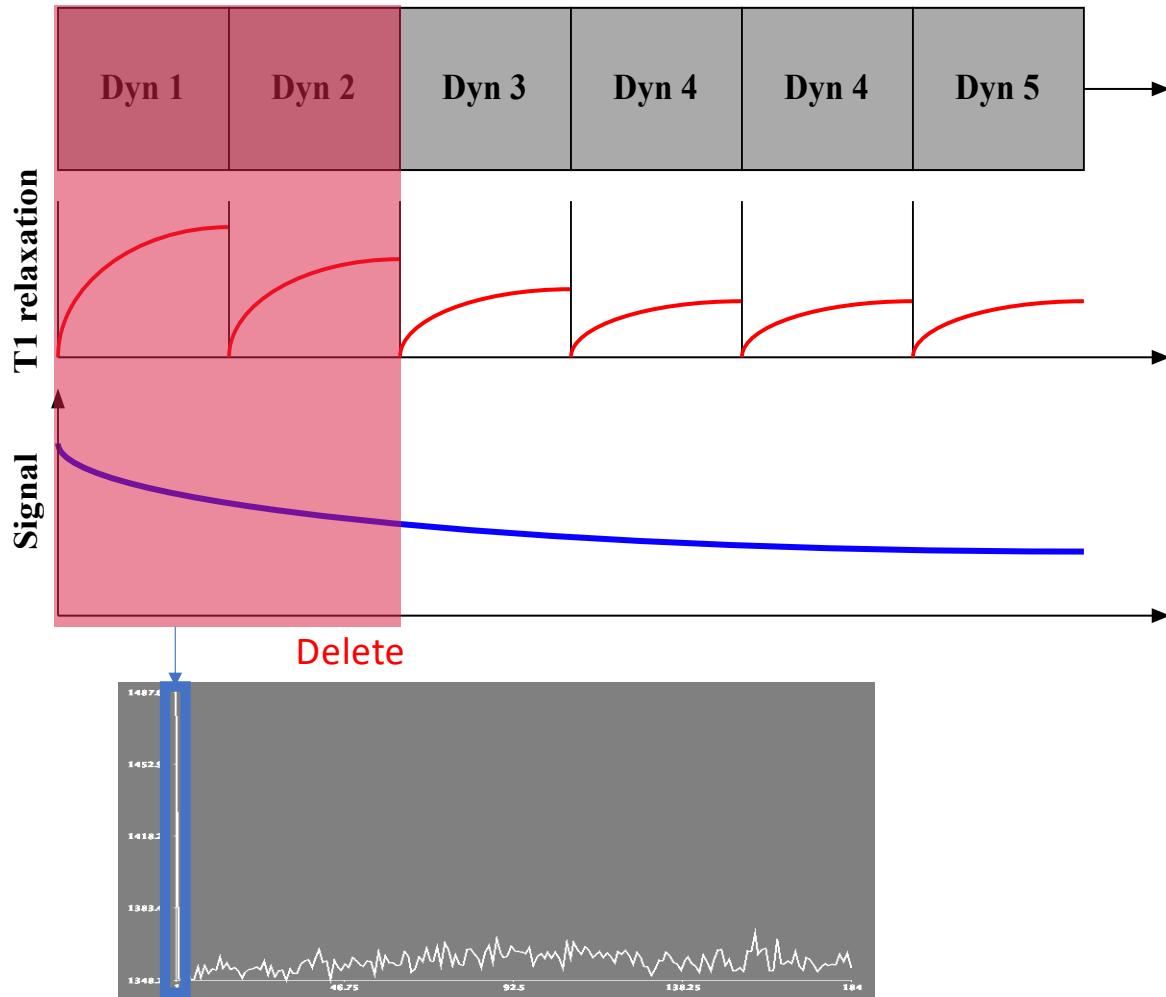


5. In the top Menus: select SPM -> Util -> Reorient Images
6. Select Images to reorient
7. Click “Dependency”
8. In the ‘Image to orient’ window: select ‘4D to 3D Conversion: Series of 3D Volumes’
9. Click ‘Ok’
10. Reorient by: select ‘Saved reorientation matrix’
11. Saved reorientation matrix: select the reorient.mat file for the func/fmap scan

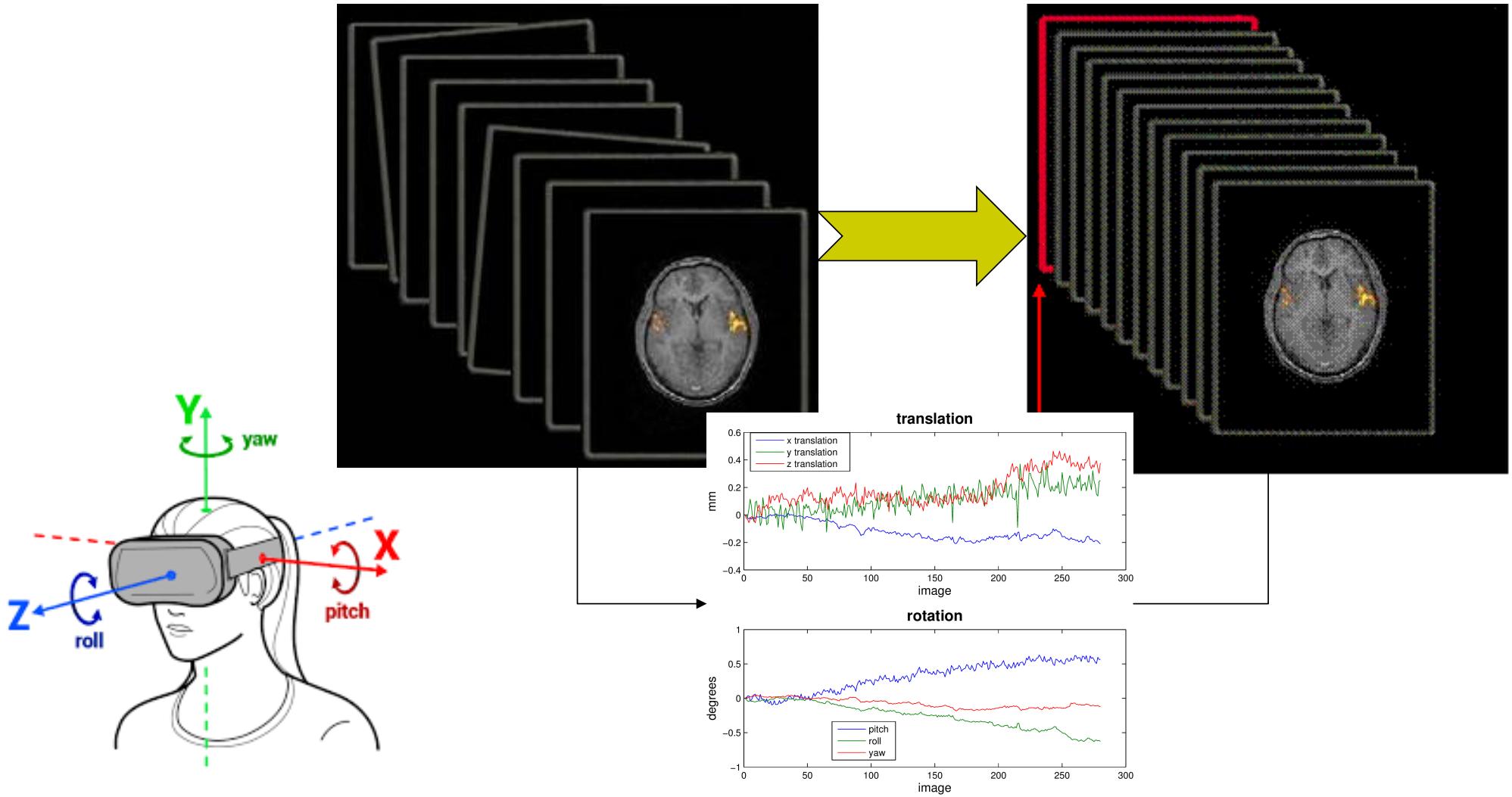
Step 1: setting the image origin and orientation



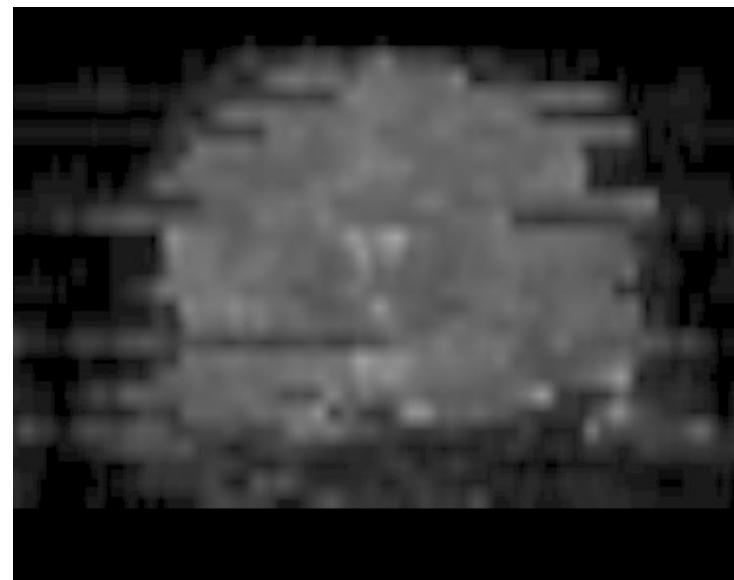
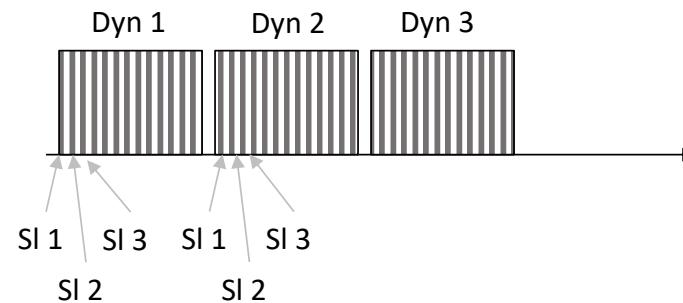
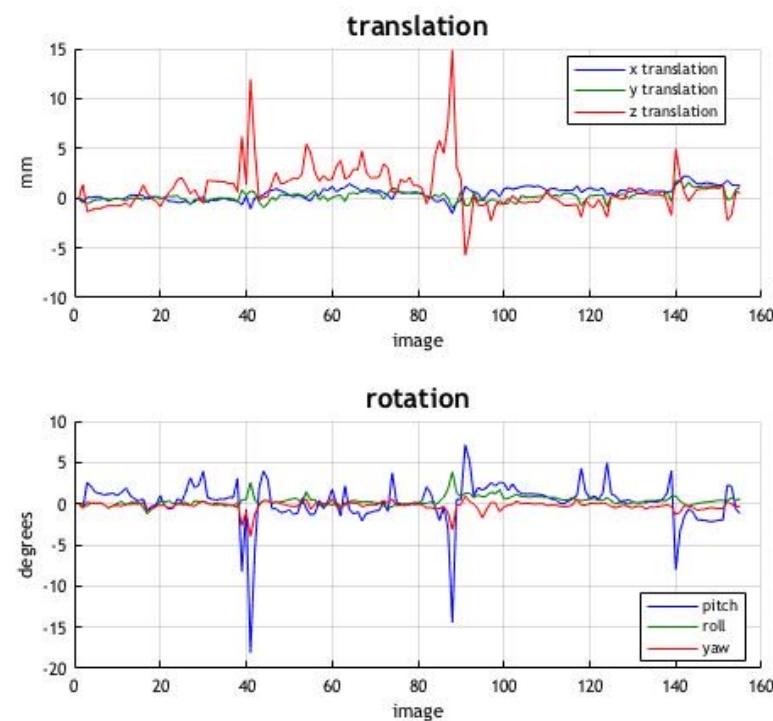
Step 2: Deleting the “dummy” scans



Step 3: Realignment: motion correction

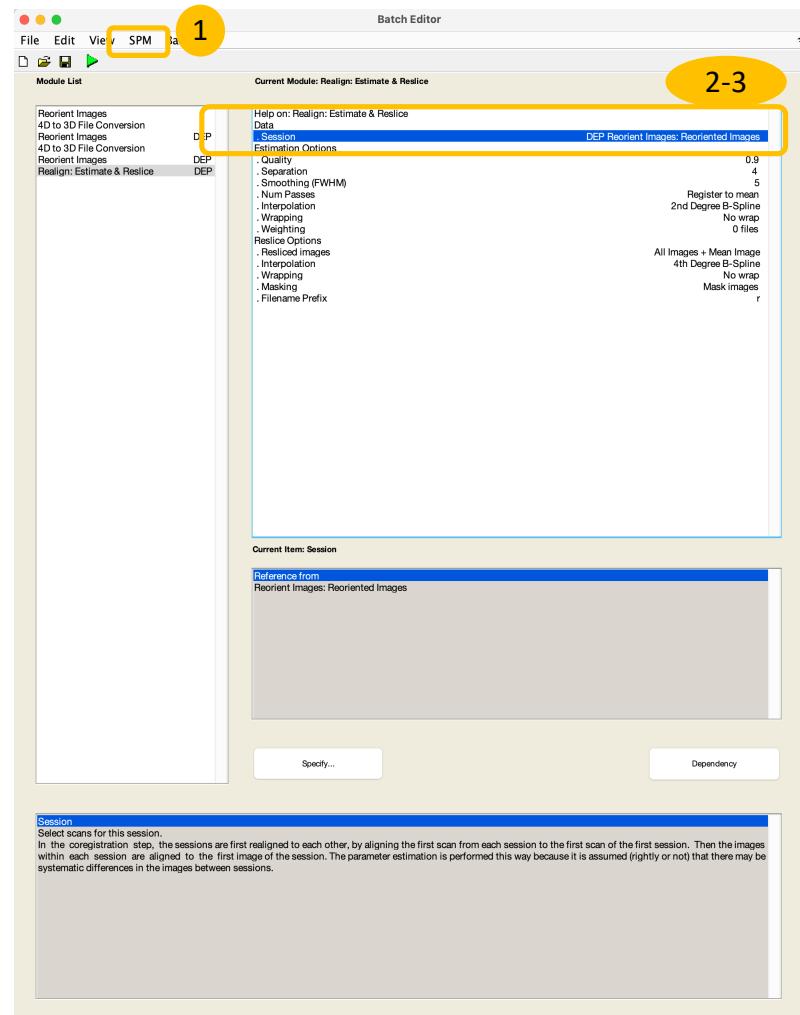


But ... if motion is too much ...

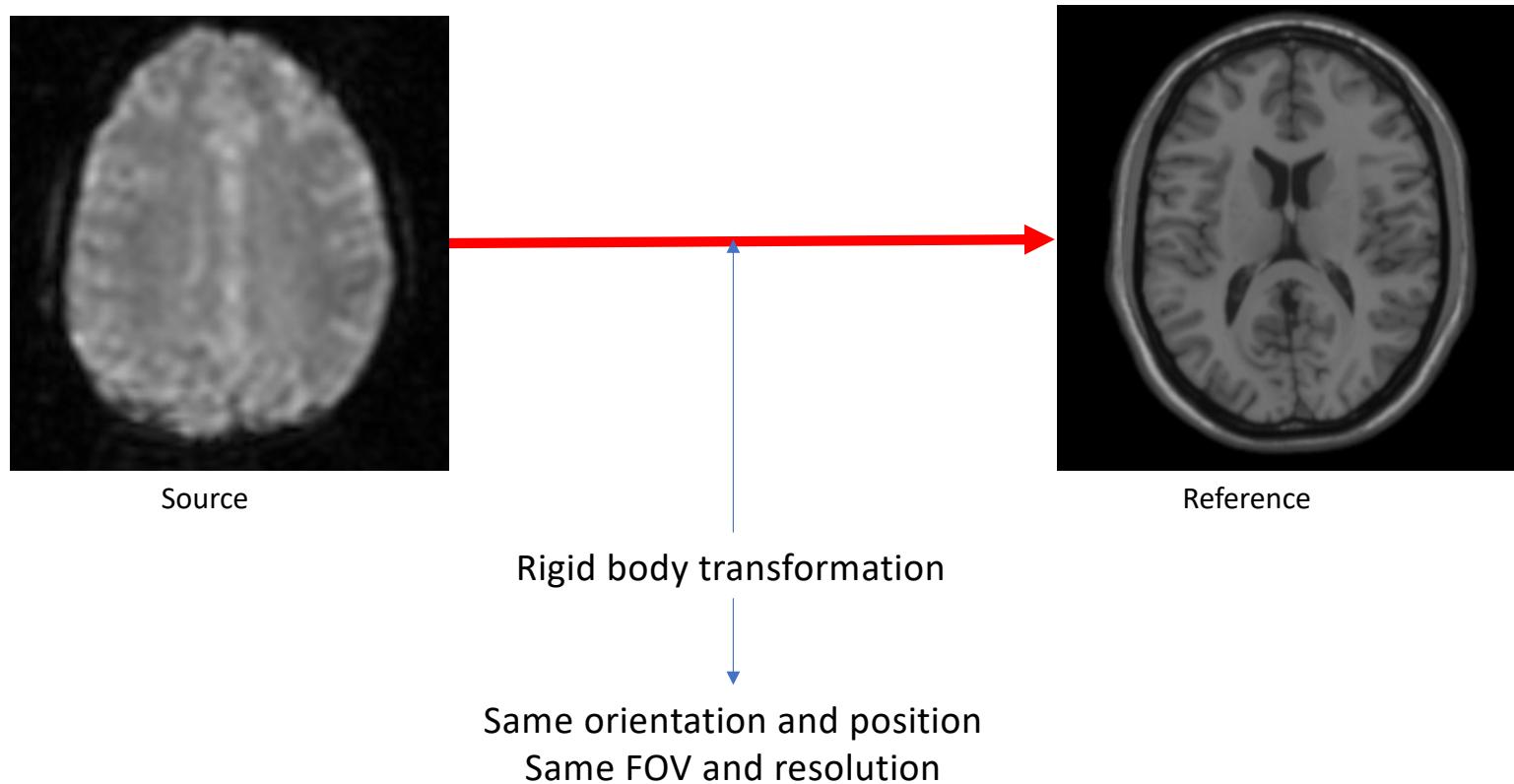


Step 3: Realignment: motion correction

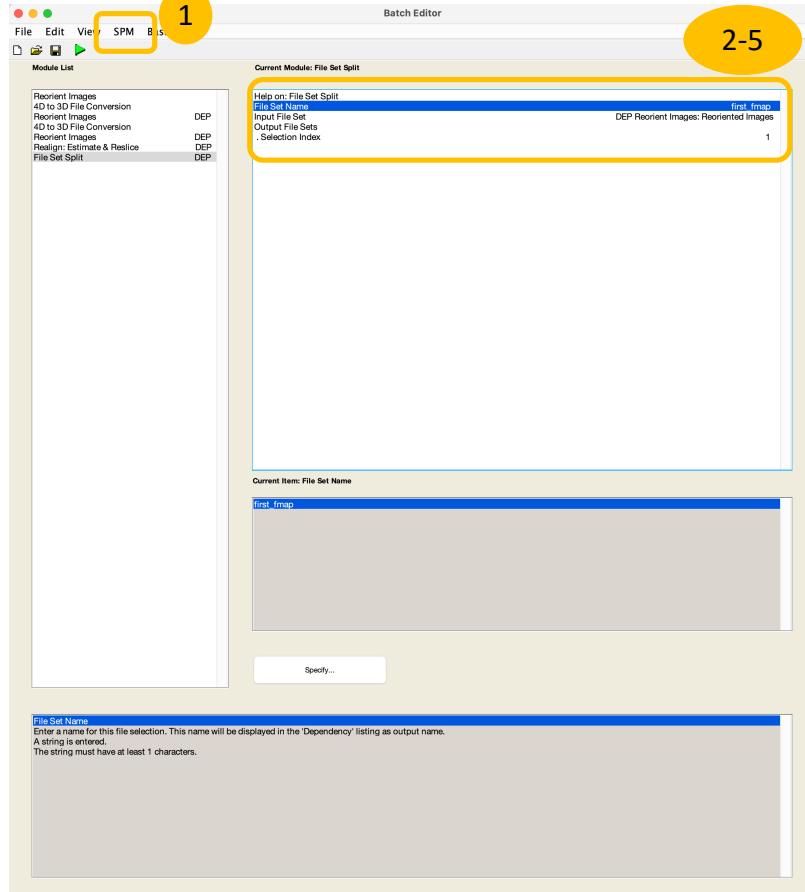
1. In the top menus: SPM -> Spatial -> Realign -> Realign: Estimate & Reslice
2. Data -> New: Session
3. Session: (using Dependency) -> Reoriented Images: Reoriented Images (from the func series!)



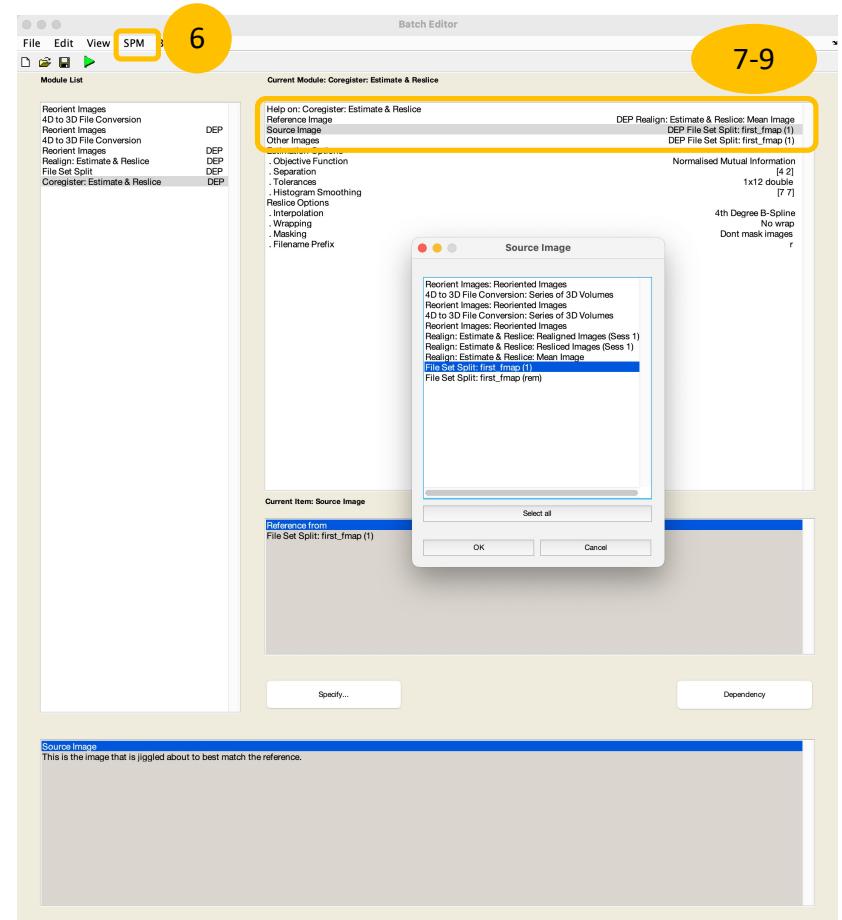
Step 4: Coregistration: within subject, between scans registration



Step 4: Coregistration: fmap to func

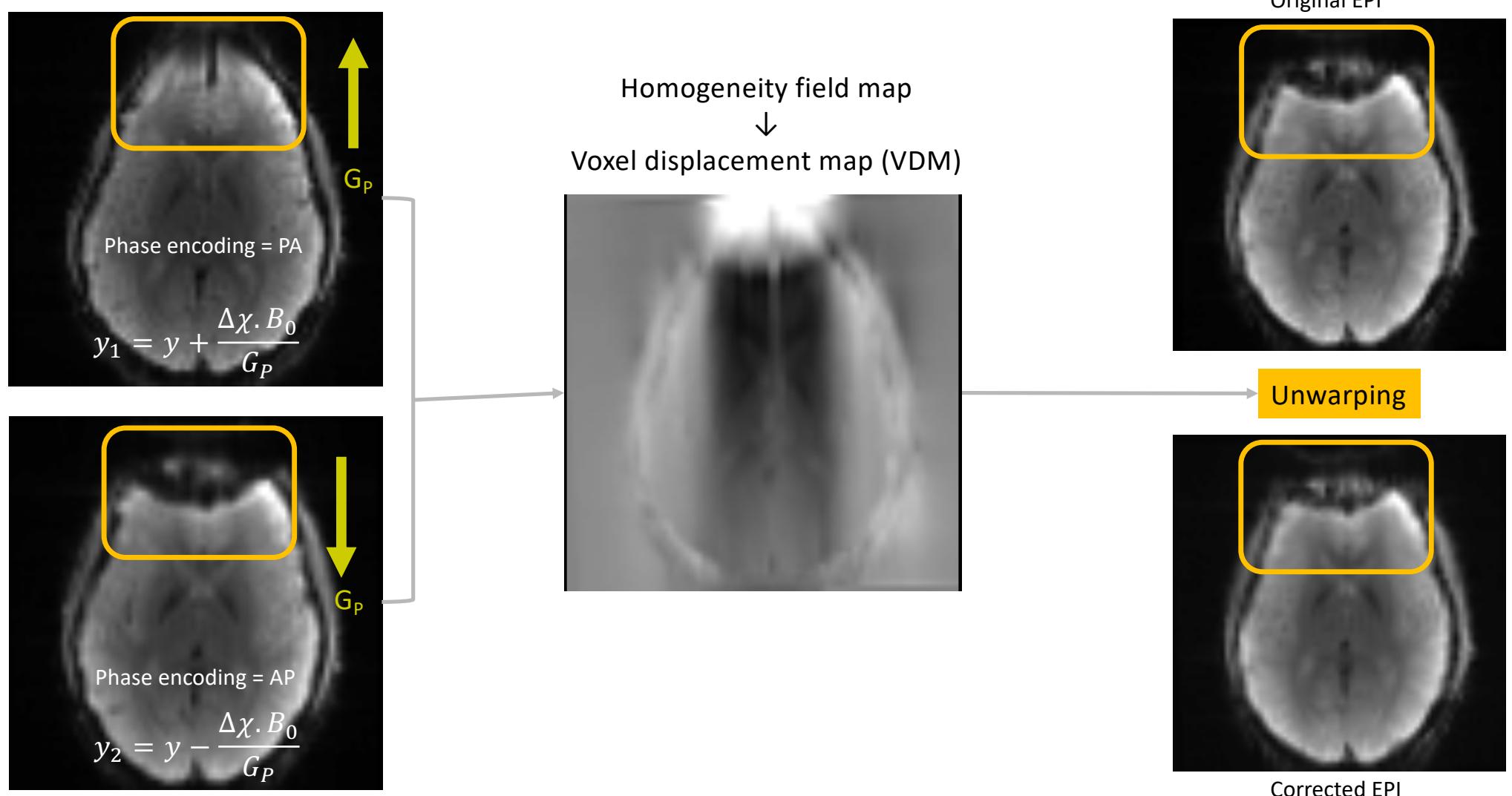


1. In the top Menus: select BasicIO -> File/Dir operations -> File Operations -> File Set Split
2. File Set Name: first_fmap
3. Input File Set: (using Dependency) Reorient Images: Reoriented Images (for the fmap data!)
4. Output File Sets: New: Selection Index
5. Selection Index: 1



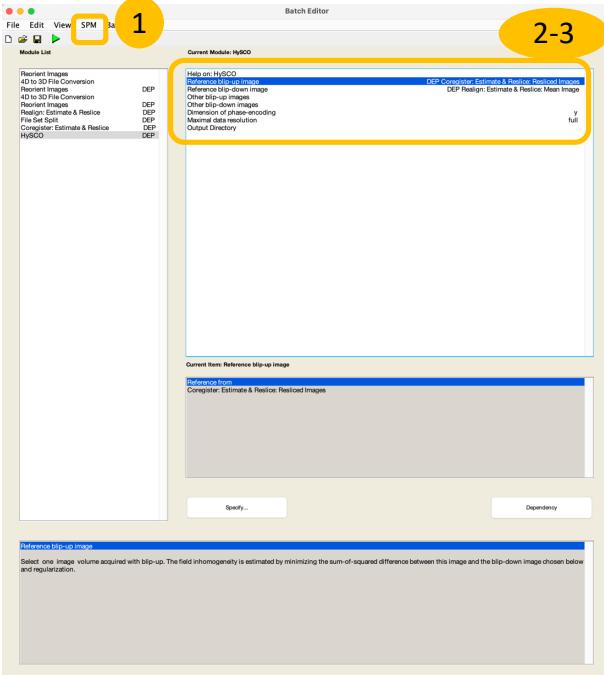
6. In the top Menus: select SPM -> Spatial -> Coregister -> Coregister: Estimate & Reslice
7. Reference Image: (using Dependency) Realign: Estimate & Reslice: Mean Image
8. Source Image: (using Dependency) File Set Split: fist_fmap (1)
9. Other Images: (using Dependency) File Set Split: fist_fmap (1)

Step 5: Correcting the geometric distortion

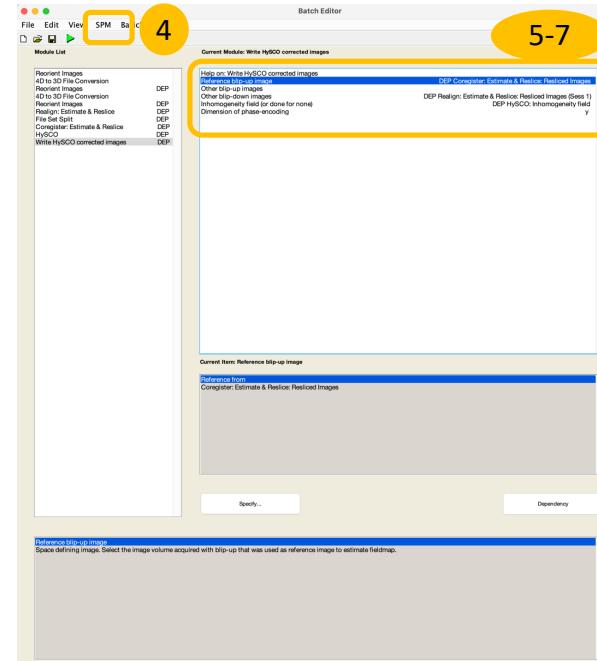


Step 5: Correcting the geometric distortion

Determine homogeneity map



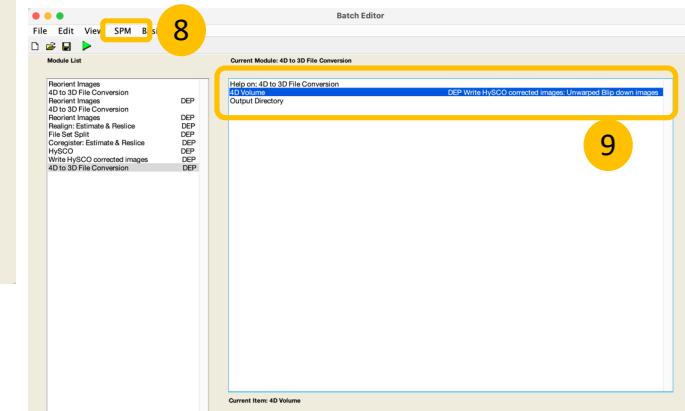
Apply to the func data



1. In the top Menus: select SPM -> Tools -> ACID Toolbox -> Pre-processing -> Choose HySCO options -> HySCO
2. Blip-up image (using Dependency): Coregister: Estimate & Resliced Images
3. Blip-down image (using Dependency): Realign: Estimate & Reslice: Mean Image

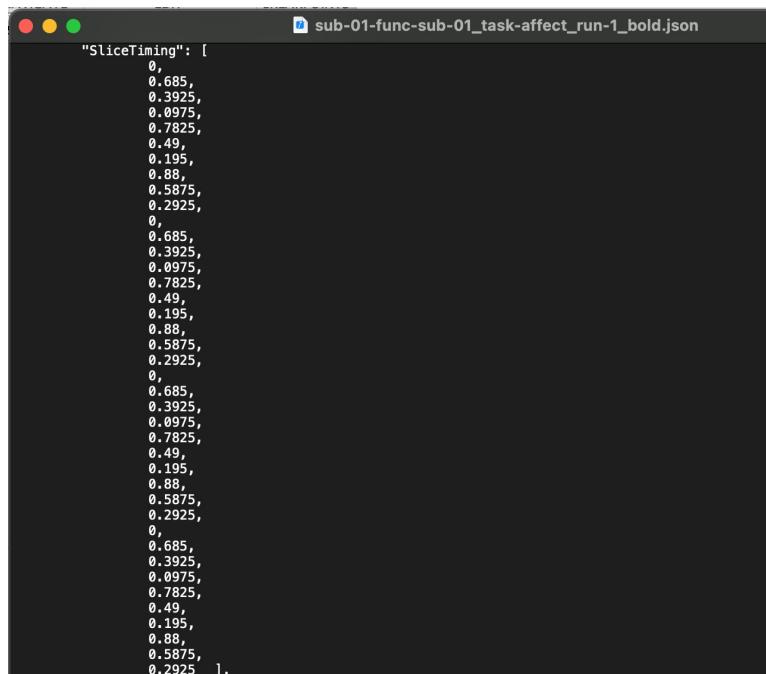
In the json file (for func and fmap):
 "PhaseEncodingDirection": "j" -> blip down
 "PhaseEncodingDirection": "j" -> blip up

4. In the top Menus: select SPM -> Tools -> ACID Toolbox -> Pre-processing -> Choose HySCO options -> Write HySCO corrected images
5. Reference blip-up image: (using dependency) Coregister: Estimate & Resliced Images
6. Other blip-down images: (using dependency) Realign: Estimate & Reslice: Resliced Images (Sess 1)
7. Inhomogeneity field (or done for none): (Using dependency) HyCO: Inhomogeneity field

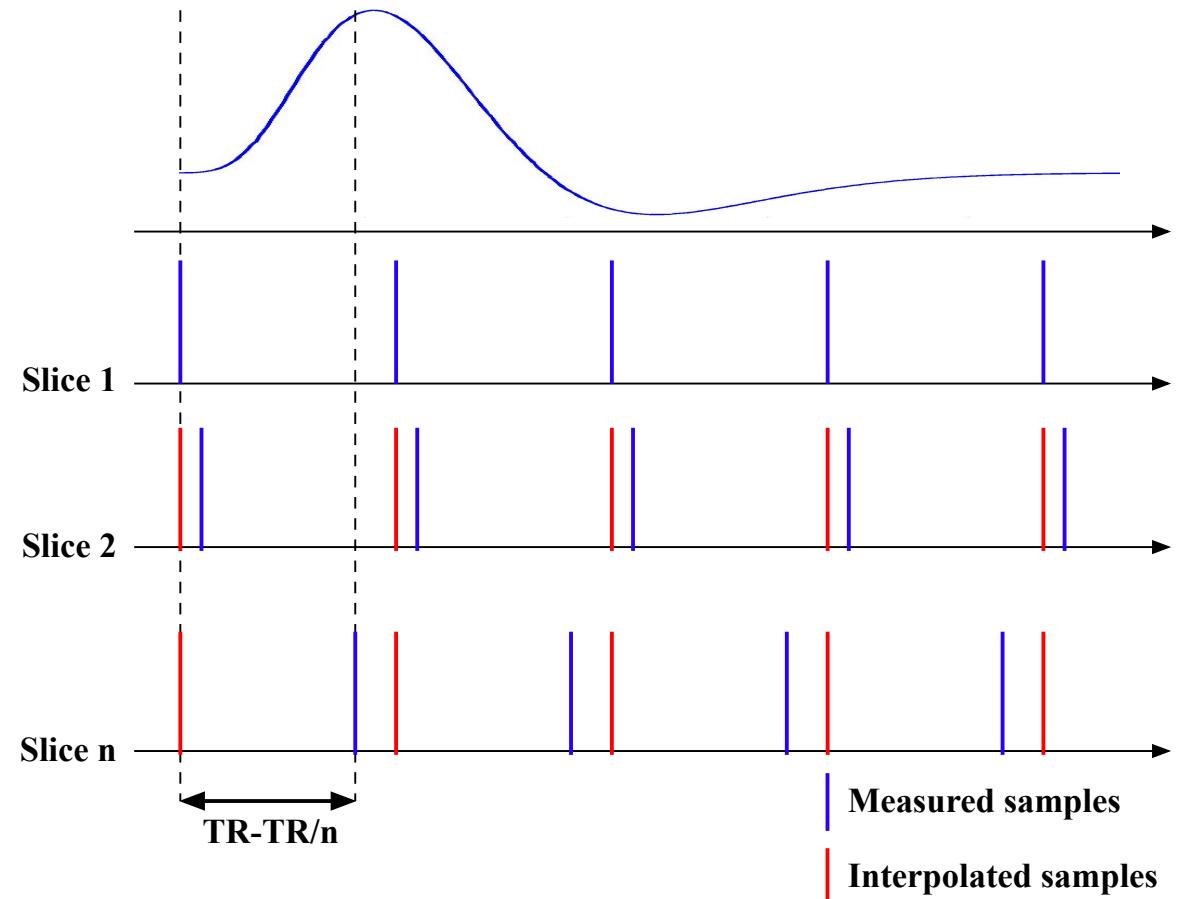


8. In the top Menus: select SPM -> Util -> 4D to 3D File Conversion
9. 4D Volume: (using dependency): Write HySCO corrected images: Unwarped Blip down images

Step 6: Slice time correction



```
sub-01-func-sub-01_task-affect_run-1_bold.json
"SliceTiming": [
    0,
    0.685,
    0.3925,
    0.0975,
    0.7825,
    0.49,
    0.195,
    0.88,
    0.5875,
    0.2925,
    0,
    0.685,
    0.3925,
    0.0975,
    0.7825,
    0.49,
    0.195,
    0.88,
    0.5875,
    0.2925,
    0,
    0.685,
    0.3925,
    0.0975,
    0.7825,
    0.49,
    0.195,
    0.88,
    0.5875,
    0.2925,
    0,
    0.685,
    0.3925,
    0.0975,
    0.7825,
    0.49,
    0.195,
    0.88,
    0.5875,
    0.2925,
    0,
    0.685,
    0.3925,
    0.0975,
    0.7825,
    0.49,
    0.195,
    0.88,
    0.5875,
    0.2925
]
```



Step 6: Slice time correction

The standard slice time correction doesn't work for data scanned with HyperBand! Use my modified function*!

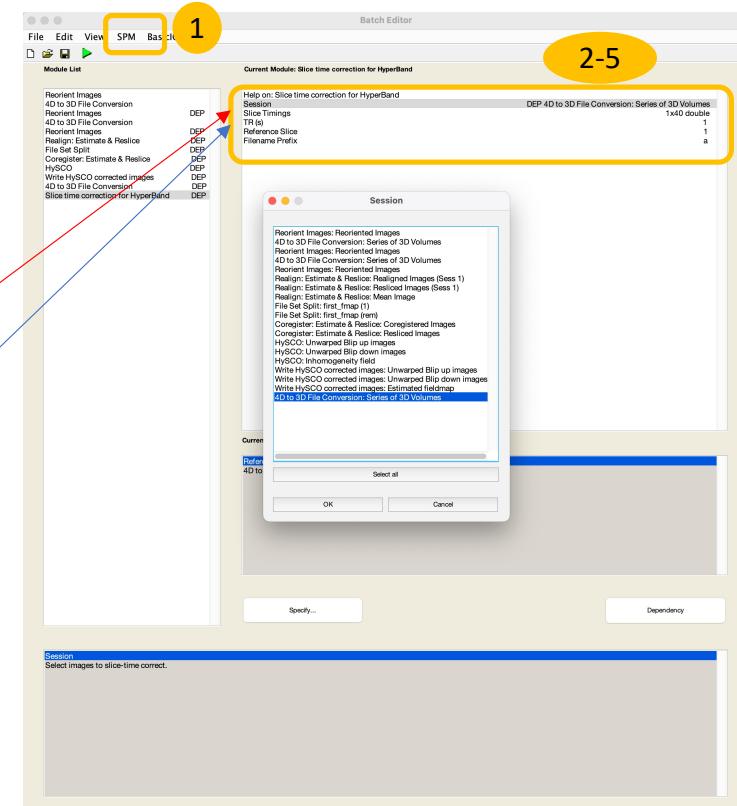
1. In the top Menus: select SPM -> Tools -> Multi echo & HyperBand -> Slice time correction for HyperBand
2. Session(using Dependency): Reoriented Images: 4D to 3D File Conversion: Series of 3D Volumes (from the previous step!)
3. Slice Timings: copy/paste the slice timings from the func.json file
4. TR (s): look up in the func.json file
5. Reference Slice: 1 (first slice)

```

sub-01/func/sub-01_task-affect_run-1_bold.json

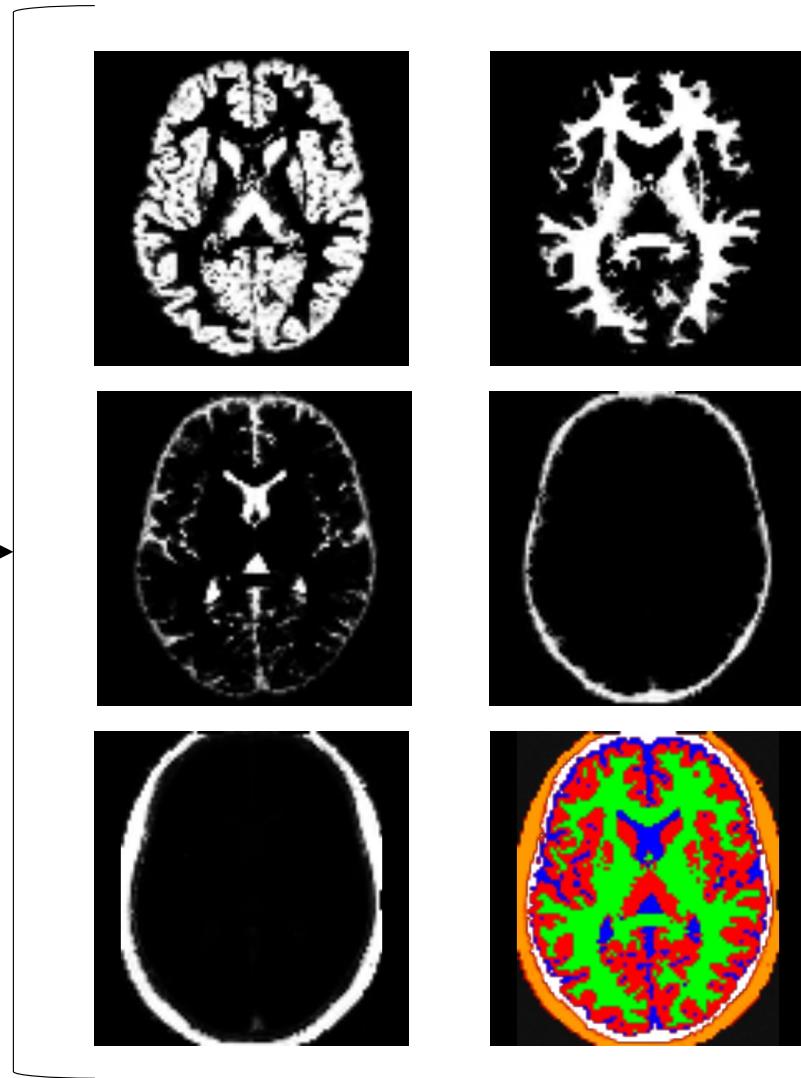
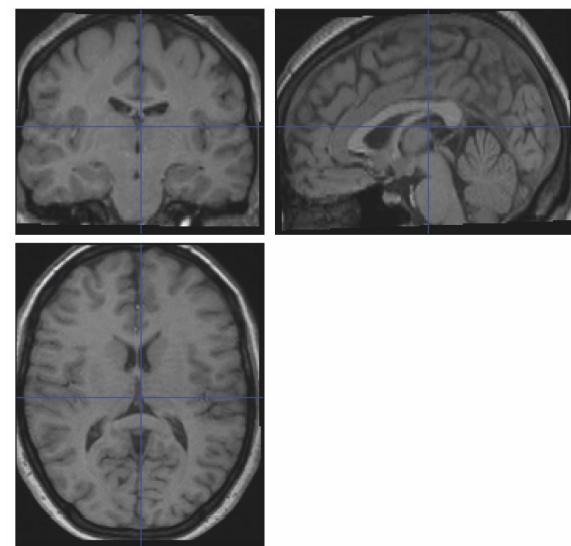
{
    "ConversionSoftware": "dicom2nii_n_20181126",
    "SeriesNumber": 3,
    "SeriesDescription": "MR1_B1_1",
    "ImageType": "ORIGINAL", "REPLICA", "TW", "WB", "ND", "MOSAIC",
    "Modality": "MR",
    "AcquisitionDateTime": "20180921141748.788000",
    "RepetitionTime": 1.0,
    "SliceTiming": [
        0,
        0.685,
        0.3925,
        0.8975,
        0.7325,
        0.49,
        0.195,
        0.88,
        0.5875,
        0.2925,
        0.7325,
        0.685,
        0.3925,
        0.8975,
        0.7325,
        0.49,
        0.195,
        0.88,
        0.5875,
        0.2925,
        0,
        0.685,
        0.3925,
        0.8975,
        0.7325,
        0.49,
        0.195,
        0.88,
        0.5875,
        0.2925,
        0,
        0.685,
        0.3925,
        0.8975,
        0.7325,
        0.49,
        0.195,
        0.88,
        0.5875,
        0.2925,
        1
    ],
    "RepetitionTime": 1,
    "EchoTime": 0.035,
    "Echotime1": 0.035,
    "deltaTE": 0.34,
    "echoTE": 0.001,
    "SliceThickness": 2.73,
    "FlipAngle": 62,
    "Manufacturer": "Siemens",
    "SoftwareVersion": "syngo MR E11",
    "MRAcquisitionType": "2D",
    "Institution": "Siemens",
    "InstitutionAddress": "Medical Center Dr 5, Columbia, SC, US, 29203",
    "DeviceSerialNumber": "670808",
    "ScanOptions": "420_1024x256_2.73",
    "SequenceVariant": "SKV\\GS",
    "ScanOptions": "FS",
    "SequenceName": "epi1024x1_78",
    "TaskName": "effect"
}

```



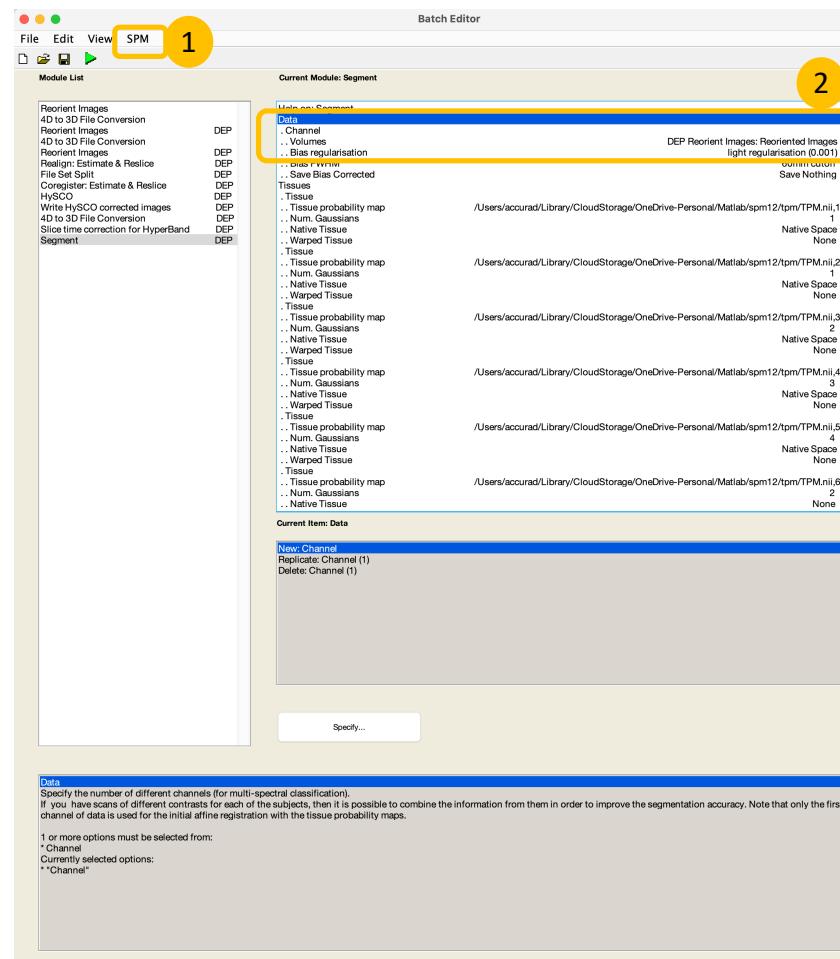
* Code available at <https://github.com/P-VS/MEHBfMRI>

Step 7: Segmentation



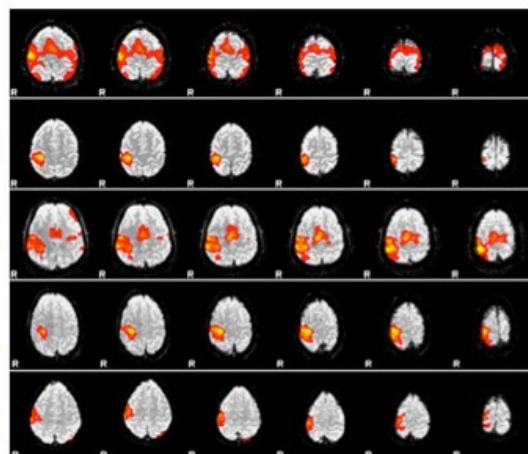
Step 7: Segmentation

1. In the top Menus: select SPM -> Spatial -> Segment
2. Volumes (using Dependency): Reorient Images: Reoriented Images (from the anatomical scan)

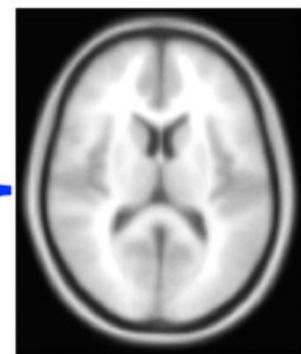


Step 8: Normalization

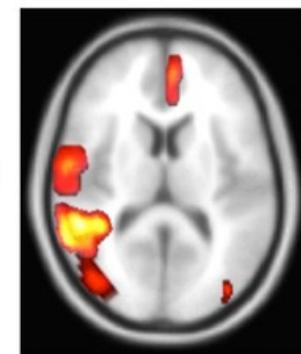
Subject 1
Subject 2
Subject 3
Subject 4
Subject 5



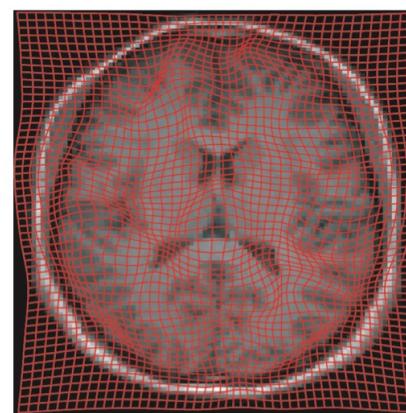
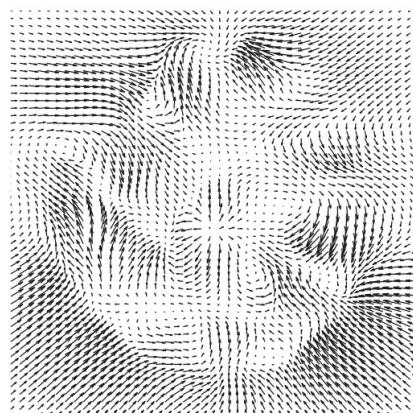
Normalization



Template

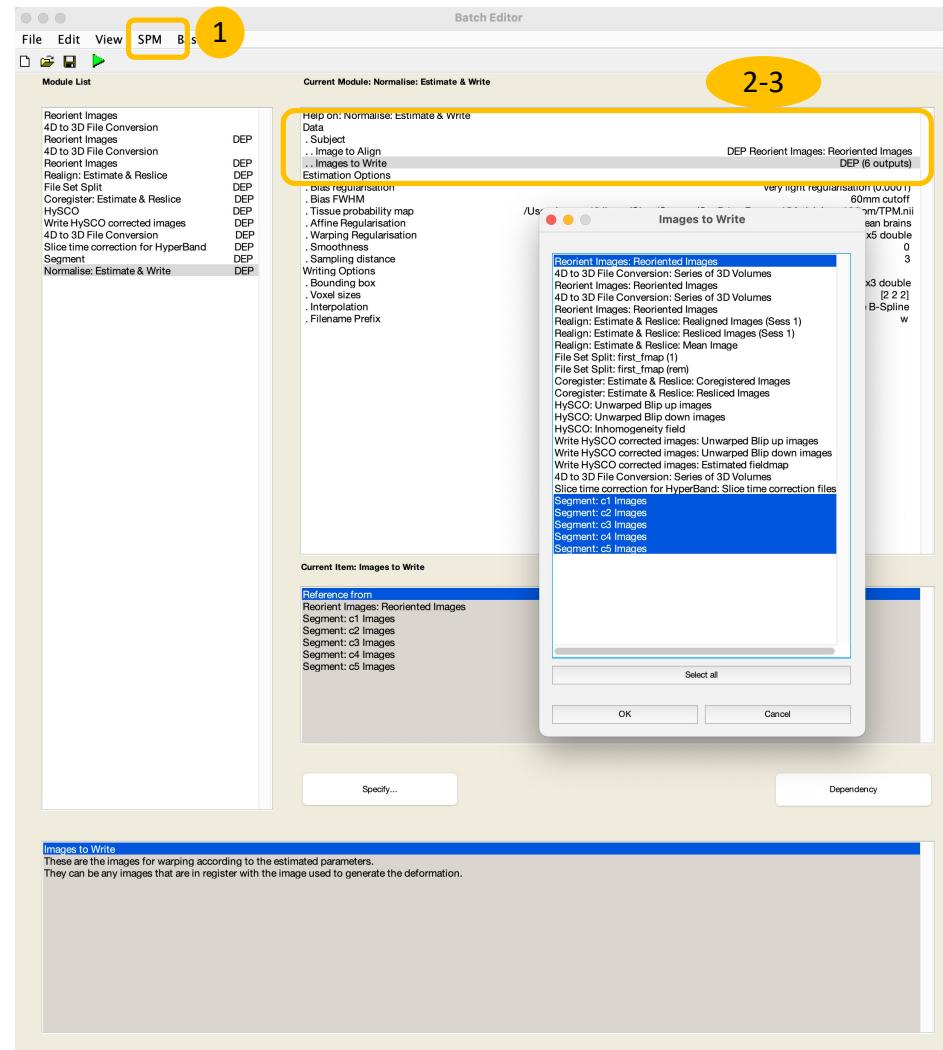


**Average
activation**



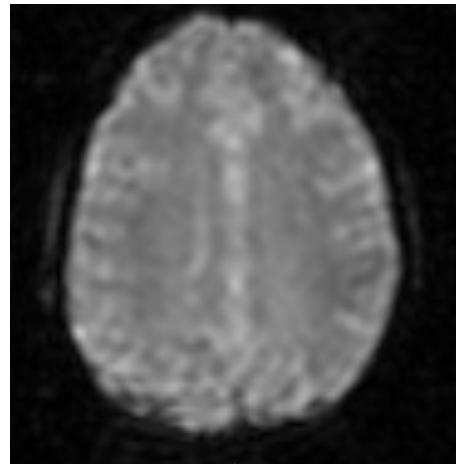
Step 8: Normalization: The anatomical scan and segmentation maps

1. In the top Menus: select SPM -> Spatial -> Normalise -> Normalise: Estimate & Write
2. Image to align: (using Dependency) Reorient Images: Reoriented Images (from anat scan!)
3. Images to write: (using Dependency) Reorient Images: Reoriented Images (from anat scan!) + Segment: c1 – c5 Images

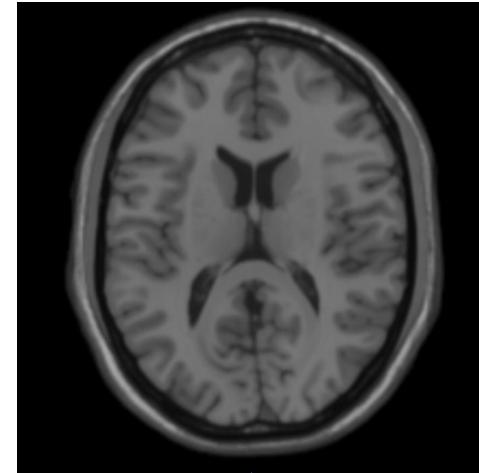


Step 8: Normalization: The fMRI scan

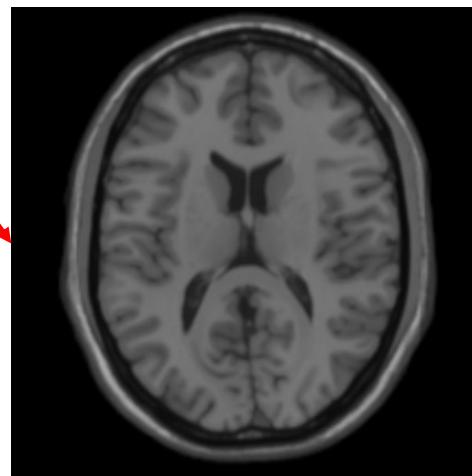
Subject
func scan



Subject
T1 scan

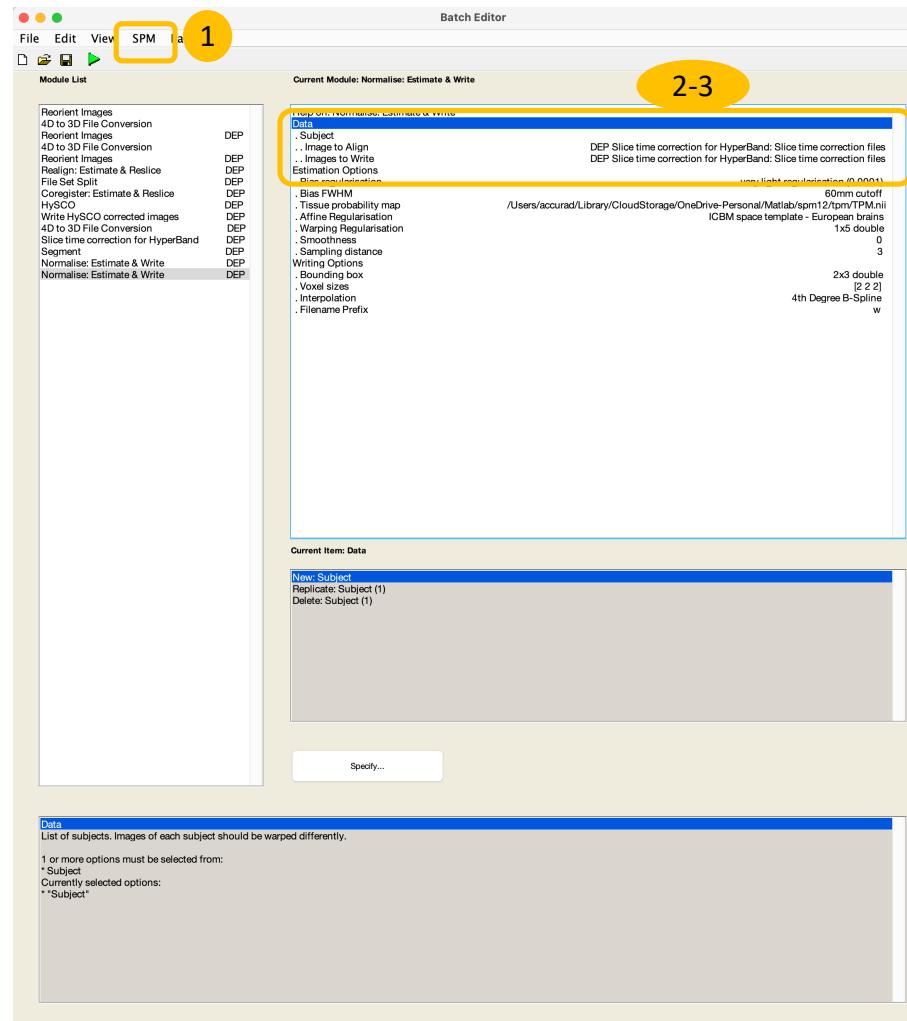


Template
T1 scan

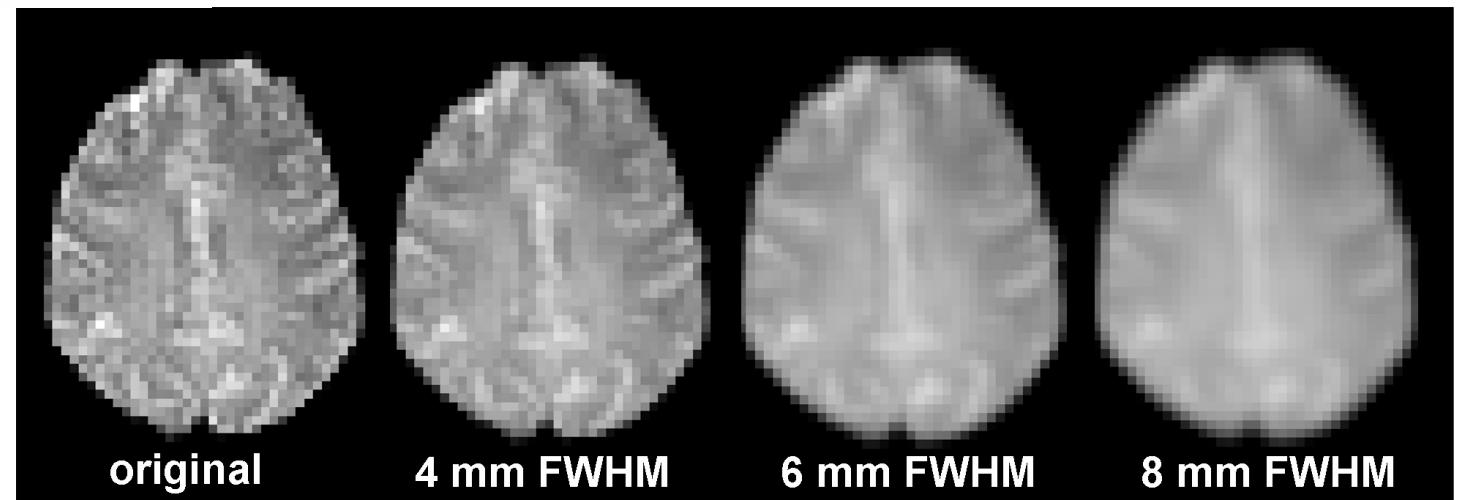
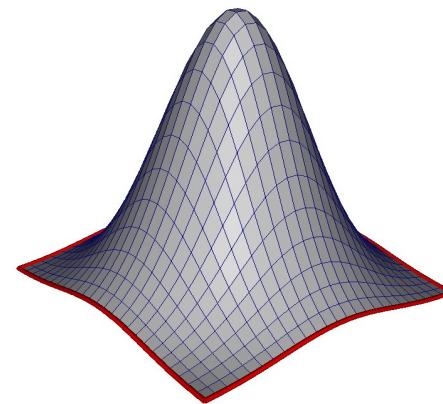
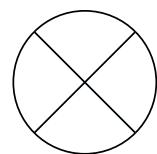
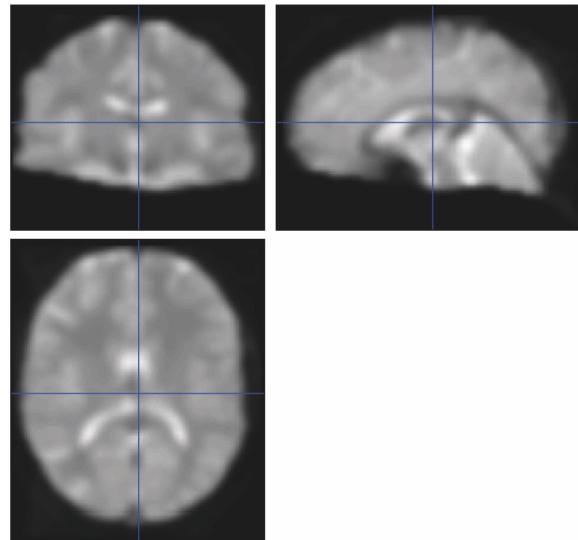


Step 8: Normalization: The fMRI data

1. In the top Menus: select SPM -> Spatial -> Normalise -> Normalise: Estimate & Write
2. Images to align: (using Dependency) Slice time correction for GyperBand: Slice time correction files
3. Images to write: (using Dependency) Slice time correction for GyperBand: Slice time correction files

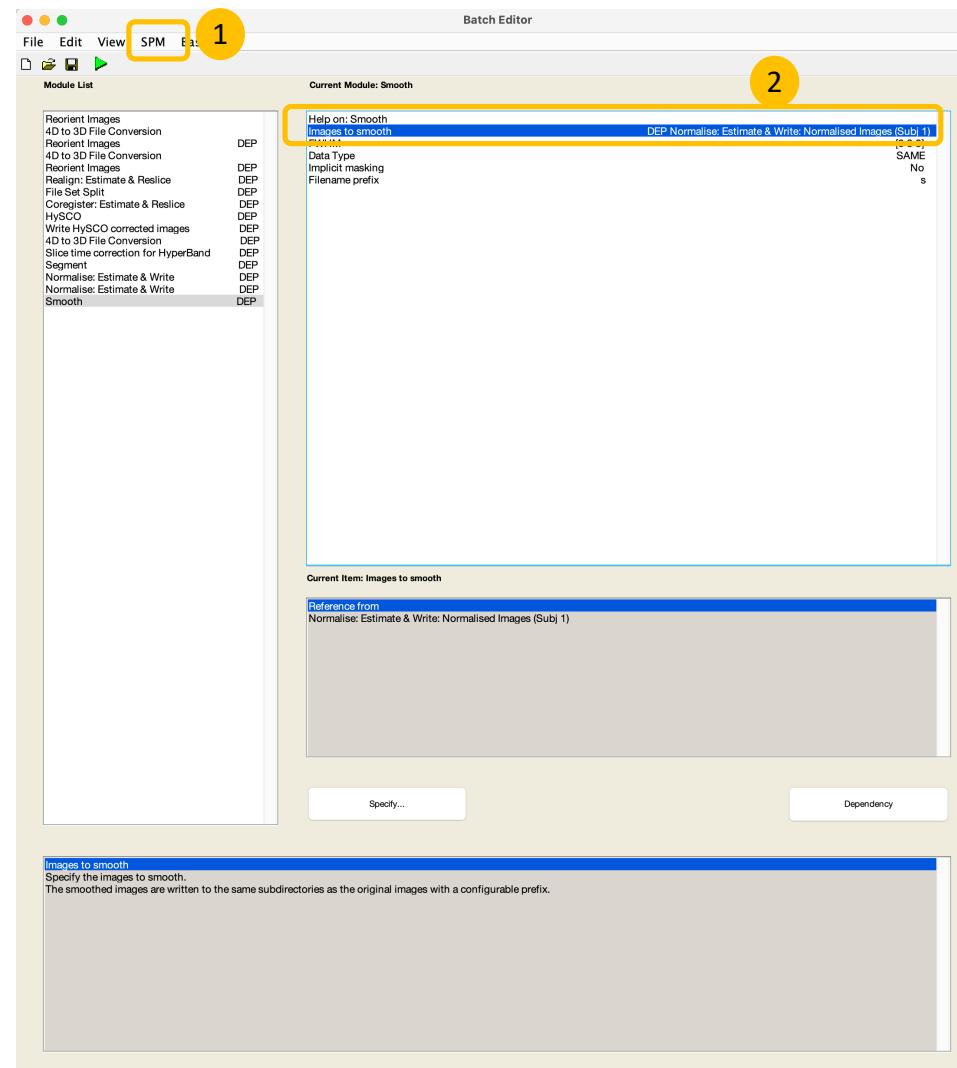


Step 9: Smoothing



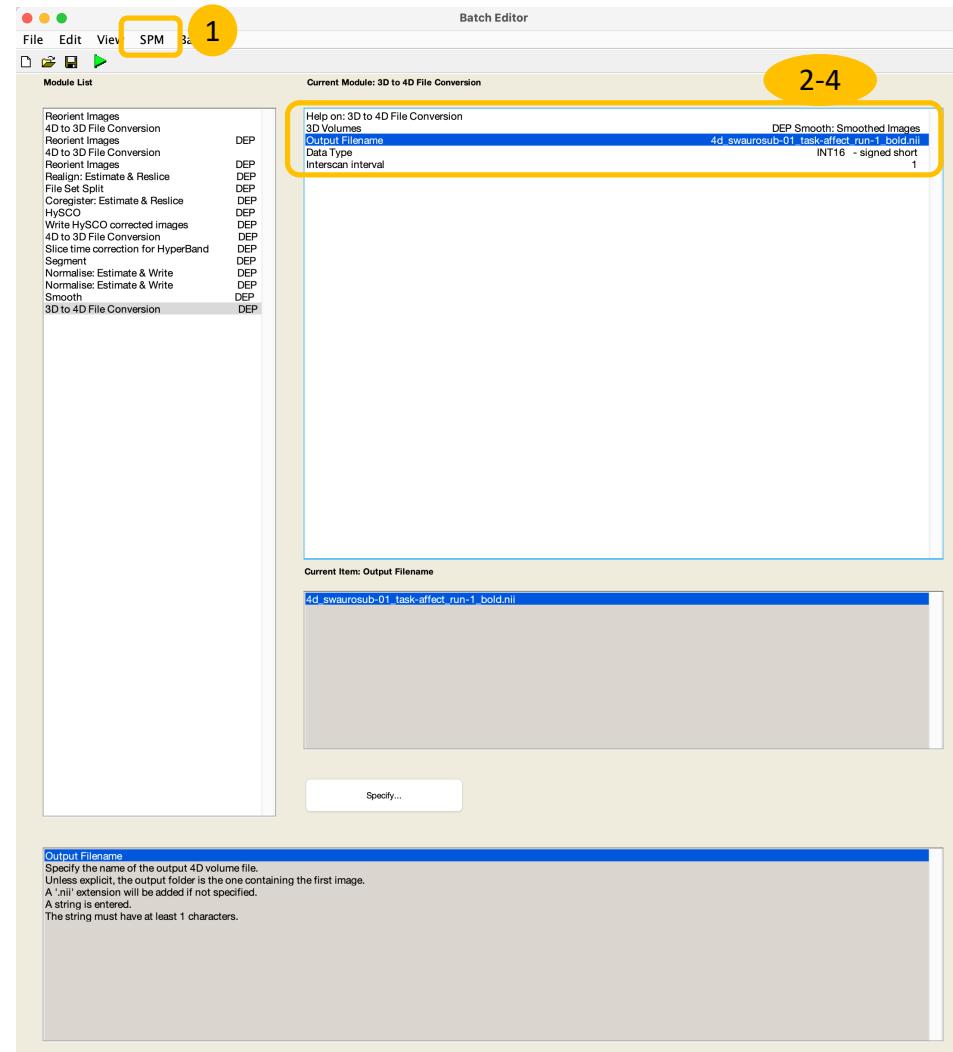
Step 9: Smoothing

1. In the top Menus: select SPM -> Spatial -> Smooth
2. Images to smooth: (using Dependency) Normalise: Estimate & Write: Normalised Images (Subj 1)



Step 10: Converting the result to a 4D nifti file

1. In the top Menus: select SPM -> Util -> 3D to 4D File Conversion
2. 3D Volume: (using dependency): Smooth: Smoothed Images
3. Output Filename: 4d_swaurosub-01_task-affect-run-1_bold.nii
4. Interscan interval: should be the TR (look up in the func.json file)

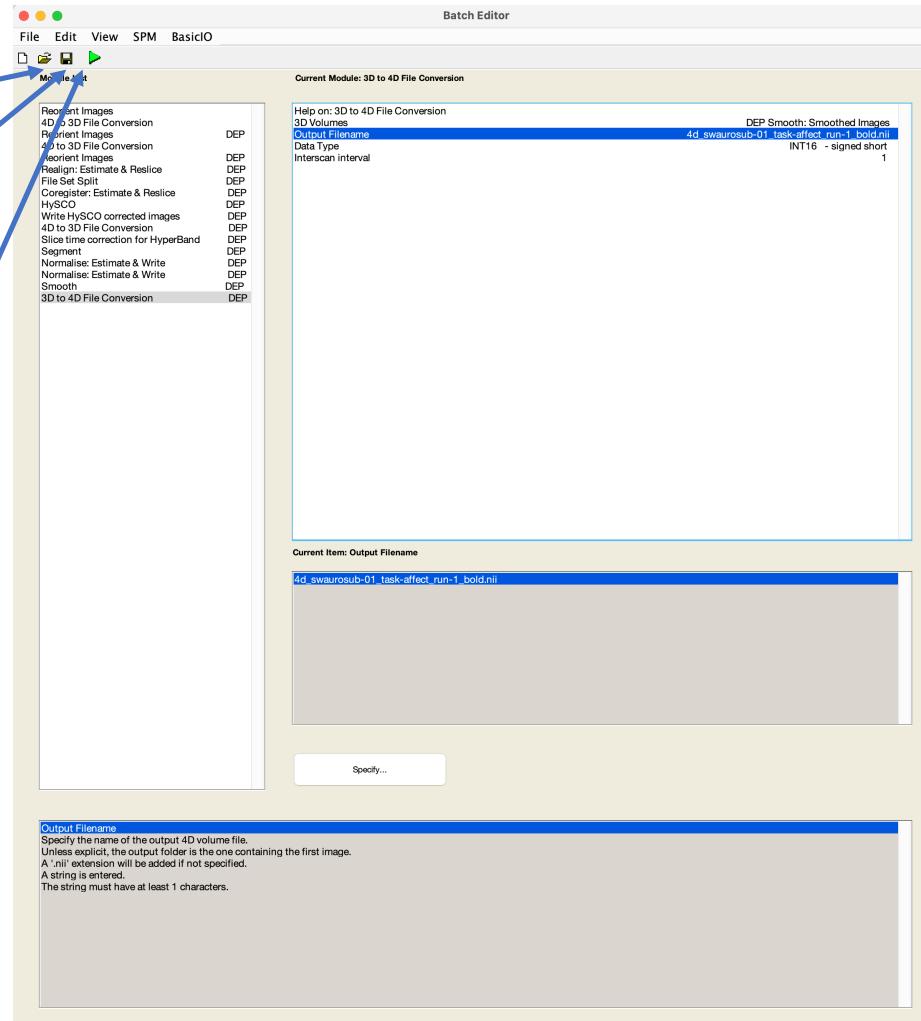


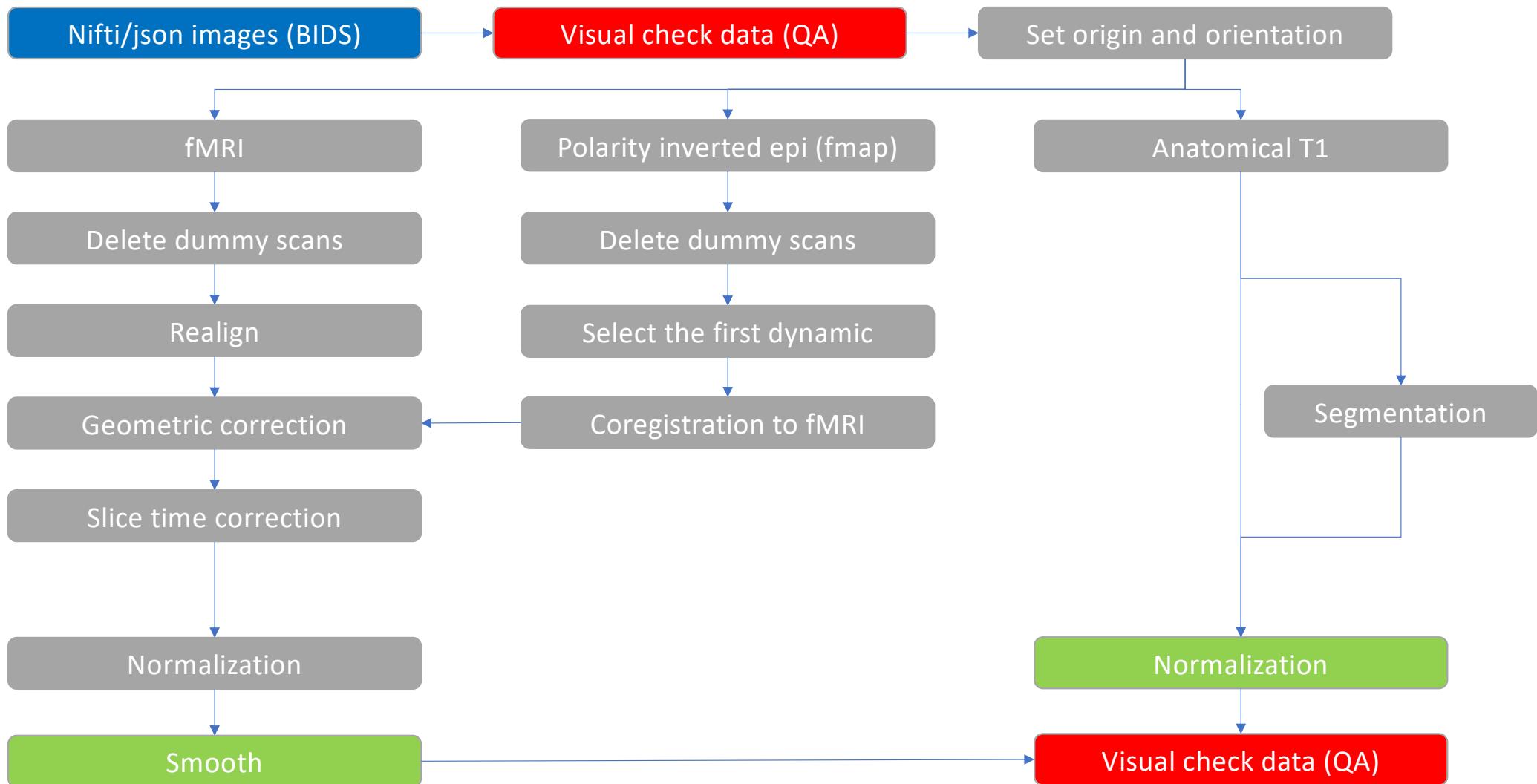
Run the batch (at home)

Load a saved BATCH file

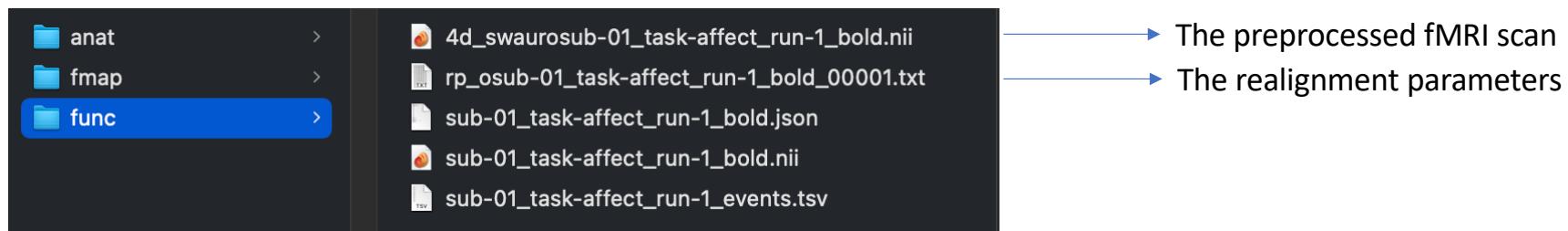
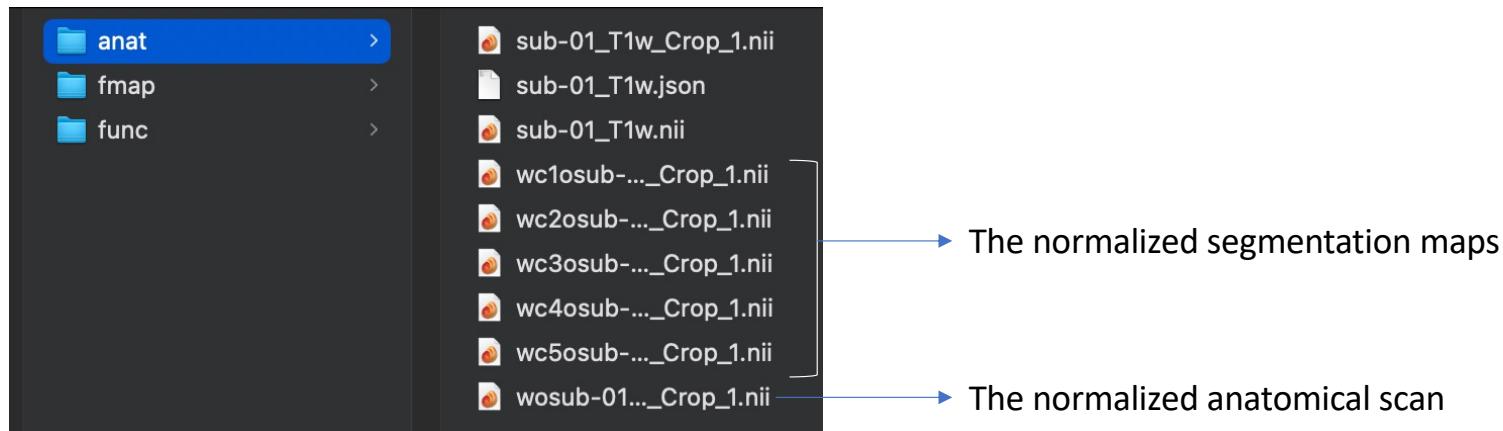
Save the BATCH as a file

Run the BATCH

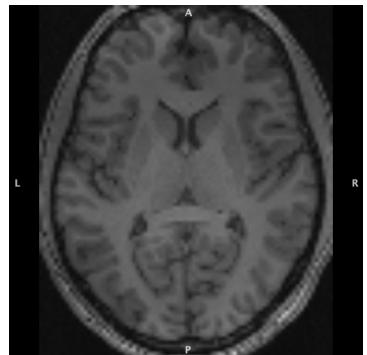




Cleaning up the results



The preprocessing results



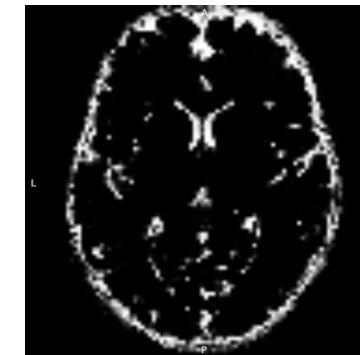
wosub-01_T1w



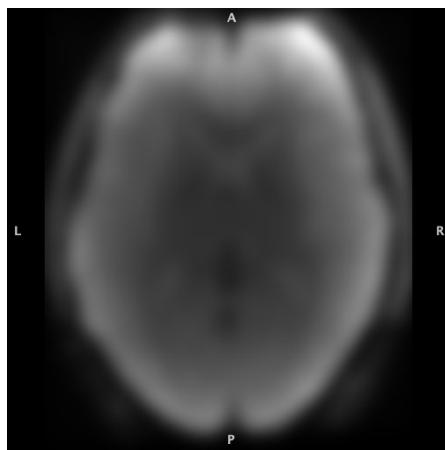
wc1osub-01_T1w



wc2osub-01_T1w



wc3osub-01_T1w



4d_swuraosub-01_task-affect-run-1_bold.nii

| | Trans x | Trans y | Trans z | Rot x | Rot y | Rot z |
|--|----------------|----------------|----------------|----------------|----------------|---------------|
| rp_aosub-01_task-affect_run-1_bold_00001.txt ~ | 0.000000e+00 | -4.7340067e-16 | 0.000000e+00 | 0.000000e+00 | 0.000000e+00 | 1.2588970e-17 |
| | 1.7513722e-02 | -6.7856195e-03 | 6.0396937e-03 | 4.4362332e-04 | -1.0208815e-04 | 3.4466021e-04 |
| | 4.8461260e-02 | -3.7386199e-02 | 6.2362634e-02 | 1.4502508e-03 | -4.0640802e-04 | 9.5685461e-04 |
| | 6.9180189e-02 | -3.9871672e-02 | 6.4310601e-02 | 1.3979599e-03 | -3.5460454e-04 | 1.4147925e-03 |
| | 5.20911583e-02 | 3.2066219e-02 | 7.7718133e-02 | 4.3498257e-04 | -9.9844301e-05 | 8.9267421e-04 |
| | 5.7427248e-02 | 1.6258788e-02 | 7.6479148e-02 | 7.0890674e-04 | 1.6059046e-04 | 7.9906206e-04 |
| | 8.6317280e-02 | -3.5120548e-02 | 7.2283943e-02 | 1.3903804e-03 | -2.0507305e-05 | 1.3339979e-03 |
| | 1.1731055e-01 | -3.0335500e-02 | 6.3979068e-02 | 1.7311331e-03 | -1.9270127e-04 | 1.7468015e-03 |
| | 8.0937031e-02 | 5.0152872e-02 | 9.1561197e-02 | 6.9045654e-04 | 2.2436062e-04 | 1.1304025e-03 |
| | 6.3606665e-02 | 3.5731932e-02 | 7.7646949e-02 | 5.5901698e-04 | 1.8457663e-04 | 8.6840523e-04 |
| | 5.2421874e-02 | -1.0953733e-02 | 1.0717907e-01 | 9.7029852e-04 | -6.1821191e-05 | 1.0495726e-03 |
| | 7.4589833e-02 | -4.0247471e-04 | 1.2329963e-01 | 7.9186069e-04 | 1.8275389e-05 | 1.1582123e-03 |
| | 1.0715947e-01 | -5.0387869e-02 | 1.0422207e-01 | 7.68870931e-04 | -7.4170782e-05 | 1.4709182e-03 |
| | 1.4121567e-01 | -7.7419048e-02 | 1.30771721e-01 | 1.4501688e-03 | -3.1955366e-04 | 1.8303812e-03 |
| | 1.7744815e-01 | -6.8792732e-02 | 5.1087038e-03 | 8.2285381e-04 | -7.5366066e-05 | 2.0172927e-03 |
| | 1.2917189e-01 | 1.7510493e-02 | 5.8319505e-02 | -2.8877083e-06 | -1.3831180e-05 | 1.5282397e-03 |
| | 1.3561558e-01 | 3.8867613e-03 | 8.8903376e-02 | 6.1257401e-04 | -2.0483346e-04 | 1.6858282e-03 |

Realignment parameters

DANK U - THANK YOU