

A clinical and research 3T MRI protocol under 30 minutes

(Yes, it's possible!)

SK Larroque, M Carrière, C Martial, S Laureys
github.com/LRQ3000/mri_protocol

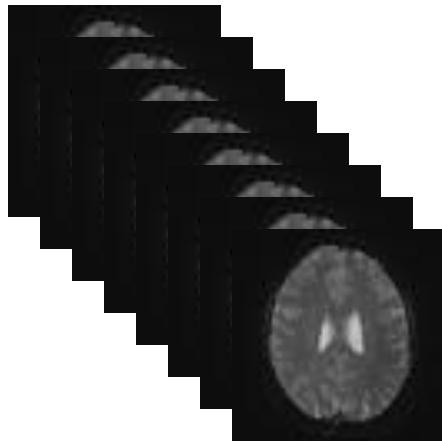


V1.0.4

Coma Science Group
GIGA Consciousness
University & Hospital of
Liège, Belgium

CME 2019
Dortmund, September 23th 2019

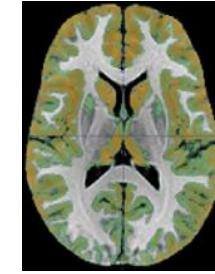
What we do: MRI analyses



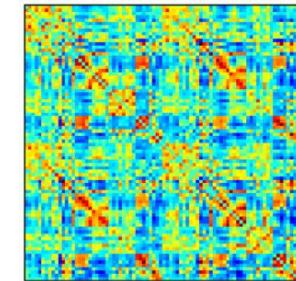
fMRI timeseries
(one per subject)



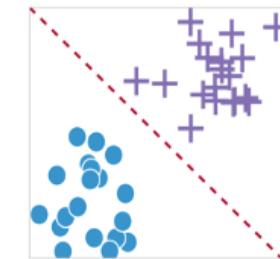
Preprocessing
(SPM12)



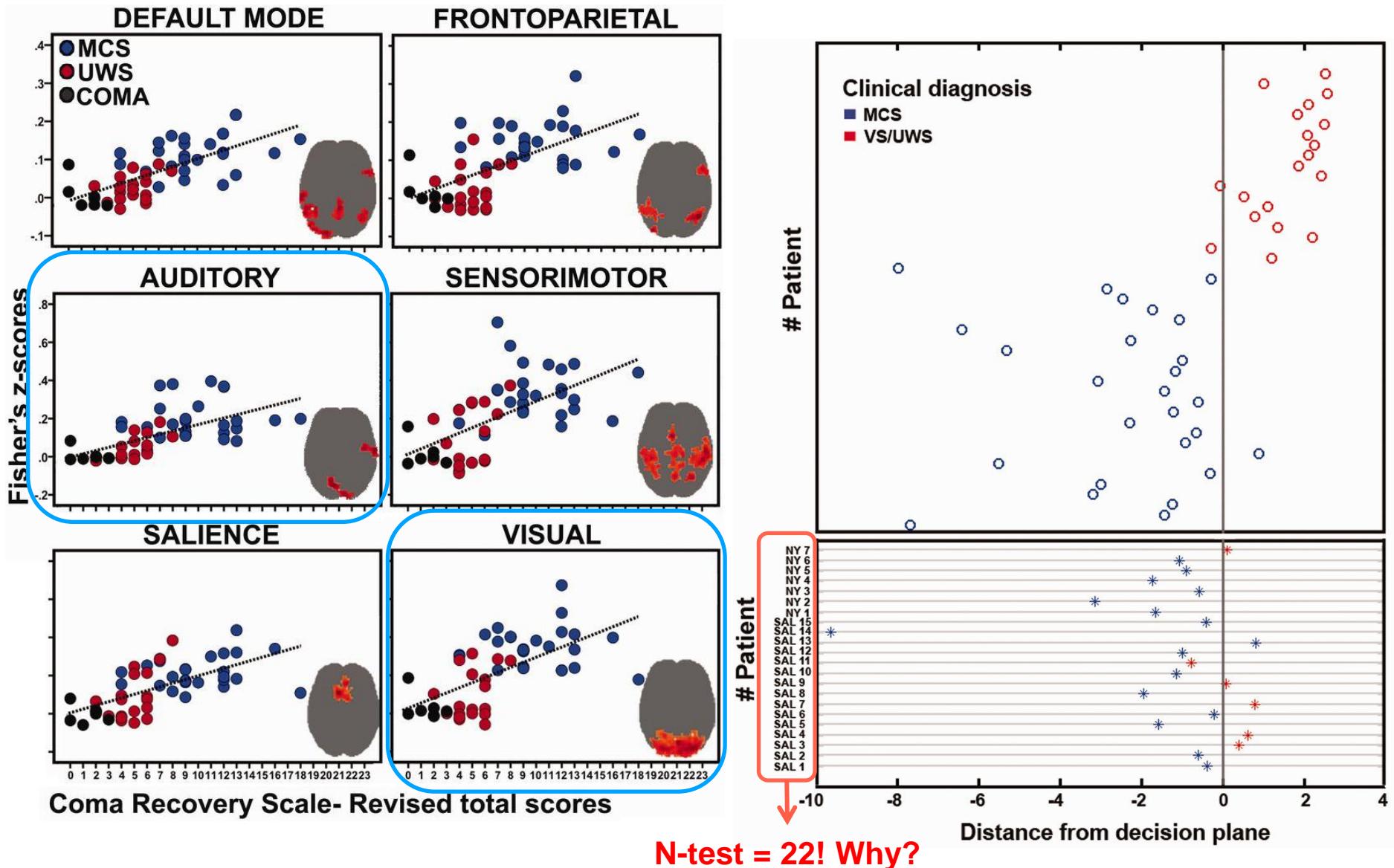
Analysis
(CONN)



Machine
learning
(SVM)



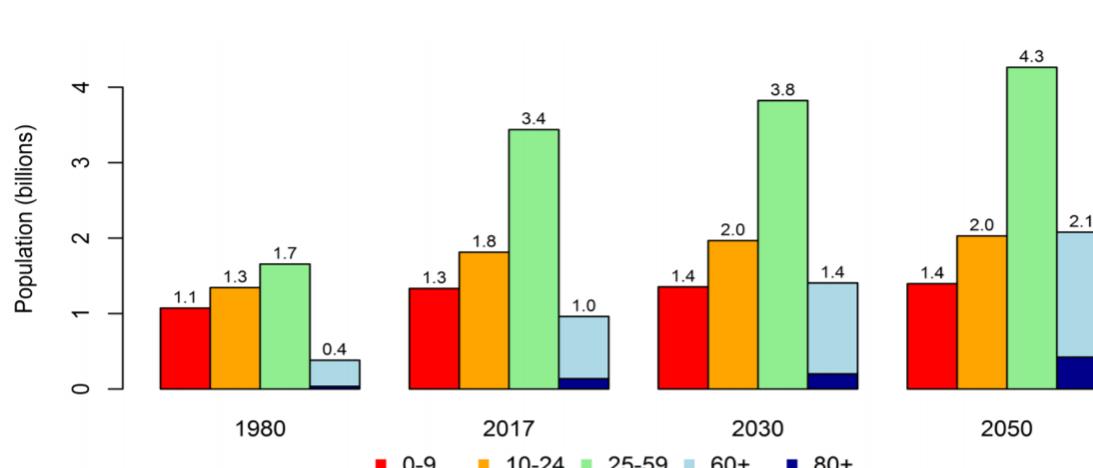
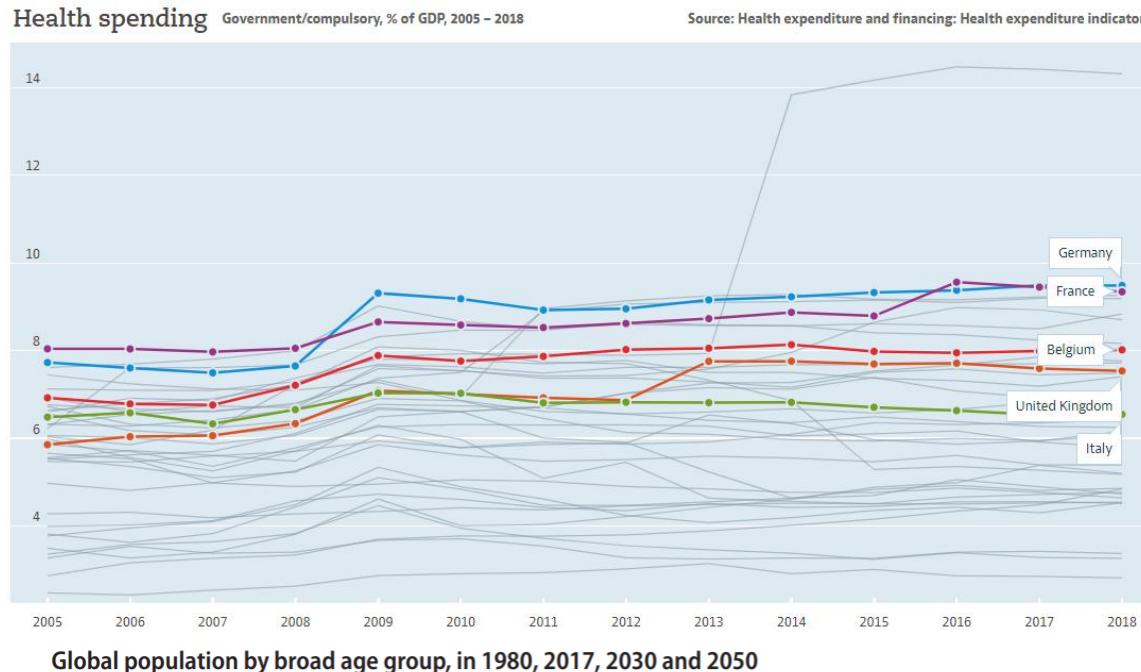
What we do: MRI analyses



Limitations to sample size



1. Time & Cost



Fee-for-service,
Diagnosis-related-
group payment^[4]

Limitations to sample size



1. Time & Cost



Healthy volunteers: compliant, cognitively autonomous

2. Motion & Sedation

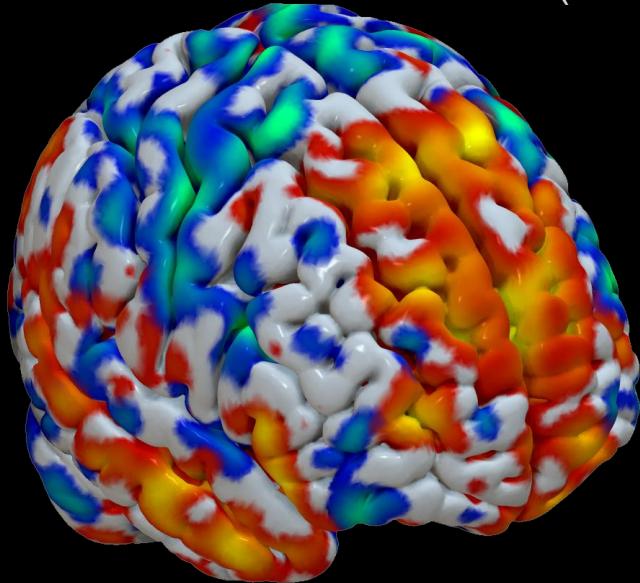
Patients: uncontrolling or non-compliant, discomfort, monitoring vital parameters

	Admitted	With MRI	Analyzable	Non-sedated
Over 10 years (%):	676 (100%)	465 (69%)	256 (38%)	~110 (16%)

→ Overcome limitations by optimizing acquisition?

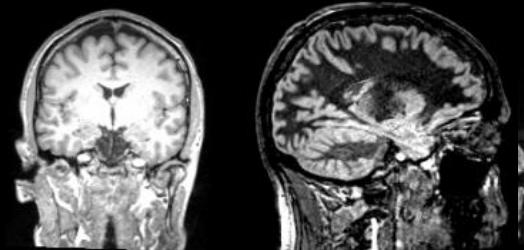
A 30 min cutting-edge, motion-resilient MRI protocol

(20-channel coil, 3T Siemens Vida)

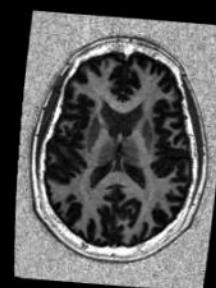


Sub-second BOLD
TR 728ms
500 vols in 6:13

T1 FLAWS
5:02

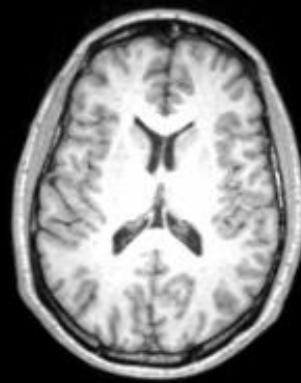
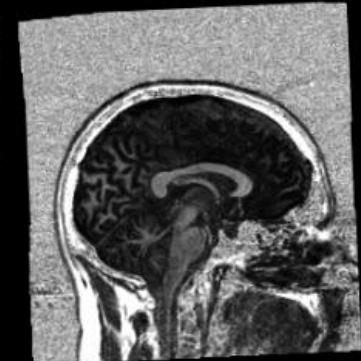
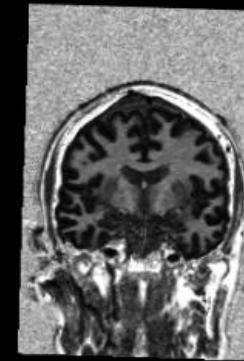
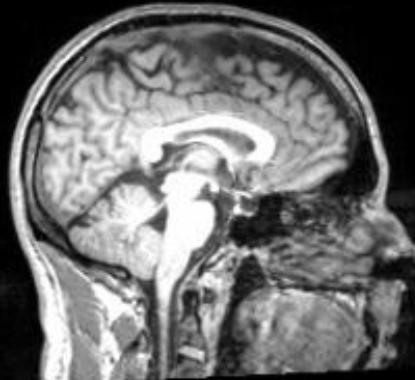
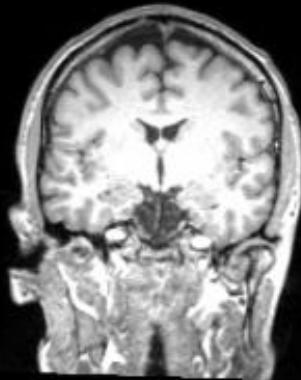


3-shells DWI
13:25

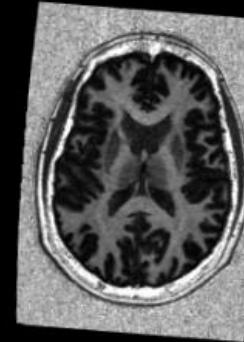


N=35 (8 test controls, 10 stable controls, 17 patients)

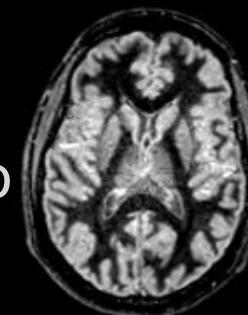
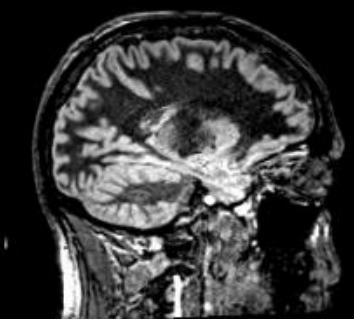
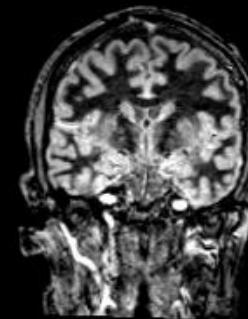
T1 FLAWS^[1,2] produces simultaneously:



MPRAGE
(inv2)
(structural, 1mm³ iso)



White Matter
(uni)



Grey Matter
(inv1)

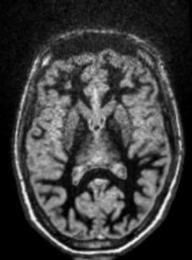
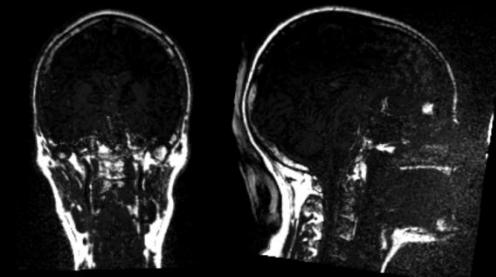
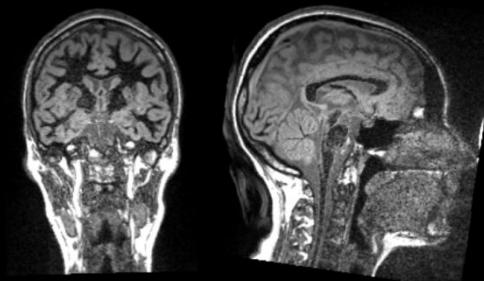
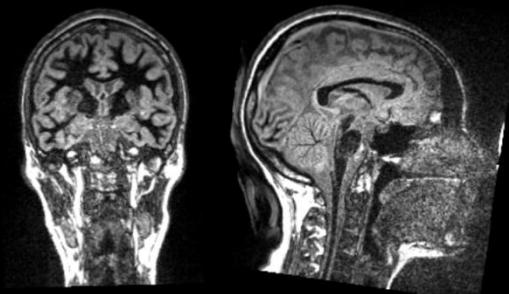
→ Physiological segmentation:

- No approximation (not computational!)
- In subject-space
- Always coregistered (even with motion)
- All in 5 min (on 3T), voxel size: 1mm iso
- More clinical infos (complement FLAIR)

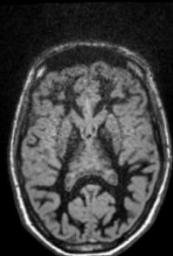
[1] Tanner et al, 2012 [2] Yishi Wang, Hua Guo, 2018

Our T1 FLAWS enhancements:

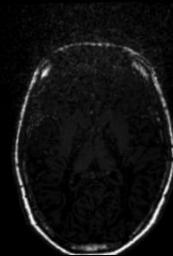
(see also alternatives in [1])



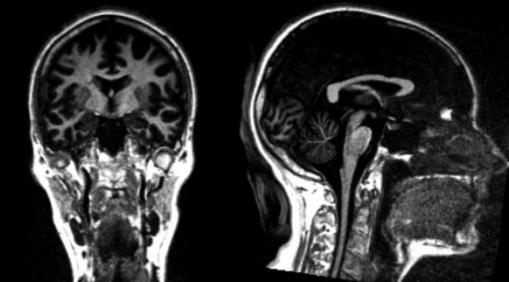
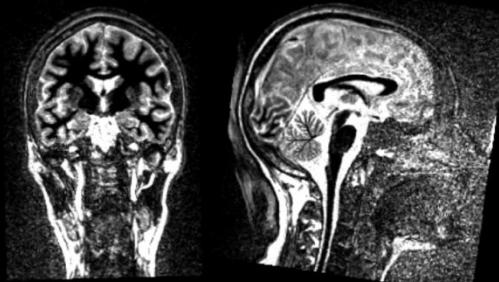
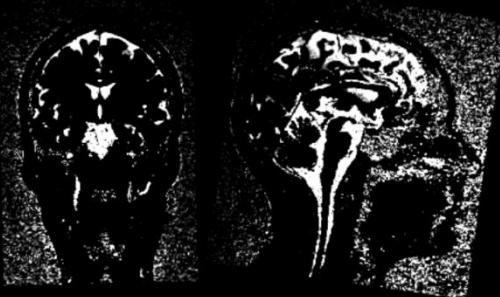
GM
 $\min(\text{inv1}, \text{inv2})$



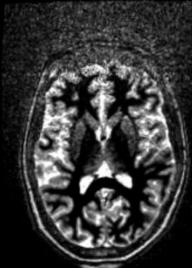
GM mIP
 $(\text{inv1} \cdot^* \text{inv2})$
 $\cdot / (\text{inv1} + \text{inv2})$



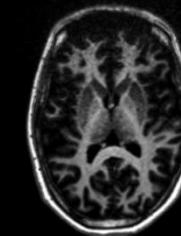
Skull
 $\text{inv1} \cdot^* \text{uni}$



CSF
 $\text{inv1} - \text{GM}$



CSF mIP
 $\text{inv1} - \text{GM mIP}$



WM denoised
 $\text{inv2} \cdot^* \text{uni}$

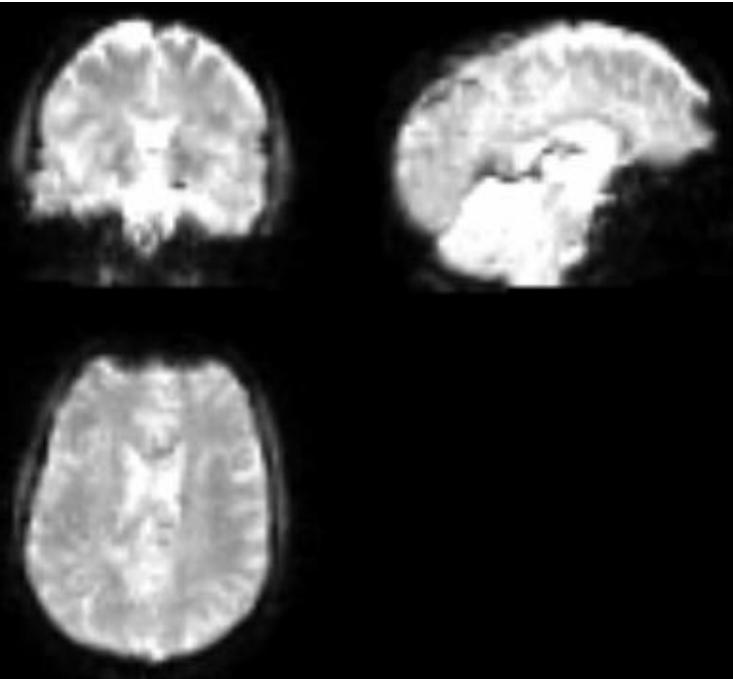
[1] Wang, Y., Wang, Y., Zhang, Z., Xiong, Y., Zhang, Q., Yuan, C., & Guo, H. (2018). Segmentation of gray matter, white matter, and CSF with fluid and white matter suppression using MP2RAGE. *Journal of Magnetic Resonance Imaging*.

Sub-second EPI Bold fMRI

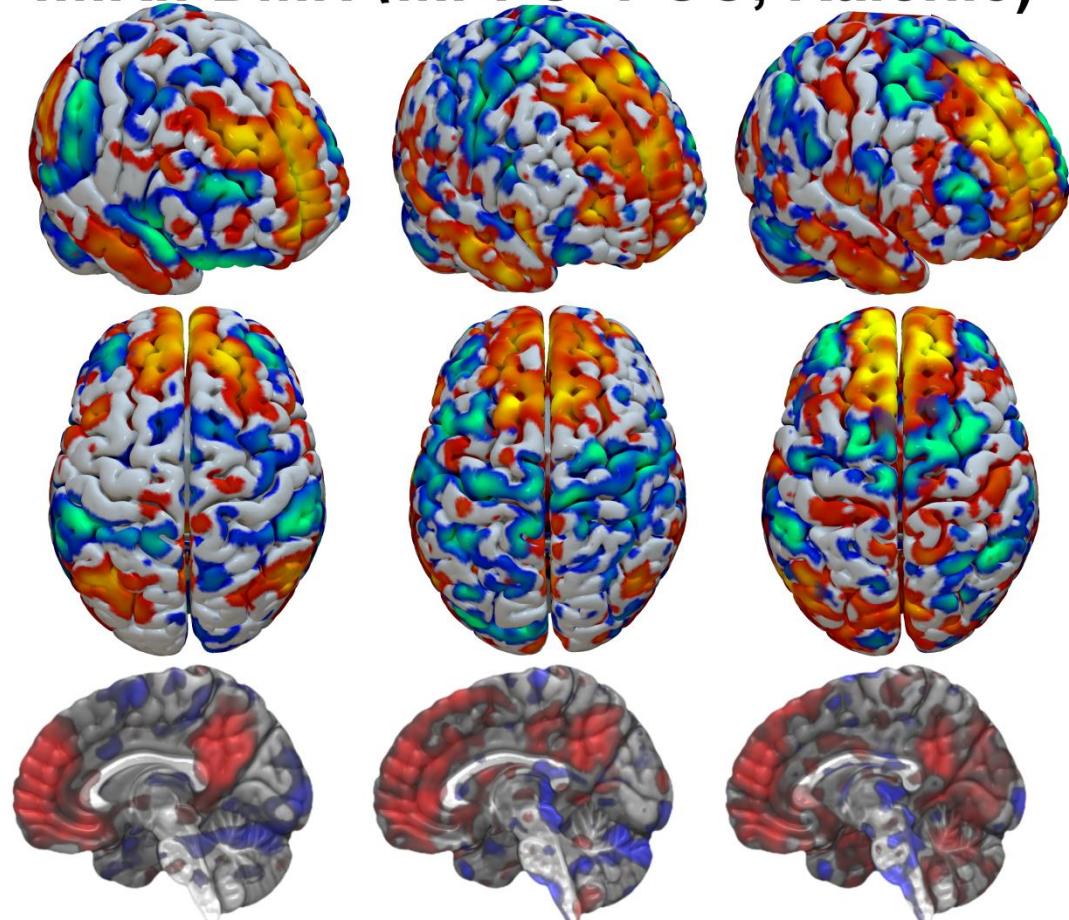
(728 ms, SMS x3, PI x2, 3mm³ iso)



First-level seed-based
fMRI: DMN (MPFC+PCC, Raichle)



- Dynamic connectivity
- Bypass HRF (<1.5s)
- Motion resilient



OLD MRI

300 vols (10:00)

TR: 2s

NEW MRI

300 vols (3:47)

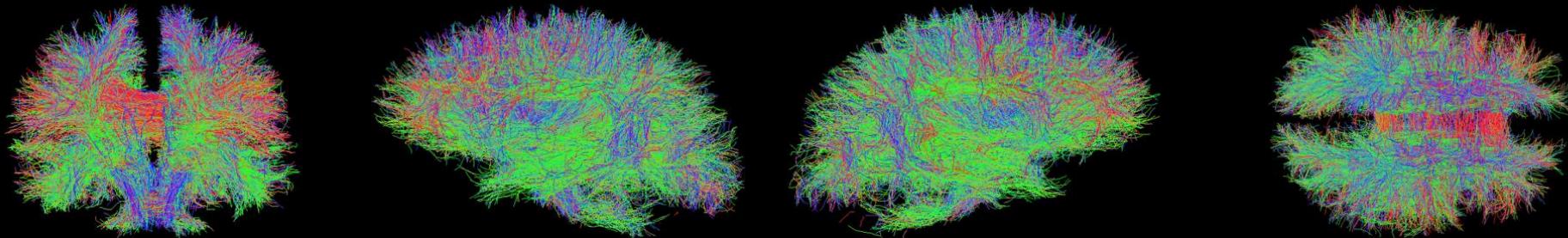
TR: 728ms

NEW MRI

500 vols (6:13)

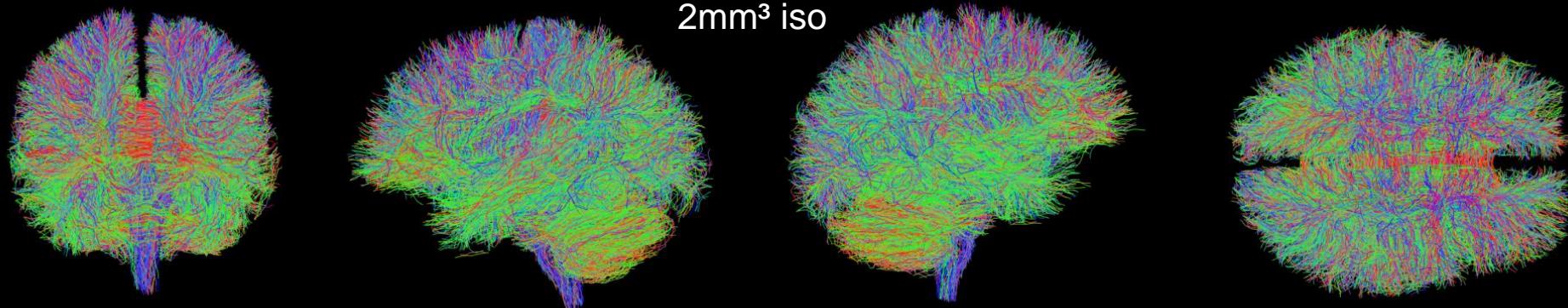
TR: 728ms

OLD MACHINE DTI (SINGLE-SHELL B1000, WITH ACT)



NEW MACHINE DTI (MULTI-SHELL 3-SHELLS, NO ACT) [1]

2mm³ iso



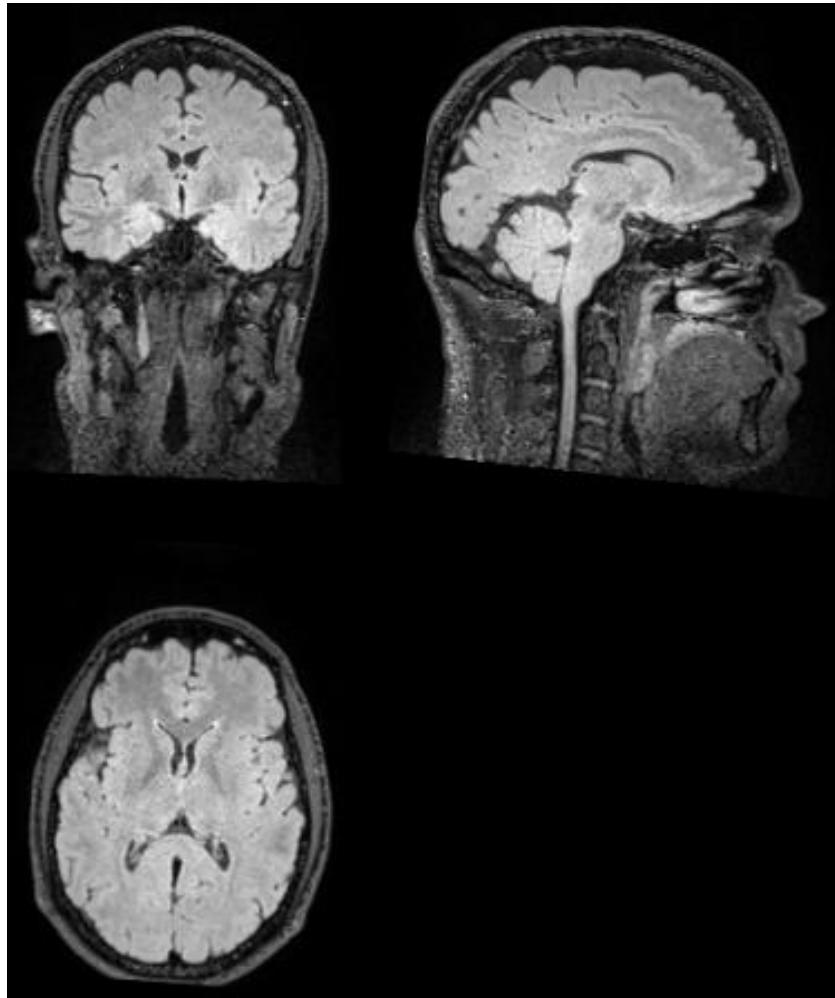
Optimizations:

- 3 shells: b700 30dir, b1000 64dir, b2000 64dir.
- b1000 is high quality (small TE), others: higher TE → faster TR.
- SMS x4.
- Partial fourier 7/8 (warning: prevents mrdegibbs!)

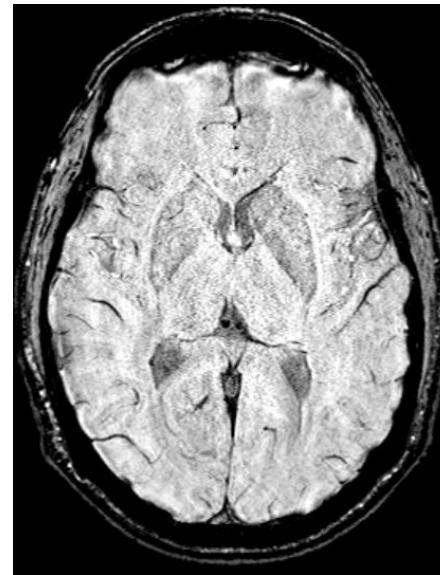
Great for:

- Clinical tissue assessment under varying diffusion bvals
- Worst case: degrades to single-shell
- Standalone (structural unnecessary)

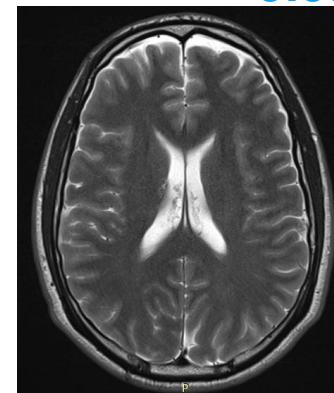
Clinical sequences: FLAIR, SWI, T2, ASL



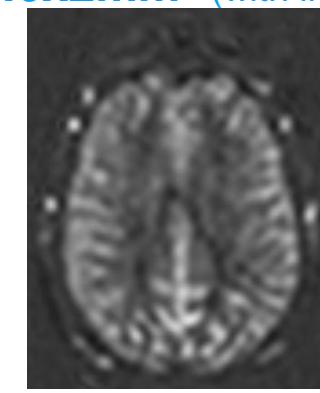
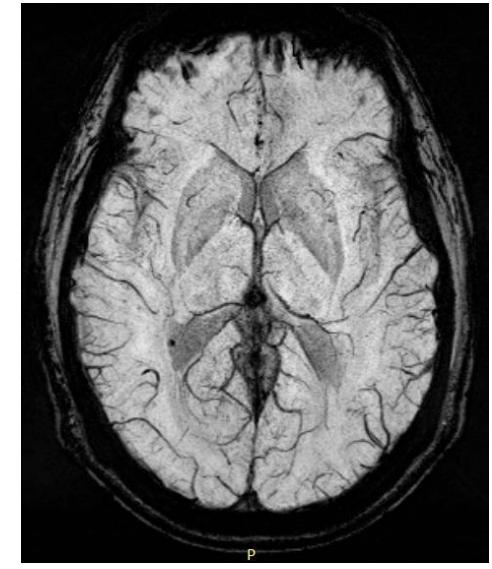
3:12, 1mm³
(with interpolation
from 0.5mm²)



3:57, 0.6x0.6x2mm³ (with interpolation)



1:21, 0.4x0.4x4.0mm³
(with interpolation)



2:17, 3mm³
(with interpolation)

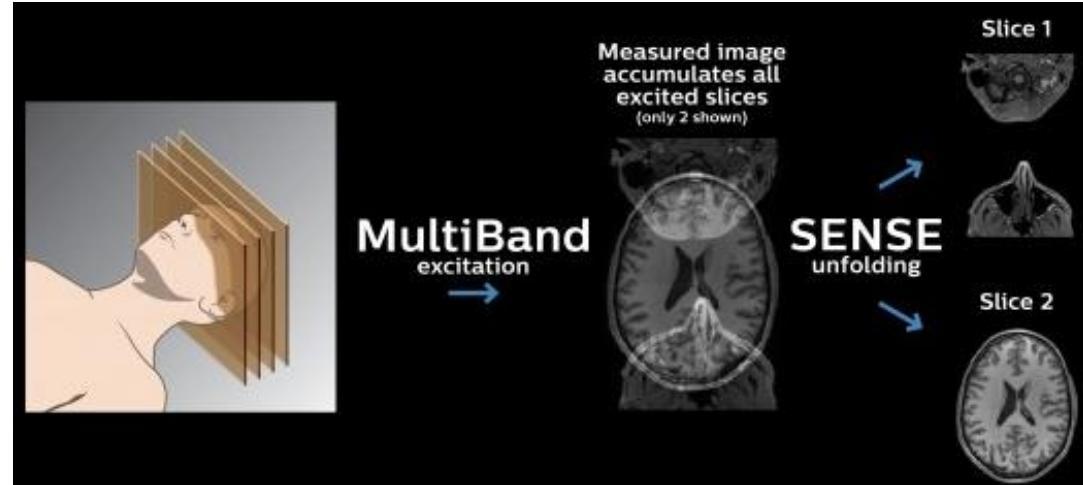
How did we make it?



1) Technological optimizations:

- Modern **acceleration**:

GRAPPA x multiband (SMS)^[1] = max x4 no loss, x6 acceptable, x8 with loss^[2,3,4]



- Literature

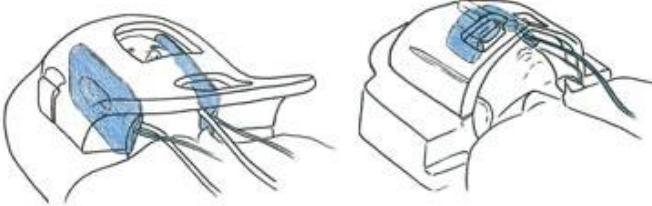
MP2RAGE FLAWS, multi-shell DTI, multi-band BOLD

- Fine-tuning: calculations + **trial-and-error**
BOLD flip angle, time of inversion, bandwidth, filters, ...

How did we make it? - 2



2) Meta-protocol optimizations:

- Protocol programming:
 - › **Maximize speed** (motion resilience, avoids sedation & reacquisitions)
 - › Acquire BOLD first (unlikely sedated)
 - › Conditional naming
- Physical devices:
 - › **3D Head immobilizer**
 - › Comfort pillows (reduces back pain), blanket, etc.





Take home message

- ▶ Cutting-edge research MRI under clinical constraints possible
- ▶ Quality-speed trade-off can be an opportunity
- ▶ **New analyses opportunities in clinical populations**
(dynamic connectivity, multi-tissues unconstrained DTI, ...)
- ▶ **Reduce risks & ethical issues by avoiding sedation**
- ▶ Future: compressed sensing, quantitative/synthetic MRI^[1], thermoplastic mask^[2], AI reconstruction^[3], multi-echo BOLD (ME-ICA)^[4]

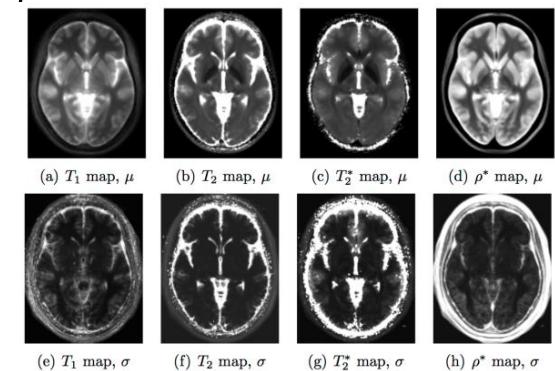


Figure: Mean and standard deviation templates of the T_1 , T_2 , T_2^* and ρ^* maps.

- Full protocol for Siemens Vida (need SMS license)
& bibliography: github.com/LRQ3000/mri_protocol
& analysis scripts: github.com/LRQ3000/csg_mri_pipelines

[1] Gonçalves, Serai, Zuccoli, 2018 [2] Mandija, Agata et al 2019 [3] Bo Zhu et al, Nature, 2018 [4] Dipasquale et al, 2017 ¹⁴



Thank you for your attention!

github.com/LRQ3000/mri_protocol

Basic analysis scripts: github.com/LRQ3000/csg_mri_pipelines

Huge thanks to Jean-Marc Léonard
at Siemens Healthineers and to
Jean-Flory Tshibanda, Nathalie
Maquet and the Liège Hospital's
Radiodiagnostic team and Pearltec
for their support!



Bonus slides

MRI: the time-quality conundrum



- ▶ Great polyvalence, for both research and clinical purposes
- ▶ Wide array of imaging contrasts: structural/function anatomy/connectivity, blood flow, lesions, etc.
- ▶ But clinical vs research needs are different:
 - Limited acquisition time (30 to 60 min) vs virtually unlimited (2h+)
 - Clinical pertinence (eg, lesions) vs cutting-edge (multi-shell DTI)
 - Uncooperative/uncontrolling patients (motion, discomfort, panic!) vs healthy volunteers (instruction compliance, no motion, calm)
- ▶ Usually results in a compromise: most sequences are clinical, some are for research with sub-optimal outdated (but faster) parameters

→ Can we make a MRI protocol both with cutting-edge research sequences and under clinical constraints?

How did we make it?



1) Technological optimization:

- Modern **acceleration** technologies:
GRAPPA parallel imaging + simultaneous multi-slice (SMS aka multi-band).
Beware of speed-quality trade-off!
- Literature for base sequences (MP2RAGE FLAWS, multi-shell DTI, multi-band BOLD)
- Calculations + **trial-and-error** to fine-tune parameters (BOLD flip angle, time of inversion, bandwidth)

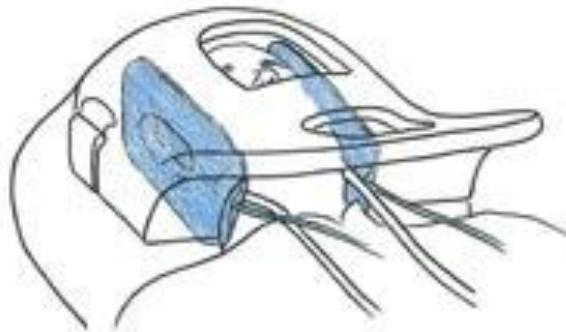
How did we make it? - 2



2) Meta-protocol optimization:

- Careful protocol programming:
 - › Maximize speed of sequence acquisition
(reduces risk of motion and need for sedation)
 - › Place BOLD first, structural/rest after
(ensures patient is awake, less distressed, always guarantees a non-sedated BOLD)
 - › Sequence renaming depending on choices (eg, sedated or not?) for automatic documentation stored in DICOMs
(bypass lack of conditional custom data storage in MRI software)
- Physical devices:
 - › Head immobilizer
 - › Comfort knee pillow (reduces back pain), blanket, etc.

Inflatable 3D head immobilizer



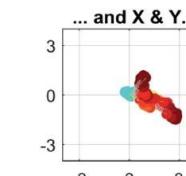
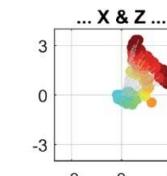
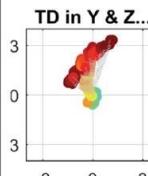
(here: Pearltec MultiPad)

Reduces:

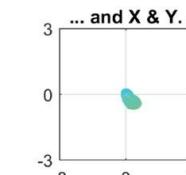
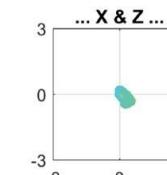
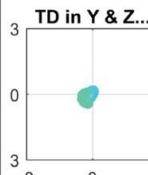
- **motion** artifacts
- need for **sedation**
(see infants studies, eg,
Yamamura & Inatomi et al,
2018)



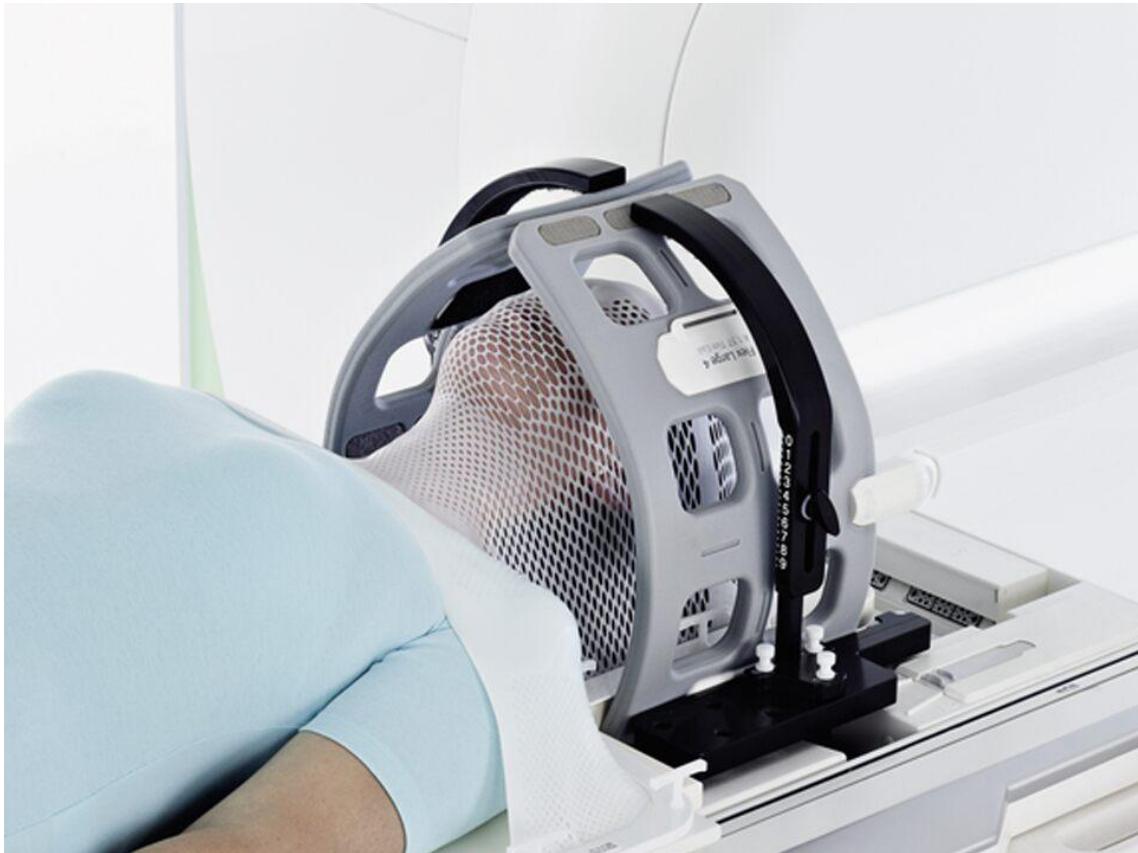
Movement profile for conventional foam



Movement profile for Pearltec positioning system



Future: Thermoplastic masks?



(Mandija, Agata
et al 2019)

Additional advices



- ▶ Enable 3D distortion correction, for all!
- ▶ Use alternate streams, allows to save non distortion corrected versions at no cost!
- ▶ Enable **Prescan Normalize** for better contrast (eases coregistration) on all sequences
- ▶ Disable other filters (Hamming, frequency/smoothing, etc)
- ▶ Disable PACE (prospective motion correction), as this prevents retrospective motion correction (ie, with external softwares such as ART)
- ▶ If lots of Gibbs noise (eg, in FLAWS or MP2RAGE), lower GRAPPA acceleration!
- ▶ For multi-shell DTI, acquire 3 different DTI sequences and bundle together with a Copy Reference to copy the acquisition parameters automatically (necessary for the multi-shell DTI to be valid)

Additional advices



- ▶ With uncooperative/uncontrollable populations, the speed-quality trade-off might be simpler: better to speed up and have a more stable (but lower resolution) image, than have a high-resolution image that fails most of the time to be acquired because of motion!
- ▶ Acquire with interpolation and rescale, eg: acquire at $0.5 \times 0.5 \times 1.0 \text{mm}$ and rescale to 1.0mm^3 , slight increase in SNR
- ▶ Increasing bandwidth reduces susceptibility to metal and chemical artifacts, useful for patients with potentially blood or metal infarcts

About free experimentation

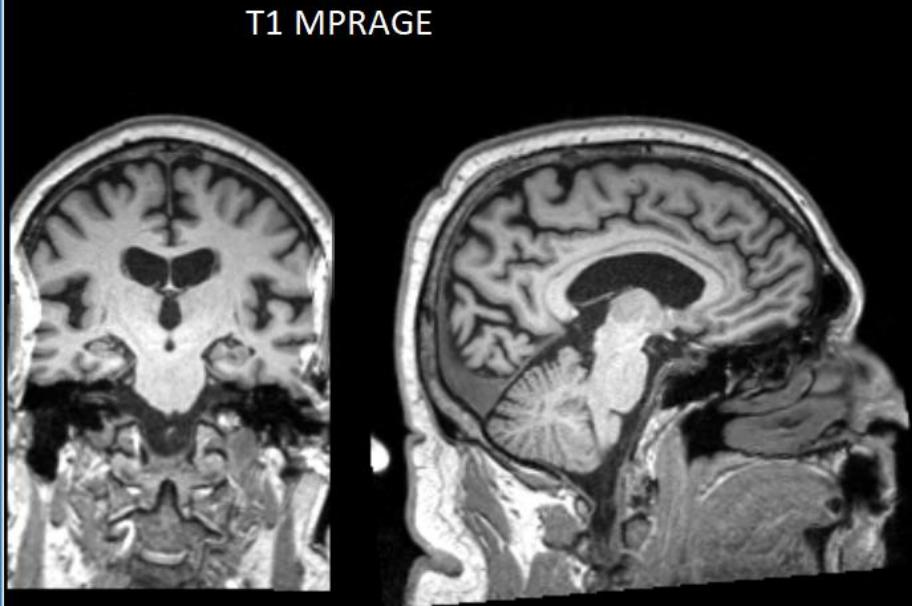


- ▶ Feel free to experiment with your protocol, often the sequences are not optimized for your machine and/or needs.
- ▶ How to proceed: no necessary need for calculations, trial and error is still the best approach (use bisection approach), but where available, calculations can save you some time instead.
- ▶ Try on a dummy or a healthy volunteer, under supervision from radiologists or MRI brand engineer to ensure no risks notably of tissue over-heating (SAR). Normally most modern machines implement safeguards that should in any case prevent these issues by warning the operator and change adequately the protocol.

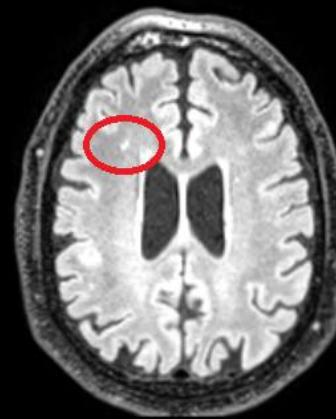
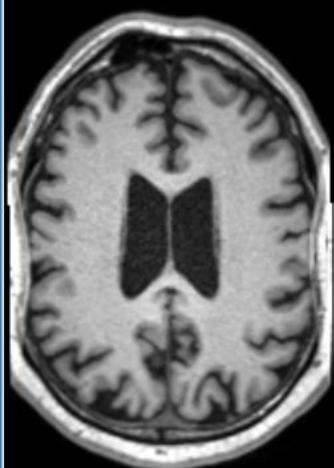
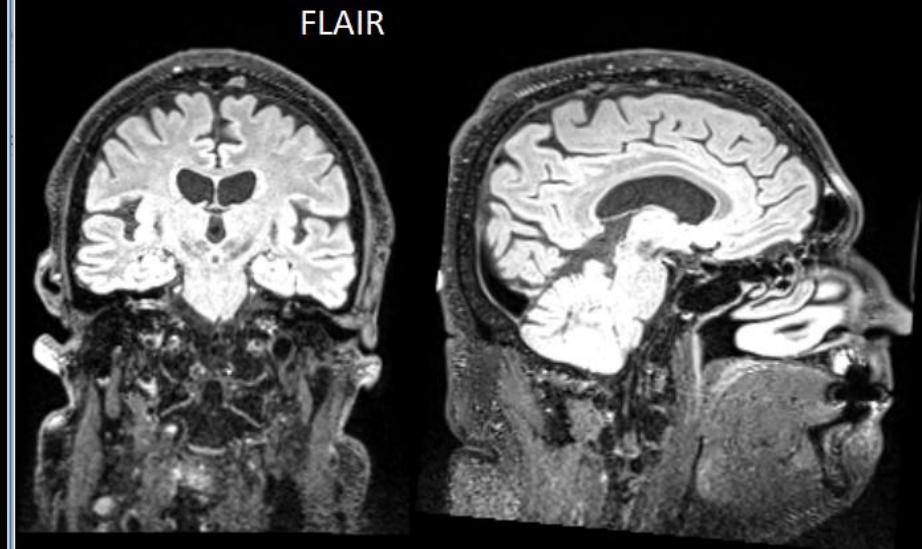
Clinical T1 FLAWS vs FLAIR



T1 MPRAGE

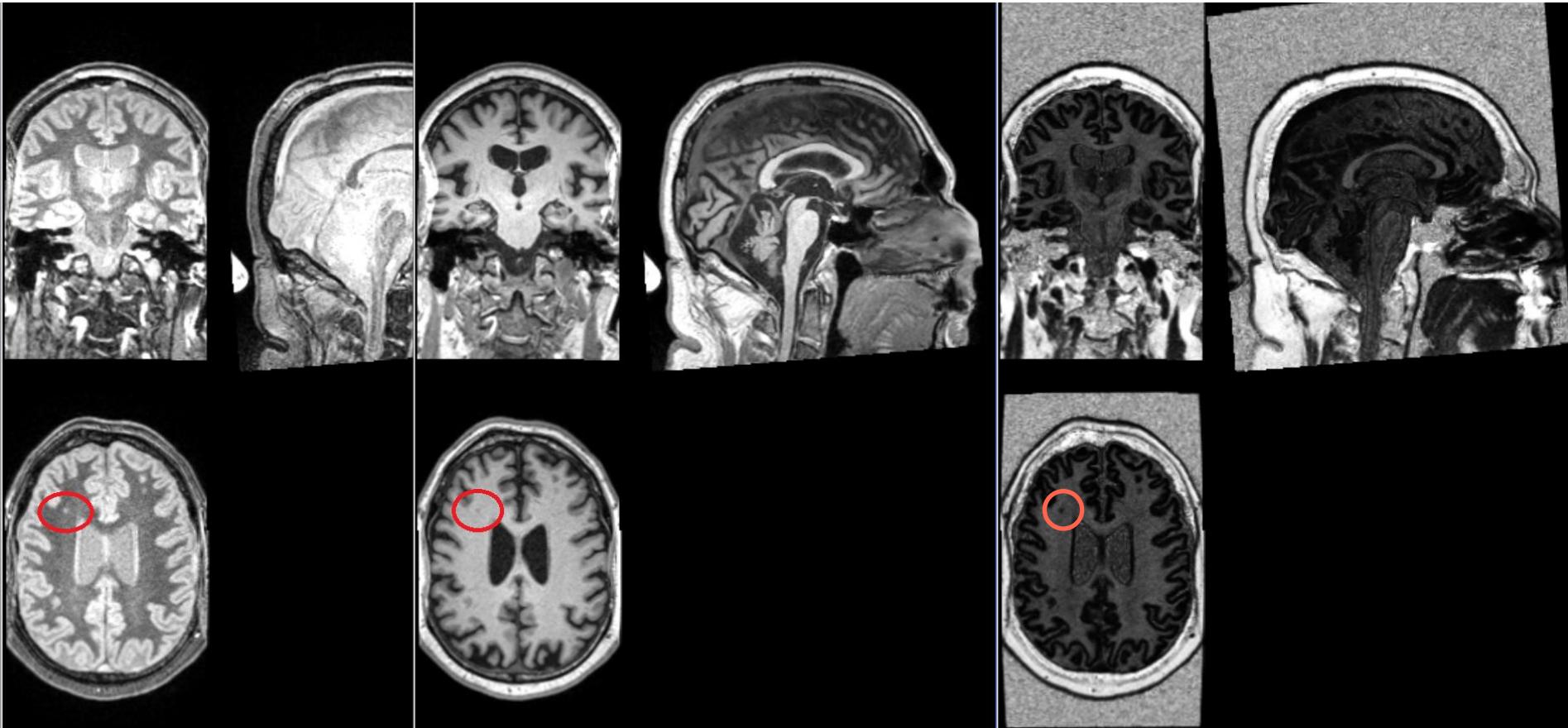


FLAIR



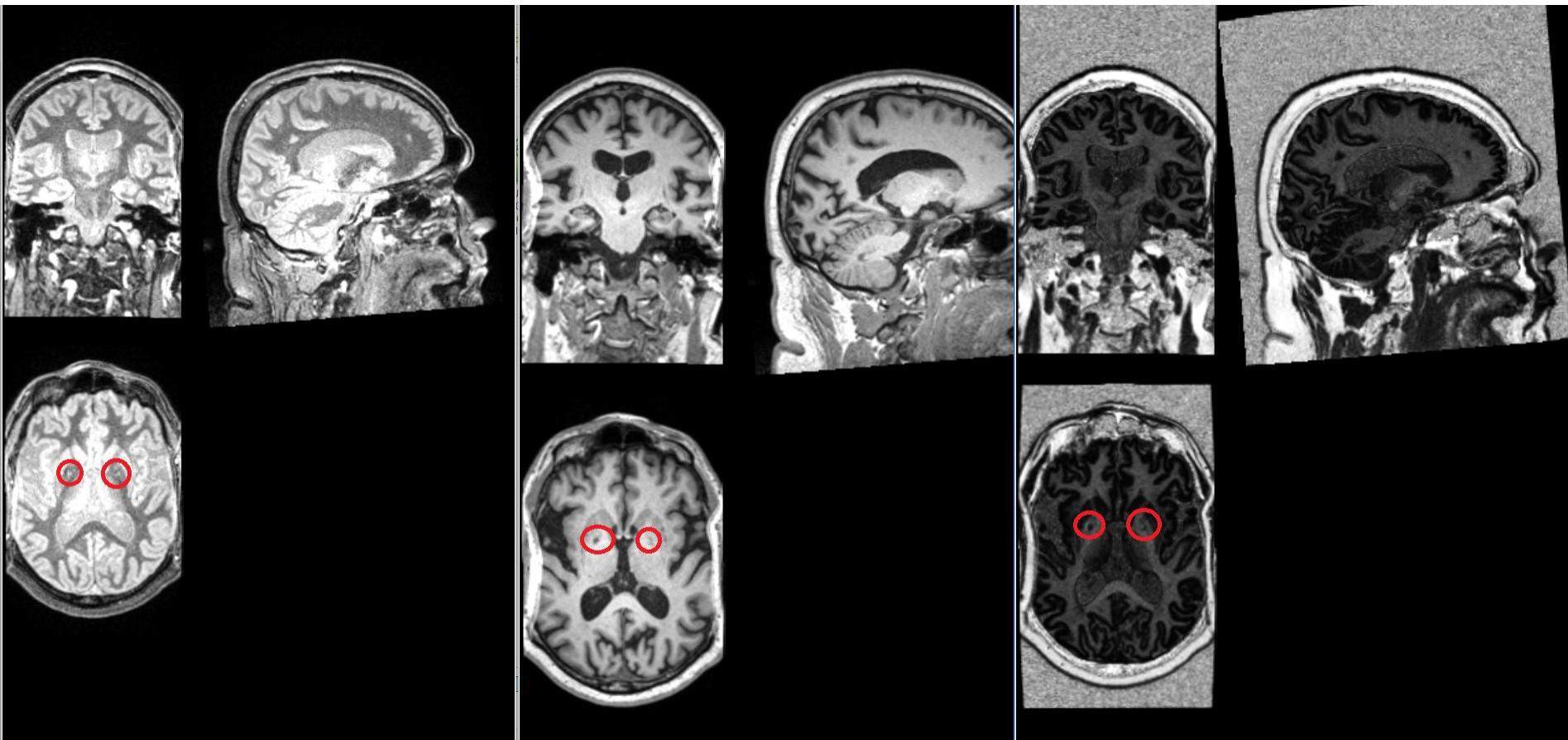
Infarct invisible on T1 MPRAGE! But is visible on FLAIR

Clinical T1 FLAWS vs FLAIR



However, with FLAWS, the infarct is visible on the other contrasts generated simultaneously with the MPRAGE! Thus can complement/replace FLAIR in some instances. In addition, the 3rd image confirms that the infarct is in the white matter.

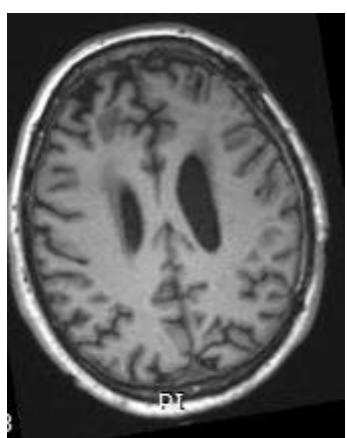
Clinical T1 FLAWS vs FLAIR



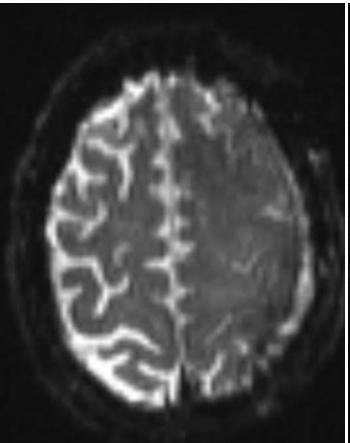
Two other infarcts of the same subject. The 3 contrasts of the FLAWS allows to confirm that the infarcts are located in the white matter.

See also: Enhanced visualization of lesions in focal cortical dysplasia using the fluid and white-matter suppression (FLAWS) sequence, Xin Chen, Tianyi Qian, Tobias Kober, Nan Chen, and Kuncheng Li, ISMRM 2017, <http://indexsmart.mirasoft.com/ISMRM2017/PDFfiles/2331.html>

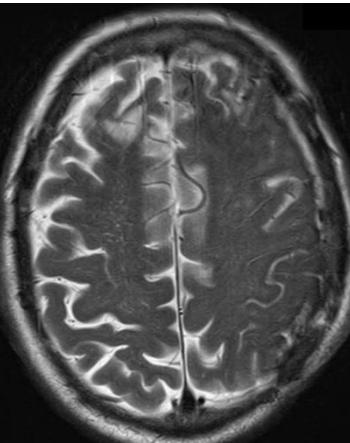
Better clinical assessment by combining modalities



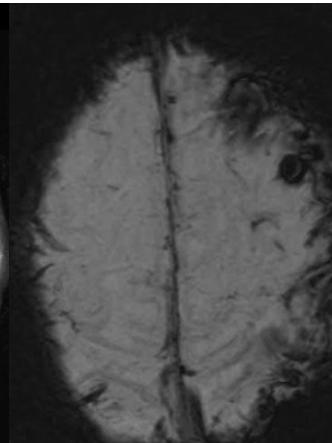
MPRAGE



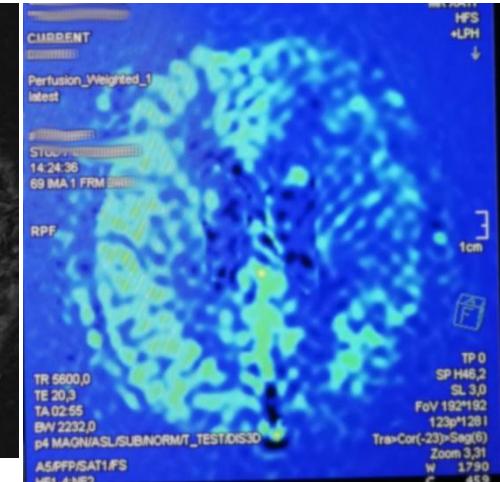
FLAIR



T2



SWI



PC-ASL
high resolution



→ Patient's craniectomy led to a decrease of vascularity and CSF fluid, only visible on FLAIR, T2 and PC-ASL, but not on MPRAGE nor SWI.

→ Can potentially impact HRF and thus PET and fMRI results.

MRI protocol decisions walkthrough (20-channel coil)



AHead_scout	00:14
	AutoAlign...
Patient anesthésie pour 1er BOLD...	
<input checked="" type="checkbox"/> no	Basic Deci...
ep2d_bold_repos_moco_s3...	03:48
<input checked="" type="checkbox"/> no	Basic Deci...
ep2d_bold_repos_moco_s3...	06:13
gre_field_mapping	00:57
t1_mp2rage_sag_p3_iso	05:15
t1_mp2rage_sag_p2_iso_F...	05:02
ep2d_diff_mddw_64_p2_s3...	02:07
ep2d_diff_mddw_64_p2_s3...	05:35
ep2d_diff_mddw_64_p2_s3...	05:43
t2_space_FLAIR_sag_p3_is...	03:57
	MPR Assi...
t2_sw_i_tra_p3_384_2mm	03:57
t2_tse_tra_512_p2	01:19
asl_3d_tra_fast	02:09
MPR Planning	
	MPR Planning

Short BOLD 3min47: Non-sedated! (except if really problematic patient)
Better have motion than sedation! (we can correct motion, but not sedation!)

Might be sedated if necessary, but please avoid

Structural: Sedation OK!

Note: If sedated, please choose « yes » in the boxes highlighted here in red.
Please do not delete or replace any sequence!
(Sequence name will change according to sedation decision set here)

Note2: 3 DTI sequences go together via a Copy Reference ALWAYS!
If you need to redo DTI, please redo all three!

All sequences can be implemented on any 3T Siemens
with multiband and MP2RAGE support (here Vida)

MRI protocol sequences list



1. AAhead_scout

2. Decision: Patient anesthetized?

Yes:

ep2d_bold_repos_moco_s3_p2_long_
avec_AG

No:

ep2d_bold_repos_moco_s3_p2_long_
sans_AG

gre_field_mapping

3. gre_field_mapping

4. t1_mp2rage_sag_p2_iso_FLAWS_fast

5. ep2d_diff_mddw_30_p2_s4_b700

6. ep2d_diff_mddw_64_p2_s4_b1000

7. ep2d_diff_mddw_64_p2_s4_b2000

8. t2_space_FLAIR_sag_p3_iso

9. t2_swi_tra_p2s2_ir_2mm

10. Decision: Acquire PC-ASL?

Yes:

pcasl_3d_tra_p2_iso_3mm_highres_fast

No: Stop.

Slice order: check in the machine's printout!

SIEMENS MAGNETOM TrioTim syngo MR B15

\\USER\\Head Lg\\Study Neuro Lg\\MyGroup Lg\\ep2d_bold_rest			
TA: 10:06	PAT: Off	Voxel size: 3.0x3.0x3.0 mm Rel. SNR: 1.00 SIEMENS: ep2d_bold	
Properties	Special sat.	None	
Prio Recon	Off	System	
Before measurement		Body	Off
After measurement		HEP	On
Load to viewer	On	HEA	On
Inline movie	Off	Positioning mode	REF
Auto store images	On	Table position	H
Load to stamp segments	Off	Table position	0 mm
Load images to graphic	Off	MSMA	S - C - T
segments		Sagittal	R >> L
Auto open inline display	Off	Coronal	A >> P
AutoAlign Spine	Off	Transversal	F >> H
Start measurement without	On	Coil Combine Mode	Adaptive Combine
further preparation		Auto Coil Select	Default
Wait for user to start	On	Shim mode	Standard
Start measurements	single	Adjust with body coil	Off
Routine		Confirm freq. adjustment	Off
Slice group 1		Assume Silicone	Off
Slices	32	! Ref. amplitude 1H	353.882 V
Dist. factor	25 %	Adjustment Tolerance	Auto
Position	Isocenter	Adjust volume	
Orientation	Transversal	Position	Isocenter
Phase enc. dir.	A >> P	Orientation	Transversal
Rotation	0.00 deg	Rotation	0.00 deg
Phase oversampling	0 %	R >> L	192 mm
FoV read	192 mm	A >> P	192 mm
FoV phase	100.0 %	F >> H	120 mm
Slice thickness	3.0 mm	Physio	
TR	2000 ms	1st Signal/Mode	None
TE	30 ms	BOLD	
Averages	1	GLM Statistics	Off
Concatenations	1	Dynamic t-maps	On
Filter	Prescan Normalize	Starting ignore meas	0
Coil elements	HEA/HEP	Ignore after transition	0
Contrast		Model transition states	On
MTC	Off	Temp. highpass filter	On
Flip angle	78 deg	Threshold	4.00
Fat suppr.	Fat sat.	Paradigm size	30
Averaging mode	Long term	Meas[1]	Baseline
Reconstruction	Magnitude	Meas[2]	Baseline
Measurements	300	Meas[3]	Baseline
Delay in TR	0 ms	Meas[4]	Baseline
Multiple series	Off	Meas[5]	Baseline
Resolution		Meas[6]	Baseline
Base resolution	64	Meas[7]	Baseline
Phase resolution	100 %	Meas[8]	Baseline
Phase partial Fourier	Off	Meas[9]	Baseline
Interpolation	Off	Meas[10]	Baseline
PAT mode	None	Meas[11]	Baseline
Matrix Coil Mode	Auto (CP)	Meas[12]	Baseline
Distortion Corr.	Off	Meas[13]	Baseline
Unfiltered images	Off	Meas[14]	Baseline
Prescan Normalize	On	Meas[15]	Active
Raw filter	On	Meas[16]	Active
Elliptical filter	Off	Meas[17]	Active
Hamming	Off	Meas[18]	Active
Geometry		Meas[19]	Active
Multi-slice mode	Interleaved	Meas[20]	Active
Series	Ascending	Meas[21]	Active
		Meas[22]	Active
		Meas[23]	Active

This « interleaved » means nothing!

Geometry

Multi-slice mode
Series

Interleaved
Ascending

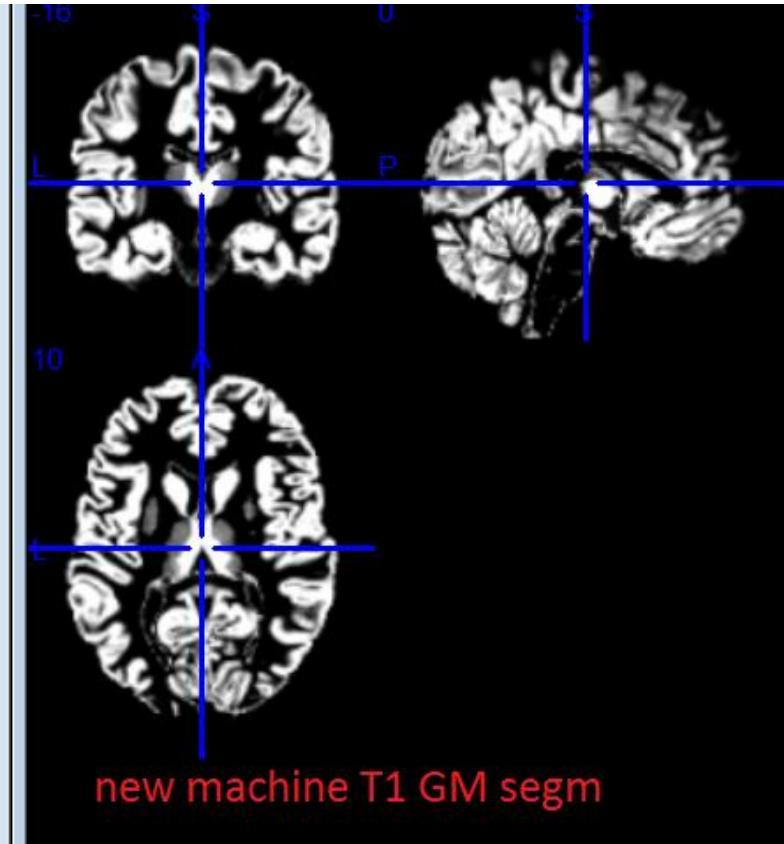
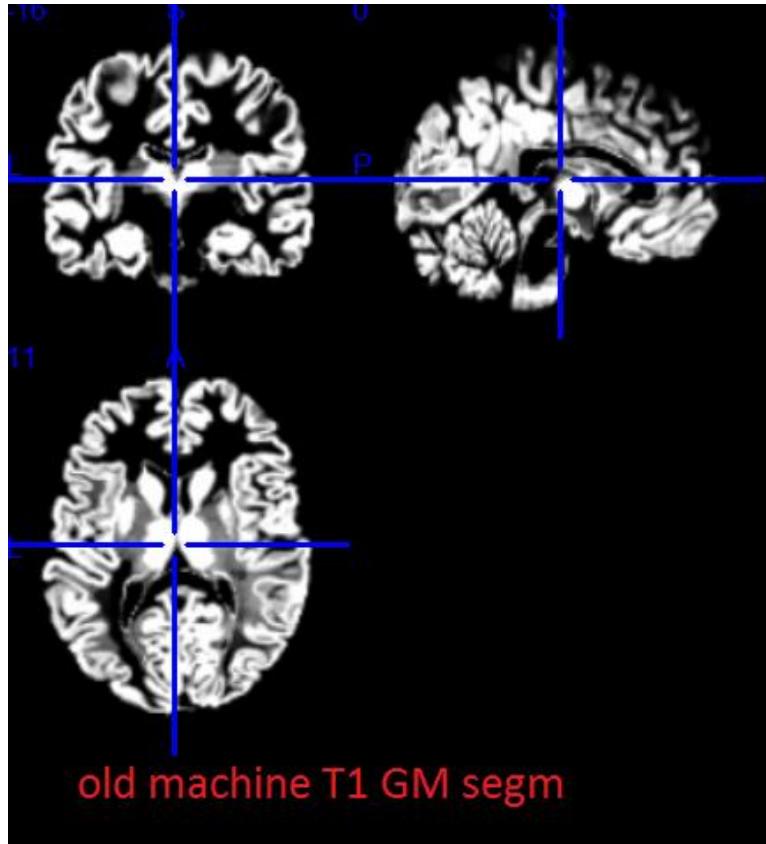


Asc员 = sequential ascending. Else it would
be « interleaved » here for interleaved ascending.

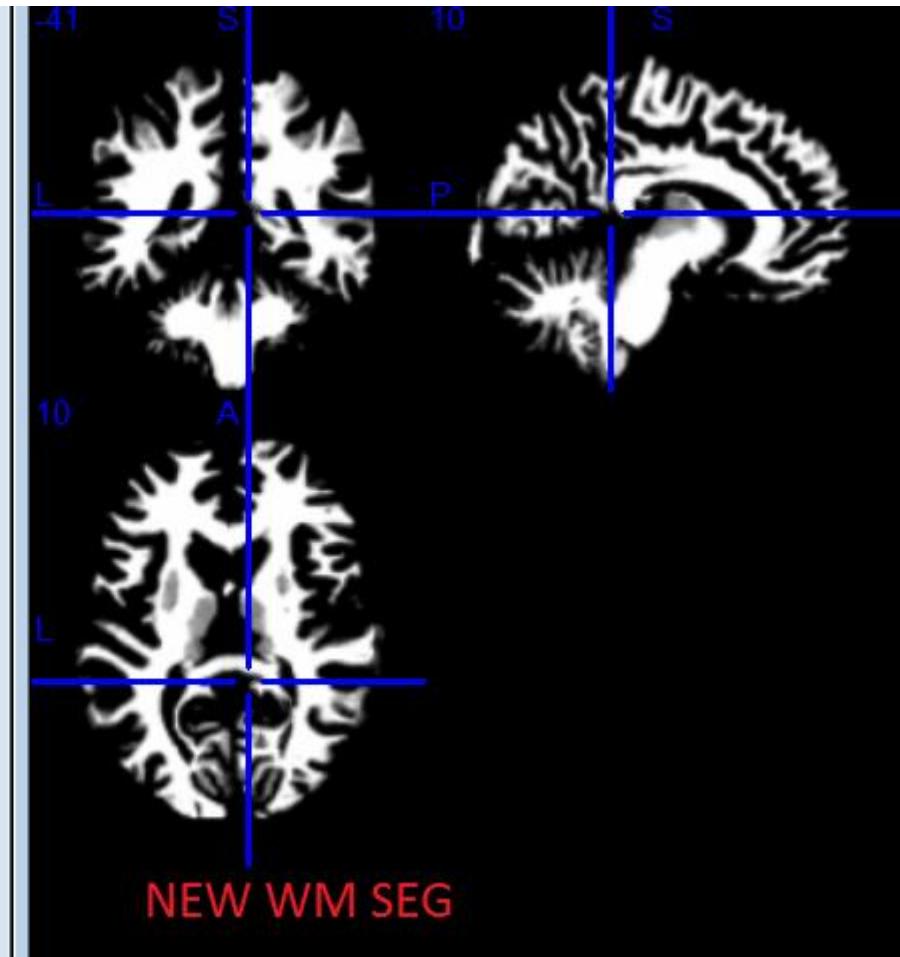
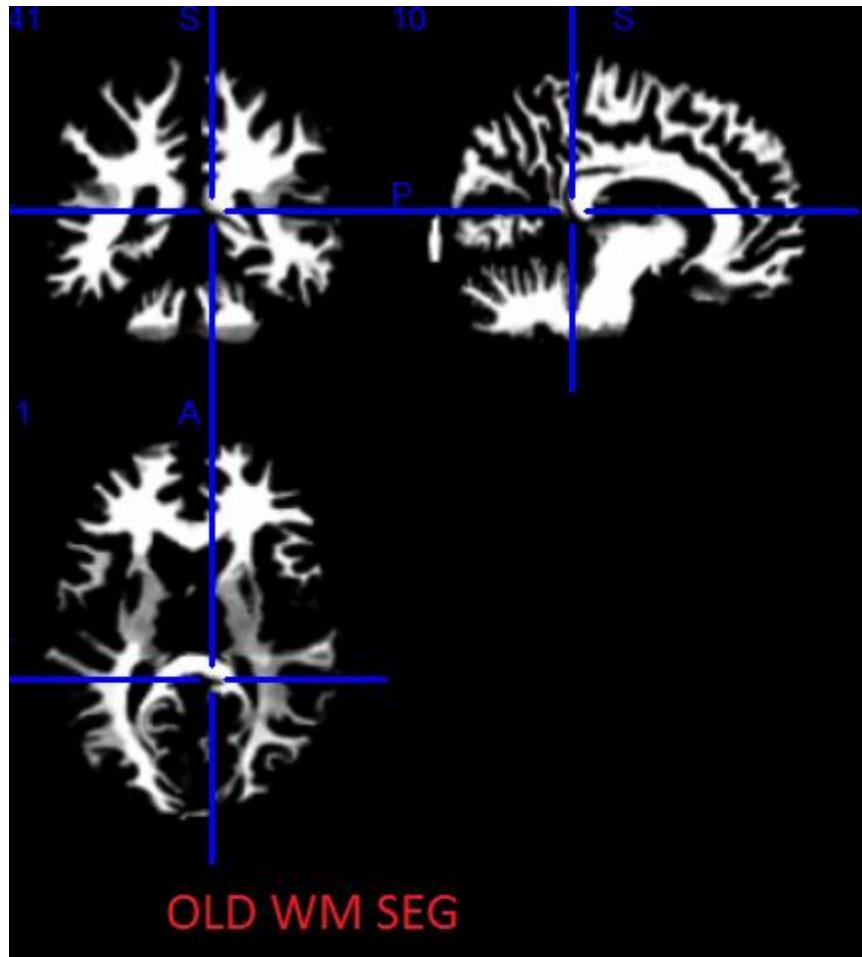
Geometry	
Multi-slice mode	Interleaved
Series	Ascending

5/+

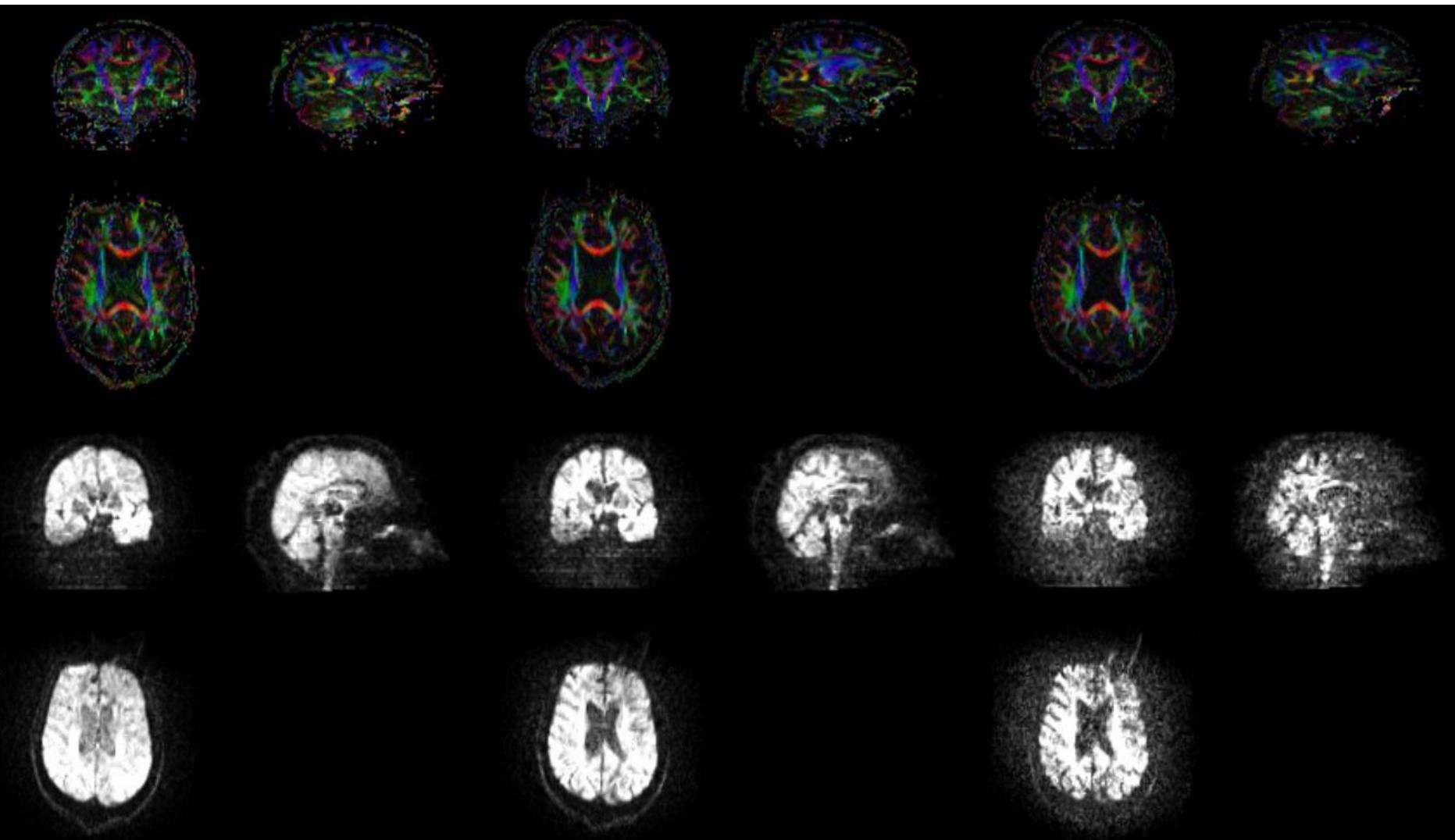
QA image example (same subject)



QA image example (same subject)



Multi-shell DTI



b700

b1000

b2000



Typical fMRI processing steps

Manual

- Select subjects, prepare demographics (age, gender, etiology, sedation, etc)
- Convert from DICOM to NIfTI
- Exclude bad subjects (too much motion, artifacts, brain surgery, metallic prosthesis, etc)

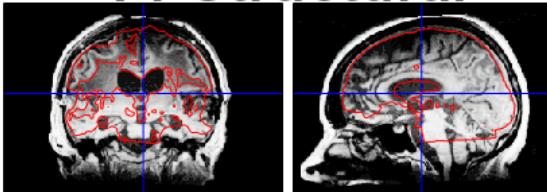
Takes > 90%
of the
analysis time!

Automatic (mostly)

- T1 reorient
- EPI/DTI manual coregistration
- Slice timing correction
- Realignment (motion correction)
- Auto coregistration
- Segmentation + Normalization (MNI 152)
- Smoothing
- Movement correction/rejection
- Denoising (PCA aCompCorr, ICA, etc.)

spm_auto_reorient_coregister: Enhanced automatic reorientation and coregistration on brain damaged patients with SPM12

T1 Structural

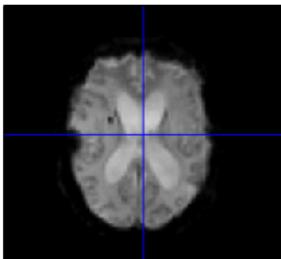
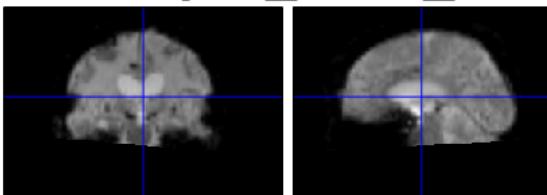


EPI BOLD



EPI BOLD

after spm_auto_coreg



→94% success rate

(11 totally off, 17 slightly
over 434 sessions, 410 subjects)

https://github.com/lrq3000/spm_auto_reorient_coregister

