Dealing with motion in fMRI scans

Jonathan Power

FMRIF Summer Course
14 August 2015

This talk is geared for post-bacs, people new to fMRI

What I want you to learn:

Big picture stuff, why motion matters in general terms

How we usually measure motion in fMRI

How we quantify the impact of motion on fMRI signals

IMAGING METHODOLOGY - Review

Magnetic Resonance in Medicine 69:621–636 (2013)

Prospective Motion Correction in Brain Imaging: A Review

Julian Maclaren,[1,2*] Michael Herbst,[1] Oliver Speck,[3] and Maxim Zaitsev[1]

NeuroImage 105 (2015) 536–551

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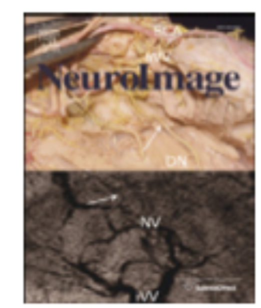
NeuroImage

journal homepage: www.elsevier.com/locate/ynimg



Review

Recent progress and outstanding issues in motion correction in resting state fMRI

Jonathan D. Power [a,*], Bradley L. Schlaggar [a,b,c,d], Steven E. Petersen [a,b,d,e,f,g]

Why motion matters:

It causes artifact, and the artifact can be influential

A problem for all major MRI modalities

task fMRI	(BOLD)
resting state fMRI	(BOLD)
diffusion imaging	(DTI, DSI)
structural imaging	(MP-RAGE)

In the last 5 years, we have realized that some findings in resting state and diffusion imaging were (mostly) not real

- developmental effects
- aging effects
- disease effects

New reports indicate that MP-RAGE-based findings may be similarly compromised (e.g., cortical thickness)

Head motion:

When people lie in the scanner, we try to minimize head motion
- padding/pillows
- thermoplastic mask (like masquerade ball)
- bite bar
- 3D-printed head mold

When people are asleep or under anesthesia, they still move

Breathing, heartbeat, yawning cause motion

The scanner can cause vibration

Within the cranium, the brain pulsates with the heartbeat
- about 50 microns at cortex, 100 microns in subcortex

Measuring head motion:

External records:
- IR cameras, lasers, optical techniques
- high temporal and spatial resolution
- sensors on the skin (often on goggle or eyeglass frames)

- skin motion is not necessarily head motion
- researchers don’t have or aren’t familiar with the equipment
- sensors can interfere with other in-scanner instrumentation
- researchers think data-derived estimates are good enough

Navigator scans:
- added to a pulse sequence, take ~50 ms
- not compatible/practical for some sequences
- no equipment needed

Field detection methods (not discussed)


http://journal.frontiersin.org/article/
10.3389/fneur.2014.00260/full


http://www.qualisys.com/wp-content/uploads/2011/05/mri-motion-capture-at-cardiff-university-2.jpg


https://www.igd.fraunhofer.de/en/Institut/Abteilungen/VHT/
Projekte/Camera-based-tracking-head-motion-MRI


http://tao.umd.edu/html/mri_head_movement_correction.html

http://www.theengineer.co.uk/news/software-for-stress-free-scans/299018.article

http://shadmehrlab.org/imaging.htm

http://www.fil.ion.ucl.ac.uk/Research/physics_info/PMC.html

Using head motion measures:

Retrospective correction:
- what we will talk about today

Prospective correction:
- there is a whole talk on this
- update the pulse sequence in real time
- can correct some motion artifacts
- is certainly promising

- not widely used in fMRI at this time
- if motion estimate wrong, image will become wrong
- complicated to assess helpfulness
  - the original “uncorrected” image doesn’t exist
  - you can’t see the motion anymore

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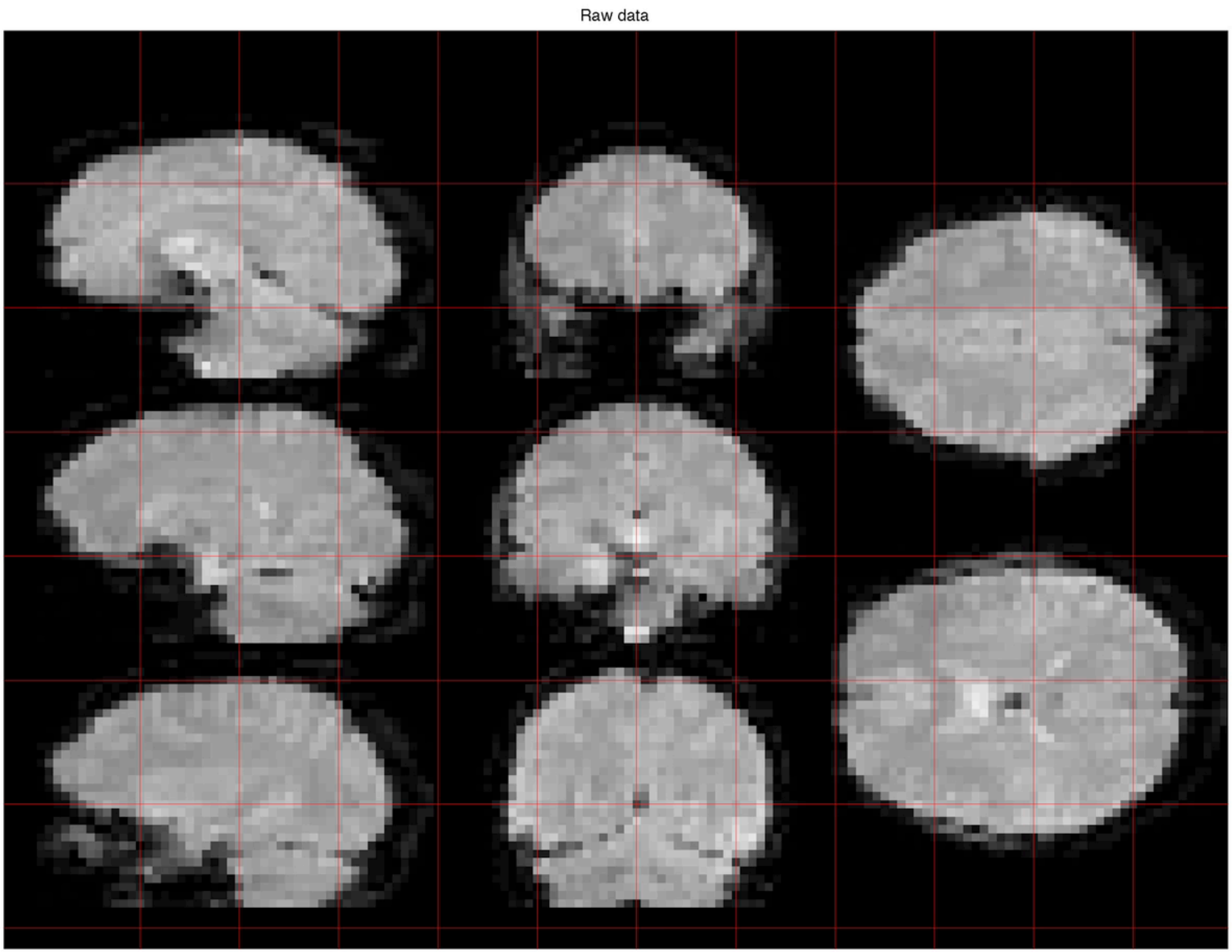

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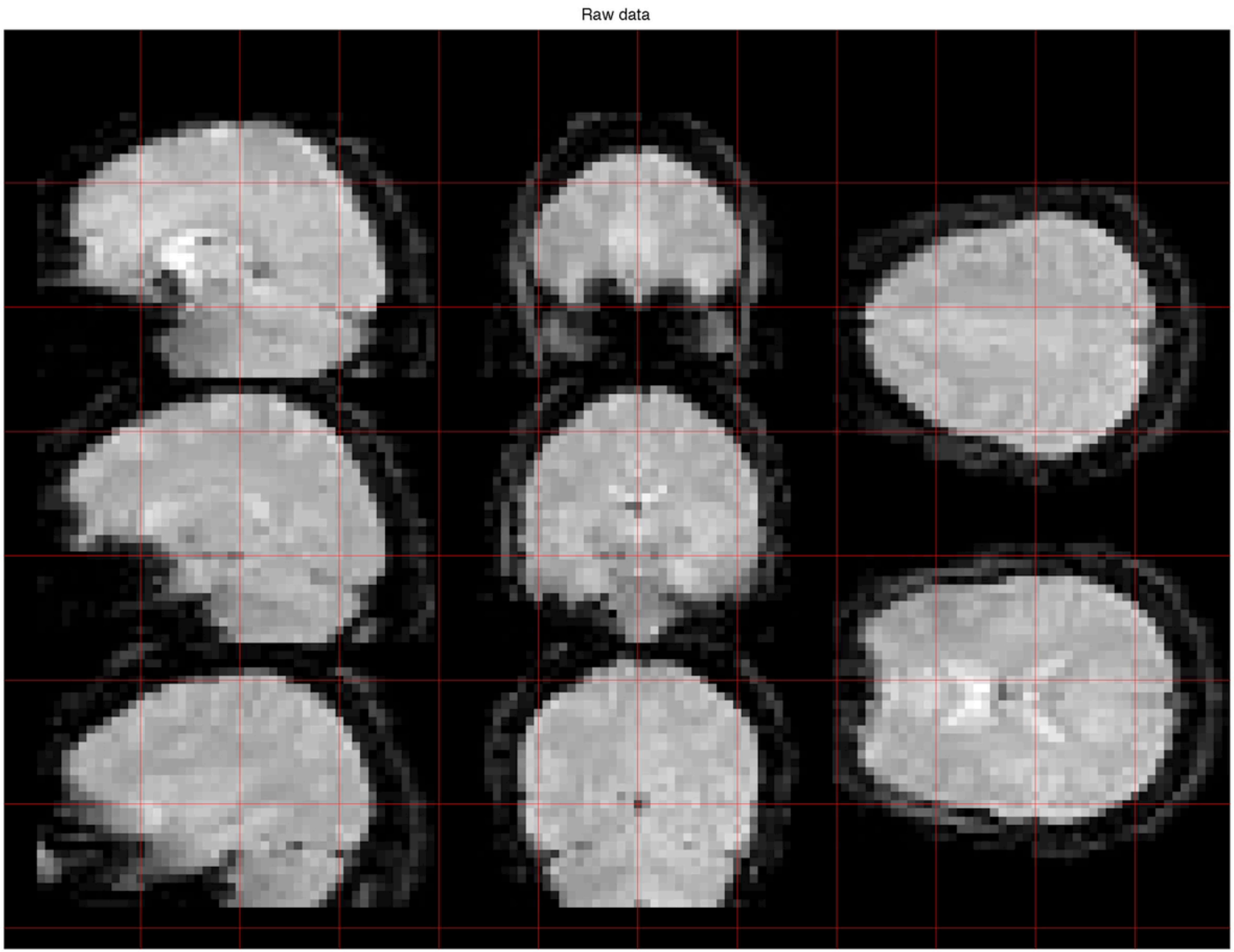

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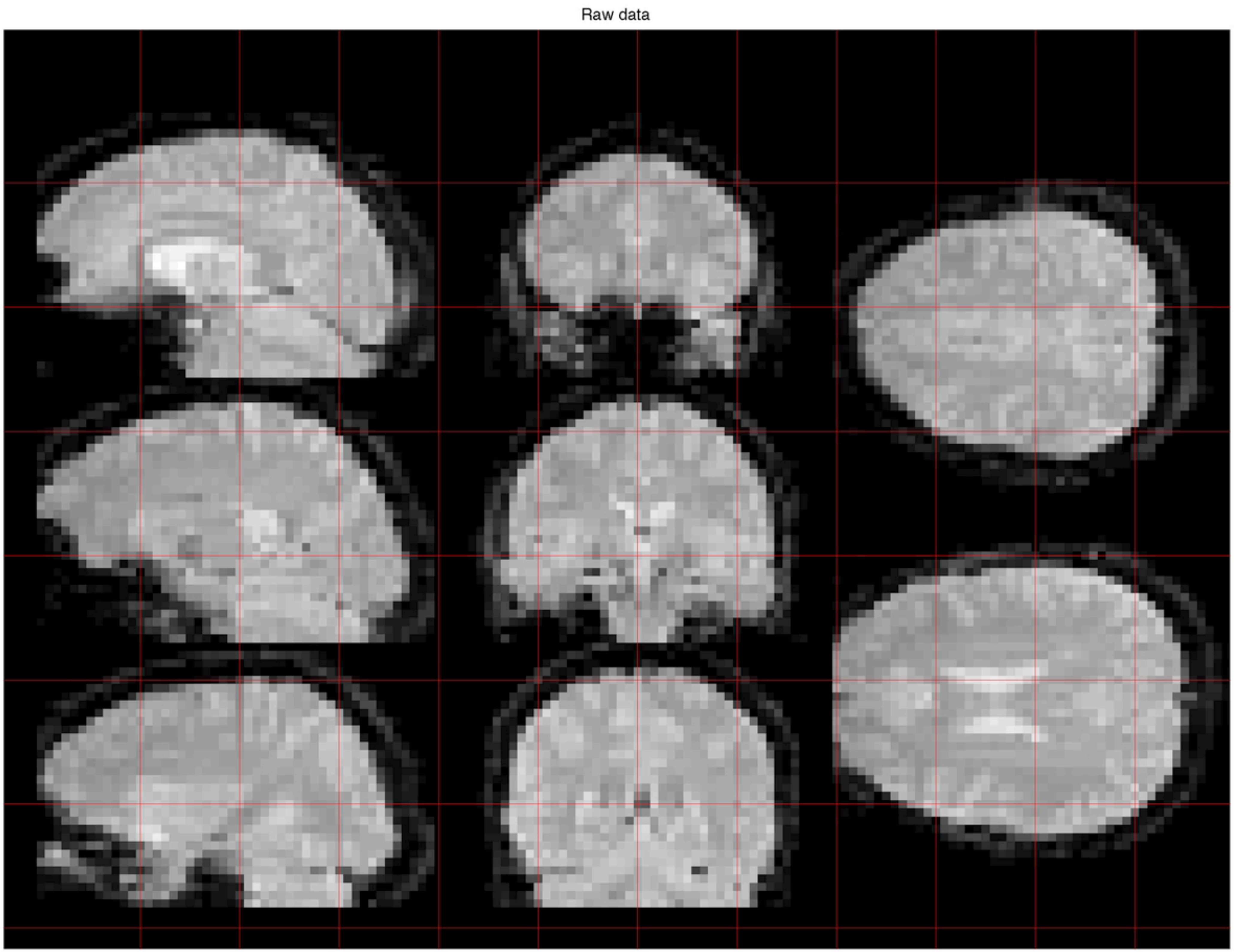

How we usually measure head motion in fMRI: from the images

It’s helpful to review how we get these images

Most people use EPI (echo-planar imaging) to get fMRI data
- You get a slice of the brain at a time
- Often the slices are interleaved

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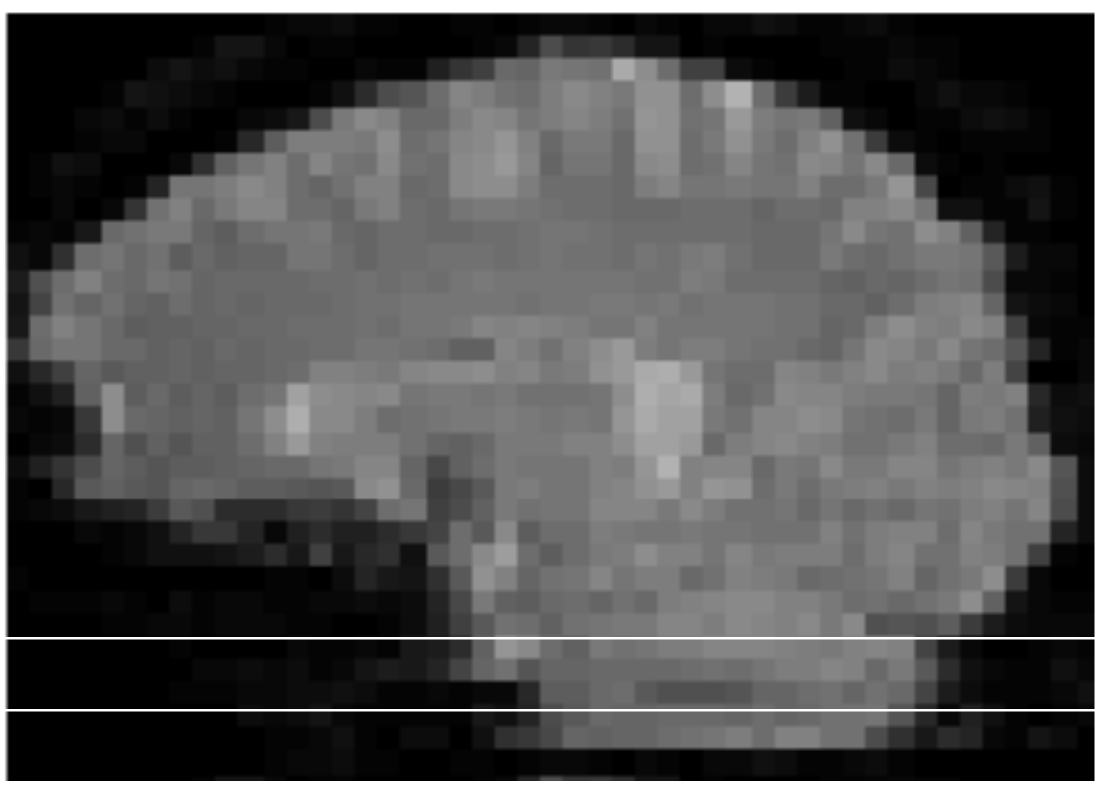

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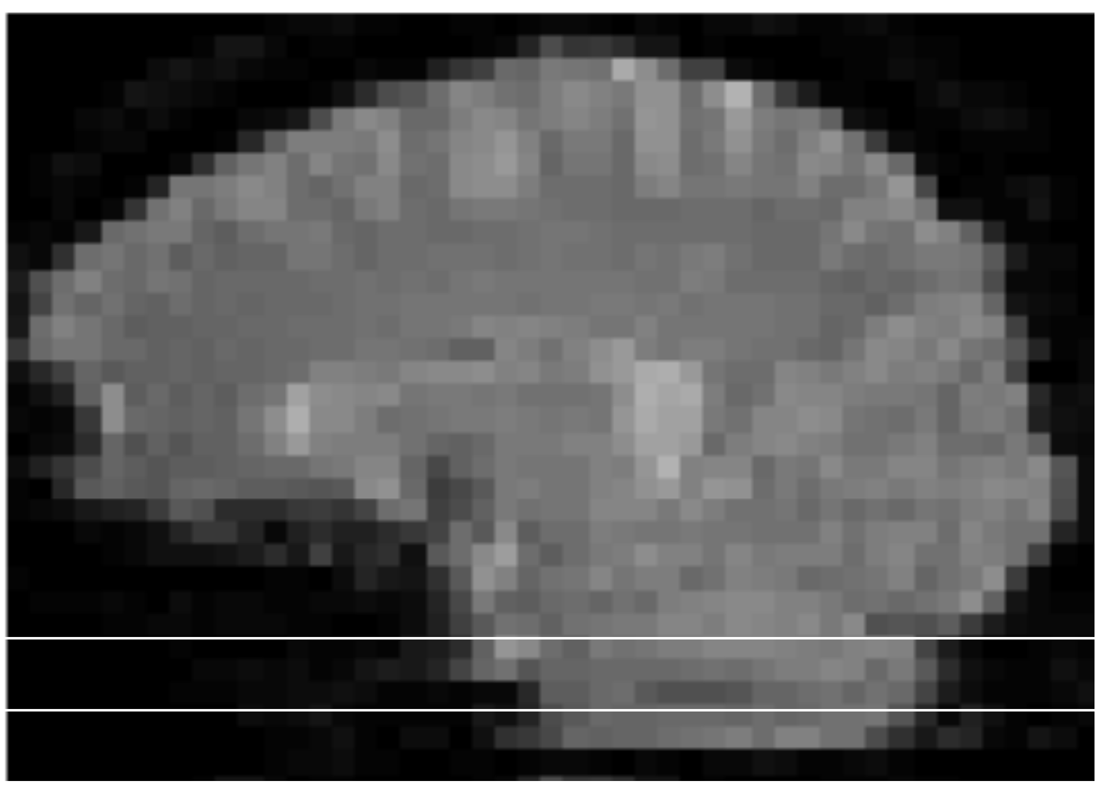

 # slices = 32
1 slice at a time
Time per slice = ~80ms
Volume time (TR) = 2500ms

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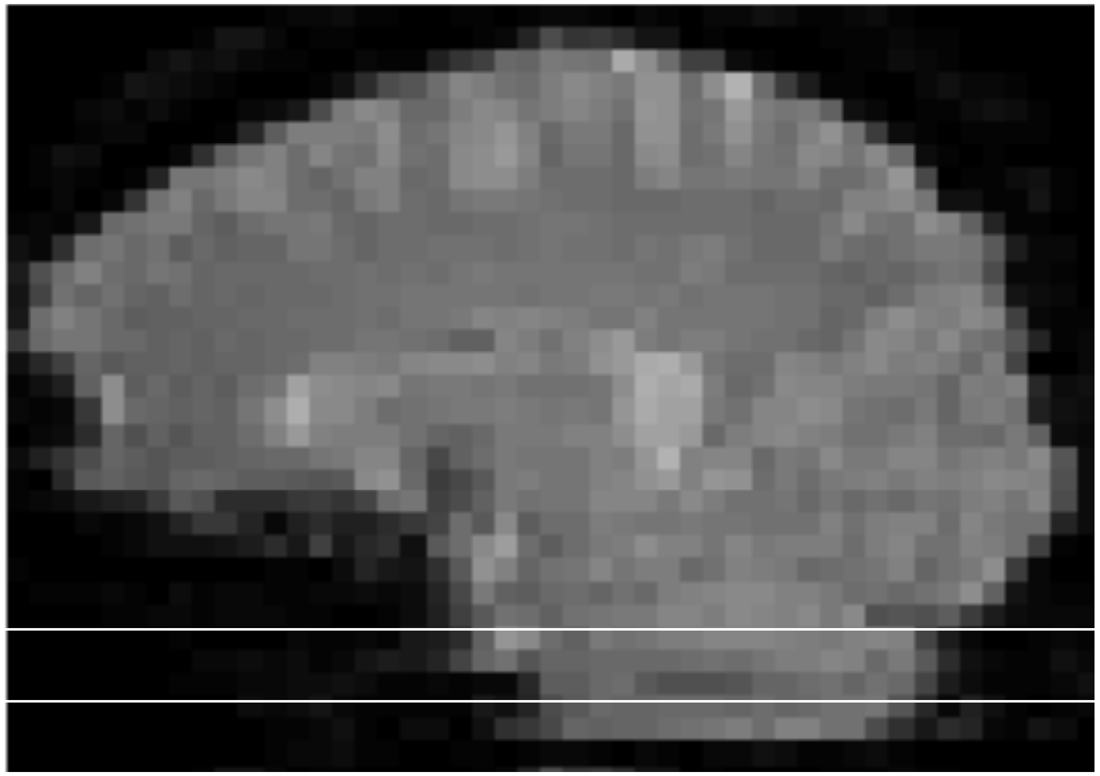

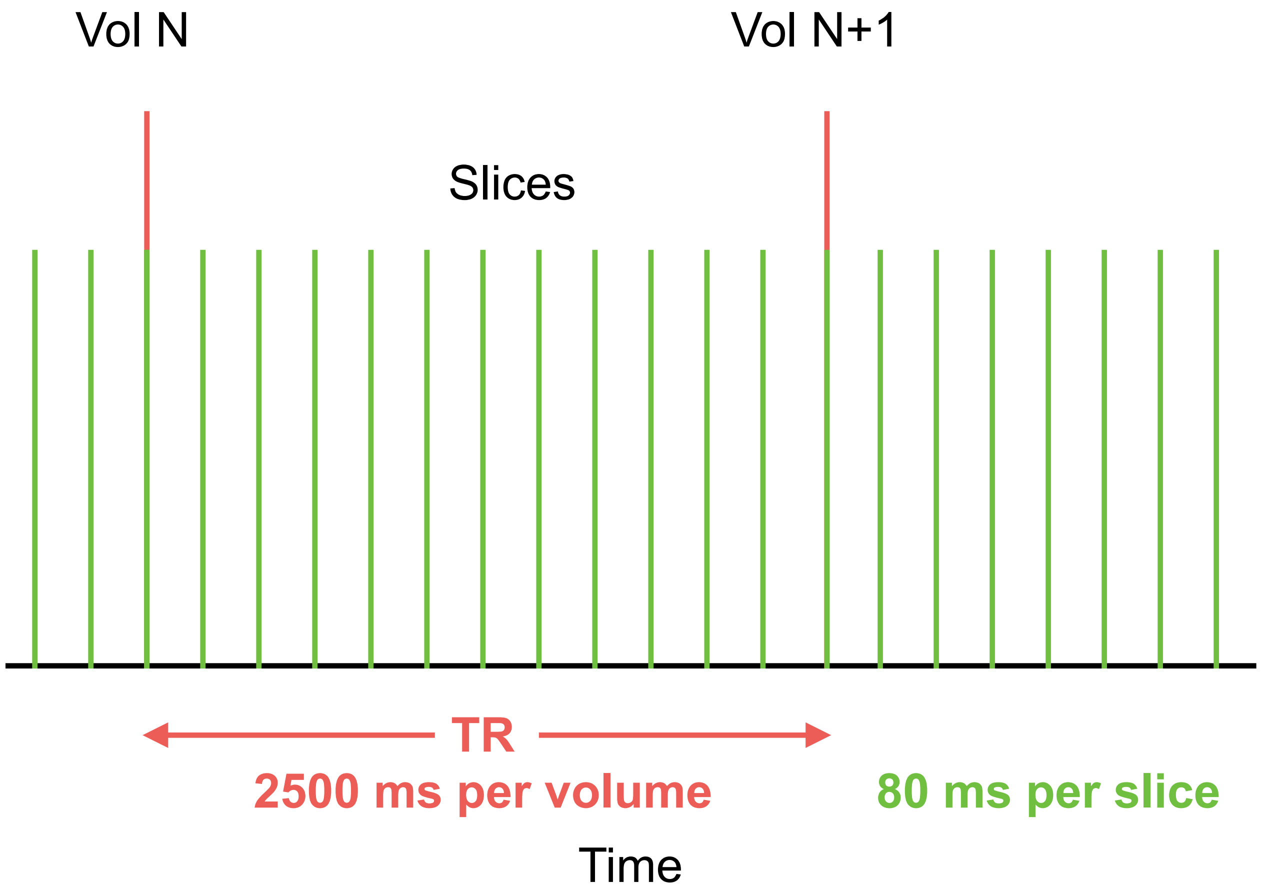

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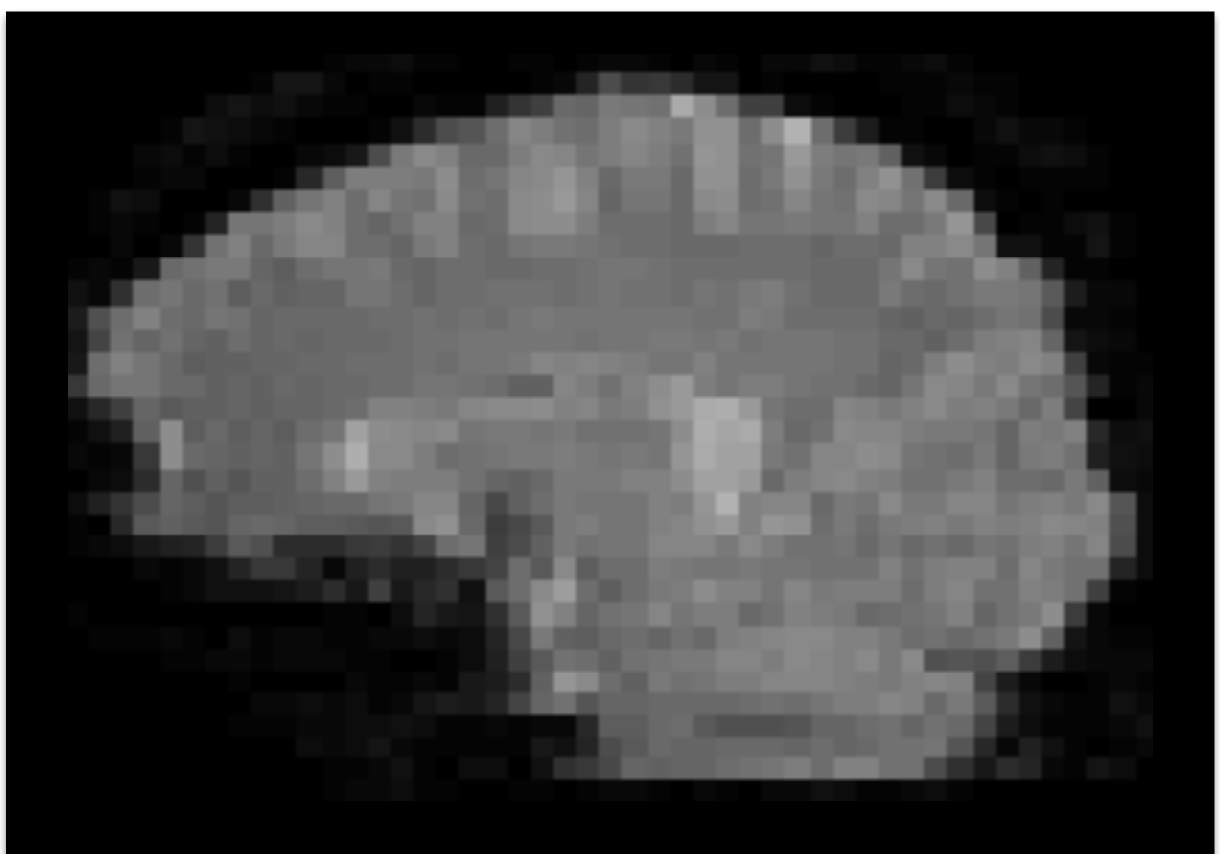

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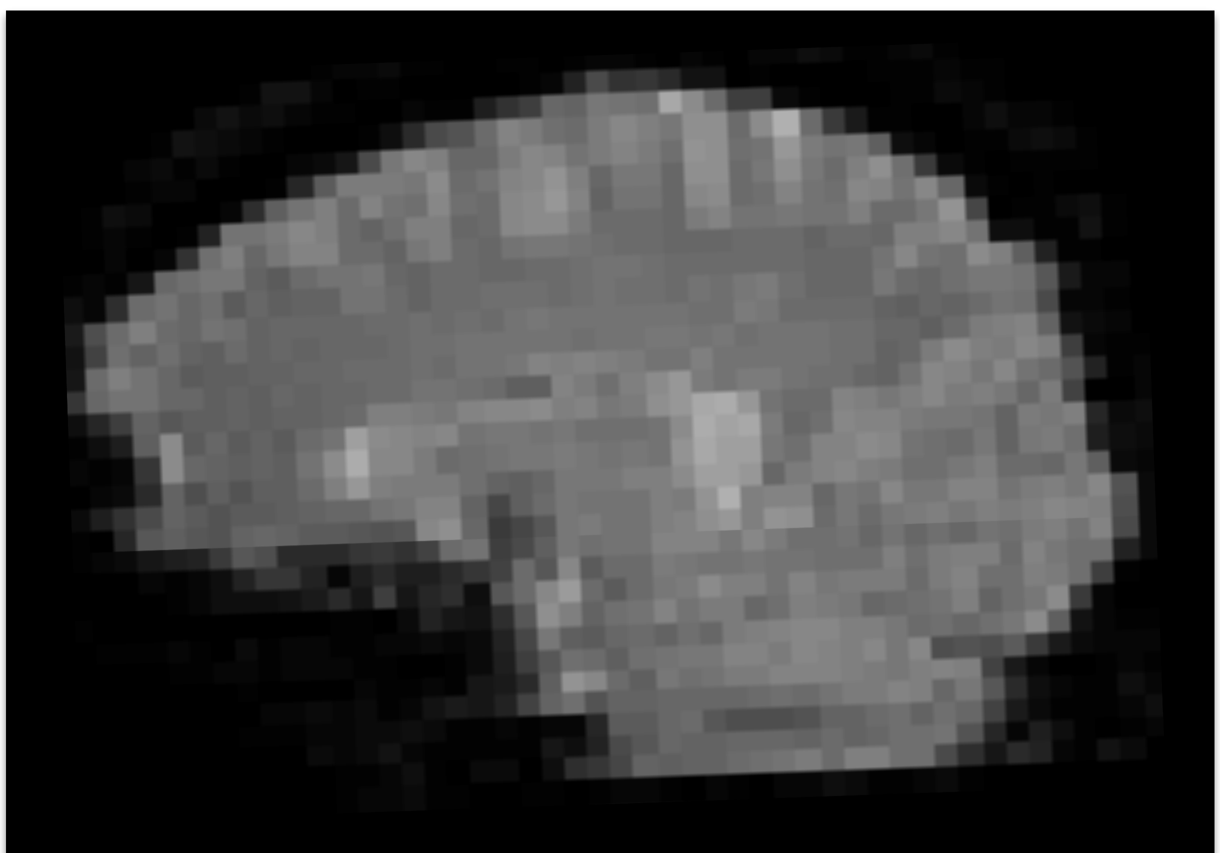

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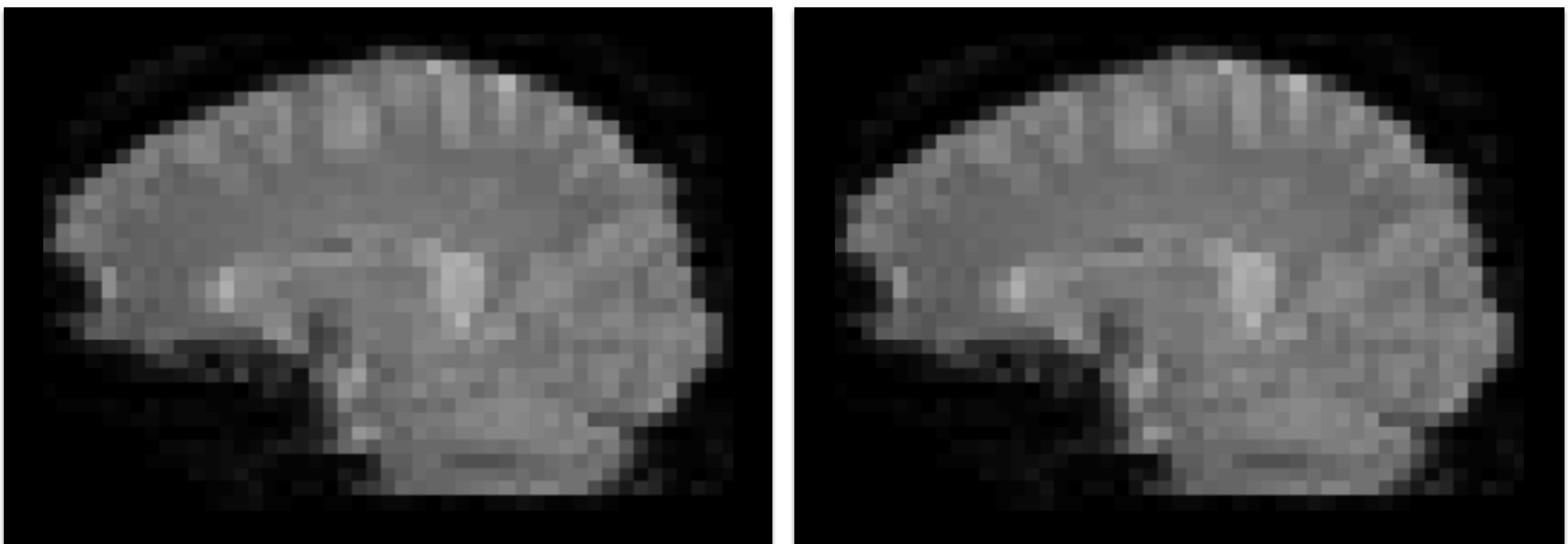

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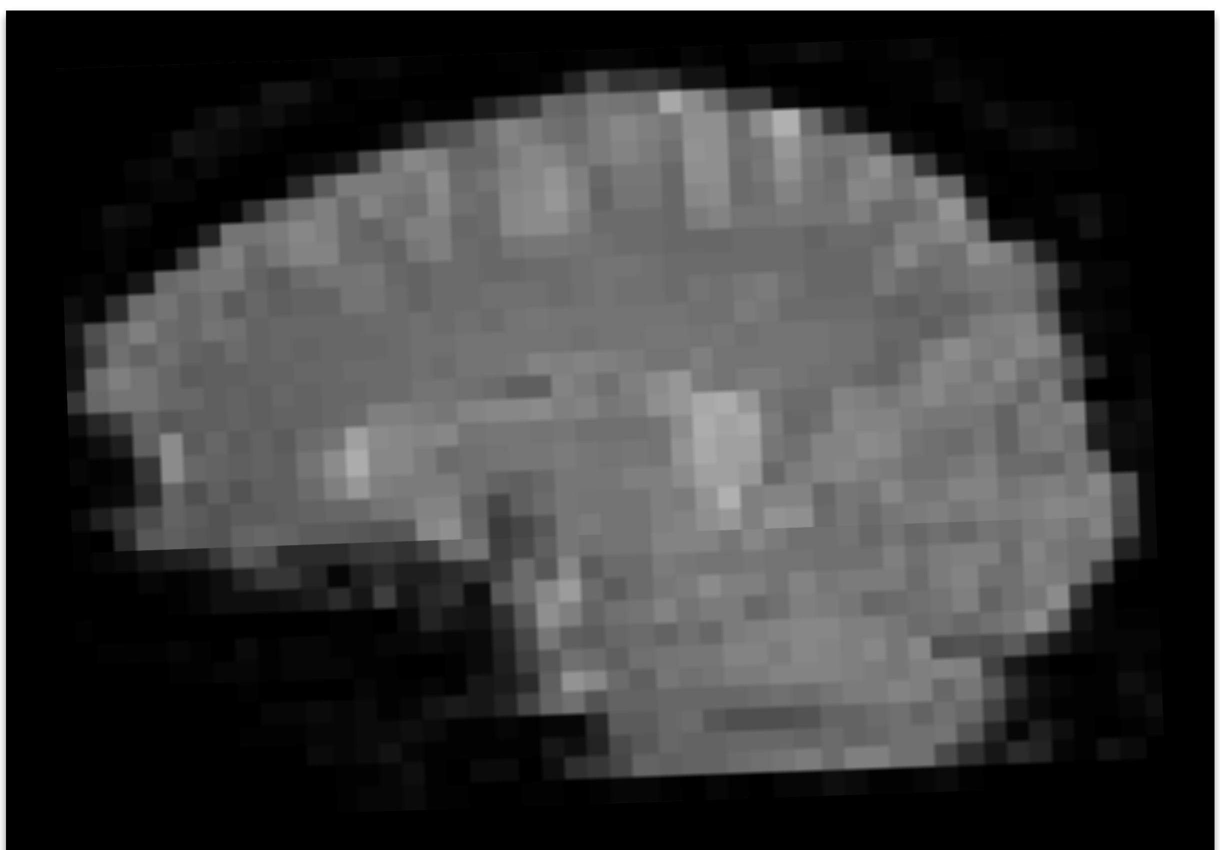

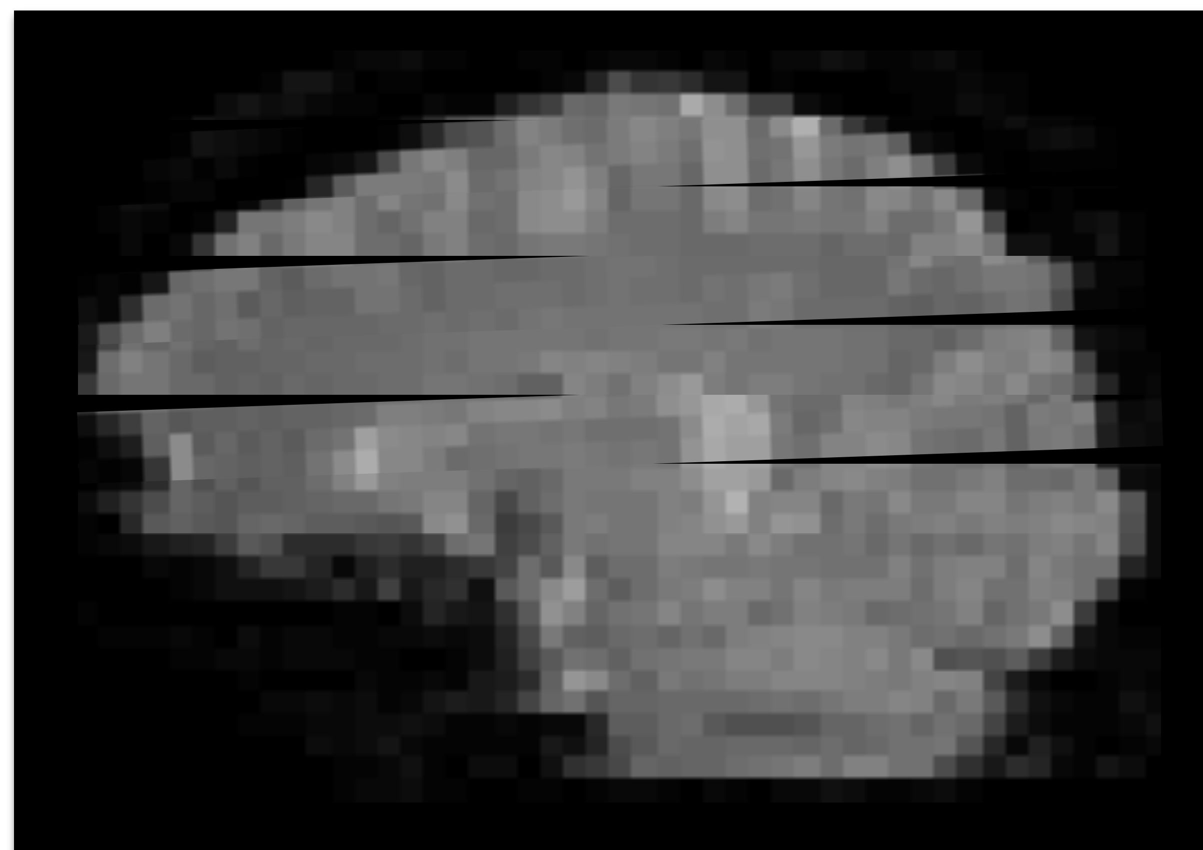

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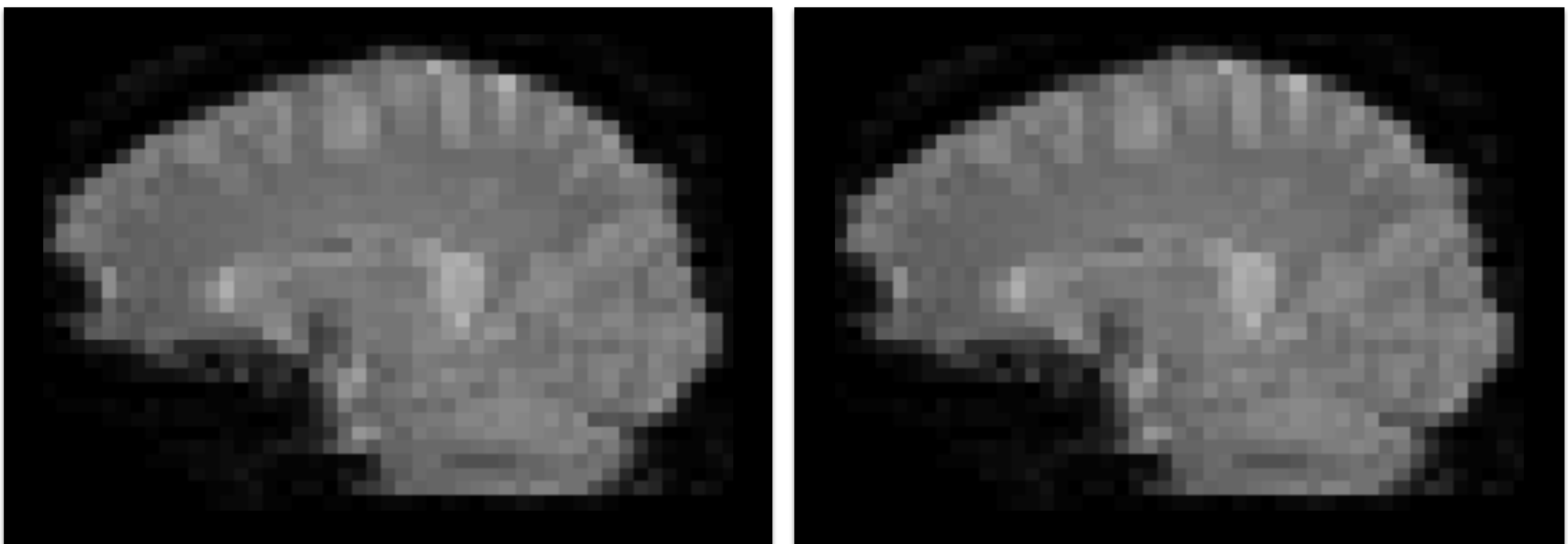

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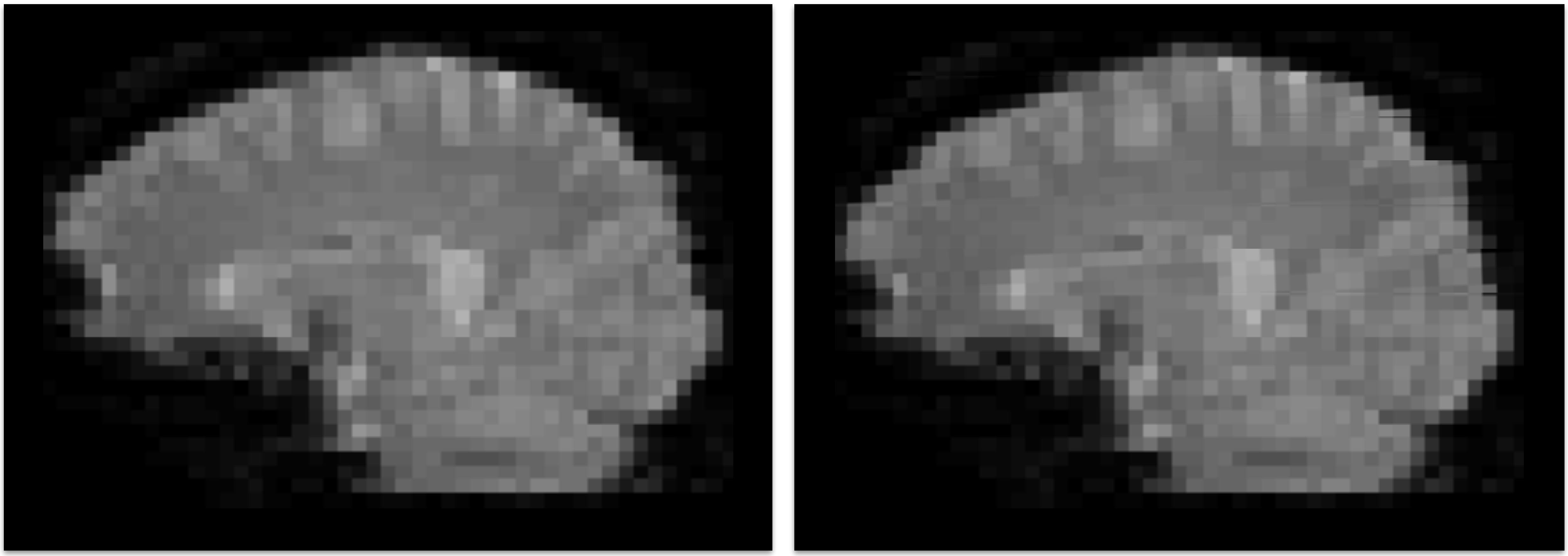

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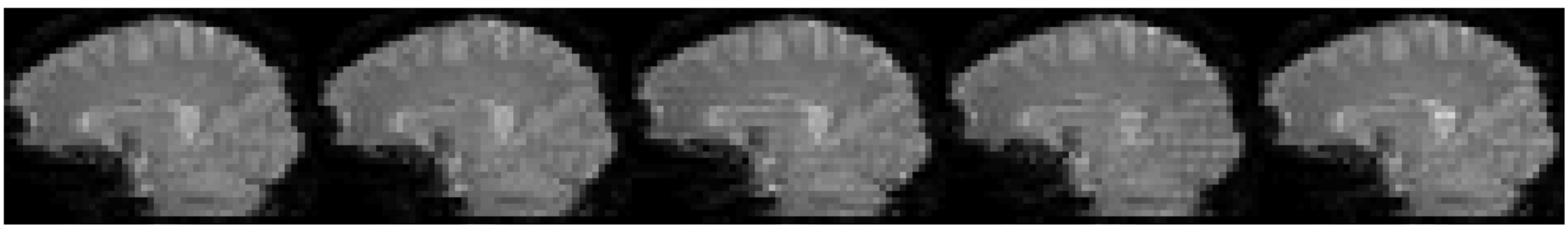

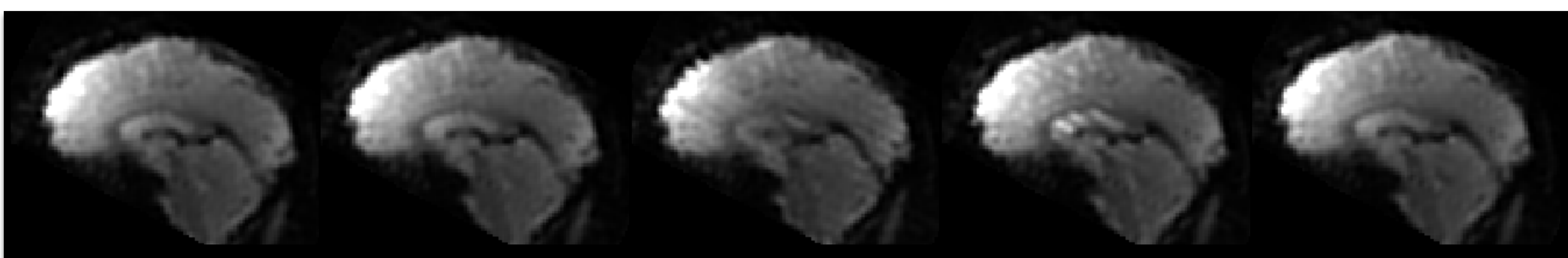

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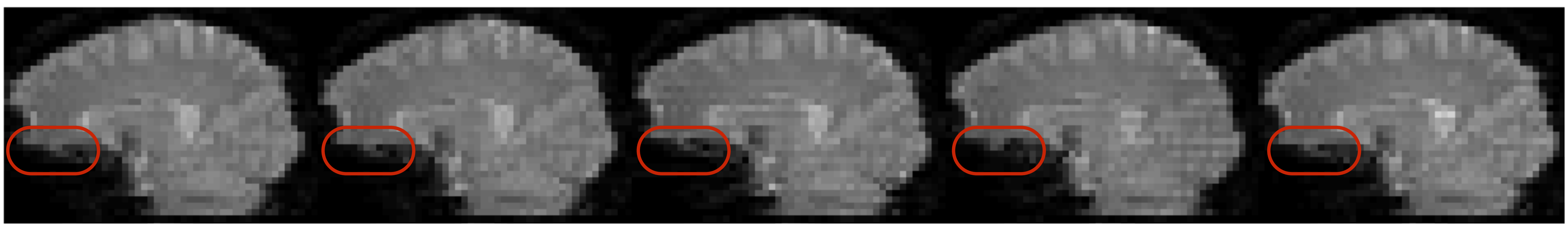

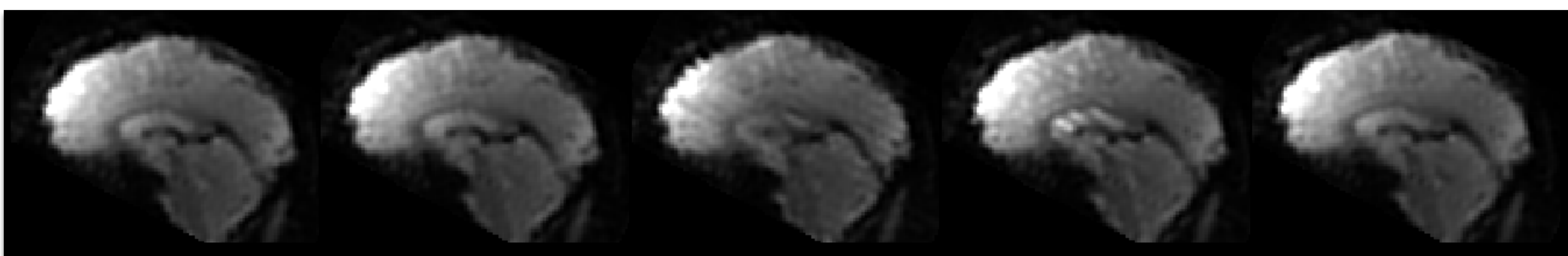

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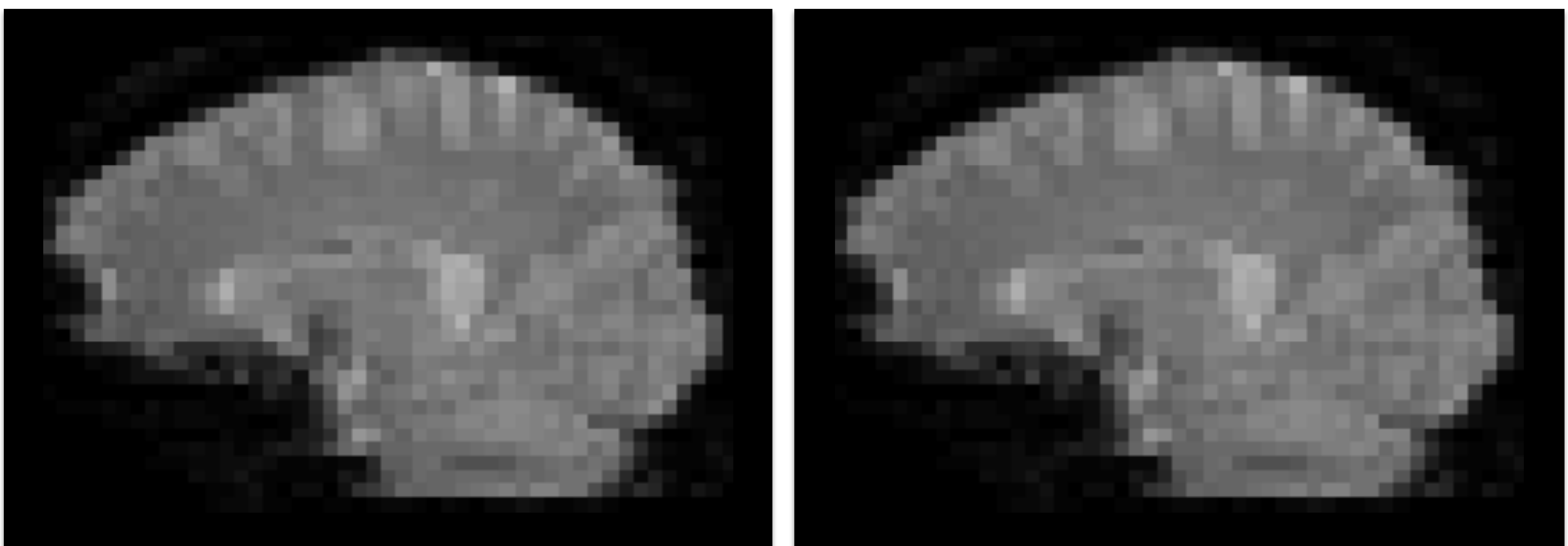

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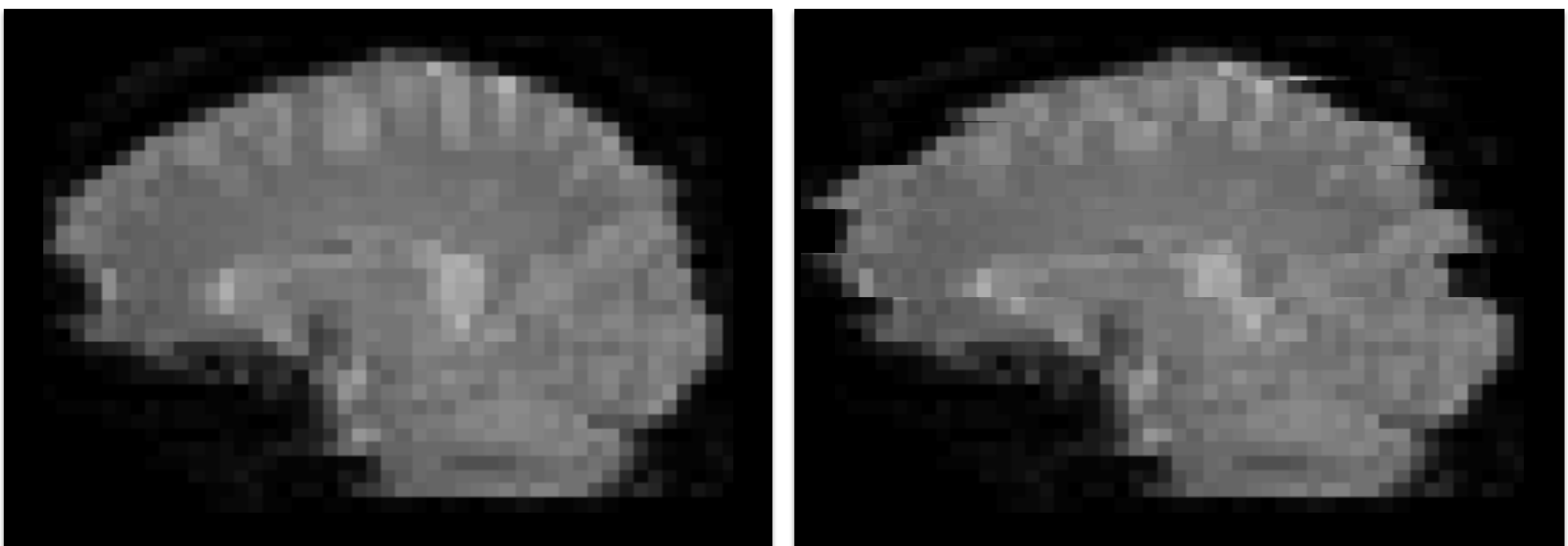


Important things so far:

You can see motion in the fMRI images

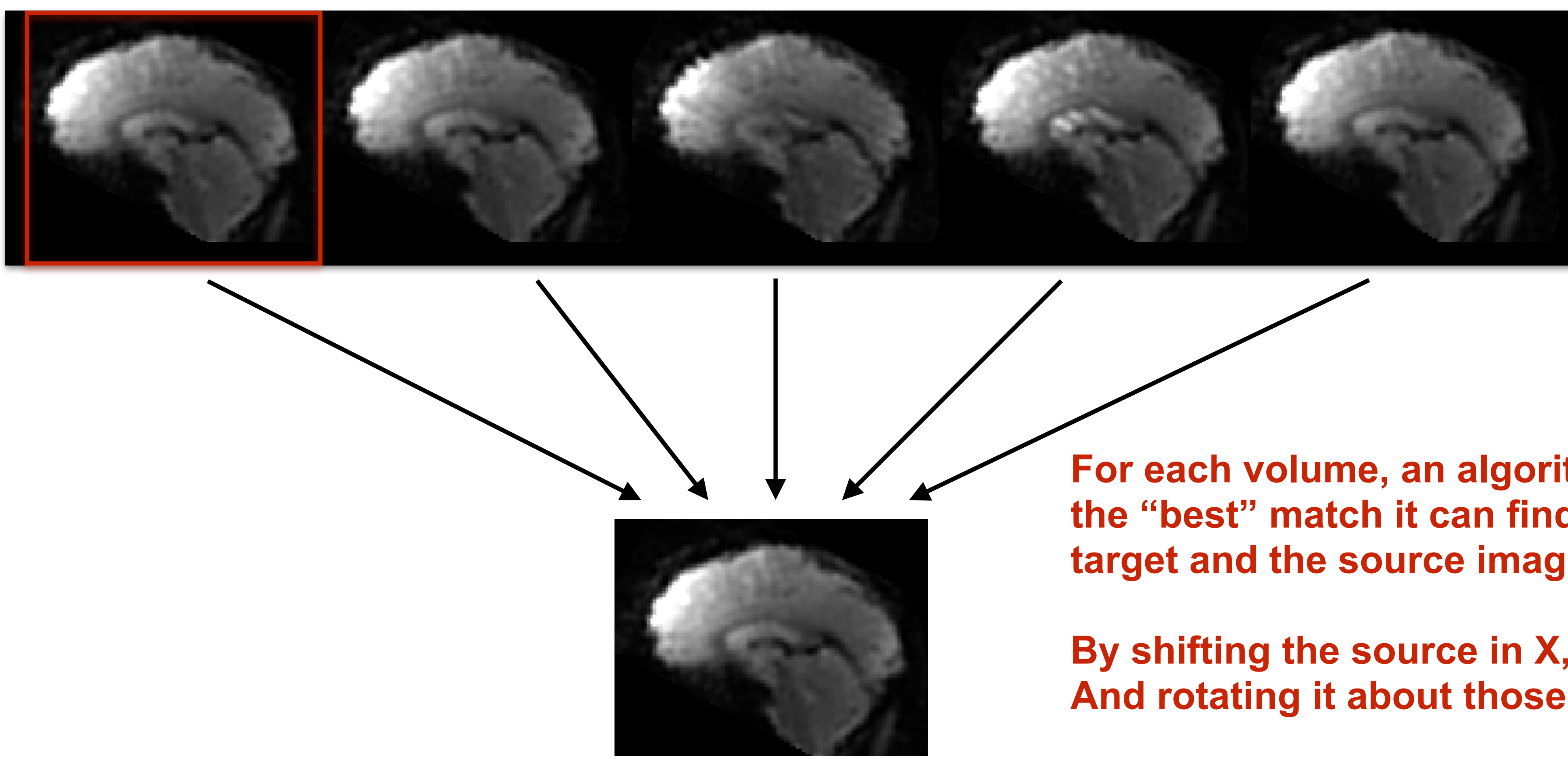
The images are staggered in time
So data-derived motion estimation can only be staggered

Slice-specific motion estimates are possible
Volume-specific motion estimates are possible
Far more common to use volume-based estimates

Brain shape may or may not be distorted
Distortion has consequences for motion estimation

How we estimate motion: via registration

An fMRI scan is just a bunch of volumes
Each of these volumes is registered to a target volume
The target volume is usually
- one of the volumes (first or middle are common)
- or a mean image of the scan



Target

For each volume, an algorithm looks for the “best” match it can find between the target and the source image

**By shifting the source in X, Y, and Z
And rotating it about those axes**

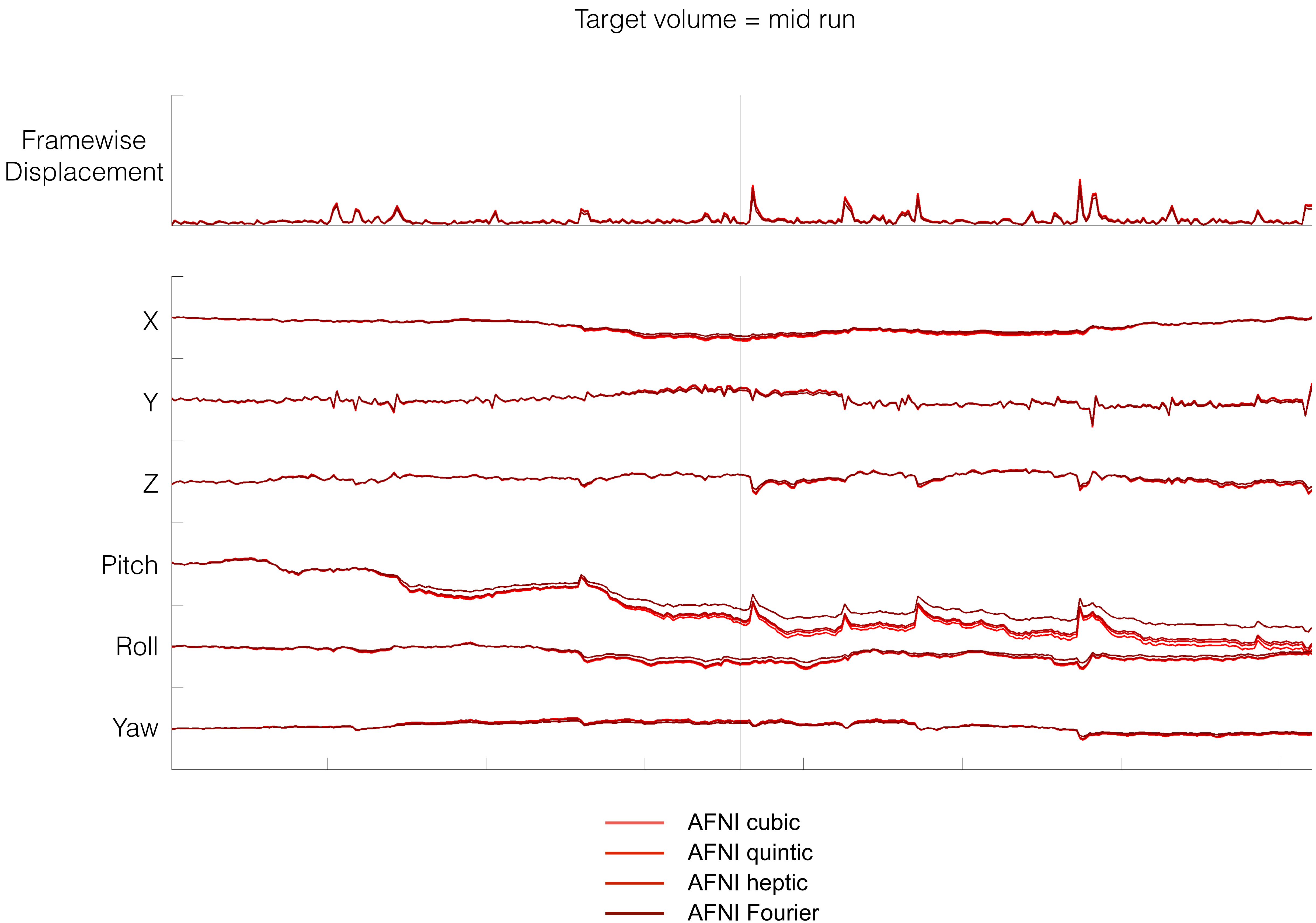
**Yielding a 6-parameter transform:
[X Y Z pitch roll yaw]**

How we estimate motion: via registration

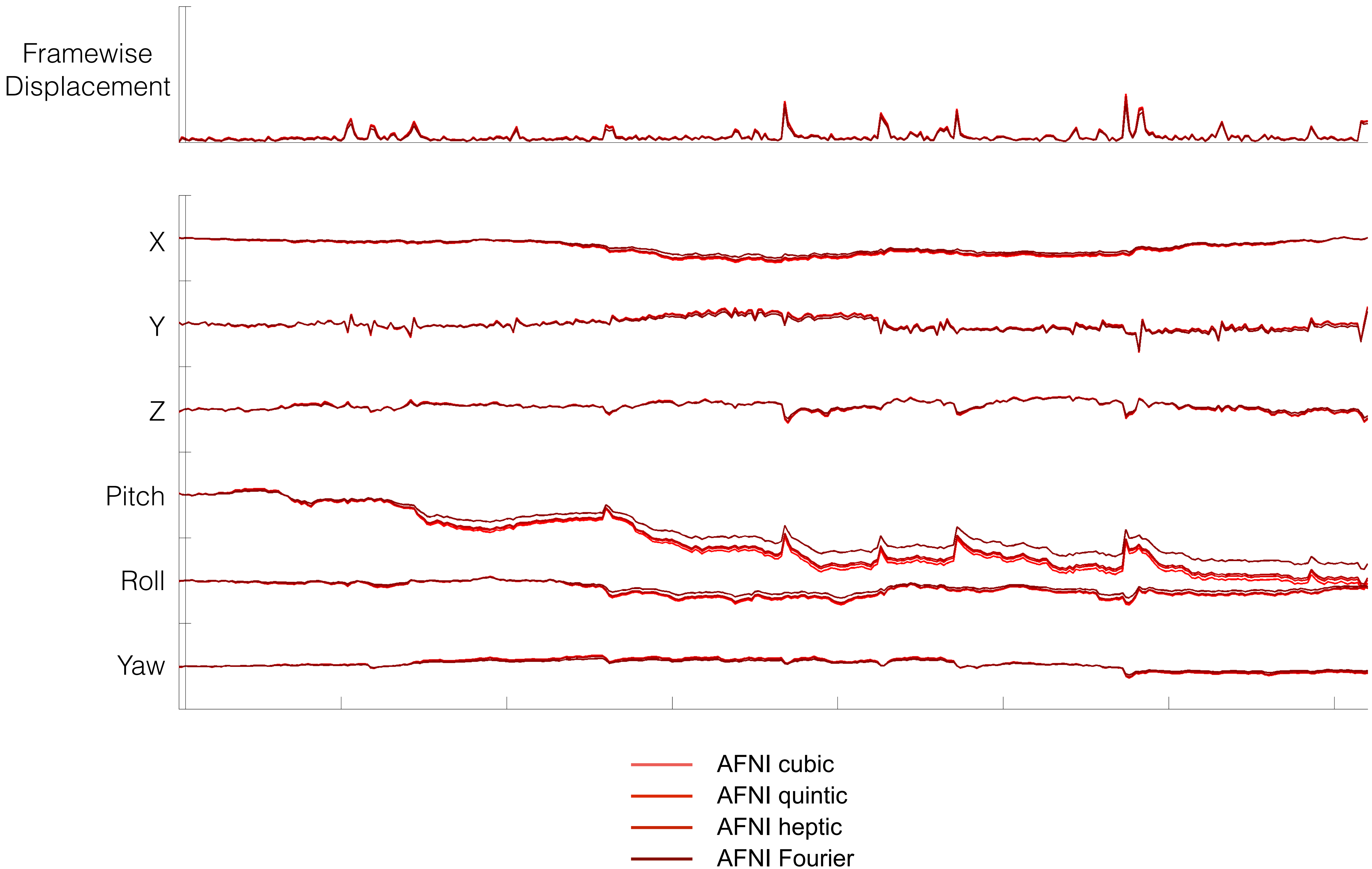
All neuroimaging software packages offer realignment:
“3dvolreg” in AFNI, “flirt” in FSL, “realign” in SPM, etc.

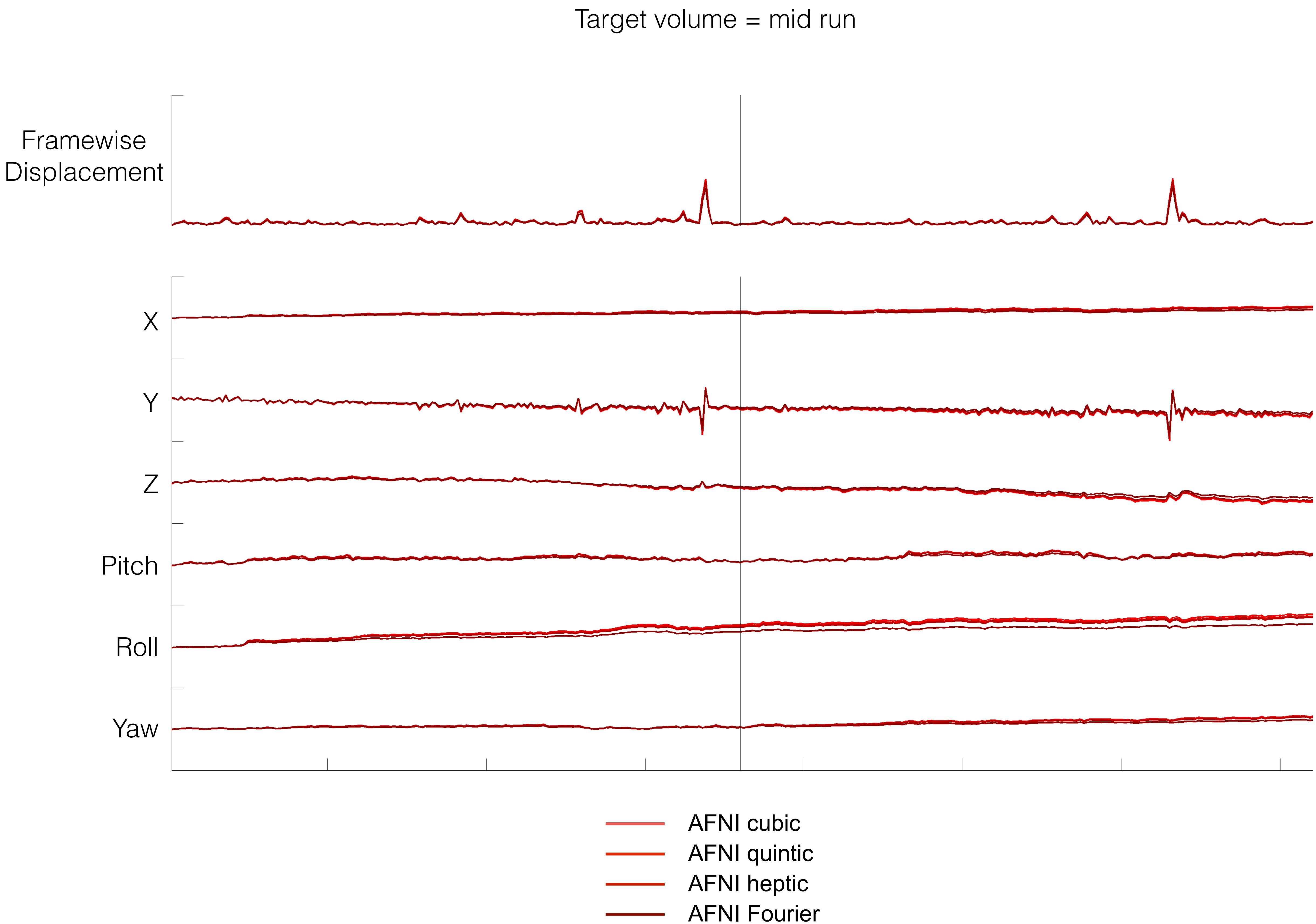
You can choose many things:
the target volume
the cost function to that defines the “best” match of images
how the transformed image is resampled

I’ll show you in AFNI the influence of
- target volume (an early vs. middle volume of a scan)
- and resampling technique (cubic, heptic, quintic, Fourier)
- and software package

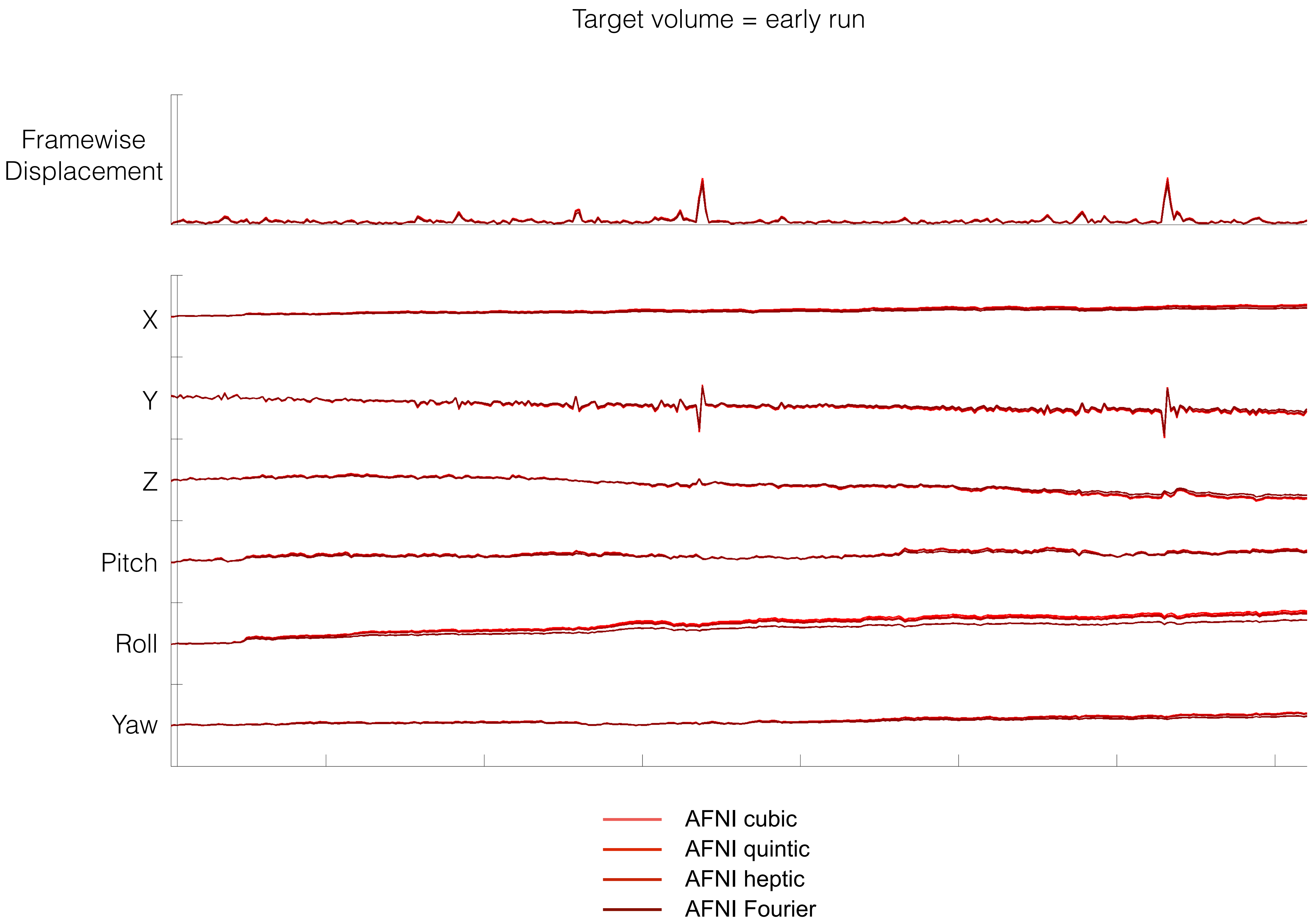

Target volume = mid run
Framewise Displacement
X
Y
Z
Pitch
Roll
Yaw
AFNI cubic
AFNI quintic
AFNI heptic
AFNI Fourier

Target volume = early run





Target volume = mid run
Framewise
Displacement
X
Y
Z
Pitch
Roll
Yaw
AFNI cubic
AFNI quintic
AFNI heptic
AFNI Fourier



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Framewise Displacement
X
Y
Z
Pitch
Roll
Yaw
AFNI cubic
AFNI quintic
AFNI heptic
AFNI Fourier

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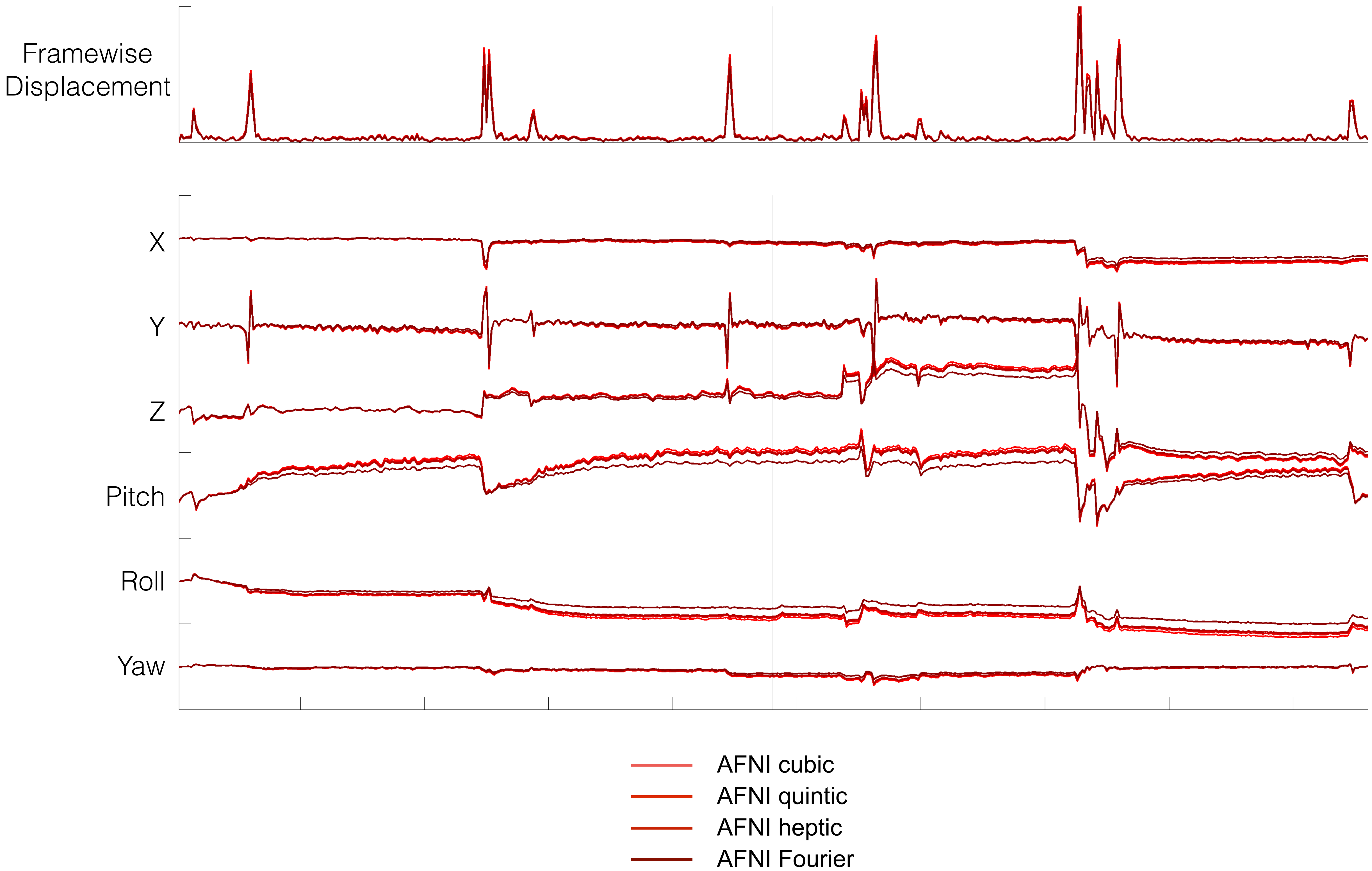

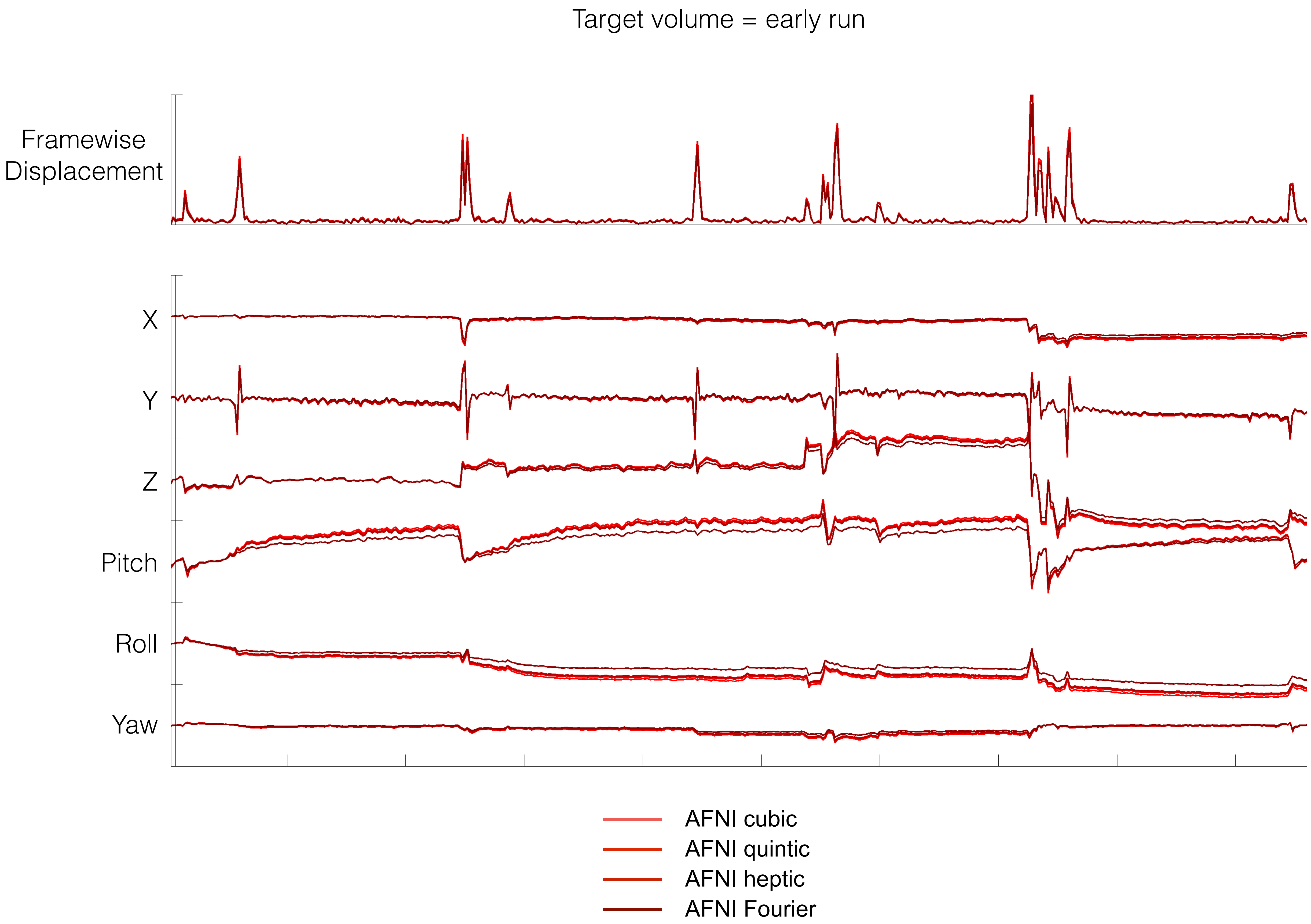
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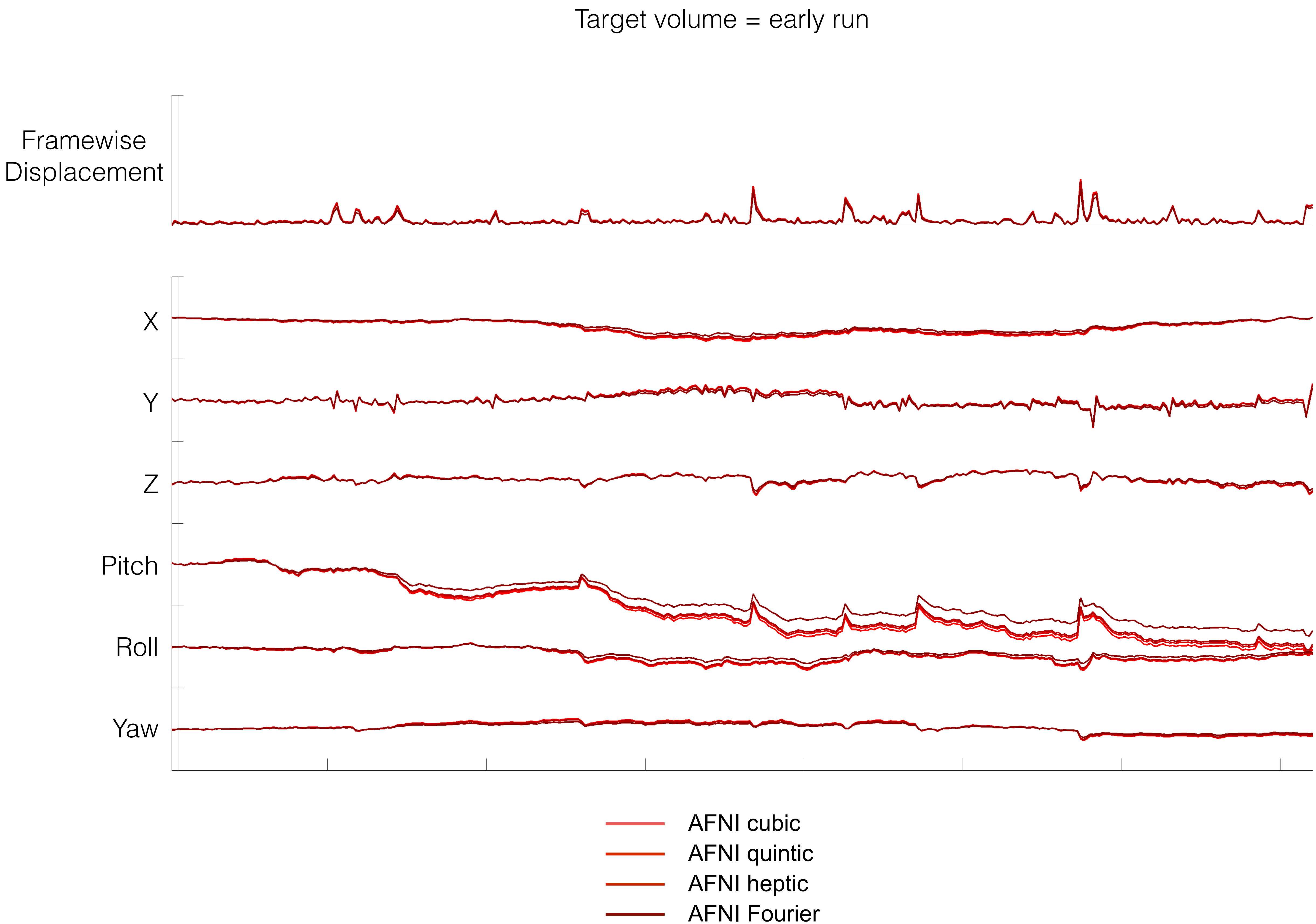
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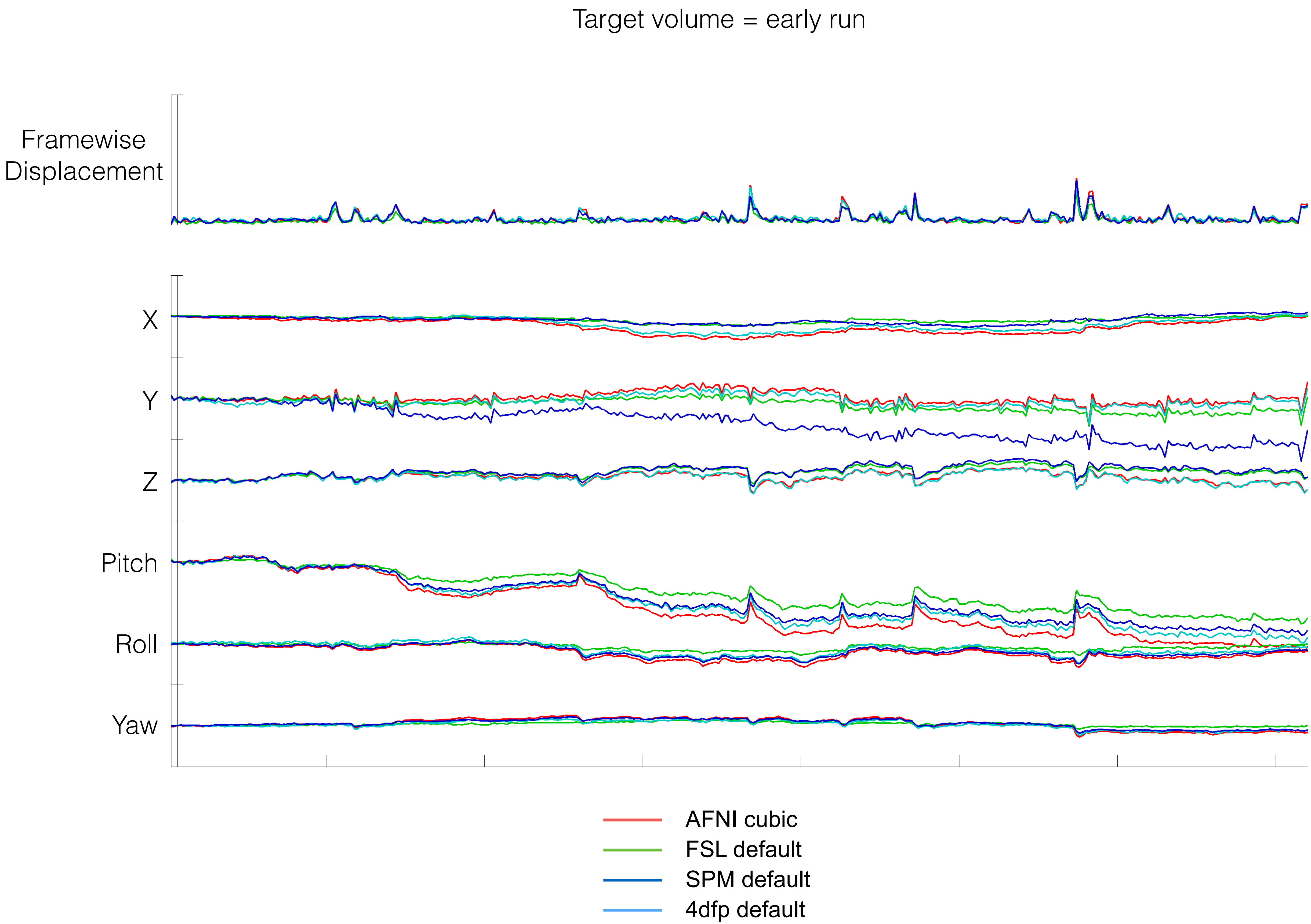
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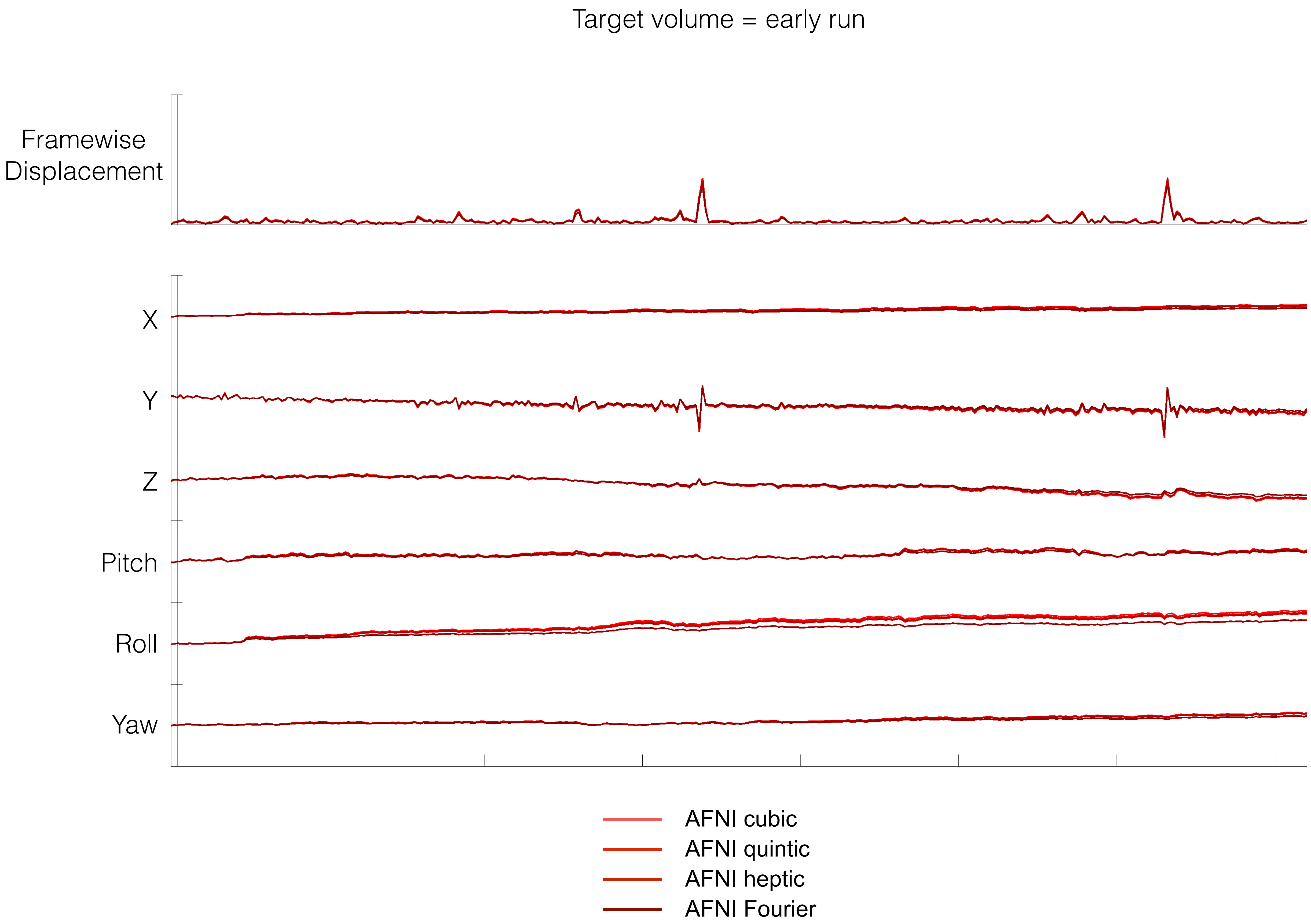
Framewise Displacement
X
Y
Z
Pitch
Roll
Yaw
AFNI cubic
FSL default
SPM default
4dfp default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Framewise
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X
Y
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Pitch
Roll
Yaw
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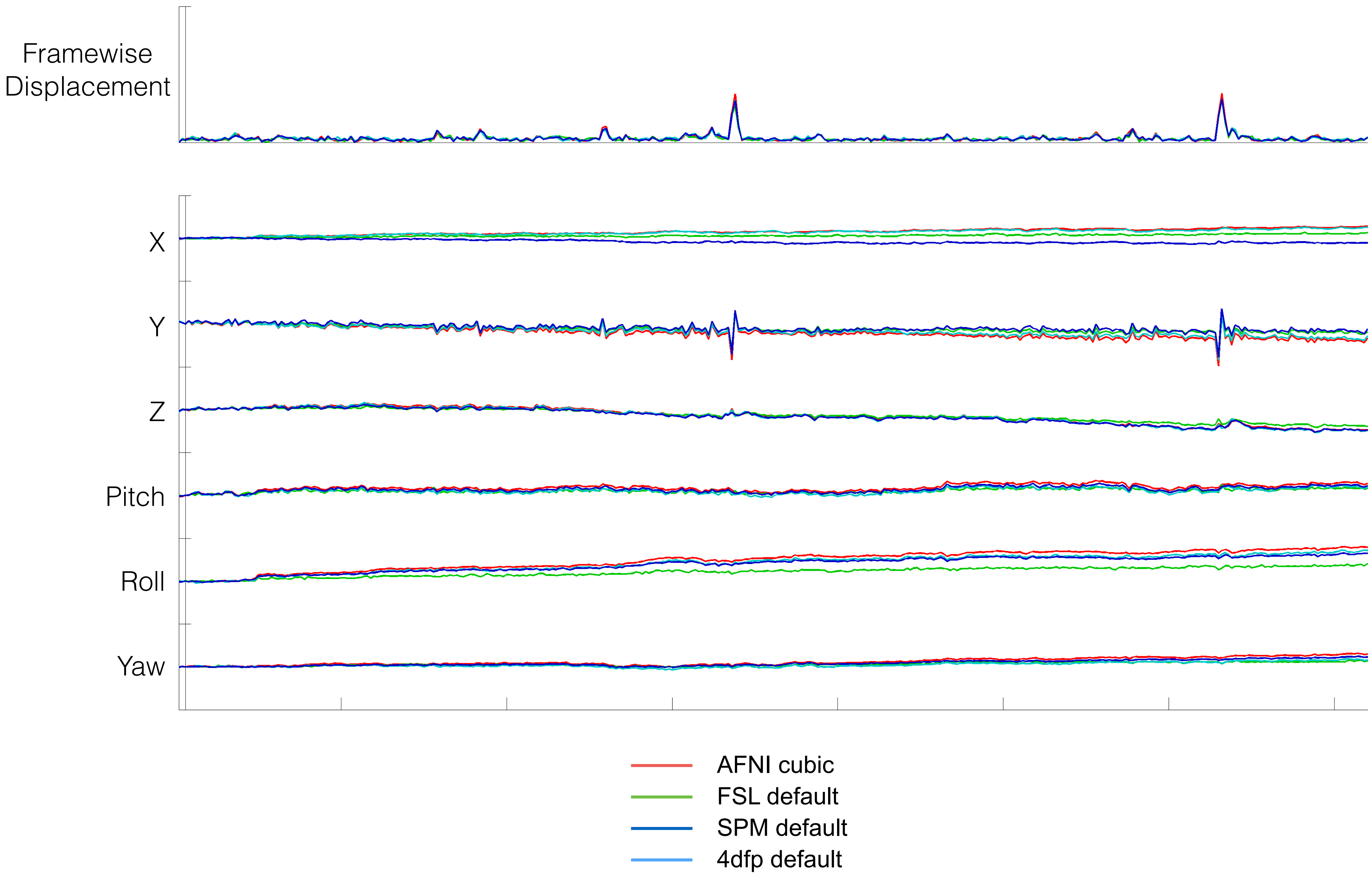

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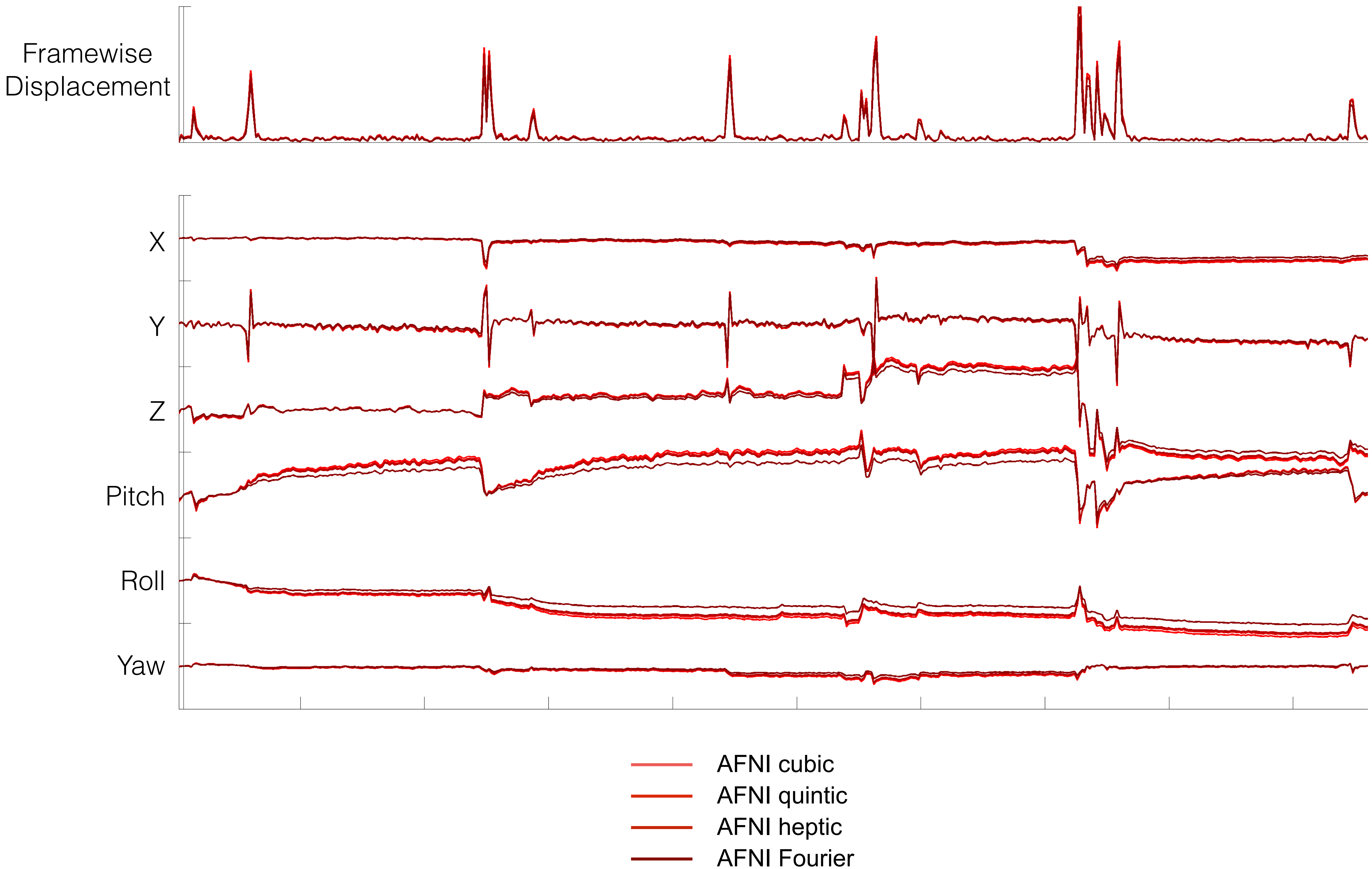
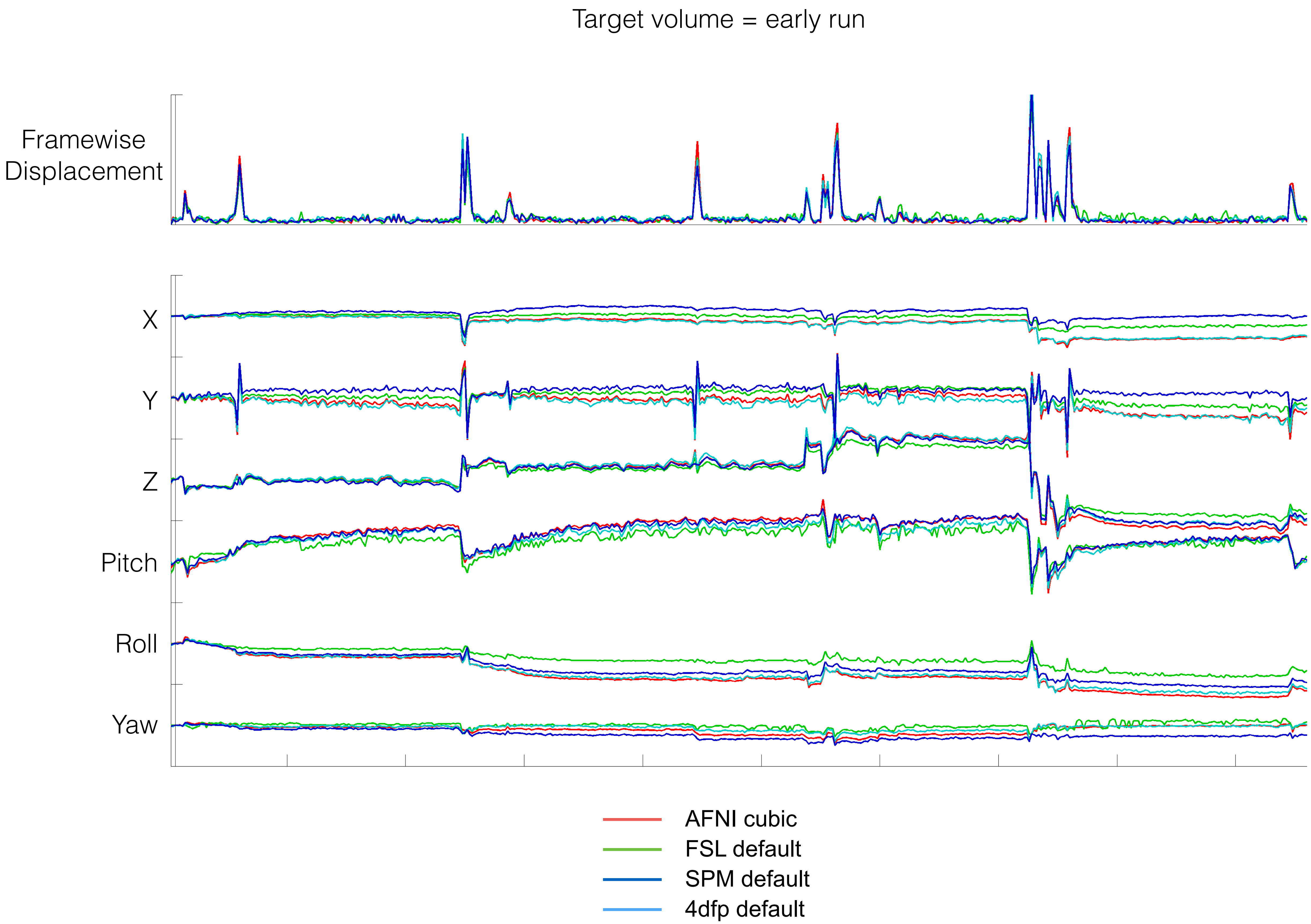




Target volume = early run
Framewise Displacement
X
Y
Z
Pitch
Roll
Yaw
AFNI cubic
FSL default
SPM default
4dfp default

Tidbits about motion estimates:

Each software package puts out 6 parameters per volume
BUT they are not ordered the same
AND axes are often flipped between software packages
AND different origins can be presumed
- e.g., center of grid space vs center of mass vs other
AND different ordering of rotations may be used
- e.g., YPR vs PRY

Even if two packages realign images identically, they may output different XYZ and PRY estimates, depending on their origins and rotational conventions.

You can figure out the “true” conversions between packages
Even without those conversions, FD estimates are close

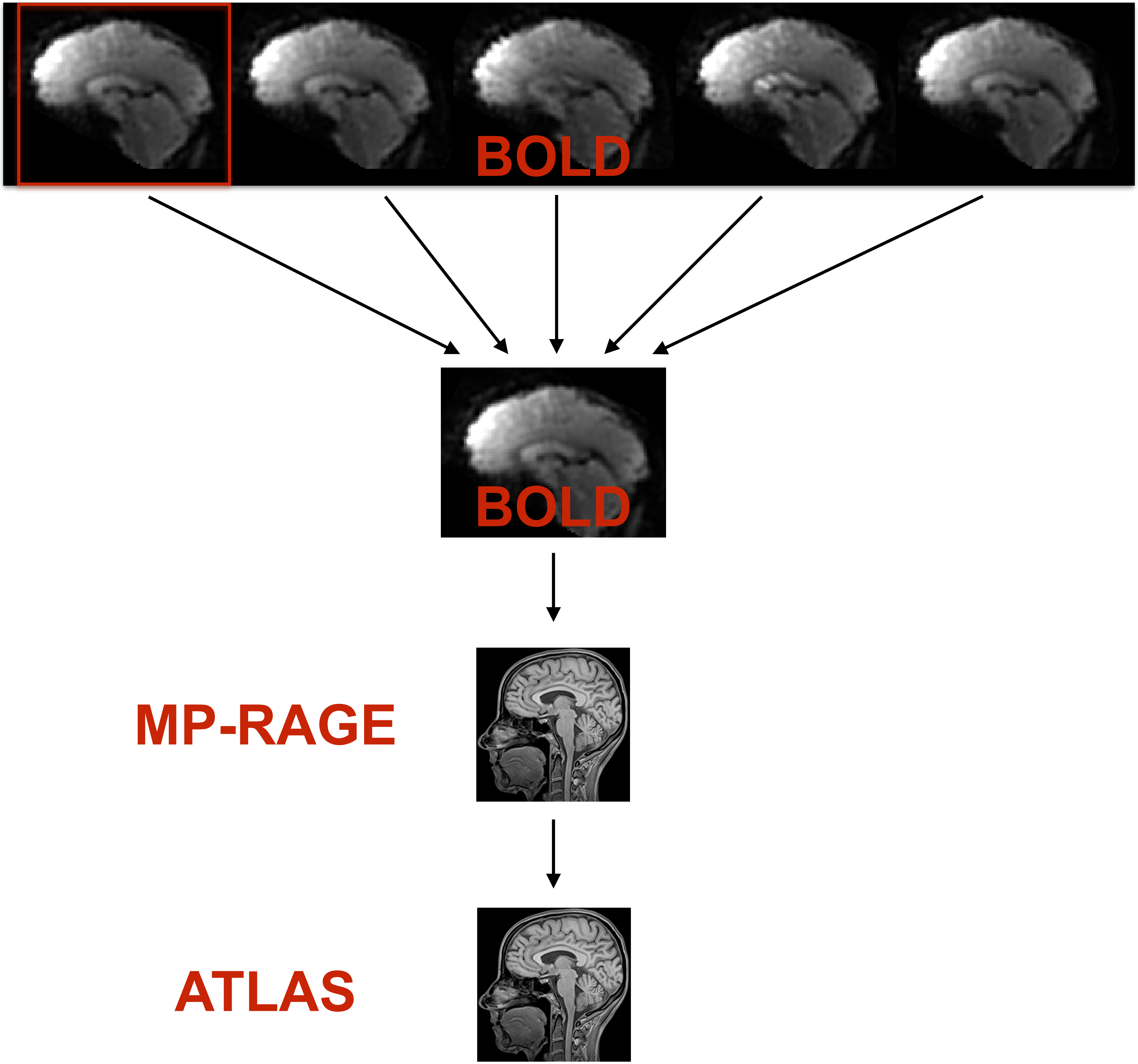
Tidbits about motion estimates:

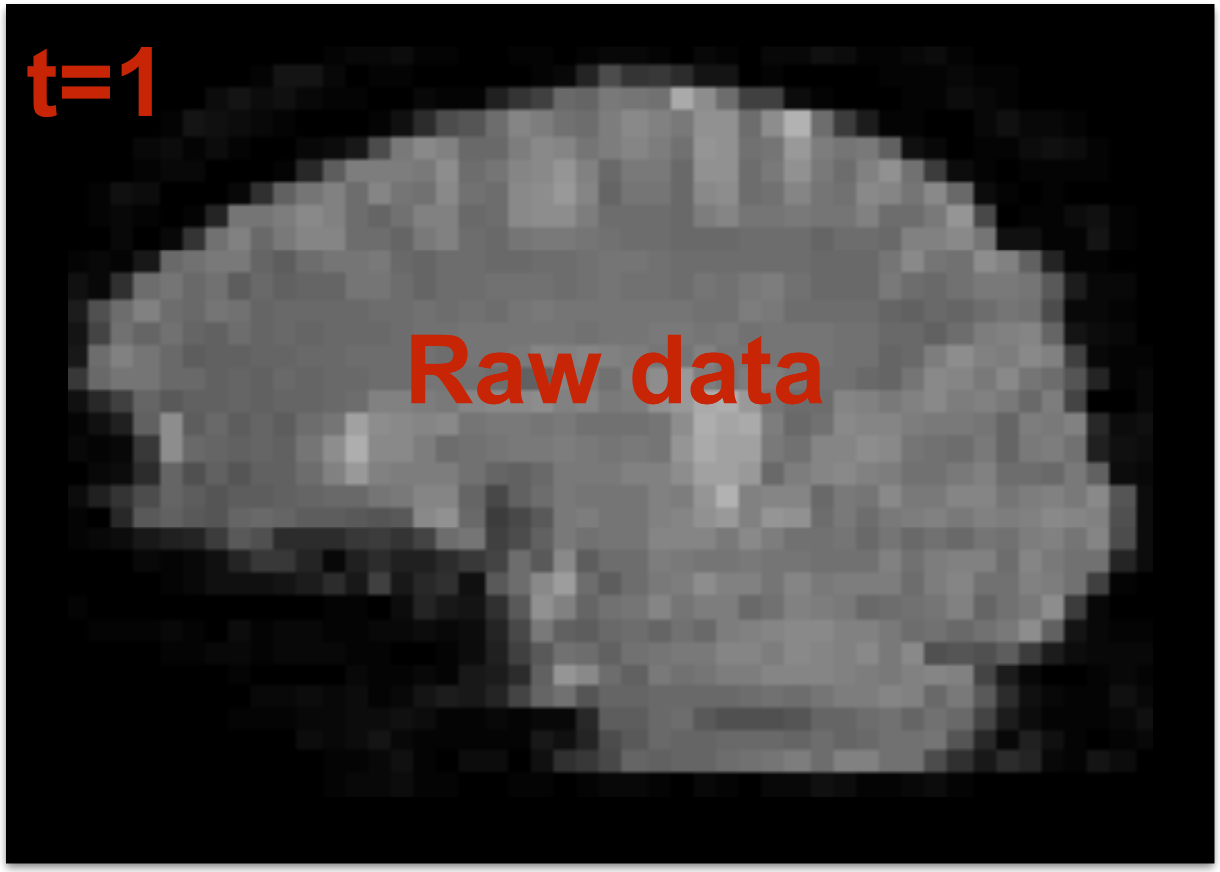
6-parameter estimates are “rigid body” transforms
Meaning they shift and rotate things like a lead pipe
The cranium is a rigid body…
The brain is practically a rigid body…
but the images we obtain may be distorted

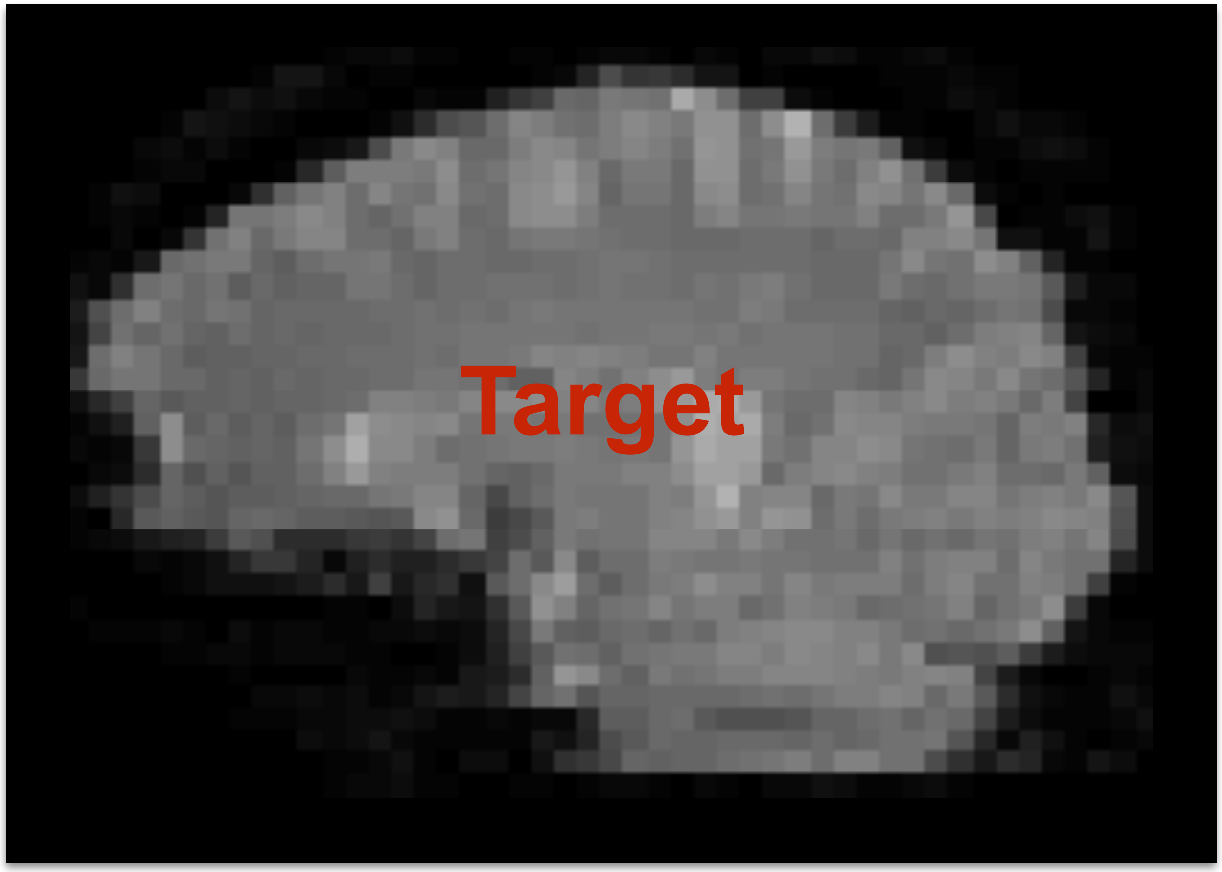
If motion distorted a brain image, there is no single “correct” estimate of motion that could ever bring the source brain in register with the target brain by rigid body transformation

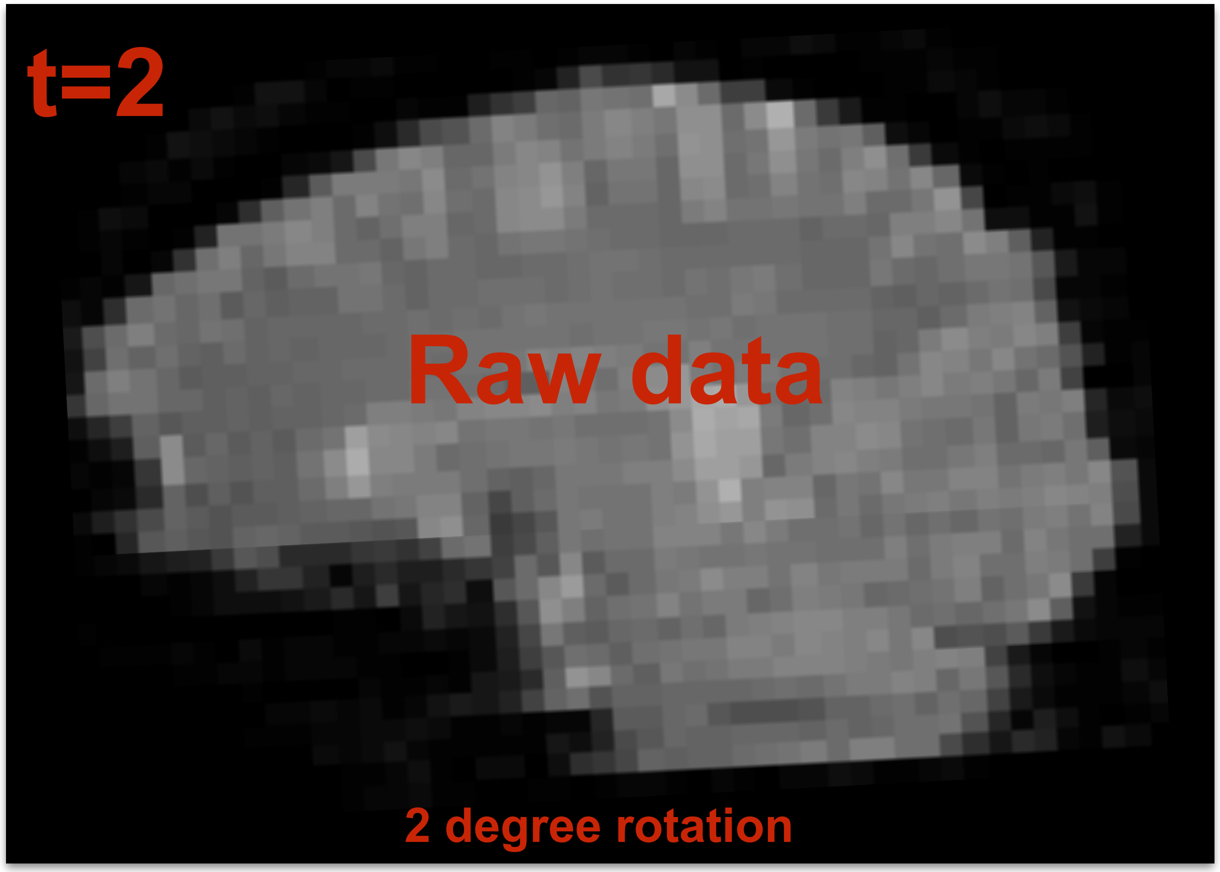
And a rigid body transformation will preserve the brain deformation even after the images are “aligned”

Implications for “realigned” images…


BOLD
BOLD
MP-RAGE
ATLAS


t=1
Raw data


Target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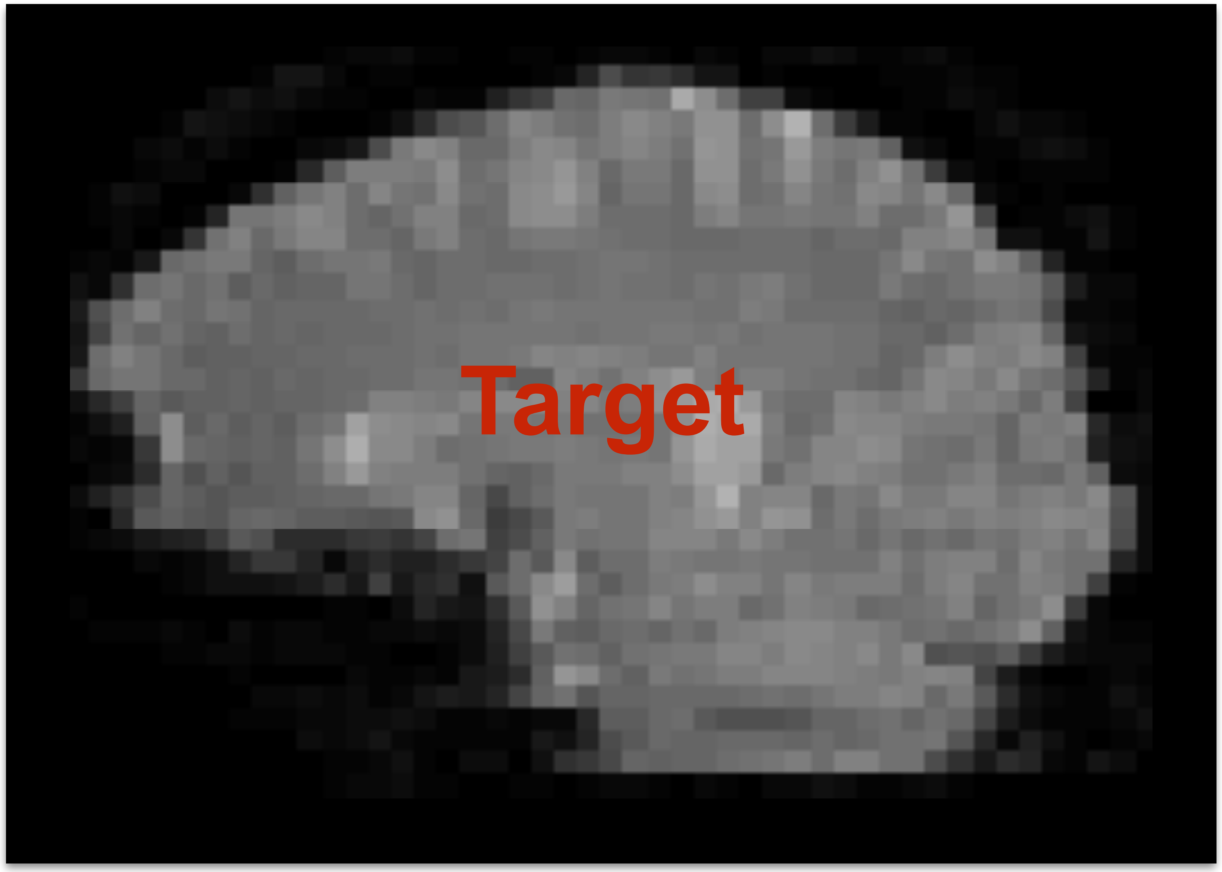
Raw data
2 degree rotation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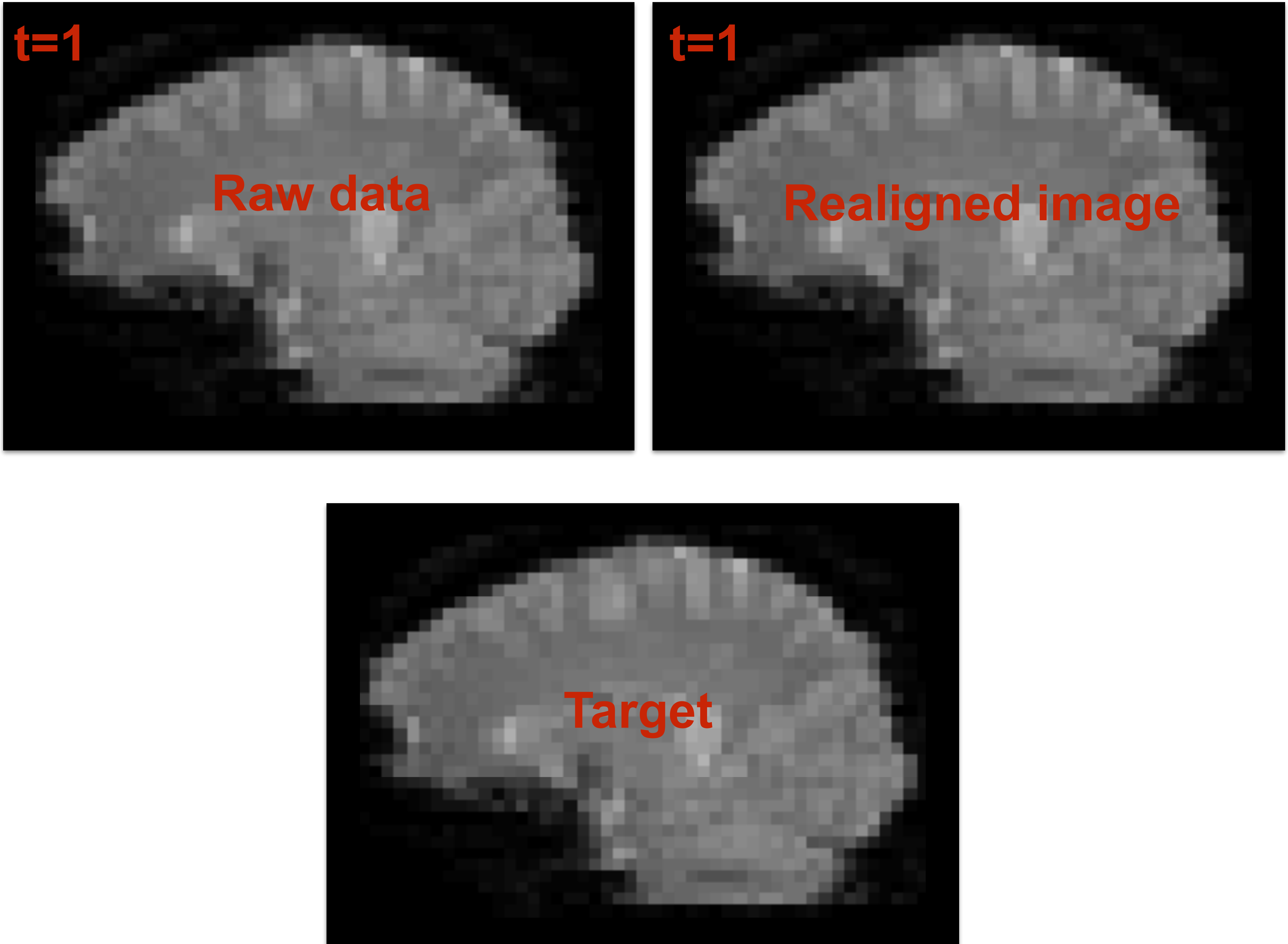
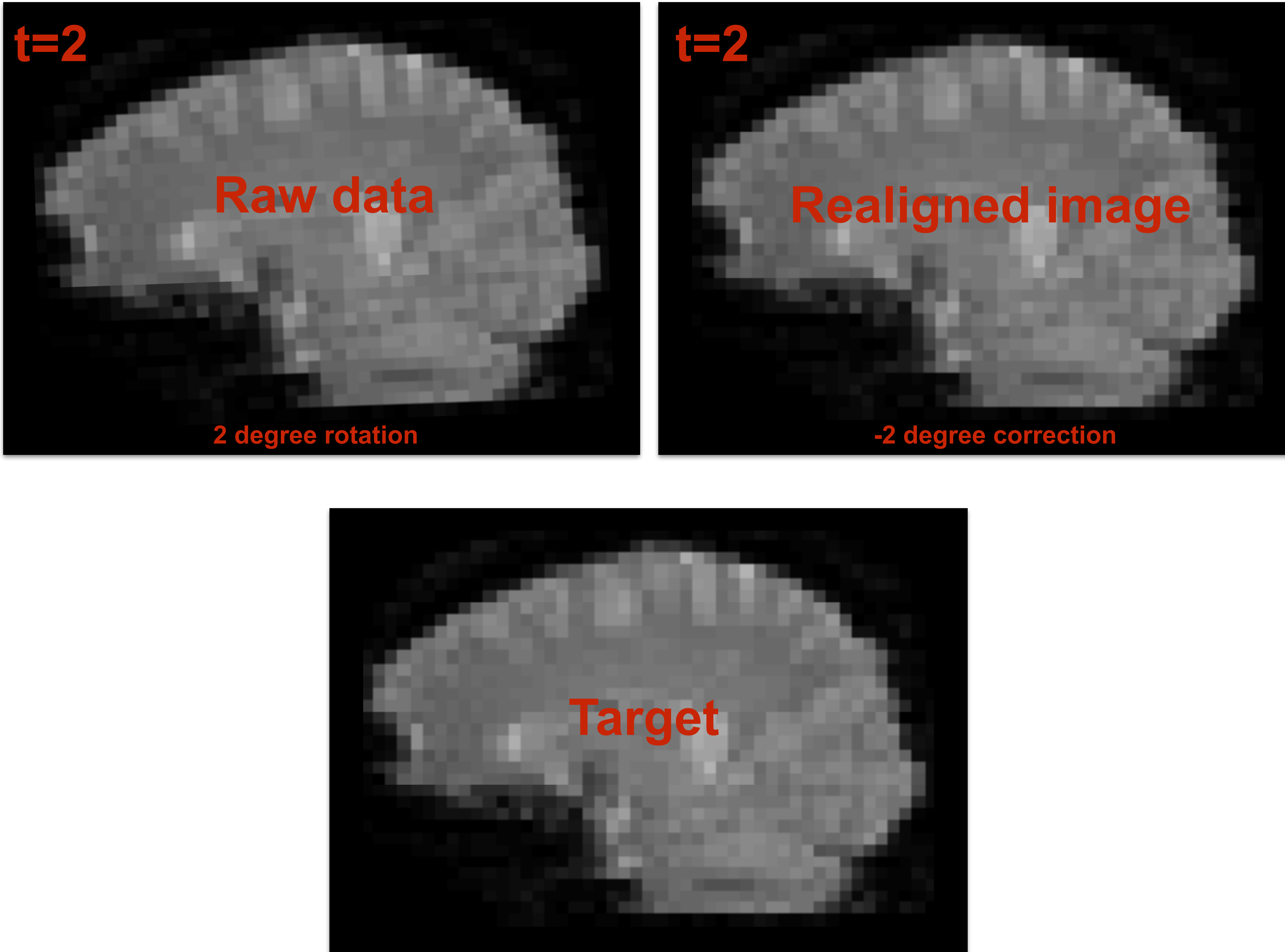
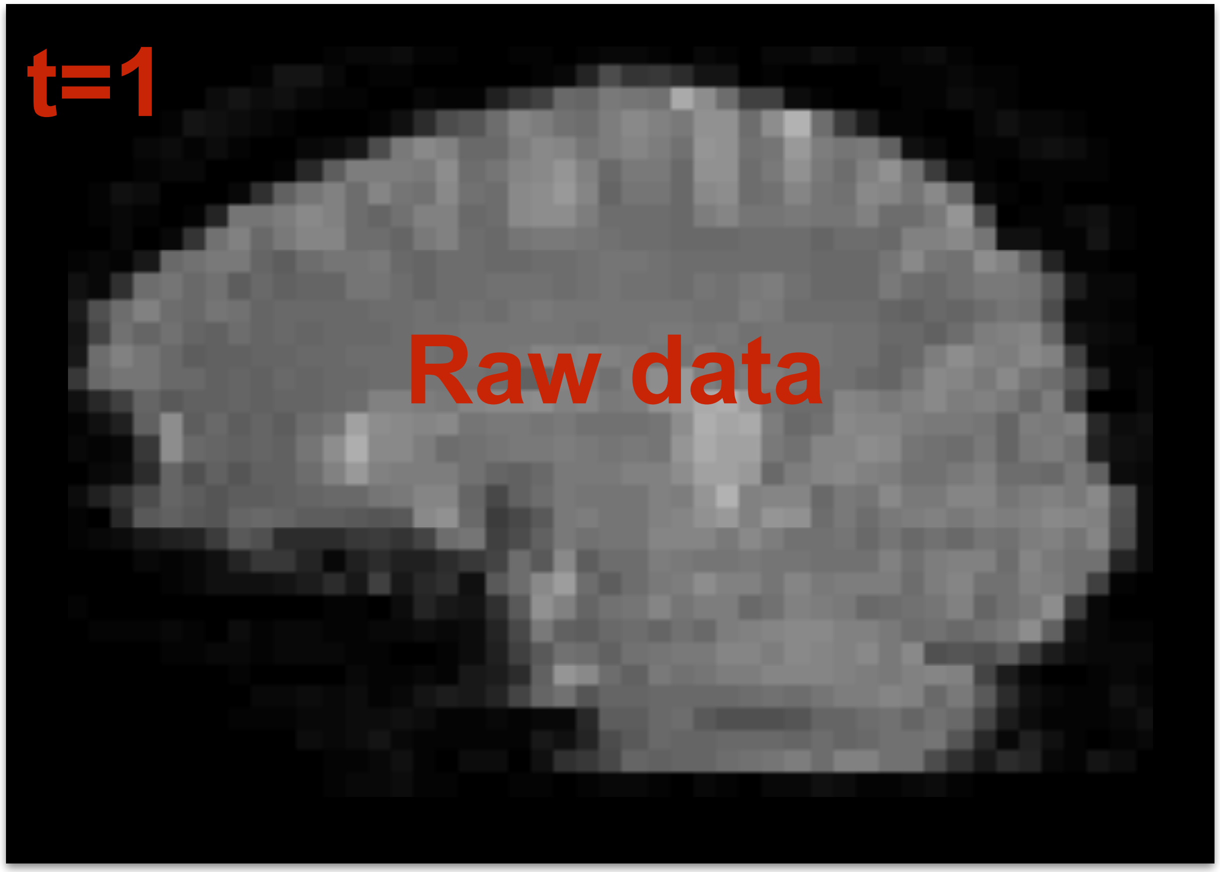
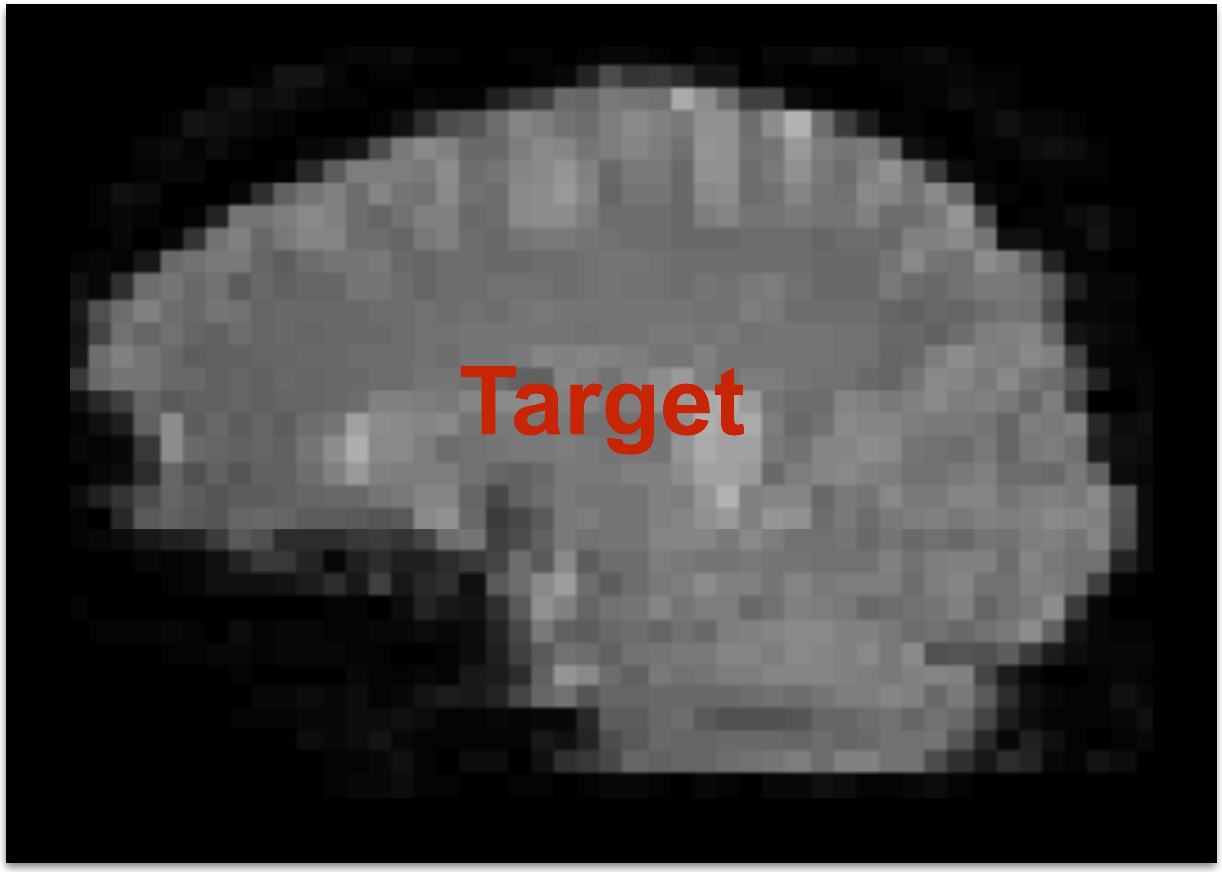
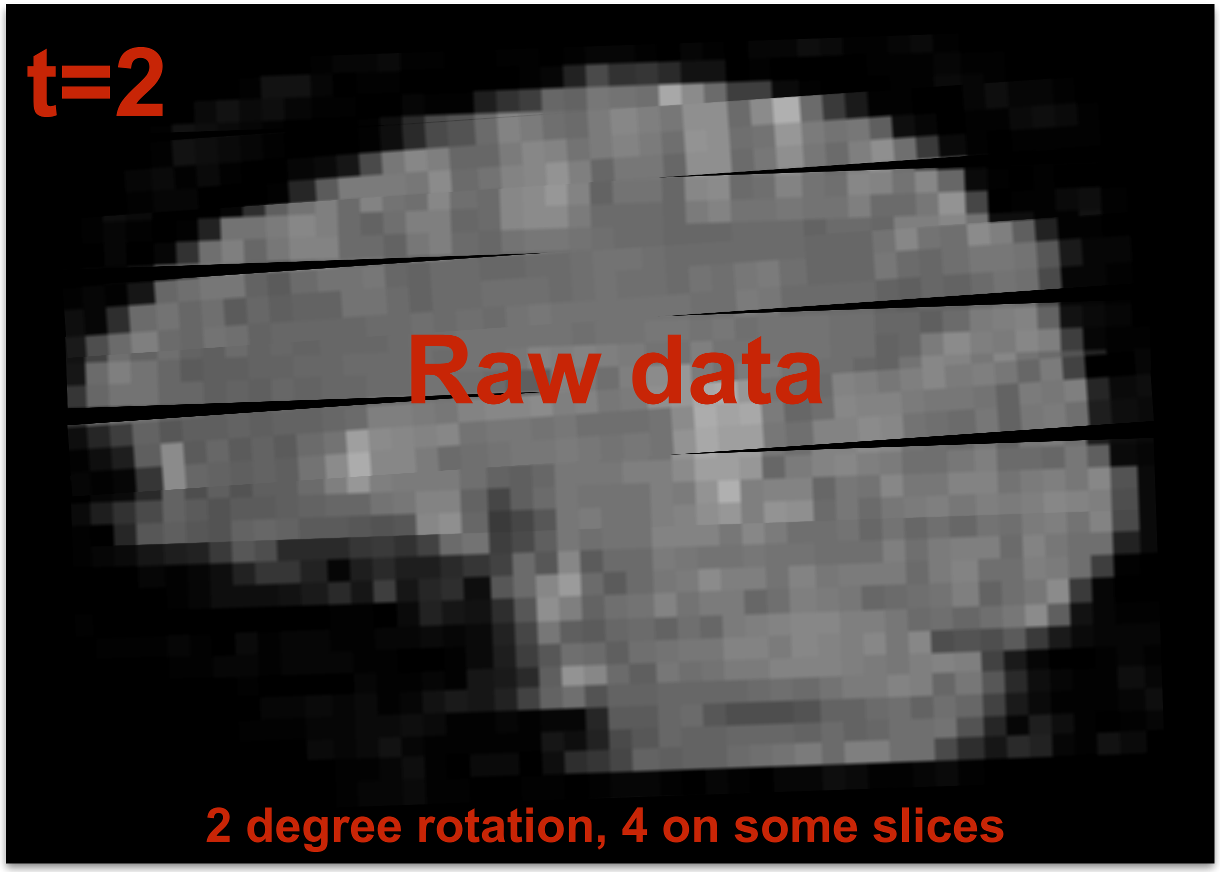
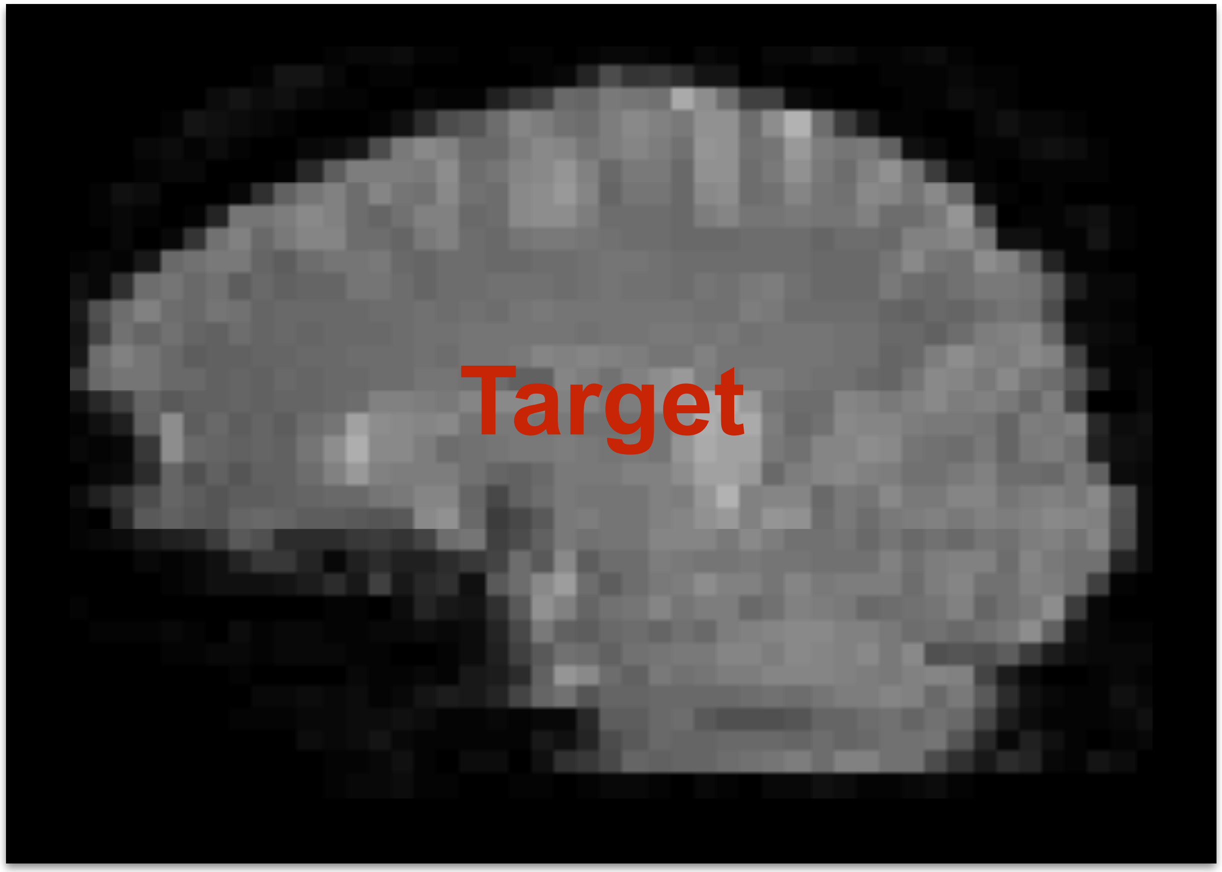

t=1
Raw data
t=1
Realigned image
Target

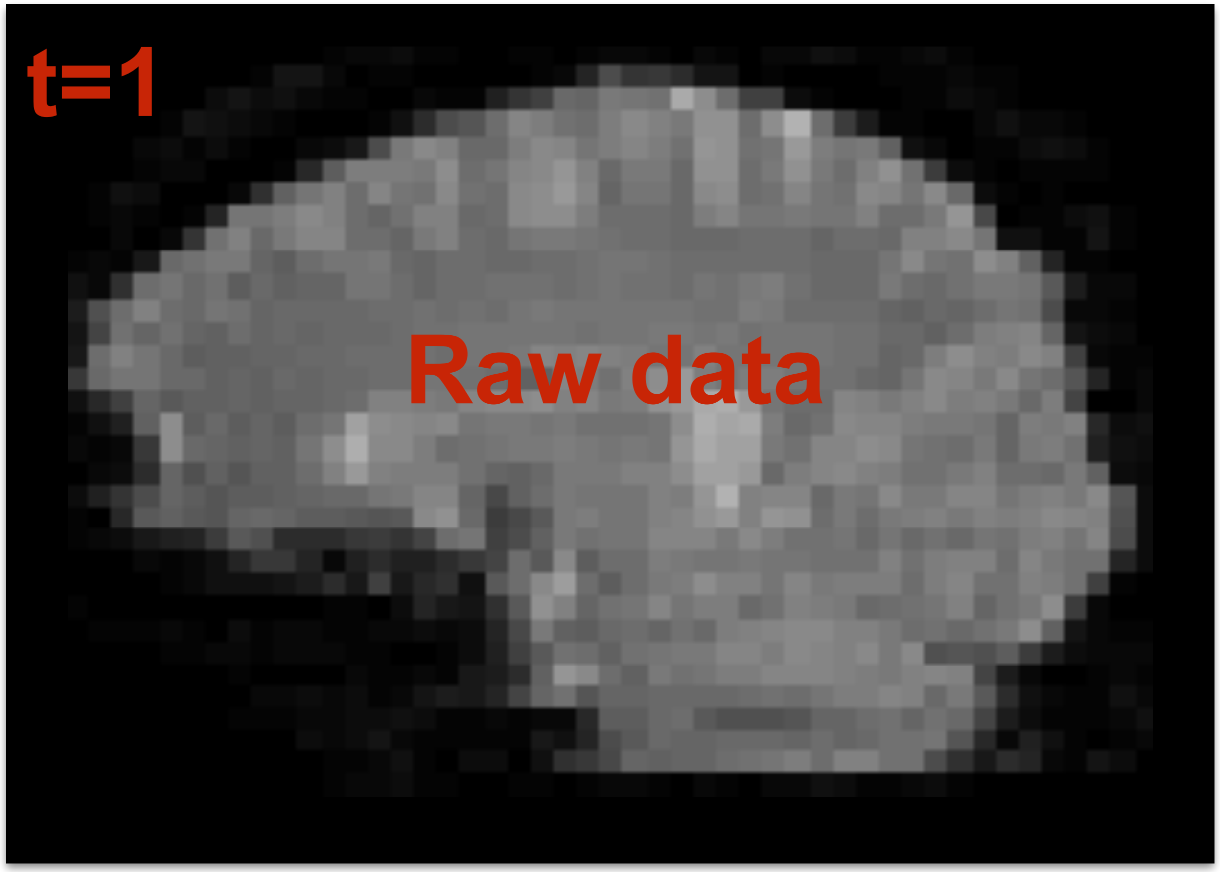

t=2
Raw data
2 degree rotation
t=2
Realigned image
-2 degree correction
Target


t=1
Raw data


Target


t=2
Raw data
2 degree rotation, 4 on some slices


Target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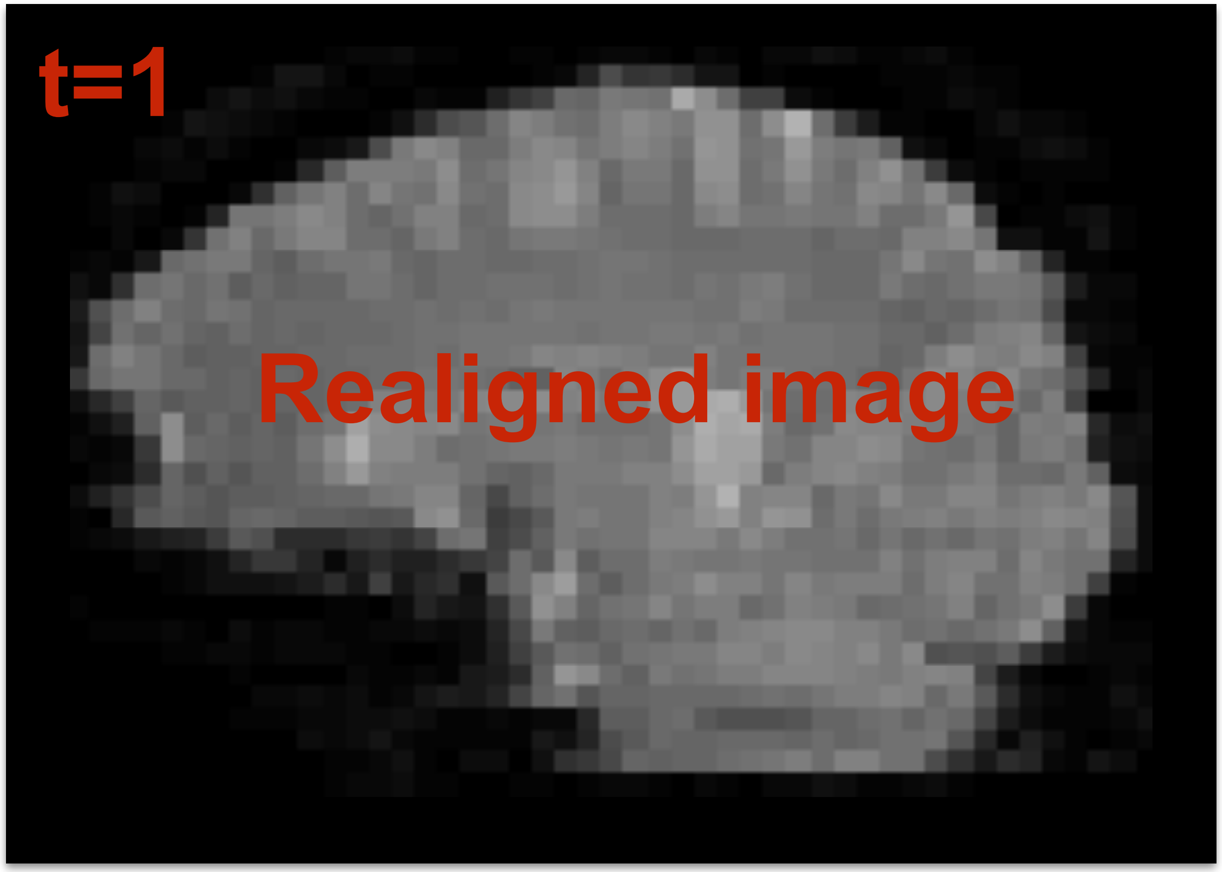
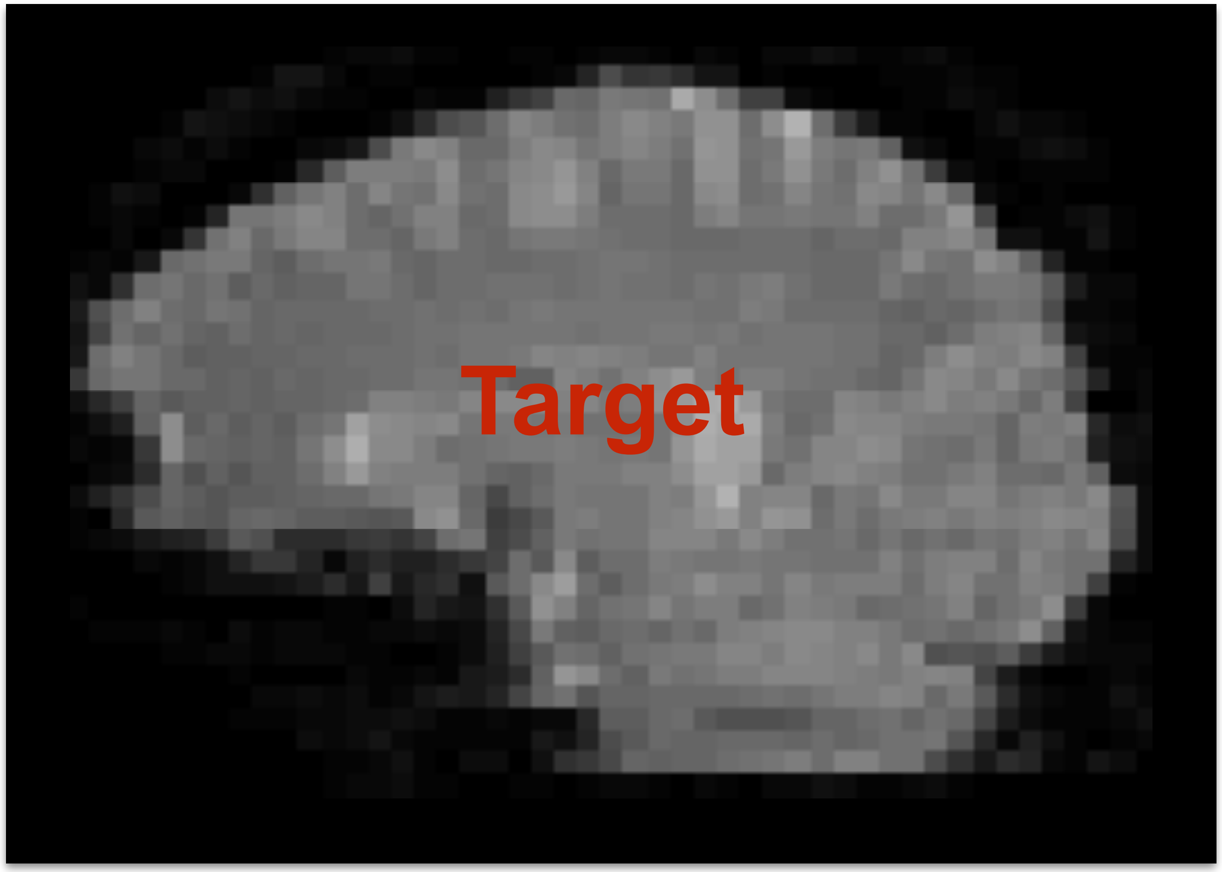
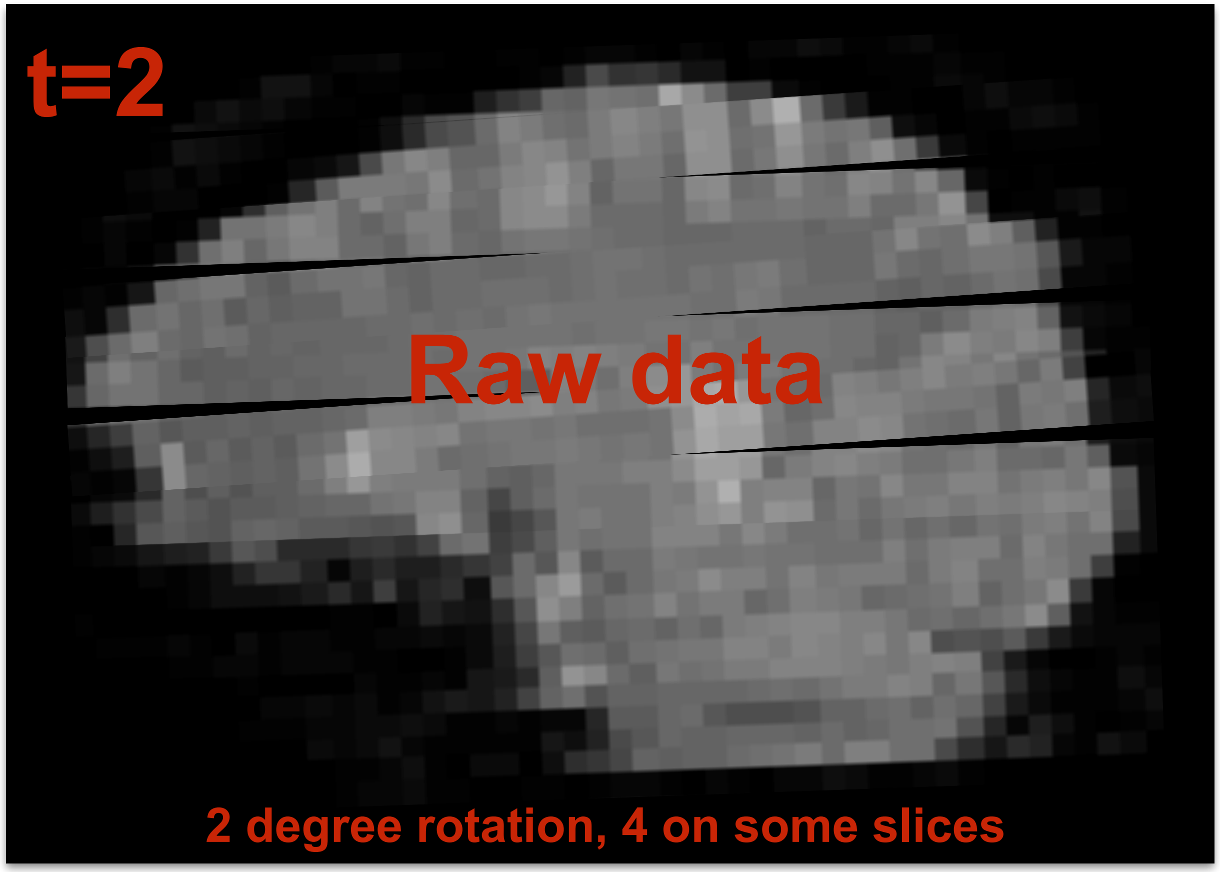
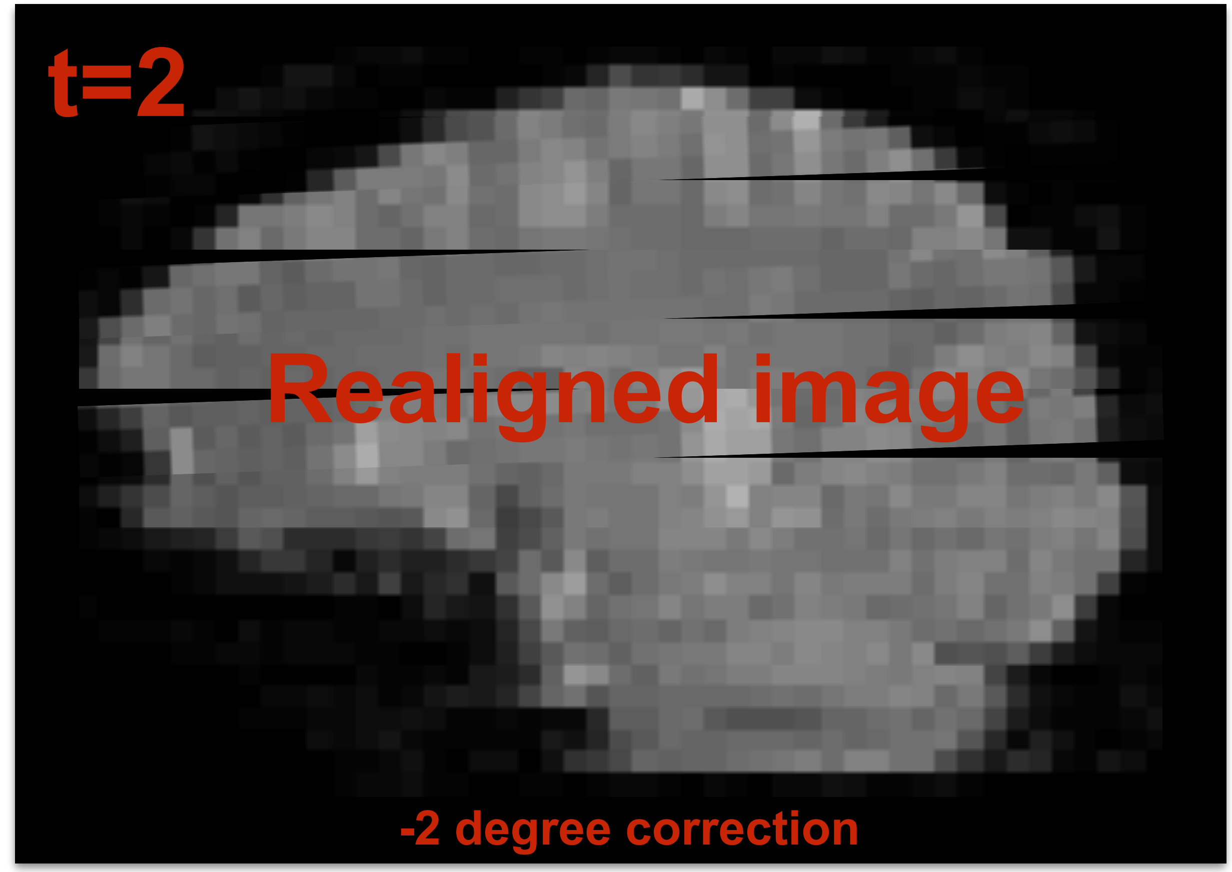
Raw data

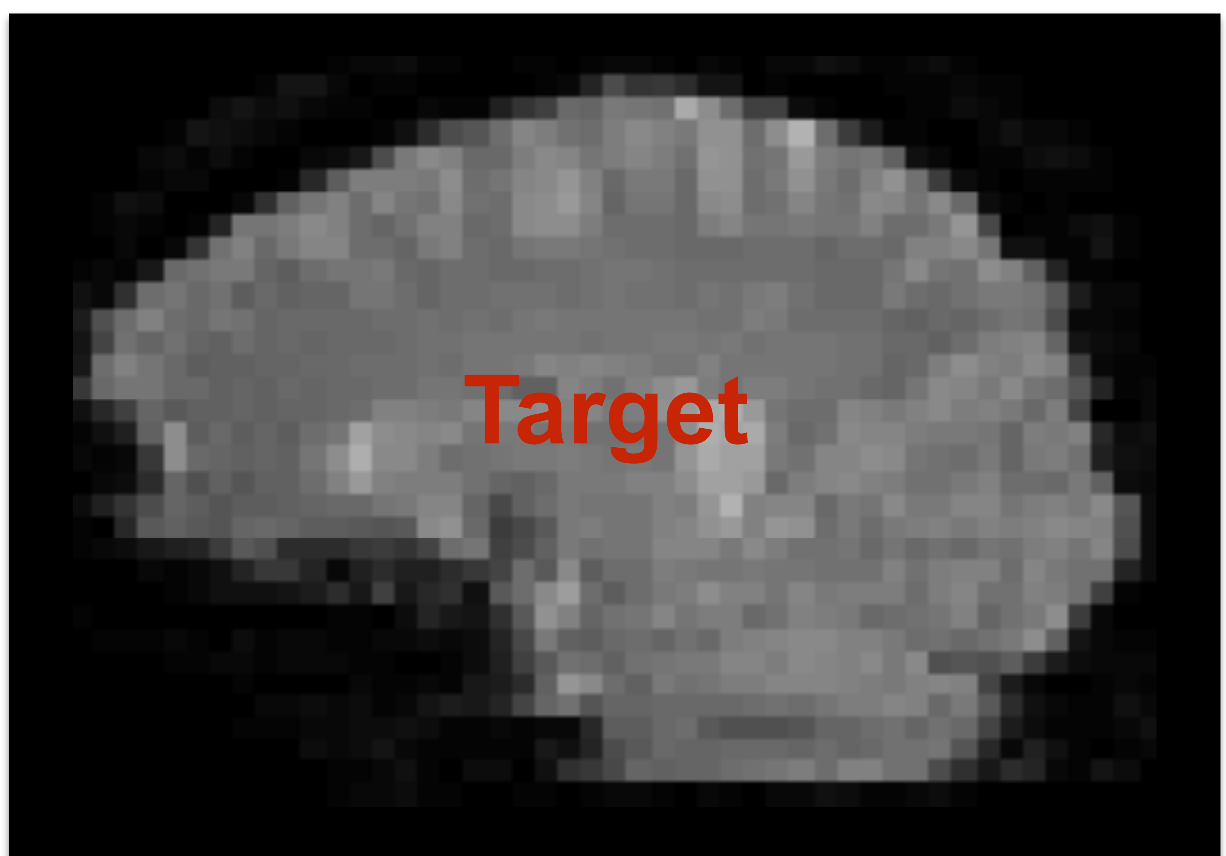

t=1
Realigned image

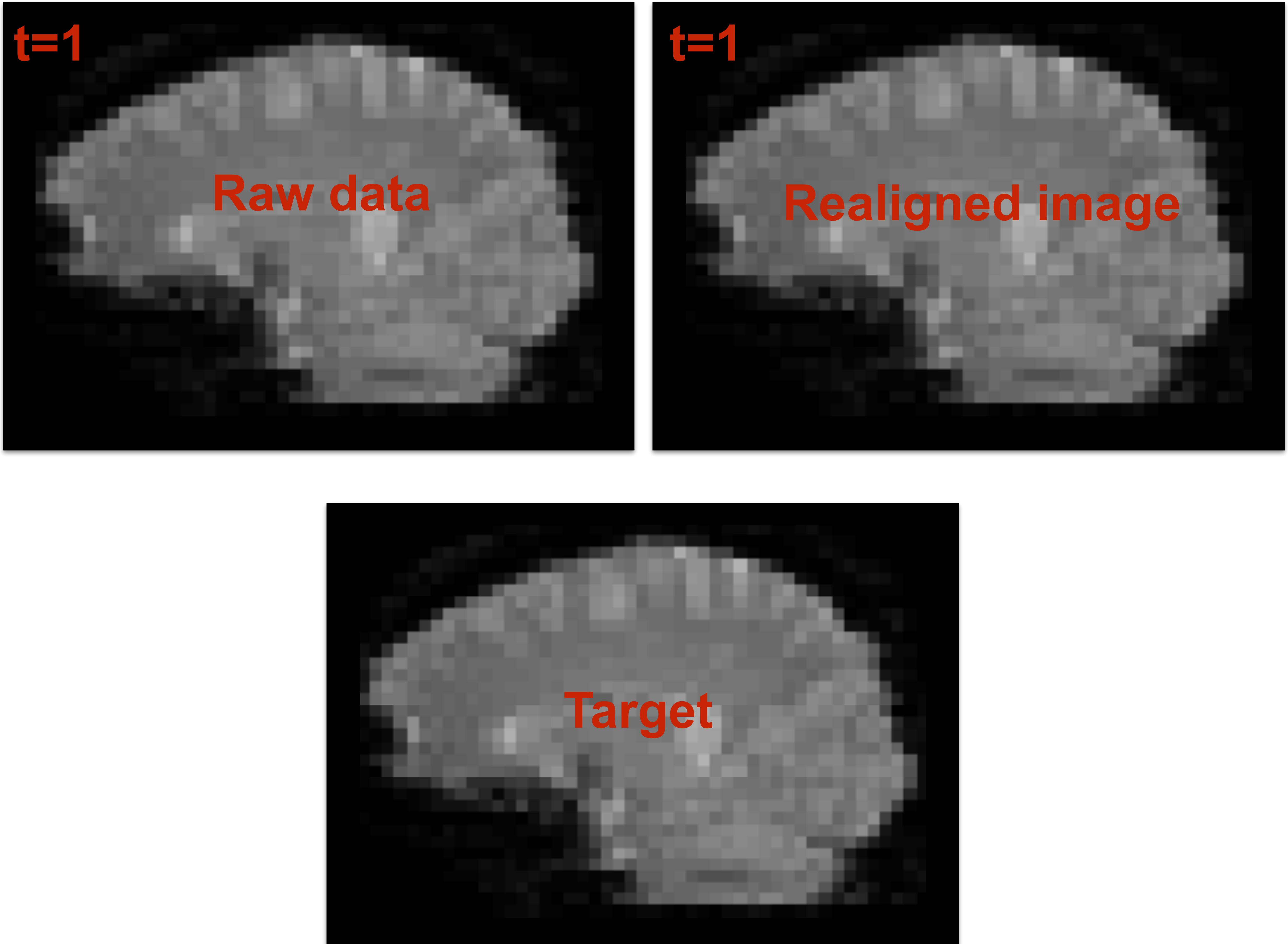

Target

The minimal “correct” rotation
Also the true correction for most slices

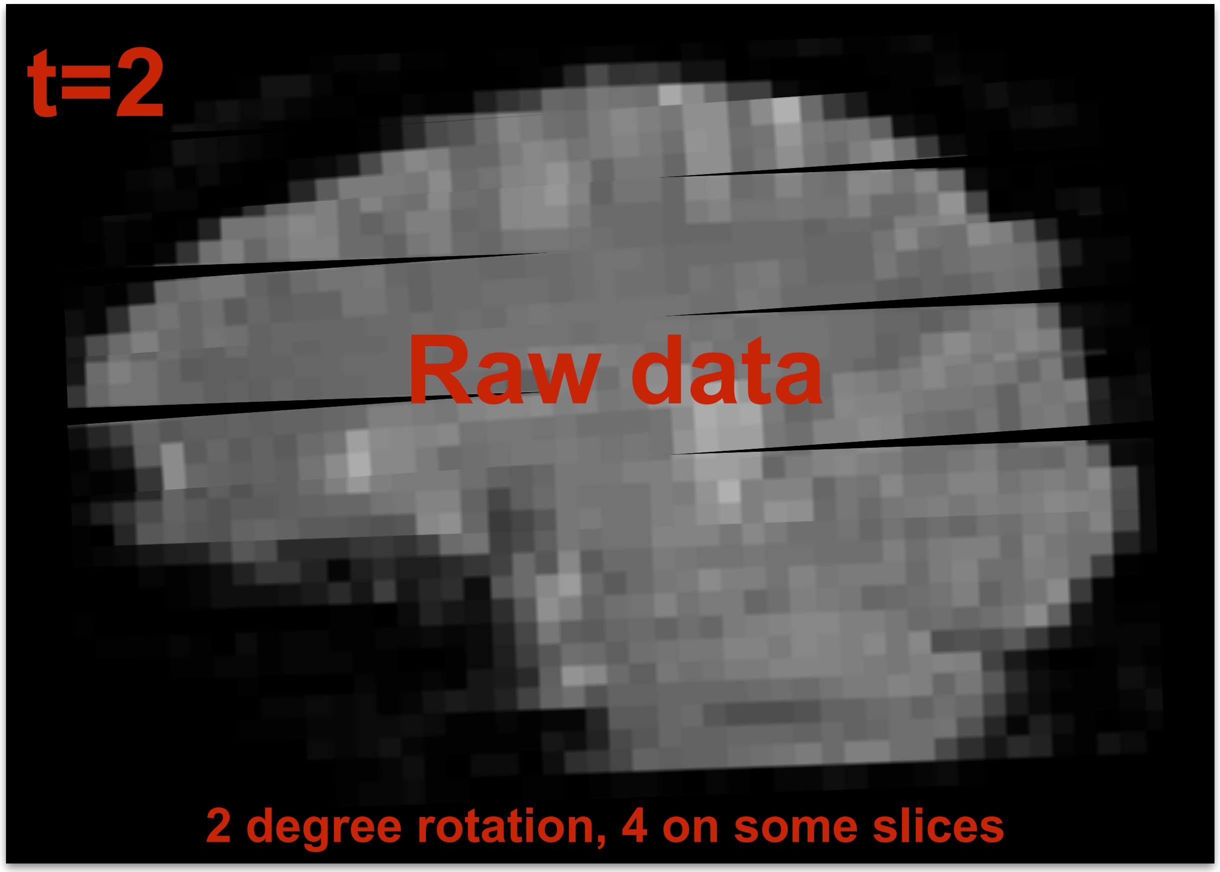


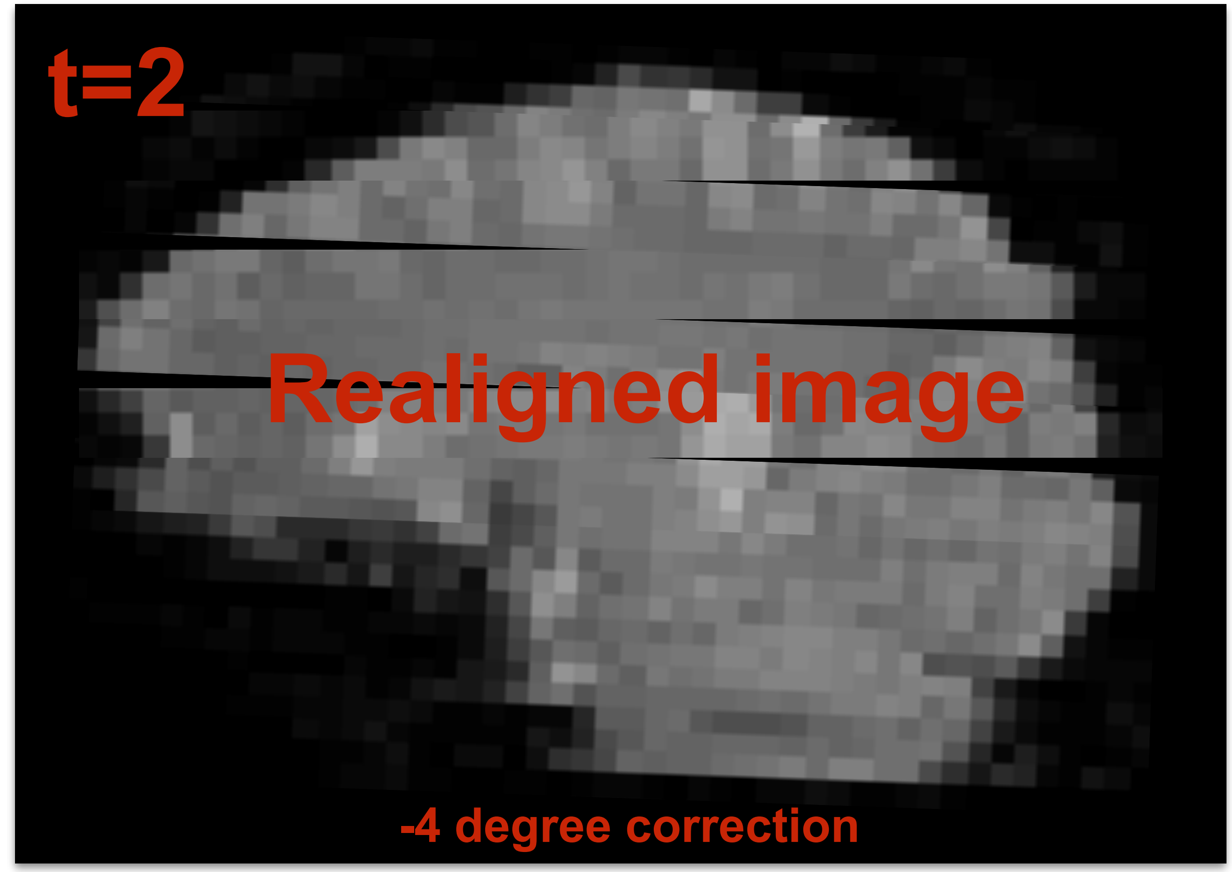


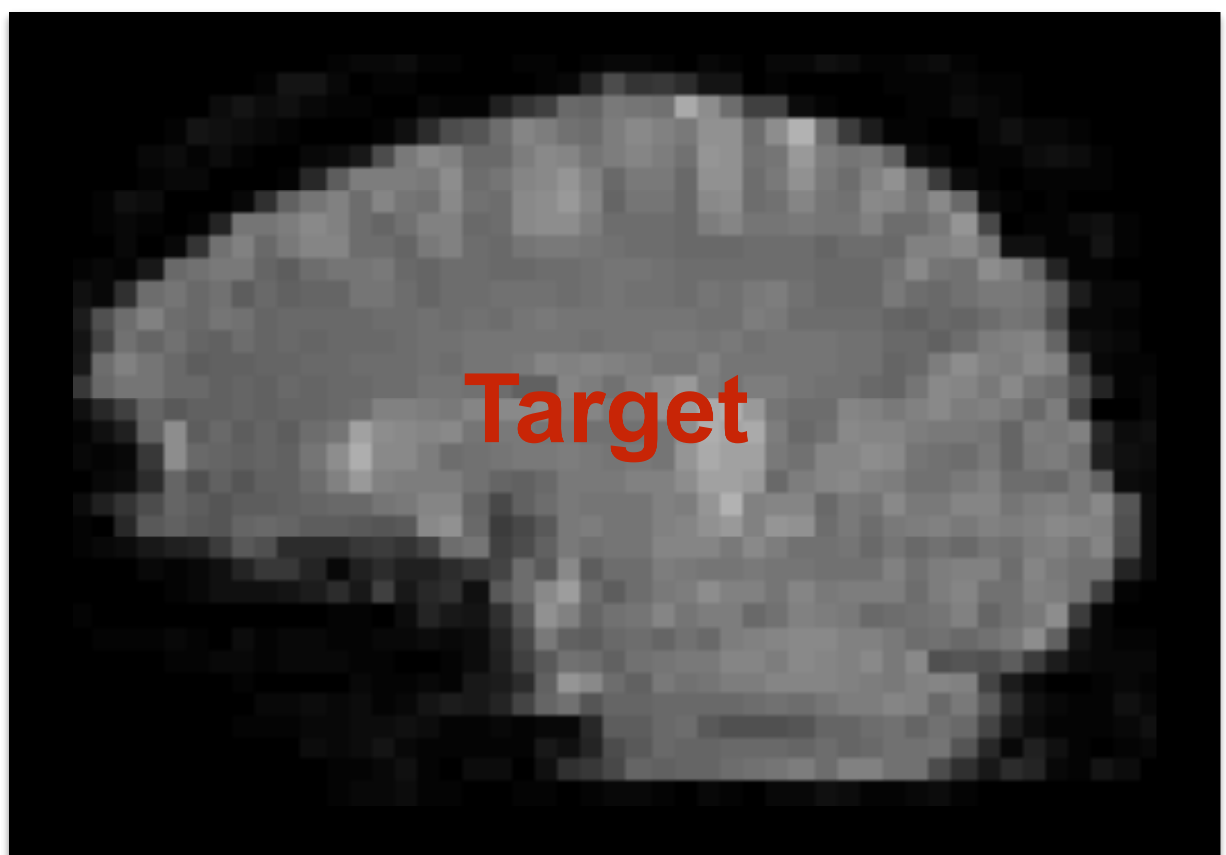


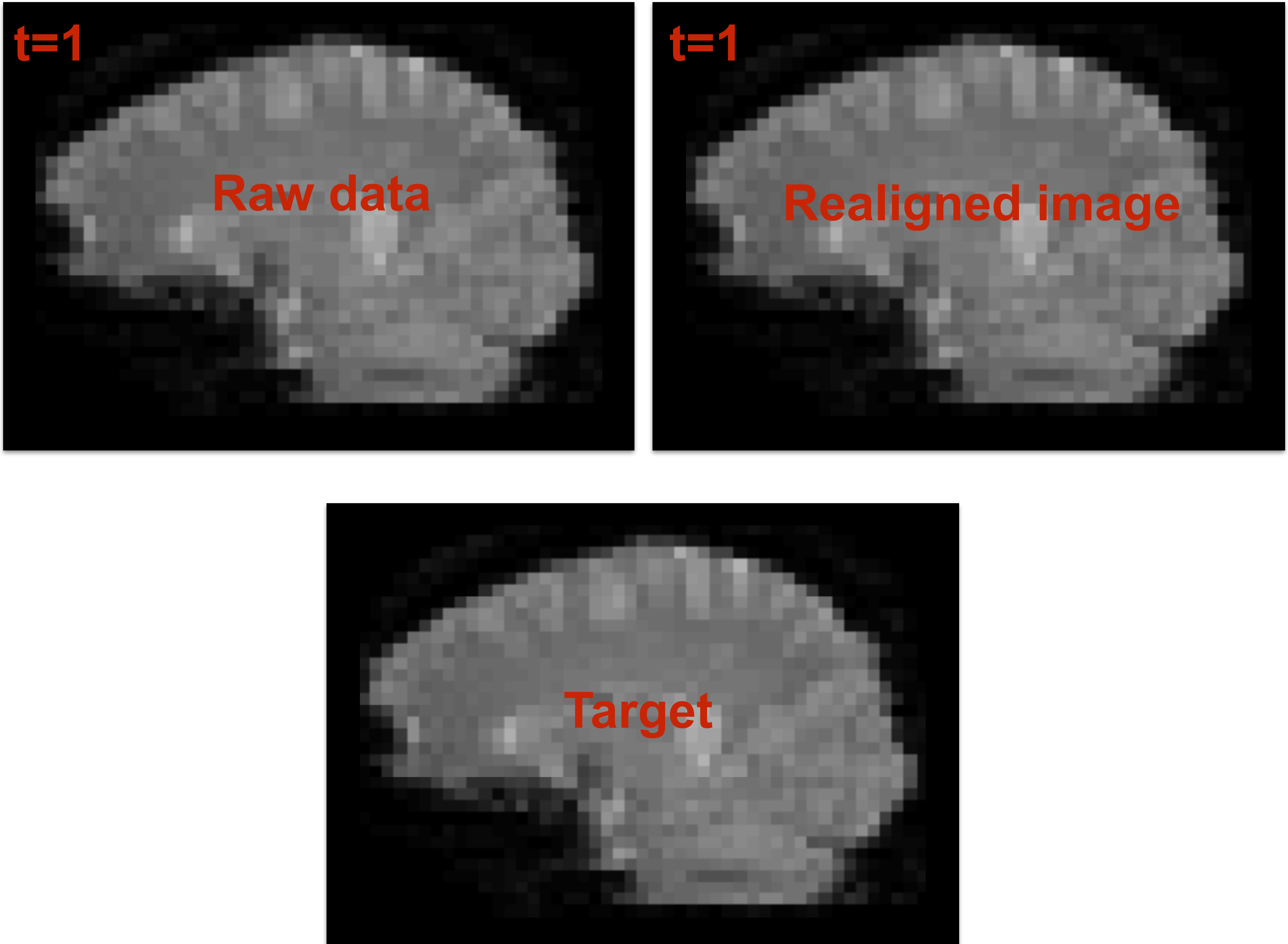

t=1
Raw data
t=1
Realigned image
Target

The maximal "correct" rotation
Also the true correction for some slices

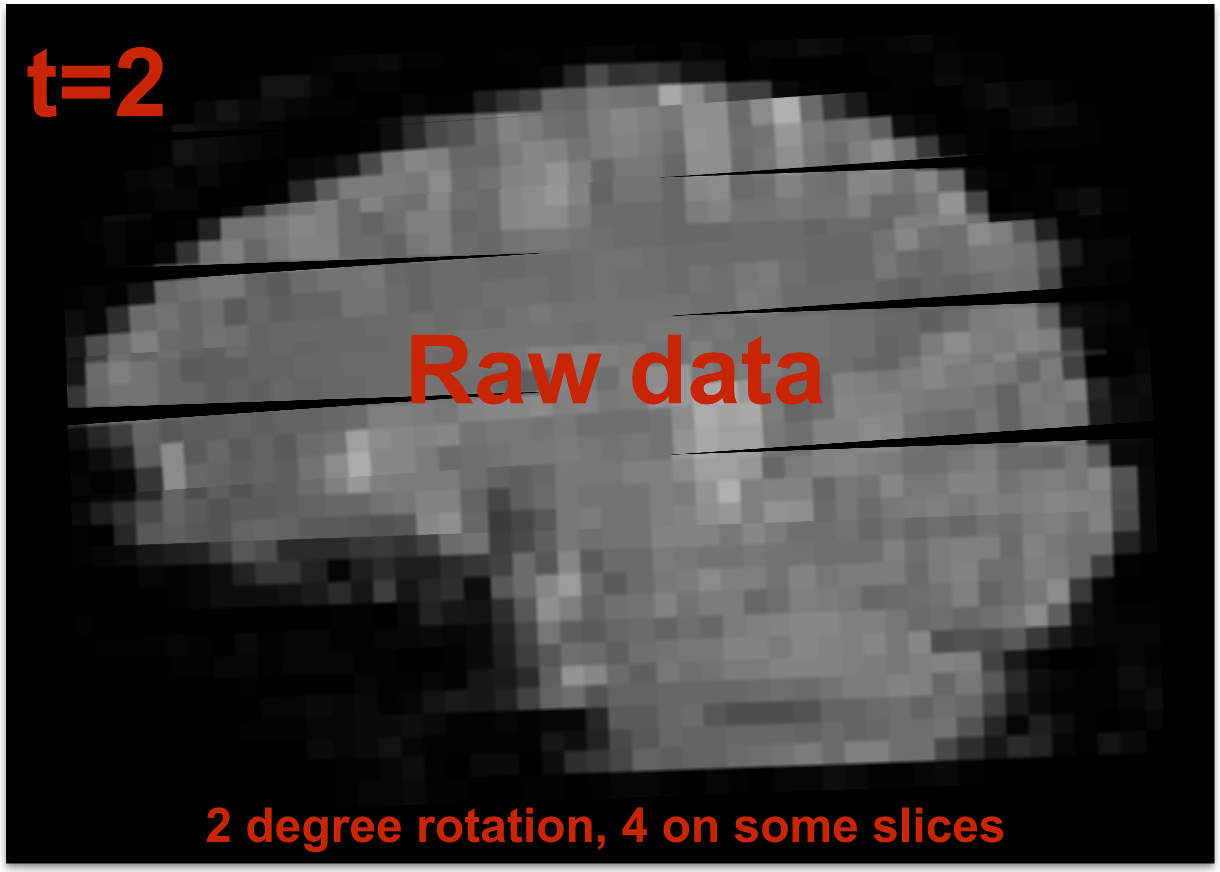


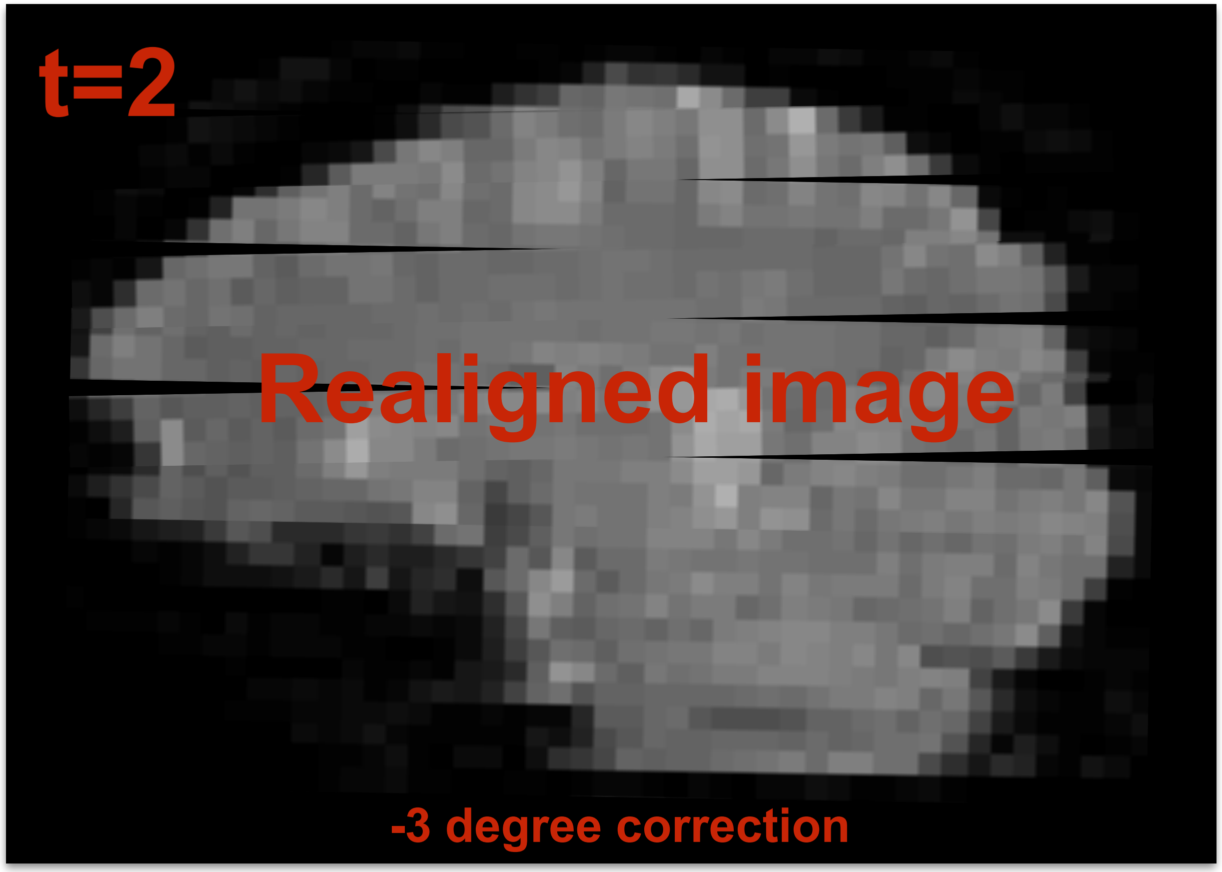


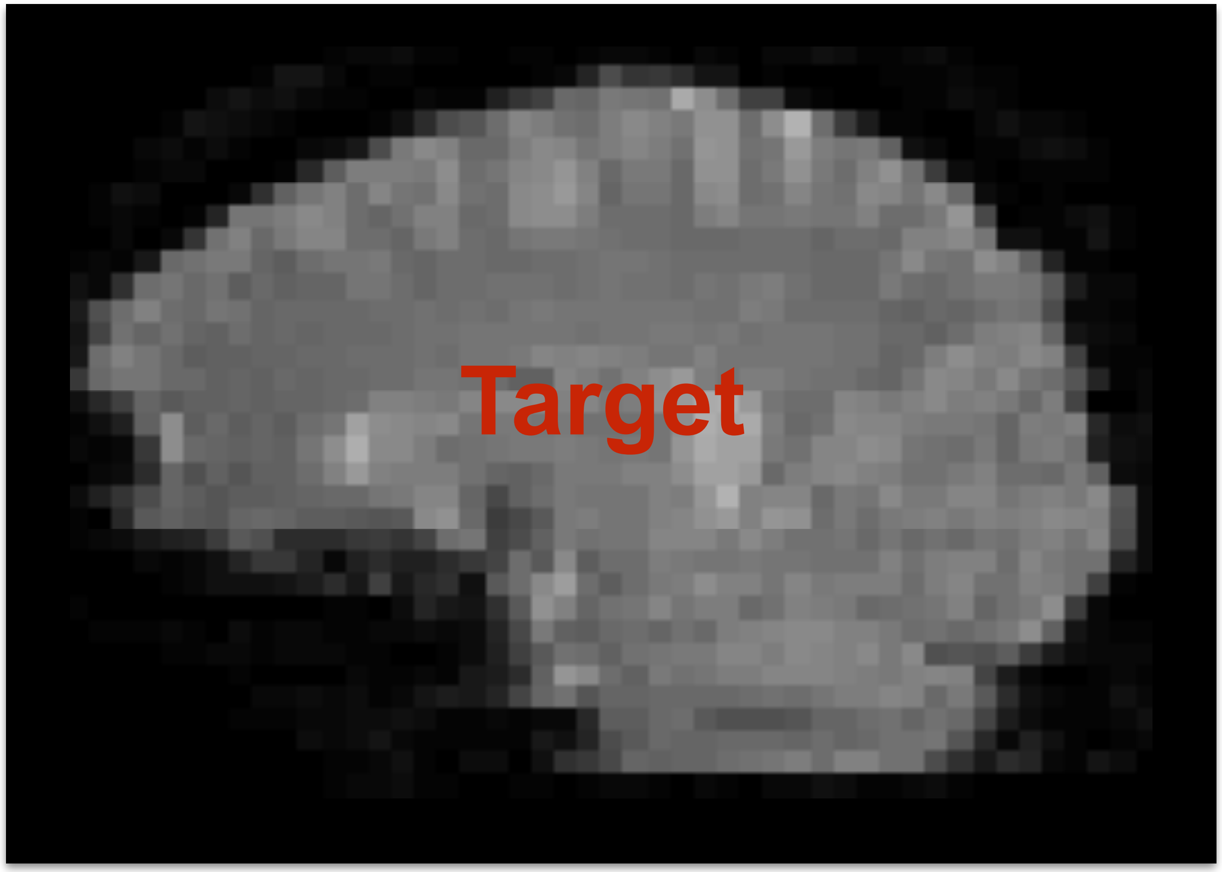



t=1
Raw data
t=1
Realigned image
Target

An intermediate "correct" rotation
Not the true correction for any slice







Examining unaligned and realigned images:

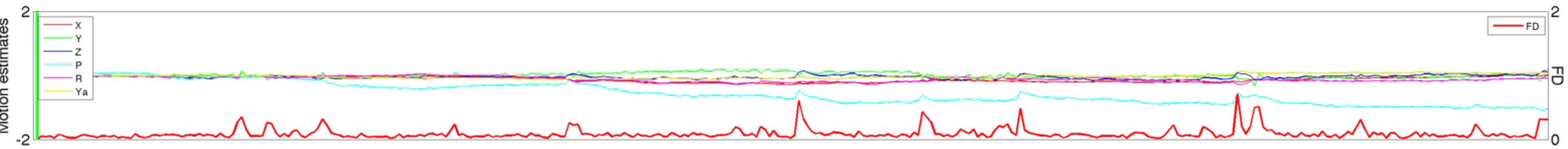
There is often no single “correct” motion estimate
Instead there is a range of “correct” estimates

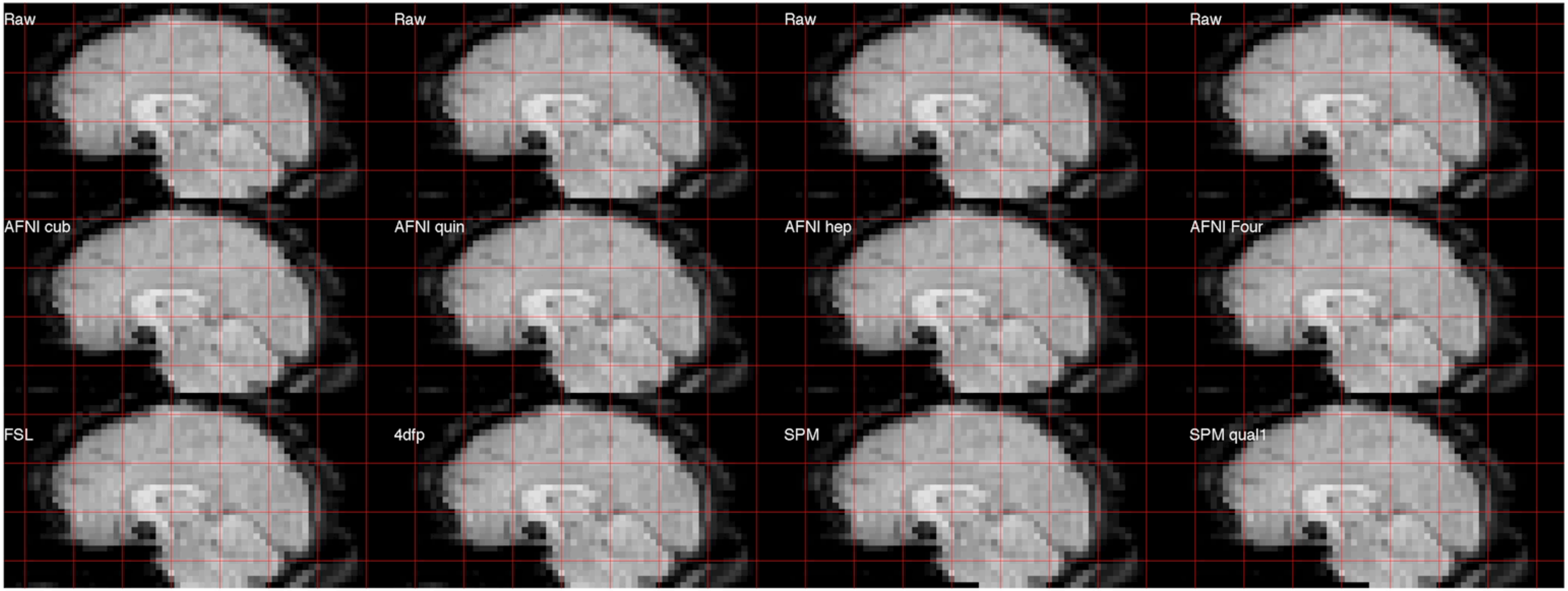
Only one value can be chosen
It is determined by the cost function

After realignment the image will remain somewhat misaligned
This will look like motion

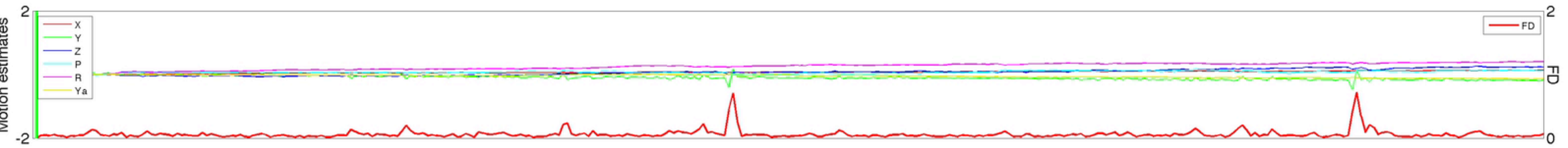
Now I’ll show examples of 3 scans before and after alignment
- unaligned in the top row
- then 4 versions of AFNI alignment (cub,quin,hept, Fourier)
- and then FSL, 4dfp, and 2 versions of SPM

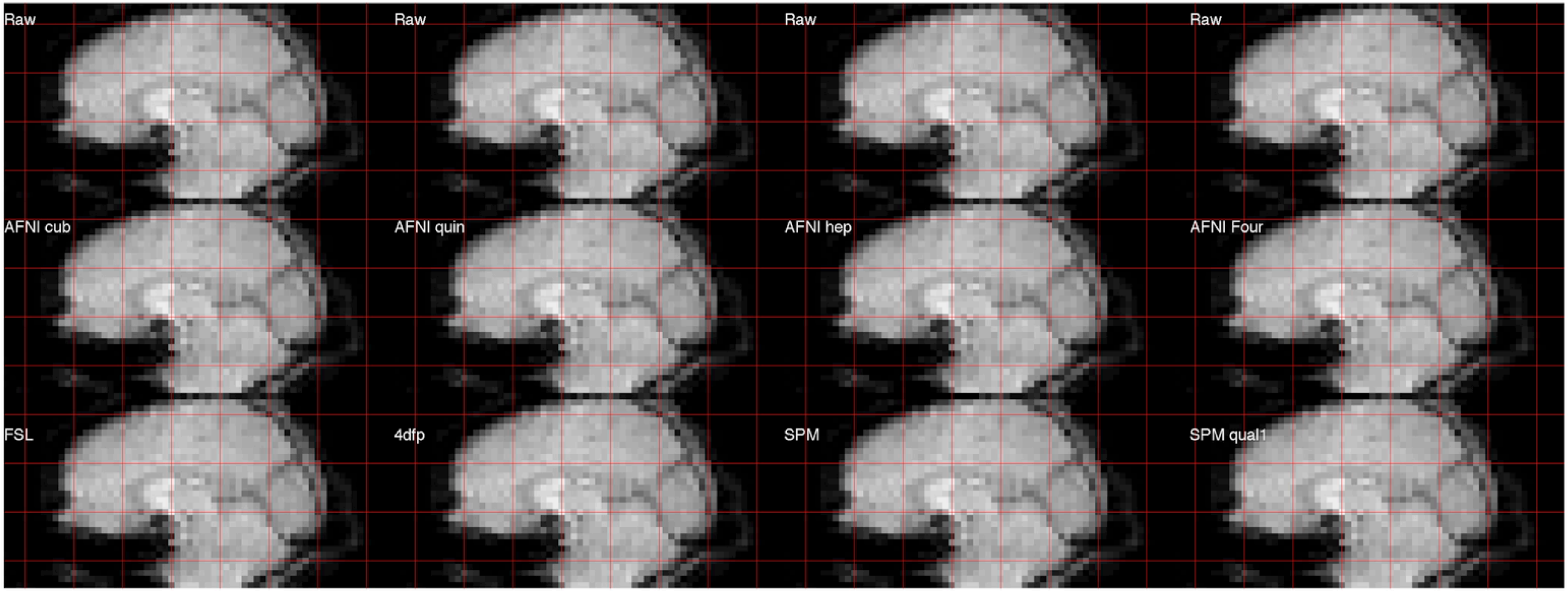
Examining unaligned and realigned images:



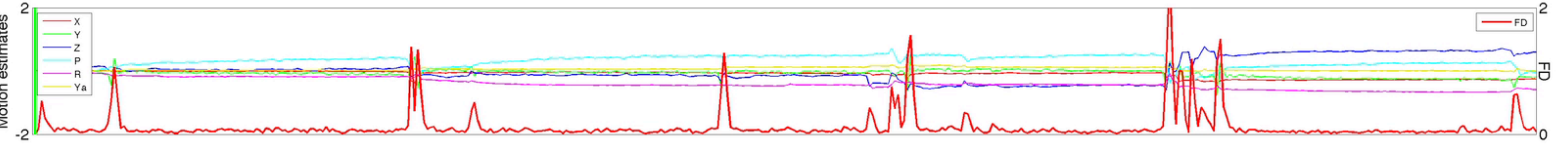


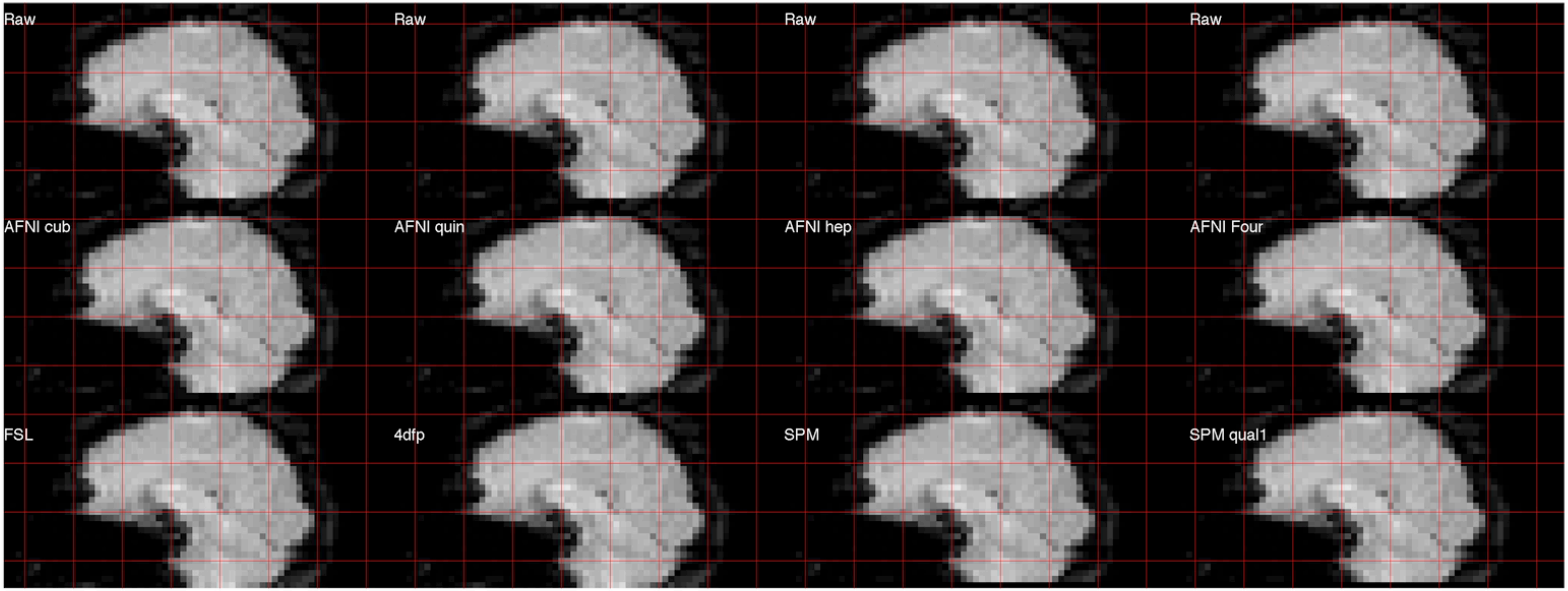
Examining unaligned and realigned images:





Examining unaligned and realigned images:





Examining unaligned and realigned images:

Positional changes are well-corrected
Meaning the brain is more or less in the right place

But during motion there is often residual misalignment
This is probably due to brain distortion
- and is probably not due to “incorrect” position estimation
- which is a fraught term for the reasons just illustrated

Examining unaligned and realigned images:

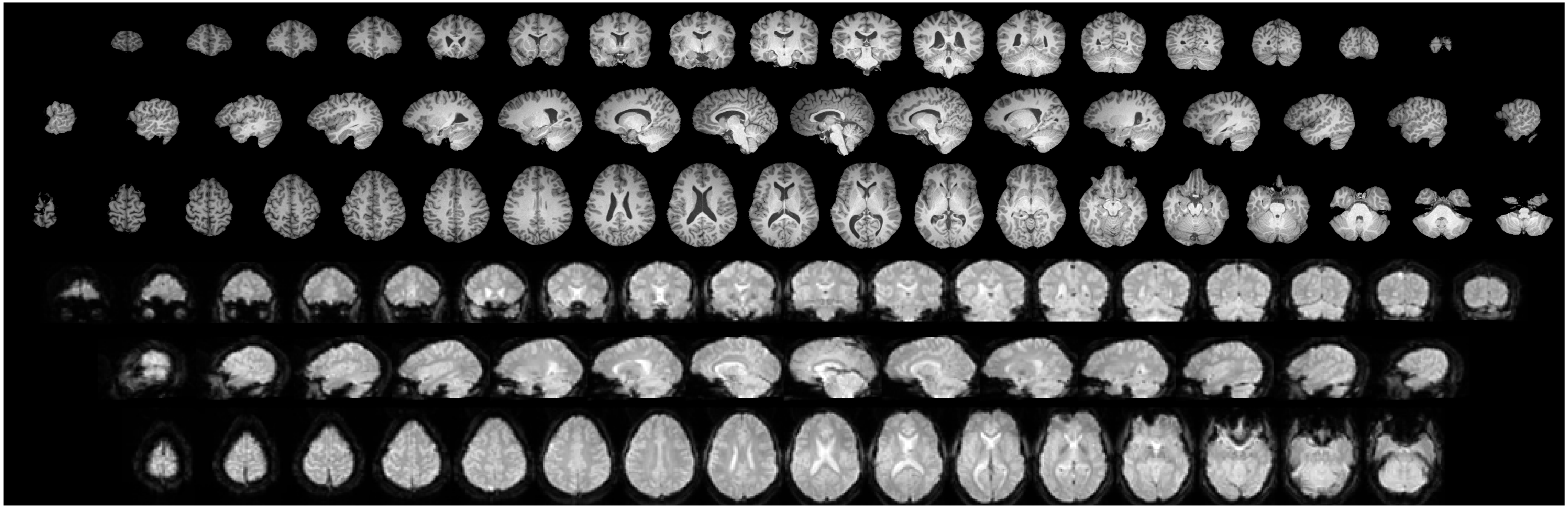
This is the “motion correction” step of processing

Volumes during motion are often not quite right
- in terms of distortion
- and in terms of signals, which we haven’t seen yet

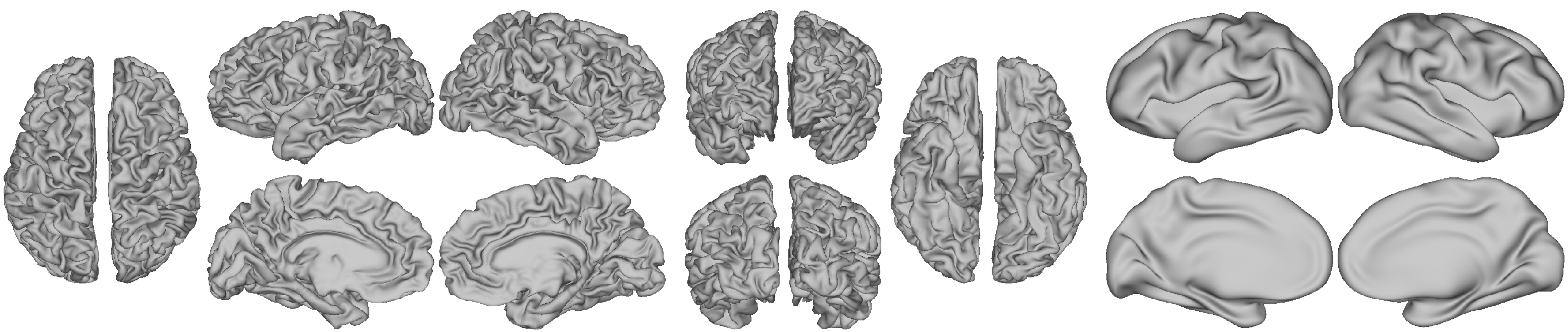
There is no way to correct these volumes
- without replacing at least some of data in some way
- e.g., interpolation in time or space
- nonlinear warps/transformations to fill in and stretch things
- beyond the scope of this talk

Let’s now look at the signals, which are the basis of FC MRI.
Signals from now on will have the mean value removed
- i.e., they will be zero-centered

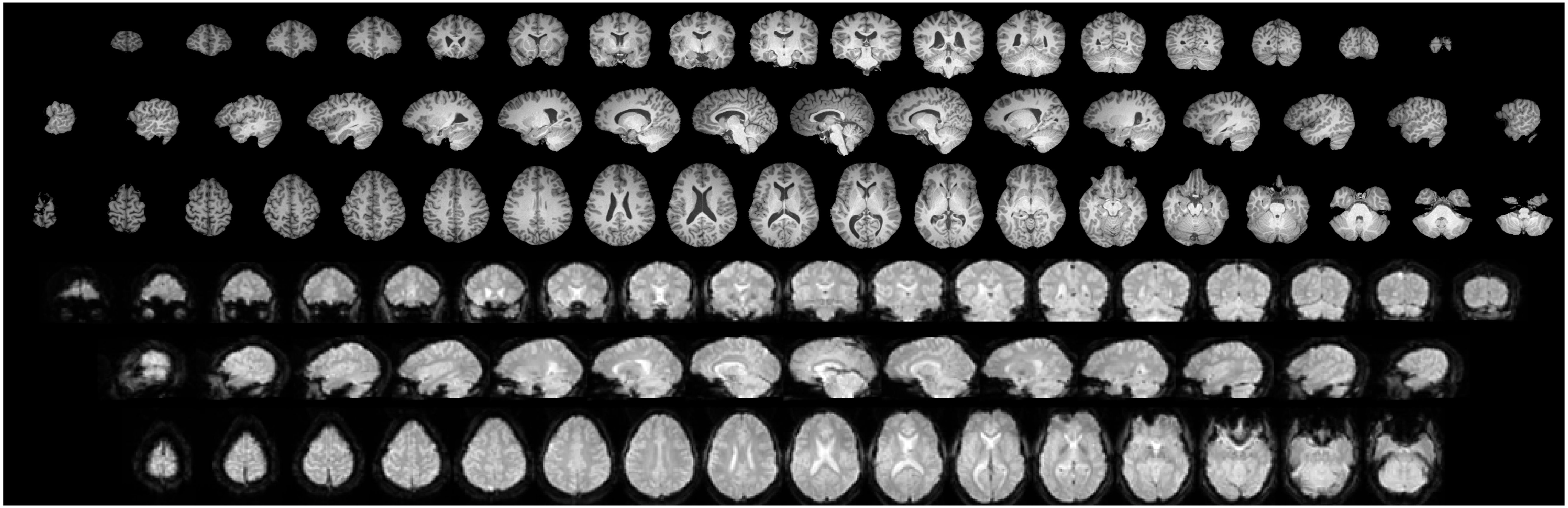
Subject 10: MP-RAGE slices (top) and mean BOLD image (bottom)



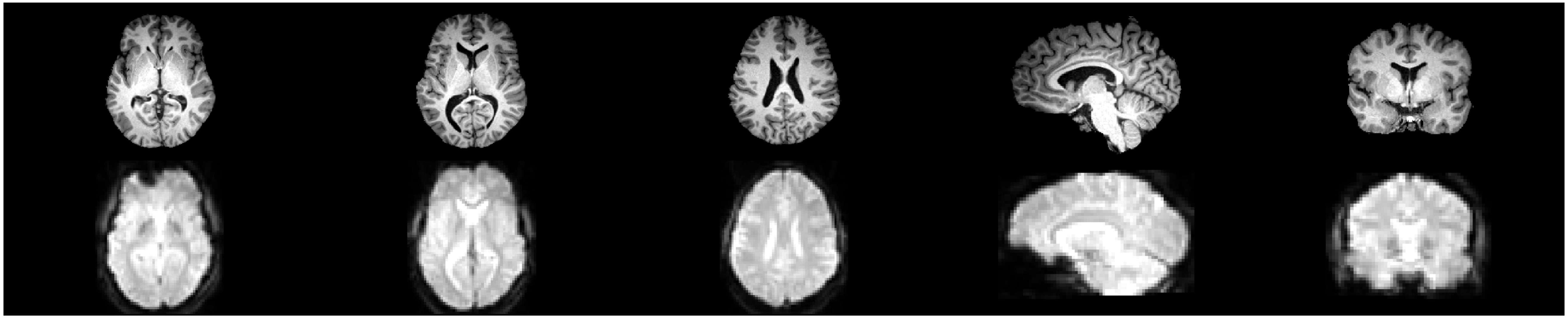
Workbench fs_LR mid-ribbon surfaces from MP-RAGE (via FreeSurfer 5.3)



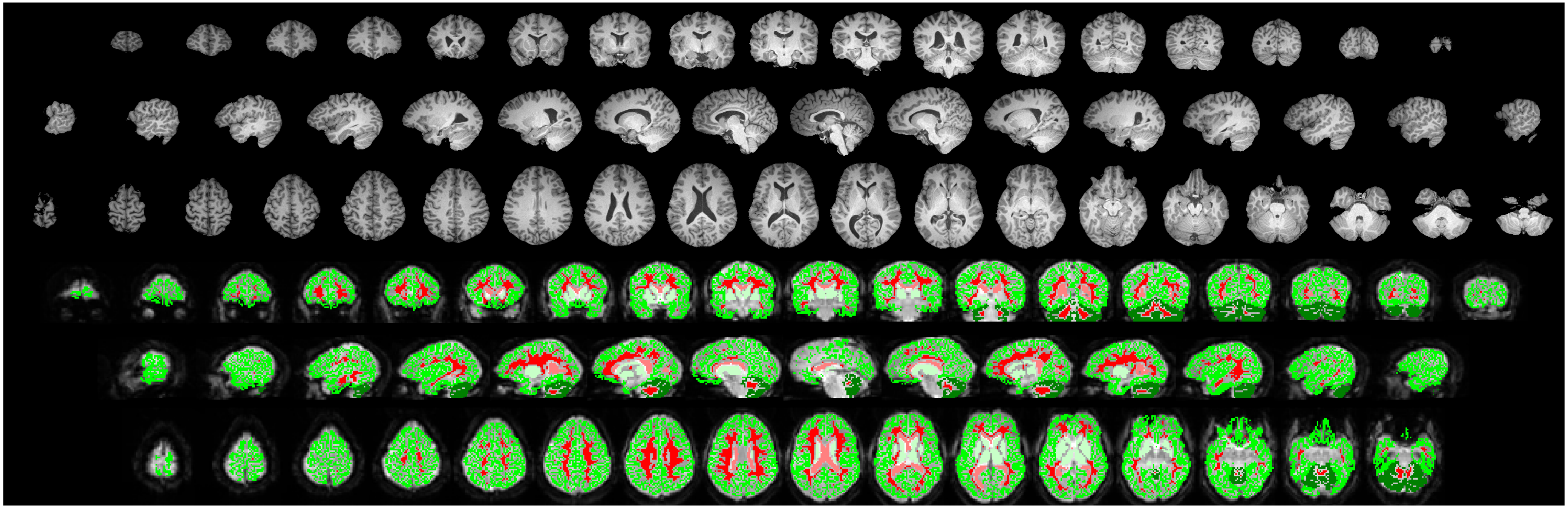
Subject 10: MP-RAGE slices (top) and mean BOLD image (bottom); FreeSurfer-derived compartments shown in colors (pink:CSF; red:WM; greens:GM)



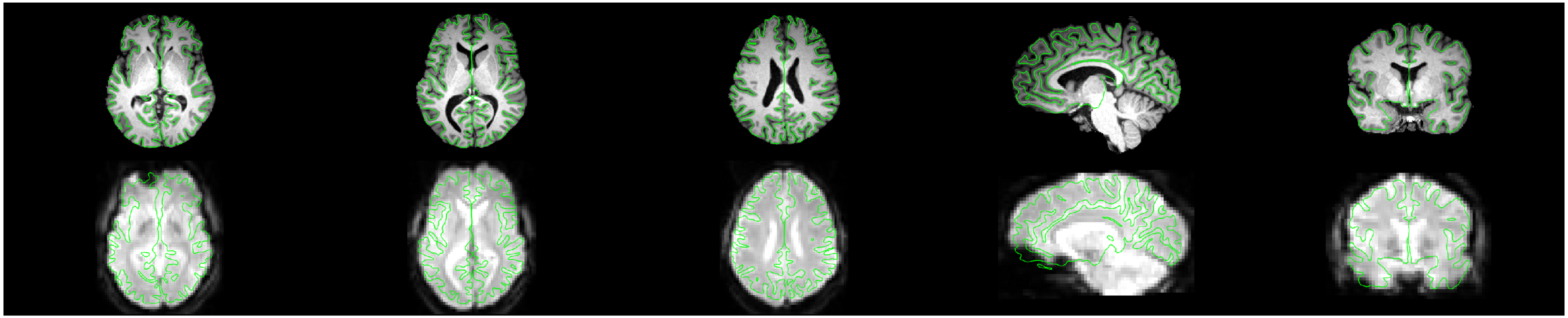
Workbench fs_LR mid-ribbon surfaces over MP-RAGE (top) and mean BOLD image (bottom)



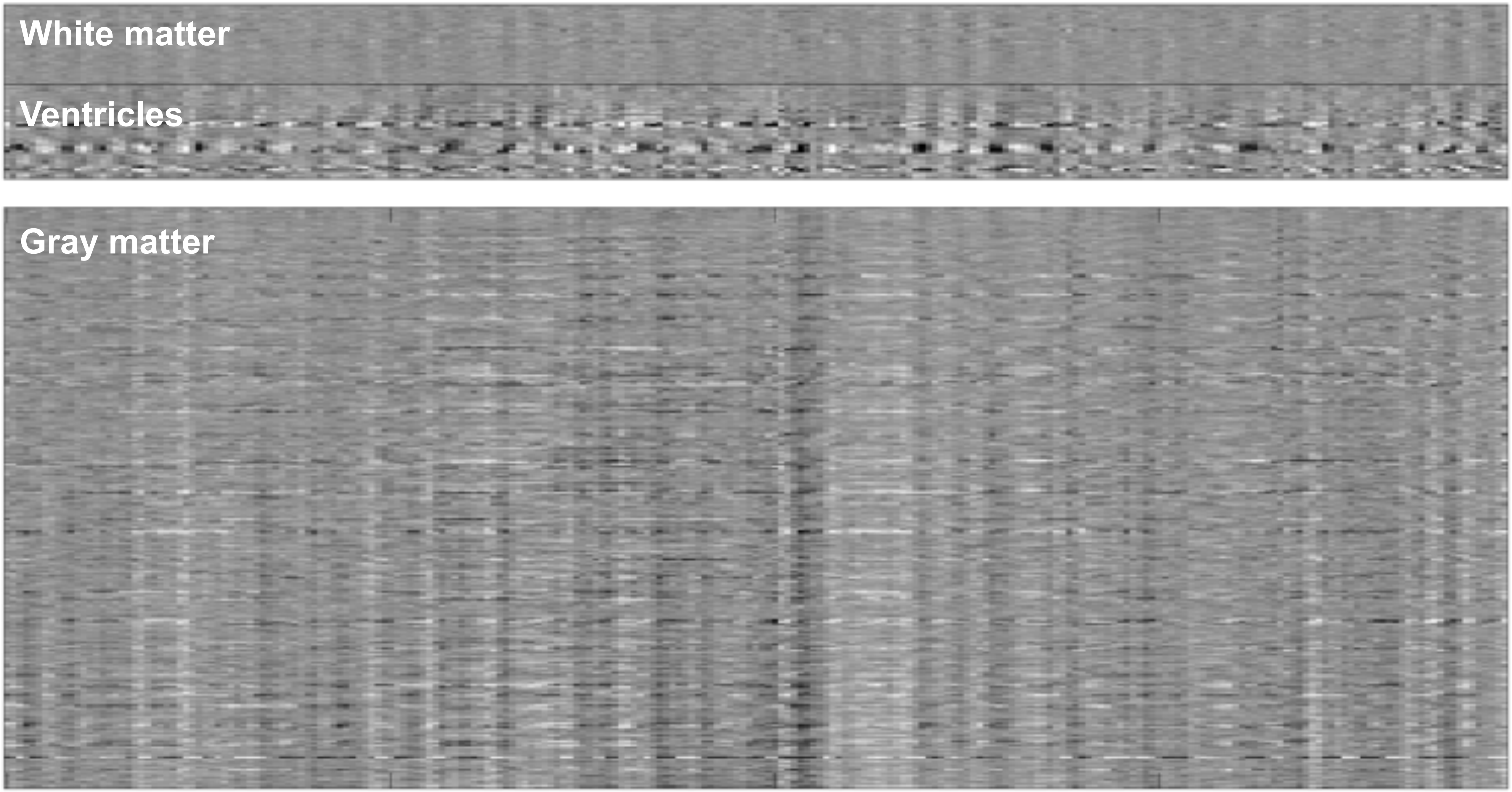
Subject 10: MP-RAGE slices (top) and mean BOLD image (bottom); FreeSurfer-derived compartments shown in colors (pink:CSF; red:WM; greens:GM)



Workbench fs_LR mid-ribbon surfaces over MP-RAGE (top) and mean BOLD image (bottom)

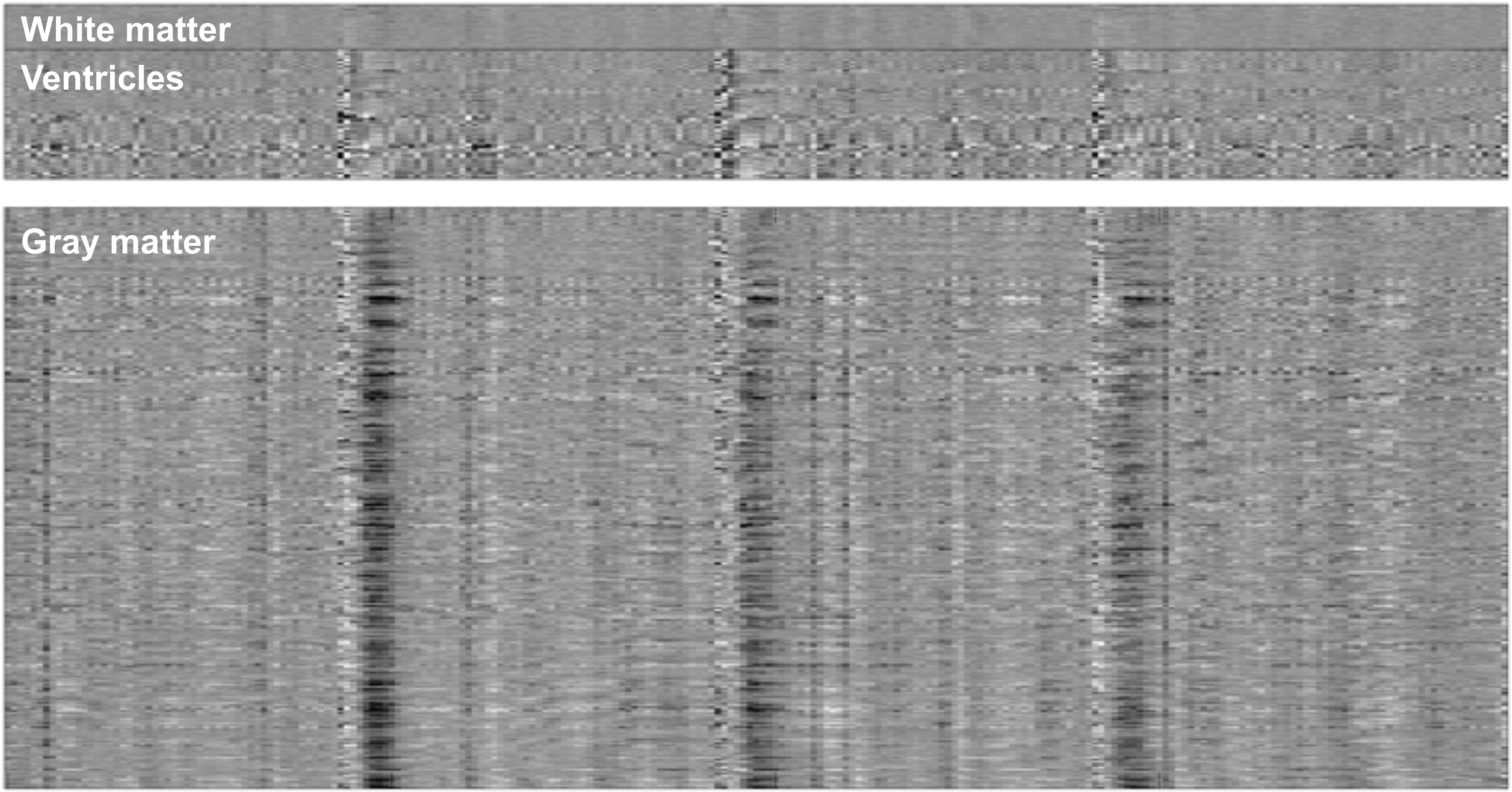


Time on x axis
Voxels on y axis (various compartments)
Heat map shows 1000s of voxel signals (-2 to 2% BOLD scale)

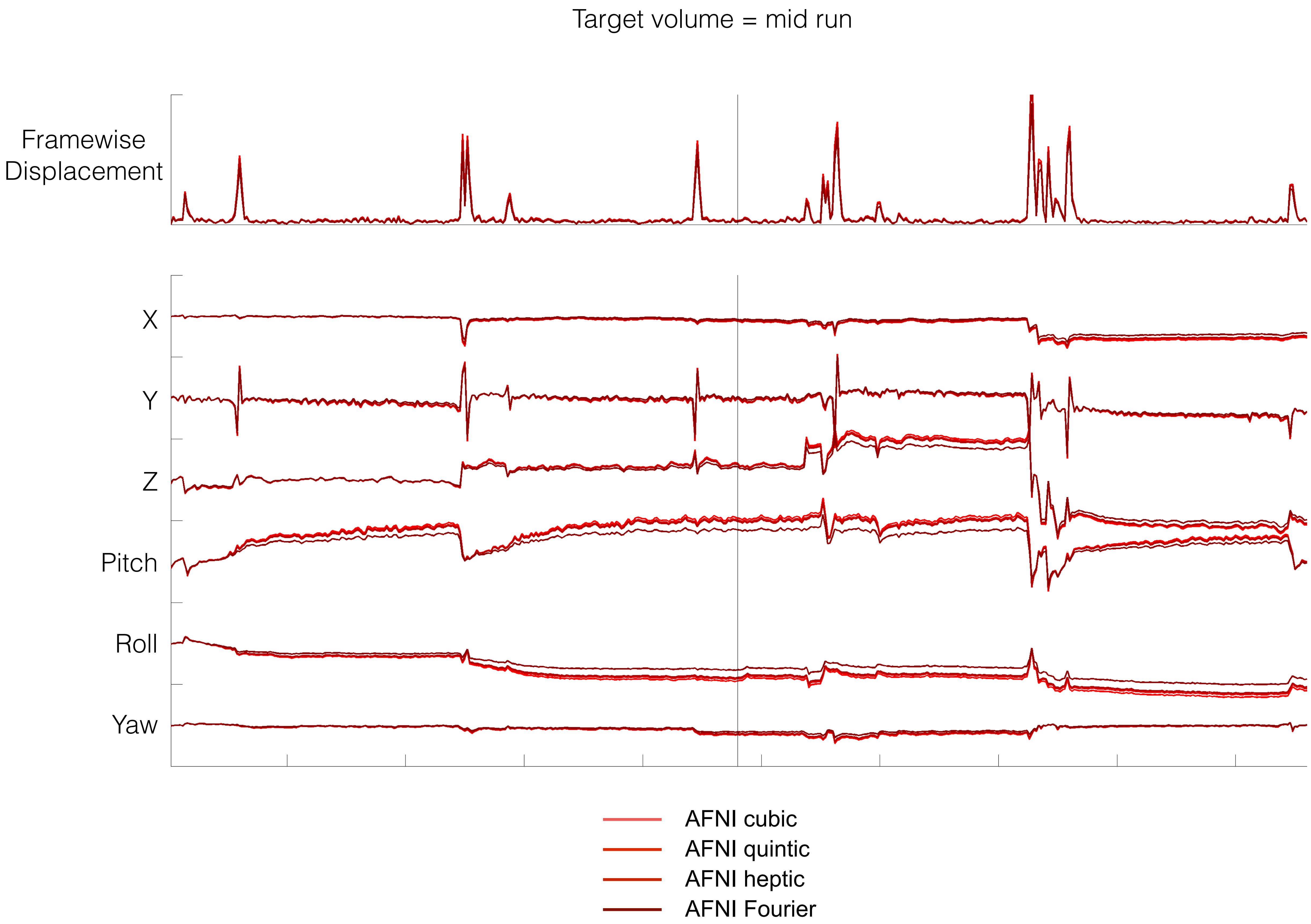


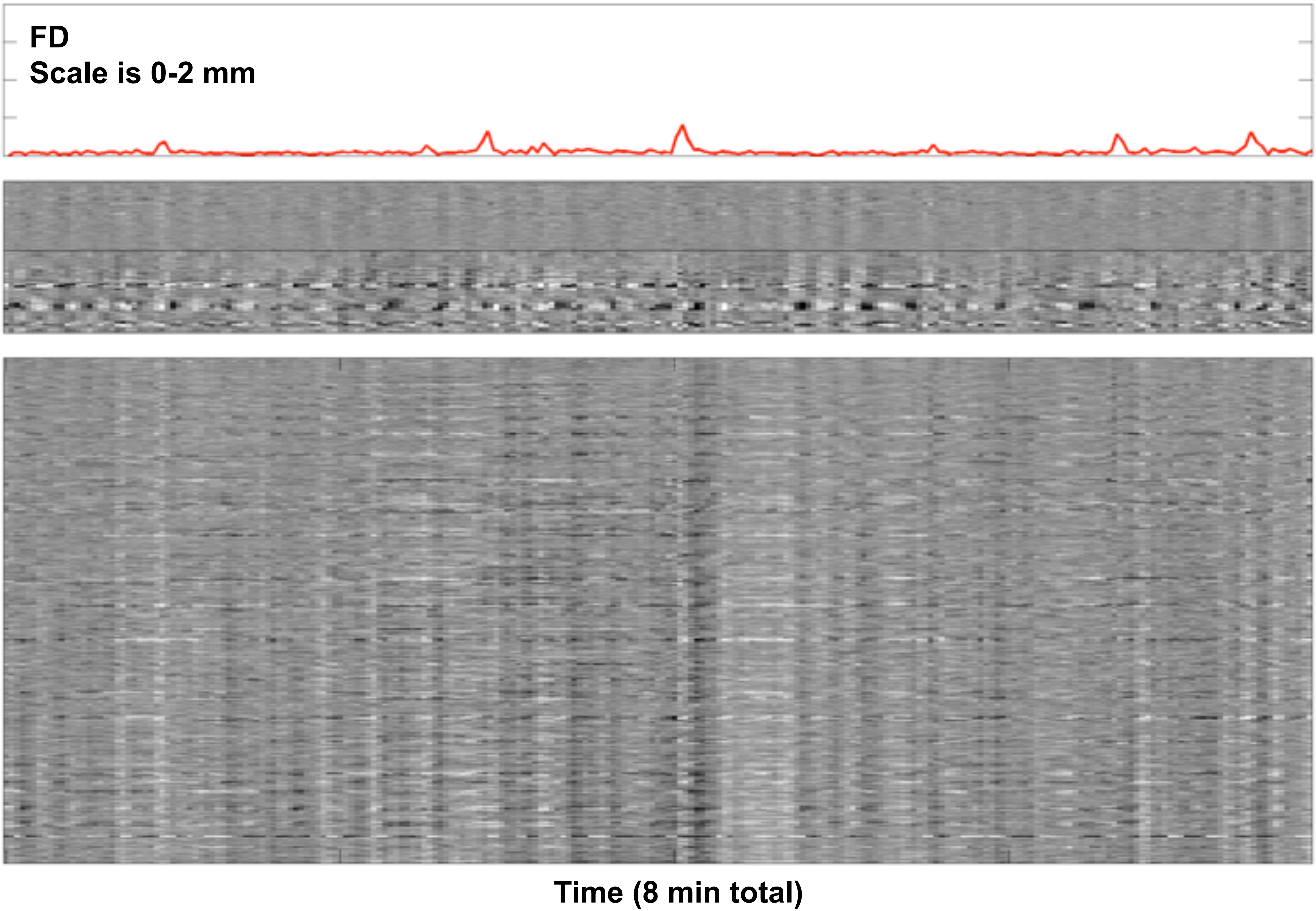
Time (8 min total)

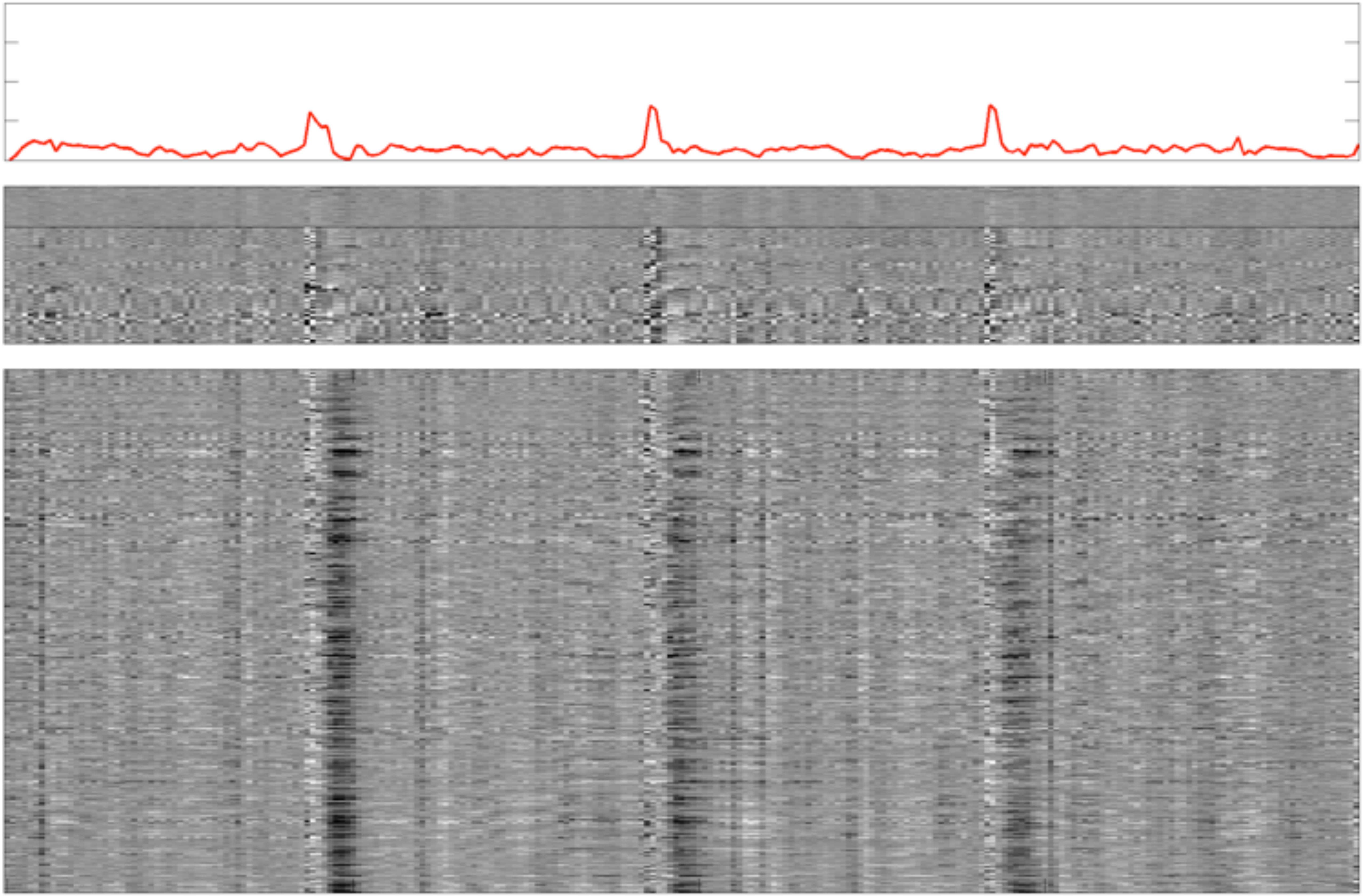
Time on x axis
Voxels on y axis (various compartments)
Heat map shows 1000s of voxel signals (-2 to 2% BOLD scale)

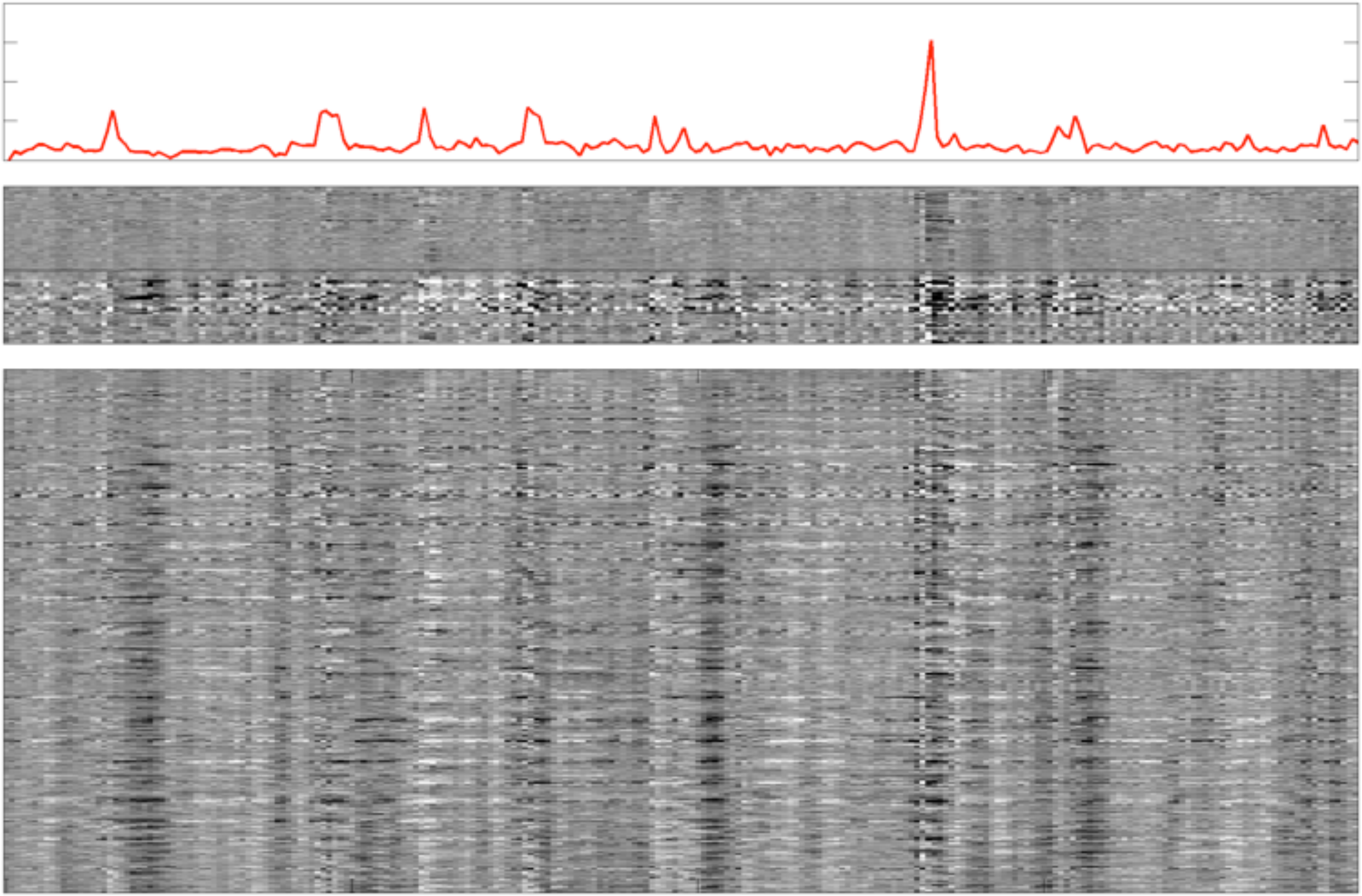


Time (8 min total)

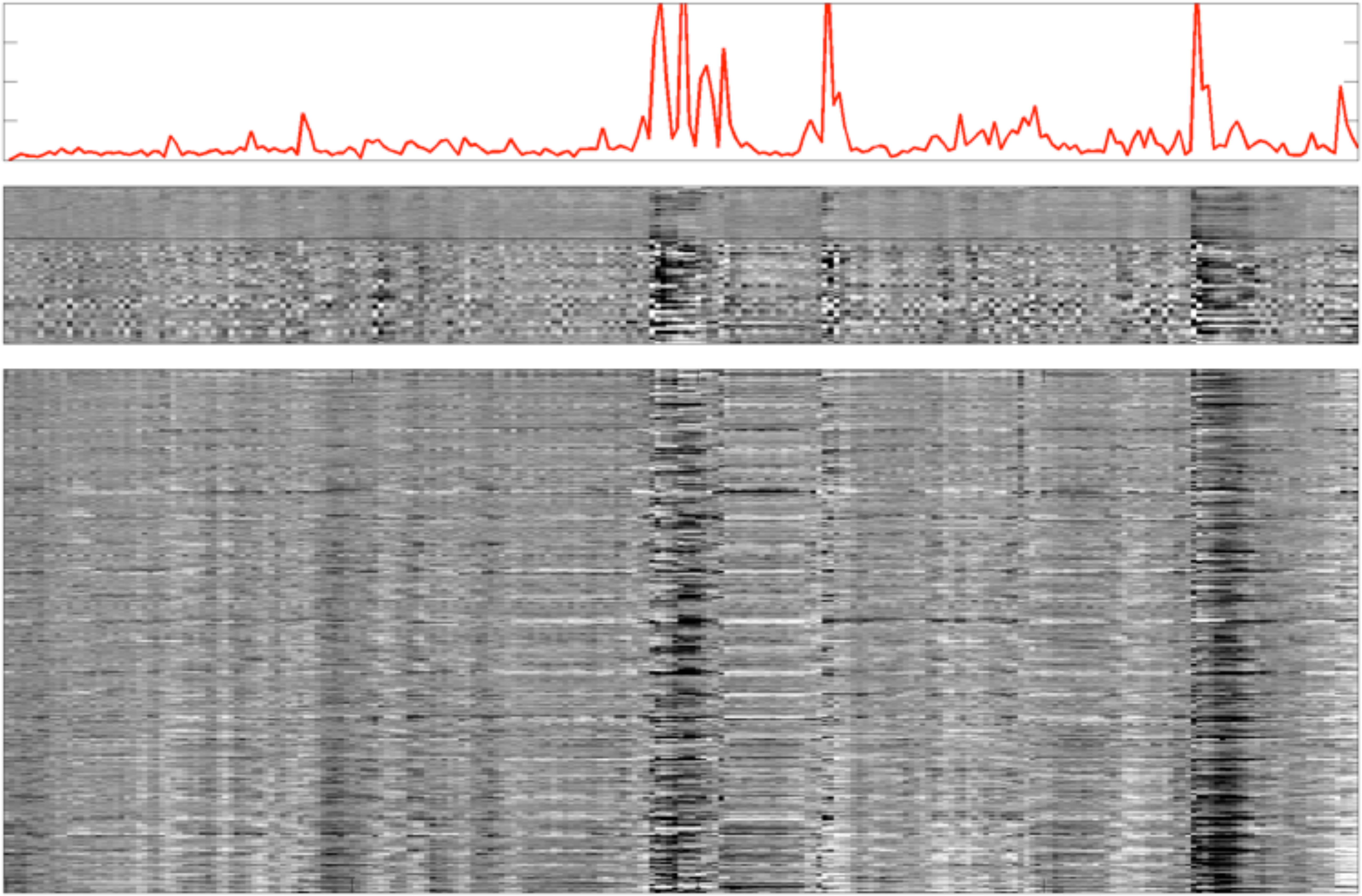

Target volume = mid run
Framewise Displacement
X
Y
Z
Pitch
Roll
Yaw
AFNI cubic
AFNI quintic
AFNI heptic
AFNI Fourier

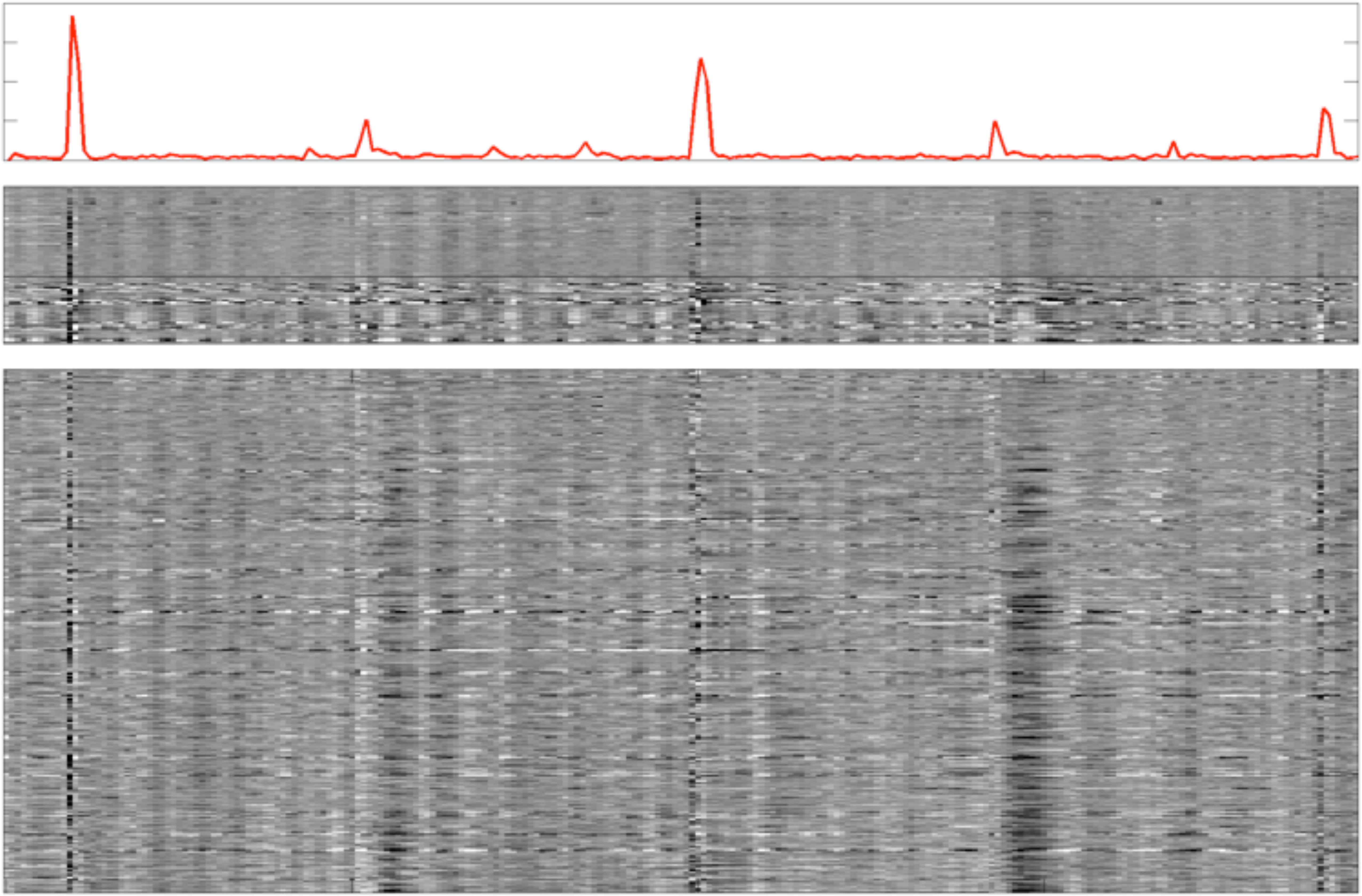

FD
Scale is 0-2 mm
Time (8 min total)

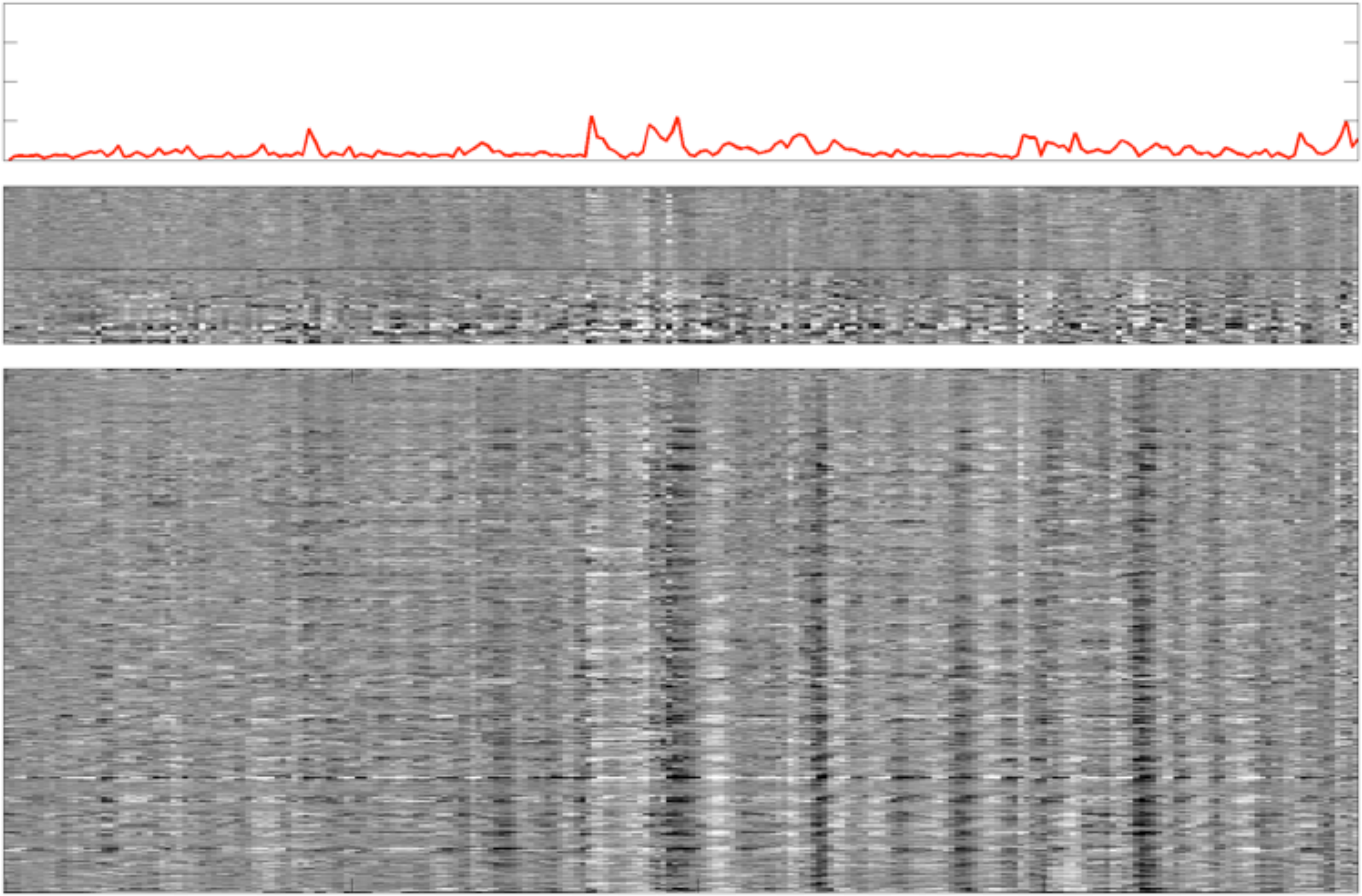

Time (8 min total)

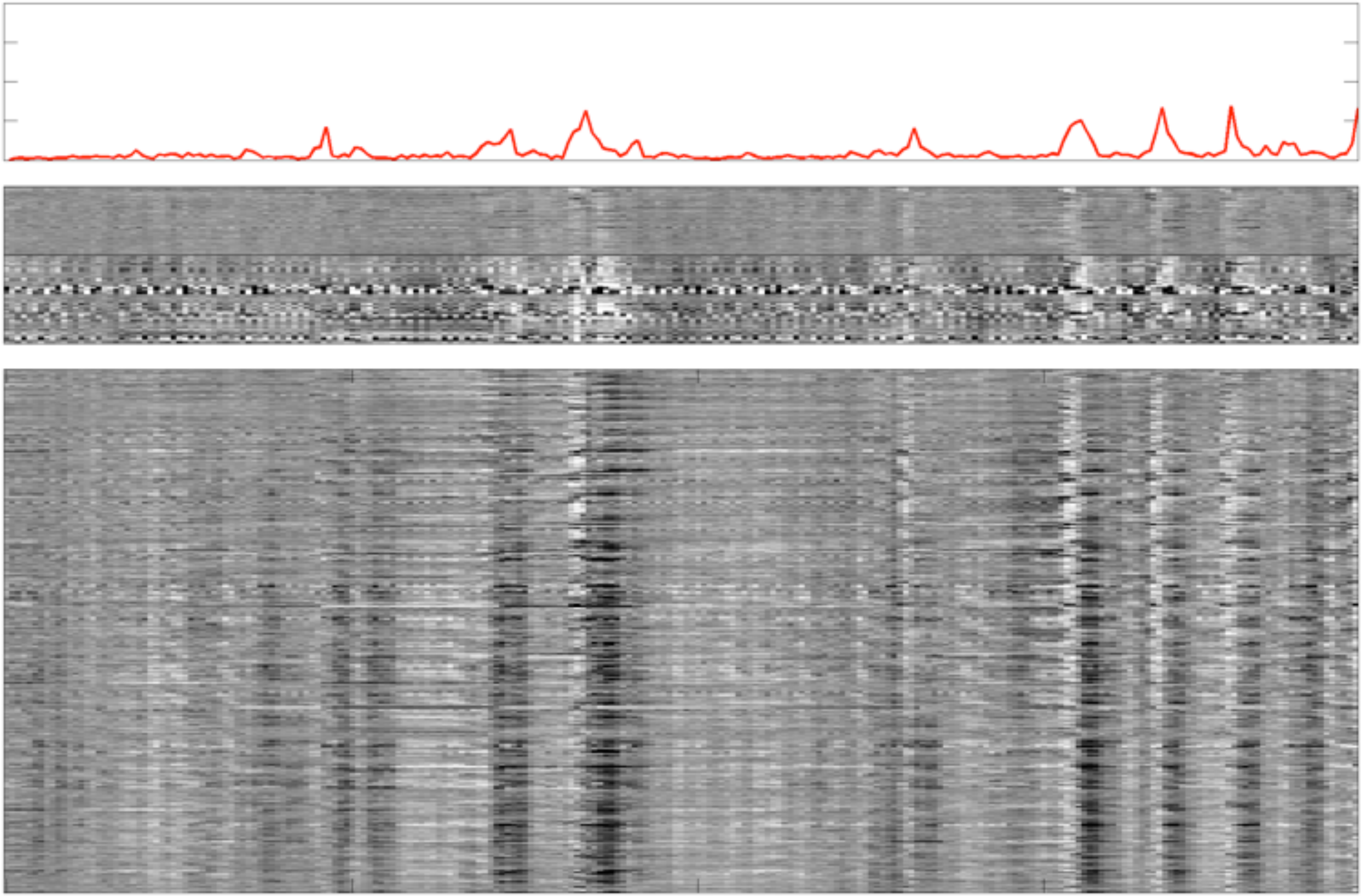


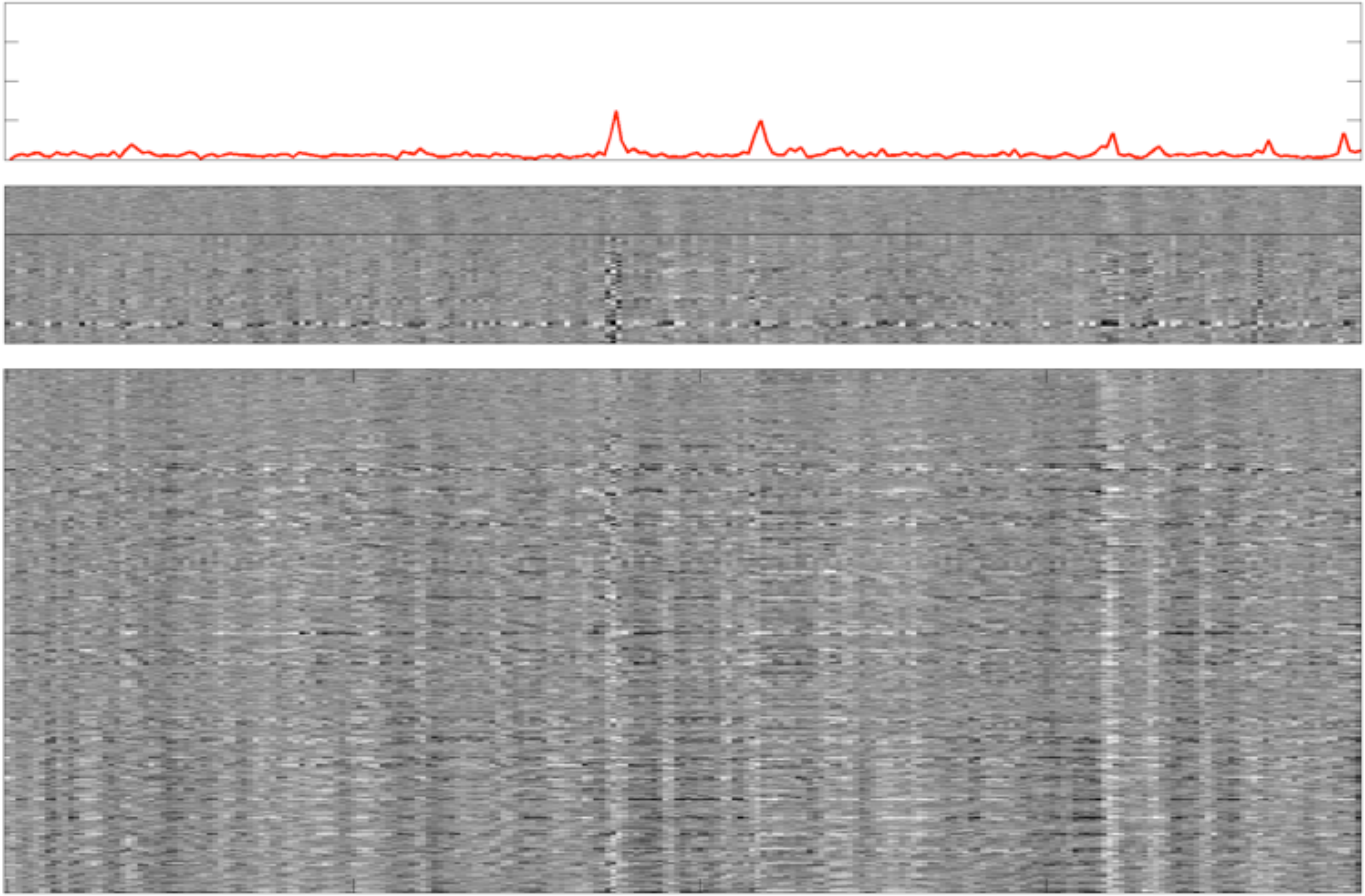
Time (8 min total)

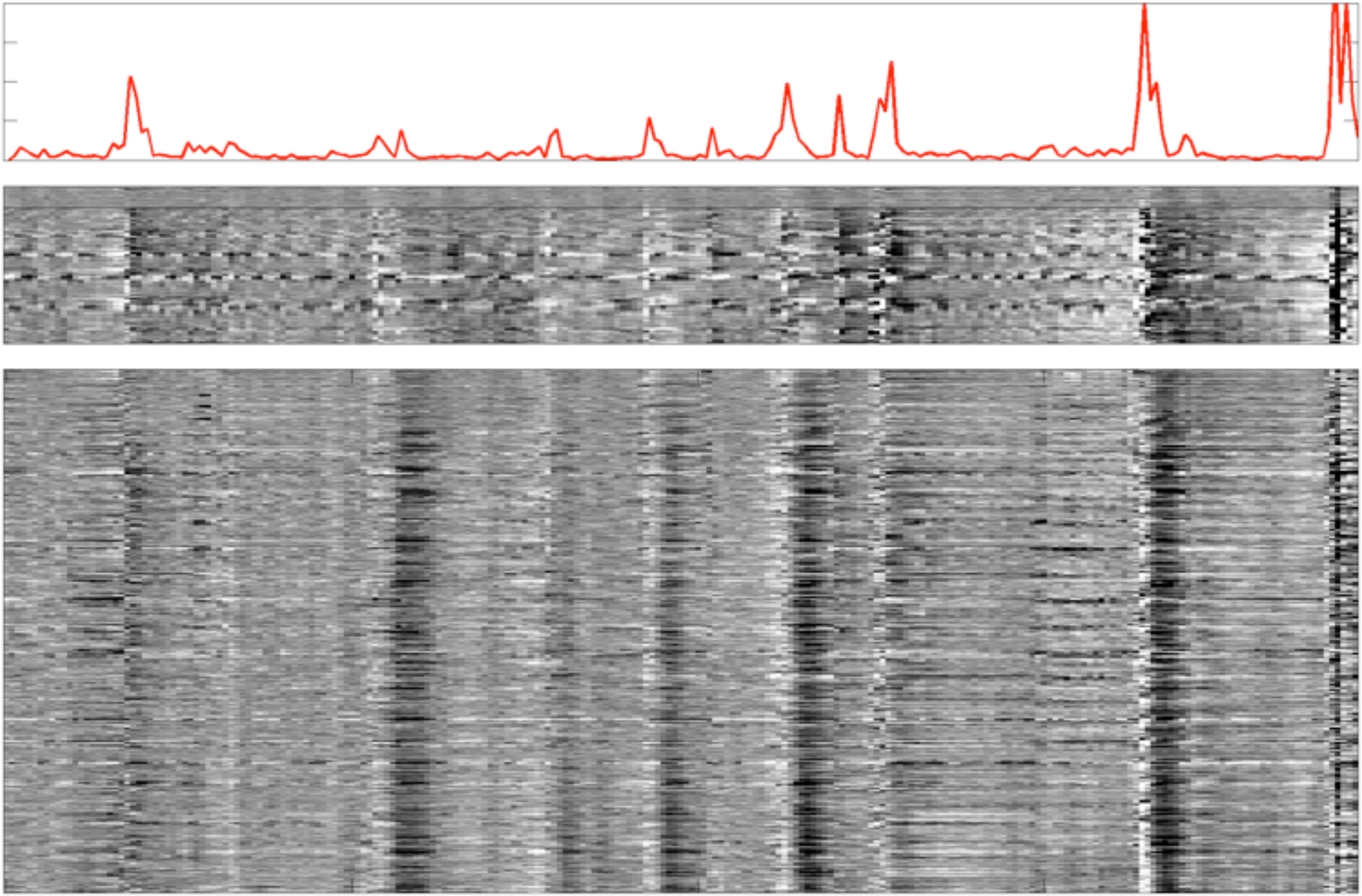


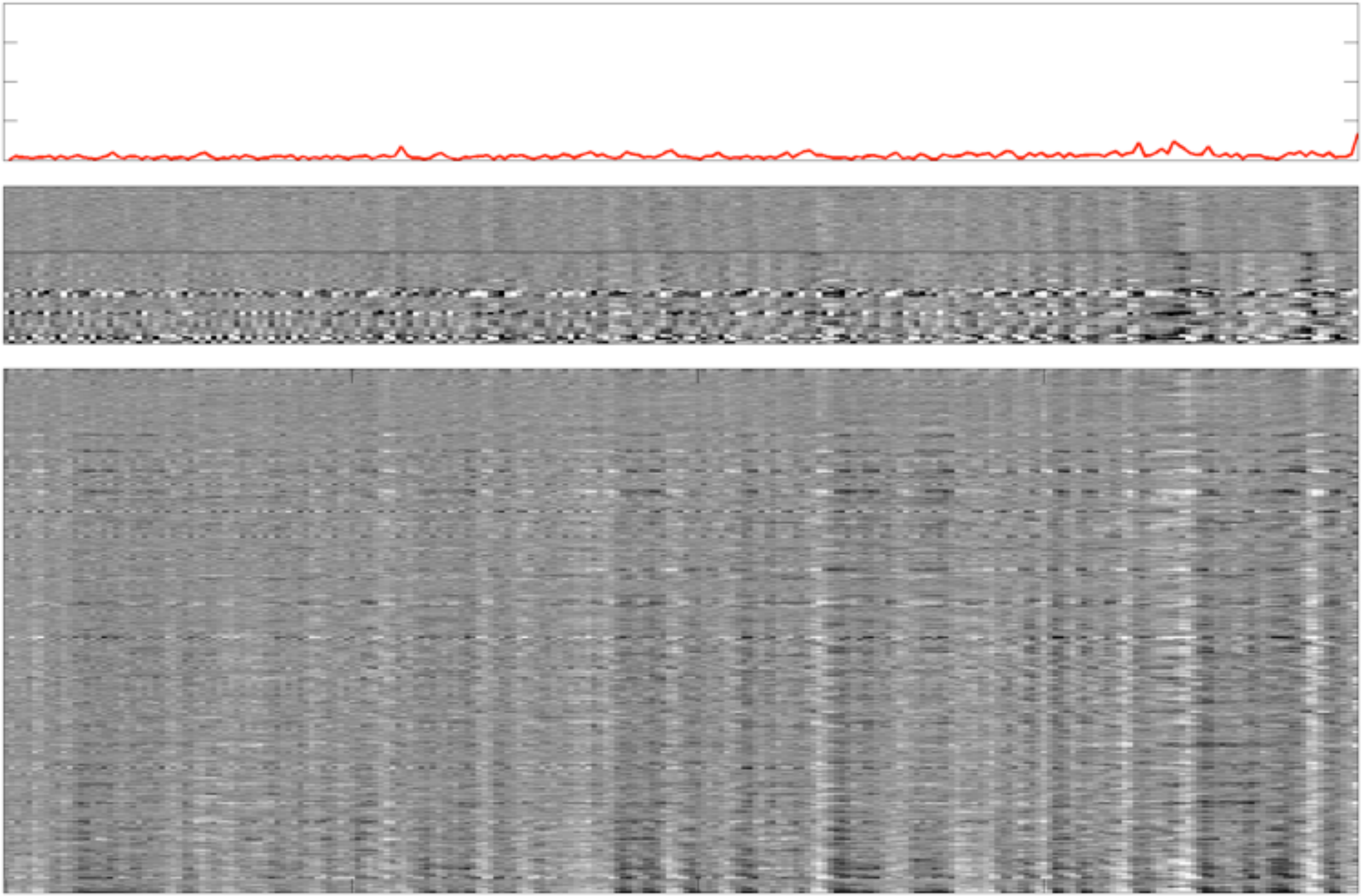


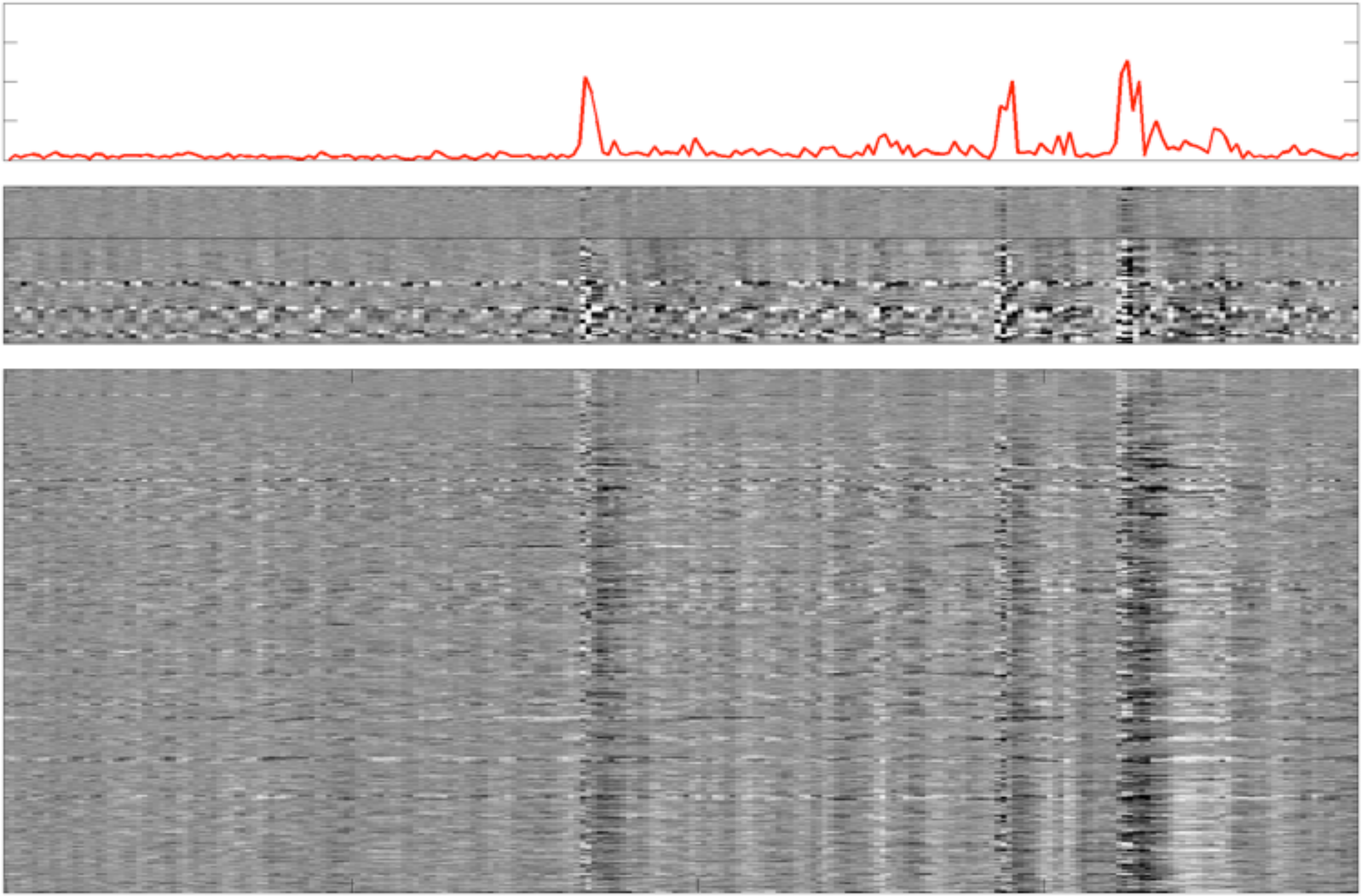


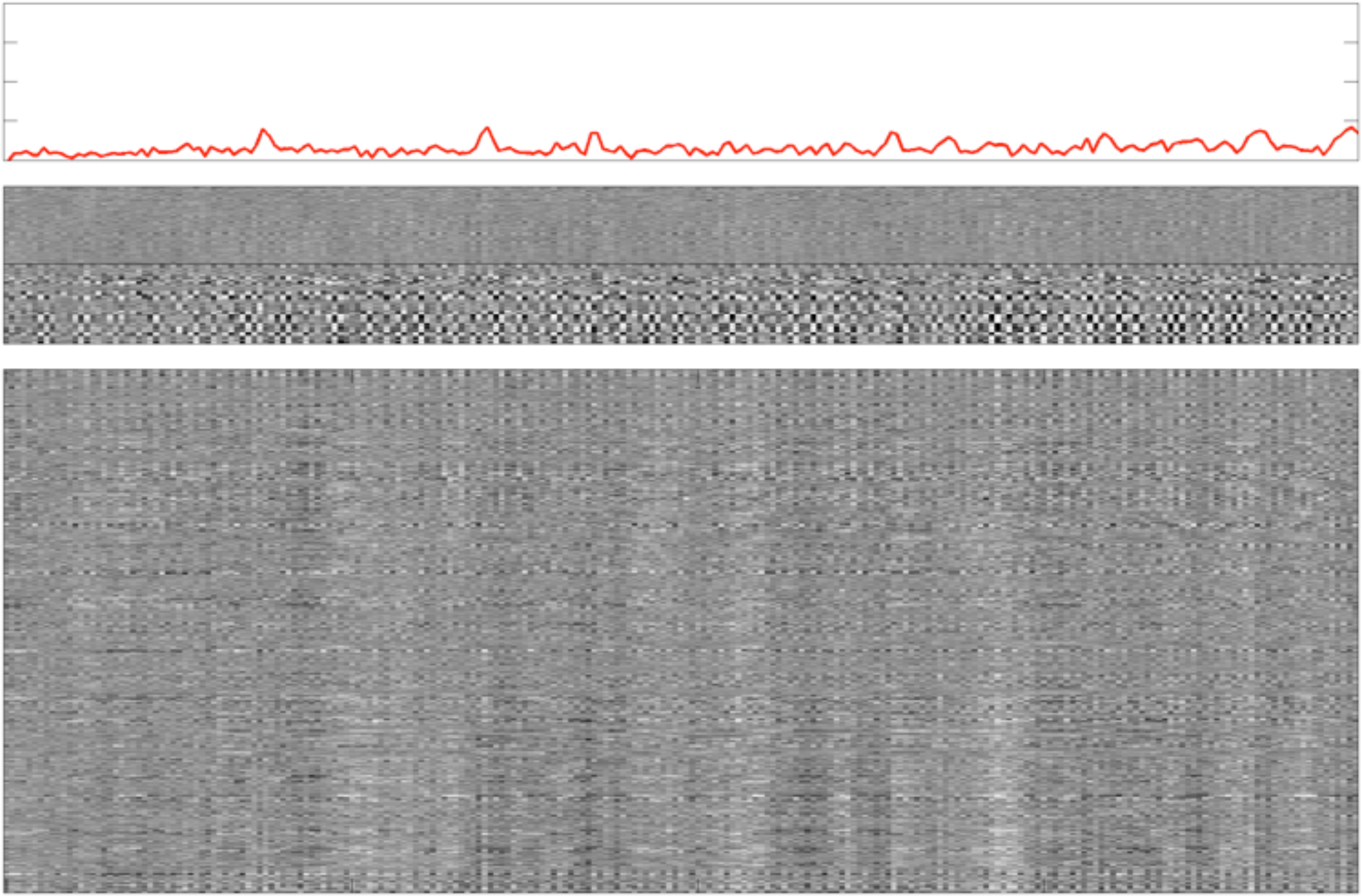


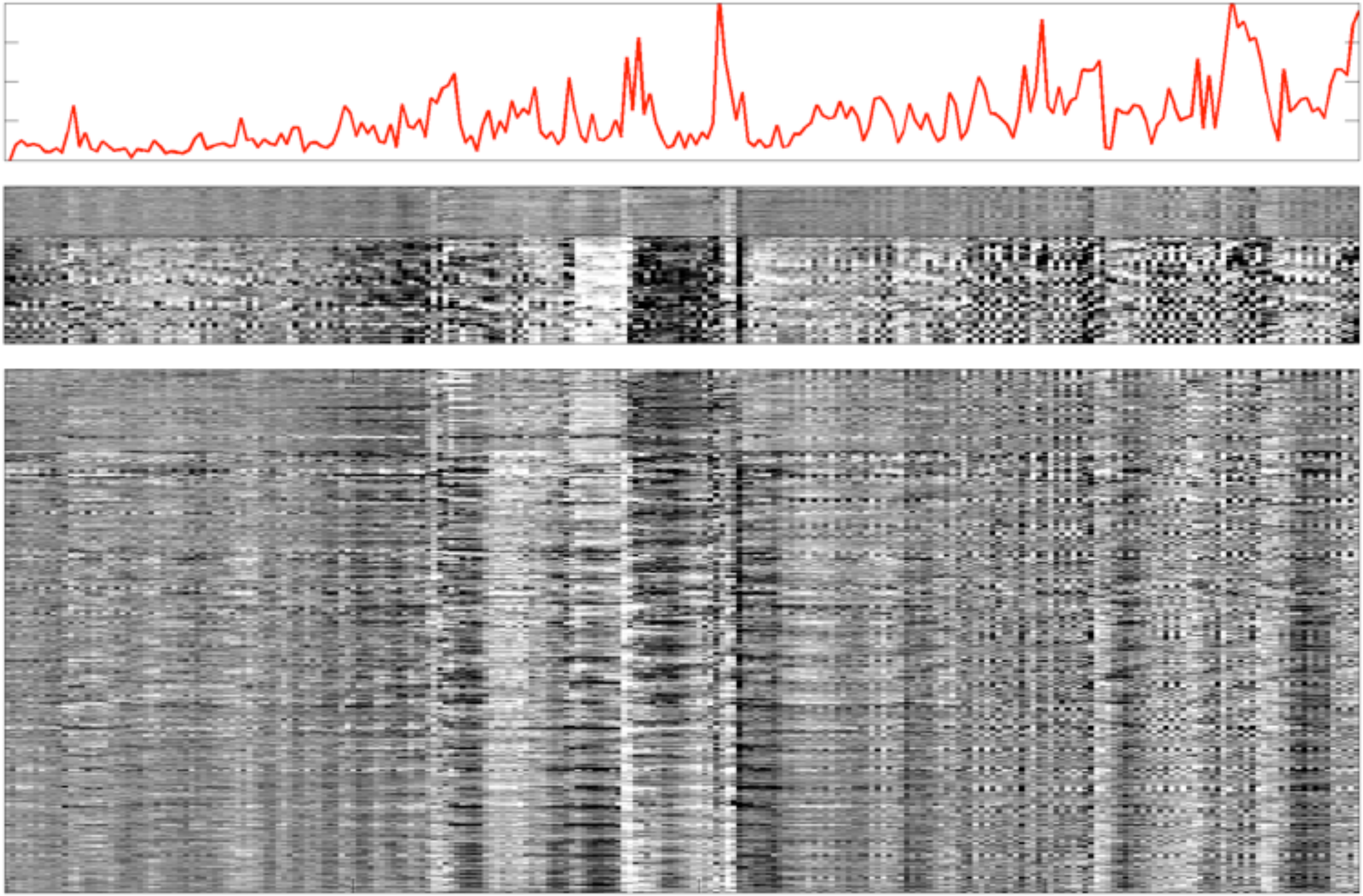












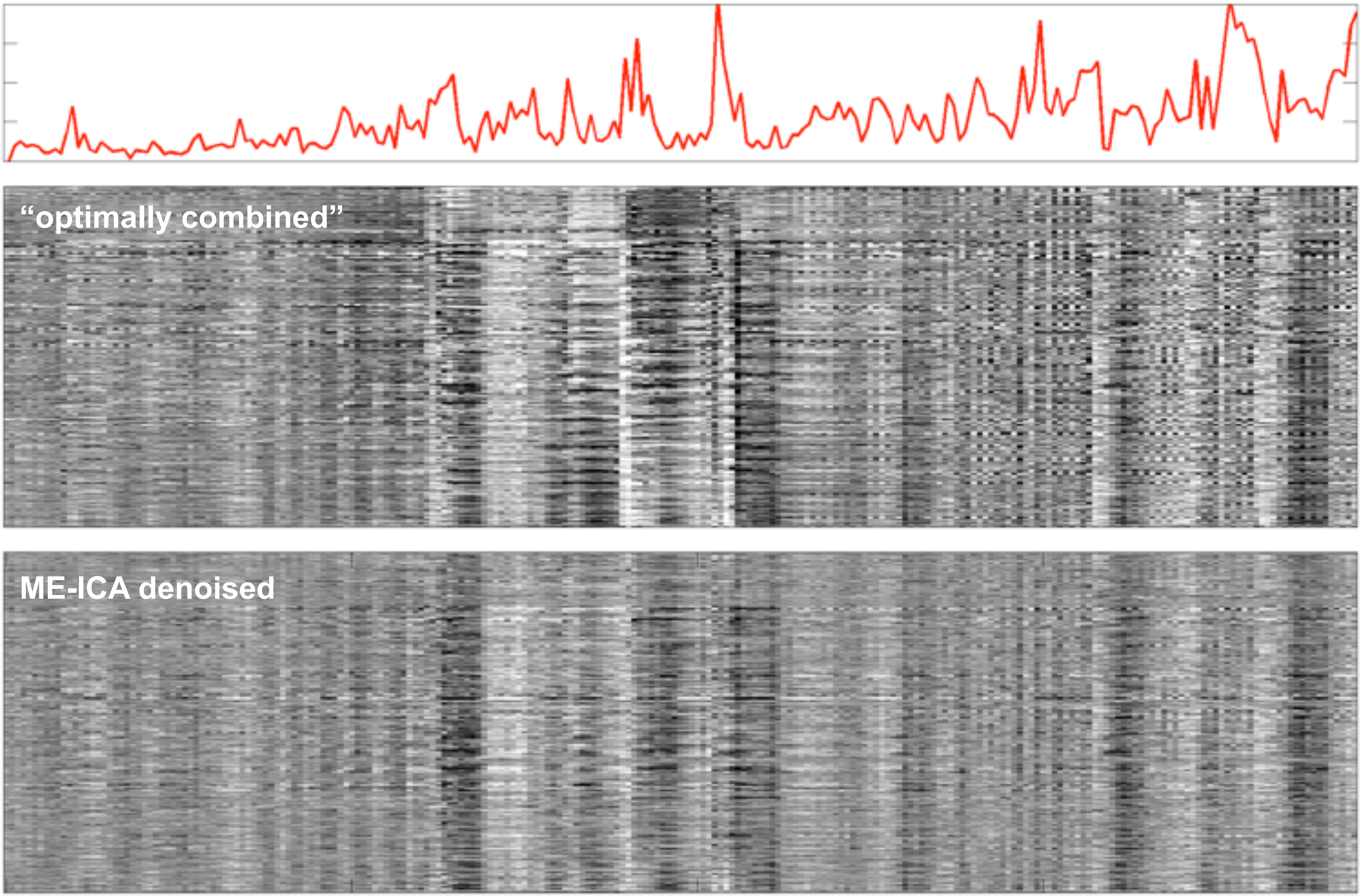
Artifact and motion

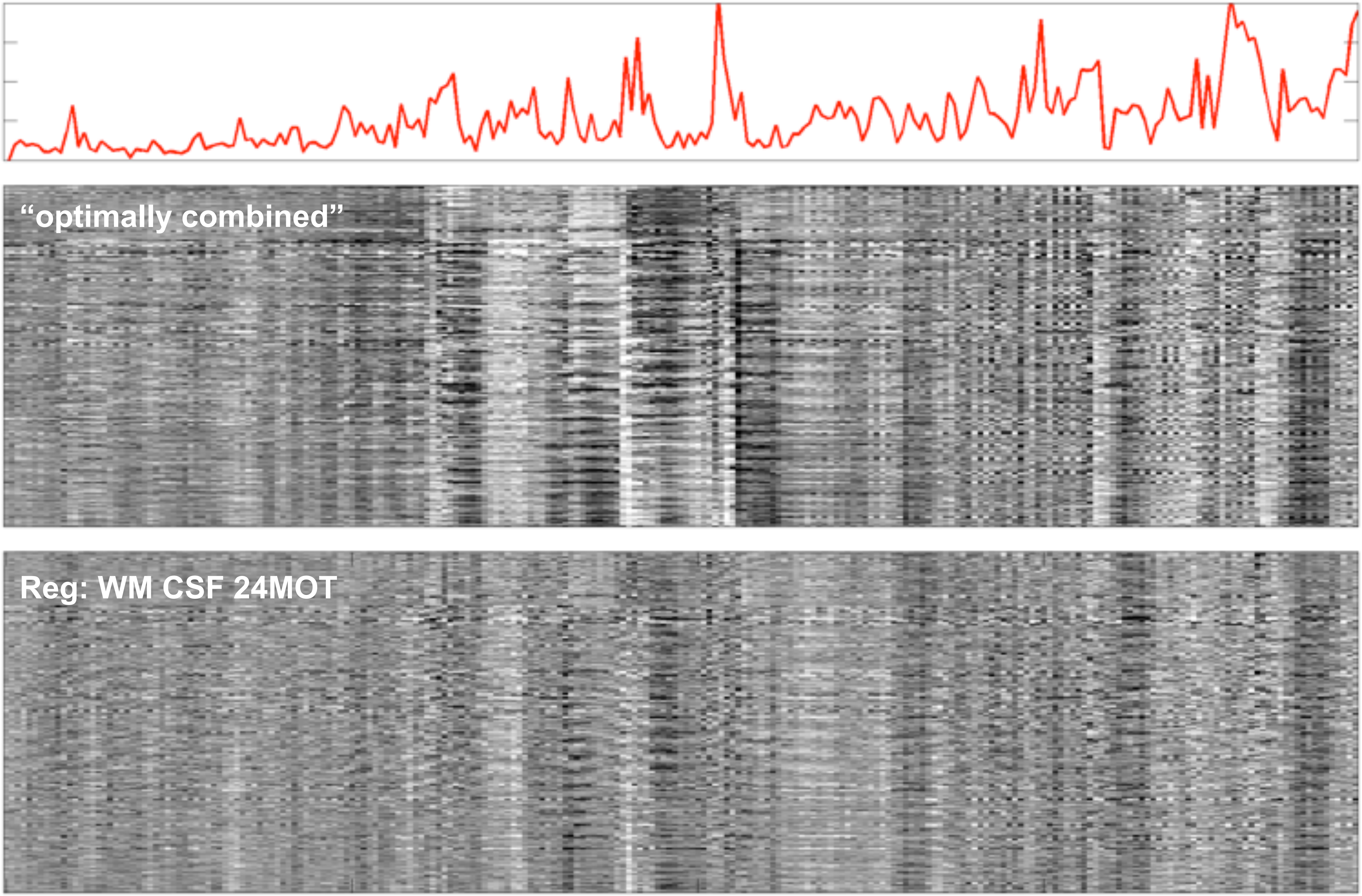
There is much artifact in these data
Much is motion-related
Much isn’t

Artifact can strongly influence correlations between signals
In the functional connectivity literature, implications for:
- development
- aging
- disease

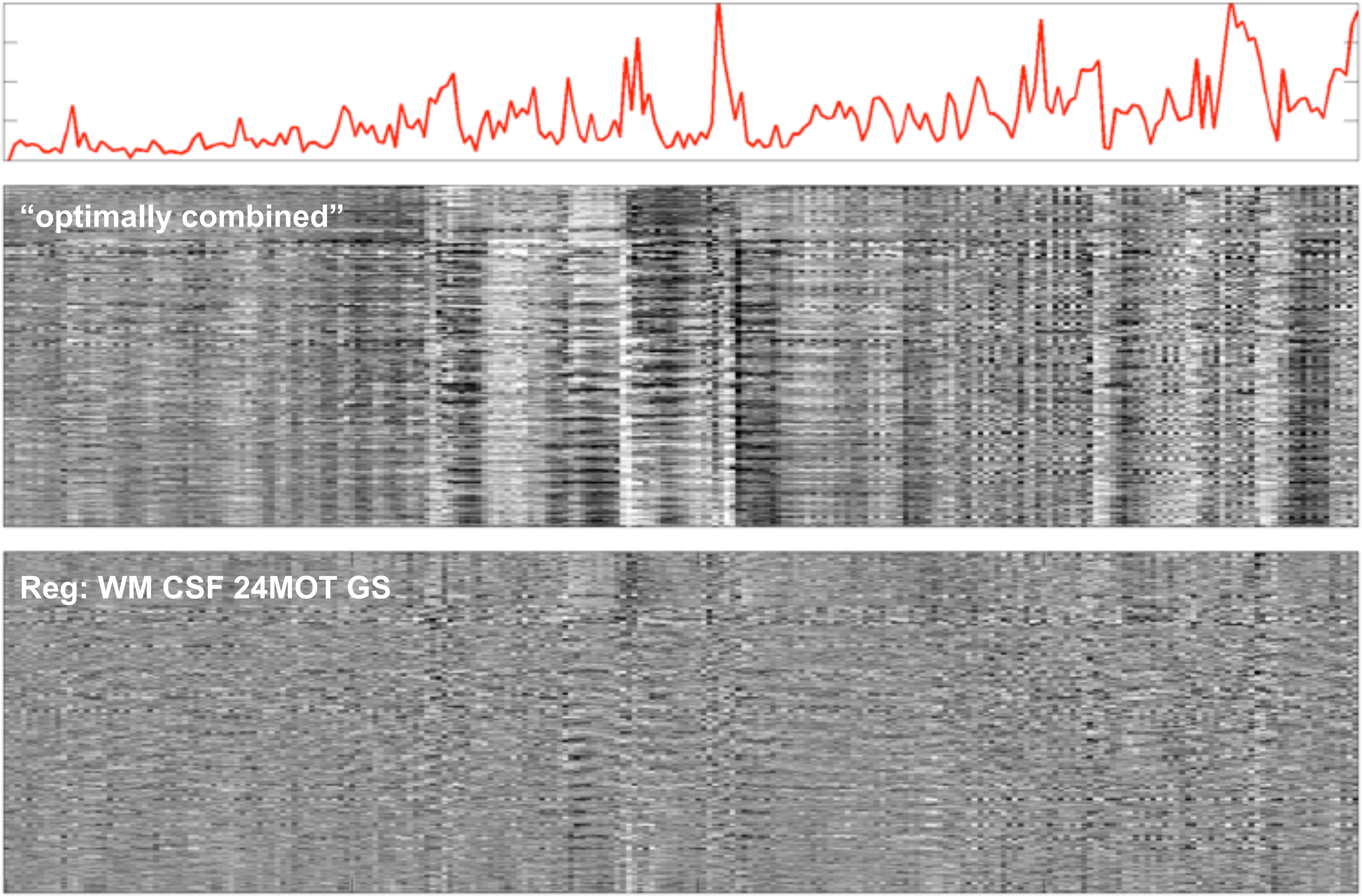
All areas where FC effects of motion were mistaken for biology

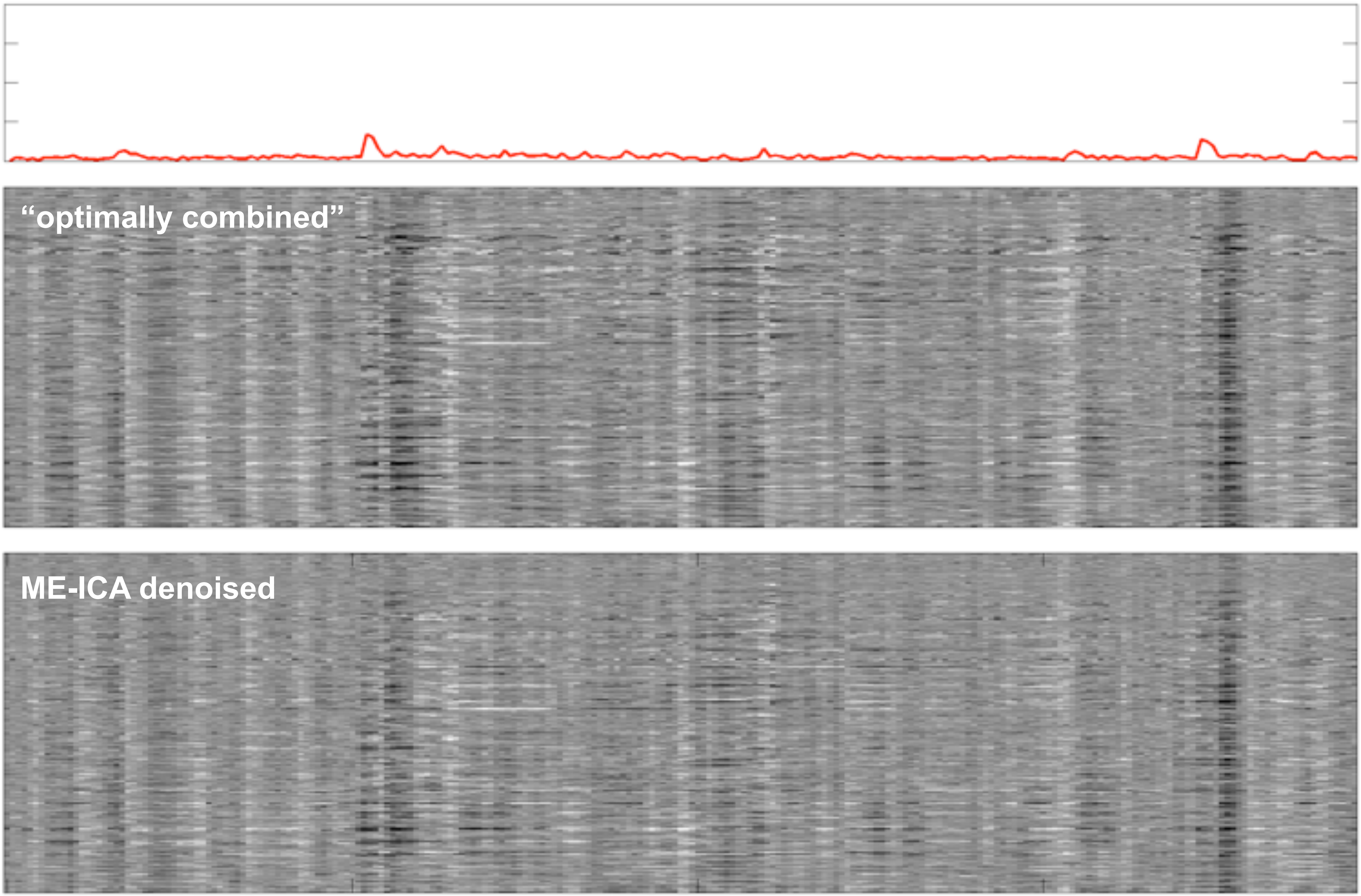
So to gauge confidence in findings, you need to know
1. How much artifact was there?
2. How much did I remove?


"optimally combined"
ME-ICA denoised

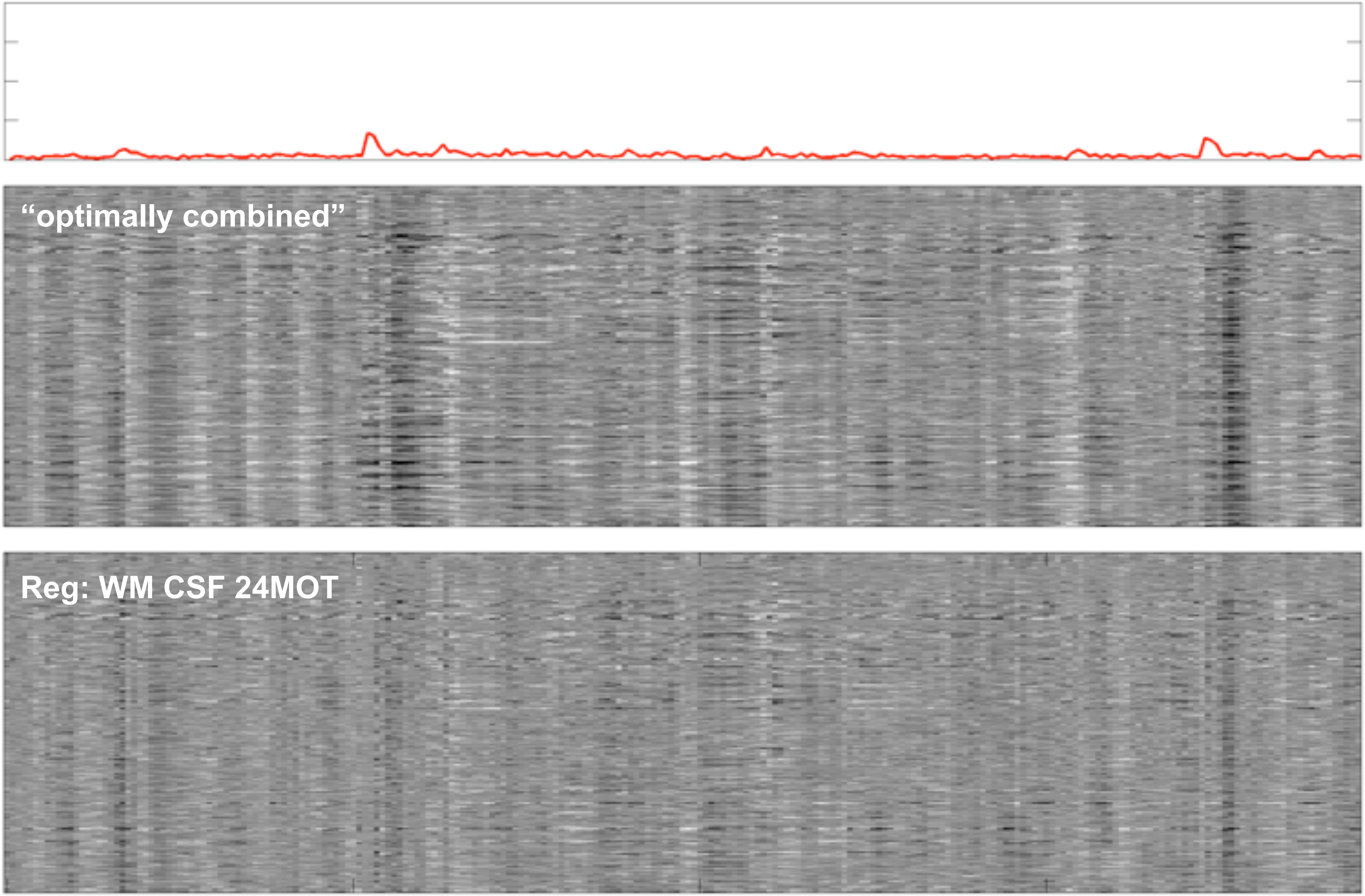


“optimally combined”
Reg: WM CSF 24MOT

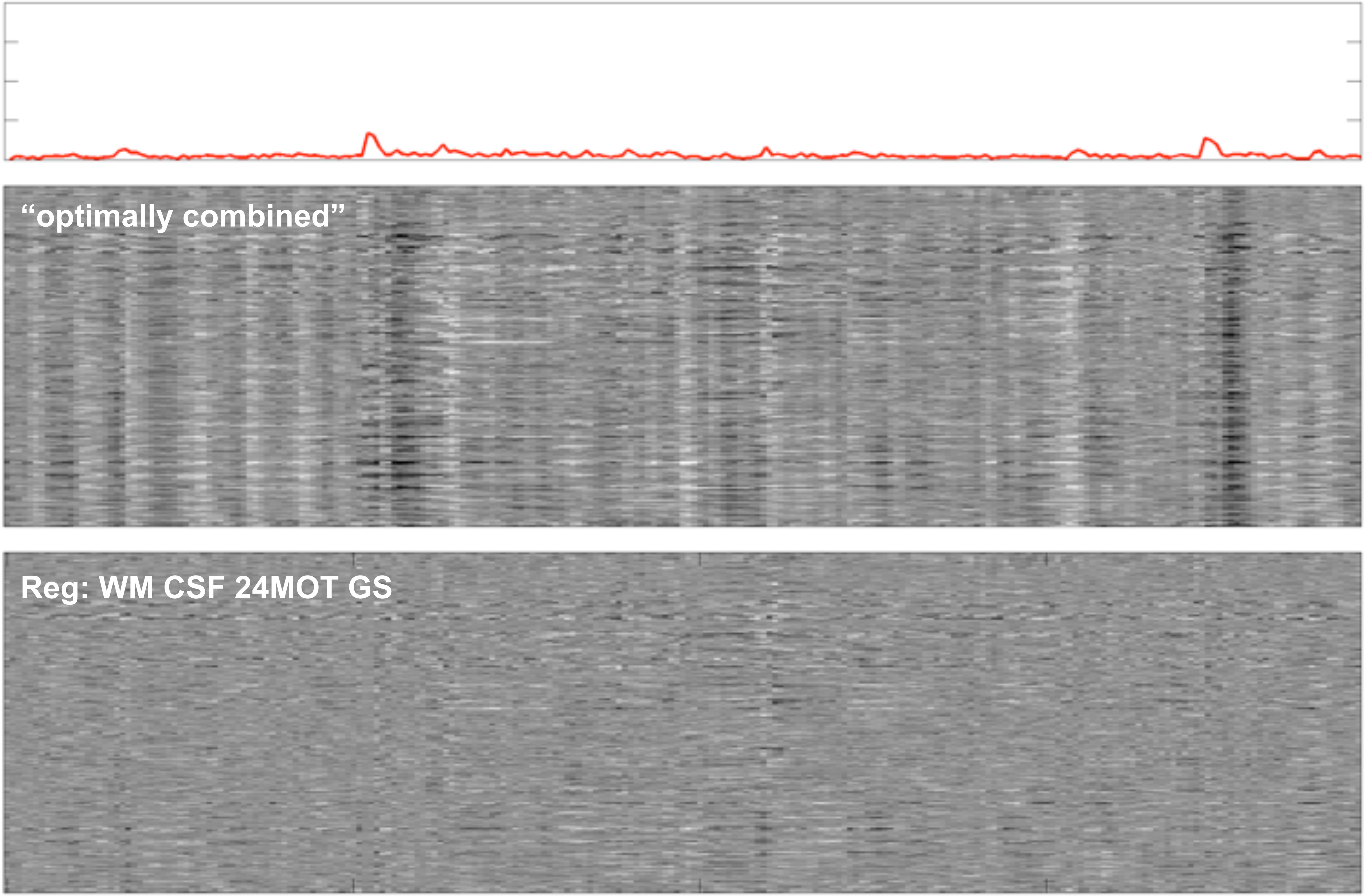

"optimally combined"
Reg: WM CSF 24MOT GS

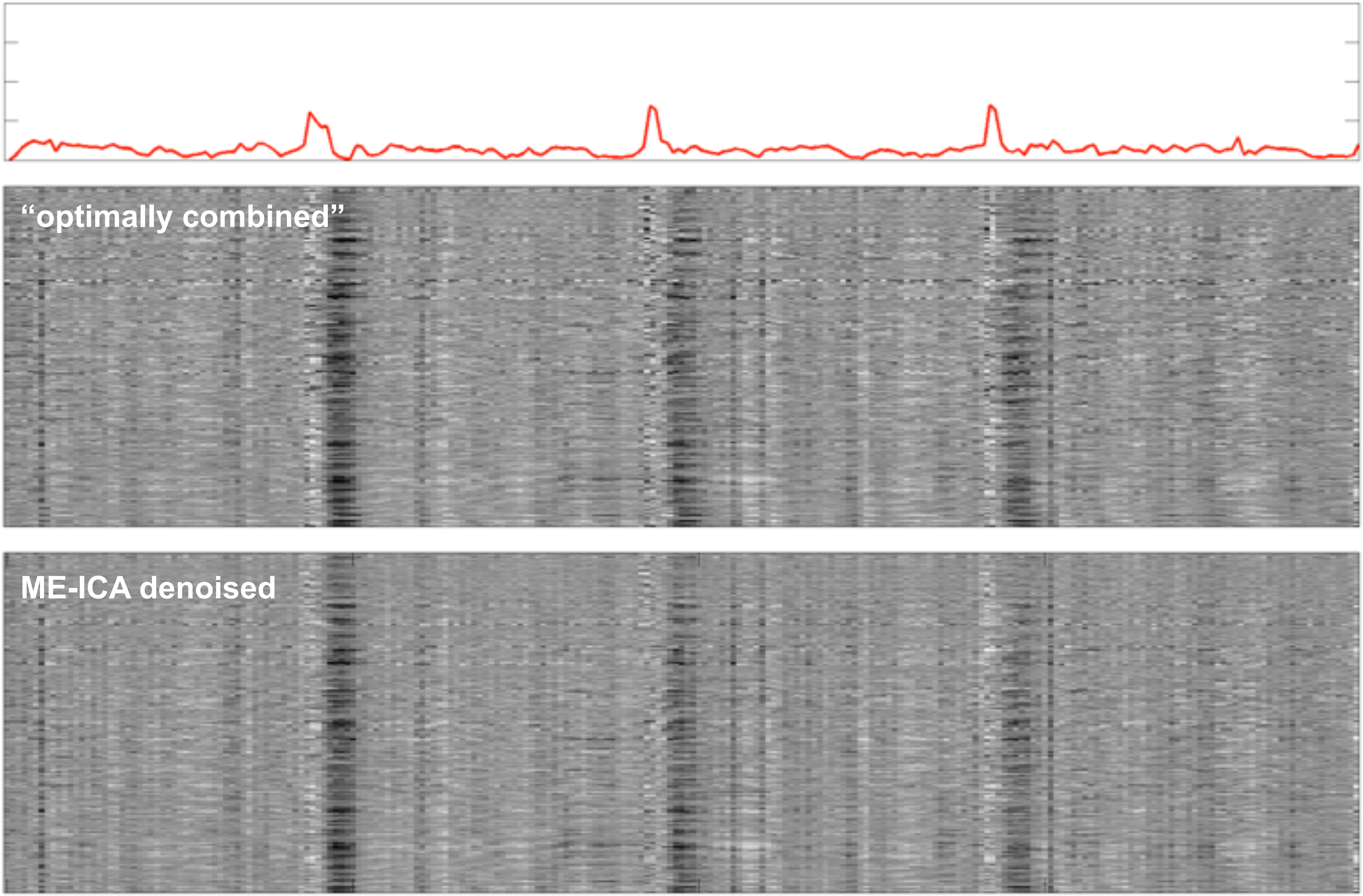


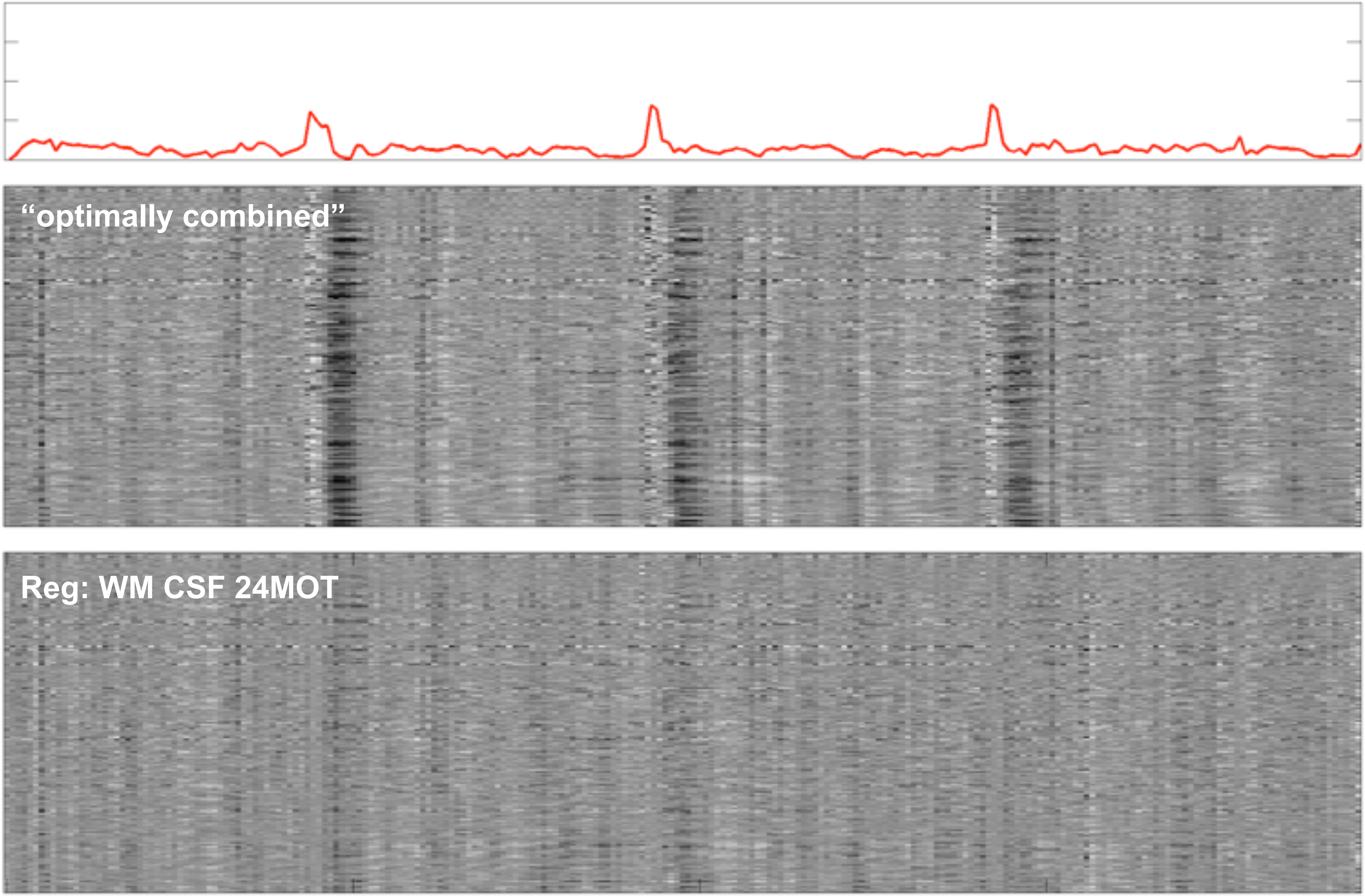
“optimally combined”
ME-ICA denoised

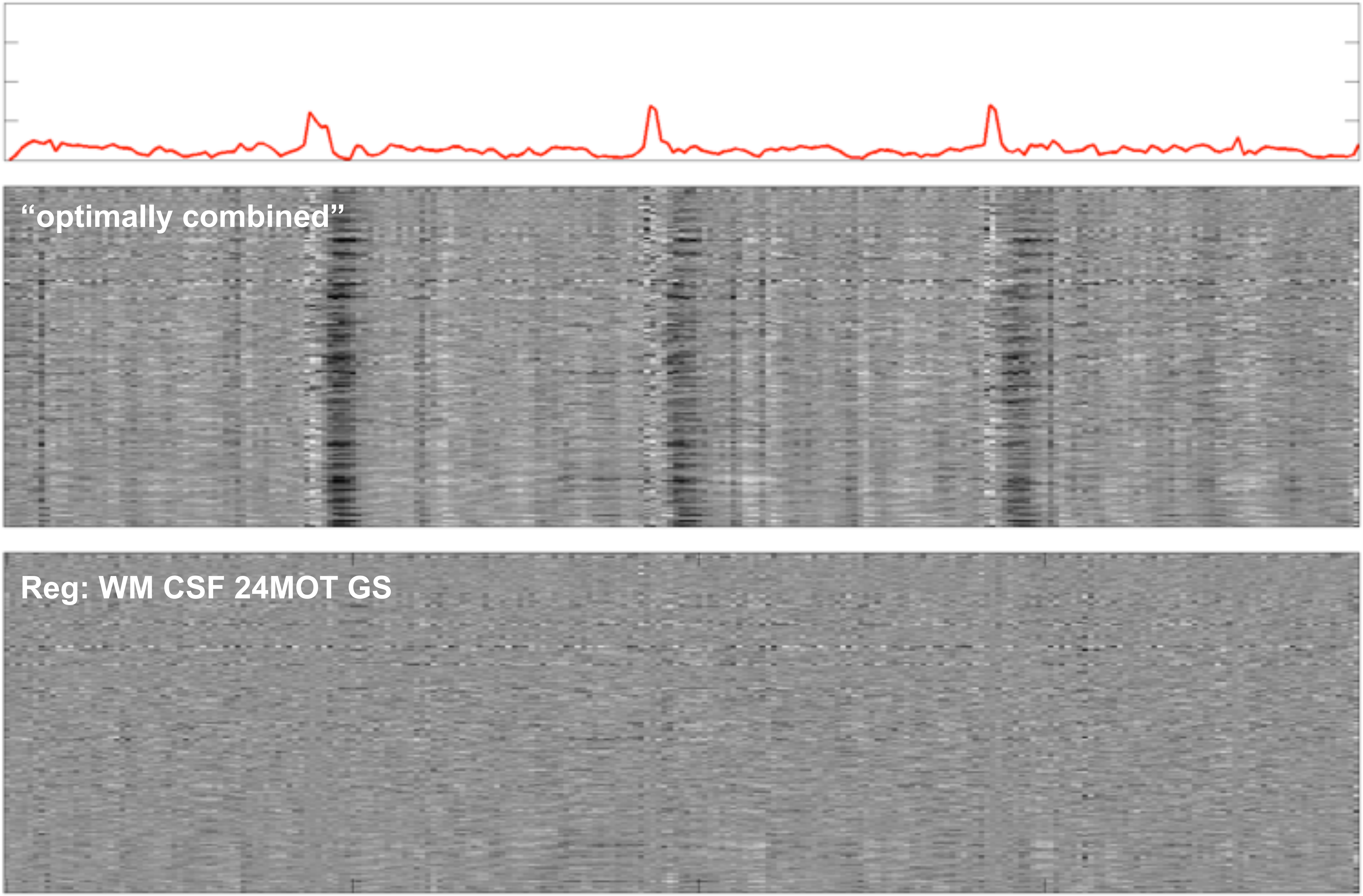


“optimally combined”
Reg: WM CSF 24MOT


"optimally combined"
Reg: WM CSF 24MOT GS


“optimally combined”
ME-ICA denoised


"optimally combined"
Reg: WM CSF 24MOT


"optimally combined"
Reg: WM CSF 24MOT GS

Take-homes:

Motion artifact is a universal problem

Motion estimation in fMRI often occurs via the data itself

Methods to “correct” motion do so in reasonable but limited ways

Data acquired during motion is often spatially distorted

Motion adds spurious and difficult-to-remove variance to the data

Motion-related variance causes spatially structured changes in signal correlations, which can easily be mistaken for an effect of interest in resting state fMRI

IMAGING METHODOLOGY - Review

Magnetic Resonance in Medicine 69:621–636 (2013)

Prospective Motion Correction in Brain Imaging: A Review

Julian Maclaren,[1,2*] Michael Herbst,[1] Oliver Speck,[3] and Maxim Zaitsev[1]

NeuroImage 105 (2015) 536–551

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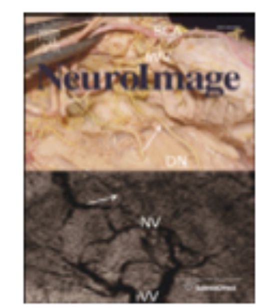
Contents lists available at ScienceDirect

NeuroImage

journal homepage: www.elsevier.com/locate/ynimg

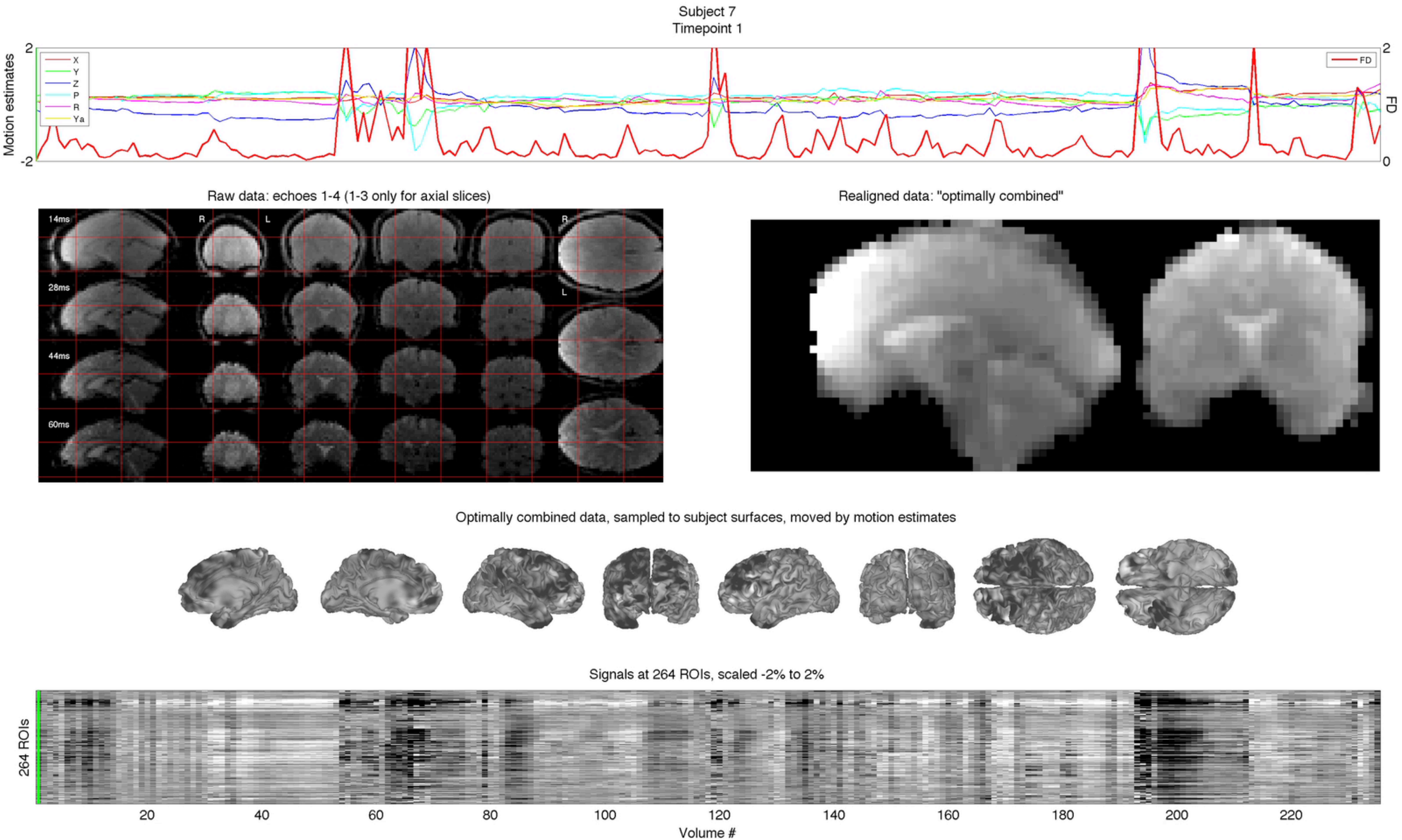


Review

Recent progress and outstanding issues in motion correction in resting state fMRI

CrossMark

Jonathan D. Power [a,*], Bradley L. Schlaggar [a,b,c,d], Steven E. Petersen [a,b,d,e,f,g]



Subject 7
Timepoint 1
Motion estimates
FD
X
Y
Z
P
R
Ya
2
-2
0
Raw data: echoes 1-4 (1-3 only for axial slices)
14ms
28ms
44ms
60ms
R
L
Realigned data: "optimally combined"
Optimally combined data, sampled to subject surfaces, moved by motion estimates
Signals at 264 ROIs, scaled -2% to 2%
264 ROIs
20
40
60
80
100
120
140
160
180
200
220
Volume #