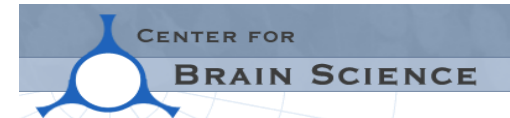


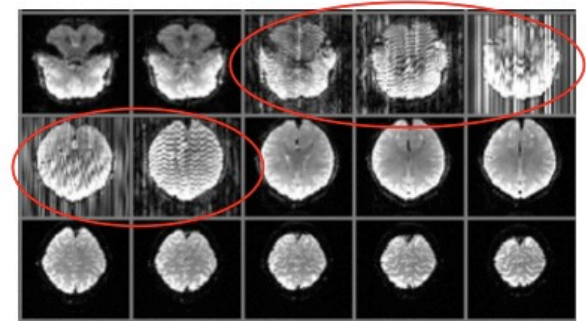
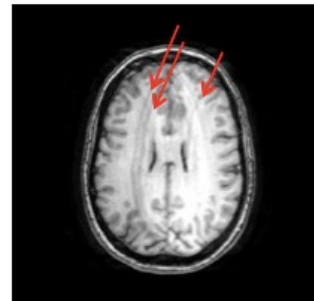
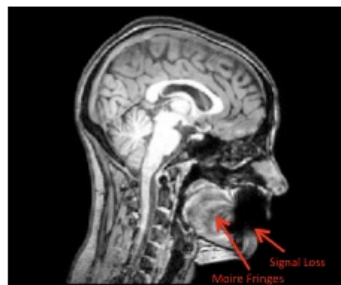
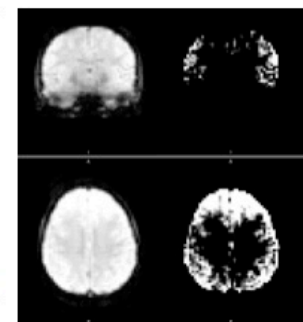
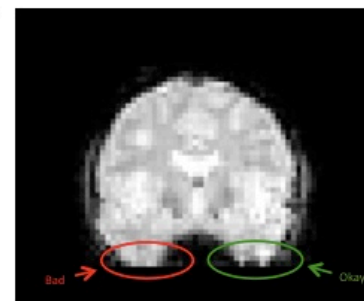
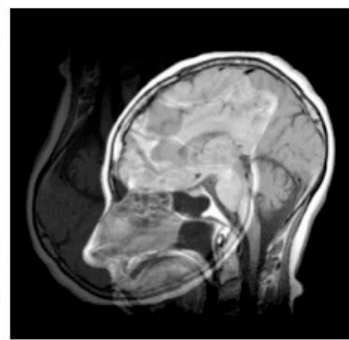
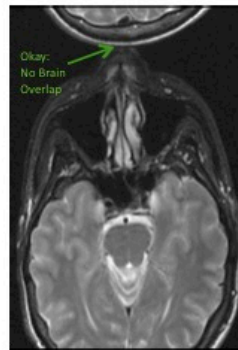


MRI Quality Control



Presented by
Natasha S. Hansen
February 20, 2013

The screenshot shows the EMBARC (EMRI-based MRI Analysis and Reporting Center) web interface. At the top, it displays the user 'nhansen' and navigation options like 'Home', 'New', and 'Upload'. The main content area is titled 'PROJECT: ENBARC' and shows a grid of image thumbnails. On the left, there is a sidebar with a 'Summary' section containing 'MR Session' details (Subject, Date Acquired: 2011-11-22), 'Parameters' (Num Volumes: 180, Num Voxels: 35545, Mask Threshold: 200.0, Slice: 0), and 'QC Overview' (Mean: 492.05, SDDev: 9.49, Slice SNR: 414.3, Voxel SNR: 66.8, Mean Rel Motion: 0.002, Max Rel Motion: 0.247, Mean Abs Motion: 0.249, Max Abs Motion: 0.44, Movements (> .2mm): 56, Movements (> .5mm): 0). Below this is an 'Assessment' section showing 'PASS' and a 'Files' list including SNR Image, Mean Image, SDDev Image, Mask Image, Mean Data, Motion Data, Slope Image, Auto-QC Report, Manual QC Report, and Slice Report. The main image area shows three columns of thumbnails with labels: 'Signal-to-Noise Ratio (SNR) 66.8', 'Mean 492.05', and 'Standard Deviation (SDDev) 9.49'. Below these are 'Slope' and 'Mask' sections, each with a grid of thumbnails and a value of 0.011.



Workshop Road Map

Where we're headed....

- Why is Quality Control (QC) Important?
- Two Kinds of QC
- Quantitative QC
 - Quantitative QC in action: EMBARC Central XNAT
- Qualitative QC
 - MRI artifacts
 - Qualitative QC in action: EMBARC scans in FSL
- Acknowledgements
- Questions & Discussion



Why is Quality Control Important?

1. Quality data are essential for good science
2. Flawed data are surprisingly common
3. Even serious flaws in data can sometimes be very difficult to detect without carefully looking for them

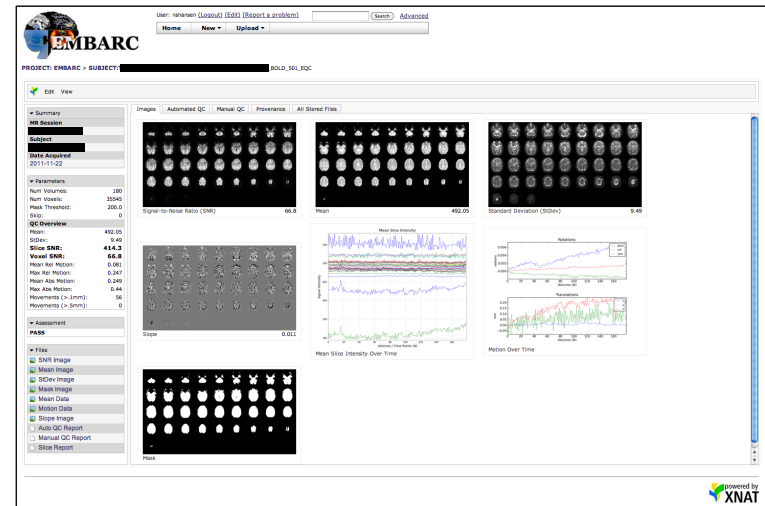


Two Kinds of QC

1. Quantitative:

By the numbers....

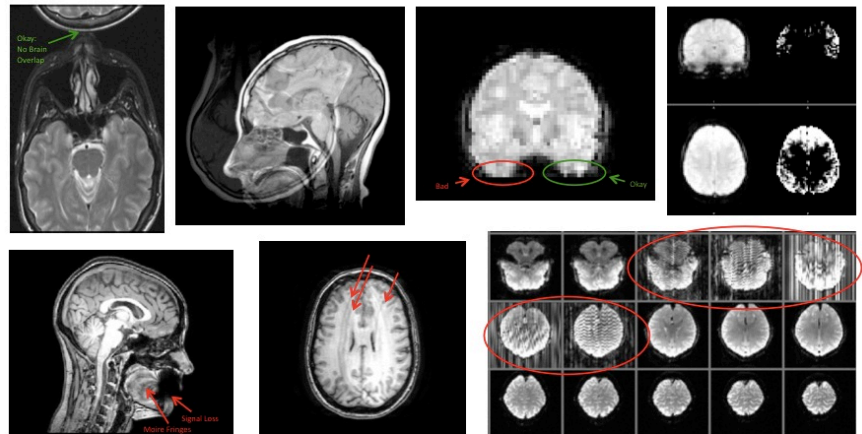
Evaluating automated system-calculated numerical values



2. Qualitative:

By the trained eye....

Manually scrolling through each slice of RAW data to look for artifacts



What is XNAT?

XNAT can calculate values used for Quantitative QC

- 3rd party neuroimaging database developed and maintained by Washington University in St. Louis
- Designed to help researchers capture, organize, and process neuroimaging data
- First developed by Dan Marcus under Randy Buckner at WUSTL (Marcus 2006)*
- Has large user community
- Visit: <http://xnat.org/>

The screenshot shows the XNAT website homepage. The header includes the XNAT logo and the tagline "the most widely-used informatics platform for imaging research". The navigation menu contains links for "About XNAT", "Download", "Documentation", "Support", "XNAT Marketplace", and "Contact Us". The main content area features a central diagram with "Imaging Data" and "Clinical Data" components. To the right, the "XNAT News" section lists several updates, including "XNAT 1.6 Is Here!", "XNAT Marketplace Launches", "XNAT 1.6 Beta RC1 Released", and "XNAT Documentation Updates". At the bottom, the "What does XNAT provide?" section lists six key features with corresponding icons: "Full DICOM Integration and Anonymization", "Secure Access & Permission Control", "Integrated Search & Reporting", "Pipeline Processing", "Modular Extensibility", and "Developer Community".

*Marcus, D. S., Olsen, T., Ramaratnam, M., & Buckner, R. L. (2006). XNAT: a software framework for managing neuroimaging laboratory data. In *Proceedings of the 12th Annual Meeting of the Organization for Human Brain Mapping Held in Florence* (pp. 11-15).



Quantitative QC

QC by the numbers.....

Examples of Quantitative QC values calculated in XNAT:

- Mean Signal Intensity
- Signal Intensity Standard Deviation
- Voxel-Based Signal to Noise Ratio (vSNR)
- Slice-based Signal to Noise Ratio (sSNR)
- Subject Motion:
 - Relative Motion & Absolute Motion
 - Mean Motion & Maximum Motion
 - # Movements $>.1\text{mm}$ & # Movements $>.5\text{mm}$



Quantitative QC in XNAT

User: nshansen (Logout) (Edit) (Report a problem) Search Advanced

Home New Upload

PROJECT: EMBARC > SUBJECT: [REDACTED] BOLD_501_EQC

Edit View

Images Automated QC Manual QC Provenance All Stored Files

Summary

MR Session

Subject

Date Acquired
2011-11-22

Parameters

Num Volumes:	180
Num Voxels:	35545
Mask Threshold:	200.0
Skip:	0

QC Overview

Mean:	492.05
StDev:	9.49
Slice SNR:	414.3
Voxel SNR:	66.8
Mean Rel Motion:	0.081
Max Rel Motion:	0.247
Mean Abs Motion:	0.249
Max Abs Motion:	0.44
Movements (>.1mm):	56
Movements (>.5mm):	0

Assessment

PASS

Files

- SNR Image
- Mean Image
- StDev Image
- Mask Image
- Mean Data
- Motion Data
- Slope Image
- Auto QC Report
- Manual QC Report
- Slice Report

Signal-to-Noise Ratio (SNR) 66.8

Mean 492.05

Standard Deviation (StDev) 9.49

Slope 0.011

Mask

Mean Slice Intensity Over Time

Motion Over Time

Rotations

Translations

powered by XNAT



Quantitative QC in XNAT

For EMBARC* Quantitative QC, we focus on:

1. Slice-Based SNR
2. Maximum Absolute Motion
3. Movements $\geq 0.5\text{mm}$

Parameter Evaluations:

Slice-Based SNR: Good = ≥ 150 , Bad = < 99

Maximum Absolute Motion: Good = < 1.49 , Bad = $> 2\text{mm}$

Movements $\geq .5\text{mm}$: Good < 5 , Bad = ≥ 5

NOTE: Remember these parameters are examples only. Consider your scanner (e.g. Siemens vs. Phillips) and head coil (e.g. 12 vs. 32 channel) to determine the right Quantitative QC parameters for your study.

Parameters	
Num Volumes:	397
Num Voxels:	36772
Mask Threshold:	200.0
Skip:	0
QC Overview	
Mean:	548.13
StDev:	11.36
Slice SNR:	341.8
Voxel SNR:	67.3
Mean Rel Motion:	0.049
Max Rel Motion:	0.154
Mean Abs Motion:	0.411
Max Abs Motion:	0.79
Movements ($> .1\text{mm}$):	19
Movements ($> .5\text{mm}$):	0

* Establishing Moderators/Biosignatures of Antidepressant Response in Clinical Care (EMBARC) is a multi-site NIMH-funded study used in the creation of these QC standards



Why these Parameters?

The Quantitative QC parameters used for EMBARC are based on research done at Massachusetts General Hospital and Harvard Medical School

Learn more about:

- How subject motion affects MRI data
- How motion values are calculated
- The relationship between Quantitative QC measures (e.g. mean vs. max motion values)
- How temporal SNR is calculated

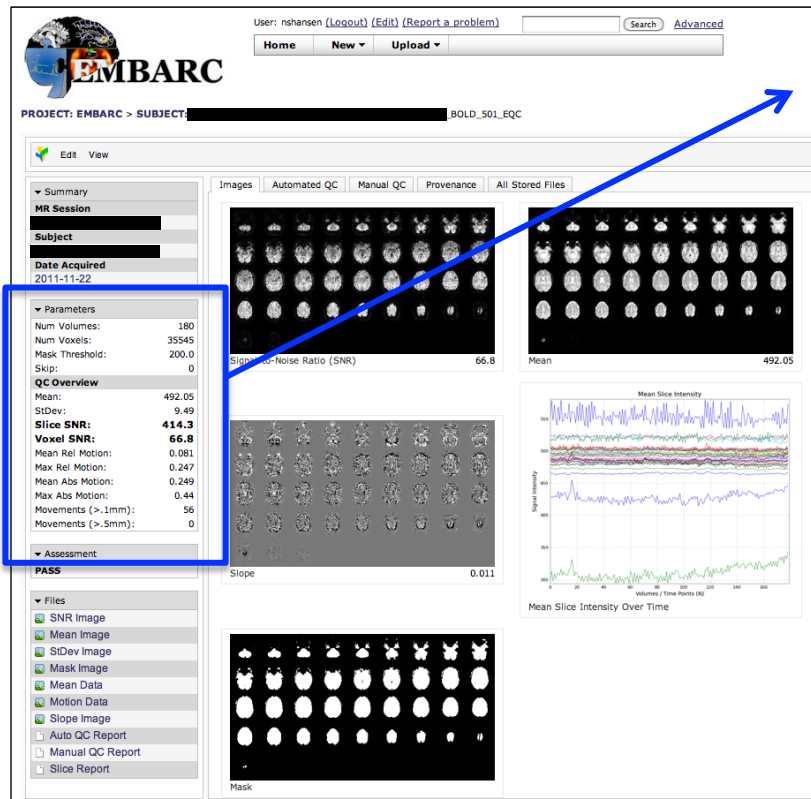
Van Dijk KRA, Sabuncu MR, and Buckner RL. (2012) The Influence of Head Motion on Intrinsic Functional Connectivity MRI. *NeuroImage*. 59(1):431-8.



Quantitative QC in Action

For EMBARC Quantitative QC, we focus on:

1. Slice-Based SNR: Good = >150 Bad = <99
2. Maximum Absolute Motion: Good = <1.49 Bad = $>2\text{mm}$
3. Movements $>.5\text{mm}$: Good <5 Bad = >5



Parameters	
Num Volumes:	180
Num Voxels:	35545
Mask Threshold:	200.0
Skip:	0
QC Overview	
Mean:	492.05
StDev:	9.49
Slice SNR:	414.3
Voxel SNR:	66.8
Mean Rel Motion:	0.081
Max Rel Motion:	0.247
Mean Abs Motion:	0.249
Max Abs Motion:	0.44
Movements ($>.1\text{mm}$):	56
Movements ($>.5\text{mm}$):	0

414.3 > 150 = Good

.44 < 1.49 = Good

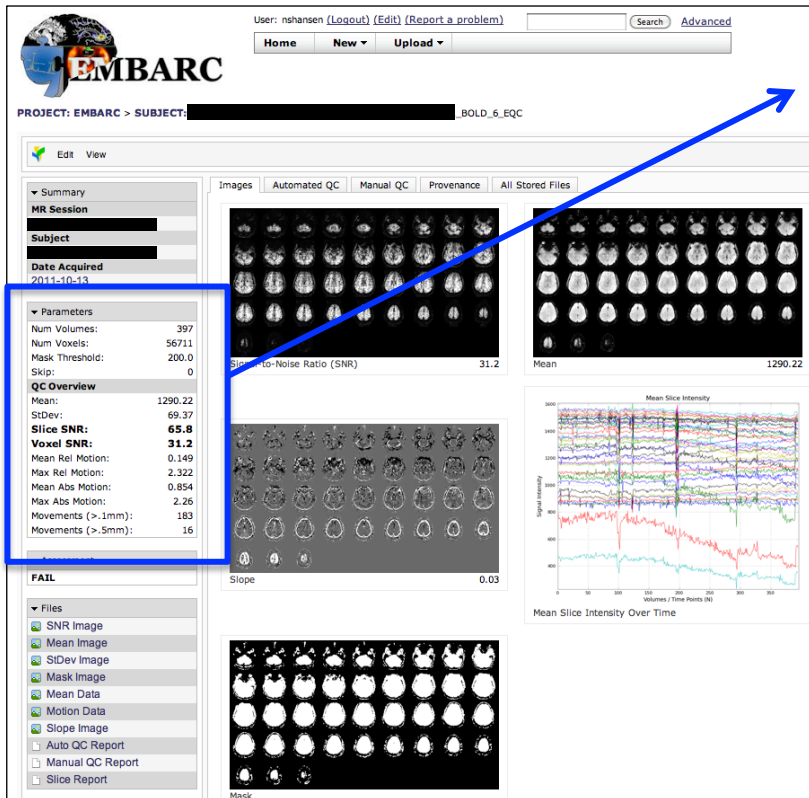
0 < 5 = Good



Quantitative QC in Action

For EMBARC Quantitative QC, we focus on:

1. Slice-Based SNR: Good = >150 , Bad = <99
2. Maximum Absolute Motion: Good = <1.49 , Bad = >2 mm
3. Movements $>.5$ mm: Good <5 , Bad = >5



Parameters	
Num Volumes:	397
Num Voxels:	56711
Mask Threshold:	200.0
Skip:	0
QC Overview	
Mean:	1290.22
StDev:	69.37
Slice SNR:	65.8
Voxel SNR:	31.2
Mean Rel Motion:	0.149
Max Rel Motion:	2.322
Mean Abs Motion:	0.854
Max Abs Motion:	2.26
Movements ($>.1$ mm):	183
Movements ($>.5$ mm):	16

65.8 < 150 = Bad

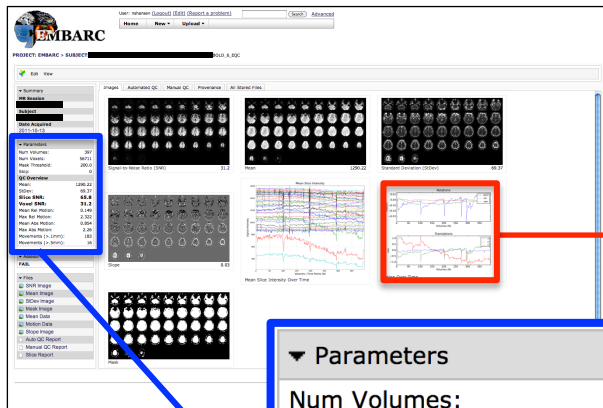
2.26 > 2 = Bad

16 > 5 = Bad

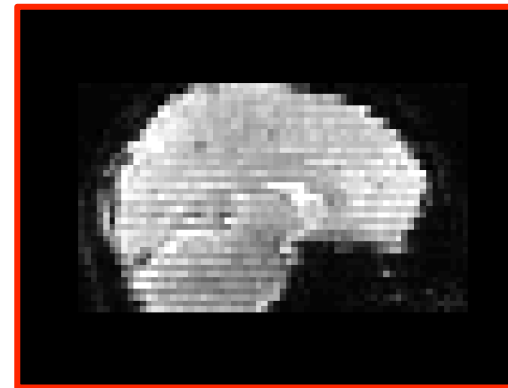
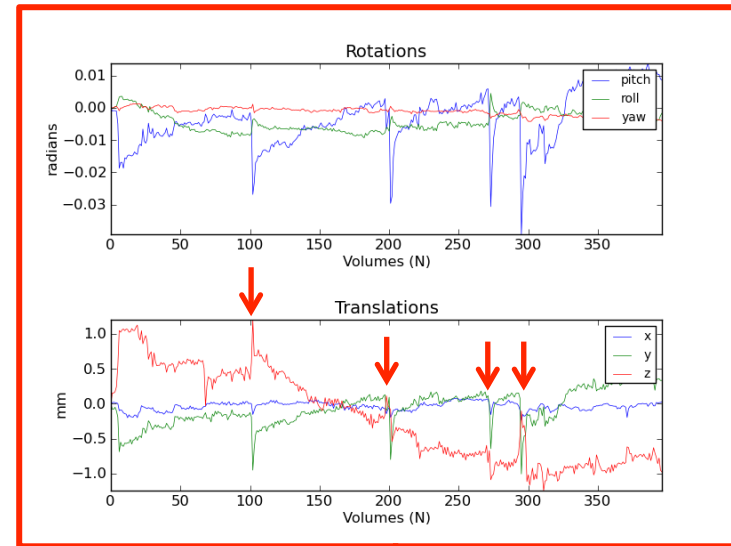


Quantitative QC meets Qualitative QC

A scan's numerical values are often reflected in its visible artifacts...

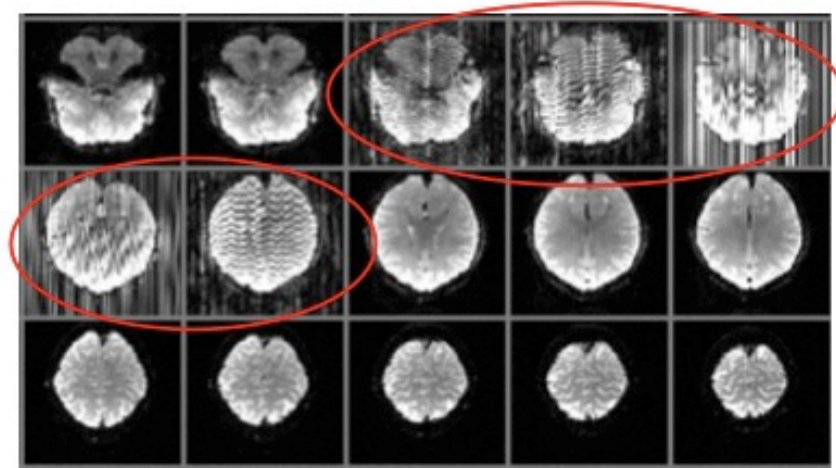
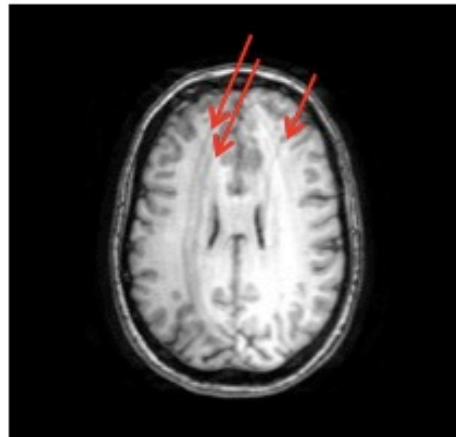
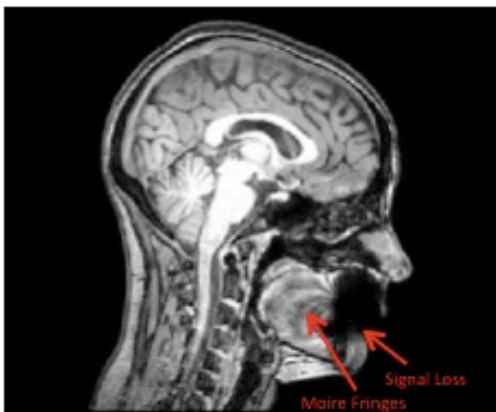
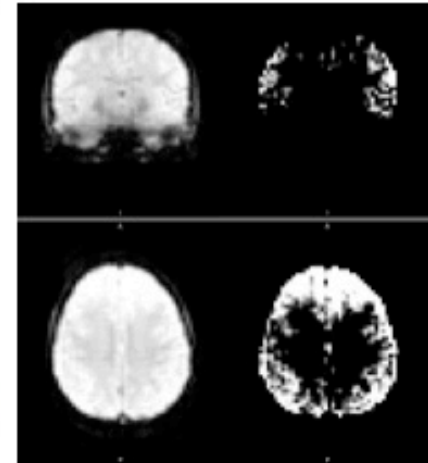
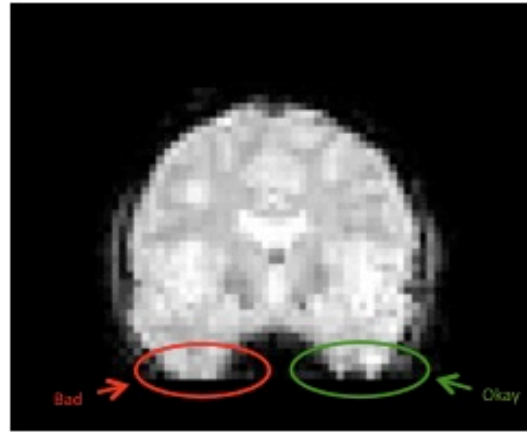
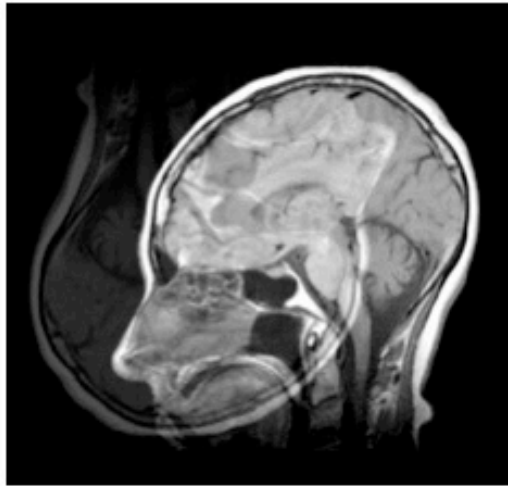
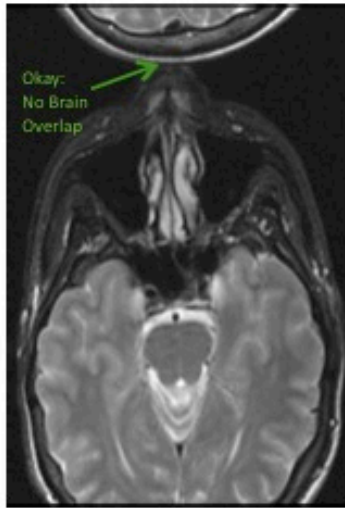


Parameters	
Num Volumes:	397
Num Voxels:	56711
Mask Threshold:	200.0
Skip:	0
QC Overview	
Mean:	1290.22
StDev:	69.37
Slice SNR:	65.8
Voxel SNR:	31.2
Mean Rel Motion:	0.149
Max Rel Motion:	2.322
Mean Abs Motion:	0.854
Max Abs Motion:	2.26
Movements (>.1mm):	183
Movements (>.5mm):	16



Qualitative Quality Control

Artifacts in Structural and Functional MRI



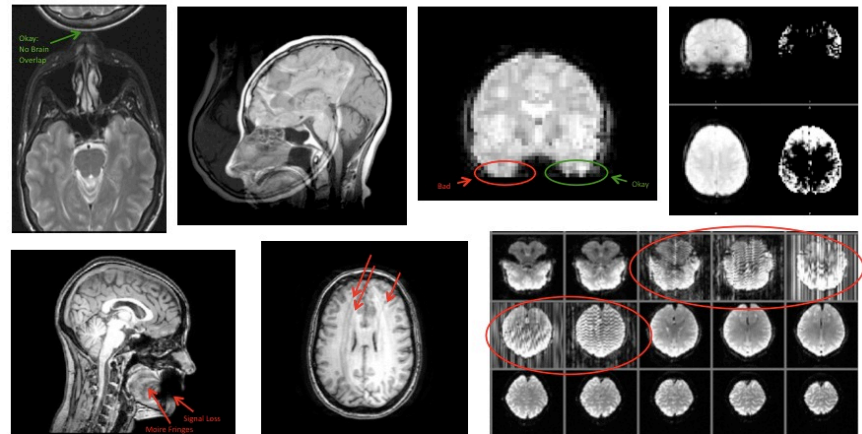
Qualitative QC

QC by the trained eye....

Some factors that can compromise data quality are so far only detectable by manually scrolling through each slice of RAW data to look for visible distortions called “**artifacts**”.

Examples of MRI artifacts:

- Field of View (FOV) clipping anatomy
- Wrapping
- Signal Loss/Susceptibility Artifact
- Ringing, Striping, or Blurring (in ANAT)
- Ghosting
- Radio Frequency Noise/Spiking
- Signal Inhomogeneity
- Motion Slice Artifact (in BOLD)



What causes MRI artifacts?

Experimenter Error:

- Field of View (FOV) positioned wrong -> brain image clipped -> “Wrapping”
- Neglected to remove all ferromagnetic metal -> signal loss -> “Susceptibility Artifact”

Subject Motion:

- Ringing, Striping, or Blurring (in structural scans)
- “Motion Slice Artifact” (in functional scans)

Problems with the Scanner/Head Coil:

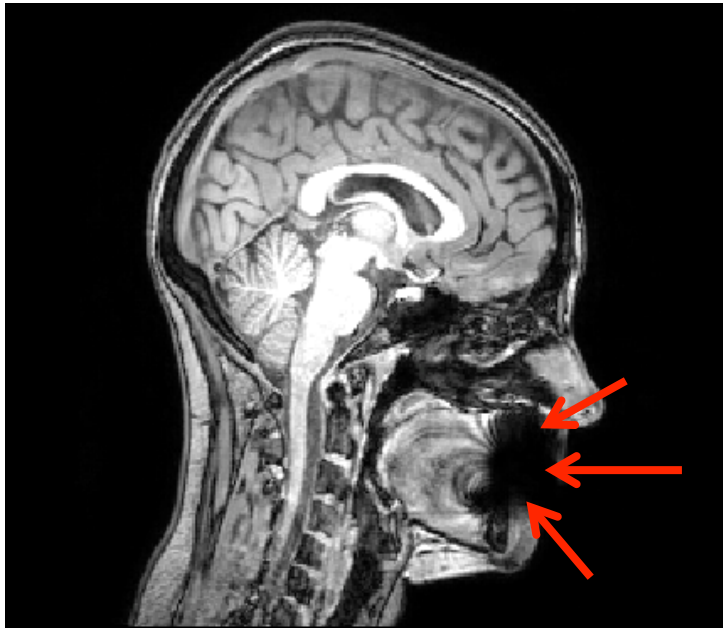
- Radio Frequency Noise/Spiking
- Signal Inhomogeneity

Artifacts from Image Reconstruction:

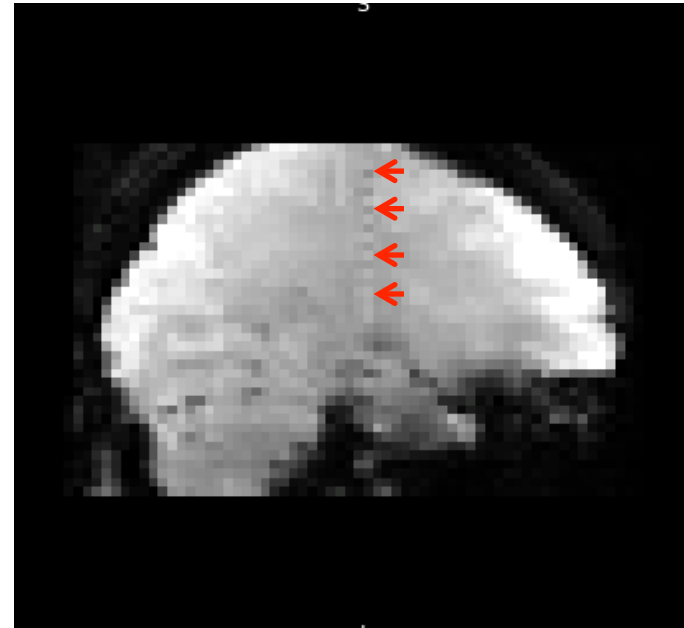
- Consistent low-level “Ghosting”
- Some types of “Ringing” (e.g. “Shadowed Arc Artifact” in structural scans)



How do you detect artifacts?

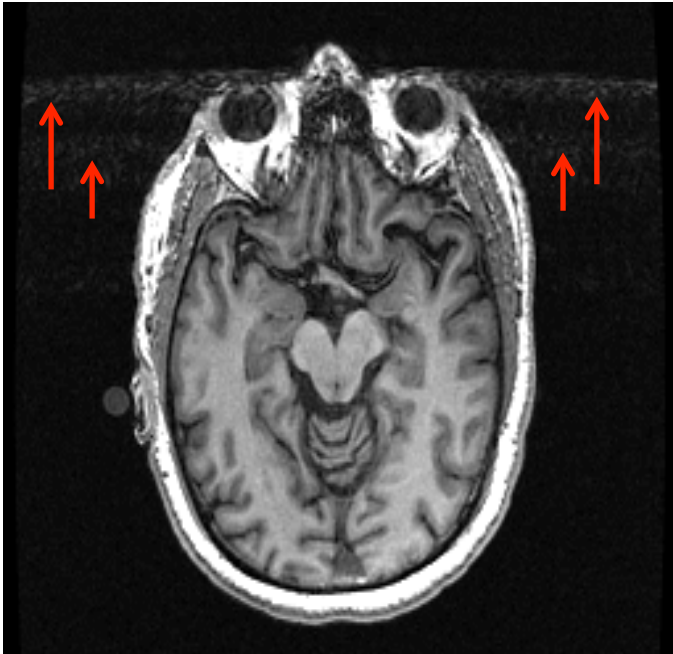


Some artifacts are hard to miss

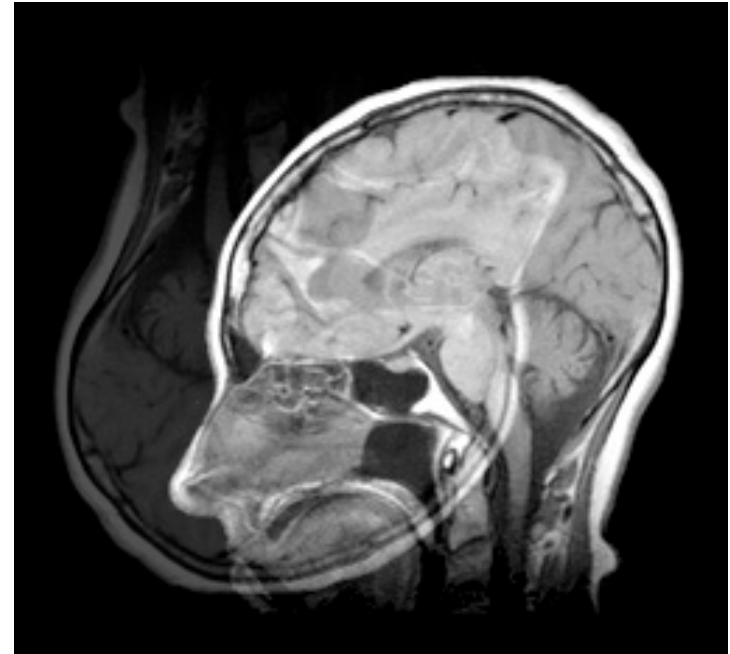


Others are incredibly subtle

When are artifacts a problem?



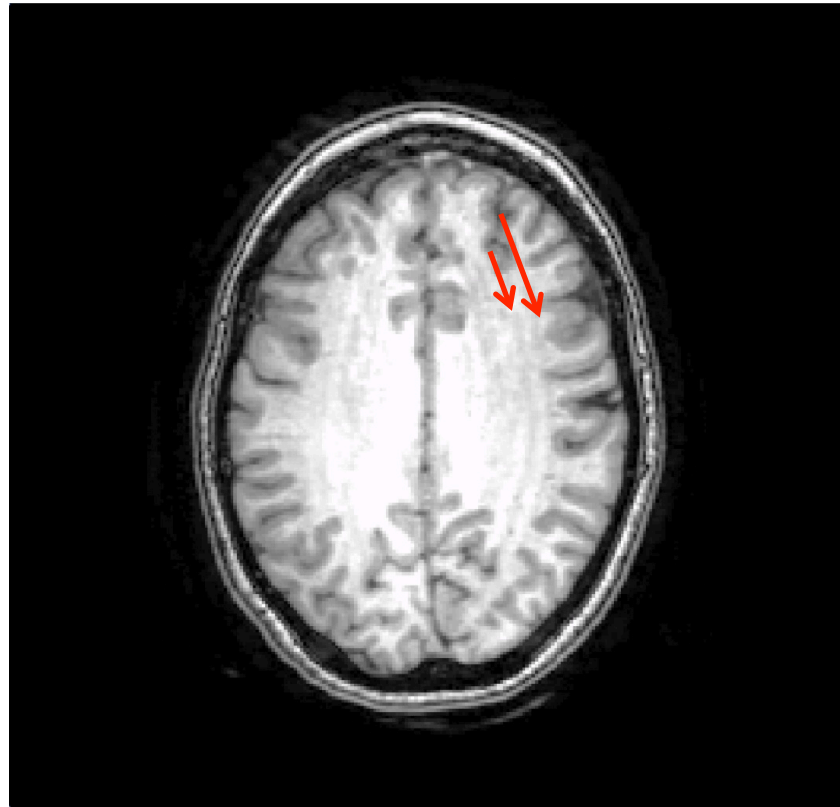
Some artifacts don't affect data quality



Others render it unusable

Training the Eye...

The intention is to familiarize you with the various types of artifacts and their levels of severity so you will be able to recognize them in your own data and make an informed decision for yourself about whether or not they affect your data quality.



MRI Qualitative Quality Control Manual

What to look for and How to look for it!

ANAT : Susceptibility Artifact



None: Susceptibility Artifact not present

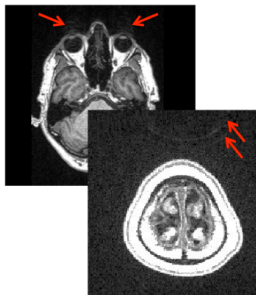
What to look for: A black area, like a hole of bright and dark ripples (called 'Moire' effect)

How to look for it: Scroll through all the slices in the brain? Do any of the distortions appear?

What causes it: A common cause is metal. Different substances (e.g. metal vs. bone) next to each other in the scanner the unit too dark (signal loss) and/or too bright (signal transmitted by the scanner, meaning



ANAT : Ghosting



Mild: Ghosting faintly detectable

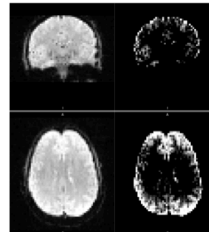
What to look for: A fainter displaced copy of the original image. A fainter displaced copy of the original image can appear anywhere in the scan. A ghost will form a streak, like cartoon motion blur.

How to look for it: Ghosting is easier to detect in areas of high contrast. Check for maximum brightness value while leaving through all the slices and time points in motion, or around eyes). Check in the brain. How clearly visible are they? Can you still see the original image?

What causes it: Ghosting comes in several forms. (Imagine fainter copies of an image or signal that are out of phase with the original, causing a mismatch in the signal channels that



BOLD : Signal Inhomogeneity



Normal Contrast **High Contrast**
None: signal intensity uniform throughout image

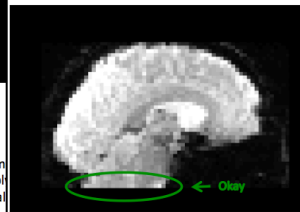
What to look for: An inconsistency/asymmetry in signal intensity. Signal homogeneity varies notably at the front and back of the brain). Signal intensity is not uniform throughout the image.

How to look for it: Signal inhomogeneity is easier to detect in areas of high contrast. Check for minimum brightness value while leaving through all the slices and time points in motion, or around eyes). Check in the brain. How clearly visible are they? Can you still see the original image?

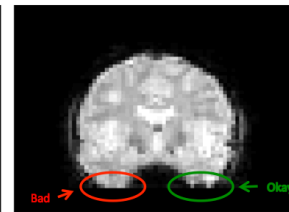
What causes it: MRI's use a receiver coil that incorrectly reads the signal as stronger in some areas. In some systems use receiver coils made up of arrays of small coils in the array have failed), in this case the signal will be weaker in those areas.



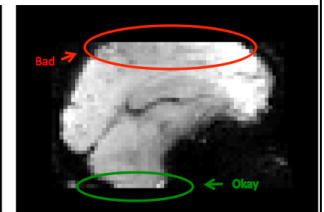
BOLD : Head Coverage



Good: EMBARC brain target area fully covered in FOV.



Questionable: FOV clips slice(s) of EMBARC brain target area.



Bad: FOV clips significant portion of EMBARC target area

What to look for: Perfect head coverage means the entire brain target area (the part of the brain you care about in your study) is clearly visible in the scan's field of view (FOV), ideally with at least one slice of black background buffer on each side. For EMBARC, the brain target area runs from the top of the brain to the bottom of the temporal lobes, and does not include the cerebellum. Note: if a subject's brain is just too large to fit in the scan's FOV, the FOV frame should be centered over the brain target area and should clip the extra slice from the *top* of the brain (not the temporal lobes) if the number of slices that must be clipped is odd.

How to look for it: Scroll through all the slices in each view of the brain. Is there any place where the brain's natural curve becomes suddenly flat as if clipped off by the black background? Is the clipped piece part of your brain target area? How much of the brain target area is clipped, only a few slices or a much larger section? Remember you will need to scroll through all the slices in the coronal (front/back) view of the brain to check if the full temporal lobe is covered since the bottom tips are not visible in all slices.

What causes it: The person operating the scanner positions the frame of MRI FOV by hand. Poor head coverage is usually caused by the scanner operator failing to reposition the FOV if a part of the brain target area is being cut off. Occasionally, the subject will cause the head coverage loss by moving out of the FOV.



© Copyright Massachusetts General Hospital 2012; all rights reserved.



© Copyright Massachusetts General Hospital &



Harvard University; all rights reserved.

Want to Reference the Manual?

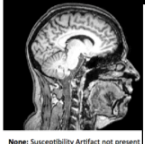
The full MRI Qualitative Quality Control Manual is available online!

Go to the Harvard Center for Brain Science Website: <http://cbs.fas.harvard.edu/>
Center for Brain Science > Neuroimaging > Information for Investigators > FAQ

MRI Quality Control Manual

What to look for and How to look for it!

ANAT : Susceptibility Artifact



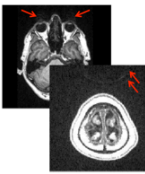
None: Susceptibility Artifact not present

What to look for: A black area, like a hole of bright and dark ripples (called "Moire") in the brain? Do any of the distortions appear?

How to look for it: Scroll through all the slices in the brain? Do any of the distortions appear?

What causes it: A common cause is metal. Different substances (e.g. metal vs. bone) react to each other in the scanner the unit too dark (signal loss) and/or too bright (signal transmitted by the scanner, meaning signal is too bright).

ANAT : Ghosting



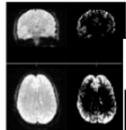
Mild: Ghosting faintly detected

What to look for: A fainter displaced copy of the brain? A fainter displaced copy of the brain? A fainter displaced copy of the brain? A fainter displaced copy of the brain? A fainter displaced copy of the brain?

How to look for it: Ghosting is easier to detect through all the slices and time points in motion, or around eyes? Check in the brain. How clearly visible are they? Can you see the original image?

What causes it: Ghosting comes in two forms: a fainter displaced copy of an image or a mismatch in the signal channels that causes the image to be blurry.

BOLD : Signal Inhomogeneity



Normal Contrast **High Contrast**

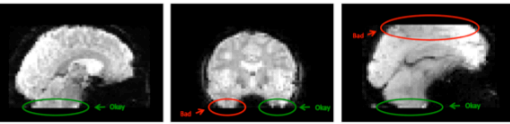
None: signal intensity uniform throughout image

What to look for: An inconsistency/symptom others. Signal homogeneity varies notably at the front and back of the brain. Signal intensity is uniform throughout image.

How to look for it: Signal inhomogeneity: minimum brightness value while leaving maximum, each time scrolling through all slices, each time scrolling through all slices, each time scrolling through all slices, each time scrolling through all slices, each time scrolling through all slices.

What causes it: MRI's use a receiver coil incorrectly reads the signal as stronger in systems use receiver coils made up of any the scanner will always read the signal as if it were a different part of the receiver coil (small coils in the array have failed), in the scanner.

BOLD : Head Coverage



Good: EMBARC brain target area fully covered in FOV.

Questionable: FOV clips slice(s) of EMBARC brain target area.

Bad: FOV clips significant portion of EMBARC target area.

What to look for: Perfect head coverage means the entire brain target area (the part of the brain you care about in your study) is clearly visible in the scan's field of view (FOV). Ideally with at least one slice of black background buffer on each side. For EMBARC, the brain target area runs from the top of the brain to the bottom of the temporal lobes, and does not include the cerebellum. Note: If a subject's brain is just too large to fit in the scan's FOV, the FOV frame should be centered over the brain target area and should clip the extra slice from the top of the brain (not the temporal lobes) if the number of slices that must be clipped is odd.

How to look for it: Scroll through all the slices in each view of the brain. Is there any place where the brain's natural curve becomes suddenly flat as if clipped off by the black background? Is the clipped piece part of your brain target area? How much of the brain target area is clipped, only a few slices or a much larger section? Remember you will need to scroll through all the slices in the coronal (front/back) view of the brain to check if the full temporal lobe is covered since the bottom tips are not visible in all slices.

What causes it: The person operating the scanner positions the frame of MRI FOV by hand. Poor head coverage is usually caused by the scanner operator failing to reposition the FOV if a part of the brain target area is being cut off. Occasionally, the subject will cause the head coverage loss by moving out of the FOV.

© Copyright Massachusetts General Hospital 2012; all rights reserved.



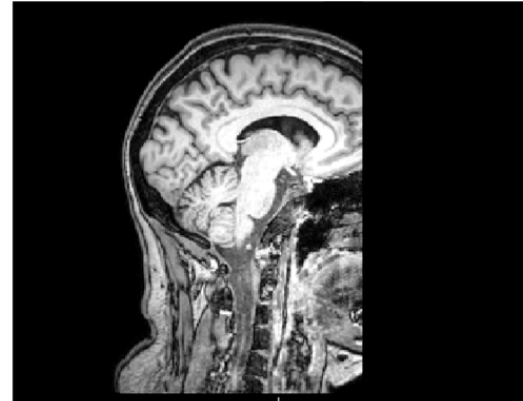
Manual Sample Page

Includes: *What to look for*, *How to look for it*, and *What causes it*

ANAT : Head Coverage



Good: brain fully covered in FOV.



Bad: FOV clips brain

What to look for: Perfect head coverage means the entire brain target area (the part of the brain you care about in your study) is clearly visible in the scan's field of view (FOV), ideally with at least one slice of black background buffer on each side. For EMBARC, the brain target area runs from the top of the brain to the bottom of the temporal lobes, and does not include the cerebellum. Note: imperfect head coverage with no wrapping is almost never seen in anatomical scans.

How to look for it: Scroll through all the slices in each view of the brain. Is there any place where the head's natural curve becomes suddenly flat as if clipped off by the black background? Does the clipping cut off any portion of the brain?

What causes it: The person operating the scanner positions the frame of MRI FOV by hand. Poor head coverage is usually caused by the scanner operator failing to reposition the FOV if a part of the brain target area is being cut off. Occasionally, the subject will cause the head coverage loss by moving out of the FOV.



ANAT : Head Coverage*



Good: brain fully covered in FOV



Bad: FOV clips brain

*Reference the MRI Qualitative Quality Control Manual for full text on each artifact



© Copyright Massachusetts General Hospital &

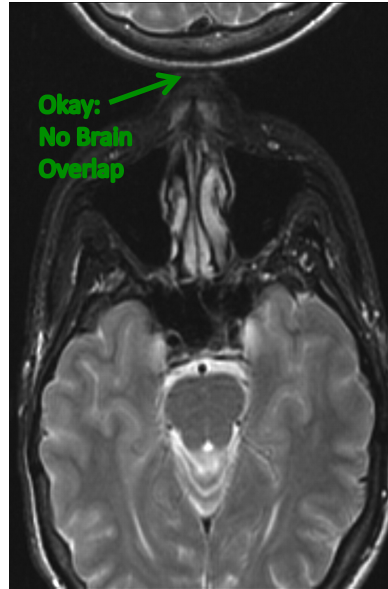


Harvard University; all rights reserved.

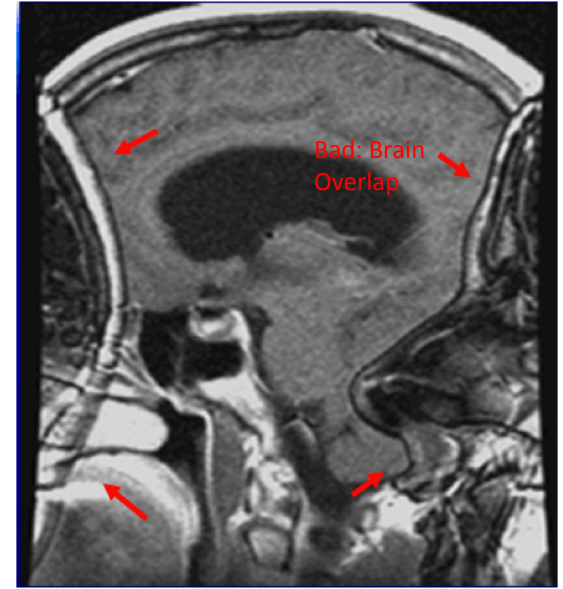
ANAT : Wrapping



Mild: head wrapping, but does not affect brain

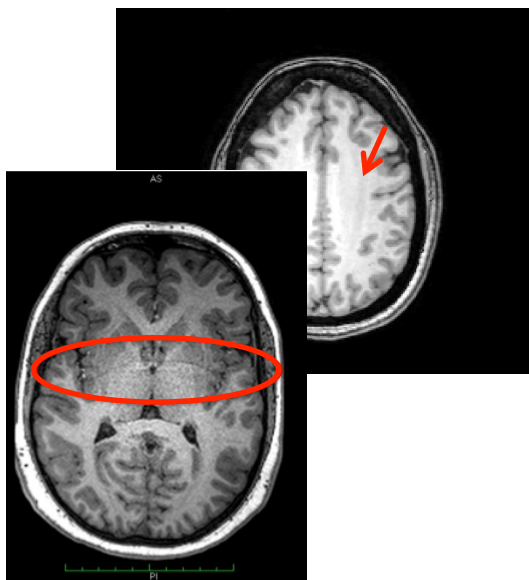


Moderate: brain wrapping but not overlapped by other anatomy

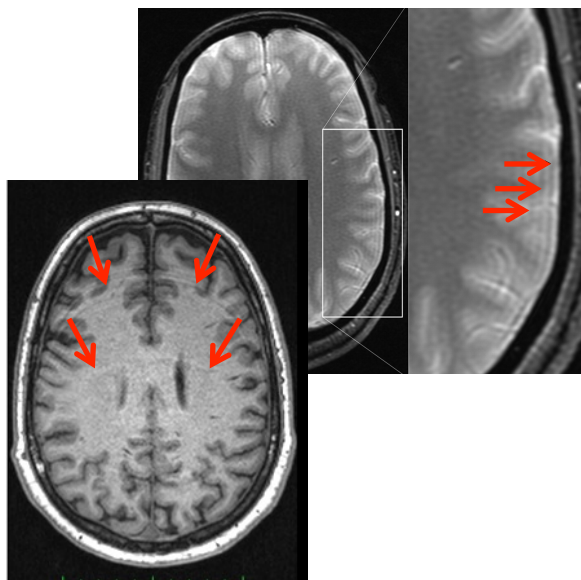


Severe: brain wrapping and overlapped by other anatomy

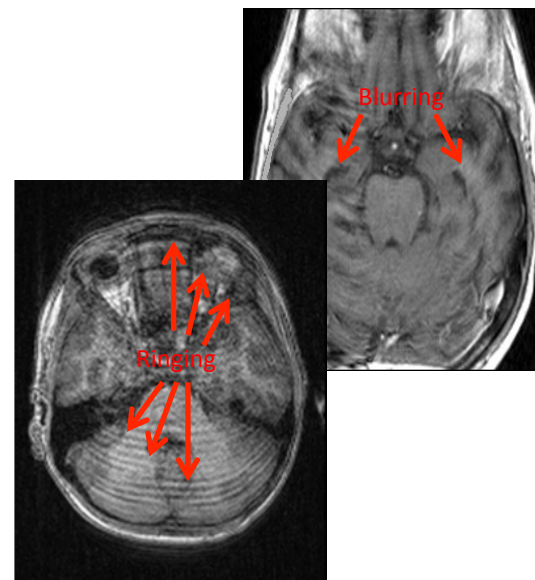
ANAT : Ringing, Striping, Blurring



Mild: Ringing, Striping, Blurring faintly detectable

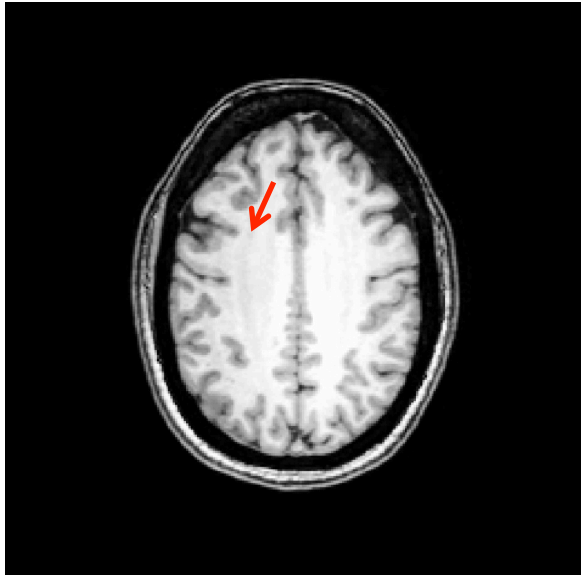


Moderate: Ringing, Striping, Blurring pronounced

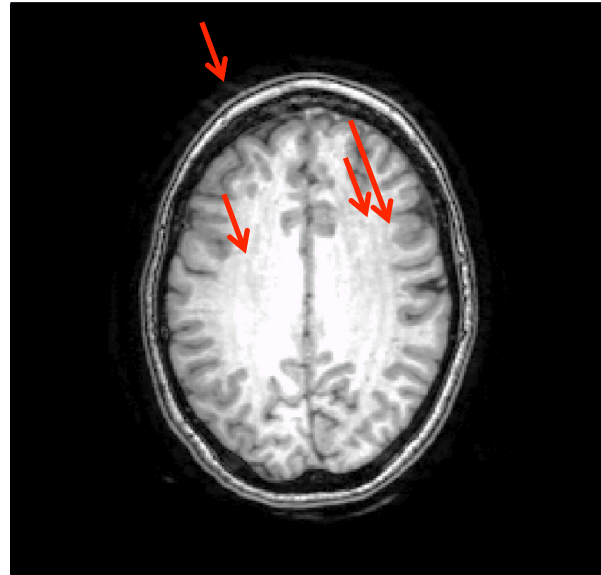


Severe: Ringing, Striping, Blurring extreme

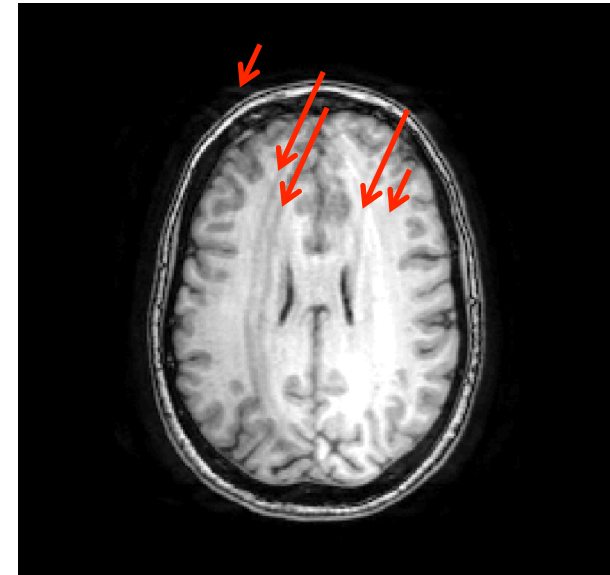
ANAT : Shadowed Arc Artifact



Mild: Shadowed Arc Artifact faintly detectable



Moderate: Shadowed Arc Artifact pronounced

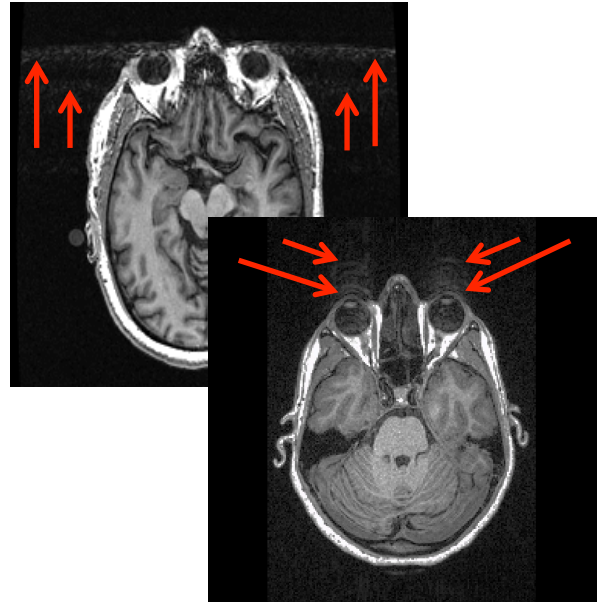


Severe: Shadowed Arc Artifact extreme

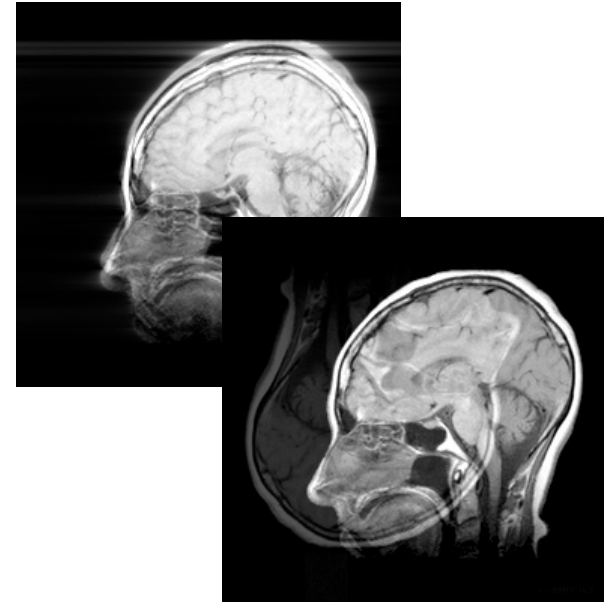
ANAT : Ghosting



Mild: Ghosting faintly detectable

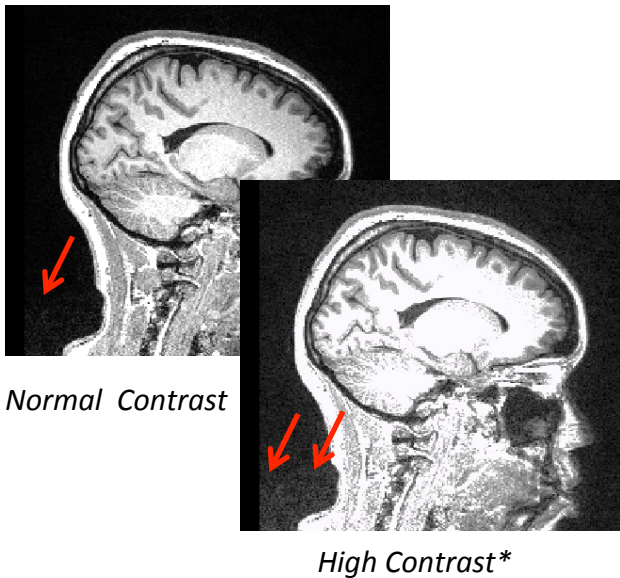


Moderate: Ghosting pronounced

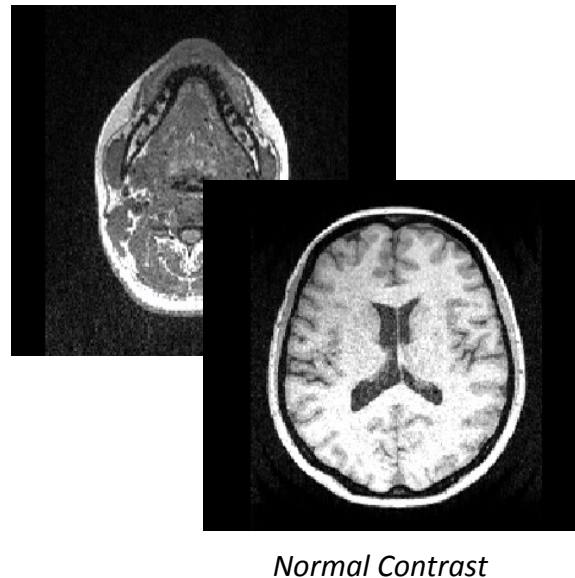


Severe: Ghosting extreme

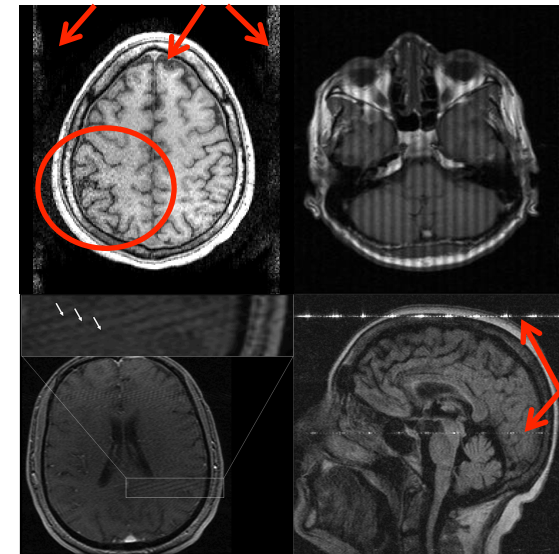
ANAT : Radio Frequency (RF) Noise (Severe = Spiking)



Mild: Low-level RF noise visible only after adjusting contrast



Moderate: RF noise prominently visible without adjusting contrast

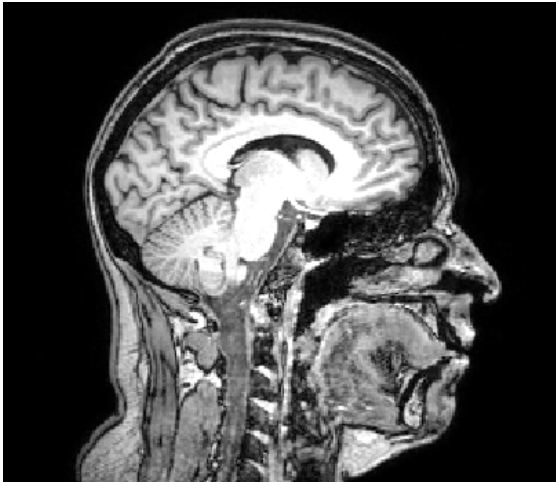


Severe: Spiking is present

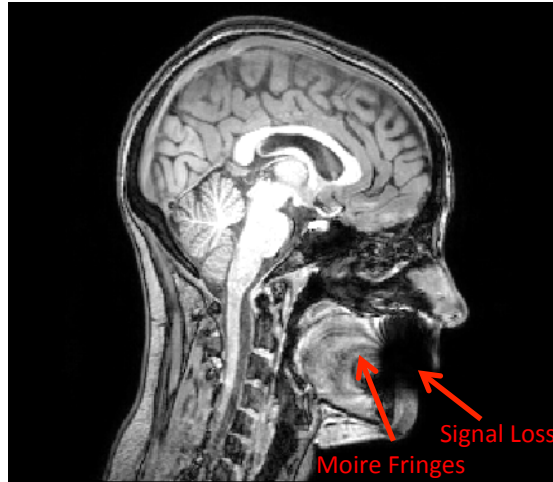
*RF Noise is most clearly visible at high contrast, adjusted by lowering the Maximum Brightness.



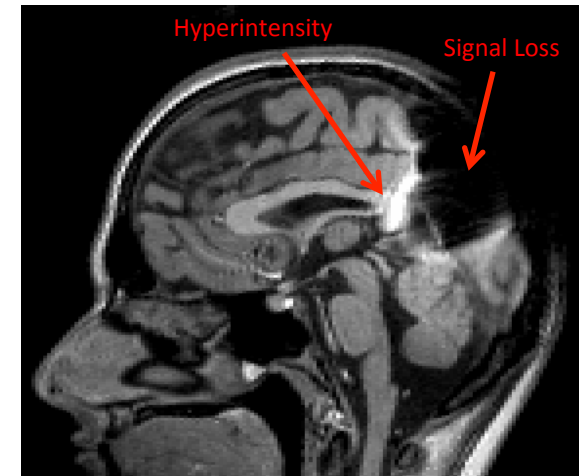
ANAT : Susceptibility Artifact



None: Susceptibility Artifact not present

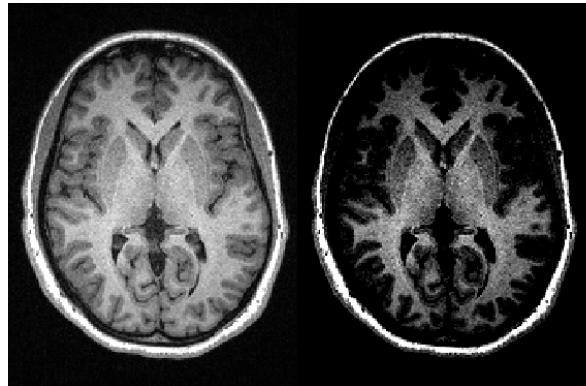


Outside Brain: Susceptibility Artifact present, but does not affect brain



Affecting Brain: Susceptibility Artifact present and affects brain

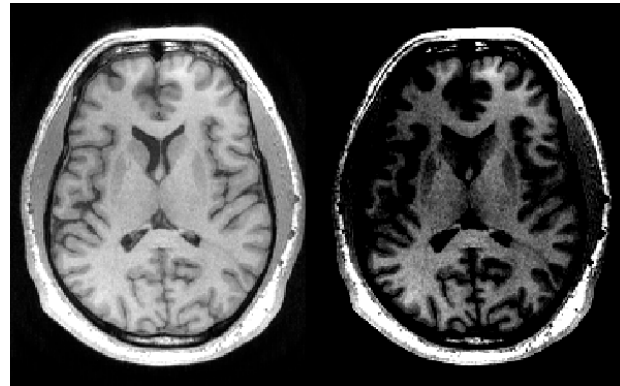
ANAT : Unexpected Inhomogeneity



Normal Contrast

High Contrast*

None: signal intensity uniform throughout image



Normal Contrast

High Contrast*

Expected: inconsistent signal intensity fits coil profile



Normal Contrast

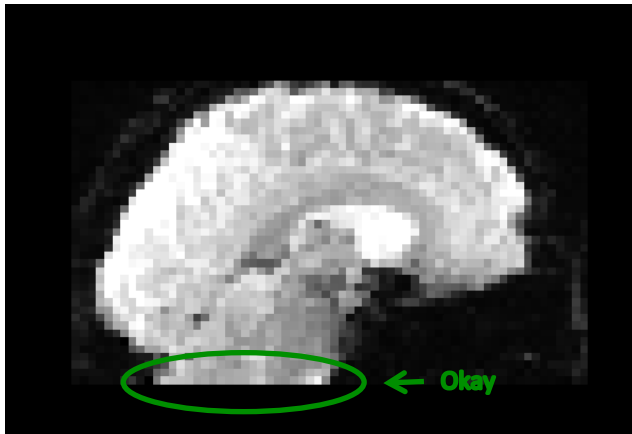
High Contrast*

Unexpected: inconsistent signal intensity does not fit coil profile

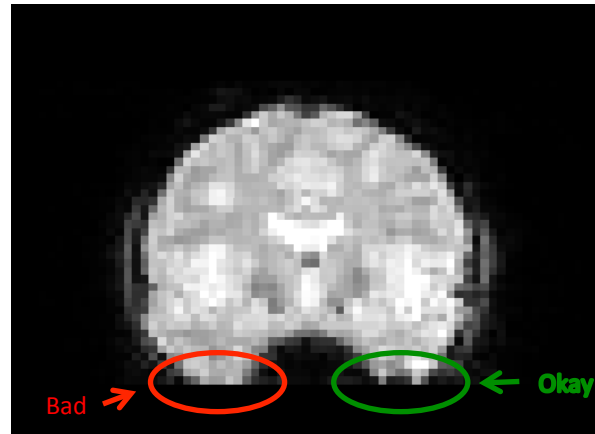
*Signal inhomogeneity is most clearly visible at high contrast, adjusted by raising the Minimum Brightness.



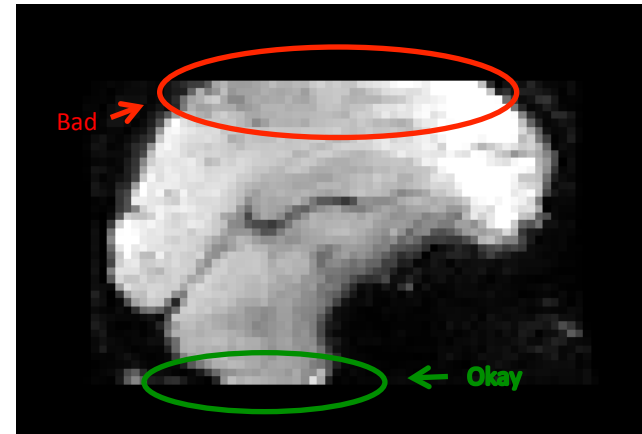
BOLD : Head Coverage



Good: EMBARC brain target area fully covered in FOV.



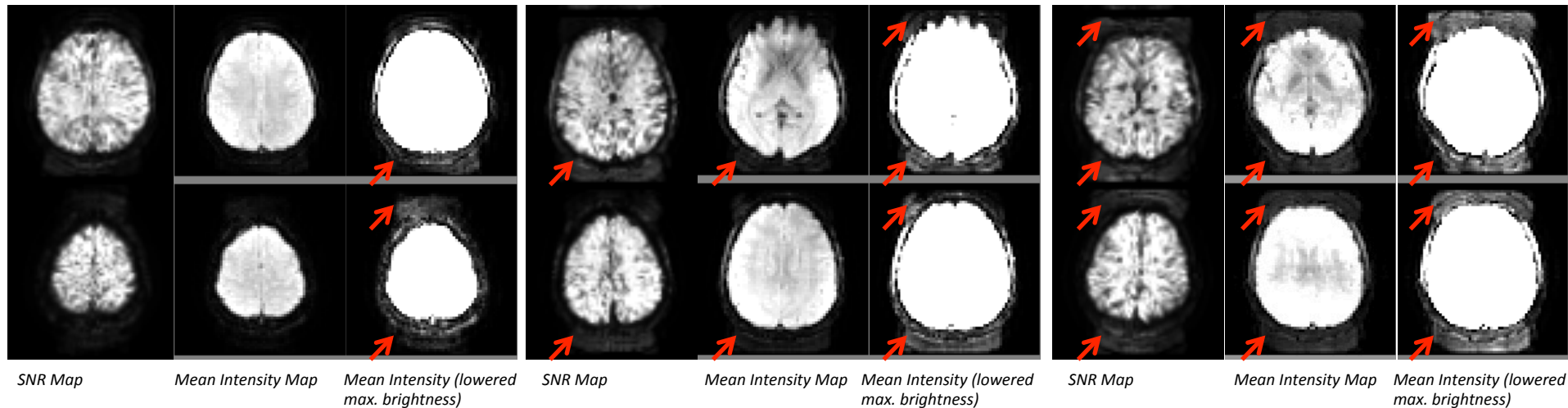
Questionable: FOV clips slice(s) of EMBARC brain target area.



Bad: FOV clips significant portion of EMBARC target area



BOLD : Ghosting

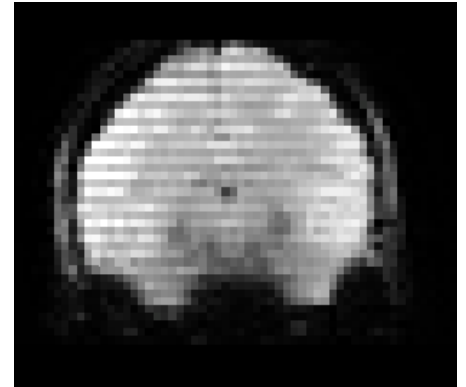
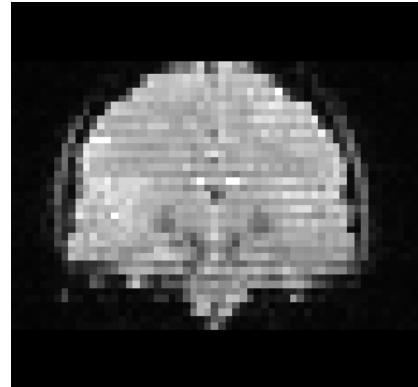
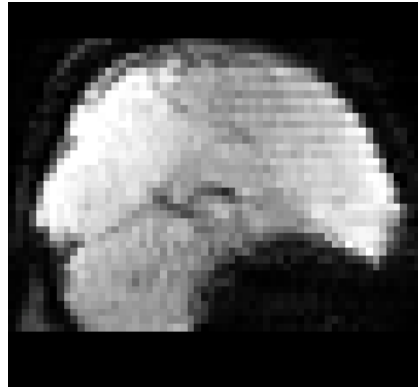


Mild: Ghosting faintly detectable only after adjusting contrast (decrease Maximum Brightness)

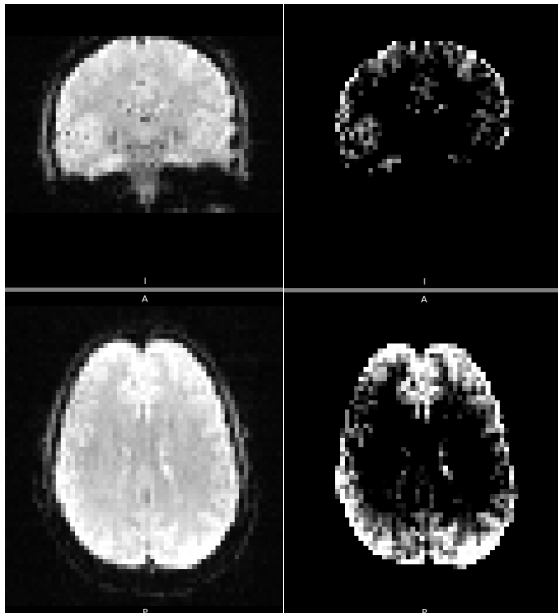
Moderate: Ghosting notably visible without adjusting contrast and prominently visible after adjusting contrast

Severe: Ghosting prominently visible without adjusting contrast

BOLD : Motion Slice Artifact



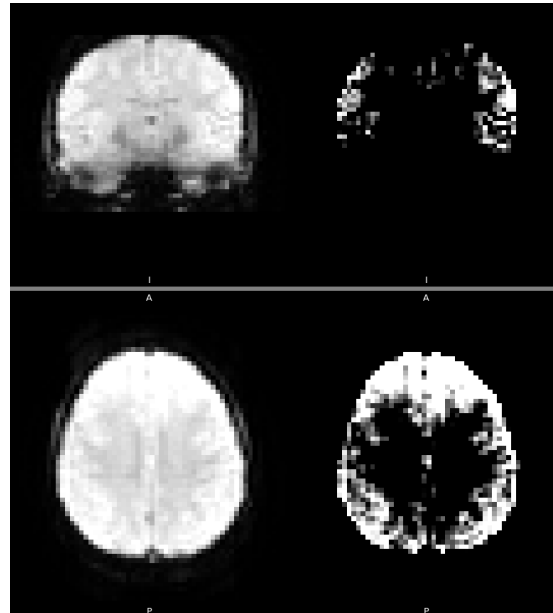
BOLD : Signal Inhomogeneity



Normal Contrast

High Contrast*

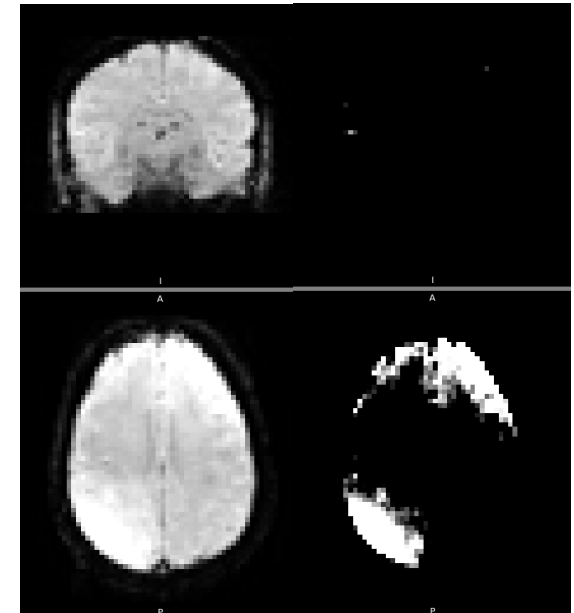
None: signal intensity uniform throughout image.



Normal Contrast

High Contrast*

Expected: inconsistent signal intensity fits scanner/coil profile



Normal Contrast

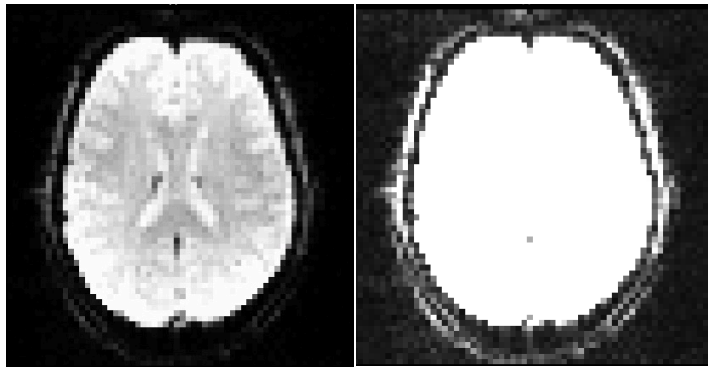
High Contrast*

Unexpected: inconsistent signal intensity does not fit scanner/coil profile

*Signal inhomogeneity is most clearly visible at high contrast, adjusted by raising the Minimum Brightness.

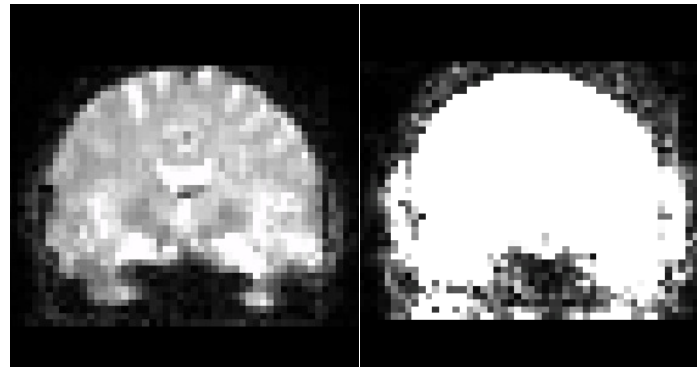


BOLD : Radio Frequency (RF) Noise (Severe = Spiking)



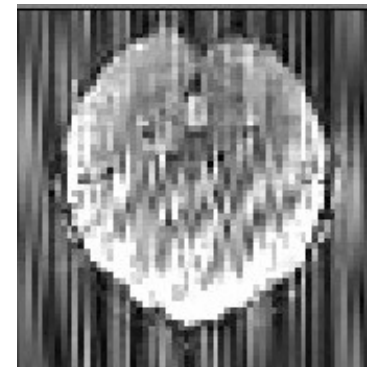
Normal Contrast

High Contrast*



Normal Contrast

High Contrast*



Normal Contrast

Mild: Low-level RF noise visible only after adjusting contrast

Moderate: RF noise prominently visible without adjusting contrast

Severe: Spiking is present

*RF Noise is most clearly visible at high contrast, adjusted by lowering the Maximum Brightness.



Make a Record

User: nshansen (Logout) (Edit) (Report a problem) Search Advanced

Home New Upload

PROJECT: EMBARC > SUBJECT: [REDACTED] BOLD_13_EQC

Edit View

Images Automated QC **Manual QC** Provenance All Stored Files

Motion
Mean Absolute Motion: 0.258
Maximum Absolute Motion: 0.532
Movements (>0.1mm): 28
Movements (>0.5mm): 0
 Good
 Questionable
 Bad

Ghosting
Affects Brain Outside of Brain
 None None
 Mild Mild
 Moderate Moderate
 Severe Severe

Overall QC Assessment
 PASS - Data passed quality control
 WARN - Data have significant quality issues
 FAIL - Data failed quality control
Save changes Do not save changes

RF Noise/Spiking
 None - no abnormal RF noise
 Mild - little static with no distinct pattern
 Moderate - low-level static with pattern (bands, spheres)
 Severe - RF spiking visible

Head Coverage
 Good - full brain coverage with ≥ 1 slice buffer
 Questionable - slight clipping or necessary clipping
 Bad - brain clipped unnecessarily or severely

Inhomogeneity
 None
 Expected
 Unexpected - moderate
 Unexpected - severe

Comments
WARN: FOV clips top
AI: Wrapping; moderate inhomogeneity; motion slice artifact @ TP's 17-23, [L49, 202-207]

Summary
MR Session [REDACTED]
Subject [REDACTED]
Date Acquired: 2012-08-01

Parameters
Num Volumes: 240
Num Voxels: 58435
Mask Threshold: 200.0
Skip: 0

QC Overview
Mean: 800.94
StDev: 19.88
Slice SNR: **289.2**
Voxel SNR: **46.9**
Mean Rel Motion: 0.065
Max Rel Motion: 0.182
Mean Abs Motion: 0.258
Max Abs Motion: 0.532
Movements (>.1mm): 28
Movements (>.5mm): 0

Assessment
WARN

Files
SNR Image
Mean Image
StDev Image
Mask Image
Mean Data
Motion Data
Slope Image
Auto QC Report
Manual QC Report
Slice Report

“Manual QC” tab in EMBARC Central XNAT

Note any information necessary to clarify broad ratings (e.g. Head Coverage -> Note: “FOV clips top”)

powered by XNAT



Qualitative QC in Action

Examples from EMBARC scans in FSL

Movie Mode cycles through Volumes

Adjust Contrast

Min 175
Max 335.46

Min 0
Max 150

Tools > Lightbox View

Pinpoint artifact location

X: 89, Y: 119, Z: 163, Intensity: 286, Volume: 1.55

Coordinate space: Scanner Anatomical

FSLView (3.1.8) - [Ortho view]

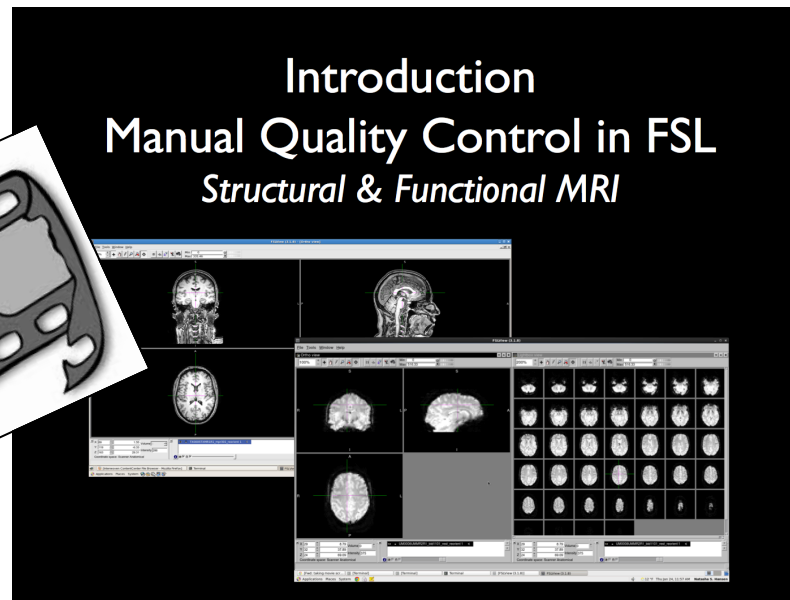
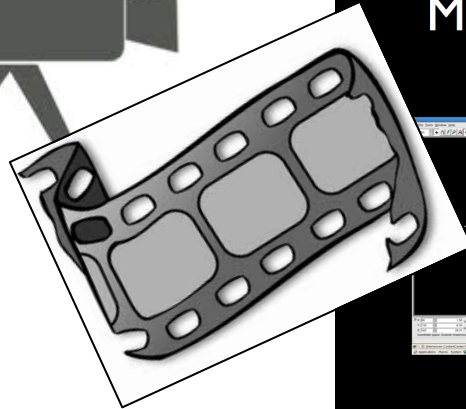
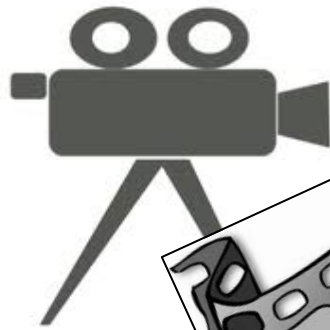


Video Tutorial

“Introduction to Quality Control Tools in FSL”

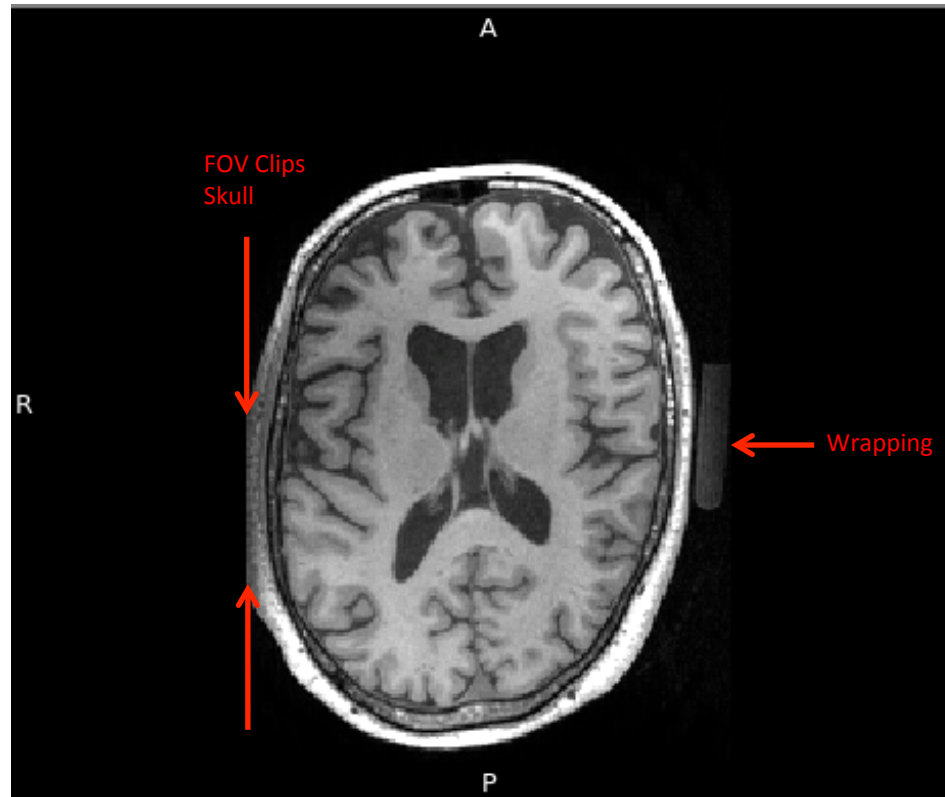
MRI quality control tutorial videos are available online!

Go to the Harvard Center for Brain Science website: <http://cbs.fas.harvard.edu/>
Center for Brain Science > Neuroimaging > Information for Investigators > FAQ



Head Coverage & Wrapping

FOV clips skull causing Wrapping



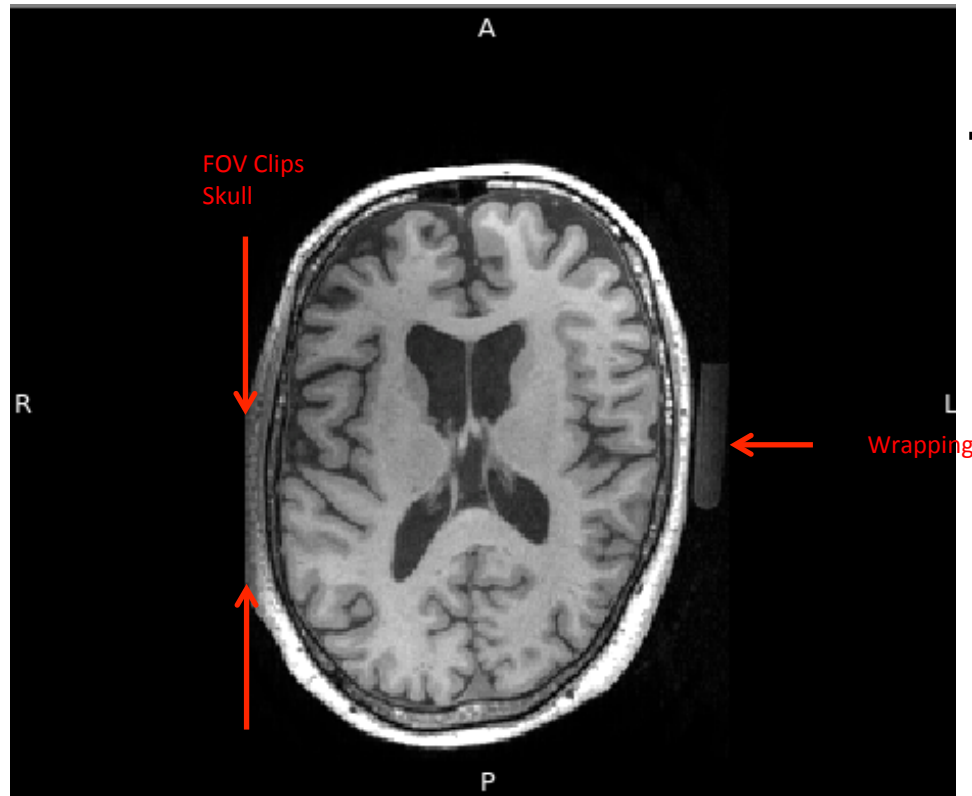
Normal Contrast



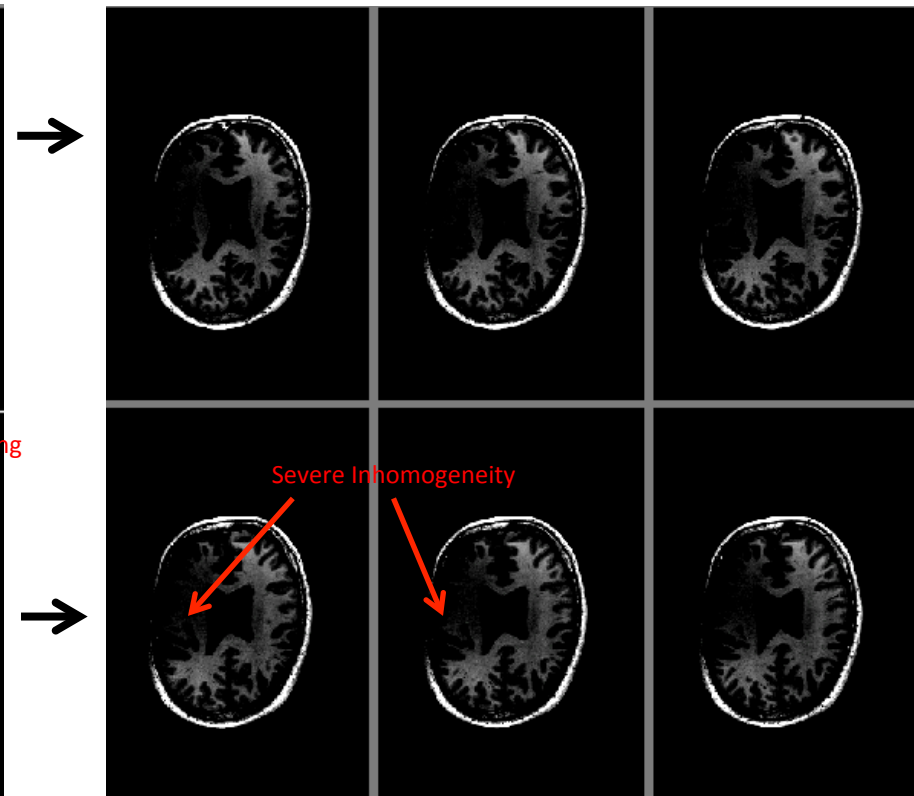
Head Coverage & Wrapping

FOV clips skull causing Wrapping

Inhomogeneity revealed at point of skull clip



Normal Contrast

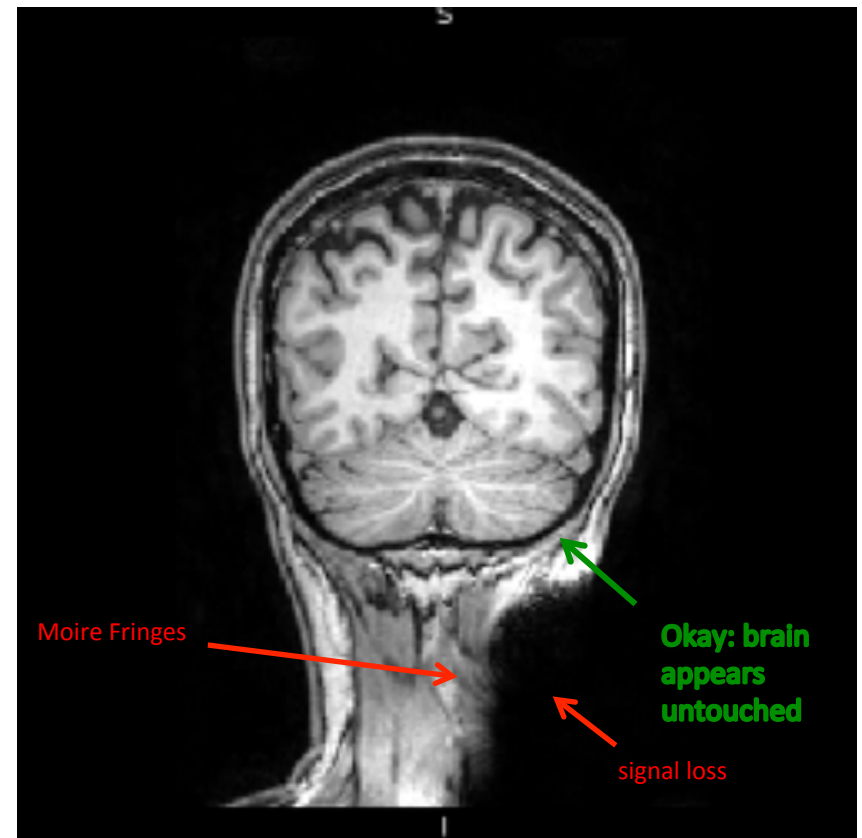


Adjusted Contrast



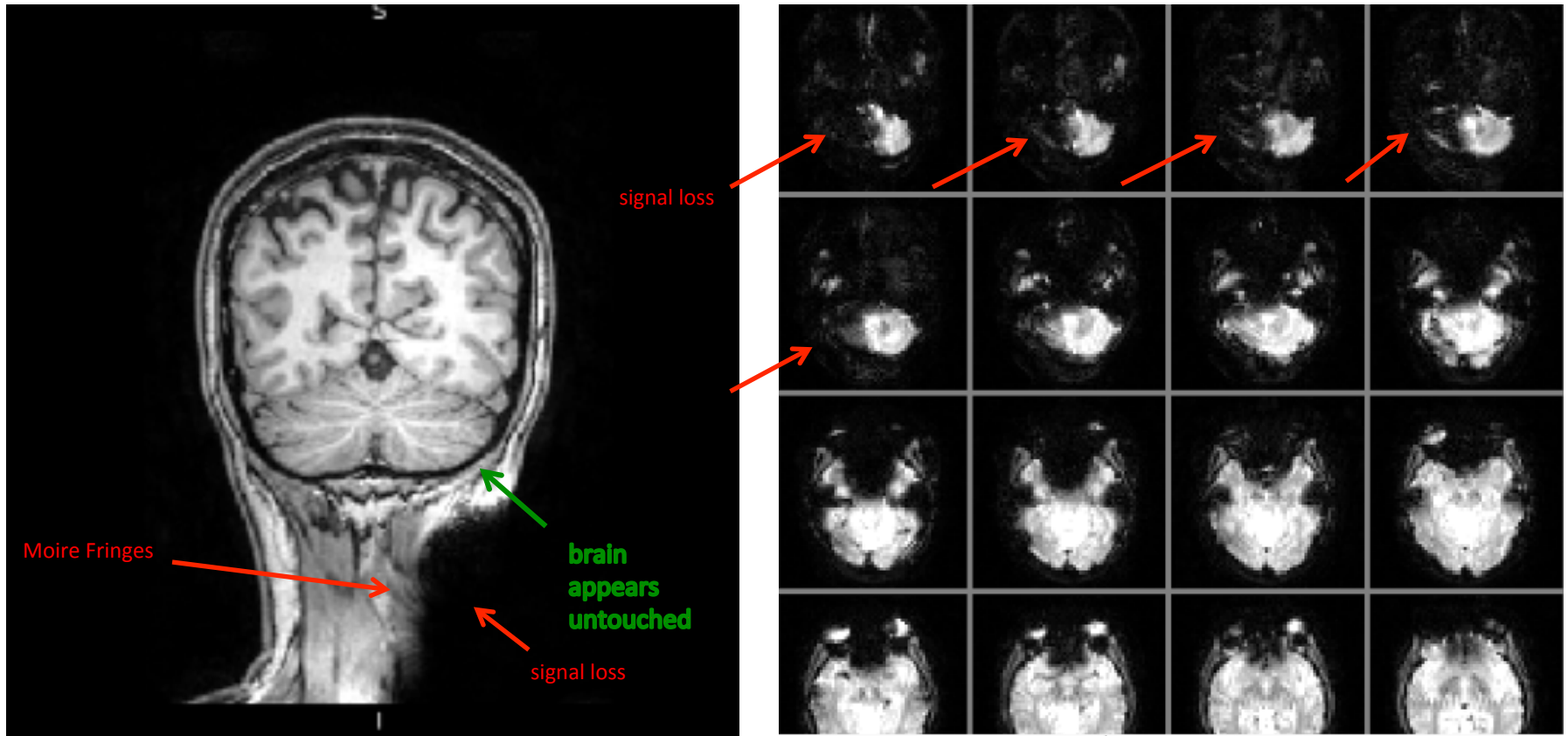
Susceptibility Artifact

Massive signal loss accompanied by “Moire Fringes” – brain appears unaffected



Susceptibility Artifact

Brain appears unaffected in by Susceptibility Artifact in structural scans, but signal drop out is visible in BOLD scans

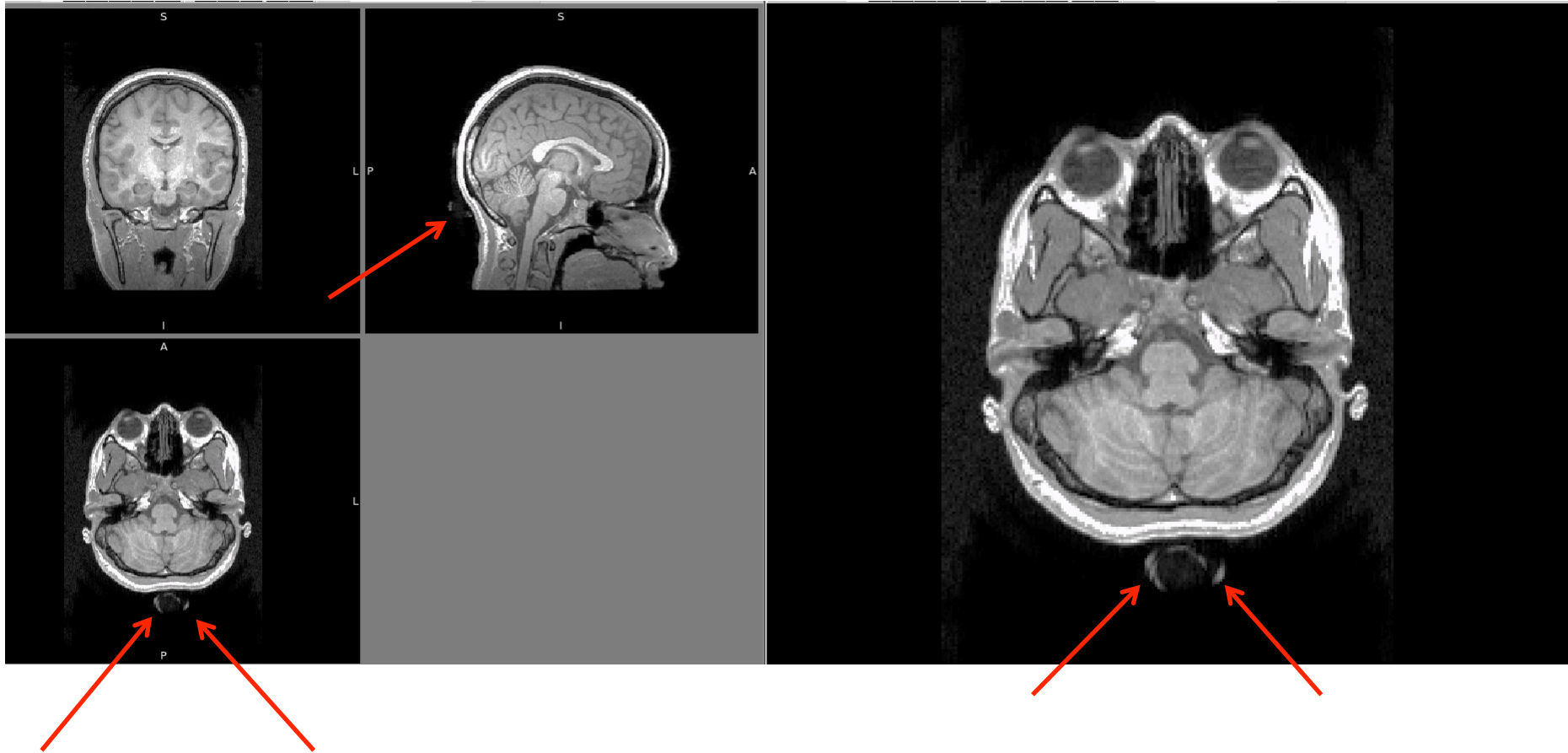


Normal Contrast



“Swirling Galaxy Artifact”!

This artifact is caused by the subject’s hair tie or greasy bun – perspective and humor are key!



Want to Learn More?

The Harvard Center for Brain Science Website has more useful information for you!

Go to: <http://cbs.fas.harvard.edu/>

Center for Brain Science > Neuroimaging > Information for Investigators > FAQ

The Qualitative QC Manual

Detailed practical QC Tutorial Videos

How to create your own measures of goodness

Preventive QC: at the scanner

What to do when you discover artifacts

MRI Quality Control Manual
What to look for and How to look for it!

ANAT : Susceptibility Artifact

ANAT : Ghosting

BOLD : Signal Inhomogeneity

BOLD : Head Coverage

© Copyright Massachusetts General Hospital & Harvard University; all rights reserved.

FAQ

NCF Questions

Getting Started

- How can I get help?
- What is the NCF?
- Who may use the NCF?
- How do I use the NCF?
- How do I get an NCF User Account?
- How do I set up my user environment/access software?
- How do I set my permissions so that everything is re-group?
- How do I access the NCF network remotely (VPN)?
- Why do I have to use an NCF designated workstation?
- How and where do I login remotely to the NCF?
- How do I connect to the NCF from a PC?
- How do I get files back and forth between the NCF?
- How do I look at and/or edit files from a workstation?

Advanced Topics

- How do I submit jobs to the compute cluster?
- Useful commands to work with submitted scripts (bsub tools).
- How do I setup VNC, which allows GUI intensive programs from my computer?
- How do I change my password?
- What if I want to VPN to the NCF from a different computer than usual?
- What software is available on the net?
- How much space will I be allocated to process and store my data?
- How do I check how much space I have left?
- How do I use the internet during VPN?
- How do I use the internet from the workstations?
- How do I change the version of my Freesurfer, Afni, FSL, or other brain analysis packages?
- How do I set or change my SPM version?

What to do if you find something.

There are several basic steps you can do to try and improve the quality of your data at the scanner.

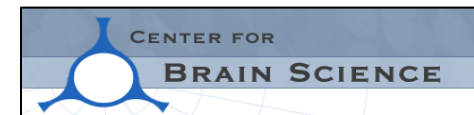
- Movement:** Provide feedback to your subject about their movement, if your paradigm permits. In general, it can be useful to provide gentle reminders that they need to stay still, or you can specifically tell them that you checked their movement and you noticed that they moved at a particular time (such as, the beginning, middle, or end of scans). This can allow the subject to realize what kind of movements aren't allowed. However, if you are studying emotions, or working with a group of participants that might not respond well to this feedback, then you may want to consider saying nothing or providing very general, generic feedback.
- Ghosting:** There is generally not a great solution for this. However, if you see severe ghosting or a change in ghosting across the run, Ross (ross@fas.harvard.edu) should be informed of the date, subject number, and run number where something was observed.
- RF Spiking:** One common source of RF interference is the button box. Make sure the subject is holding the box down by their side and not up in the scanner bore near their head, and make sure they are keeping it stationary. This should also be reported to Ross (ross@fas.harvard.edu) with the date, subject number, and run number where observed.

How to check for correct coverage.

It is important to make sure that every part of the brain you want to collect information about is inside the field of view (yellow box).

Structural

For the structural, this means making sure the top, bottom, and sides of the brain are in the yellow box, and that the nose isn't being cut off. Anything that falls just outside of the yellow FOV will 'wrap around' to the other side. For example, the nose would show up in the occipital lobe. If you use autoalign, then this will usually come up correctly for you, but it is always wise to look closely.



Acknowledgements

MRI Qualitative Quality Control Manual written and created by:

Natasha Hansen, Garth Coombs, Thilo Deckersbach, & Randy Buckner

Special Thanks to:

Primary Investigator

Randy Buckner, PhD

EMBARC Quality Control Team

Thilo Deckersbach, PhD

Kristen Ellard, PhD

Sharmin Ghaznavi, MD, PhD

Natasha Hansen, BA

Garth Coombs, BA

Neuroinformatics Team

Gabriele Fariello, MA

Victor Petrov, BA

Timothy O'Keefe, BA

MR Physics Consultant

Ross Mair, PhD

Neuroimaging Consultants

Stephanie McMains, PhD

Erik Kastman, BS

Sophia Mueller, MD



Questions and Discussion...

