SCAN MR

- SCAN provides service to NIA/ADCs
- Outline:
  - Illustrate ADNI/clinical trial approach to MR
  - similarities and differences proposed for SCAN

MR in clinical trials or ADNI environment

Site survey and protocol development – propose same for SCAN

- technical survey of scanners at each site – pick best
- Create generic non-platform-specific protocol
  - Select sequence types, order, some sequence-specific parameters
- Create a vendor and operating system-specific protocol for each scanner in the study
  - pilot the protocol on every platform prior to site distribution
  - ADNI: 60 scanners, 17 different vendor/OS platforms

ADNI 3 generic protocol

- 3D T1 volume
- 3D FLAIR
- T2* GRE (3 echoes for Siemens – QSM)
- ASL
- TF-fMRI –advanced (SMS) or basic versions
- dMRI – advanced (SMS) or basic versions
- Coronal high resolution T2 – for hippocampal subfields

Sagittal 3D MPRAGE

TA: 5:12 PM: ISO Voxel size: 1.0x1.0x1.0mmPAT:2 Rel. SNR: 1.00 : tfl

Properties

Prio recon	Off
Load images to view	On
Inline movie	Off
Auto store images	On
Load images to stamp segments	On
Load images to graphic segments	Off
Auto open inline display	Off
Auto close inline display	Off
Start measurement without further Preparation	Off
Wait for user to start	Off
Start measurements measurement	Single

Routine

Slab group		1
Slabs		1
Dist. Factor		50 %
Position mm		L0.0 P5.4 H26.4
Orientation		Sagittal
Phase enc. Dir	A > > P	
Auto Align		--
Phase oversampling		0 %
Slice oversampling		0.0 %
Slices per slab	208	
FOV read		256
FOV phase		93.8 %
Slice thickness		1.00 mm
TR		2300.0 ms
TE		2.98 ms
Averages		1
Concatenations		1
Filter (3D),		Distortion Corr. Prescan Normalize
Coil Elements	HC1-7; NC 1, 2	

Contrast- Common

TR		2300.0 ms
TE		2.98 ms
Magn. Preparation		Non-sel. IR
TI		900 ms
Flip angle		9 deg
Fat suppr.		None
Water suppr.	None	

Contrast- Dynamic

Averages		1
Averaging mode		Long term
Reconstruction		Magnitude
Measurements	1	
Multiple series	Each measurement	

Resolution – Common

FoV read		256 mm
FoV phase		93.8 %
Slice thickness		1.00 mm
Base resolution		256
Phase resolution		100 %
Slice resolution		100 %
Phase partial Fourier		Off
Slice partial Fourier		Off
Interpolation	Off	

Resolution - iPAT

PAT mode		GRAPPA
Accel. Factor PE		2
Ref. lines PE	32	
Accel. Factor 3D		1
Reference scan mode		Integrated

Resolution – Filter Image

Image Filter		Off
Distortion Corr.		On
Mode		3D
Unfiltered images		Off
Prescan Normalize		On
Unfiltered images		Off
Normalize		Off
B1 filter		Off

Resolution – Rawdata

Raw filter		Off
Elliptical filter	Off	

Geometry - Common

Slab group		1
Slabs		1
Dist. Factor		50 %
Position		L0.0 P5.4 H26.4 mm
Orientation		Sagittal
Phase enc. Dir	A >> P	
Slice oversampling		0.0 %
Slices per slab		208
FoV read		256 mm
FoV phase		93.8 %
Slice thickness		1.00 mm
TR		2300.0 ms
Multi-slice mode		Single shot
Series		Ascending
Concatenations		1

Geometry – Navigator

Geometry – AutoAlign

Slab group		1
Position		L0.0 P5.4 H26.4 mm
Orientation		Sagittal
Phase enc. Dir	A >> P	
AutoAlign		---
Initial Position	L0.0 P5.4 H26.4 mm	
L		0.0 mm
P		5.4 mm
H		26.4 mm
Initial Rotation	0.00 deg	
Initial Orientation		Sagittal

System – Miscellaneous

Positioning mode		ISO
Table position	H	
Table position	26 mm	
MSMA		S-C-T

System – Miscellaneous

Sagittal	L >> R
Coronal	A >> P
Transversal	F >> H
Coil Combine Mode	Adaptive Combine
Save uncombined	Off
Matrix Optimization	Off
AutoAlign	---
Coil Select Mode	On - AutoCoilSelect

System – Adjustments

B0 Shim mode Standard	
B1 shim mode TrueForm	
Adjust with body coil	Off
Confirm freq. adjustment	Off
Assume Dominant Fat	Off
Assume Silicone	Off
Adjustment Tolerance	Auto

System – Adjust Volume

Position	L0.0 P5.4 H26.4 mm
Orientation	Sagittal
Rotation	0.0 deg
A >> P	240 mm
F >> H	256 mm
R >> L	208 mm
Reset	Off

System – pTx Volumes

B1 Shim mode	TrueForm
Excitation	Non-sel.

System – Tx/Rx

Frequency 1H	123.251925 MHz
Img. Scale Cor.	1.000
Reset	Off
? Ref. amplitude 1H	0.000 V

Physio – Signal1

1st Signal/Mode	None
TR	2300.0 ms
Concatenations	1

Physio – Cardiac

Magn. Preparation	Non-sel. IR
TI	900 ms
Fat suppr.	None
Dark blood	Off
FoV read	256 mm
FoV phase	93.8 %
Phase resolution	100 %
Correction factor	1
Gain	Low

Physio – PACE

Resp. control	Off
Concatenations	1

Inline - Common

Subtract	Off
Measurements	1
StdDev	Off
Save original images	On

Inline – MIP

MIP-Sag	Off
MIP-Cor	Off
MIP-Tra	Off
MIP-Time	Off
Save original images	On

Inline - Composing

Distortion Corr.	On
Mode	3D
Unfiltered images	Off

Sequence – Part 1

Introduction	On
Dimension	3D
Elliptical scanning	Off
Reordering	Linear
Asymmetric echo	Off
Flow comp.	No
Multi-slice mode	Single shot
Echo spacing	7.1 ms
Bandwidth	240 Hz/Px

Sequence – Part 2

RF pulse type	Fast
Gradient mode	Normal
Excitation	Non-sel.
RF spoiling	On
Incr. Gradient spoiling	Off
Turbo factor	208

Sequence – Assistant

Mode	Off

150 parameters/sequence x 7 sequences/exam = 1050 parameters/exam

MR in clinical trials/ADNI environment

site certification- propose same for SCAN

- Send and load protocol by efile
- Scan on phantom/human volunteer
- QC – did site execute protocol correctly
- Certify site – one scanner per site

MR in clinical trials/ADNI environment

participant exam - propose same for SCAN

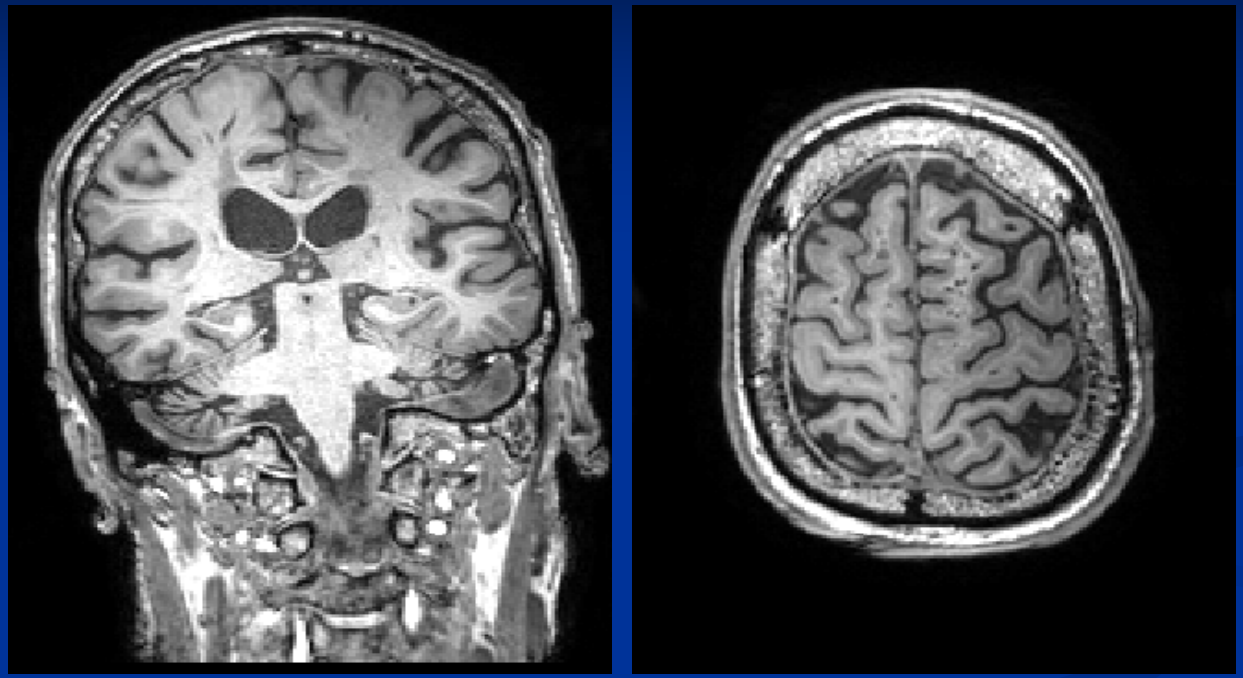
- Scan participant, send to central repository, pull by Mayo
- Automated QC
  - Correct (certified) scanner
  - Correct patient (serial)
  - protocol correctly executed – DICOM check parameters
    - ~ 1000 parameters to check per exam

MR in clinical trials/ADNI environment

Manual review of images in each exam - propose same for SCAN

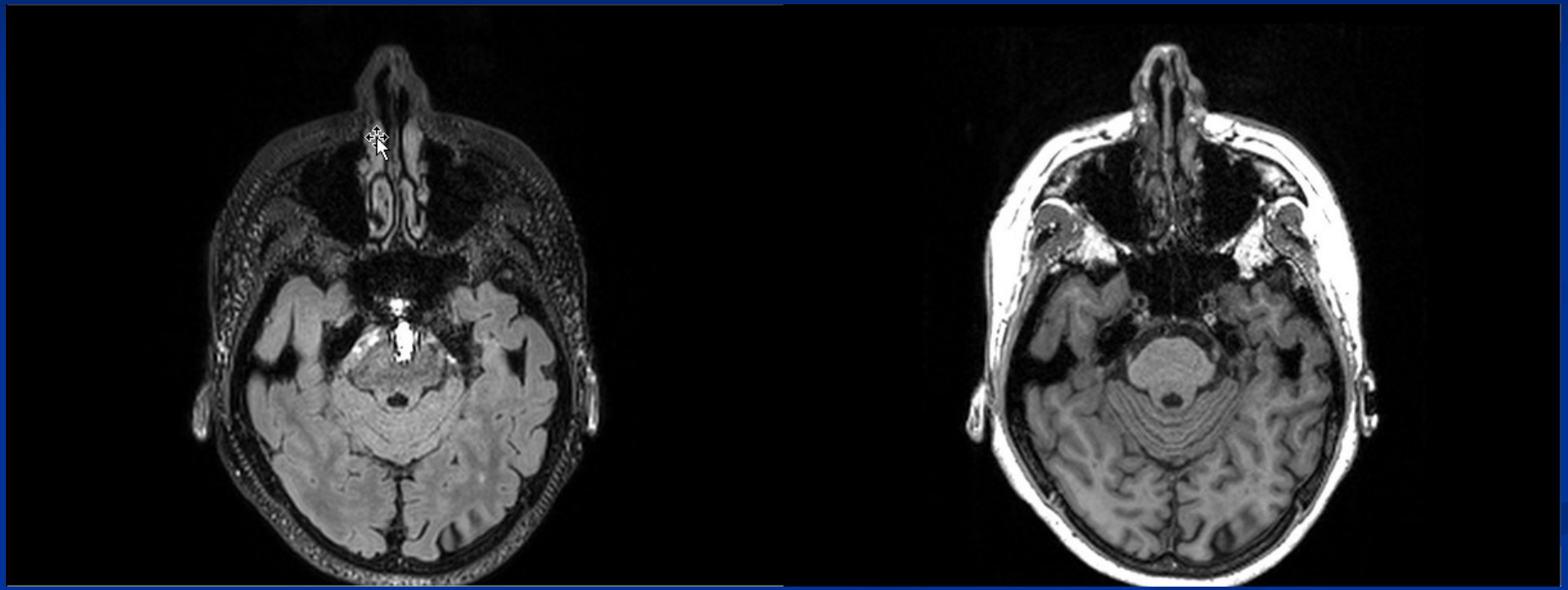
- Medical findings – safety – notify site/study if needed
  - Local MR interpretation still needed
- Visual QC
  - Scanner problem – eg. SNR, coil drop out
  - Tech errors – eg. copy FOV prescription error, intensity normalize off
  - Quality – e.g. motion

Coil Drop Out

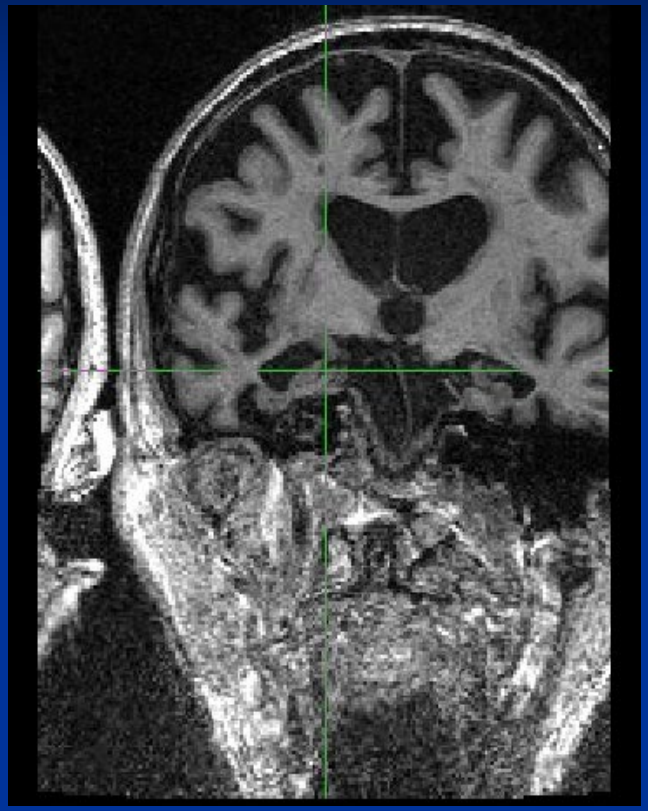


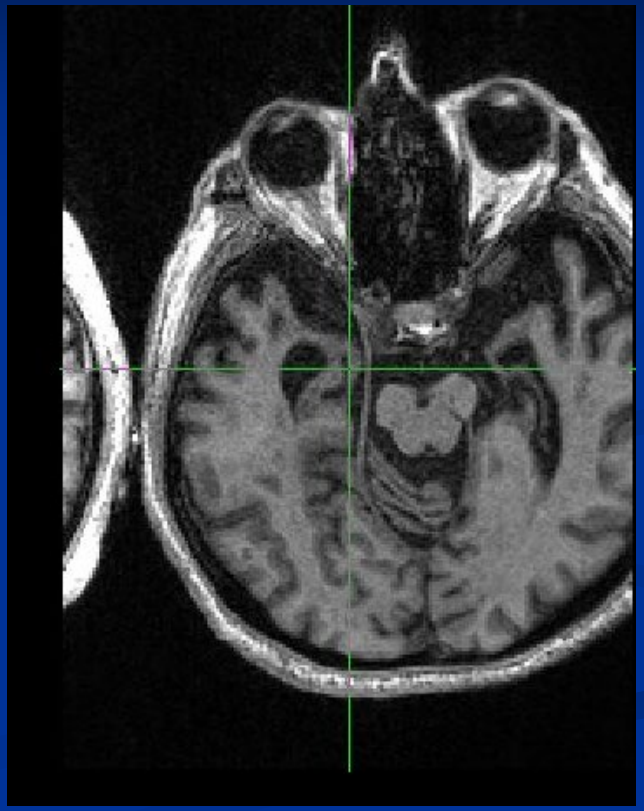
inhomogeneity due to bad element in multi-channel head coil

Wrong acquisition plane

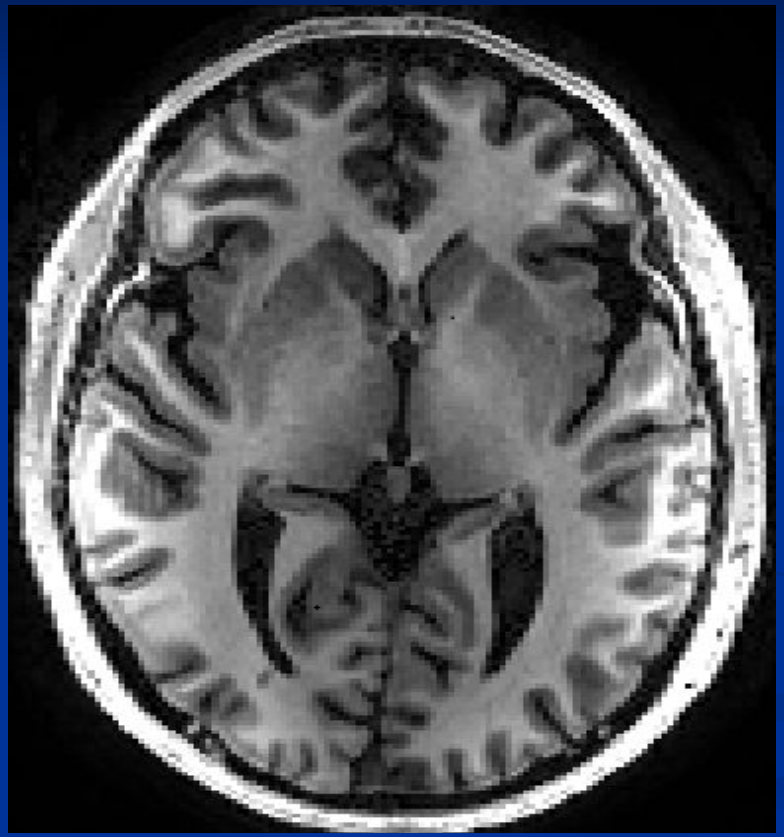


Copy FOV Prescription Error





Intensity Normalization - Off



Plan for SCAN

- Front end (up to image analysis) - Mayo
- Image analysis – DeCarli and Mayo
- Image analysis – create numeric information, send to NACC
  - WMH volume calculation (FLAIR)
  - ROI-wise cortical volume thickness

How to operationalize MR for SCAN

- Some aspects of clinical trial/ADNI operationalization may be problematic for SCAN
  - One certified scanner per site
    - Scans done on non certified scanners do not "count" in ADC tally
  - Pick best scanner at site for SCAN
    - OK for new imaging cohorts
    - Continue on current for established longitudinal imaging cohorts
  - protocol

ADNI 3 protocol ~ 1 hr (45 min gradient time)

- 3D T1 volume
- 3D FLAIR
- T2* GRE (3 echoes for Siemens – QSM)
- ASL
- TF-fMRI –advanced (SMS) or basic versions
- dMRI – advanced (SMS) or basic versions
- Coronal high resolution T2 – for hippocampal subfields

Inherent conflict

- require everyone to do exactly the same protocol
  - study-wide harmonization
- Free form
  - innovation, flexibility and consistency at site level

SCAN protocol options

- No harmonization
  - Accept all data generated at sites using their existing protocols
- Rigid harmonization
  - Require all 7 exact ADNI sequences
- Compromise

Proposed compromise – site can choose

- #1) Site only required to do 2 ADNI sequences: T1 & FLAIR
  - First 10 minutes of exam belongs to NIA
  - Remainder of exam belongs to site
  - SCAN would only collect and analyze T1 (enables ATN) and FLAIR
- #2) OR site may do T1, FLAIR & add'l ADNI sequences
  - esp. sites that have do not now have a formal ADC imaging program
  - SCAN would collect and analyze all sequences

Option 1: SCAN protocol

- 3D T1 volume
- 3D FLAIR

- Site specific sequences

Option 2: SCAN protocol

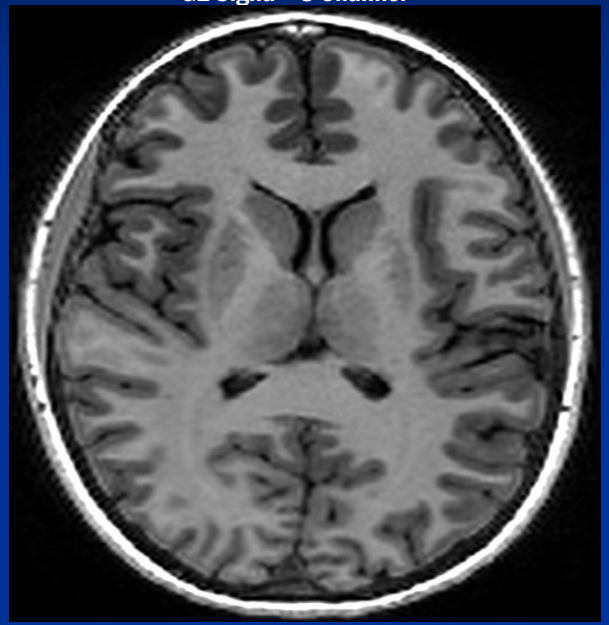
- 3D T1 volume
- 3D FLAIR

Options for SCAN standards

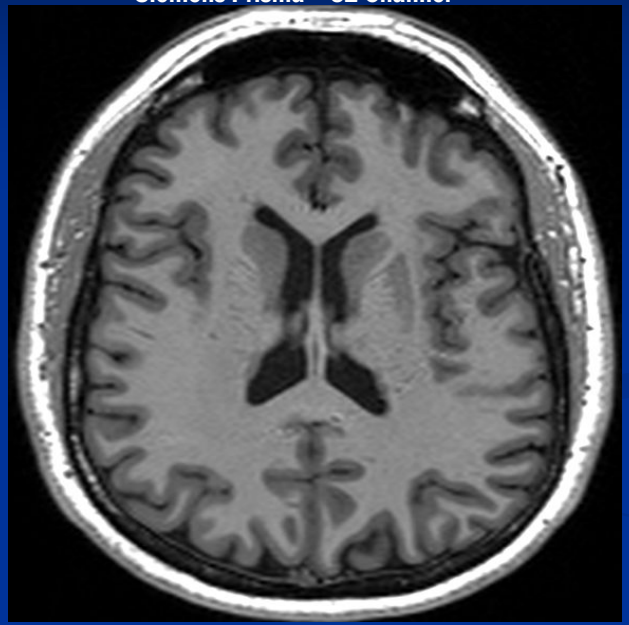
- T2* GRE
  - 2D GRE vs SWI/SWAN vs multi echo P/F QSM, SWI (Siemens and Philips >5X) ?
- dMRI – advanced (SMS) or basic versions ?
- ASL – 3D only
- TF-fMRI – advanced (SMS) or basic versions ?
- Coronal high resolution T2 – for hippocampal subfields ?

Limitations to harmonization

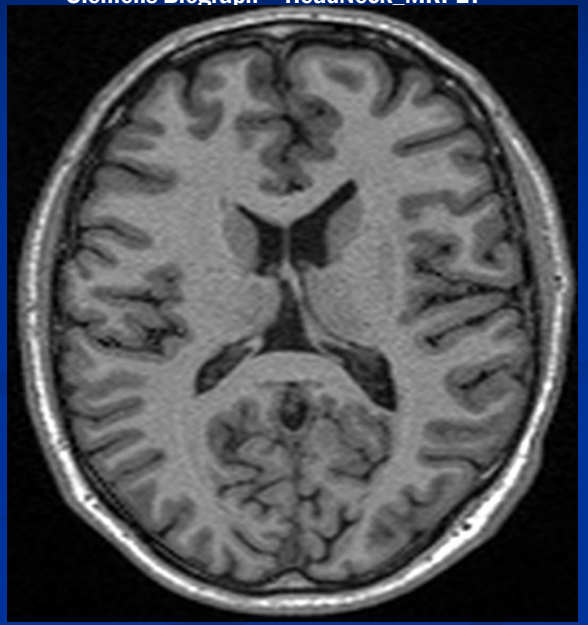
GE Signa - 8 Channel



Siemens Prisma – 32 Channel

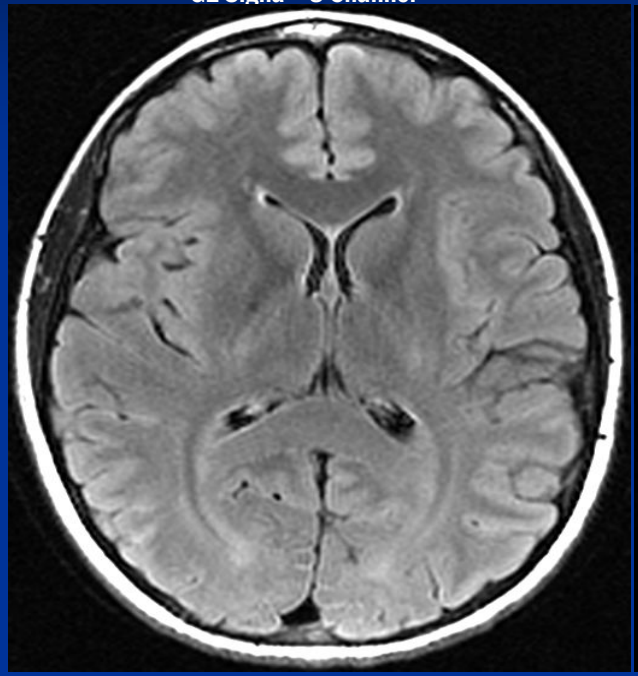


Siemens Biograph – HeadNeck_MRPET

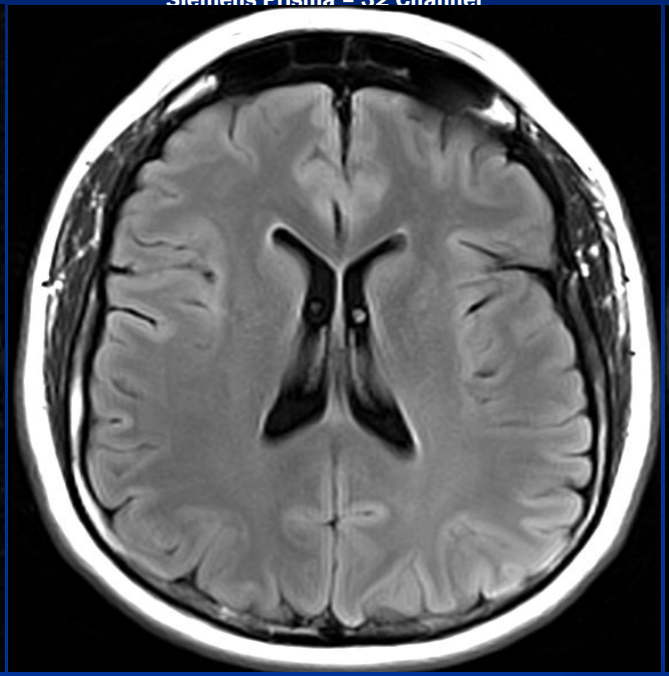


Limitations to harmonization: FLAIR

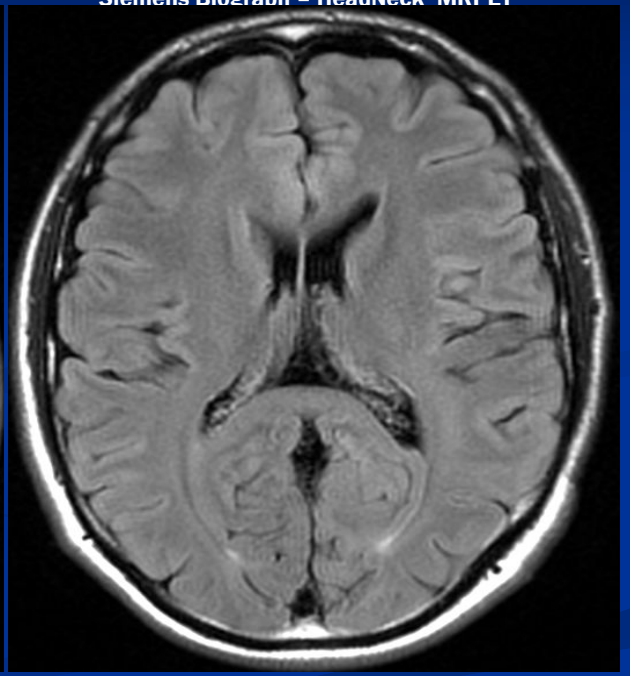
GE Signa - 8 Channel



Siemens Prisma – 32 Channel

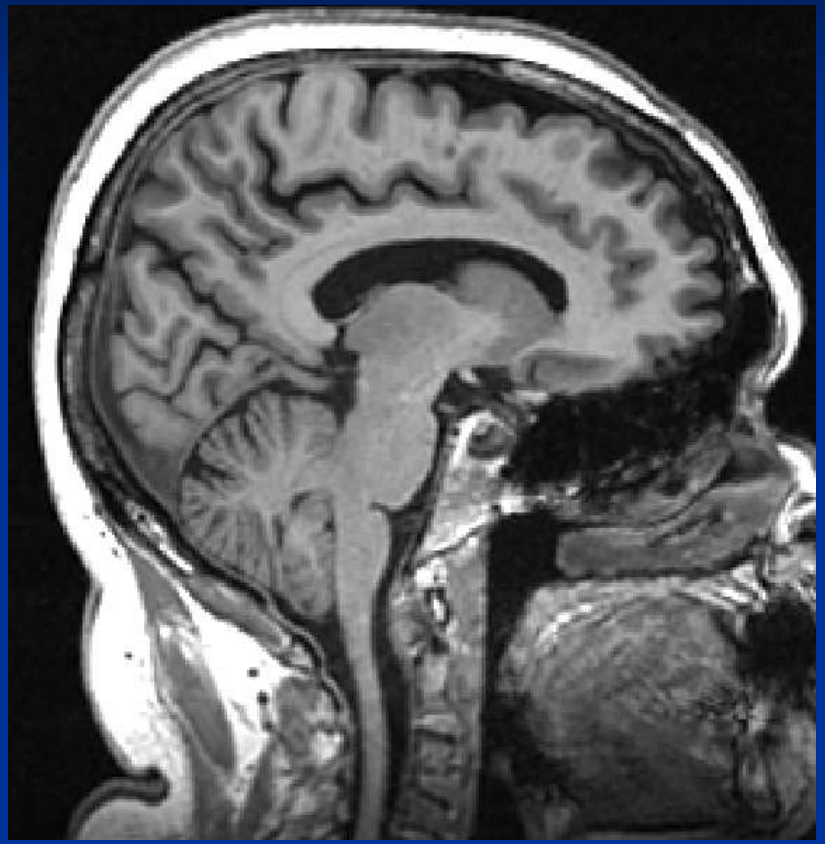


Siemens Biograph – HeadNeck MRPET

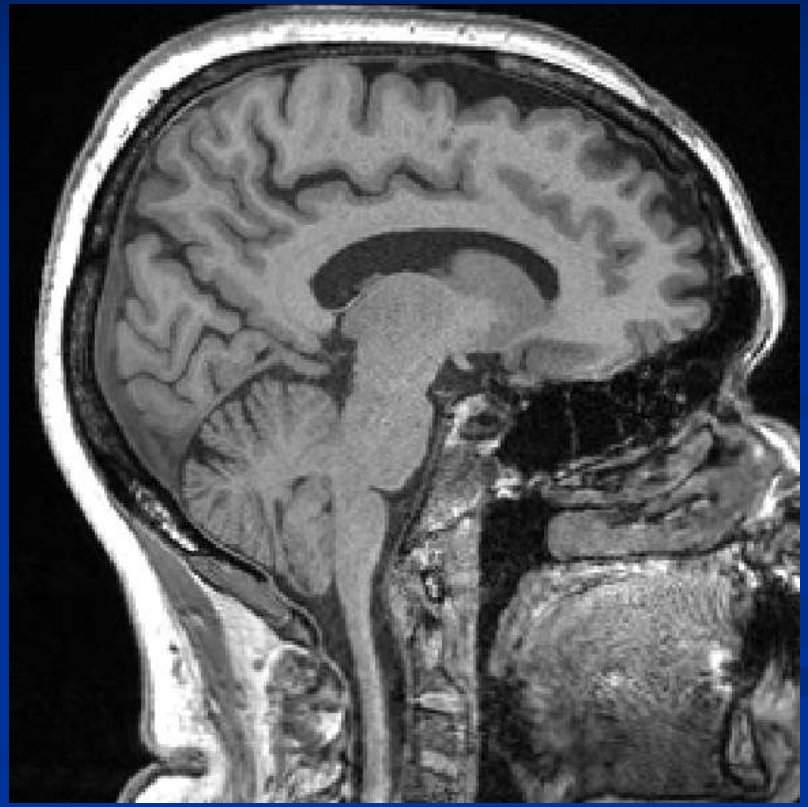


Same volunteer: effect of manufacturer/ parameters on cortical segmentation – Gunter

GE

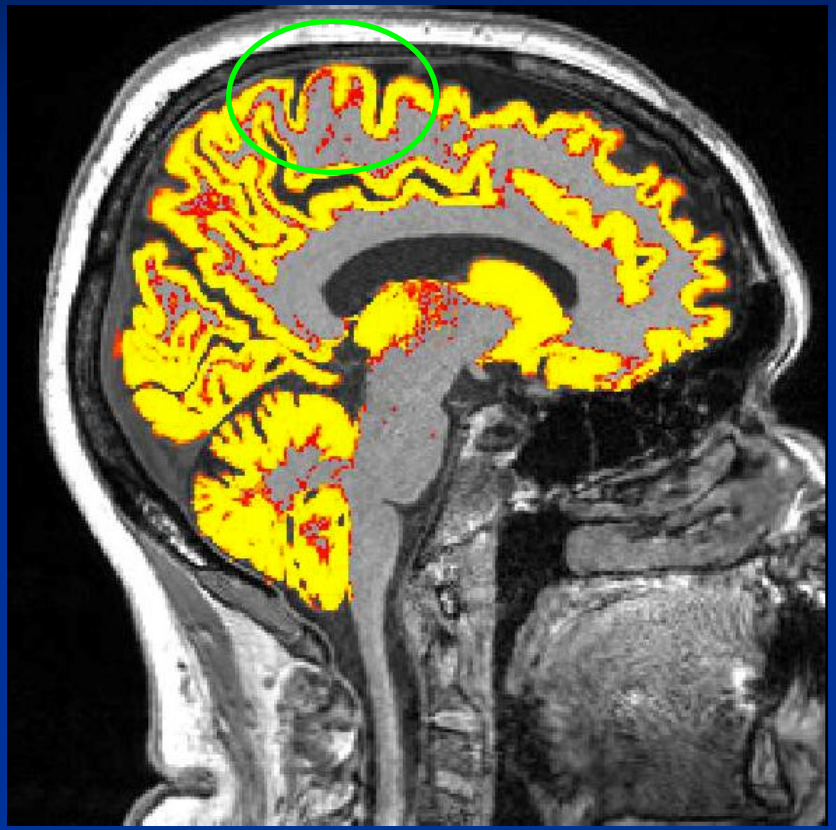


Siemens



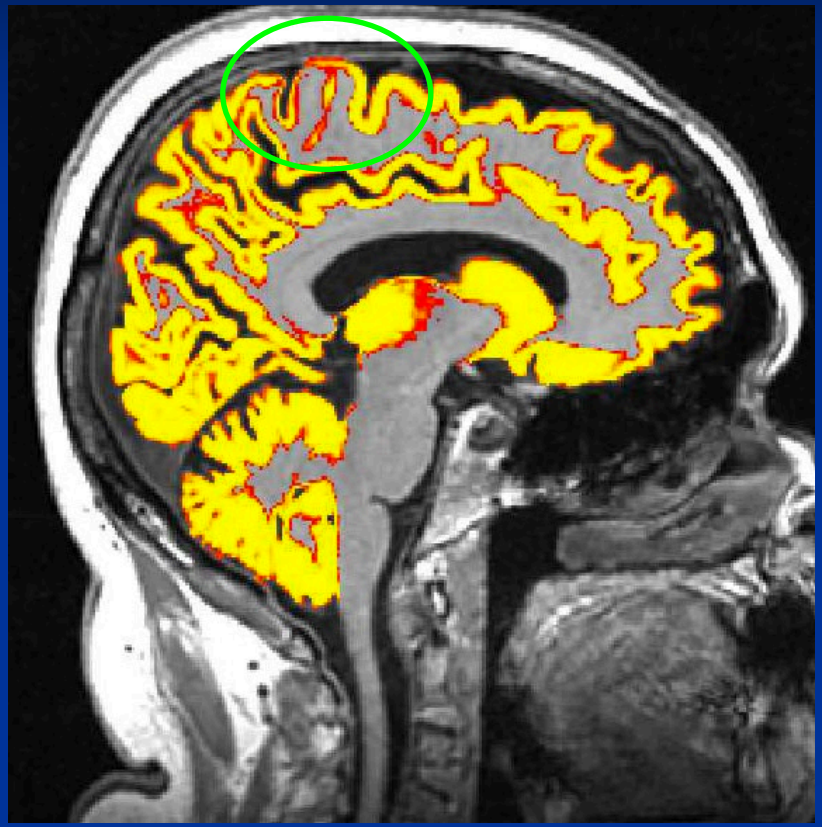
Siemens

Yellow = cortical ribbon segmentation



GE

Yellow = cortical ribbon segmentation



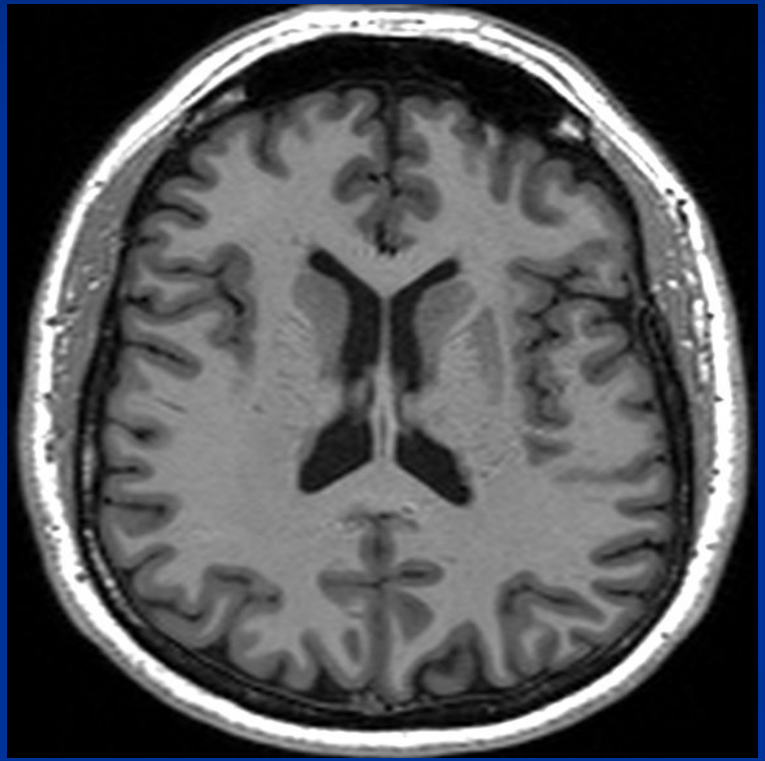
Solutions to data heterogeneity
Paul Thompson

1. Meta-analysis of effects from each site (early ENIGMA)
2. Fit the site/scanner effect using random effects regression (needs centralized data)
3. Use ComBat to adjust data histograms before pooling across sites/scanners
4. Use Variational Autoencoder (site free data+site code) with Generative Adversarial Networks that make it hard to tell which site the data came from (Moyer et al., Magn Res Med 2020)

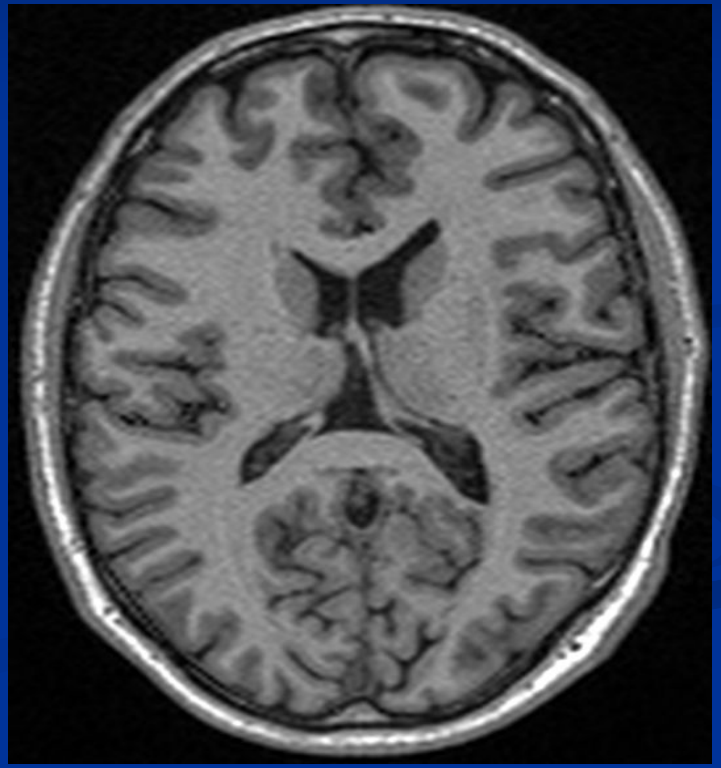
https://www.youtube.com/watch?v=KI3nRPFLqps&feature=youtu.be&t=898

Site may want to optimize sequence for their scanner: e.g. SNR resolution trade off

Better SNR



Worse SNR

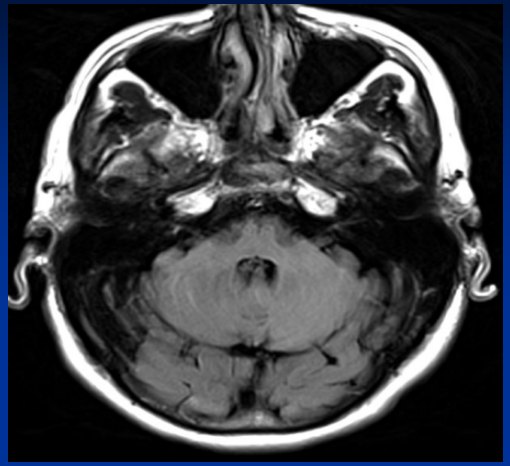


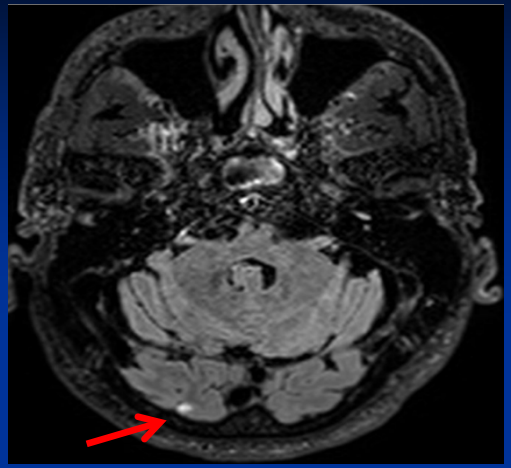
2D FLAIR Compared to 3D FLAIR Infarction Detection

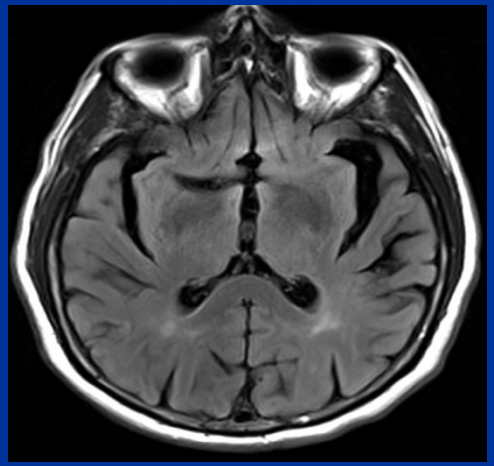
Same person for All Images

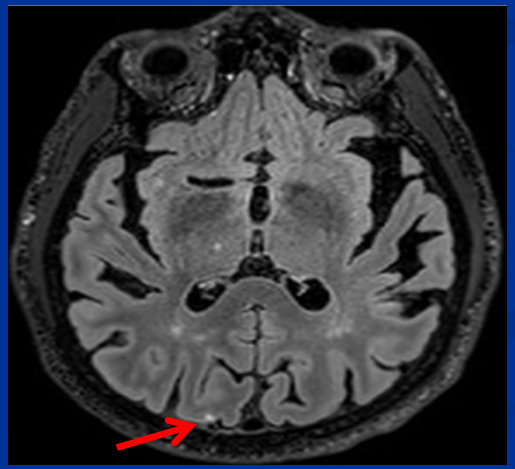
2D FLAIR

3D FLAIR









Site may want to keep protocol constant over time

Possible evolution of SCAN/ADC protocol

- Multi shell DTI
- high resolution 3D T2 -perivascular spaces
- circle of Willis MR angiogram
- Multi echo read out GRE – SWI/QSM