

Phantom QA Results: 32 CH

Date:01/09/2017

Dartmouth Brain Imaging Center (DBIC)

| Measurement | Value | Comments |
|---|-------|--|
| Signal-to-Noise Ratio (SNR) (fig 2) | 250.4 | |
| Signal-to-Fluctuation-Noise ratio (SFNR) (fig 2) | 252.1 | |
| Radius of Decorrelation (RDC) (fig 3) | 10.0 | |
| Drift (fig 1) | 0.28 | |
| Percent Fluctuation (fig 1) | 0.04 | |
| Fourier analysis of the residuals (fig 2) | <2 | |
| Ghost Mean Percentage (fig 10) | 2.52% | Better than the recommended level (3% <) in ref 2: |

Table 1: Key measurements

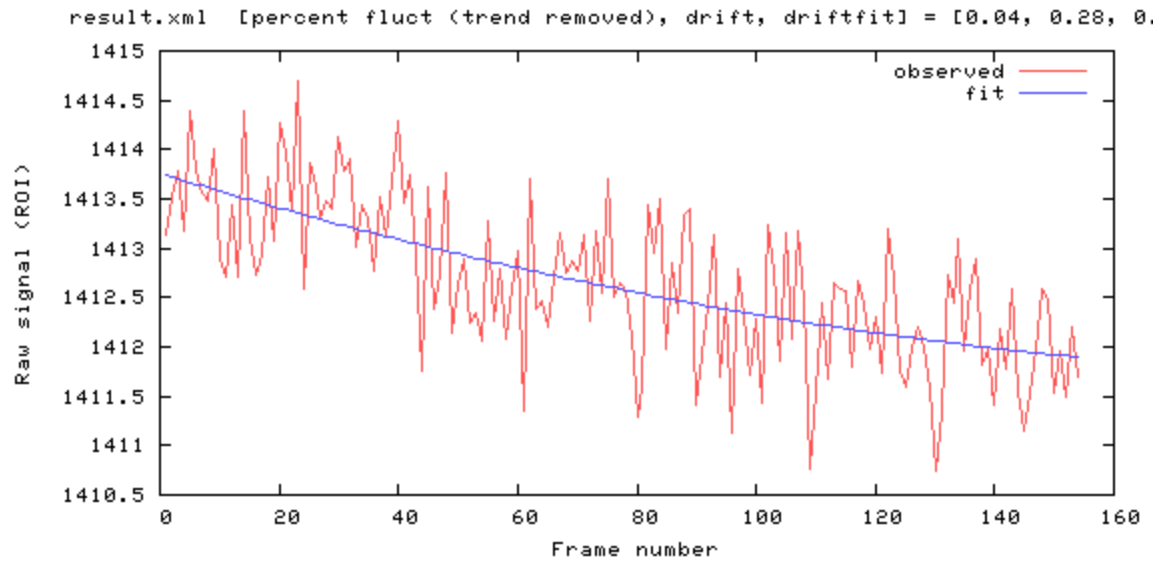


Figure 1

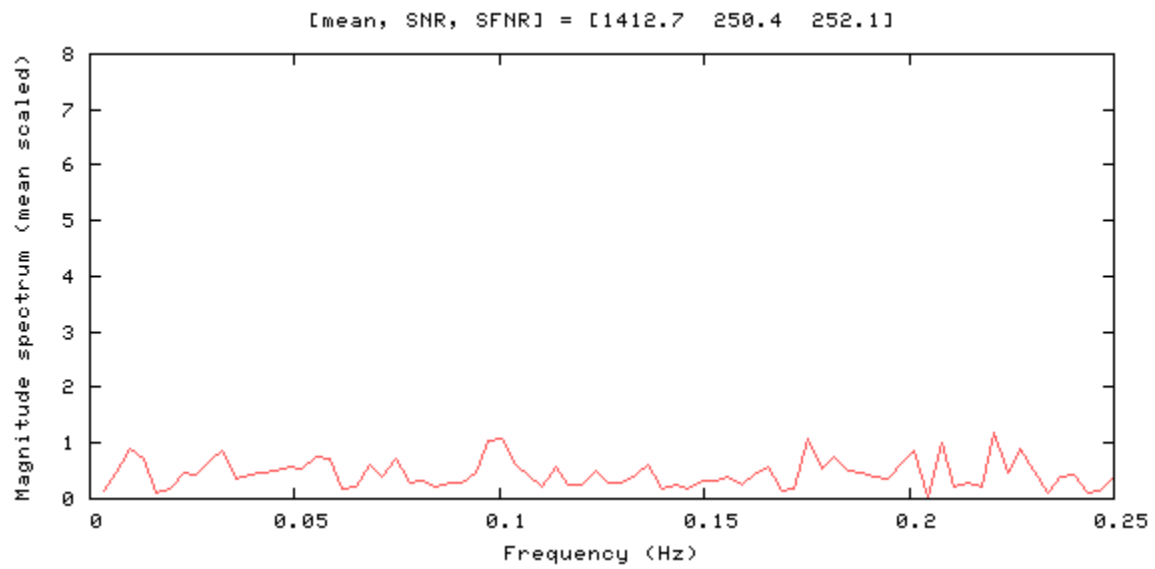


Figure 2

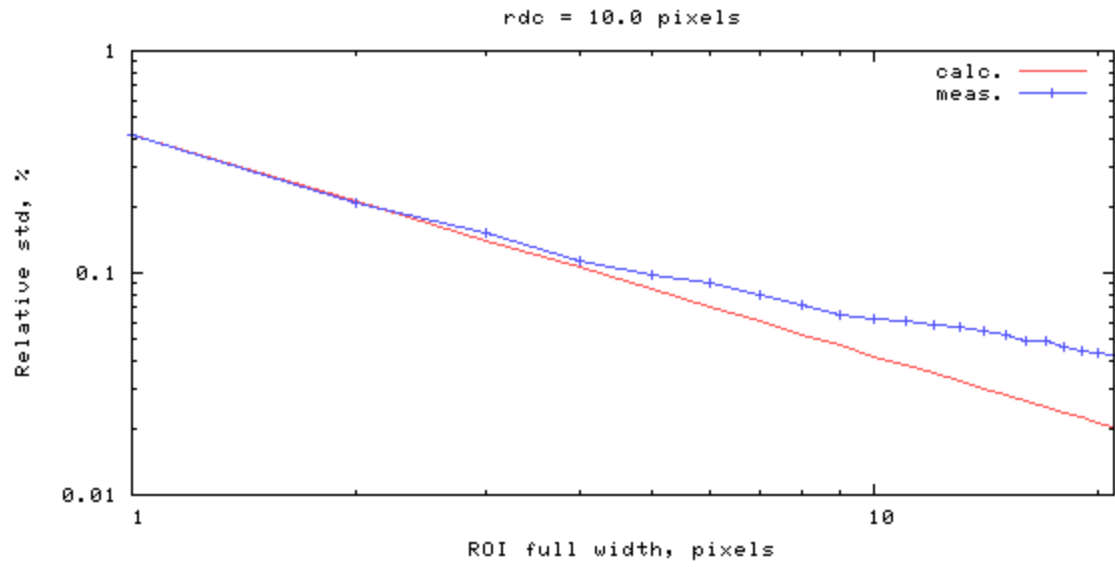


Figure 3

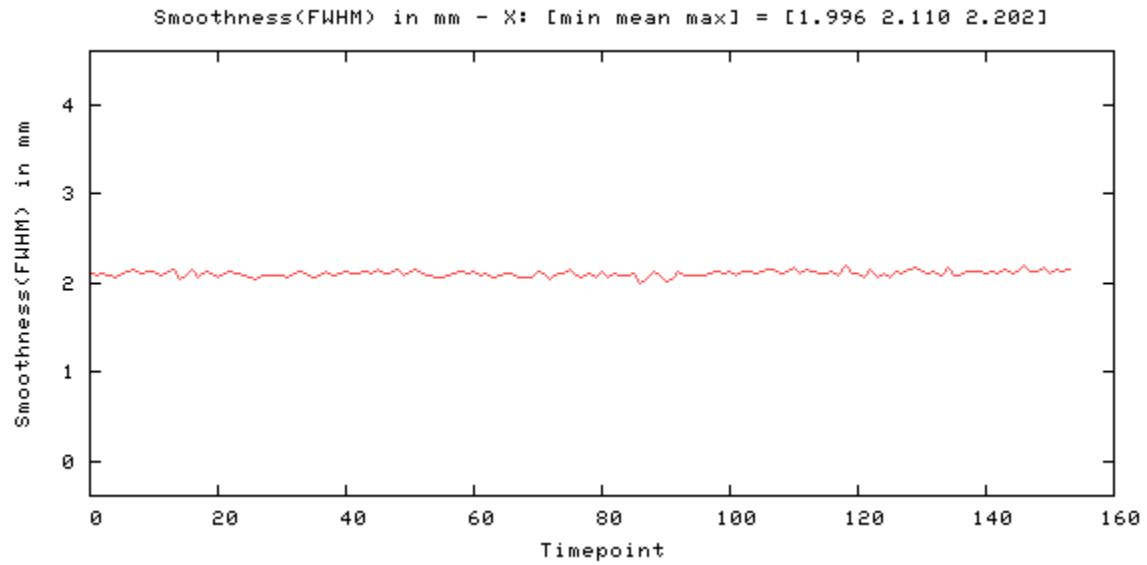


Figure 4

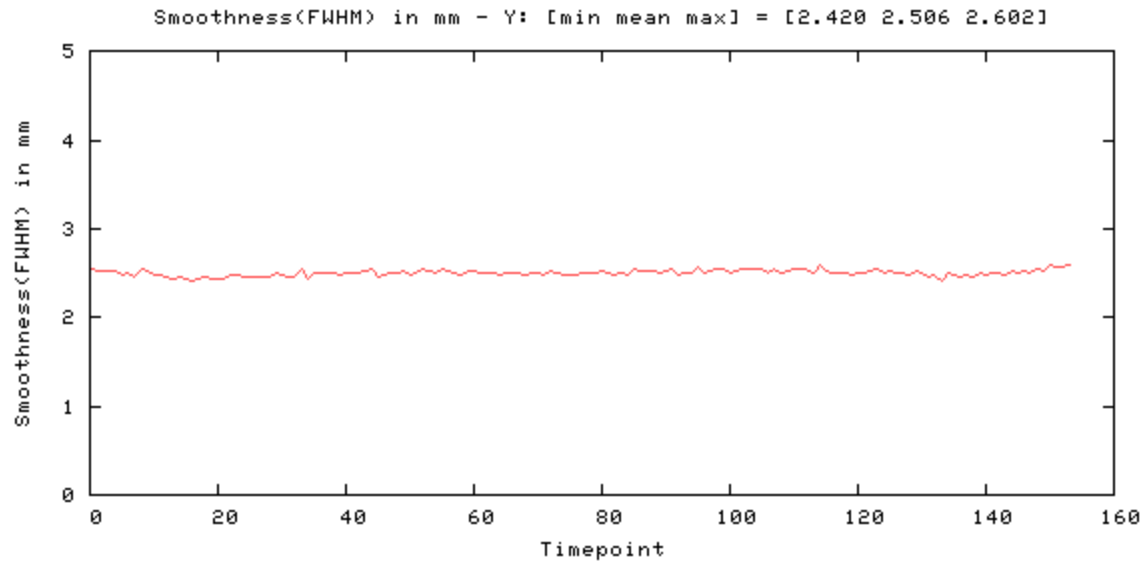


Figure 5

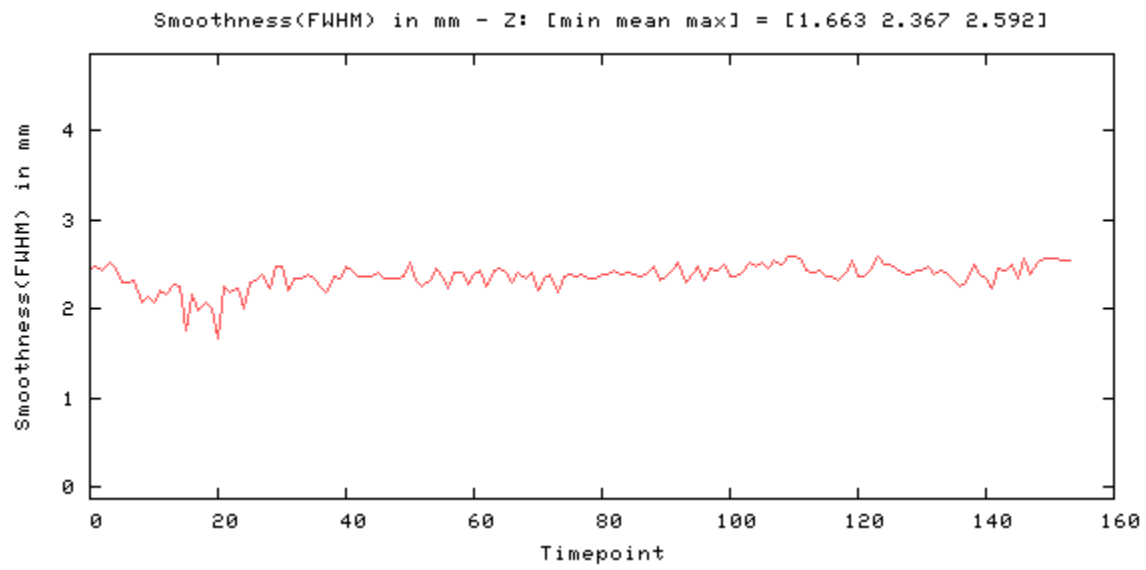


Figure 6

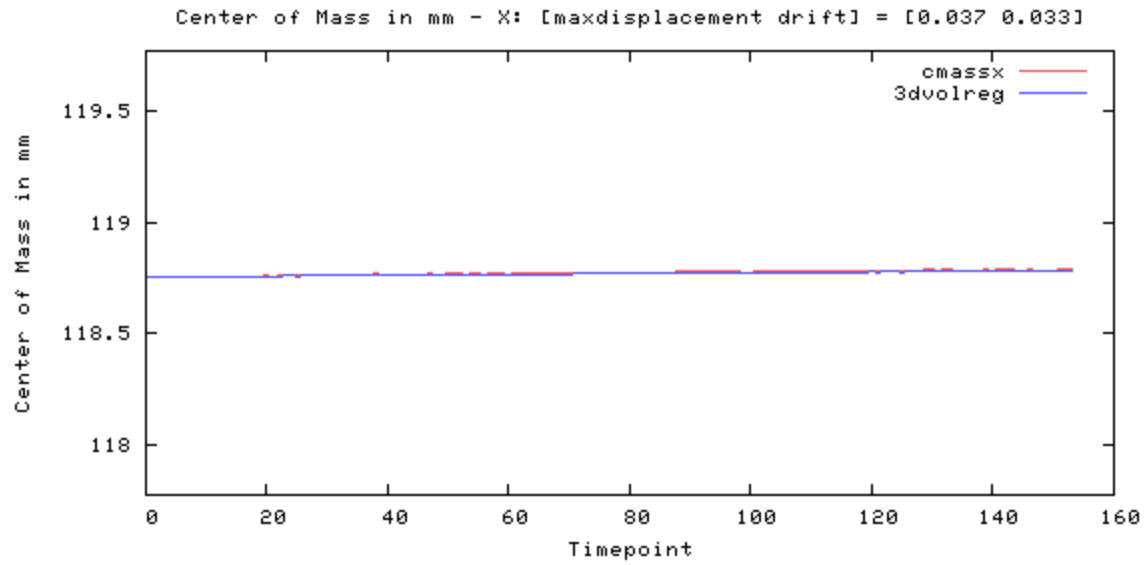


Figure 7

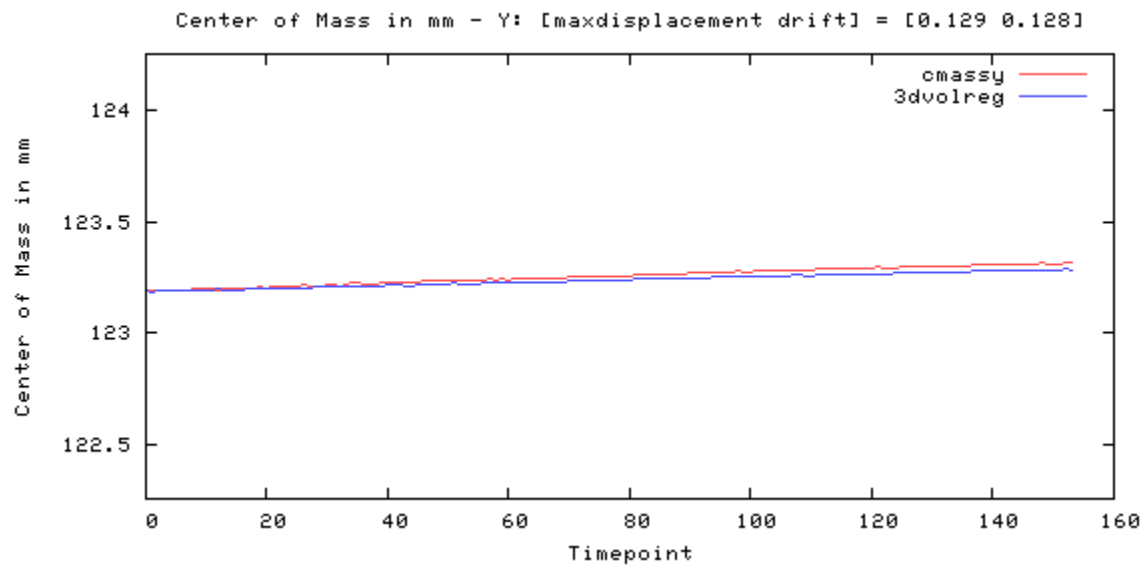


Figure 8

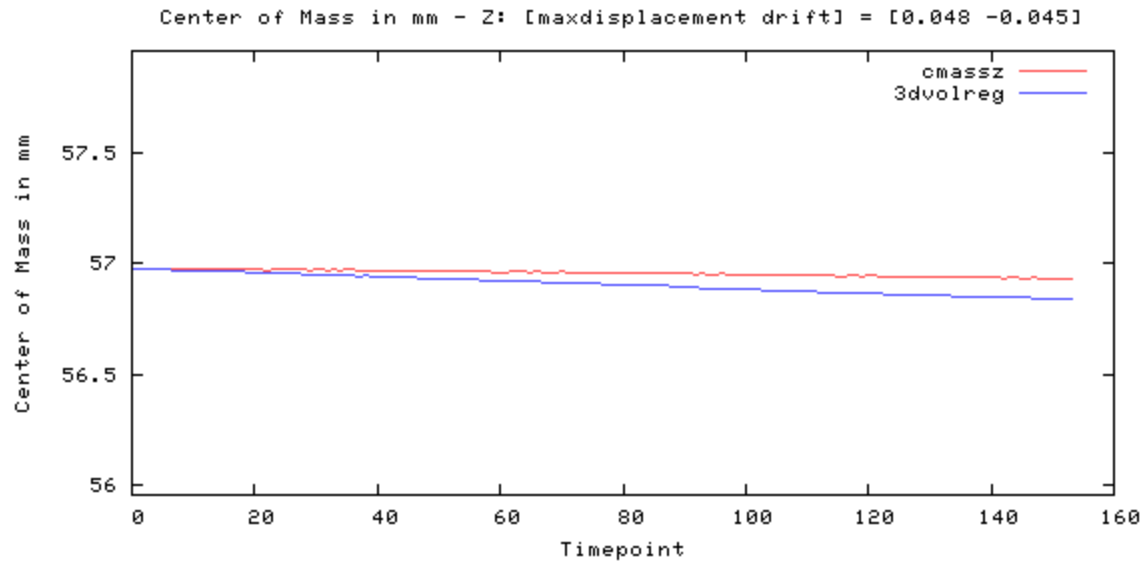


Figure 9

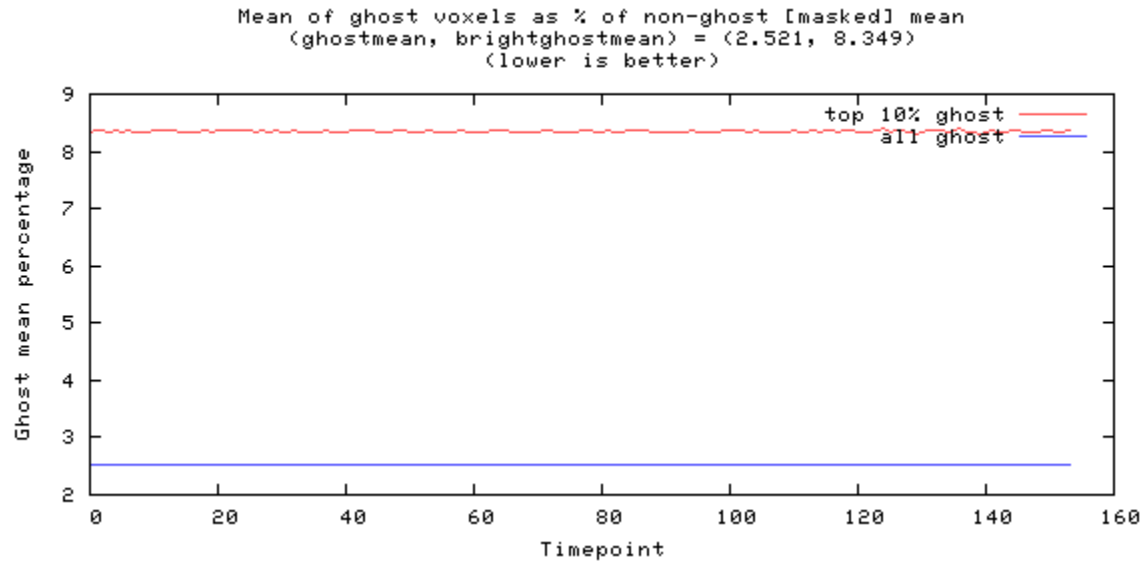


Figure 10

Odd-even difference image



image min: -190, image max: 207

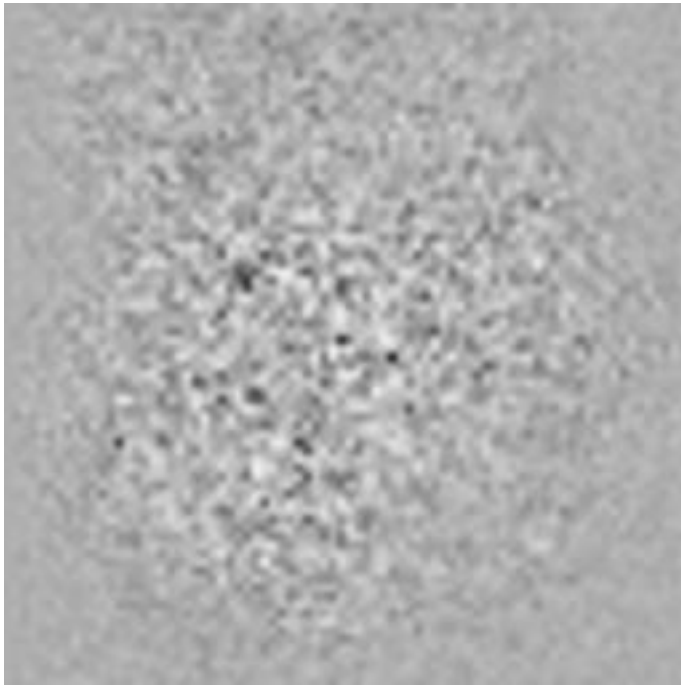


Figure 11

Mean image



image min: 0, image max: 2153.74

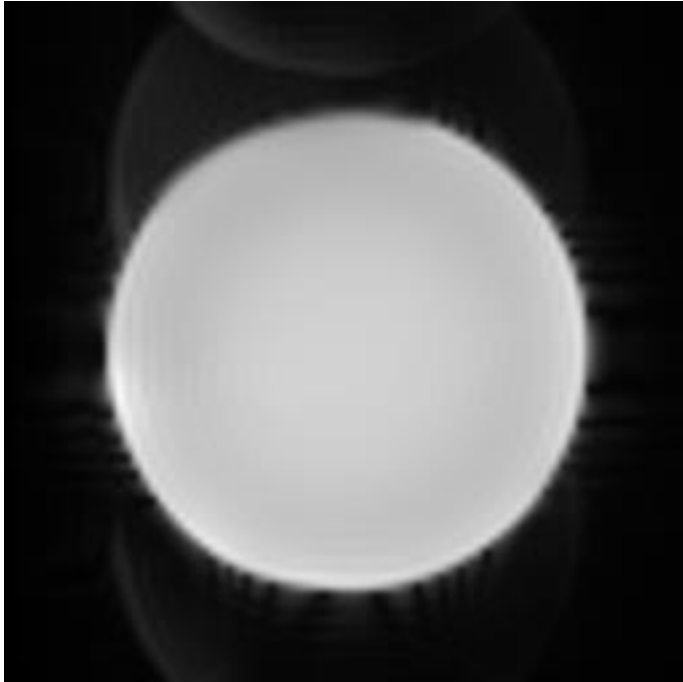


Figure 12

Standard Deviation image



image min: 0, image max: 8.48059

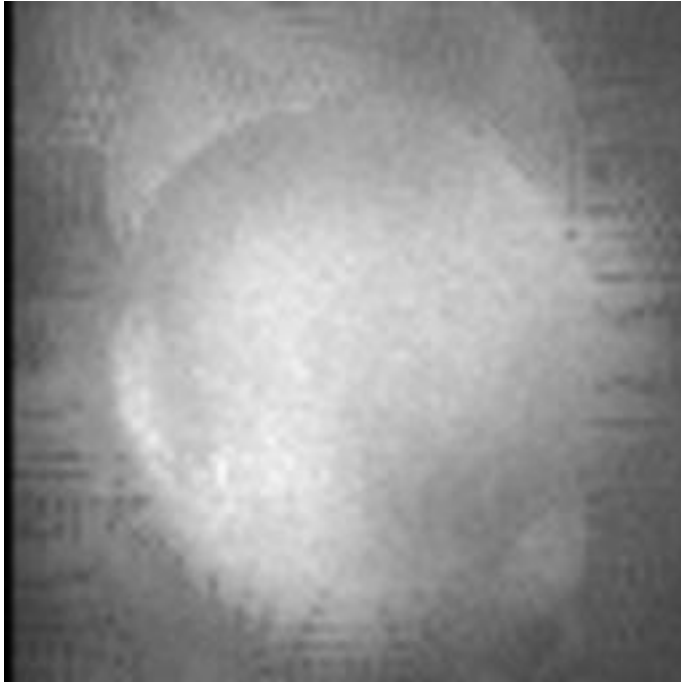


Figure 13

SFNR image



image min: 0, image max: 853.492

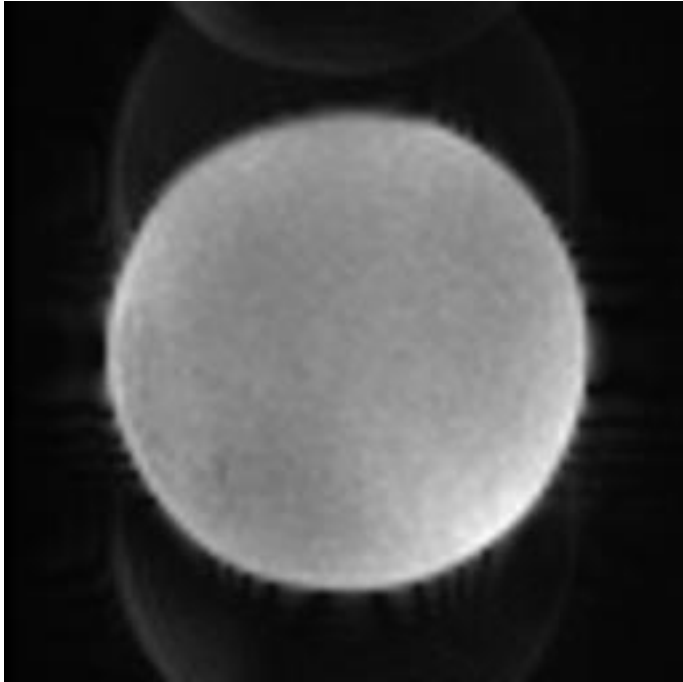


Figure 14

Acquisition parameters

| | |
|------------------------|-------------------------|
| dimensions | 80x80x30x157 |
| spacing | 3mmx3mmx3.99mmx2000ms |
| gap | 0mmx0mmx0.49mmx0ms |
| scanner | AWP66112 |
| psdname | %SiemensSeq%\ep2d_bold |
| examnumber | 20 |
| studyid | QA |
| seriesnumber | 5 |
| runnumber | 1 |
| scanningsequence | EP |
| sequencevariant | SK |
| magneticfield | 3 |
| description | BOLD_p2 |
| scandate | 2017-01-09 |
| scantime | 10:28:21 |
| tr | 2000 |
| te | 35.000000 |
| flipangle | 90 |
| prescribedslicespacing | 3.99 |
| frequencydirection | 1 |
| acquisitionmatrix | 80 80 |
| bandwidth | 185.2 |
| transmitcoilname | Body |
| institution | Dartmouth College - PBS |
| examdescription | dbic^QA |
| scanner | AWP66112 |
| scannermanufacturer | SIEMENS |
| scannermodelname | Prisma |
| fieldofview | 240 240 |
| psdname | %SiemensSeq%\ep2d_bold |
| protocolname | BOLD_p2 (BOLD_p2) |

| | |
|--------------------------------|-------------------------------|
| institutionaddress | Maynard 3,Hanover,NH,US,03755 |
| institutionaldepartment name | Department |
| scanoptions | FS |
| mracquistiontype | 2D |
| sequencename | *epfid2d1_80 |
| angioflag | N |
| numaverages | 1 |
| imagingfrequency | 123.252535 |
| imagednucleus | 1H |
| spacingbetweenslices | 3.9900001720566 |
| numphaseencodingsteps | 79 |
| echotrainlength | 39 |
| percentsampling | 100 |
| percentphasefieldofview | 100 |
| scannerserialnumber | 66112 |
| softwareversions | syngo MR E11 |
| inplanephaseencoding direction | COL |
| variableflipangleflag | N |
| sar | 0.05572343375316 |
| dBdt | 0 |
| acquisitionnumber | 1 |
| instancenumber | 1 |
| samplesperpixel | 1 |
| photometricinterpretation | MONOCHROME2 |
| rows | 480 |
| columns | 480 |
| bitsallocated | 16 |
| bitsstored | 12 |
| highbit | 11 |
| pixelbandwidth | 2315 |
| otherinfo | |

| | |
|------------|--|
| sliceorder | 2,4,6,8,10,12,14,16,18,20,22,24,26,28,30,1,3,5,7,9,11,13,15,17,19,21,23,25,27,29 |
|------------|--|

References:

1. Friedman L, Glover GH. Report on a multicenter fMRI quality assurance protocol. J Magn Reson Imaging. 2006a; 23(6):827–839. [PubMed: 16649196]
2. Acceptance Testing and Quality Assurance Procedures for Magnetic Resonance Imaging Facilities, AAPM Report No. 100
3. https://www.nitrc.org/projects/bxh_xcede_tools