



# Vendor-Neutral Implementation of SNR-Efficient Fat Quantification in Pulseq

---

Jiayi Tang

Quantitative Imaging Methods Lab

Departments of Medical Physics and Radiology

University of Wisconsin-Madison





# Acknowledgements

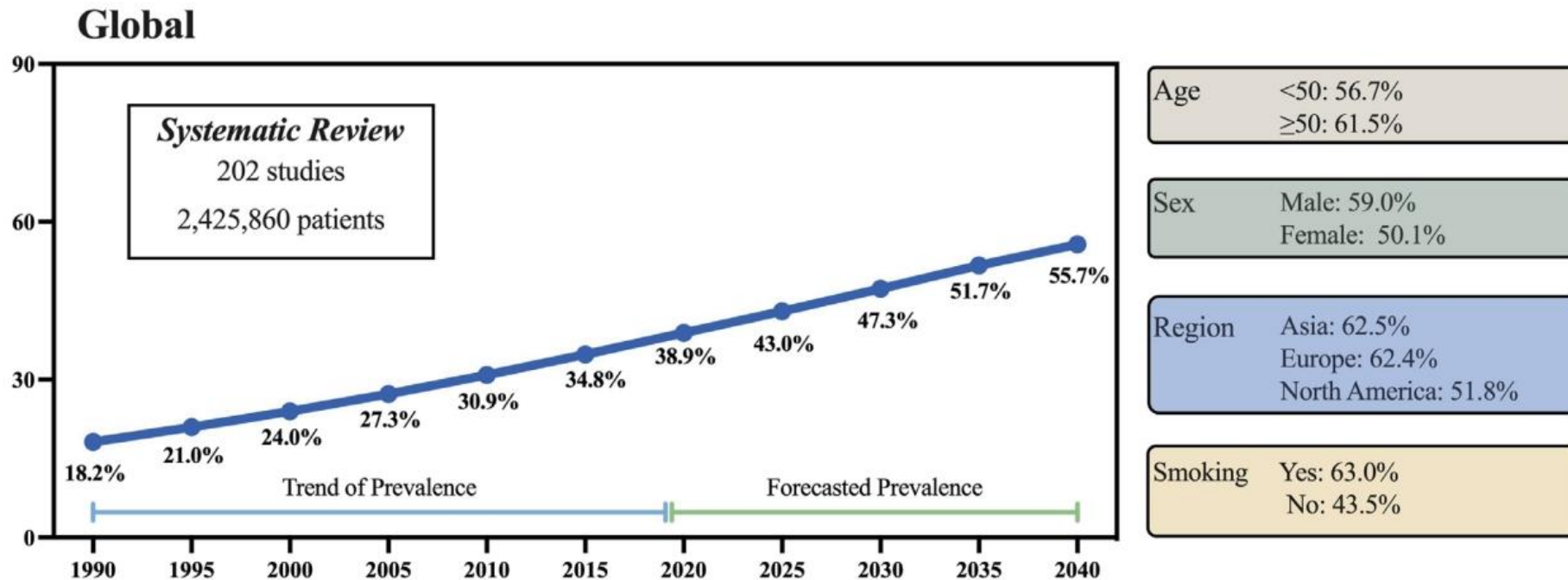
- UW-Madison
  - Daiki Tamada
  - Jitka Starekova
  - Alan McMillan
  - Scott B Reeder
  - Diego Hernando
- Martinos Center
  - Xingwang Yong
  - Yuting Chen
  - Shohei Fujita
  - Berkin Bilgic
- Calimetrix, LLC
  - Jeff Kammerman
  - Jean H Brittain
- U of Michigan
  - Jon-Fredrik Nielsen
- U of Freiburg
  - Maxim Zaitsev
- QIML/LIRP  
[qiml.radiology.wisc.edu](http://qiml.radiology.wisc.edu)
  - Collin Buelo
  - Sheena Chu
  - Garrett Fullerton
  - David Harris
  - Andrea Houck
  - Yavuz Muslu
  - Aidan Tollefson
  - Lucky Volety
- Ruiyang Zhao et al
  - Zhao R, Zhang Y, Wang X, et al. Motion-robust, high-SNR liver fat quantification using a 2D sequential acquisition with a variable flip angle approach. *Magn Reson Med*. 2020;84(4):2004-2017. doi:10.1002/mrm.28263

# Disclosures

- NIH grants R44EB025729 and R01EB031886
- Dr. Hernando and Dr. Reeder are co-founders of Calimetrix, LLC, which manufactured and loaned to the authors the phantom used for this study.
- Dr. Reeder is the John H. Juhl Endowed Chair of Radiology.
- Jiayi Tang is a shareholder of GE HealthCare.
- GE HealthCare provides research support to the University of Wisconsin.

# Motivation

## Forecasted NAFLD Prevalence in 2040

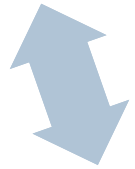


Motion-robust, accurate, **cross-vendor reproducible**  
MR-based fat quantification urgently needed

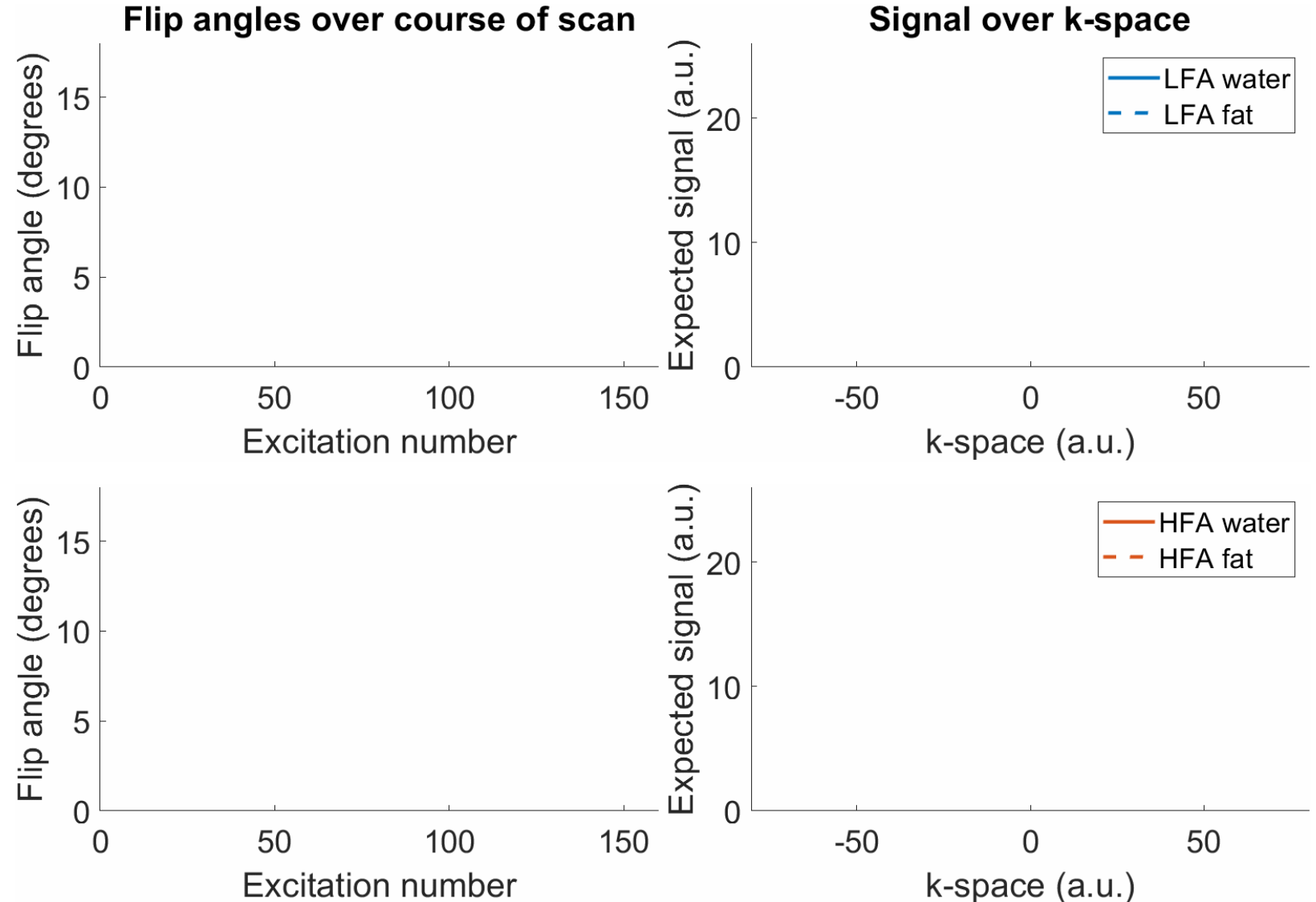
# Constant FA, Linear Encoding (Steady State)

2D sequential 6-echo spoiled gradient echo sequence

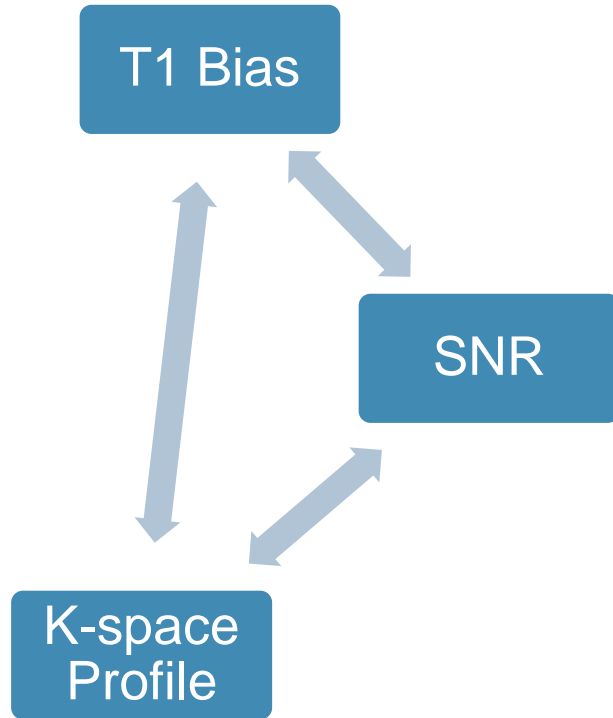
T1 Bias



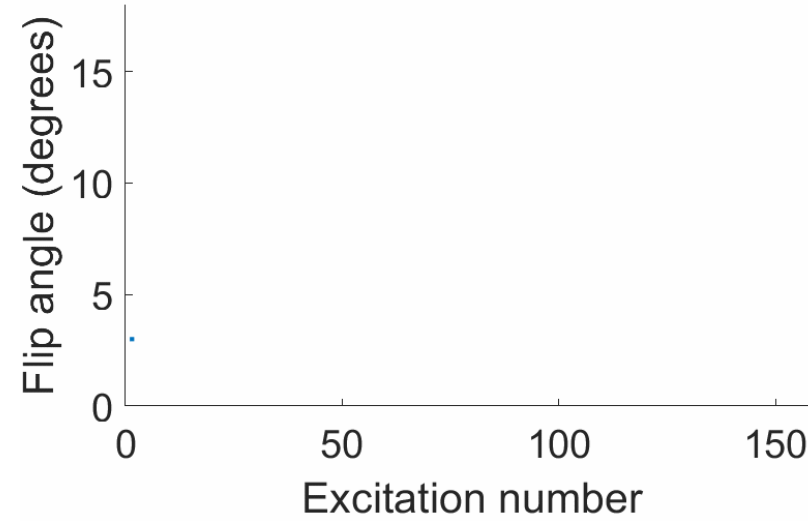
SNR



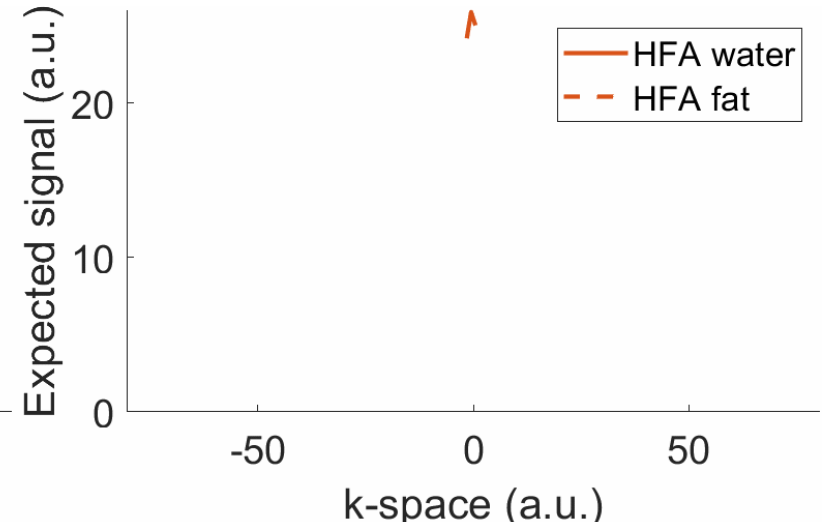
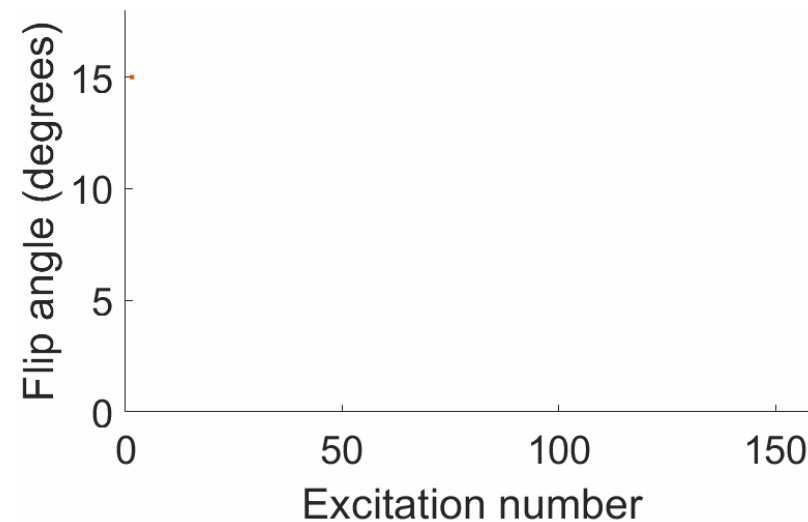
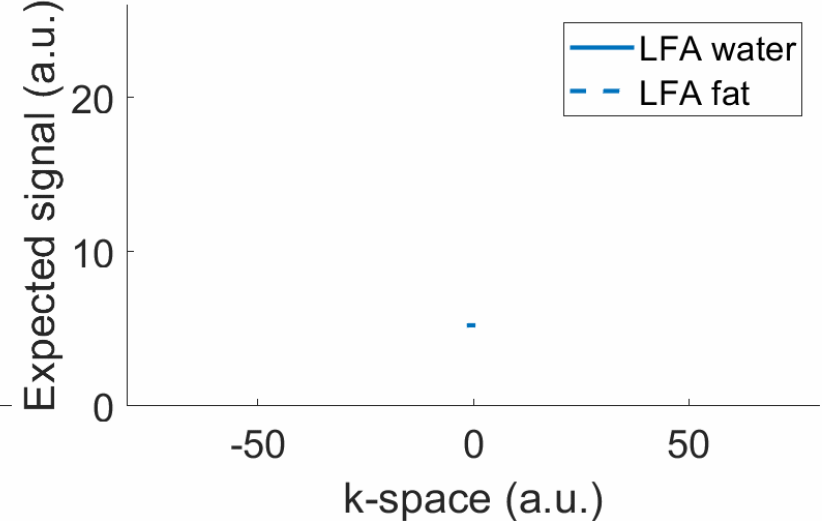
# Constant FA, **Centric Encoding** (Non-Steady State)



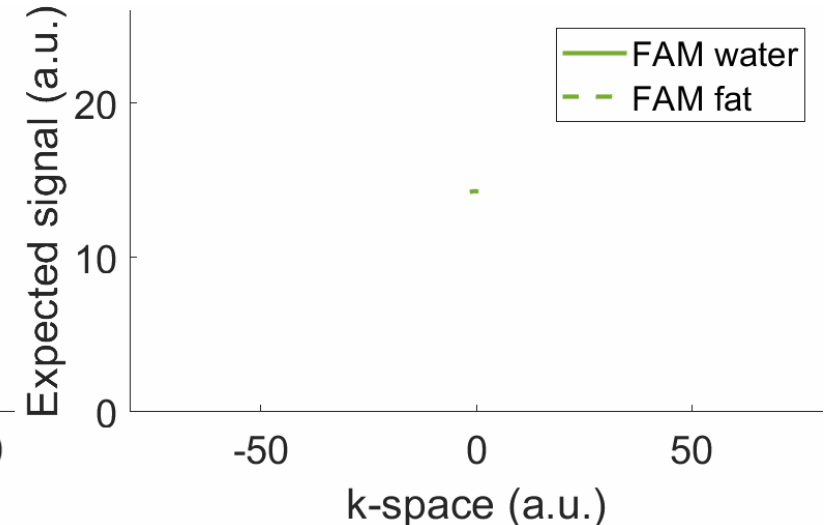
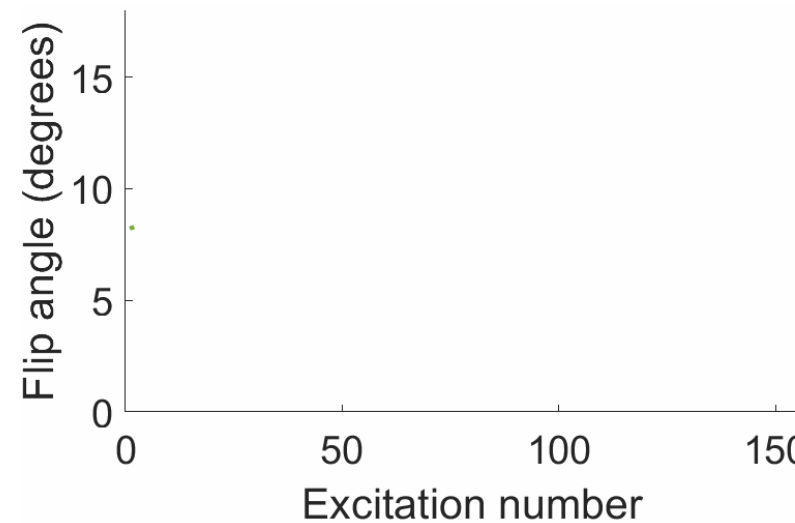
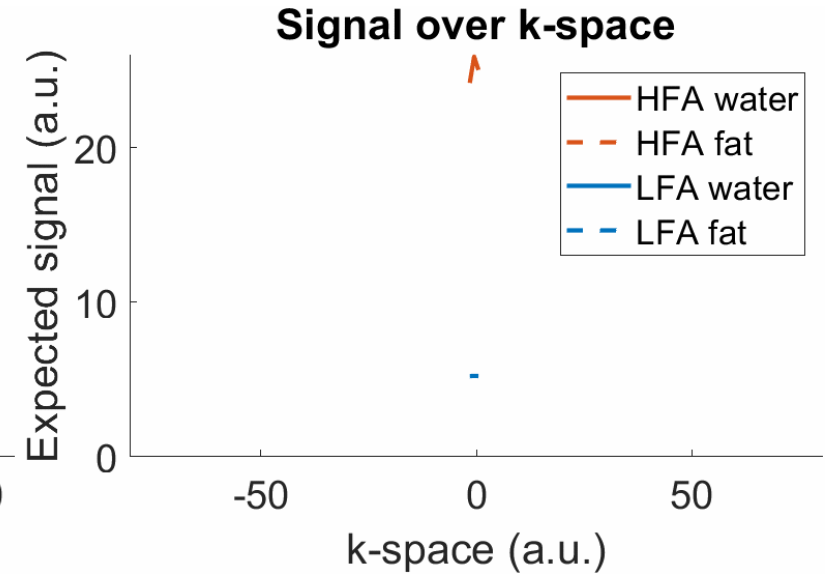
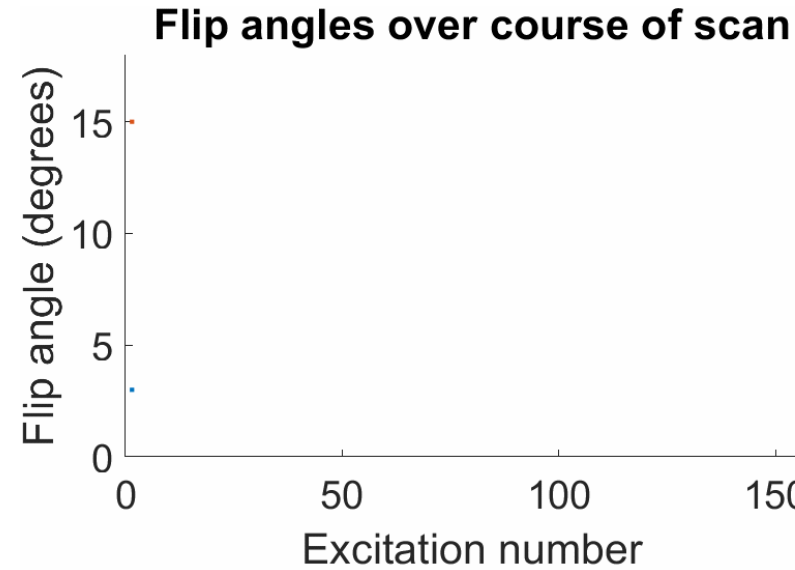
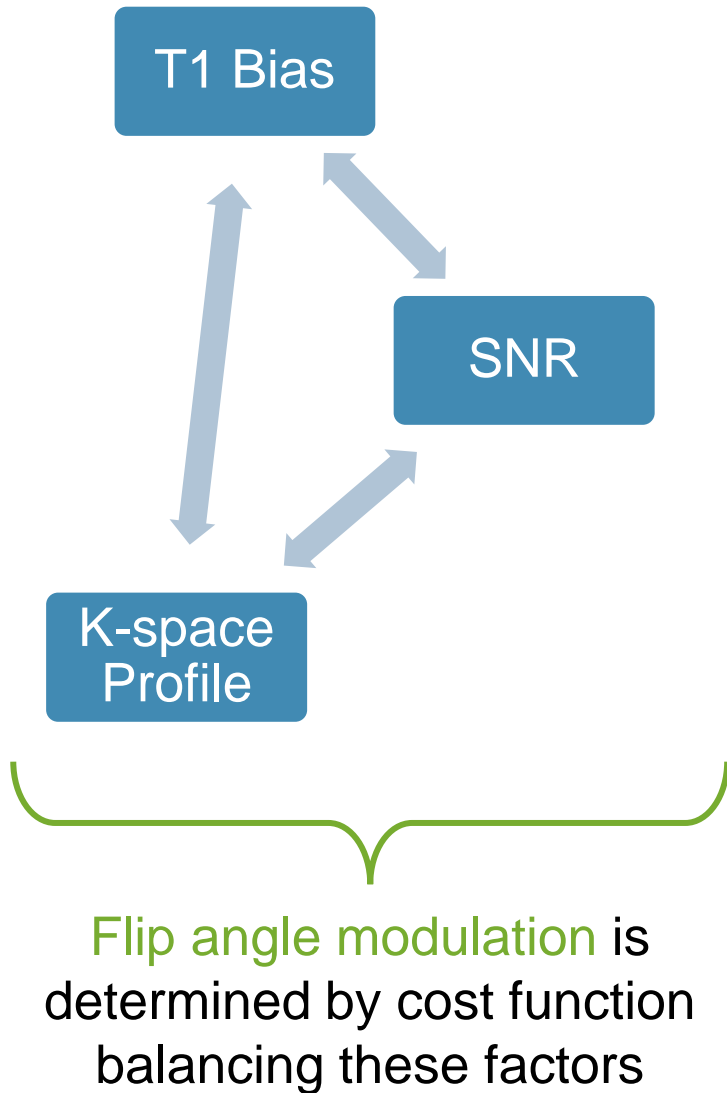
Flip angles over course of scan



Signal over k-space



# Flip Angle Modulation, Centric Encoding (Non-Steady State)





```
if FA_SCHEME == "v"
    fam_alphas = [ 9.17745046  9.26863982  9.36001542  9.45565493  9.54323117  9.63717383 ...
    9.71881626  9.81095649  9.88708398  9.97803693 10.04897537 10.13895461 ...
    10.20463764 10.29354696 10.35368694 10.44131505 10.49561803 10.58178627 ...
    10.63000632 10.71458573 10.75654003 10.83944674 10.87499766 10.95616004 ...
    10.98517414 11.06450891 11.08685388 11.16426104 11.179797  11.25515225 ...
    11.26372629 11.3368954  11.33836008 11.40919305 11.4034025  11.47175452 ...
    11.45857155 11.52429318 11.5036031  11.56654912 11.53825032 11.59828036 ...
    11.56228751 11.6192647  11.57551346 11.62930094 11.57774259 11.62821752 ...
    11.56882282 11.61586343 11.54863153 11.59212317 11.51706819 11.55691375 ...
    11.47408212 11.51019576 11.41966515 11.45197632 11.35385439 11.38231916 ...
    11.27674969 11.30134313 11.18850774 11.20923648 11.08935538 11.10625052 ...
    10.97958058 10.9927064  10.85954423 10.86899179 10.72966915 10.73556036 ...
    10.59044077 10.59292221 10.44240274 10.44164722 10.28614811 10.28235005 ...
    10.12231138 10.115683   9.95156309  9.94232983  9.77459298  9.76299006 ...
    9.59210564  9.57837584  9.40481165  9.38919749  9.21331334  9.19606455 ...
    9.0183434   8.99968503  8.82062638  8.80078979  8.62081667  8.60002103 ...
    8.41953837  8.39799767  8.21738969  8.19530071  8.01492841  7.99247797 ...
    7.8126774   7.79003545  7.61111636  7.58843817  7.41068654  7.38810925 ...
    7.21178416  7.18943146  7.01476457  6.99274054  6.81994028  6.79833525 ...
    6.62758367  6.606473   6.43793022  6.41737406  6.25117977  6.23122585 ...
    6.06749793  6.04818298  5.88702148  5.86837114  5.70986029  5.69189036 ...
    5.53610058  5.51881886  5.36580564  5.34921431  5.19902353  5.18311812 ...
    5.03578451  5.02055651  4.87610557  4.86154183  4.71999379  4.70607922 ...
    4.5674436   4.55416079  4.41844462  4.40577316  4.27297649  4.26089451];
    % optimized variable flip angles for res = 144, TR = 12 ms, field strength = 3T, no parallel imaging acceleration
elseif FA_SCHEME == "h"
    fam_alphas = repmat(15, [1 144]); % for high flip angle
elseif FA_SCHEME == "l"
    fam_alphas = repmat(3, [1 144]); % for low flip angle
else
    error("FA_SCHEME must be 'v', 'h', or 'l'")
end
```



```
if ENCODING_SCHEME == "1"
    peScales = peScales - (peScales(1) + peScales(end))/2;
elseif ENCODING_SCHEME == "c"
    peScalesTemp=peScales;
    peScales(1:2:end) = peScalesTemp(length(peScalesTemp)/2+1:end);
    peScales(2:2:end) = peScalesTemp(length(peScalesTemp)/2:-1:1); % rearrange for centric encoding
    peScales = peScales + peScales(3)/2; % to make the k-space sampling along PE direction symmetric
else
    error("ENCODING_SCHEME must be 'c' or '1'")
end
```

Implementing centric encoding is easy  
(just remember to reorder data in reconstruction)





```
for i=1:Ny
    [rf, gz] = mr.makeSincPulse(fam_alphas(i)*pi/180, 'Duration', rfDuration, ...
        'SliceThickness', sliceThickness, 'apodization', 0.42, 'timeBwProduct', 4, 'system', sys);
    % ...
    seq.addBlock(gxPre, mr.scaleGrad(gyPre, peScales(i)), gzReph);
    % ...
    seq.addBlock(mr.makeDelay(delayTR(c)), gxSpoil, mr.scaleGrad(gyPre, -peScales(i)), gzSpoil);
end
```

Adding FAM is easy too!

# Rapid Prototyping and Experiments

Aug

- Single slice and multi-slice FAM developed

Sept

- Debugging/refinement at UW
- Shorten TEs and add dummy slices

Oct

- Experiments with flip angle/encoding schemes
- Multi-repetition, internal test-retest

Nov

- Send to Martinos Center for cross-center/vendor reproducibility
- Submit ISMRM abstract



# Two-Center, Two-Vendor Study

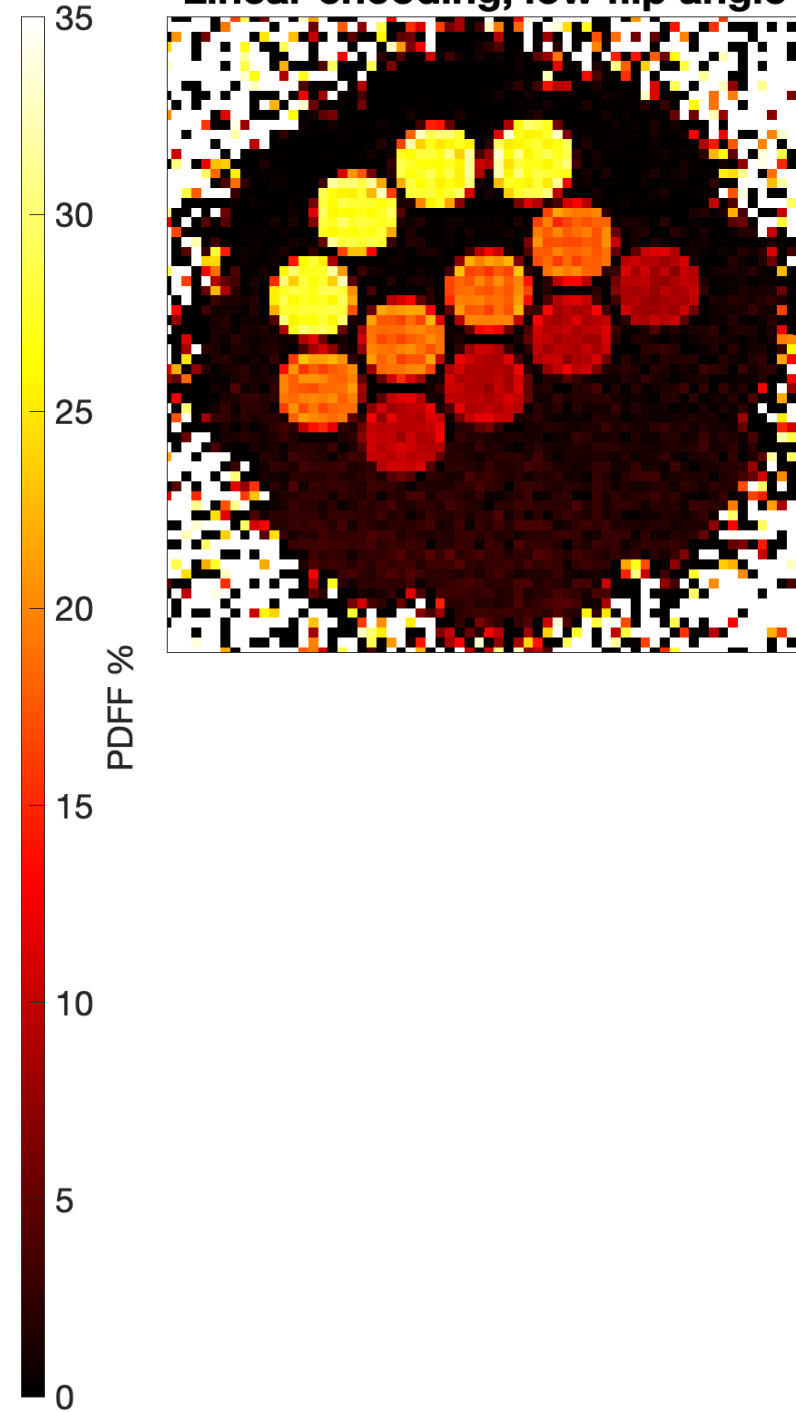
Site	Center 1 UW-Madison	Center 2 Martinos Center
Scanner	GE Signa Premier	Siemens MAGNETOM Skyra
Field Strength	3.0 T	2.89 T
TE <sub>1</sub> , initial echo time (ms)	1.73	1.53

Pulse sequence parameter	Values
TE, echo time	TE <sub>1</sub> = variable by vendor, $\Delta$ TE = 1.3 ms, N <sub>TE</sub> = 6
TR, repetition time (ms)	12
Total bandwidth (kHz)	500
Flip angle	Varies by sequence
Voxel size (mm × mm × mm)	2.0 × 2.0 × 8.0
Dummy slices / acquired slices	2 / 6
Acquisition matrix	144 × 144
Acquisition duration	14 s
Temporal footprint per slice	1.7 s

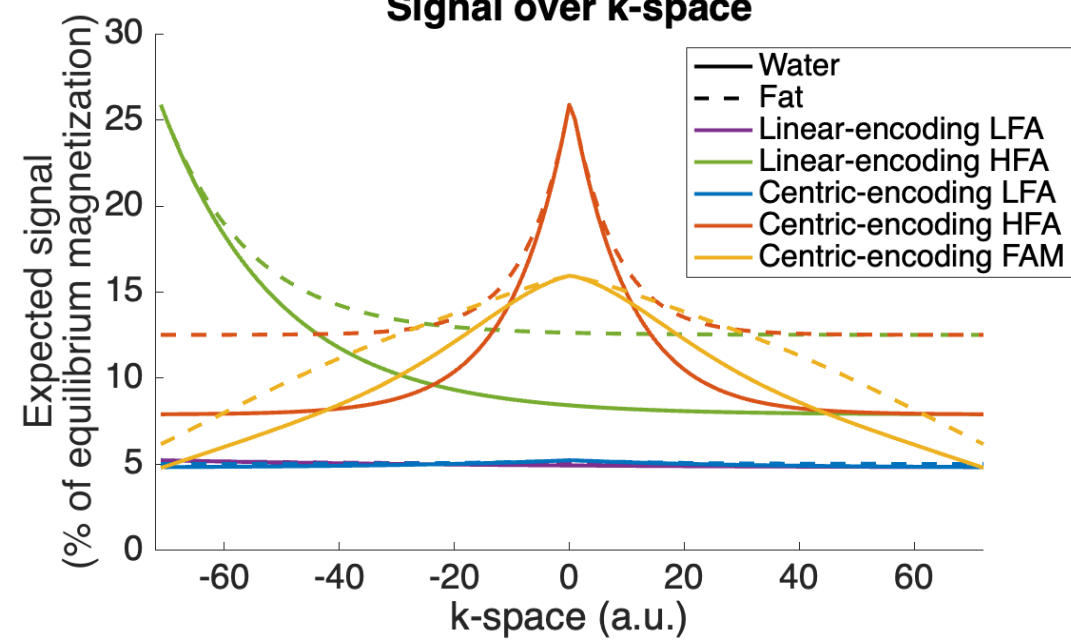
Berkin Bilgic, Xingwang Yong, Shohei Fujita, Yuting Chen  
Athinoula A. Martinos Center for Biomedical Imaging

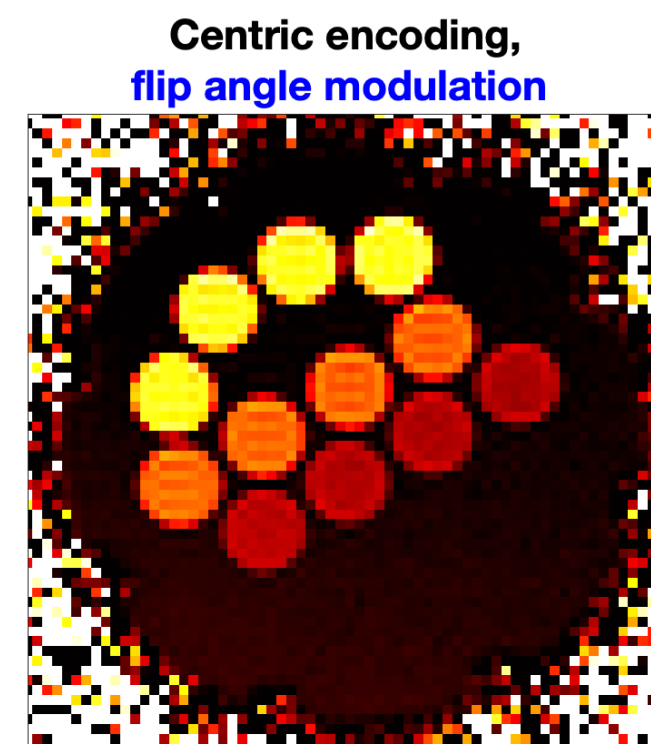
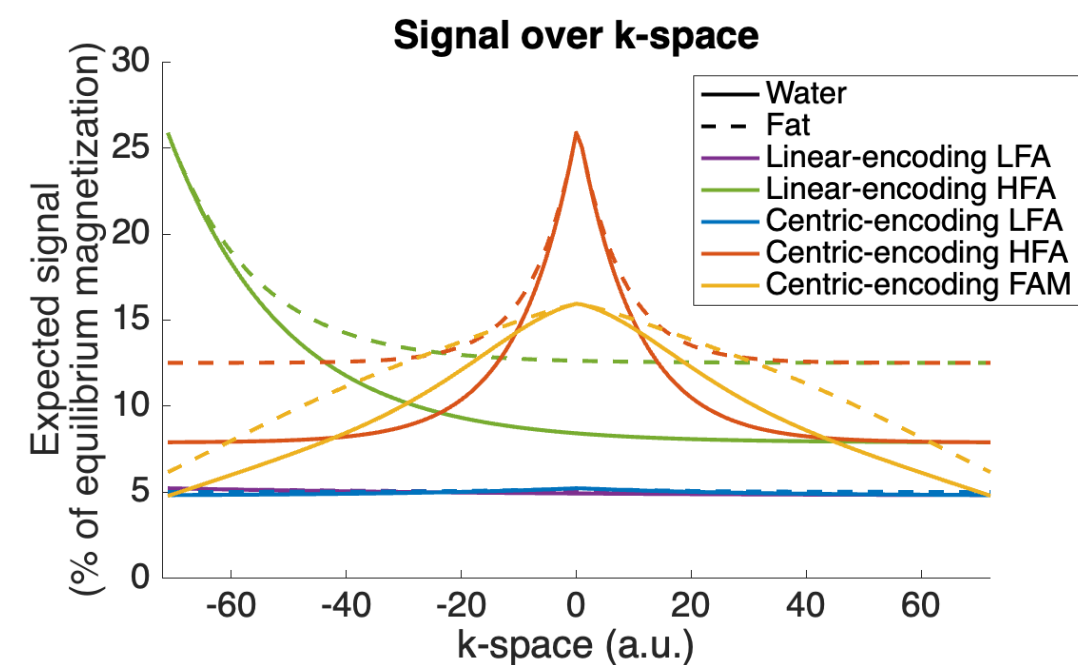
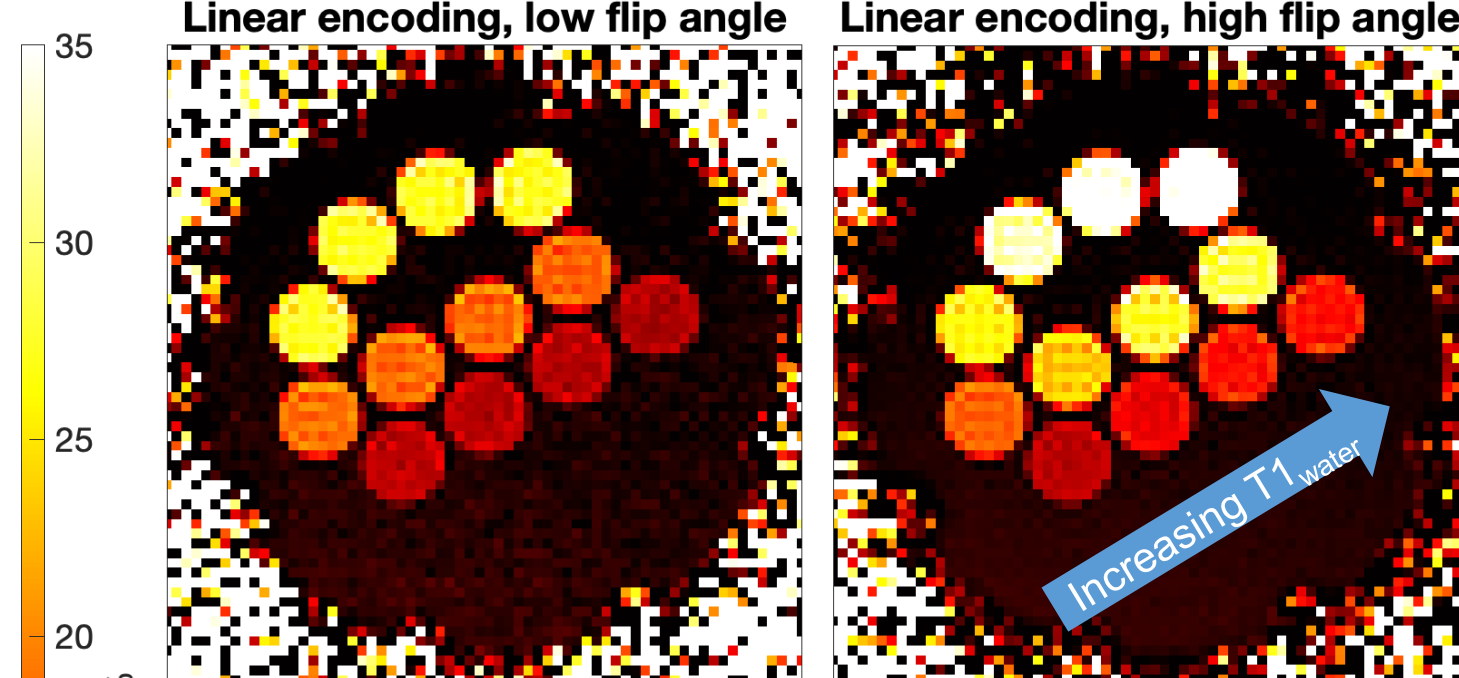


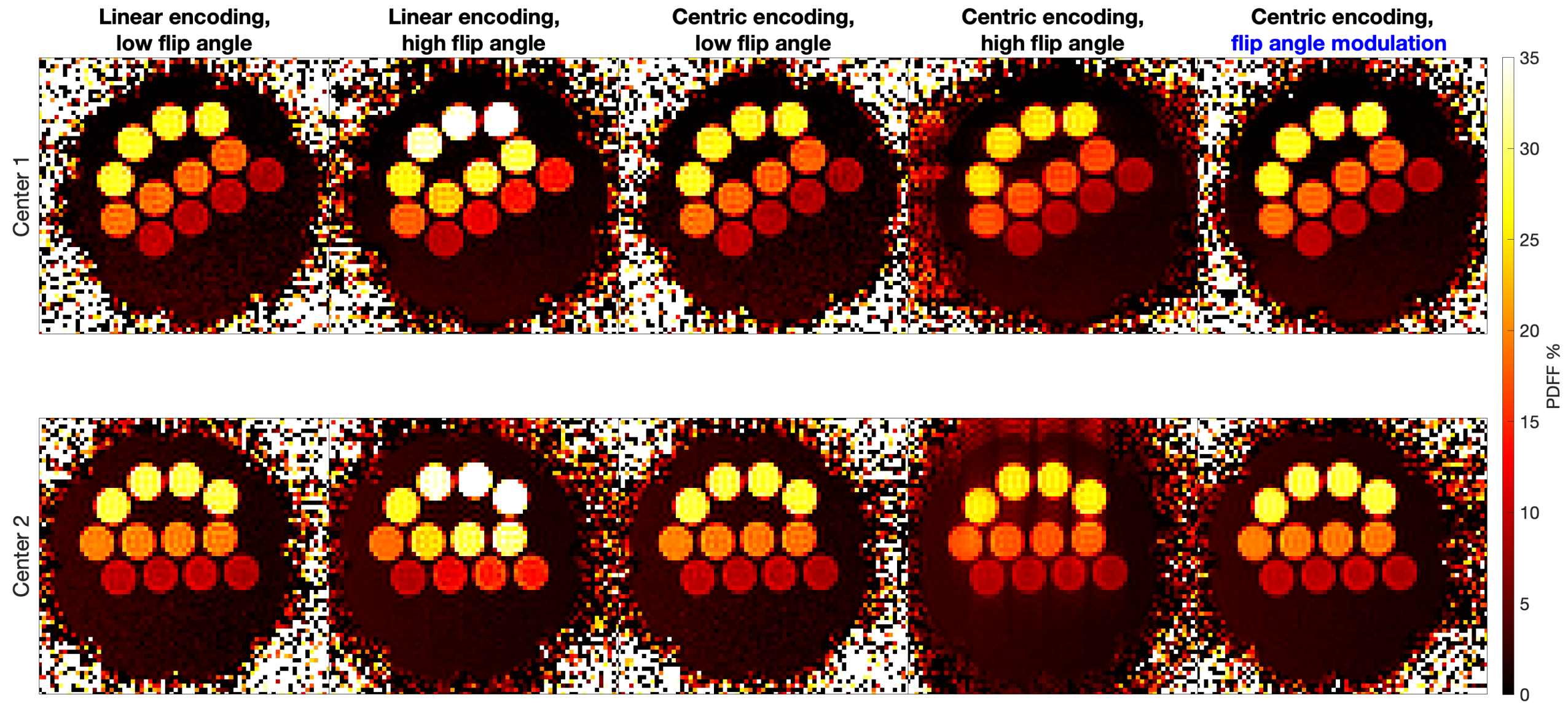
Linear encoding, low flip angle



Signal over k-space





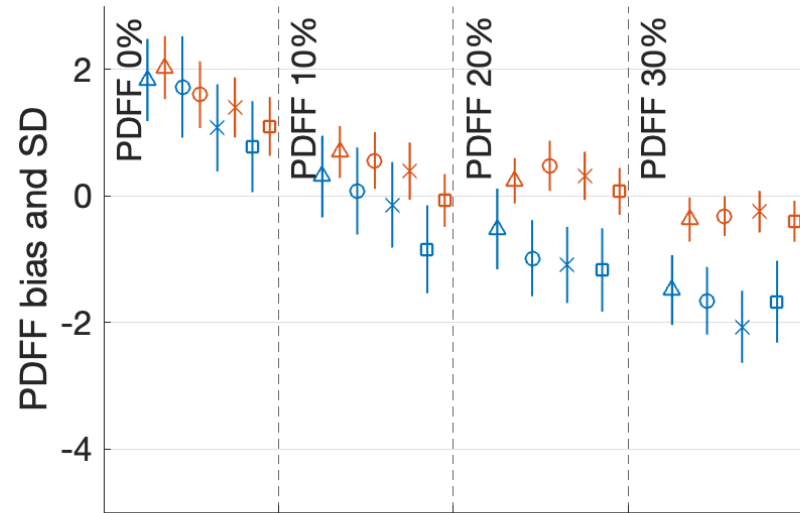


# Pulseseq-FAM has low bias and good SNR

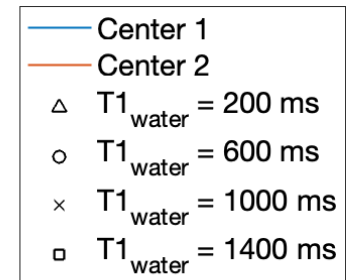
Linear encoding, low flip angle

Center 1 mean SD = 0.65

Center 2 mean SD = 0.41

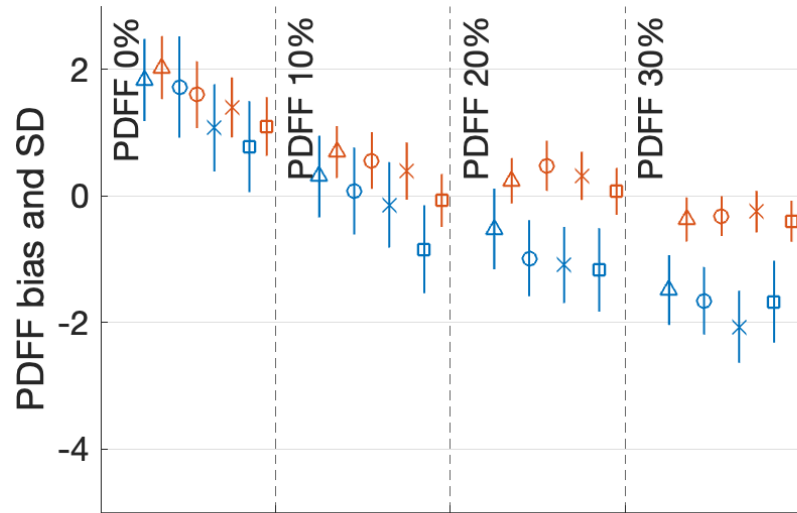


Note all plots except linear encoding, high flip angle share y-axis scaling.

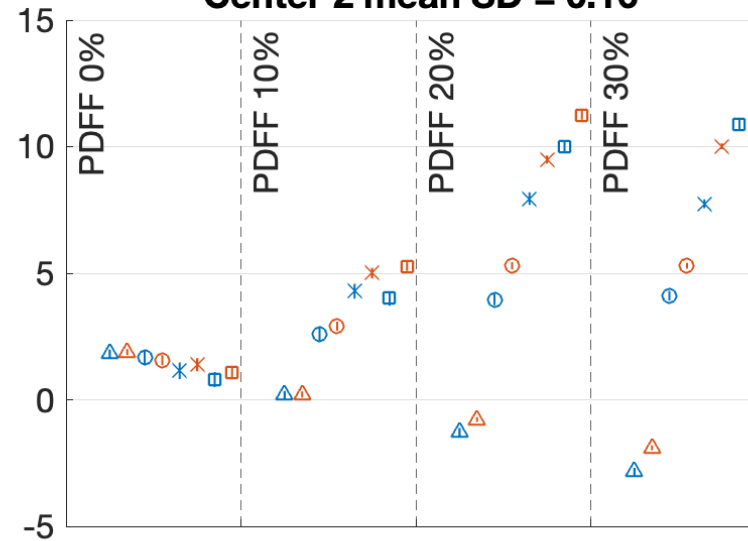


# Pulseseq-FAM has low bias and good SNR

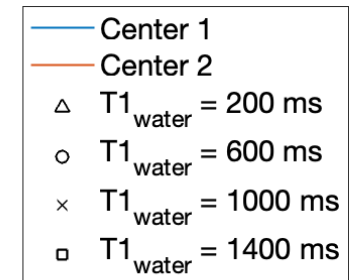
**Linear encoding, low flip angle**  
Center 1 mean SD = 0.65  
Center 2 mean SD = 0.41



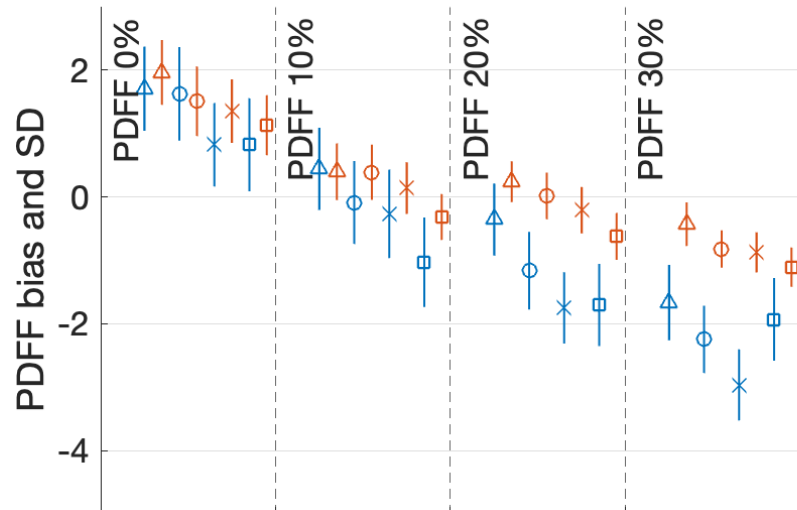
**Linear encoding, high flip angle**  
Center 1 mean SD = 0.23  
Center 2 mean SD = 0.16



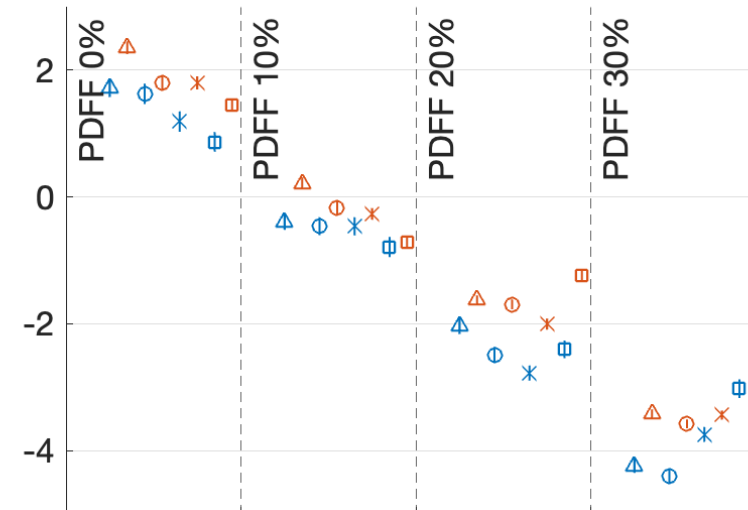
Note all plots except linear encoding, high flip angle share y-axis scaling.



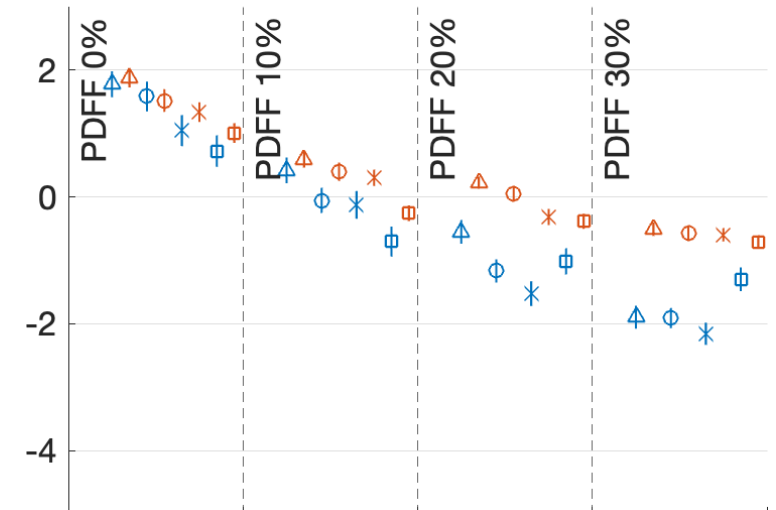
**Centric encoding, low flip angle**  
Center 1 mean SD = 0.64  
Center 2 mean SD = 0.40



**Centric encoding, high flip angle**  
Center 1 mean SD = 0.14  
Center 2 mean SD = 0.08



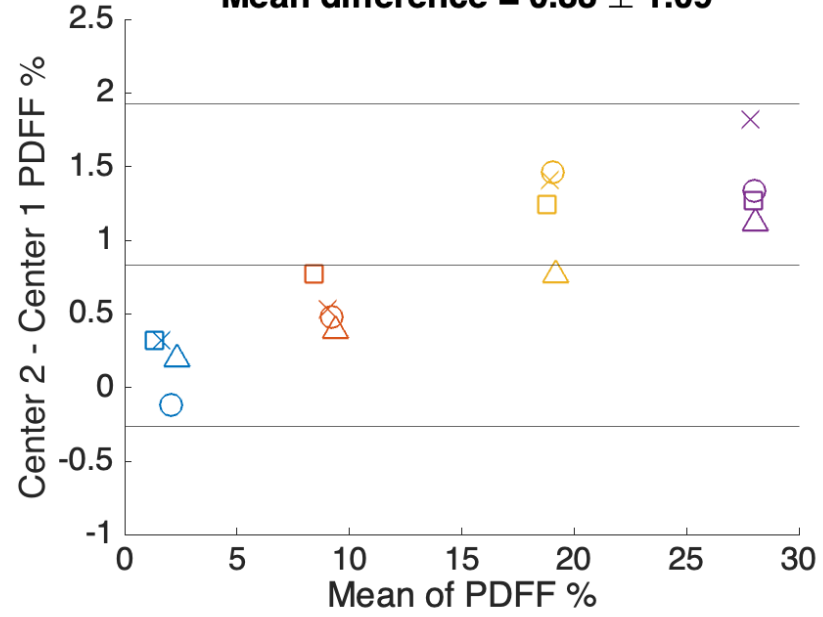
**Centric encoding, flip angle modulation**  
Center 1 mean SD = 0.20  
Center 2 mean SD = 0.13





# Pulseseq-FAM has good repeatability

Linear encoding, low flip angle  
Mean difference =  $0.83 \pm 1.09$

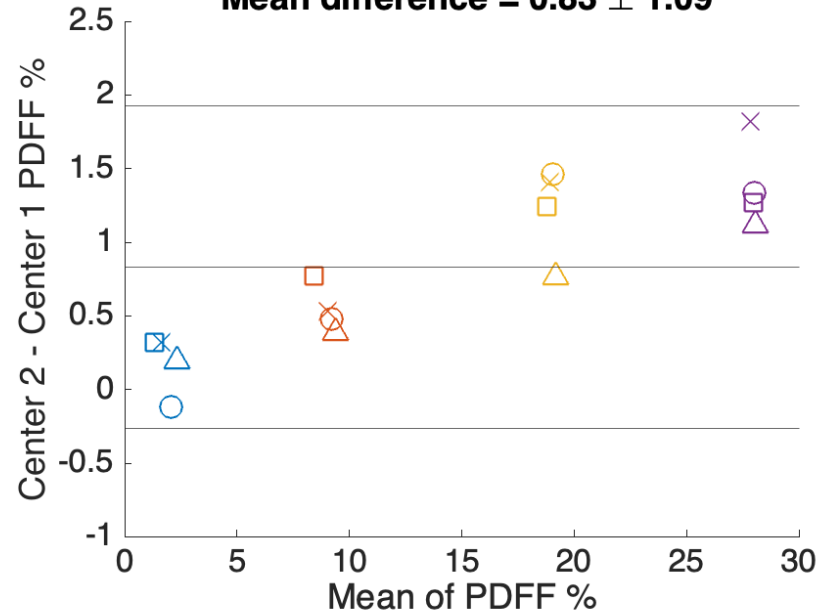


Note all plots except linear encoding,  
high flip angle share x-axis scaling.

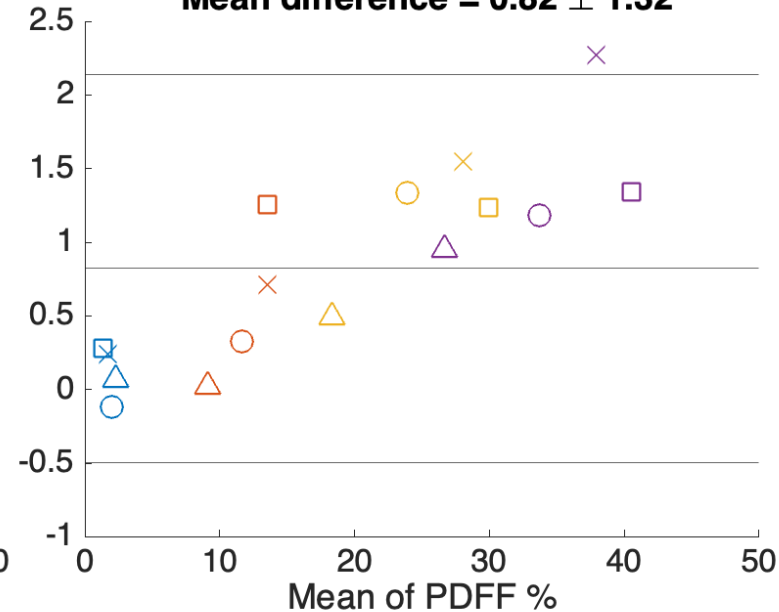
- △ T1<sub>water</sub> = 200 ms
- T1<sub>water</sub> = 600 ms
- × T1<sub>water</sub> = 1000 ms
- T1<sub>water</sub> = 1400 ms

# Pulseq-FAM has good repeatability

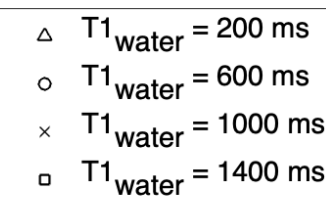
**Linear encoding, low flip angle**  
**Mean difference =  $0.83 \pm 1.09$**



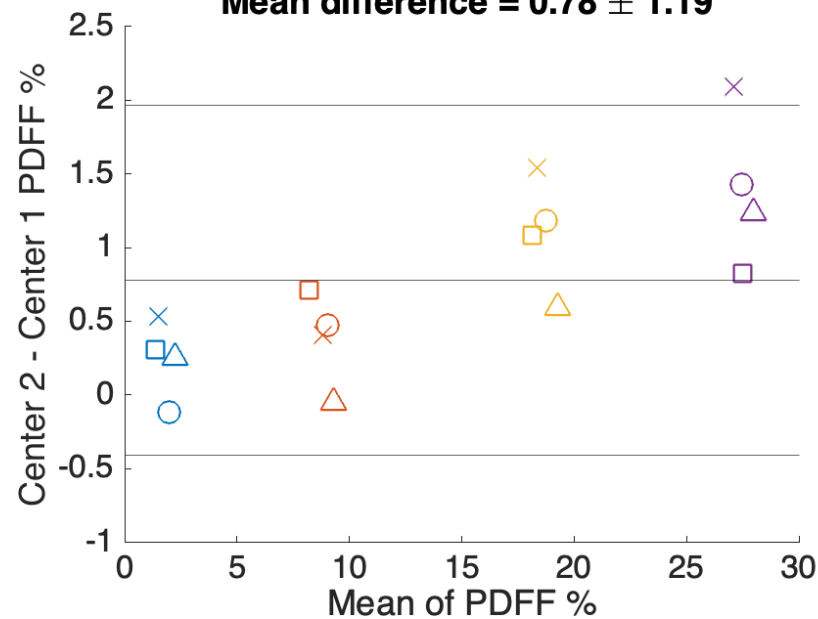
**Linear encoding, high flip angle**  
**Mean difference =  $0.82 \pm 1.32$**



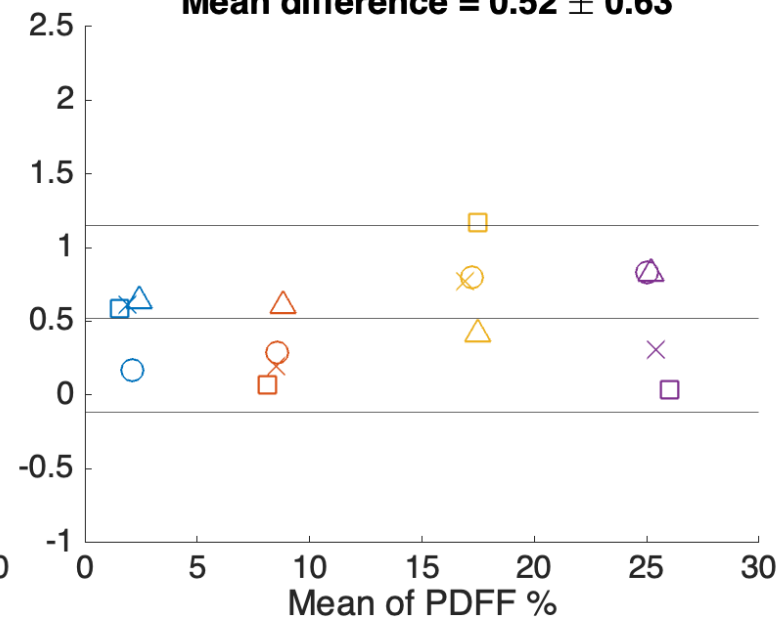
Note all plots except linear encoding, high flip angle share x-axis scaling.



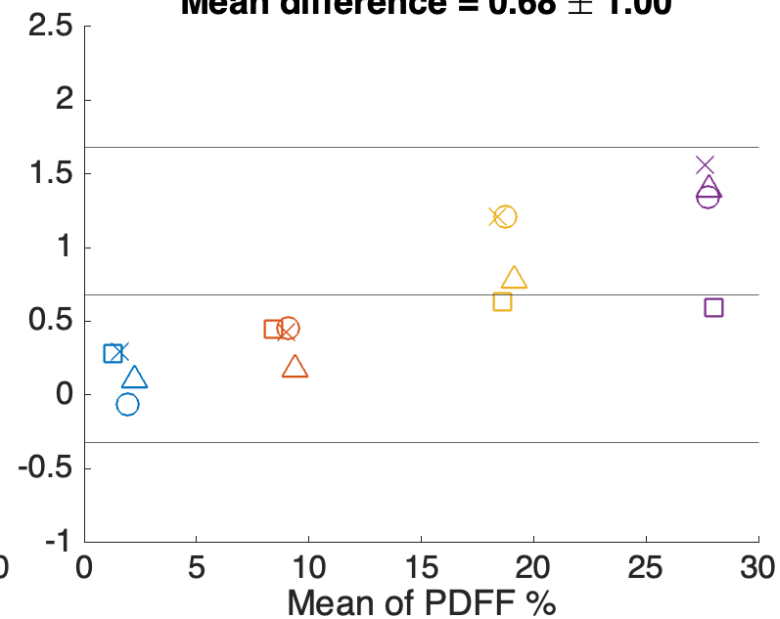
**Centric encoding, low flip angle**  
**Mean difference =  $0.78 \pm 1.19$**



**Centric encoding, high flip angle**  
**Mean difference =  $0.52 \pm 0.63$**



**Centric encoding, flip angle modulation**  
**Mean difference =  $0.68 \pm 1.00$**



# Pulseseq-FAM is feasible in vivo with free breathing (two different volunteers)

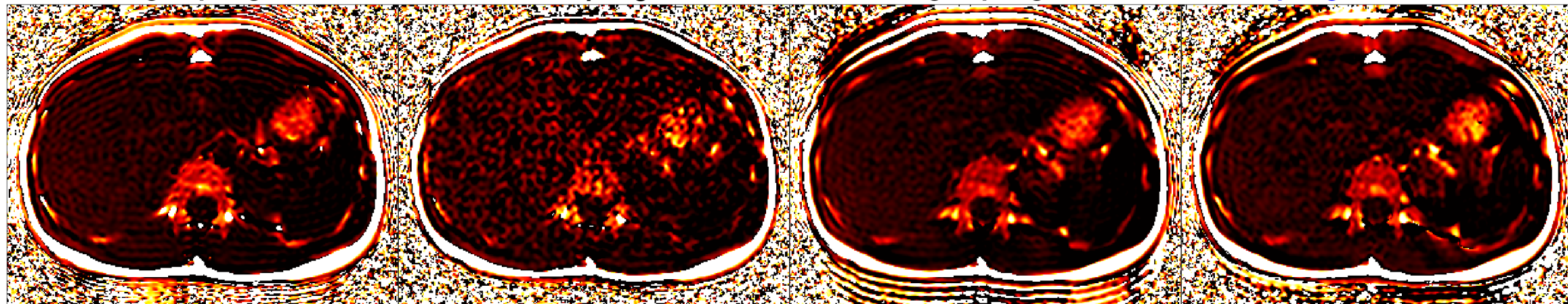
Linear encoding,  
high flip angle

Centric encoding,  
low flip angle

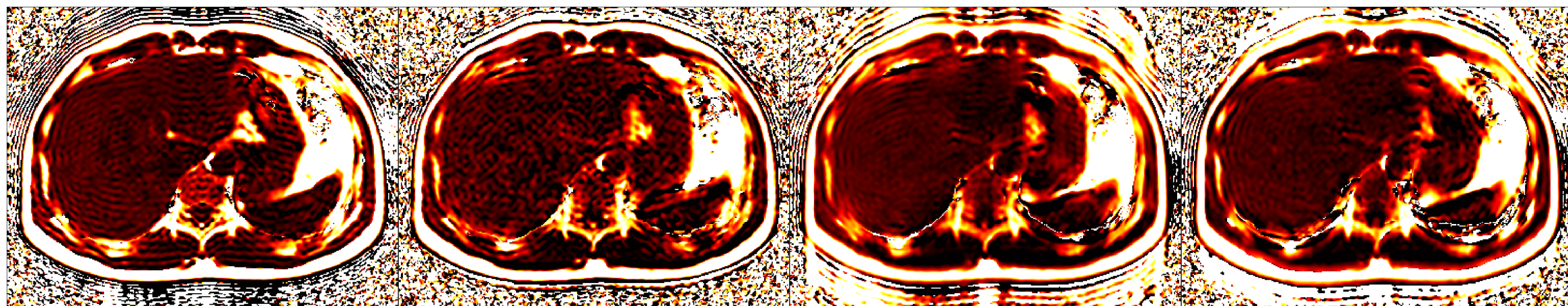
Centric encoding,  
high flip angle

Centric encoding,  
flip angle modulation

Volunteer 1 at Center 1



Volunteer 2 at Center 2

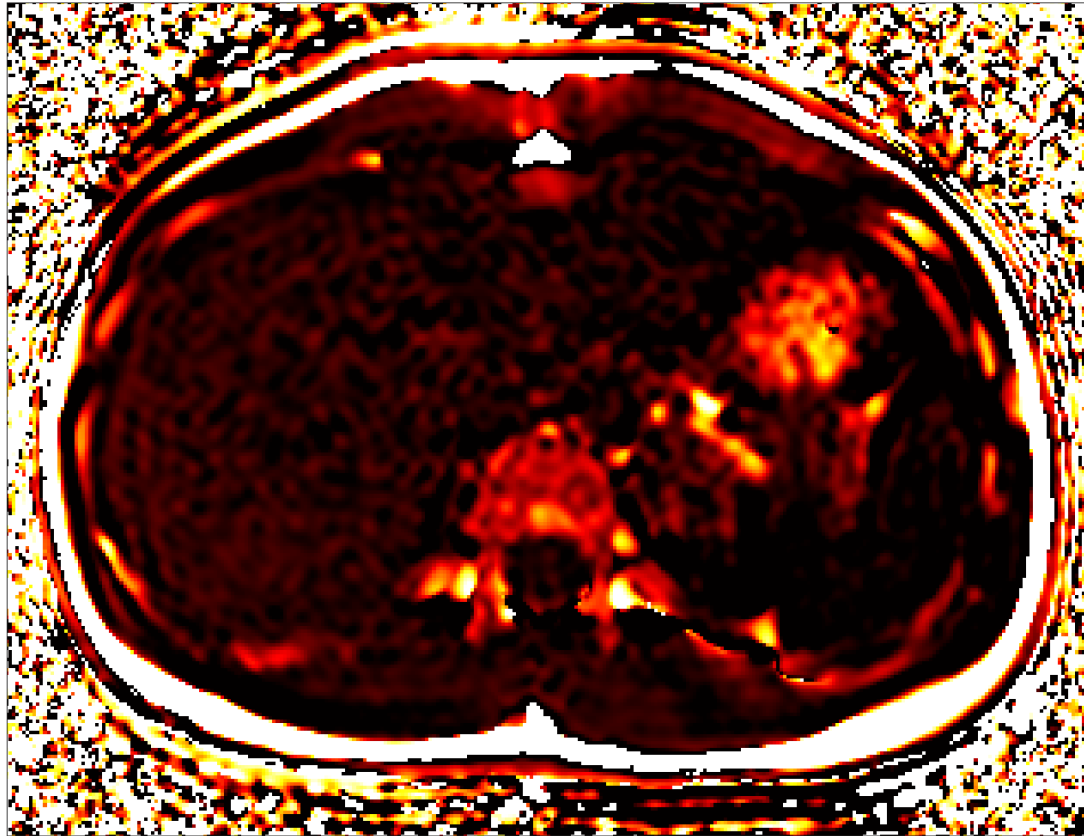


PDF %

# Free-Breathing Pulseseq-FAM: Centric Encoding, Flip Angle Modulation

Volunteer 1 at Center 1

GE Signa Premier 3.0T



Volunteer 2 at Center 2

Siemens MAGNETOM Skyra 2.89T





## Discussion

---

- Successful, straightforward implementation of FAM in Pulseseq
- SNR and accuracy of FAM matches predictions in phantoms
- Free breathing in vivo feasibility demonstrated

## Future Directions

---

- Larger scale in vivo study
- More centers and field strengths
- Study timing mechanisms deeply to harmonize TEs
- Add scanner GUI and live recalculation of FAs
- Parallel imaging, simultaneous-multi-slice





Thank you!

Jiayi Tang

[jiayi.tang@wisc.edu](mailto:jiayi.tang@wisc.edu)