

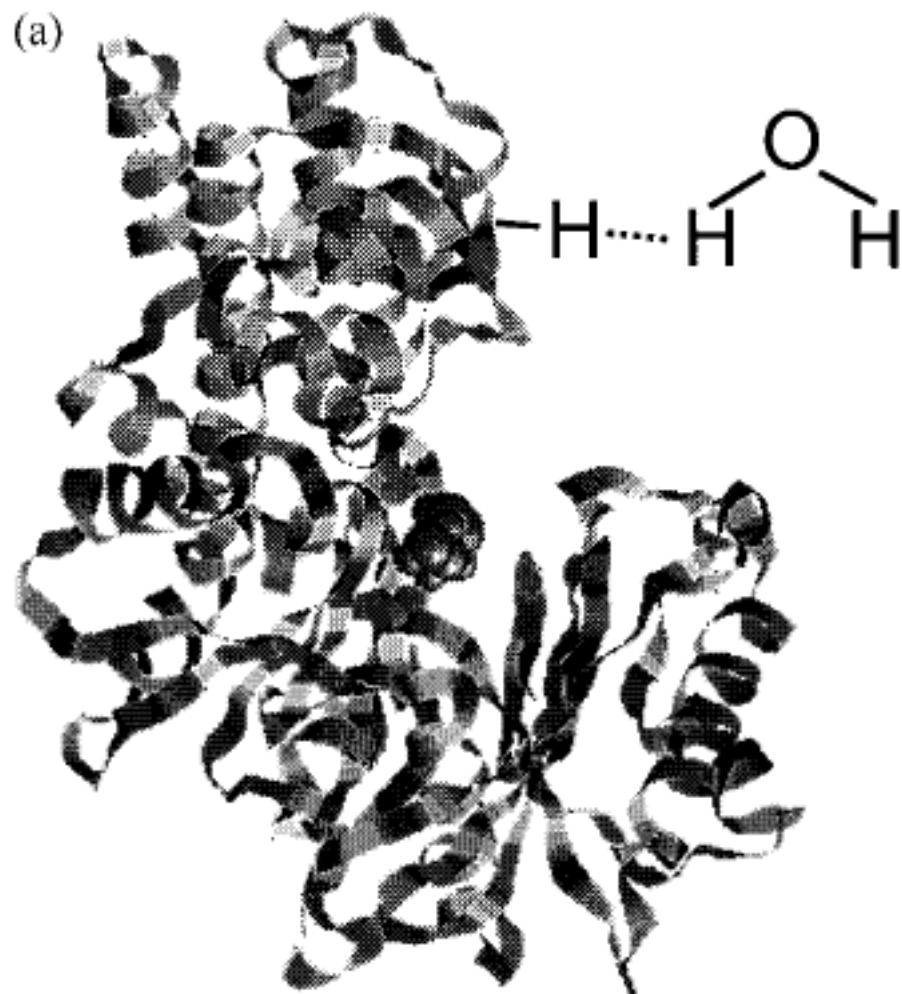
Analysis of B_1 -sensitivity of qMT parameters when using two different T1 methods

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MRIL Lab Meeting

September 29th 2014

Hydrogen in myelin can't be directly measure with MRI



2-Pool Magnetization Transfer Model

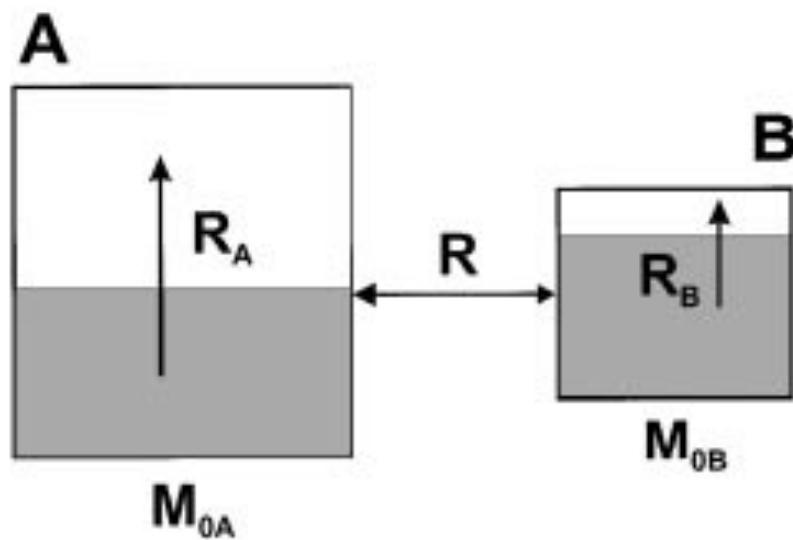
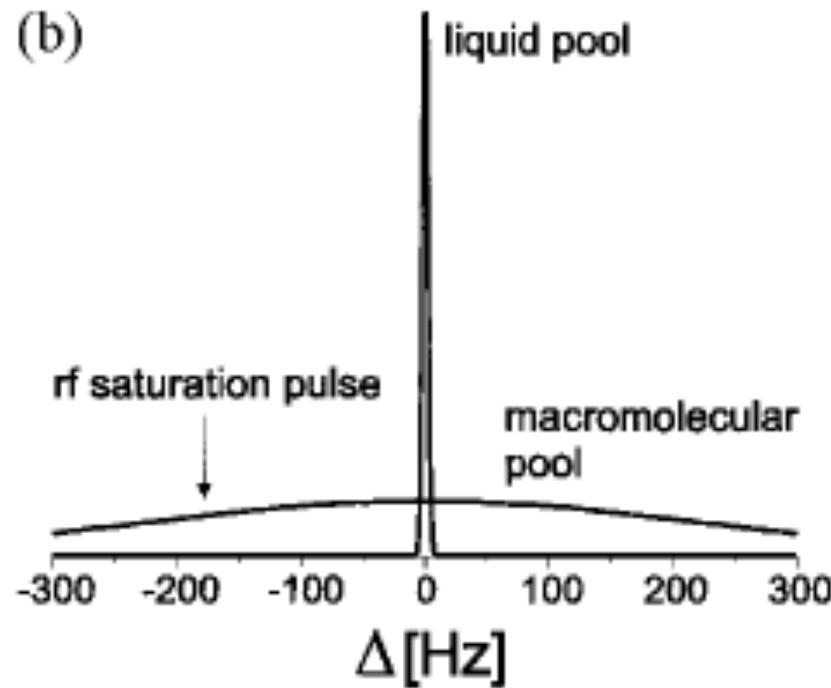


Figure 2. A two-pool model of magnetization transfer exchange. The shaded region in each pool represents saturated spins. R_A and R_B represent longitudinal relaxation rates in liquid and macromolecular pools respectively. R denotes magnetization transfer exchange between the pools

Prepare magnetization using off-resonance saturation



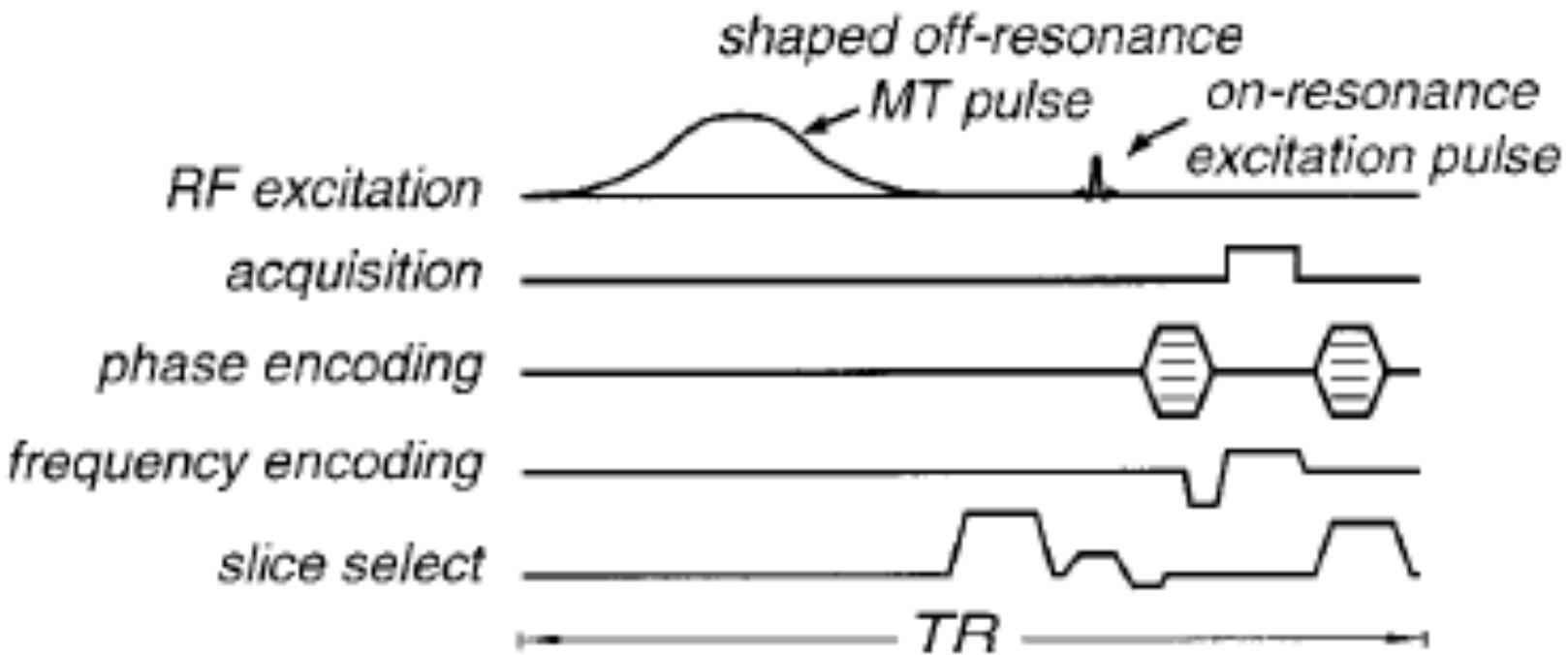


FIG. 1. An MT-weighted spoiled gradient echo pulse sequence with shaped off-resonance saturation pulses.

$$\frac{dM_{x,f}}{dt} = -\frac{M_{x,f}}{T_{2,f}} - \Delta M_{y,f} - \text{Im}(\omega_1)M_{z,f} \quad [1]$$

$$\frac{dM_{y,f}}{dt} = -\frac{M_{y,f}}{T_{2,f}} + \Delta M_{x,f} + \text{Re}(\omega_1)M_{z,f} \quad [2]$$

$$\begin{aligned} \frac{dM_{z,f}}{dt} = & R_{1,f}(M_{0,f} - M_{z,f}) - k_f M_{z,f} + k_r M_{z,r} + \text{Im}(\omega_1)M_{x,f} \\ & - \text{Re}(\omega_1)M_{y,f} \quad [3] \end{aligned}$$

$$\frac{dM_{z,r}}{dt} = R_{1,r}(M_{0,r} - M_{z,r}) - k_r M_{z,r} + k_f M_{z,f} - WM_{z,r} \quad [4]$$

$$W = \pi \omega_1^2 G(\Delta) \quad [5]$$

$$G(2\pi\Delta) = T_{2,r} \int_0^1 \frac{1}{|3u^2 - 1|} \exp\left(-2\left(\frac{2\pi\Delta T_{2,r}}{3u^2 - 1}\right)^2\right) du. \quad [6]$$

$$R_{1,f} = \frac{R_1^{obs}}{1 + \left(\frac{\left[\frac{k_f}{R_{1,f}} \right] (R_{1,r} - R_1^{obs})}{(R_{1,r} - R_1^{obs}) + k_f/F} \right)}. \quad [7]$$

5 Fitted parameters

- F – pool size ratio (correlates with myelin density)
- k_f – Magnetization transfer exchange rate
- T_{2r} – T_2 of restricted pool
- T_{2F} – T_2 of free pool
- T_{1F} – T_1 of free pool

(T_{1R} always set to 1, model not sensitive to this parameter)

qMT processing code: www.github.com/sharktank-bic/qMTLab/

Measurements

- 11 qMT measurements
 - 1 MT off
 - 10 MT point design (e.g. UK, 2 MT angles, 5 logarithmic off-resonance frequencies)
- B0 – For off resonance frequency correction
- B1 – For MT and excitation pulse correction
- T1 – Additional measurement to further constrain the MT mathematical model

Measurements

- But T1 measurements can depend on B1
- B1 independent
 - Inversion recovery
 - Look-Locker (can be)
- B1 dependent
 - Variable Flip Angle/DESPOT1

transmission, expected to reduce transmit field inhomogeneities (35), the applied corrections were still important. A different choice of method for $T_{1\text{obs}}$ mapping (e.g., the variable flip-angle method (36)) may also result in greater sensitivity to B_1 inhomogeneity that could propagate to the QMTI parameters, especially R_{1f} .

Parameter estimation with a subset of the MT data (the “reduced” protocol) introduced a bias in the parameter

Levesque I., MRM, 2010

B_1 error propagation pathways

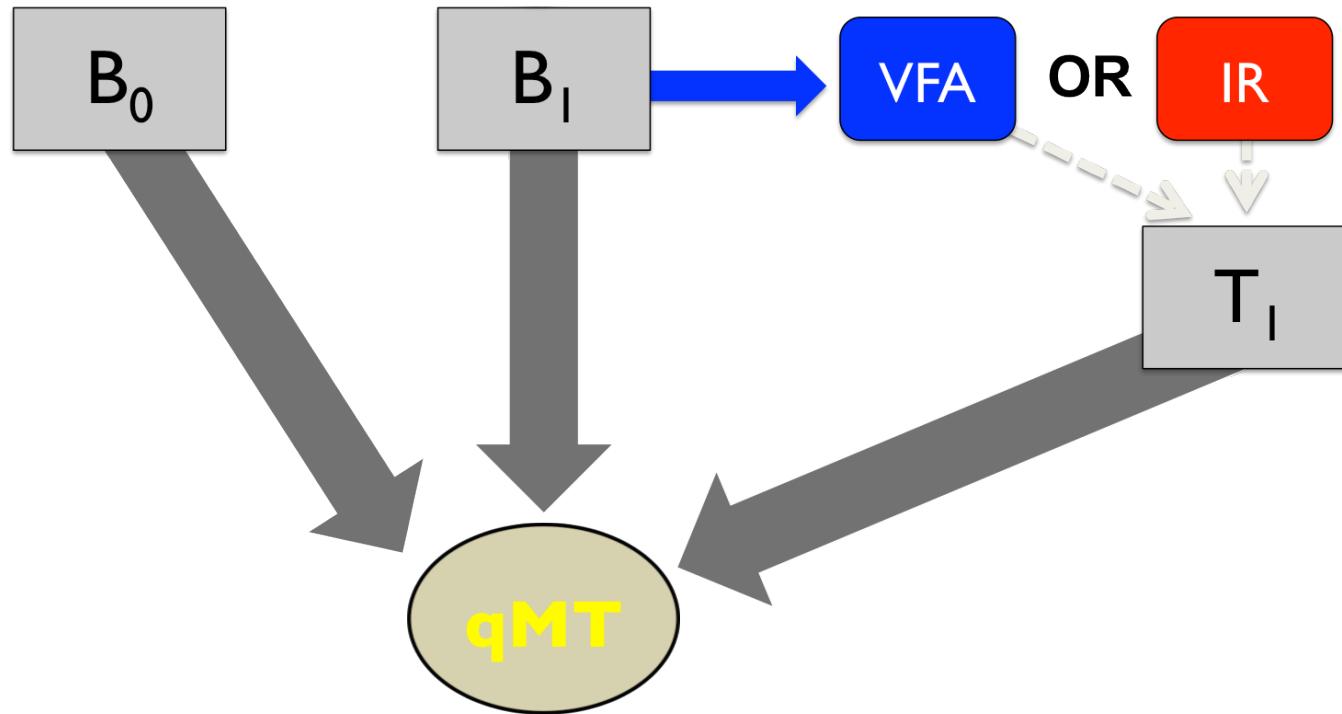


Figure I. Quantitative MRI protocol processing hierarchy.

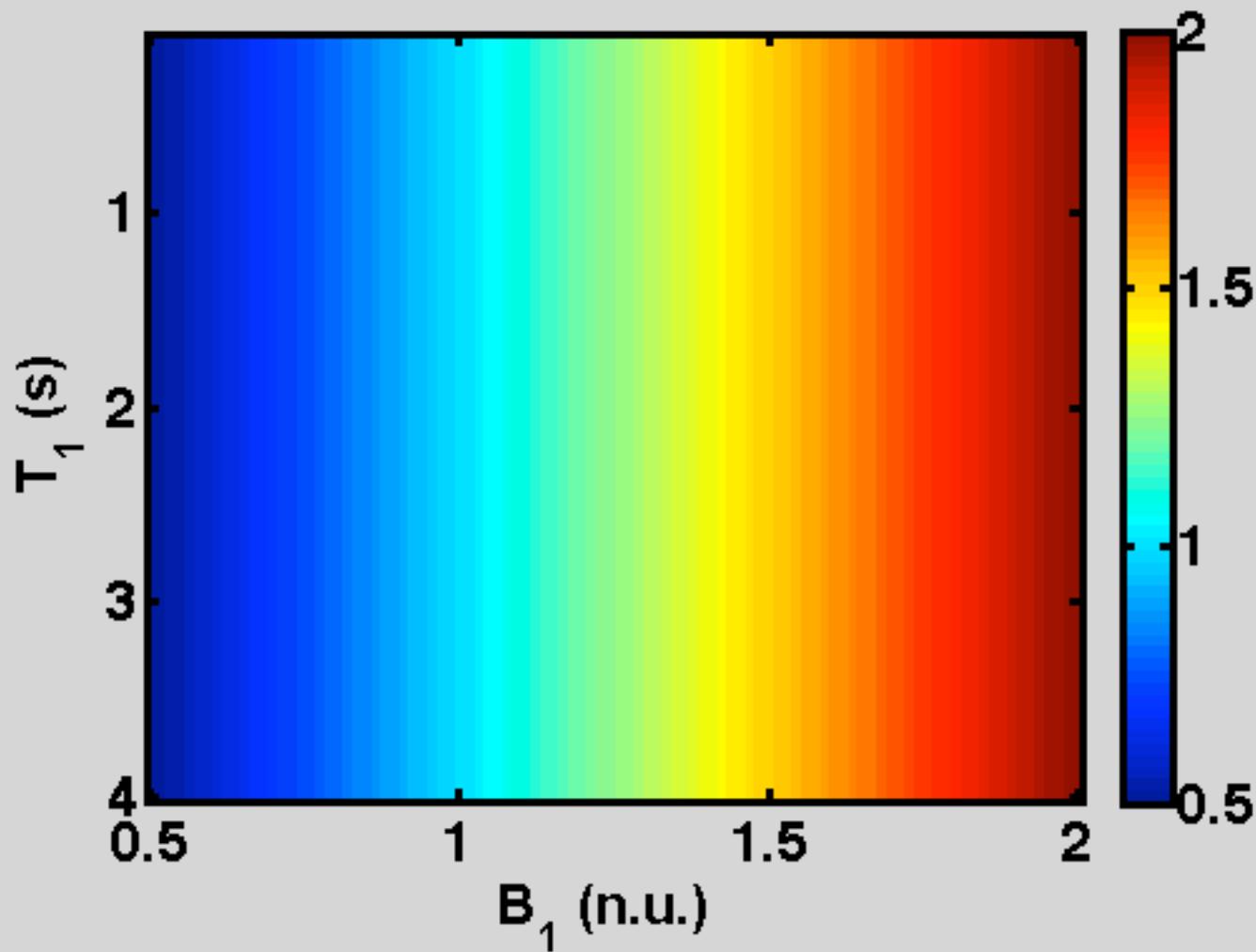
Questions

1. How do qMT fitted parameter (F , k_f) behave when B_1 errors occur when using:
 - IR: B_1 independent T1 method
 - VFA: B_1 dependent T1 method
2. Does this relationship hold in vivo (noise, range of tissue MR parameters, etc.)
3. Does it hold for abnormal tissue parameters (e.g. MS lesions).

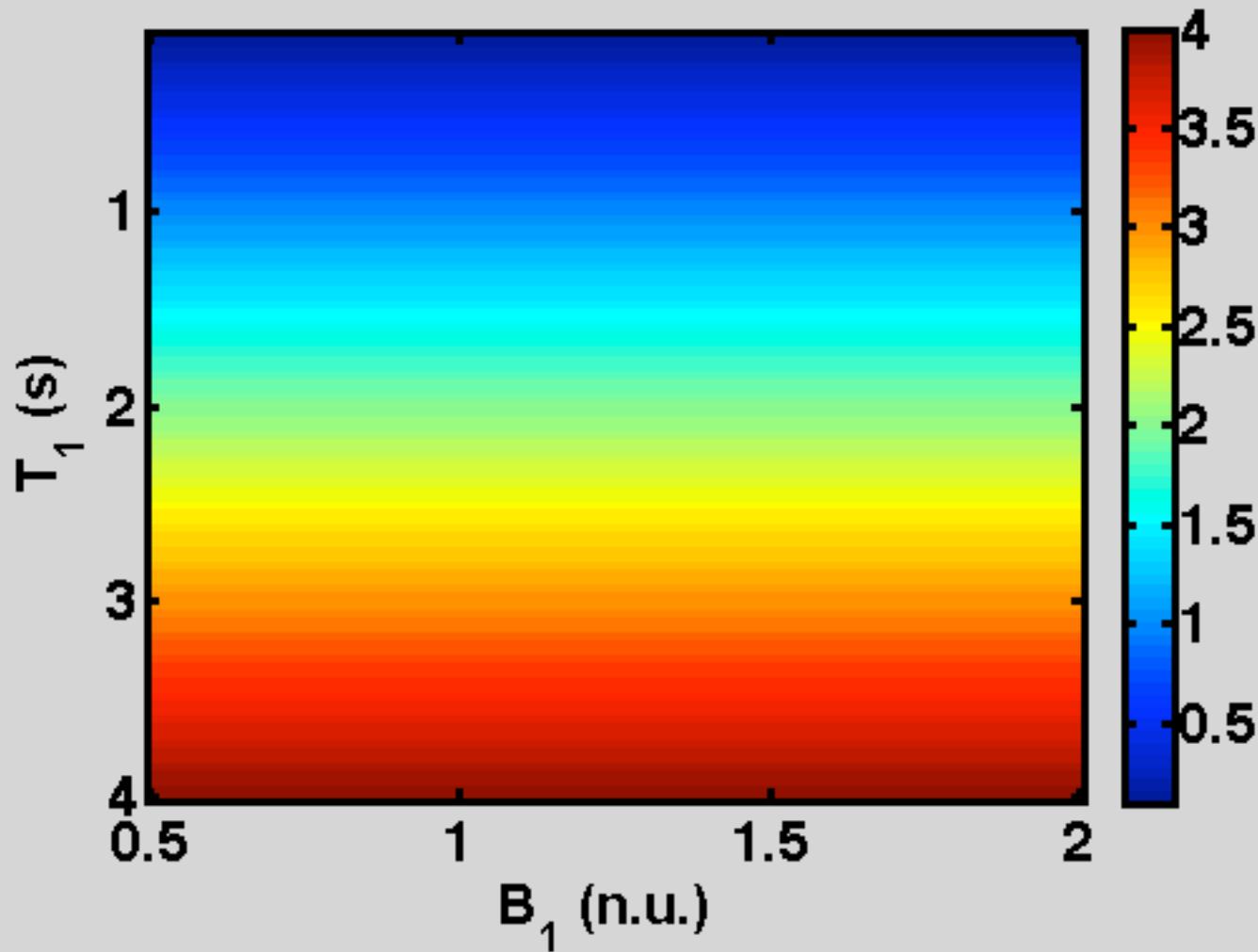
Stage 1: Simulations

- UK qMT protocol
- Healthy WM tissue parameter
- True $T_1 = 900$ ms
- True $B_1 = 1$ (n.u.).

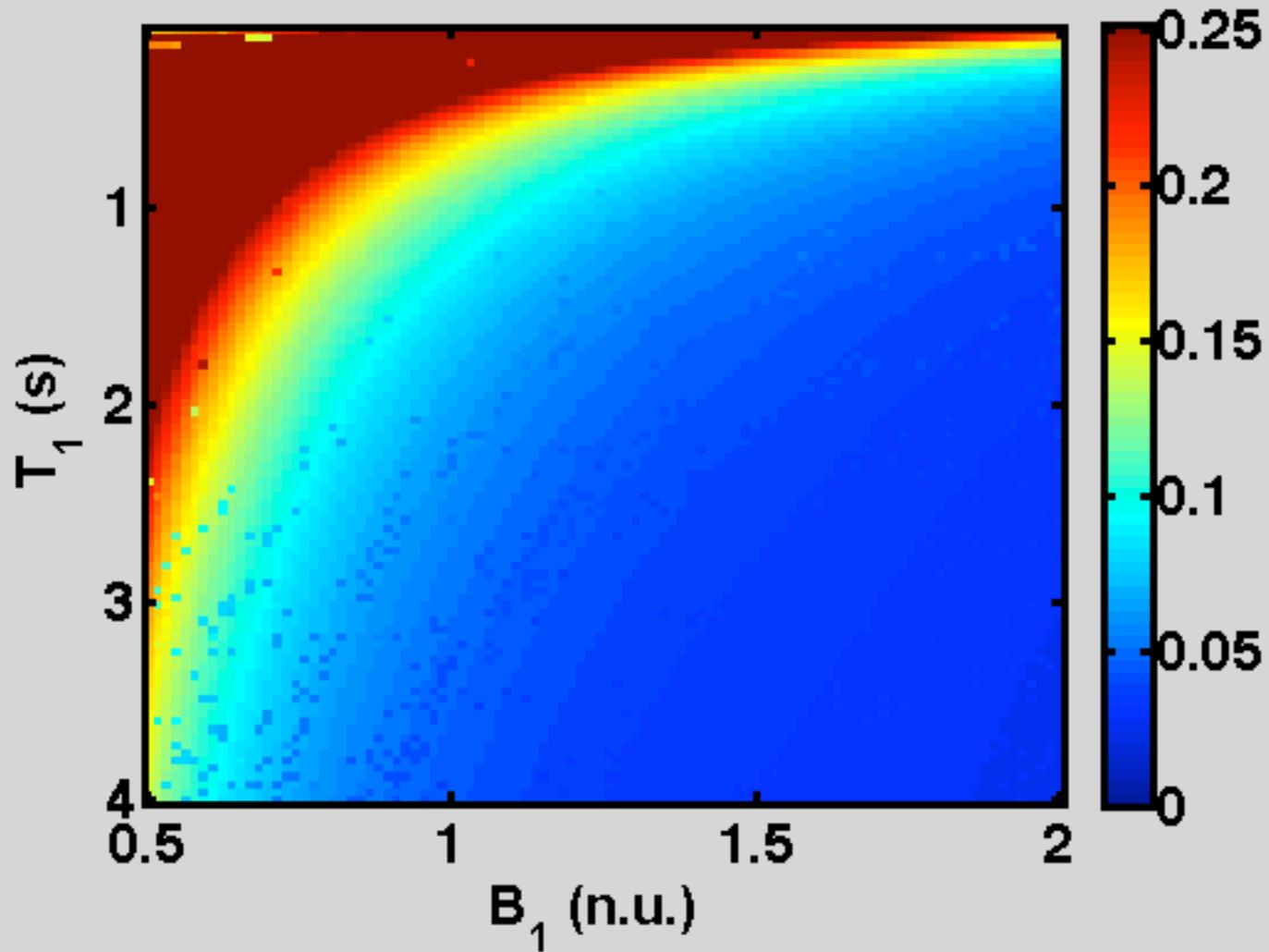
Map of B_1 values used in Stage 1



Map of T_1 values used in Stage 1

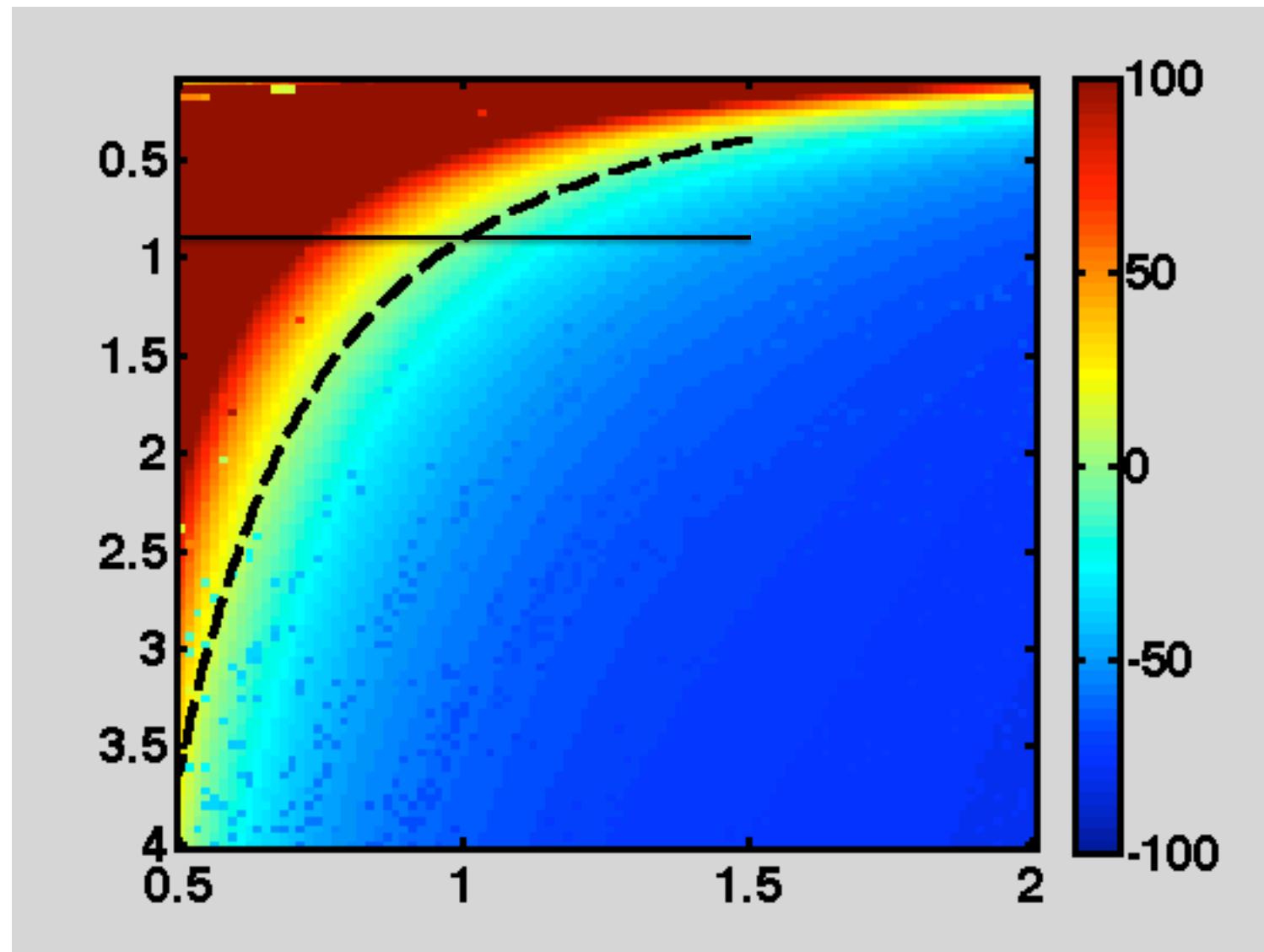


Map of fitted F values in Stage 1



Fitted qMT F error %

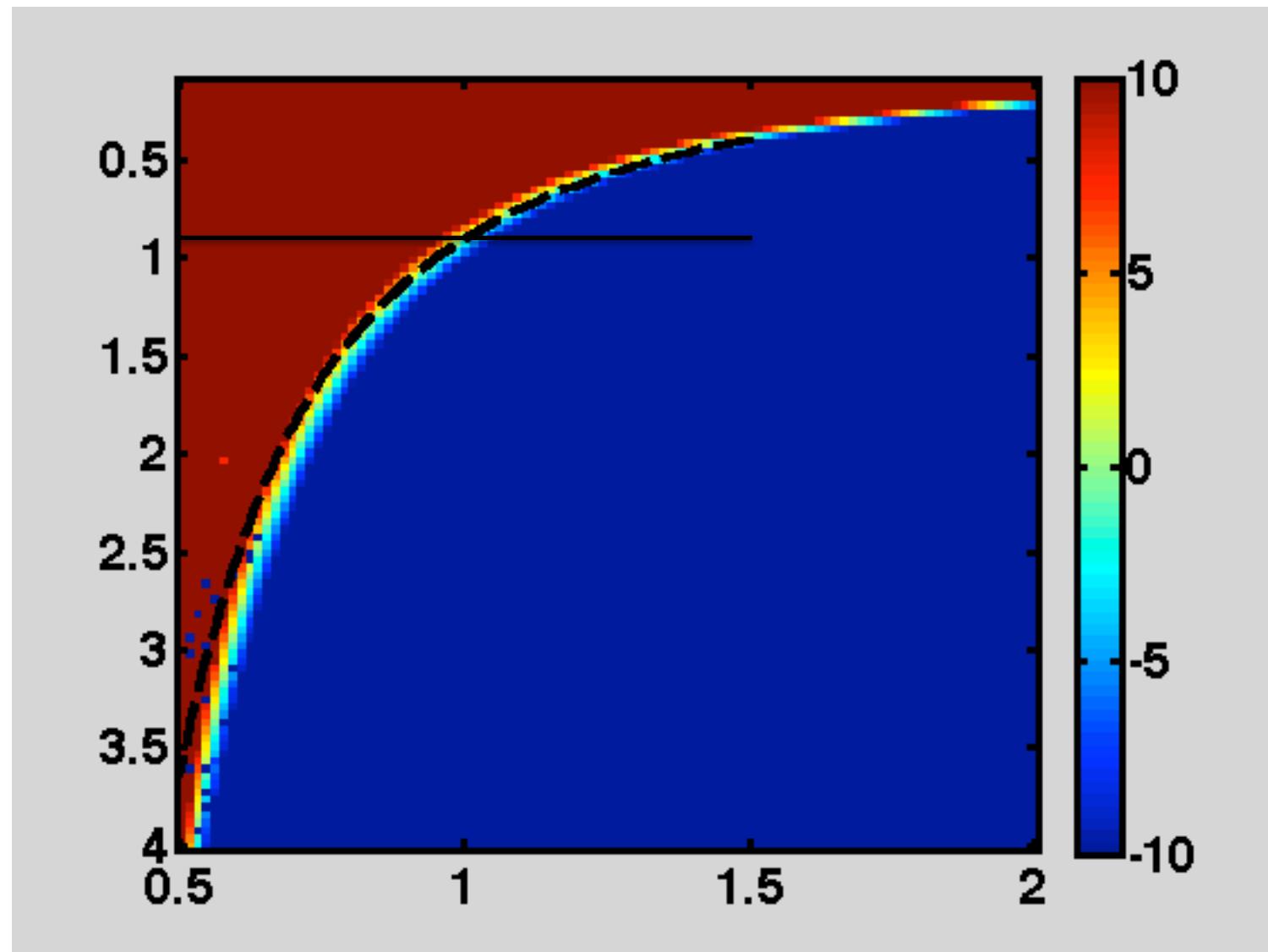
T_1 (s) error (true value 0.9)



B_1 error

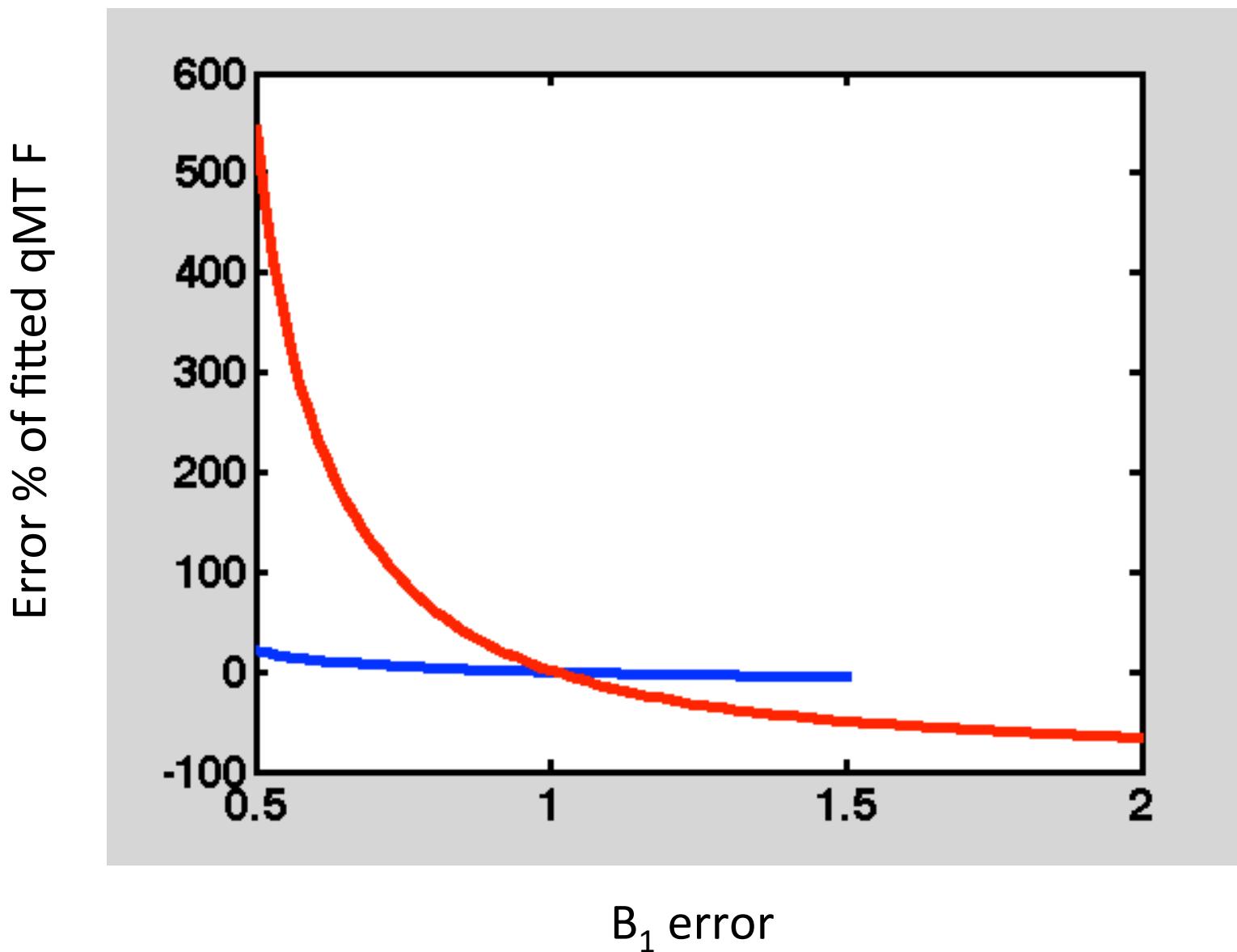
Fitted qMT F error %

T_1 (s) error (true value 0.9)

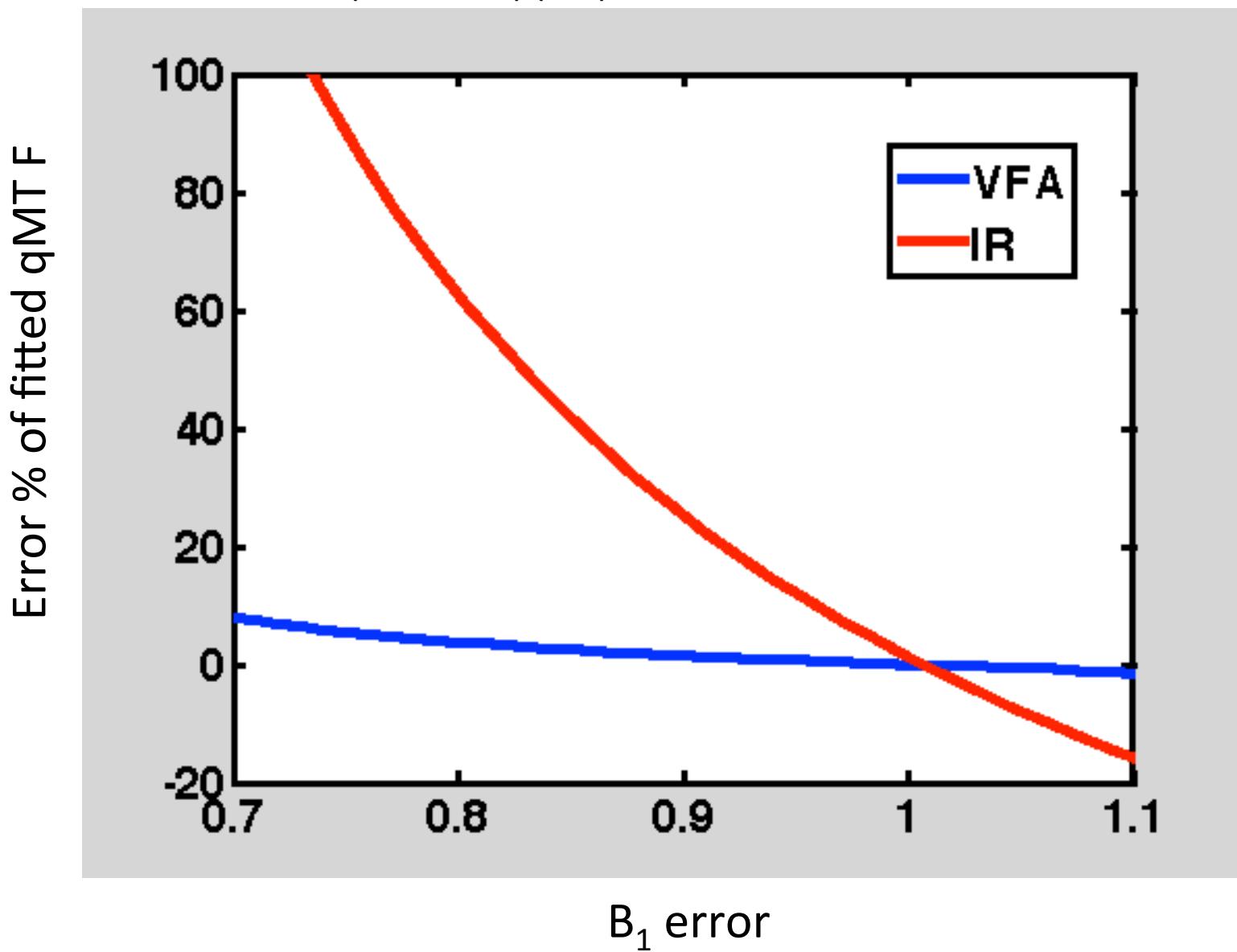


B_1 error

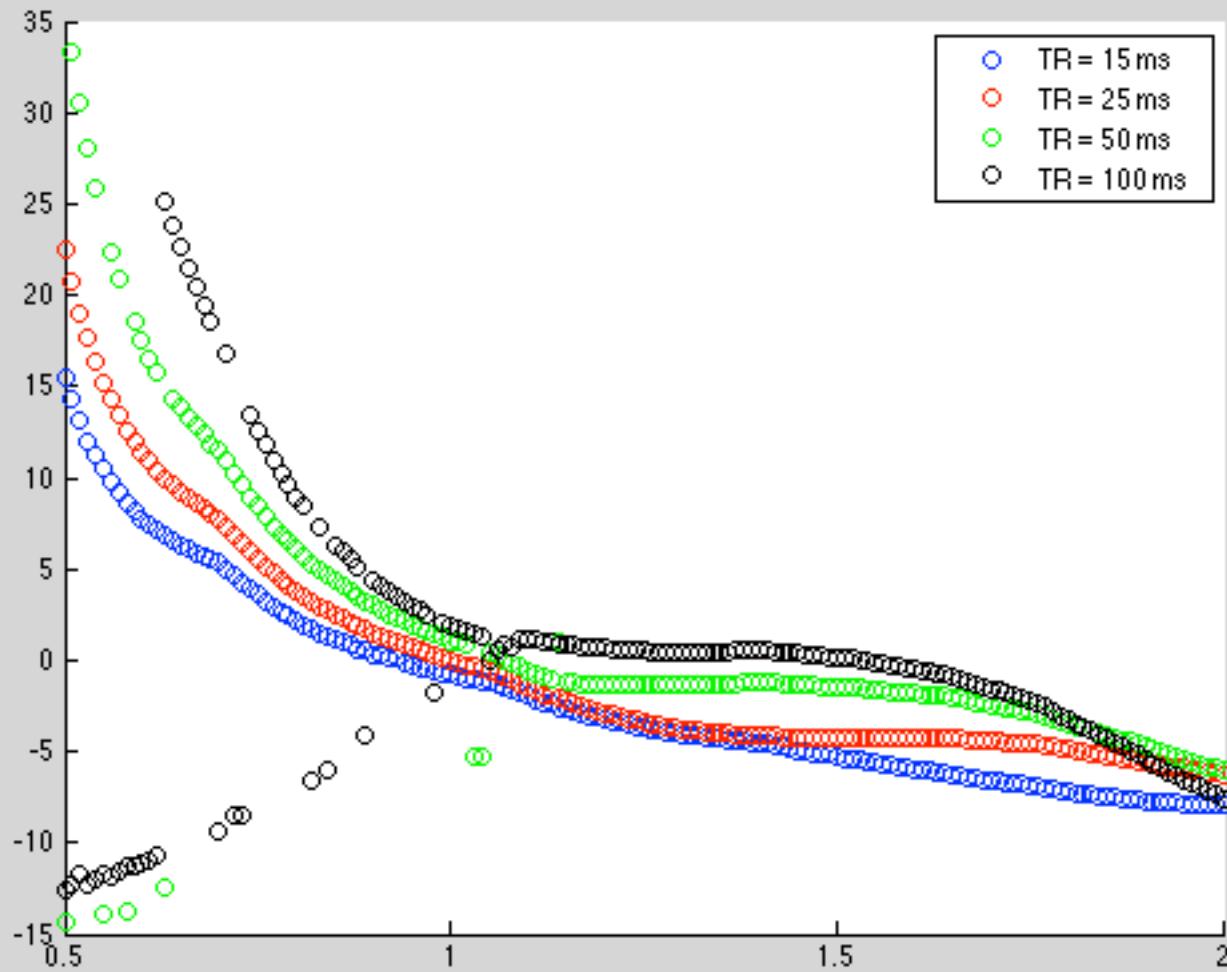
Simulated qMT F % error vs B1 errors using VFA (blue) T1 maps and fixed T1 value (such as IR) (red)



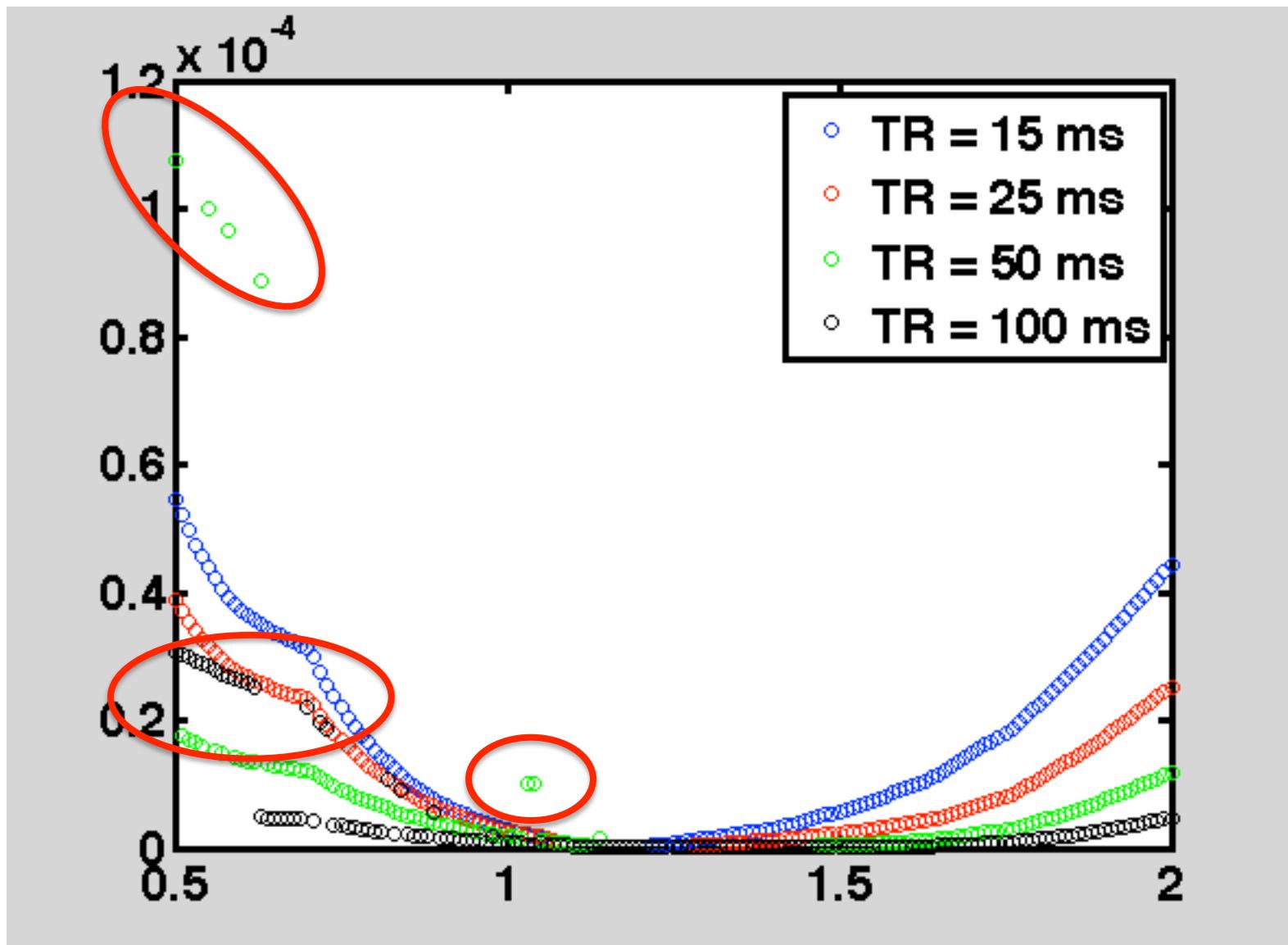
Simulated qMT F % error vs B1 errors using VFA (blue) T1 maps and fixed T1 value (such as IR) (red)



Error % of fitted qMT F

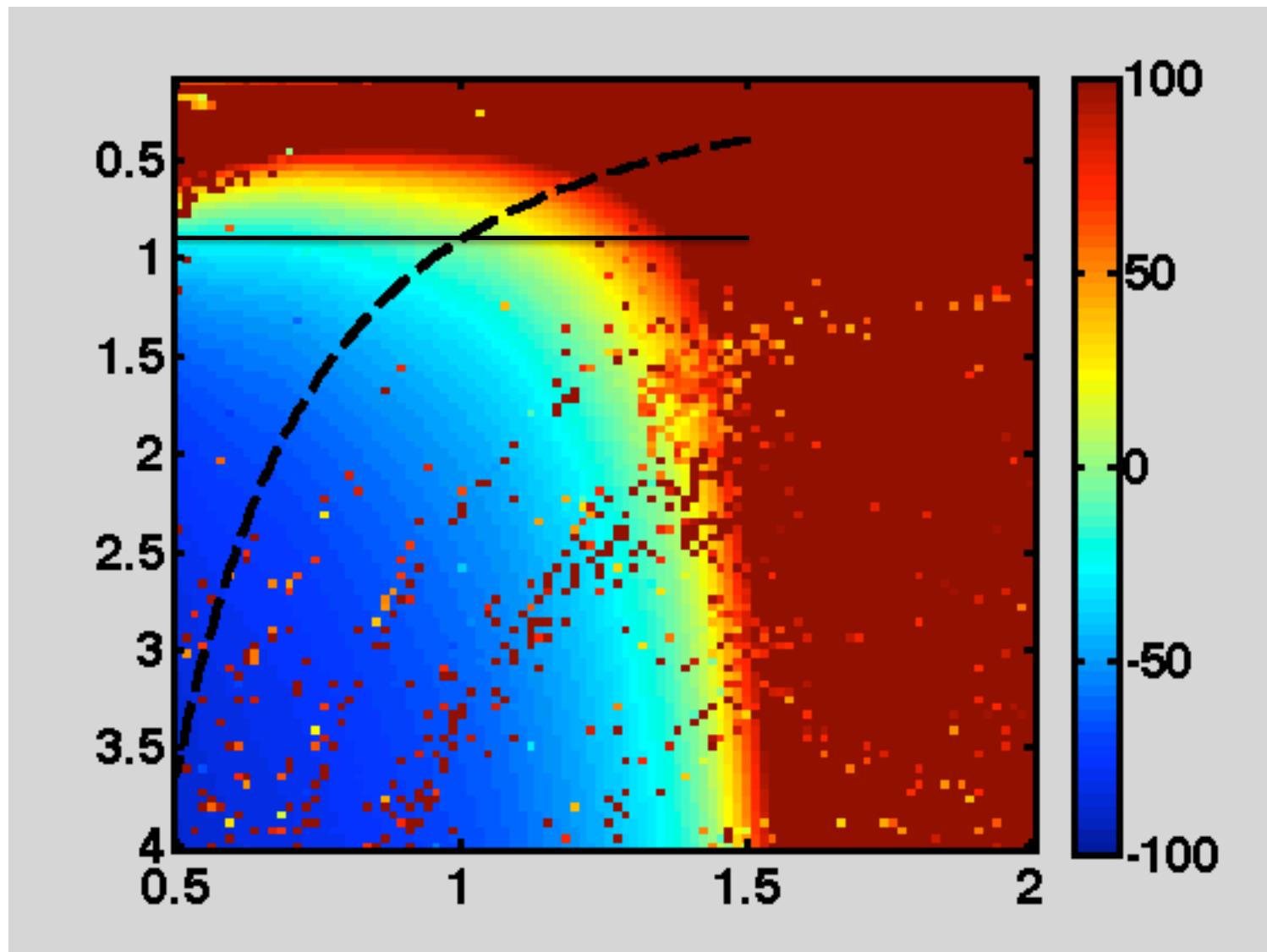


Fit root mean square error



Fitted qMT kf error %

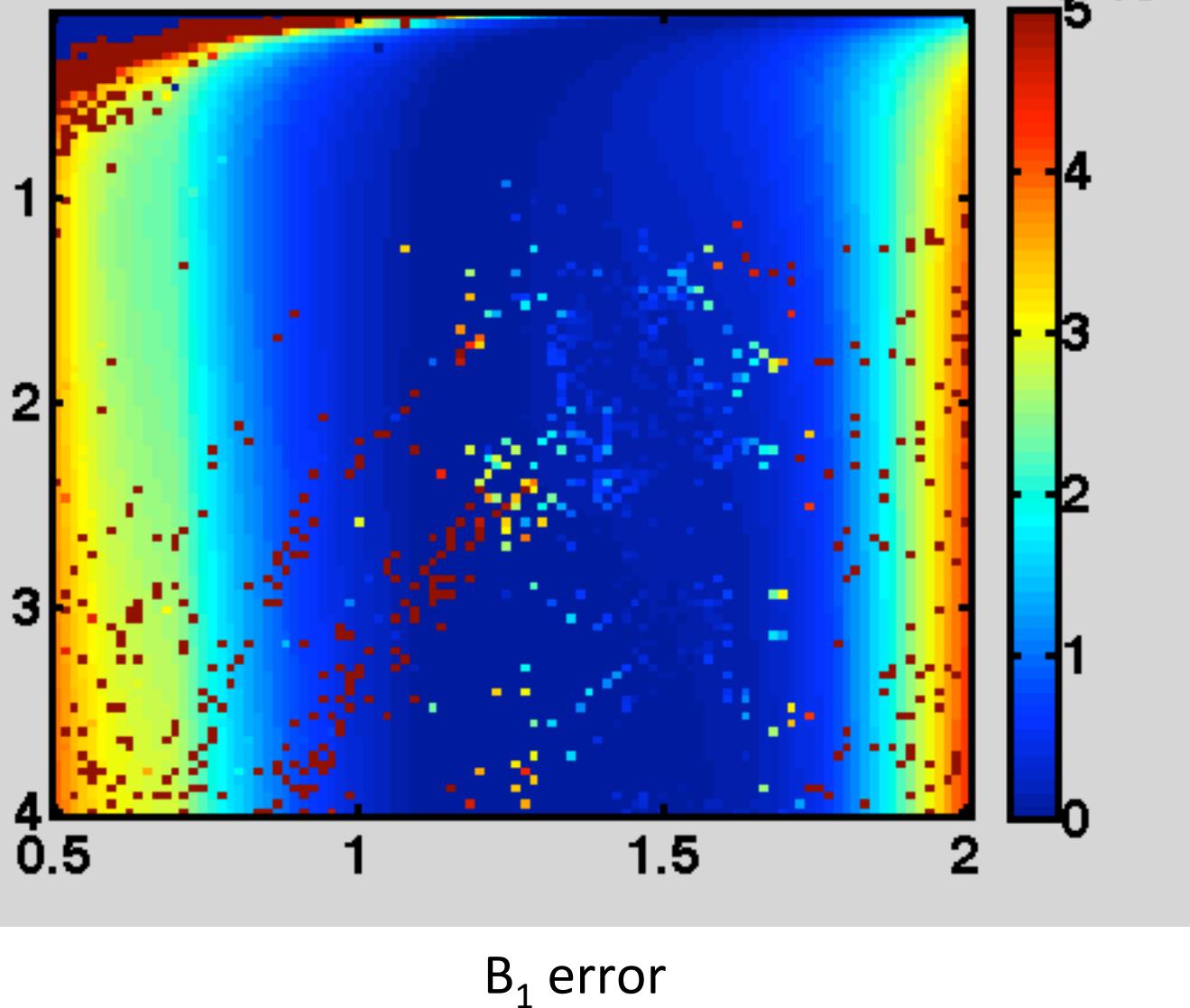
T_1 (s) error (true value 0.9)



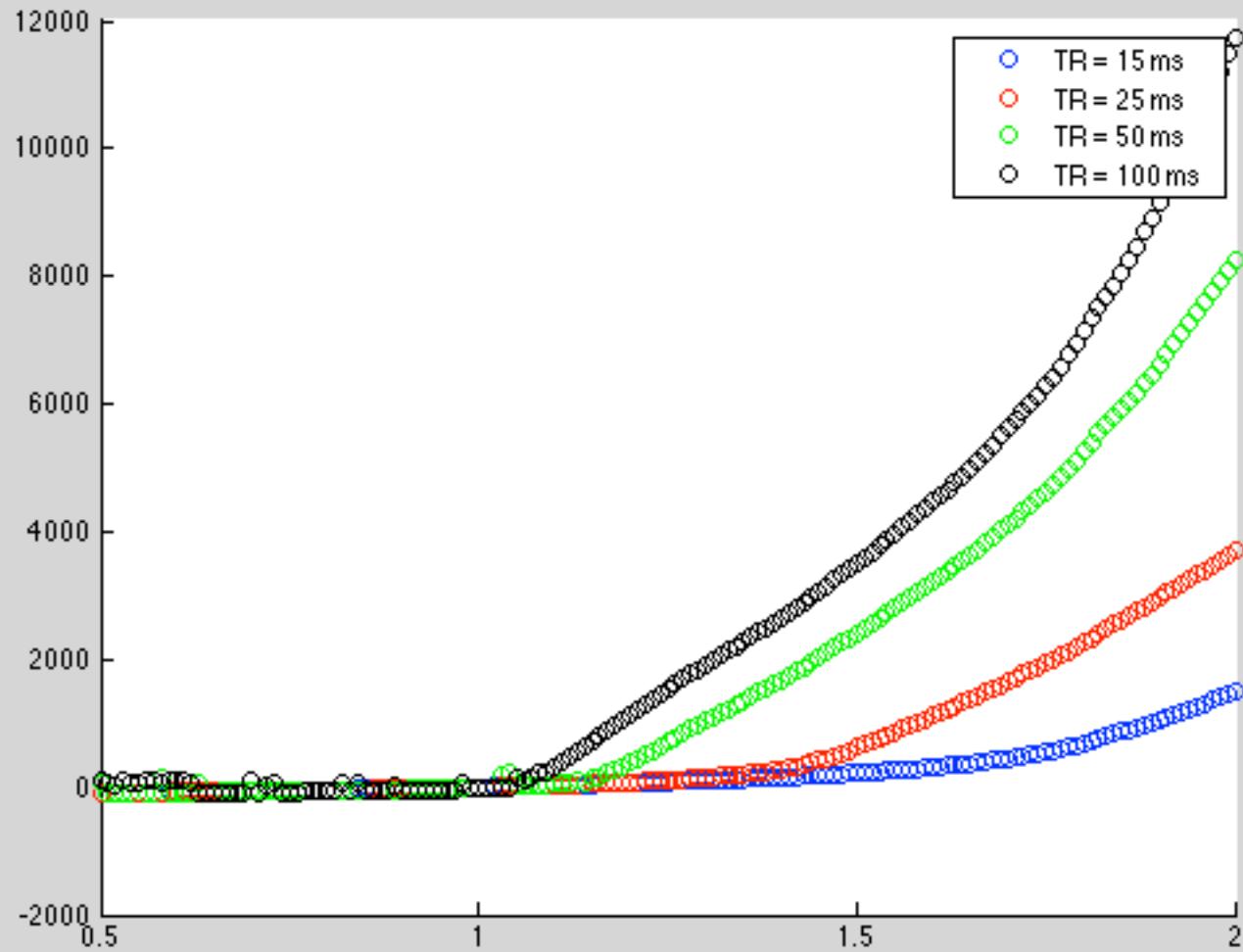
B_1 error

T_1 (s) error (true value 0.9)

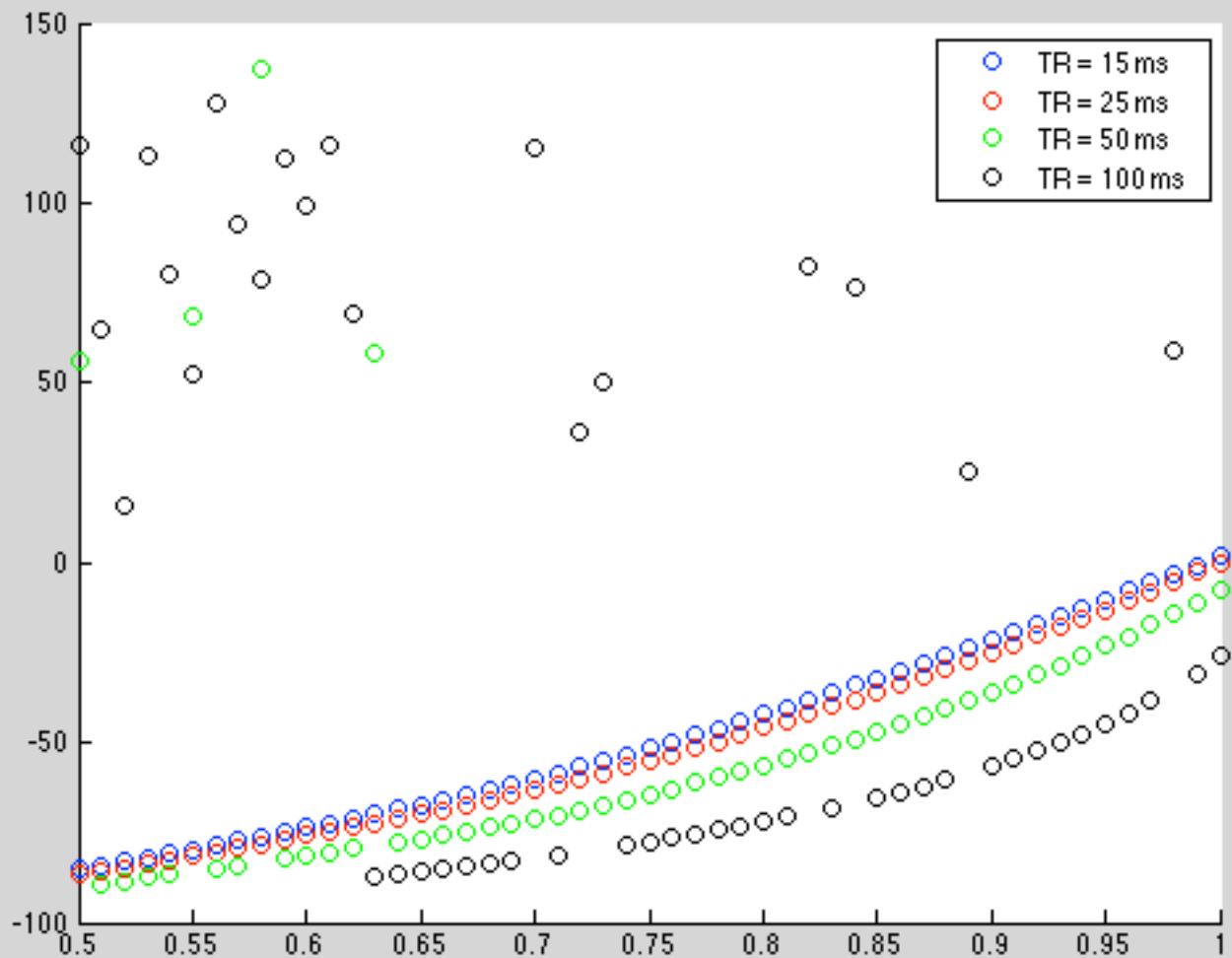
Root mean square error of fit



Error % of fitted qMT kf



Error % of fitted qMT kf



Noise simulations

- Omited

Stage 2: In vivo, Normal Subjects

- 3 Healthy subjects
- Single Slice
- T1: IR and VFA
- qMT: UK and Opt

B_1 error propagation

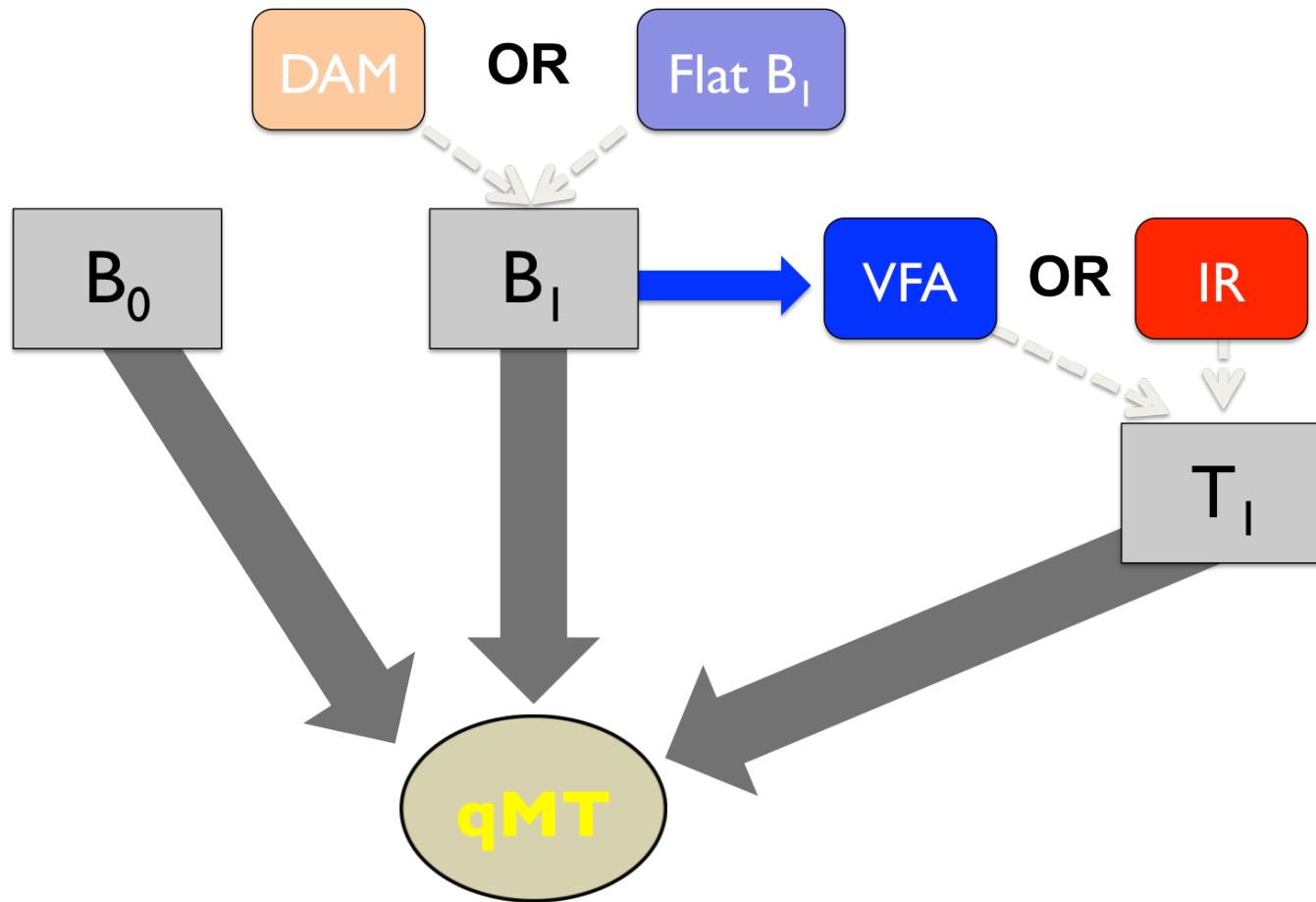


Figure I. Quantitative MRI protocol processing hierarchy.

Results – Measured B_1 vs. Nominal FA

Opt qMT protocol

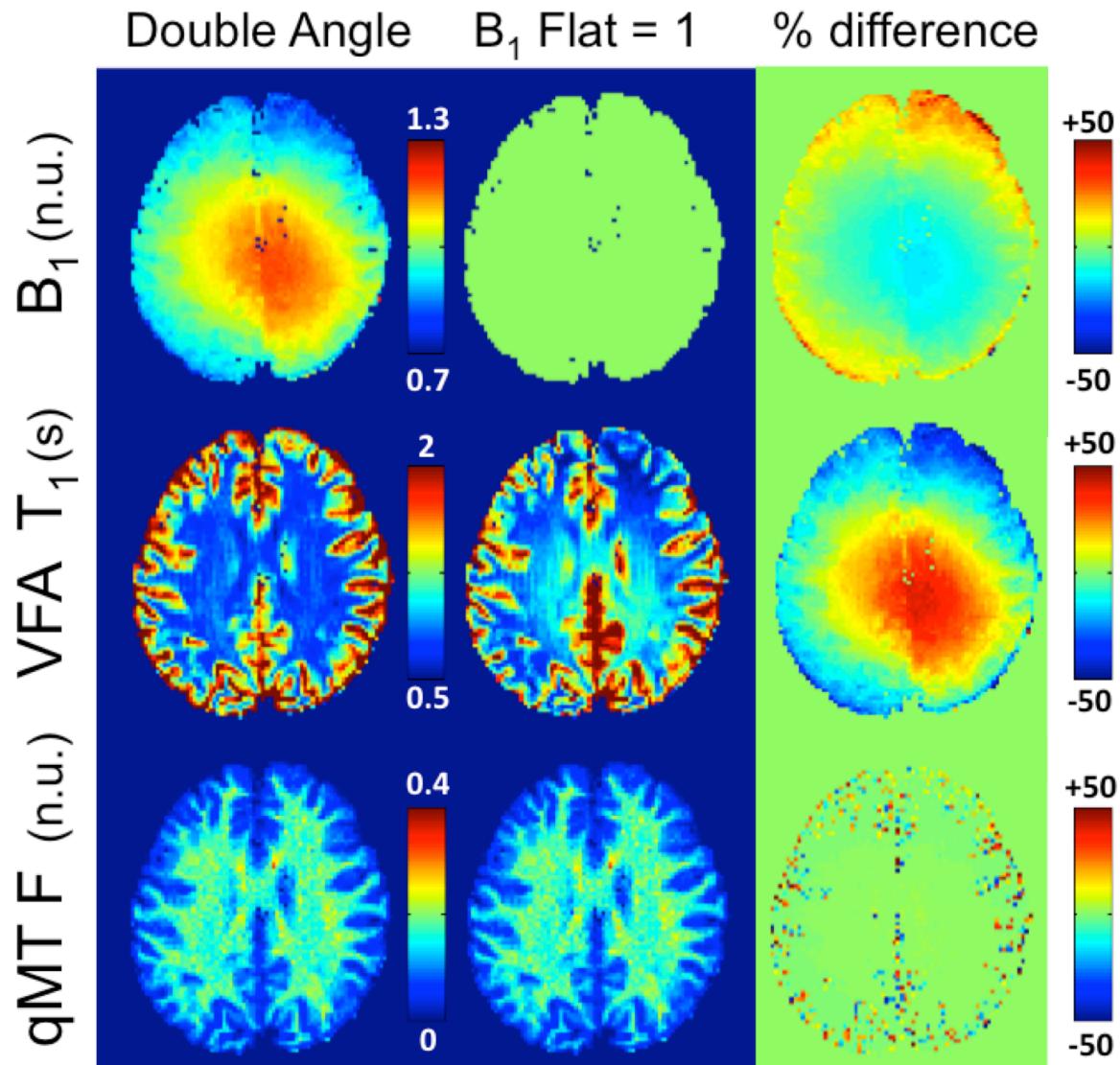


Figure 2. Comparison of VFA T_1 and qMT F maps using measured (DA) and nominal (B_1 flat = 1) B_1 maps.

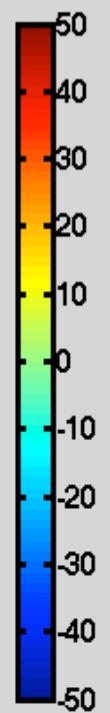
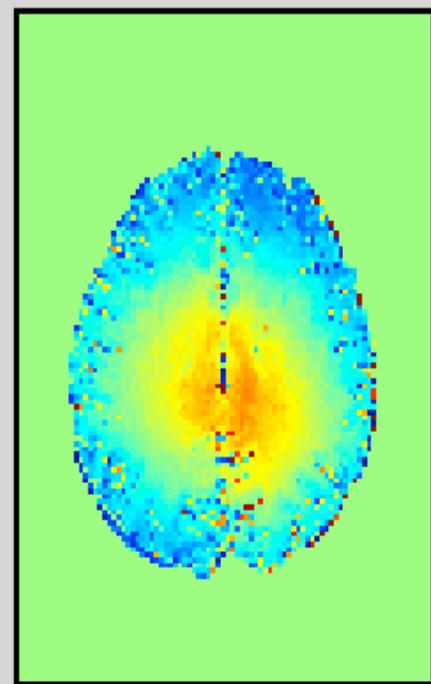
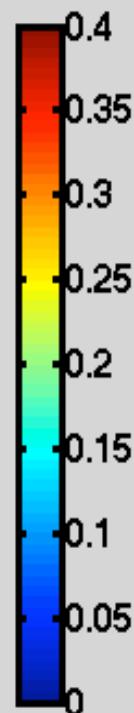
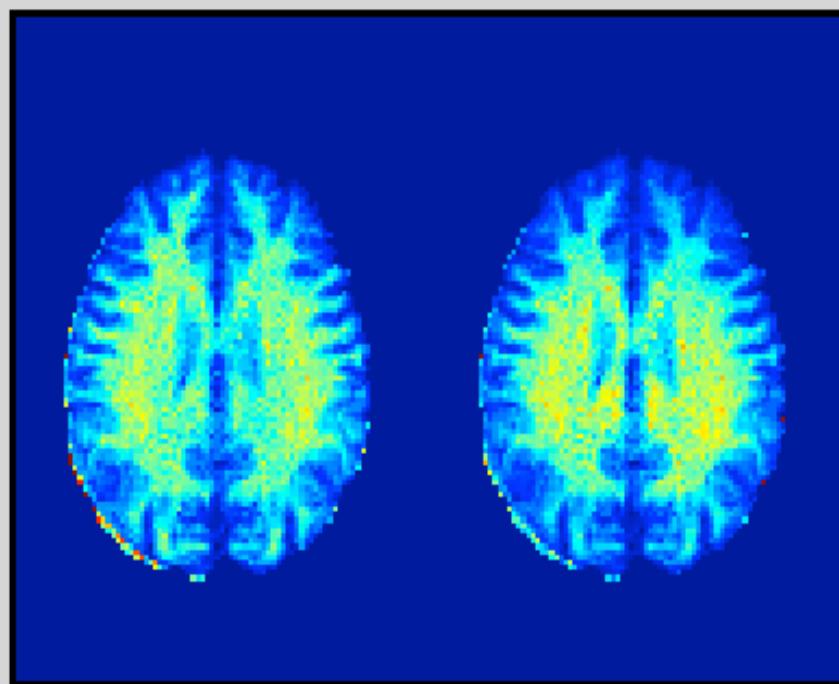
Opt qMT protocol

qMT F map

IR+(B1=DA)

IR+(B1=1)

% Difference

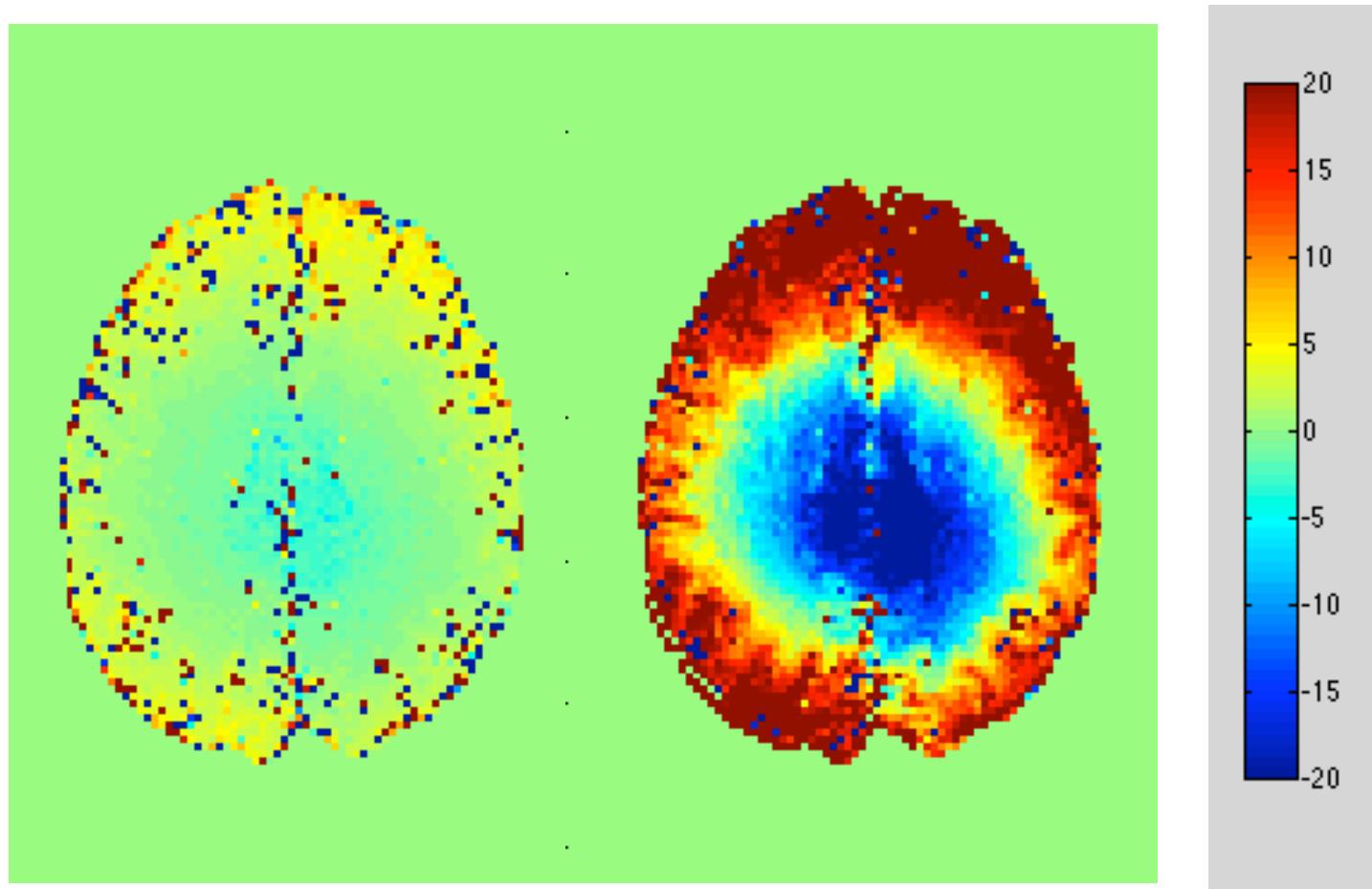


Error % in qMT F (UK Protocol)

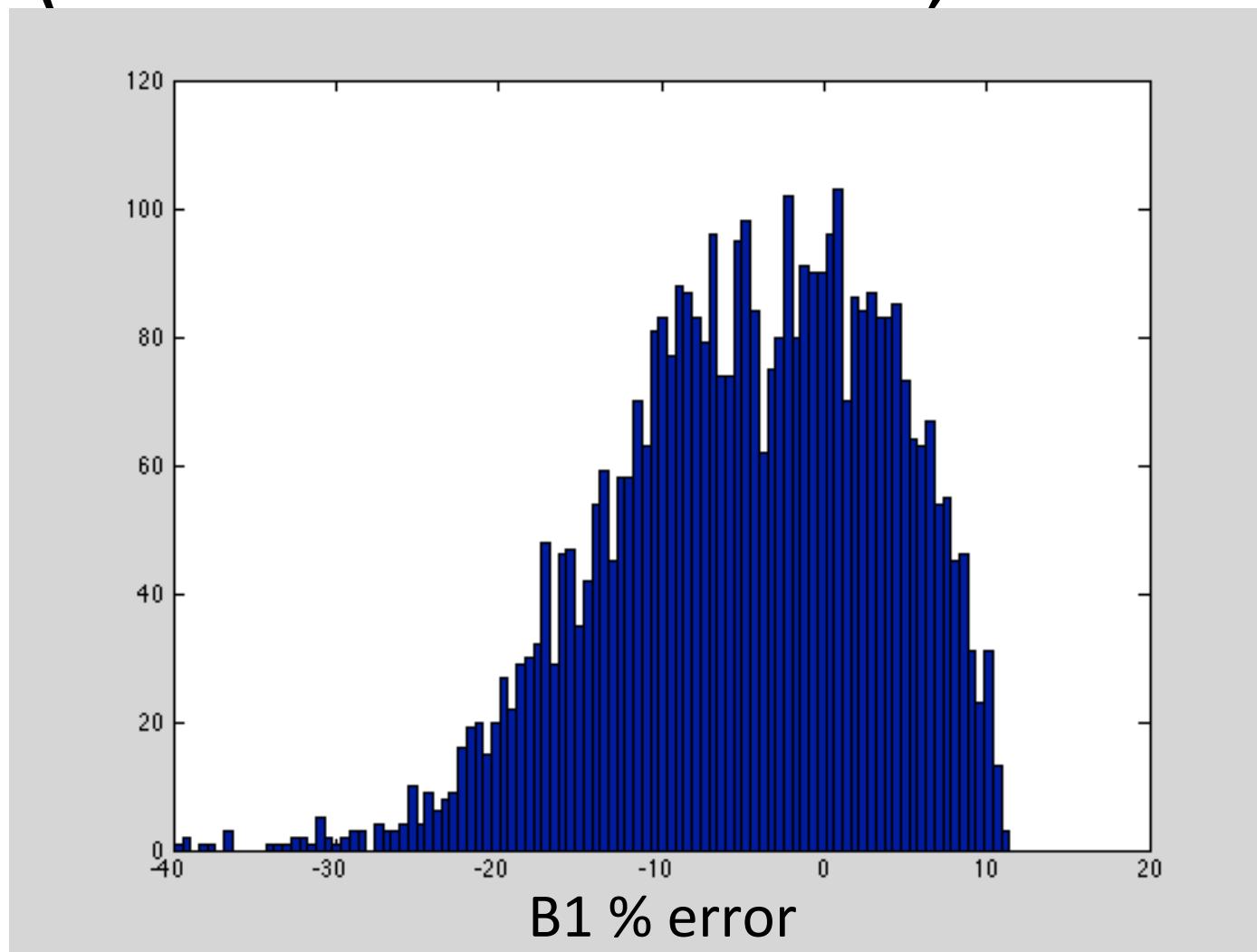
VFA

IR

*Scale bar changed
from last slides

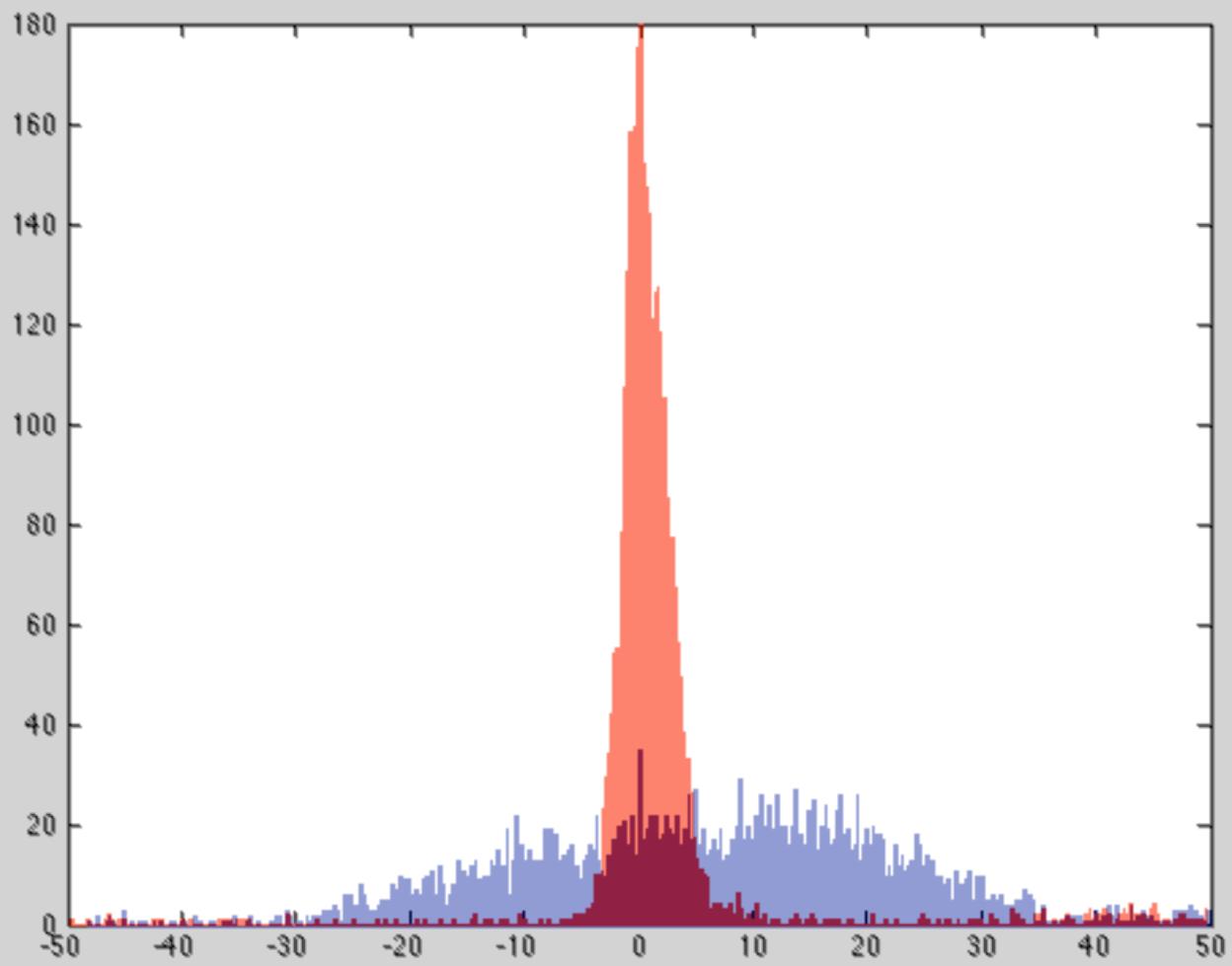


B1 % error in brain (relative to nominal FA, i.e. B1=1)



Error % in qMT F between
B1=Measured and B1=1 (flat/nominal)
(UK Protocol, 1 subject)

Red- VFA
Blue - IR



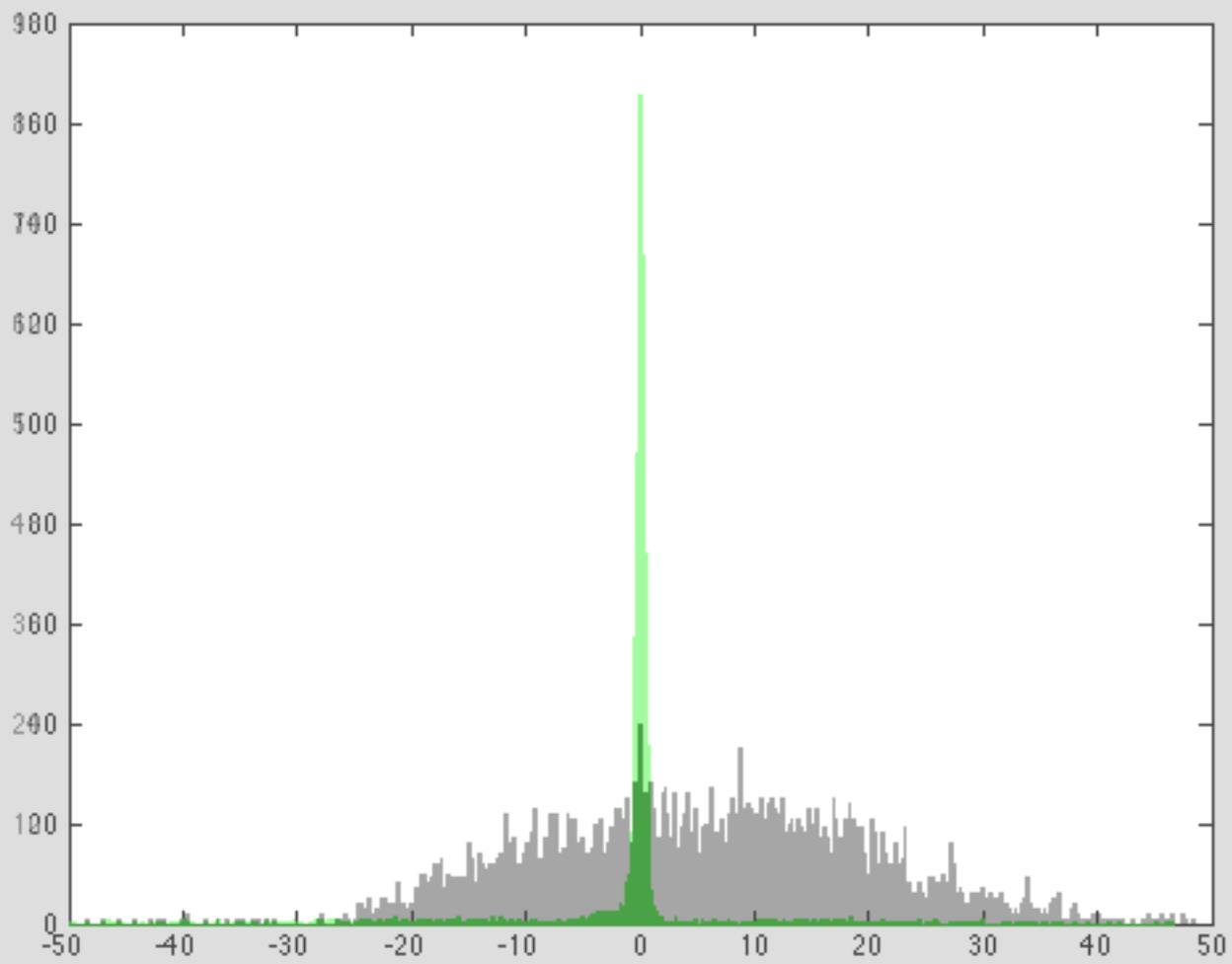
Error % in qMT F between

B1=Measured and B1=1 (flat/nominal)

(Opt protocol for green and black, 1 subject)

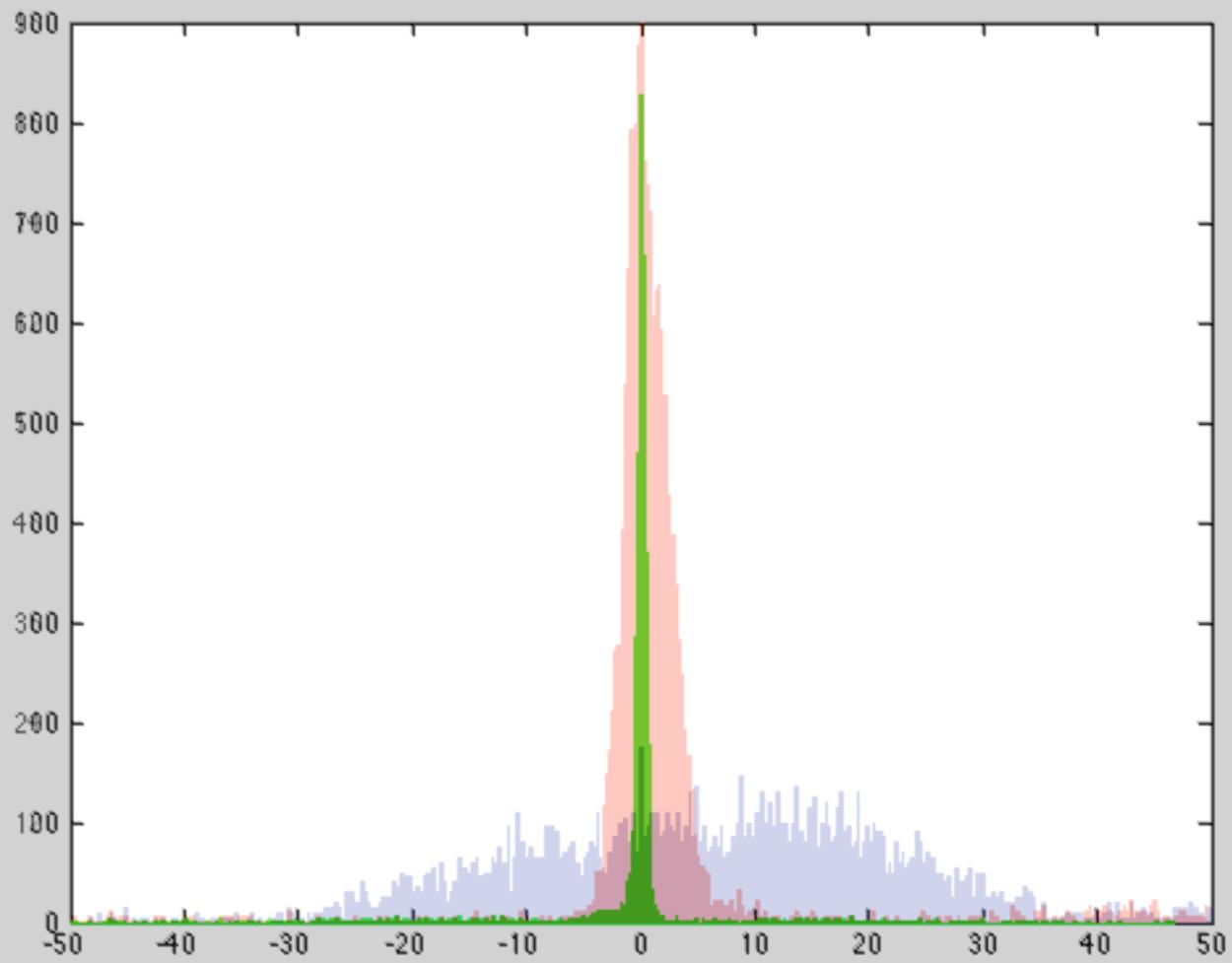
Green- VFA

Black - IR



Error % in qMT F between
B1=Measured and B1=1 (flat/nominal)
(UK Protocol for red and blue*, 1 subject)

*Green –VFA
& Opt 10 pt
qMT protocol



Opt qMT
protocol

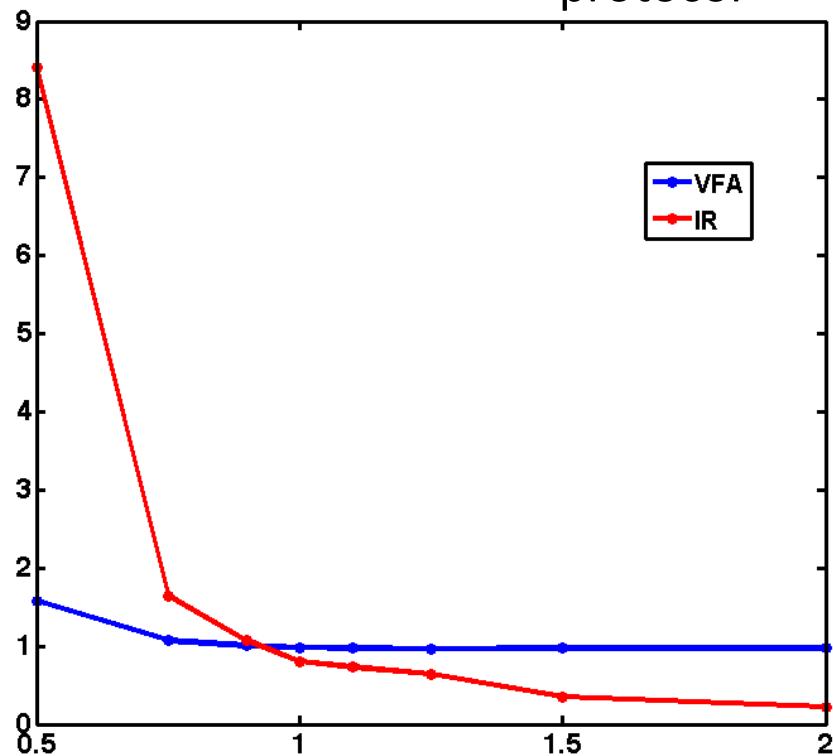
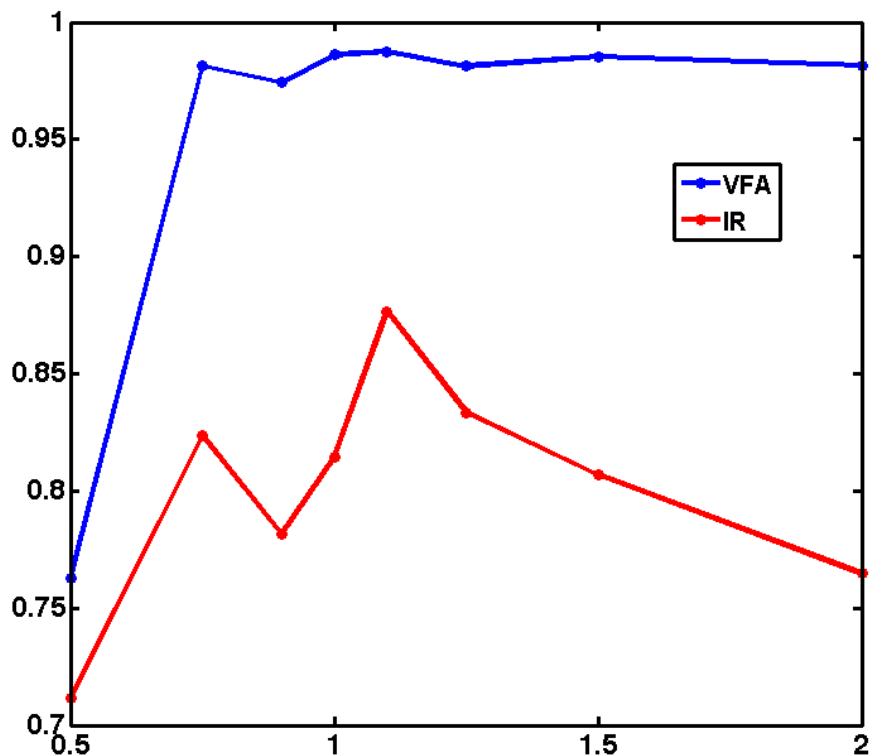
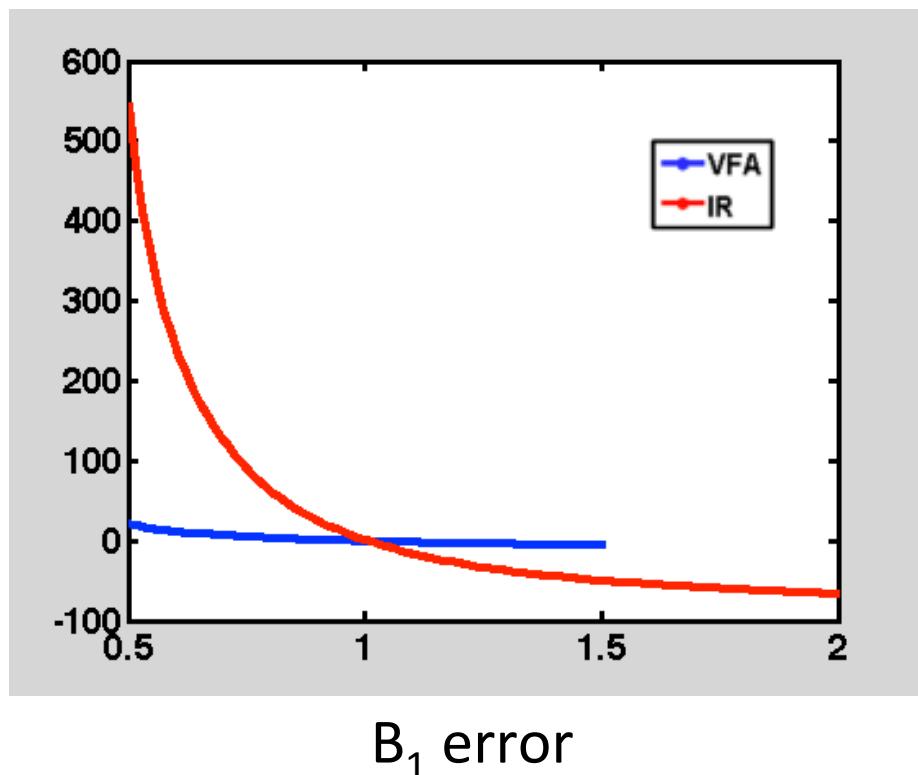


Figure 3. Linear regression analysis of the voxelwise qMT F parameter, comparing measured DA B_1 and a range of flat B_1 (VFA T_1 , blue; IR T_1 , red).

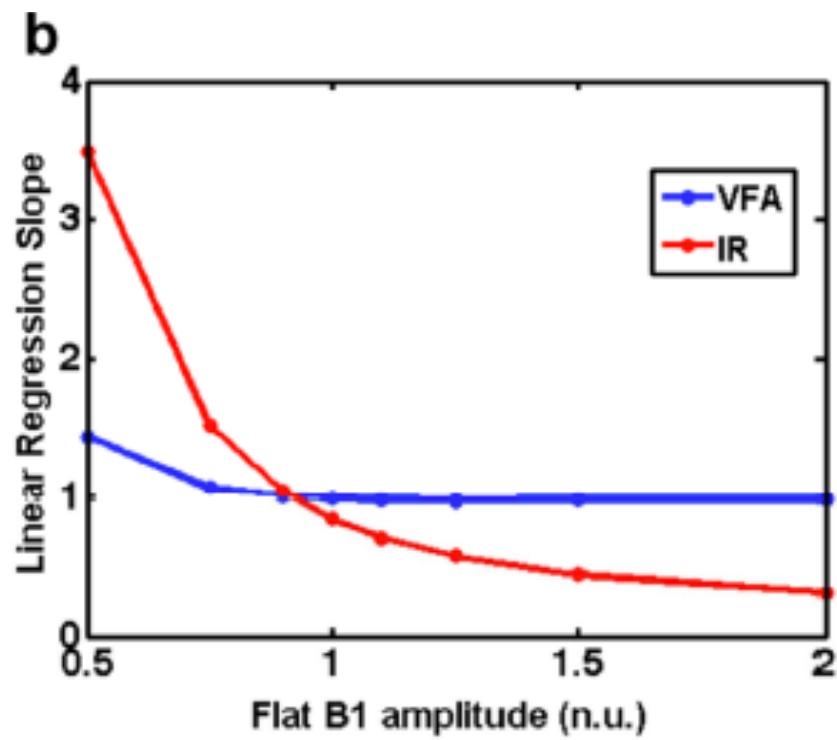
UK qMT
protocol

Simulated WM F % error



Opt qMT
protocol

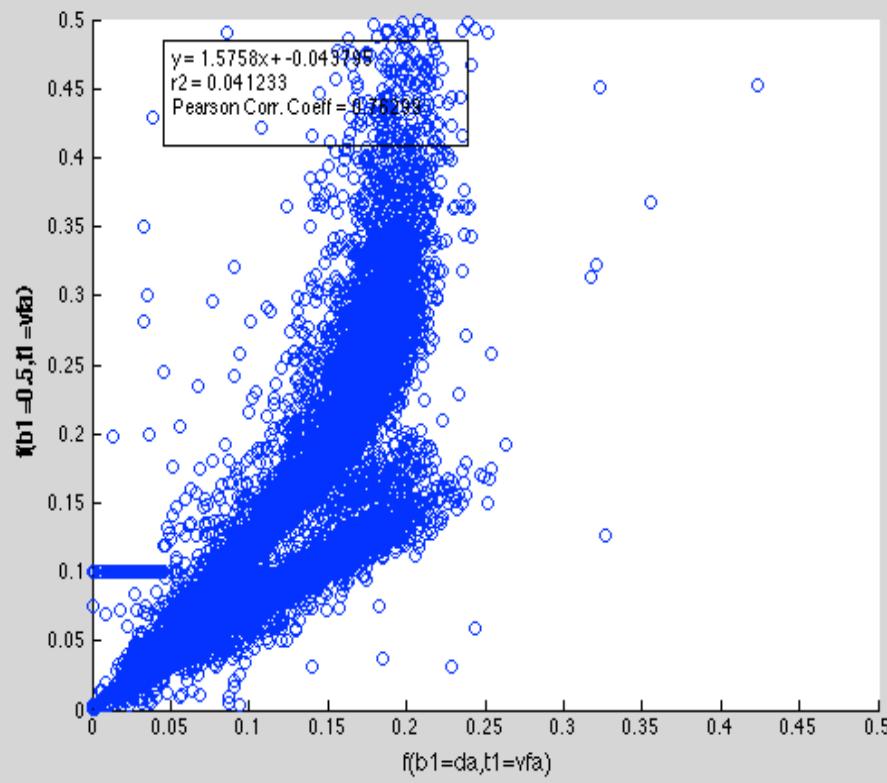
In Vivo Whole-Brain F



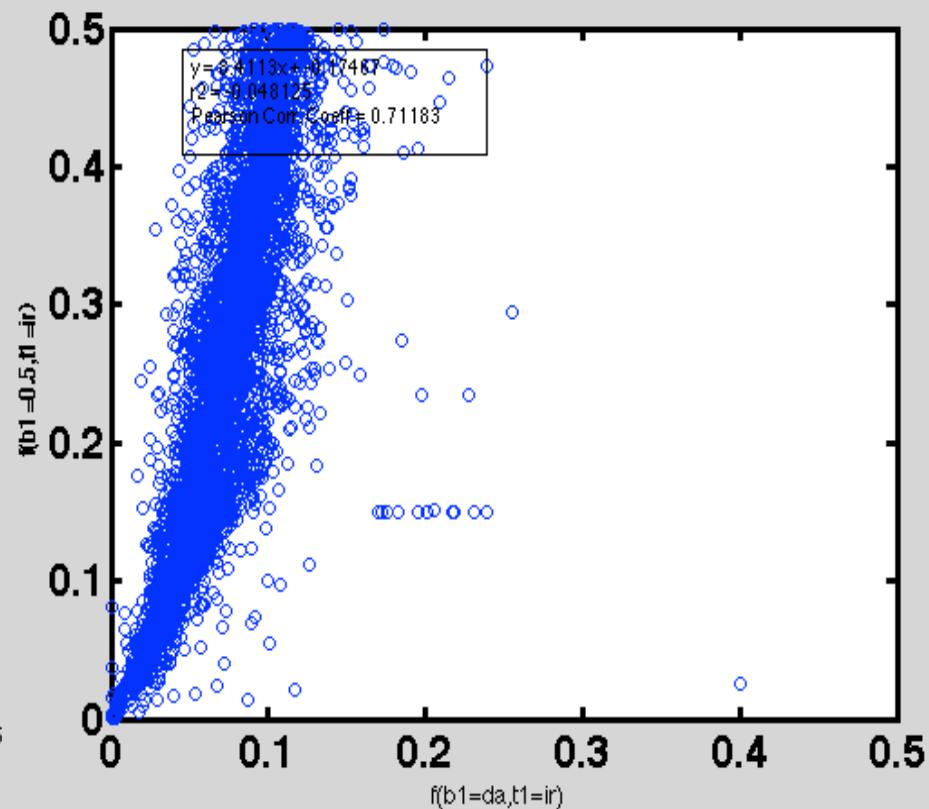
qMT F parameter comparison

B1 measured vs. B1 flat = 0.5

VFA



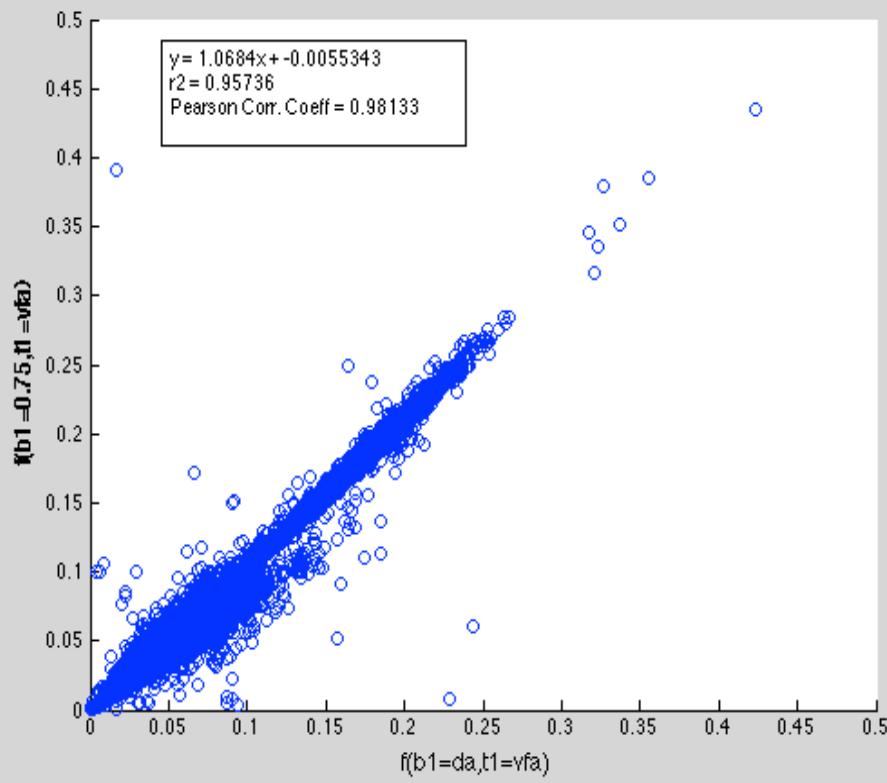
IR



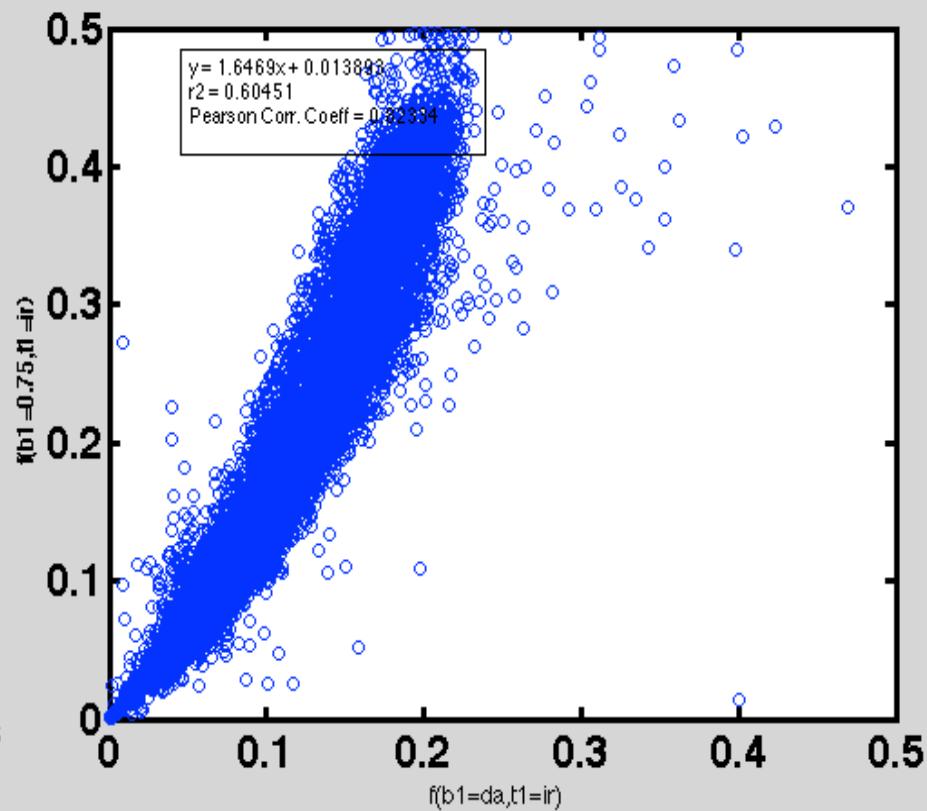
qMT F parameter comparison

B1 measured vs. B1 flat = 0.75

VFA



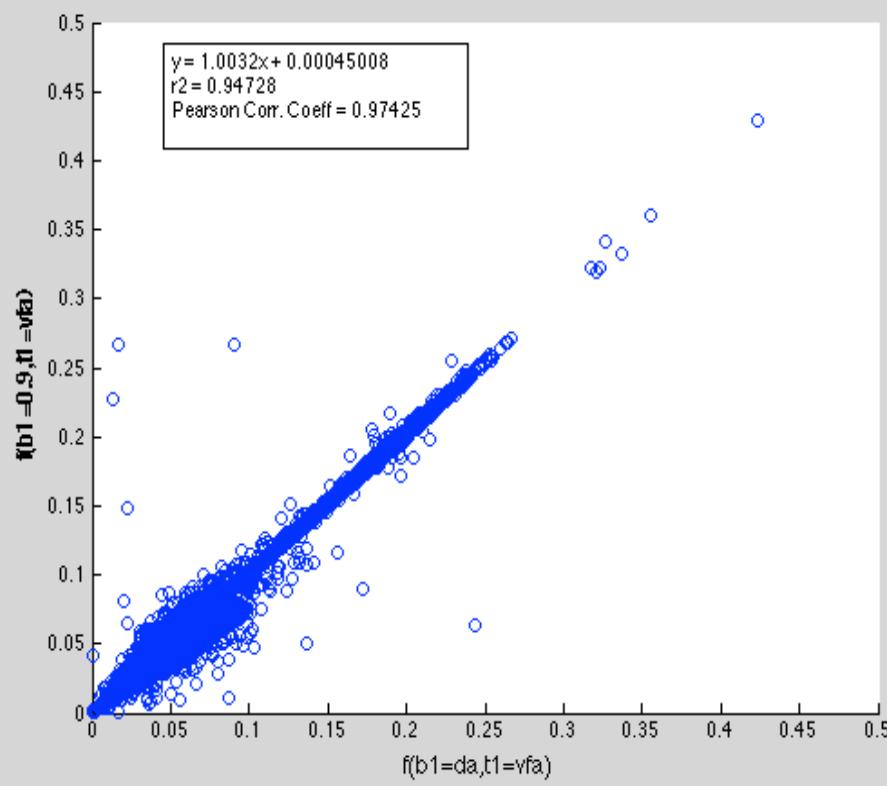
IR



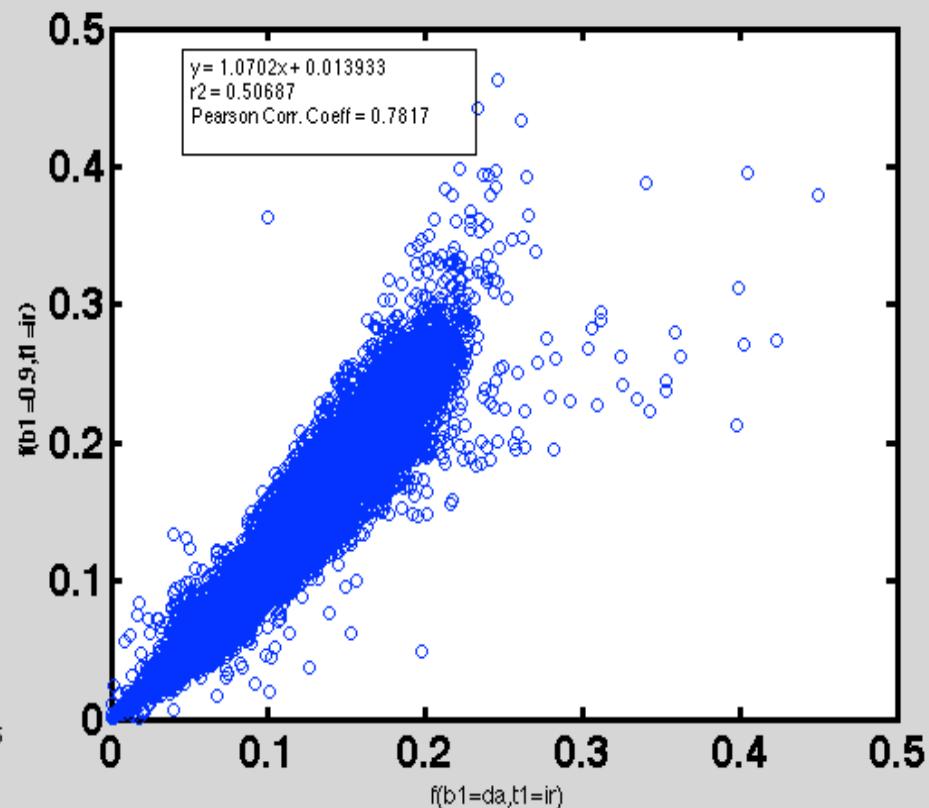
qMT F parameter comparison

B1 measured vs. B1 flat = 0.9

VFA



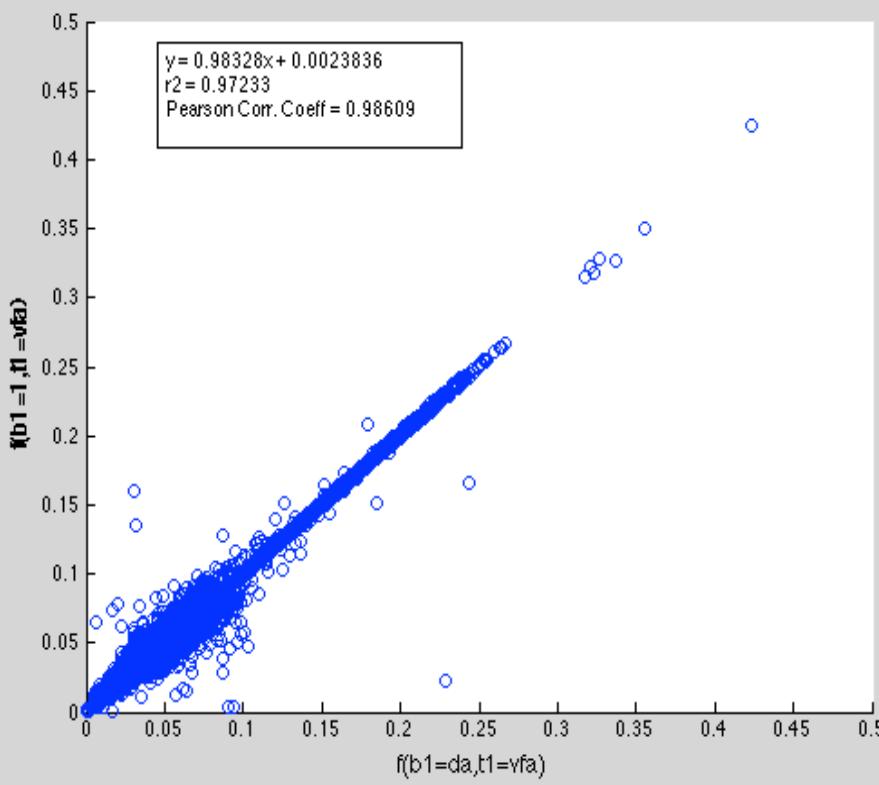
IR



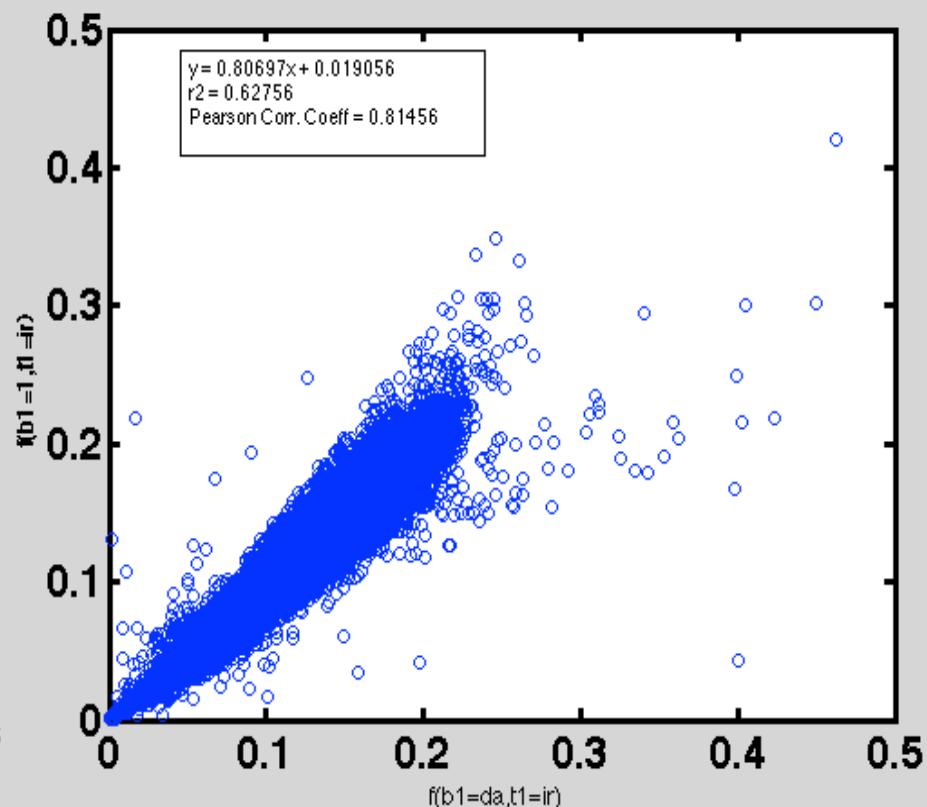
qMT F parameter comparison

B1 measured vs. B1 flat = 1

VFA



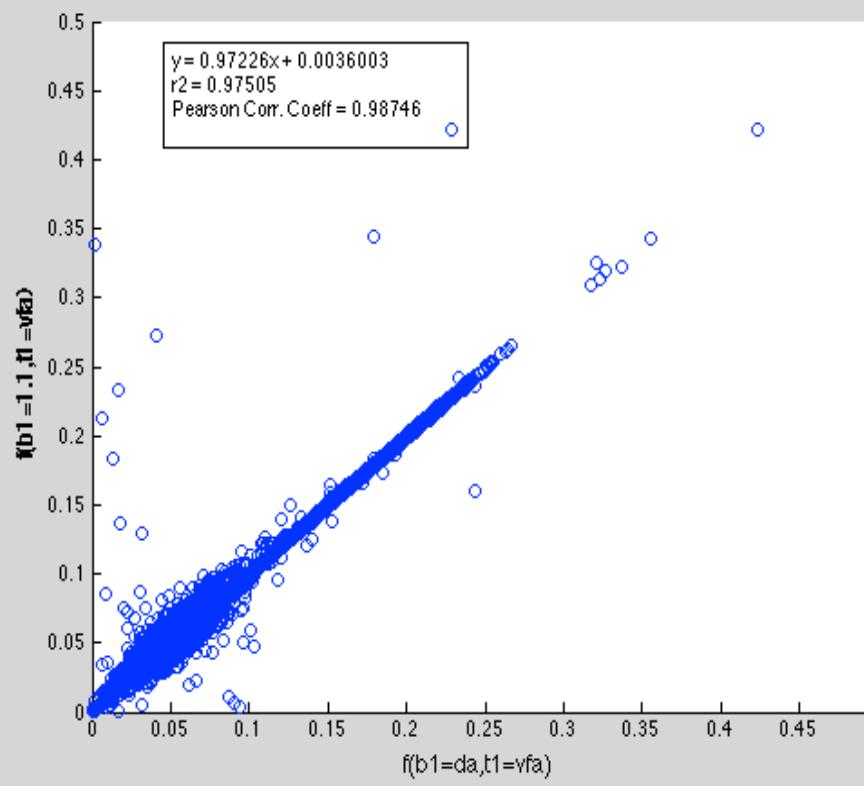
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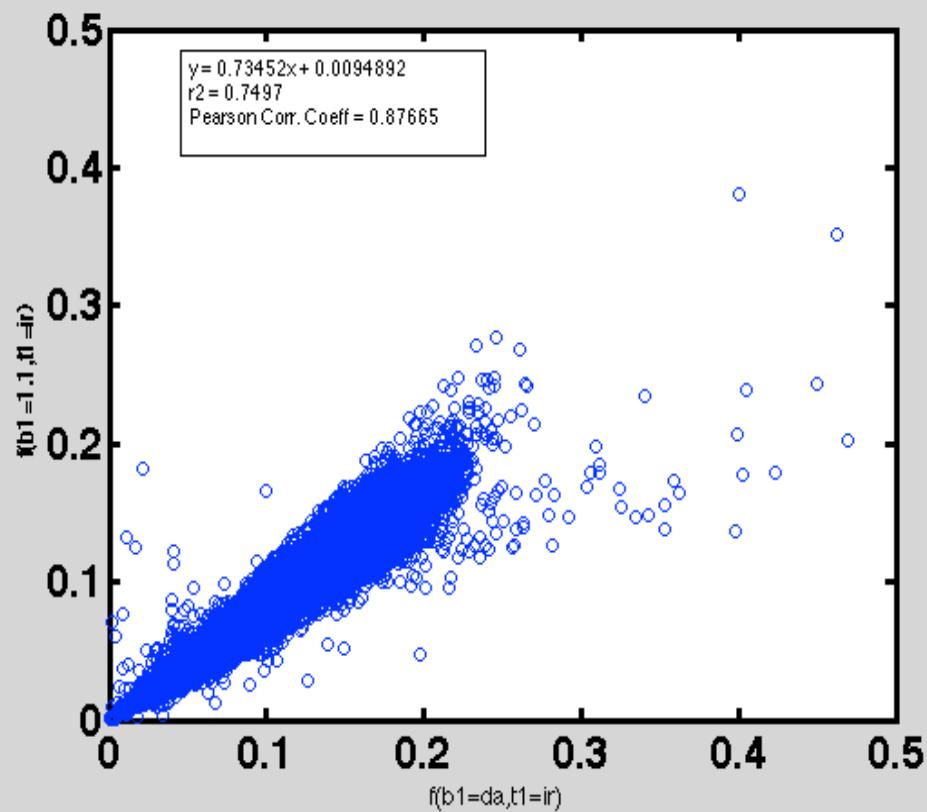
qMT F parameter comparison

B1 measured vs. B1 flat = 1.1

VFA



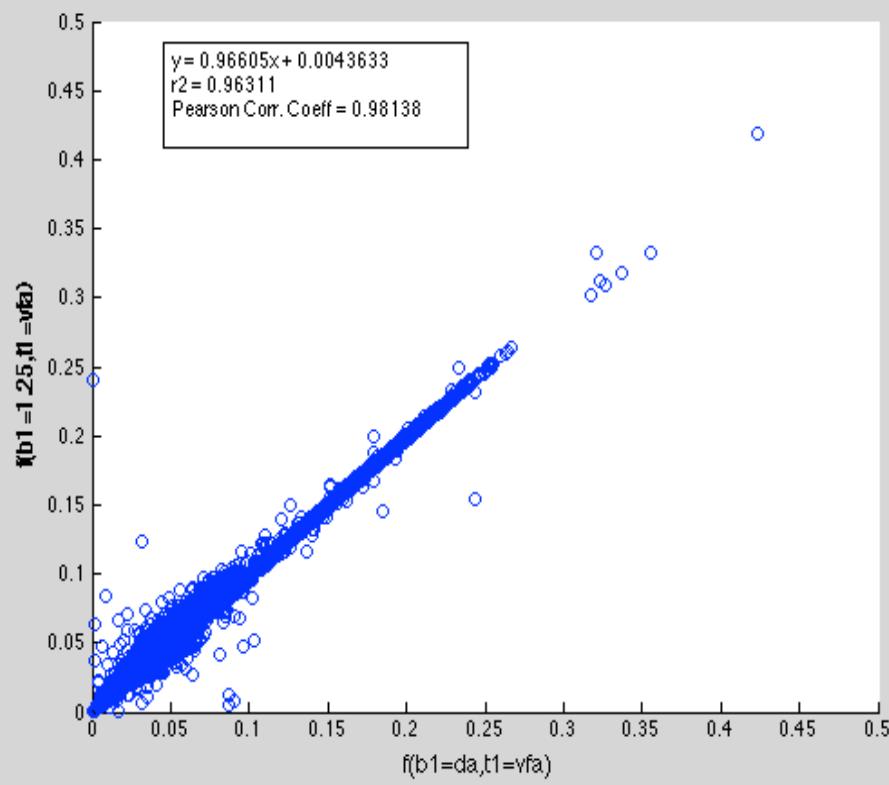
IR



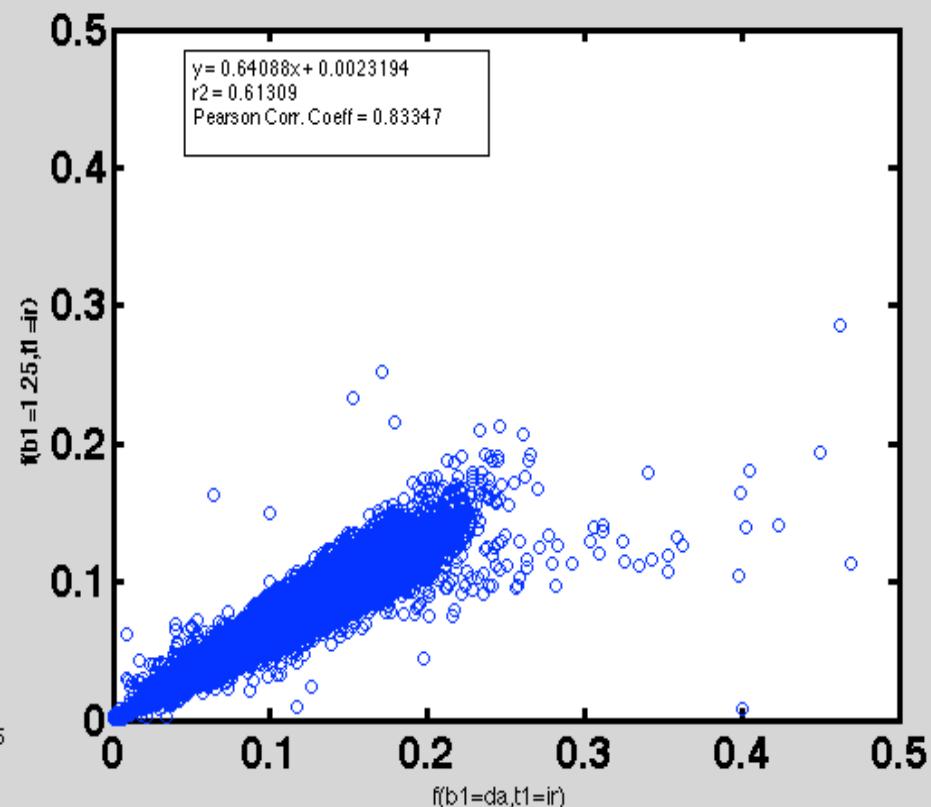
qMT F parameter comparison

B1 measured vs. B1 flat = 1.25

VFA



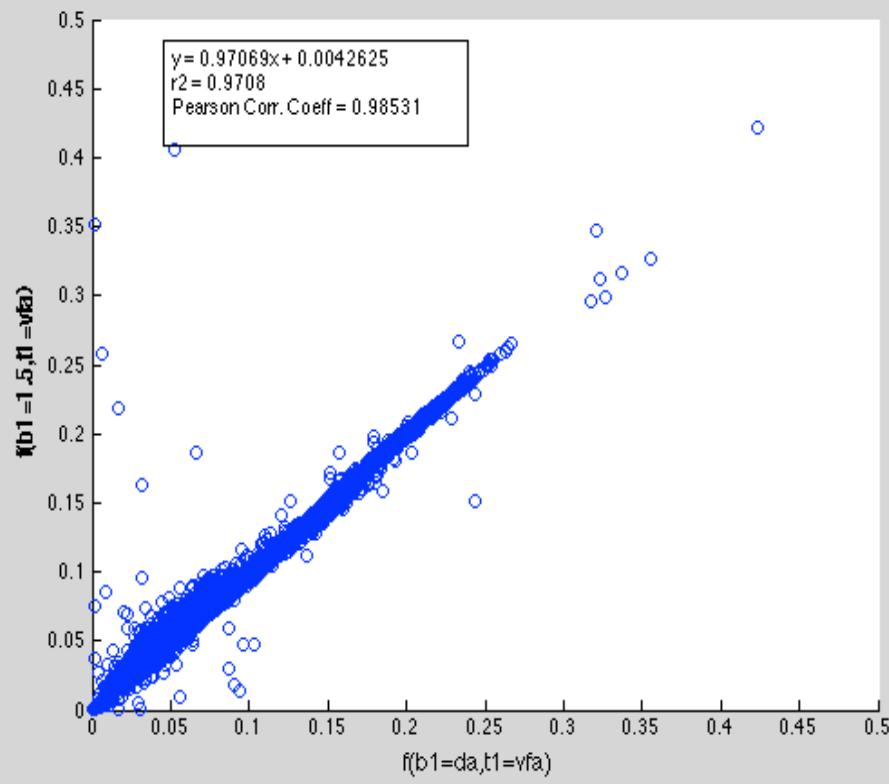
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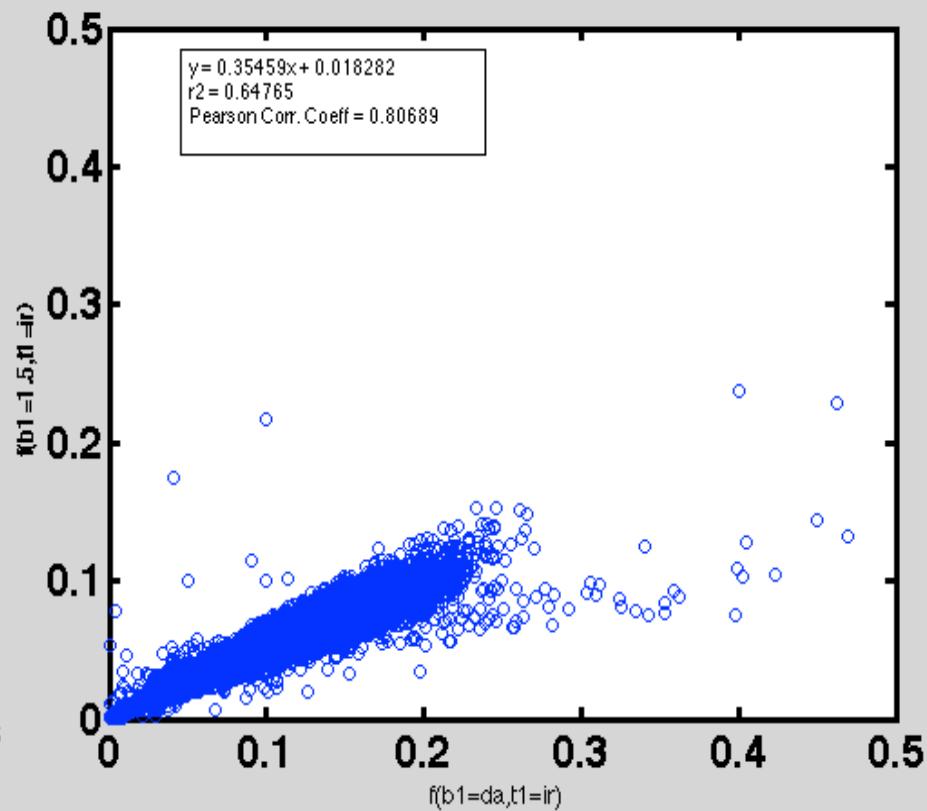
qMT F parameter comparison

B1 measured vs. B1 flat = 1.5

VFA



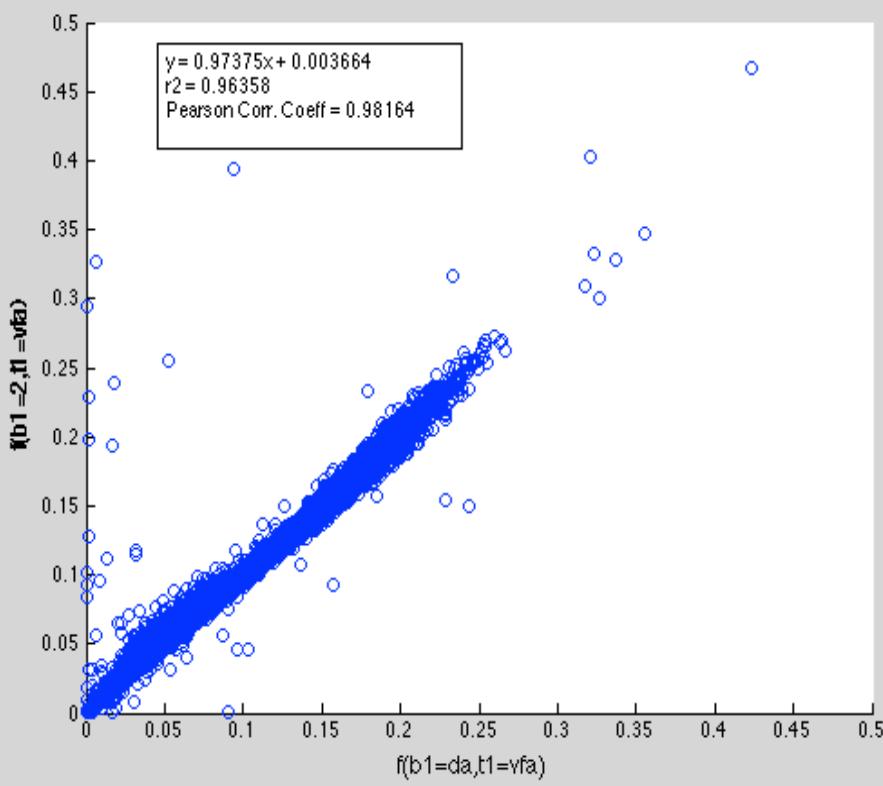
IR



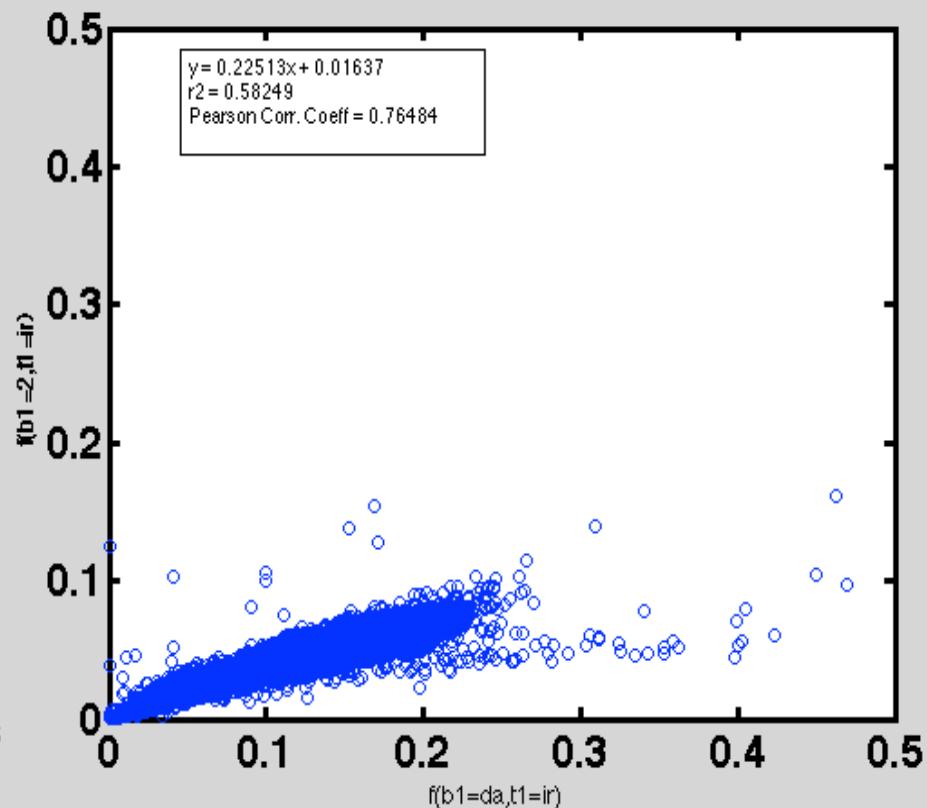
qMT F parameter comparison

B1 measured vs. B1 flat = 2

VFA

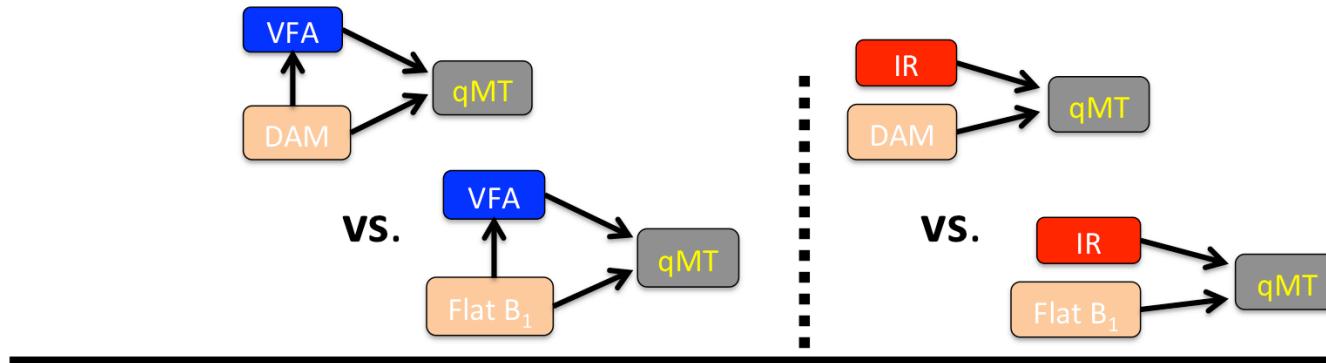


IR



Results – qMT Parameters

Table I. Voxelwise linear regression analysis of all fitted qMT parameters, using each T_1 method (VFA - left, IR-right), and a comparison of the measured (DA) and nominal FA (B_1 flat = I) maps.

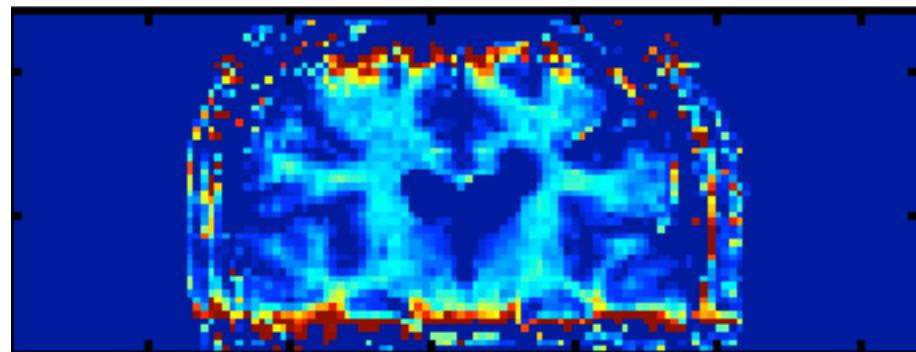
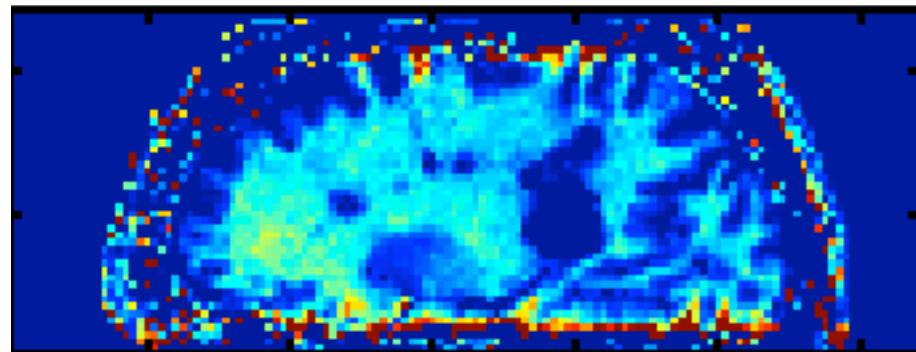
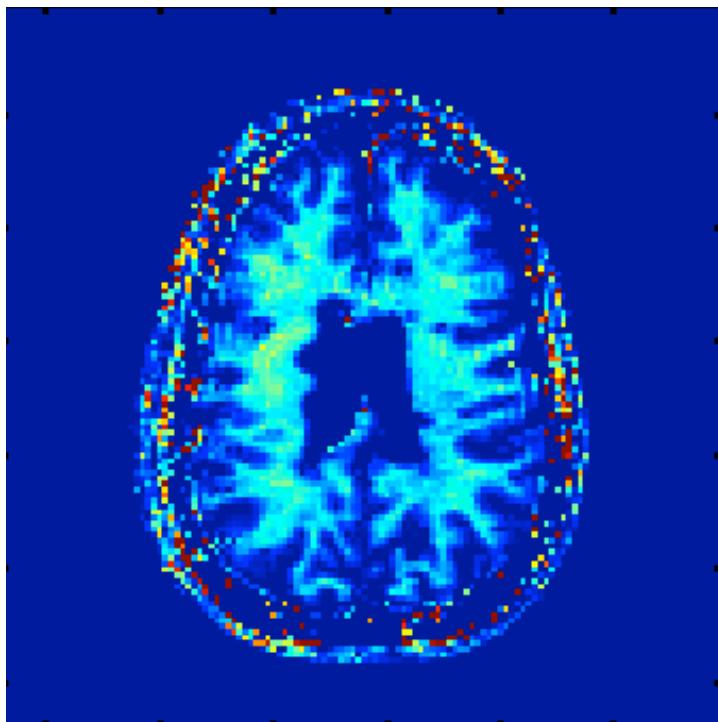
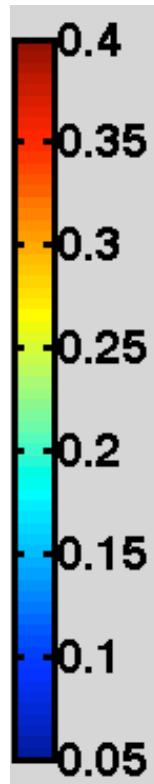


qMT	Pearson ρ	Slope	Pearson ρ	Slope
F	0.99	0.98	0.81	0.81
k_f	0.32	0.31	0.52	0.57
R_{1f}	0.81	0.98	0.78	0.71
T_{2f}	0.99	0.95	0.93	1.02
T_{2r}	0.92	0.90	0.87	0.91

Stage 3: MS Patient

- 3D data already acquired for another study at 3T
- Am I allowed to use this data? Which ethics form was used?
- To process with B1 flat+lesion masks

Relapse Remitting MS Patient



To do with $B_1=1$ (flat) + lesion masks

