Liver ^{1}H MR spectroscopy.

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MRS in the Liver

- Historically ^{1}H MRS used to estimate PDFF in liver.

- We are using MRS to estimate the type of fat or rapidly measure relaxation parameters.

- We have developed a STEAM sequence that collects spectra at multiple TRs and TEs in single breath-hold.

- A single breath-hold increases the ease of collecting the values.
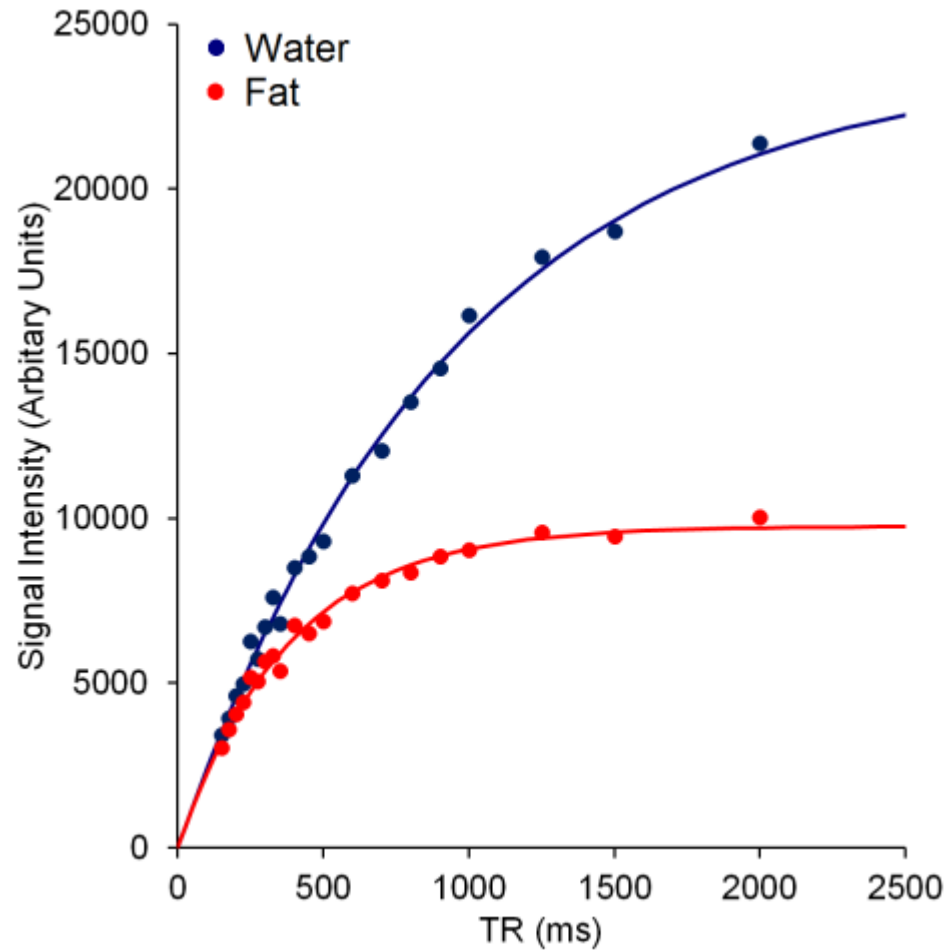
The Multi TR-TE sequence

- Acquire 32 spectra acquired in 21 s.

- TR range: 150 – 2000 ms

- TE Range: 10 – 110 ms

- Spectra analyzed using the AMARES algorithm in the MRUI software package.

- Use non-linear model to fit signal function
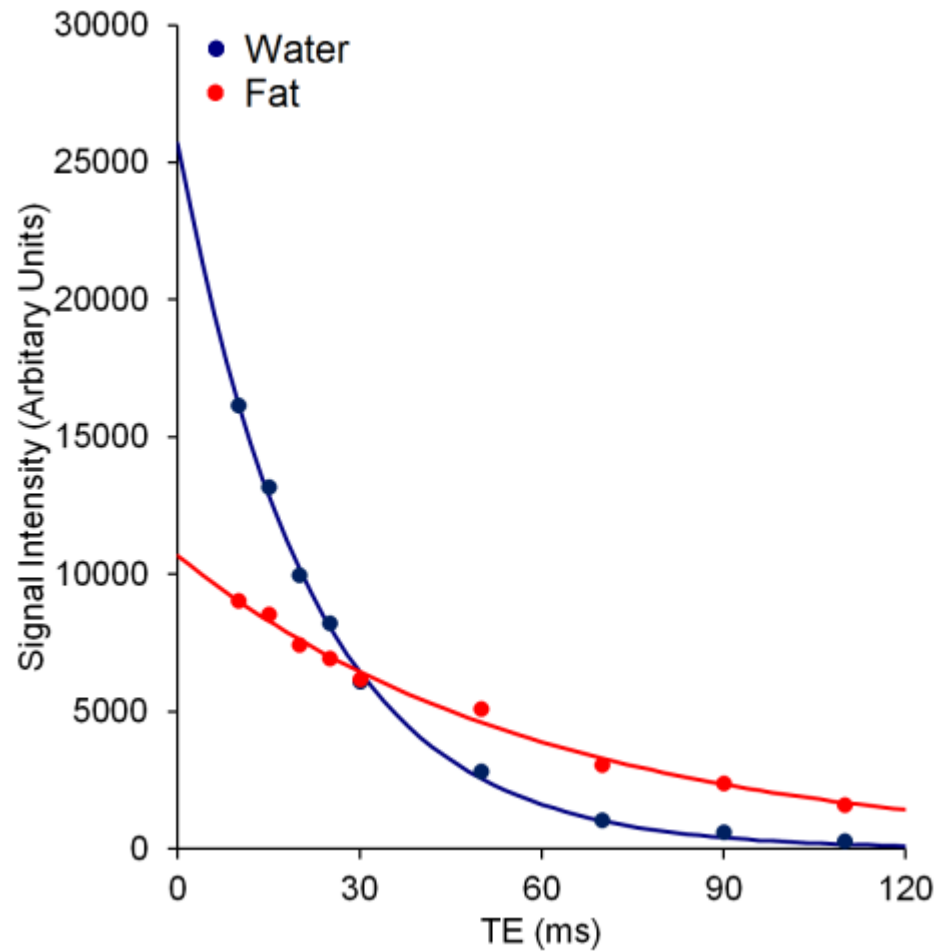 - $S = S_0(1 - \exp(-TR/T1)).\exp(-TE/T2)$
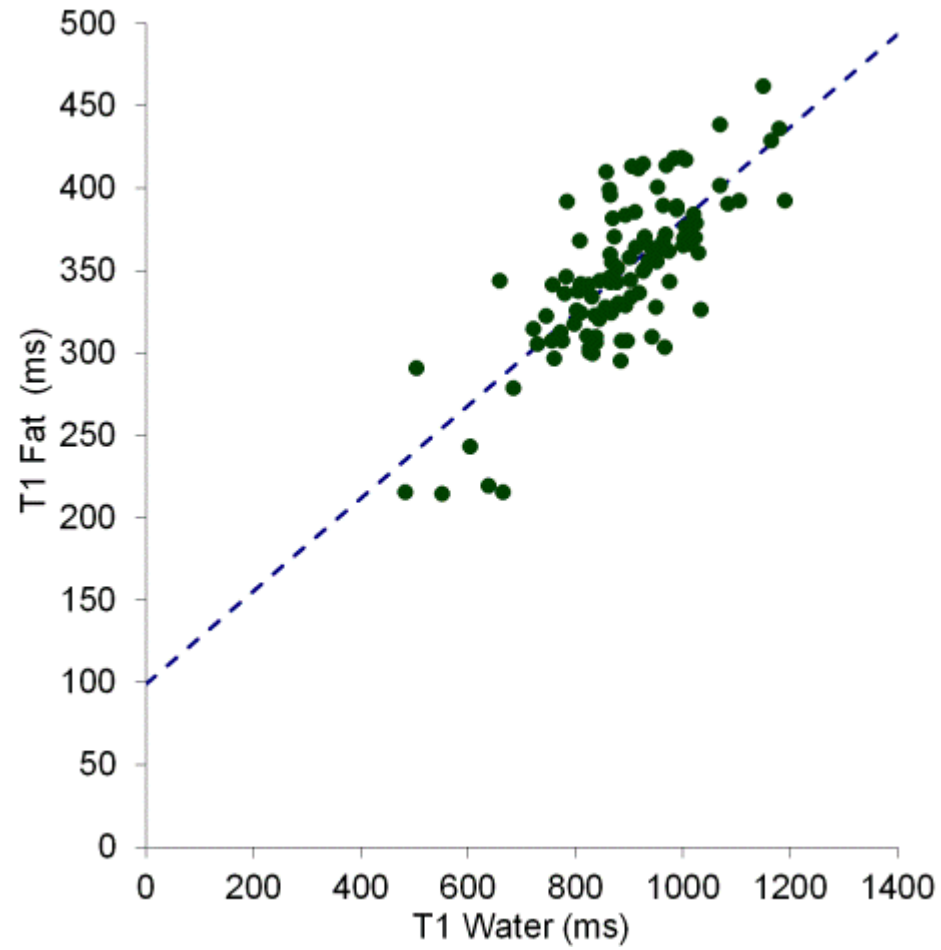
The Multi TR-TE sequence
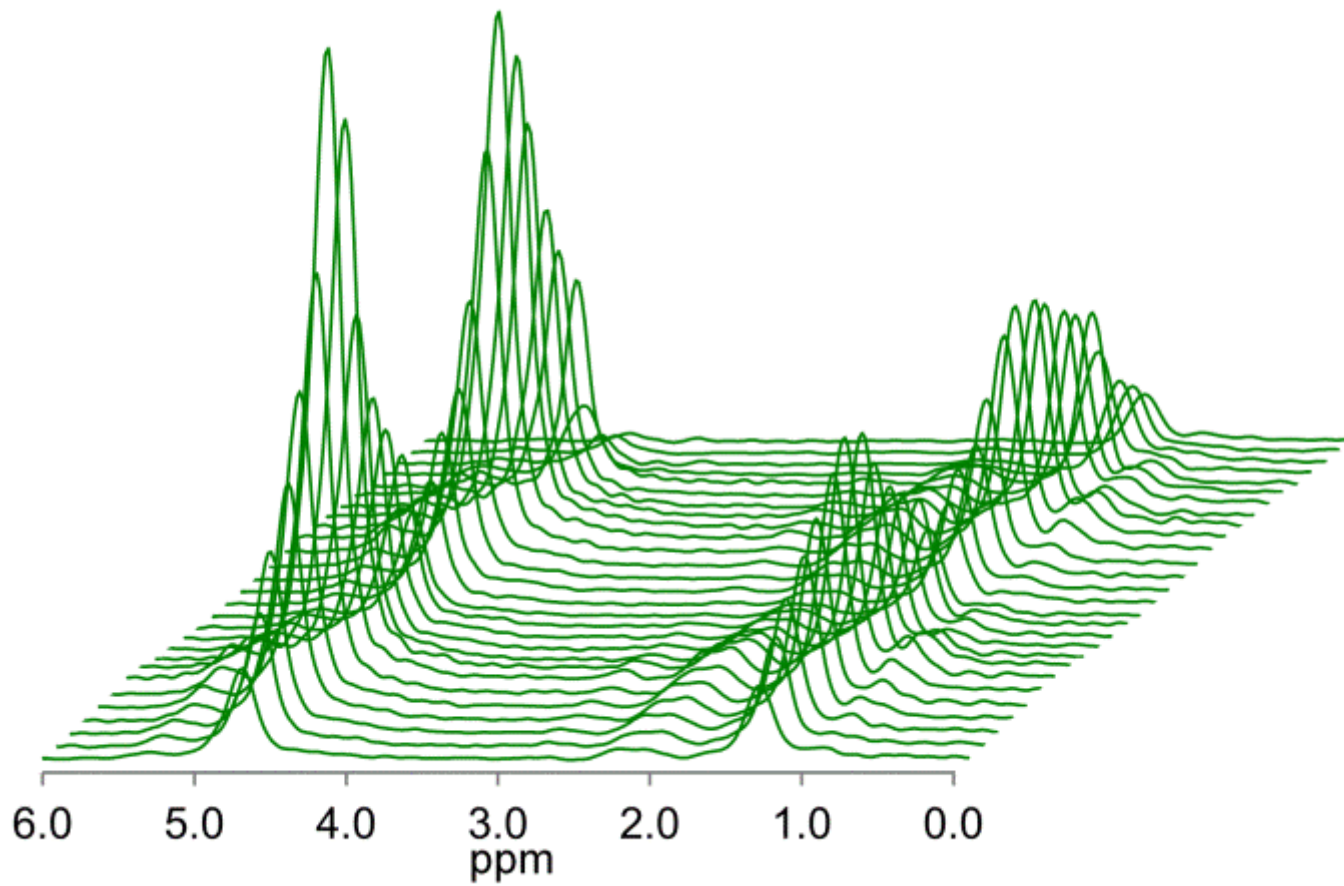
T1 measurement

T2 measurement

Fat T1 v Water T1

The Multi TR-TE sequence

- Sequence gives T1 and T2 of fat and water and liver proton density fat fraction in single breath-hold.

- Can measure T1 and T2s of liver water unconfounded by the amount of fat.

- Assessed by other sites for quantifying the amount of iron the liver.

- Have seen changes in water T1 with liver fibrosis.

Thank you