Using Artificial Intelligence to Assist in NMR Scanning

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Abstract. Nuclear Magnetic Resonance (NMR) data acquisition and processing is complex with many parameters that require the user to input to get valid results. For example, a simple CPMG T_2 measurement required no less than 22 parameters to be inputted by the user. Most of these parameters can be automatically calculated as a "best guess". For example, the measurement time (tau) is usually set to the minimum allowed by the instrument (which can be calculated). Other parameters such as recycle delay depend on the NMR properties of the sample being studied and thus cannot be determined ahead of time. Users follow work flows for determining these NMR properties to make educated guesses at these parameters. We have attempted to utilize Artificial Intelligence to put these workflows and "best guesses" into our software so the end user does not have to select any (or very few) parameters. Where direct relationships do not exist, we will utilize training sets to determine these values with the goal of obtaining "good" results 95% of the time. For more complex NMR measurements like 1D profiles or imaging the situation is even more complex as there are multiple NMR techniques (sequences) that can be used, each with advantages and disadvantages depending on the sample.

To implement the AI Scanning and Processing a series of "prescans" or simple NMR measurements are used to automatically determine some of the NMR properties. The values derived from these scans are then used to automatically select scanning and processing parameters. Investigations into which prescans to run and which NMR properties need to be defined were performed. For example, testing found that the NMR properties T_1, T_2, and T_2* were required to be measured by the prescans. Initially, it was first assumed that an iterative approach would be required to determine these properties (i.e. take one measurement, examine the results and try again). However, investigation and testing revealed that these properties could be determined by acquiring the prescans assuming the longest values expected for our samples (as defined by the user). Particular care was taken to monitor the additional scanning time required to run these prescans to prevent the total scanning time to become too long for practical use.

Armed with the information learned from honing the prescan process, a framework and design plan for AI assisted NMR scanning has been implemented. During the prescan process, the NMR properties T_1, T_2, and T_2* are measured automatically and then all the required parameters are calculated either based on these prescan values or "best practices". These prescan properties are measured using a Saturation recovery for T1, CPMG for T2, and a Free Induction Decay for T2*. These measurement techniques were chosen for their robustness and speed. Test measurements have also been performed to test the design and demonstrate its robustness. We are now working towards the final goal of having all scans and processing "AI enabled".

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1 Introduction

Nuclear Magnetic Resonance (NMR) core analysis has become a fixture in core analysis labs around the world [1]. It can yield vital information such as porosity, pore size distribution [1], bound vs. free fluid [1], wettability [2], saturation profile [3], 2D and 3D images [4]. Because NMR can yield so much different information and so many different NMR measurements exist, NMR data acquisition and processing is complex with many parameters that require the user to input to get valid results. For example, a simple Carr-Purcel-Meiboom-Gill (CPMG) T_2 measurement [5] required no less than 22 parameters to be inputted by the user. Without the correct parameters, the NMR measurements will give erroneous results leading to bad interpretation of the core analysis data. Experienced users know how to set these parameters correctly to optimize scan times and get the best results out of the NMR data. We have set out this year to automate this experience making it easier for all users to achieve the optimal scan times and get the best results irrespective of NMR experience.

2 Results of Poor Choices of NMR Parameters

Figure 1 shows three examples where a poor choice of NMR parameters for a CPMG T_2 measurement can lead to flawed results. Figure 1 (a) shows three different T_2 distributions each taken with three different tau values. Tau is the spacing between the pulses in a CPMG sequence. The shorter the tau value, the shorter the minimum T_2 value that can be measured. It is important to select your tau value small enough so that the smallest pores (with the shortest T_2 values) are fully measured. As can be seen from Figure 1 (a), a CPMG sequence with a 100 µs tau (Figure 1 (a) – Black trace) fully observes the entire T_2 distribution. As the tau value is increased to 300 µs (Figure 1 (a) – Blue trace) and then 600 µs (Figure 1 (a) – Red trace), less and less of the short T_2 components are observed. This can lead to a reduction in the observed pore volume. For example, increasing the tau value from 100 µs to 600 µs can decrease the observed by approximately 20%.

Figure 1 (b) shows four T_2 distributions each recorded with a different recycle delay. The recycle delay is the wait time between the end of data acquisition of the last CPMG sequence and the next first radiofrequency (RF) pulse of the next CPMG pulse sequence. In a typical NMR core analysis measurement, a CPMG pulse sequence is repeated multiple times to attain a sufficient signal to noise ratio and waiting between sequences allows the nuclei in the sample to return to equilibrium. If the recycle delay is not long enough the nuclei will not return to equilibrium and the RF pulses of the next CPMG sequence will not excite these nuclei leading to a reduction of observed signal. As is shown in Figure 1 (b), as the recycle delay is decreased (from 5000 ms to 100 ms) the observed signal is also decreased. This decrease in signal is most evident in the longer T_2 components which take longer to relax back to equilibrium.

Finally, Figure 1 (c) shows four T_2 distributions each recorded with a different T_2 max. T_2 max is the maximum T_2 value that the CPMG pulse sequence is capable of measuring. Essentially, it is the length of the CPMG pulse train. It should be chosen long enough such that all the T_2 components in the distribution are fully measured. As can be seen from Figure 1 (c), if the T_2 max value is not long enough the longest T_2 components will not be fully encapsulated by the CPMG measurement. This will lead to a strange appearance of the T_2 distribution for the longest T_2 components. Stated another way, the CPMG pulse sequence is not fully measuring the T_2 decay curve. All the nuclei have not fully relaxed before the CPMG pulse sequence is finished. It is lacking any measurement of the longest decay components. Without this data the T_2 distributions cannot be accurately determined.

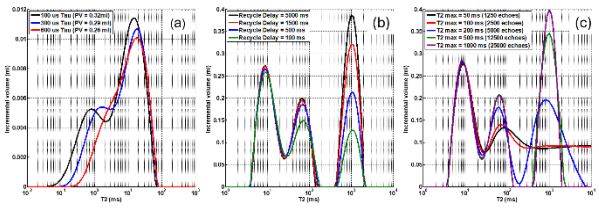

Fig. 1. Three sets of T_2 distributions each showing how the wrong CPMG parameters can lead to inaccurate data. Figure 1 (a) shows three different T_2 distributions each taken with three different tau values. The shorter the tau value, the shorter the minimum T_2 value that can be measured ensuring that the smallest pores (with the shortest T_2 values) are fully measured. Figure 1 (b) shows four T_2 distributions, each recorded with a different recycle delay. If the recycle delay is not long enough the nuclei will not return to equilibrium and the RF pulses of the next CPMG sequence will not excite these nuclei leading to a reduction of observed signal. Figure 1 (c) shows four T_2 distributions each recorded with a different T_2 max. T_2 max is the maximum T_2 value that the CPMG pulse sequence is capable of measuring. It should be chosen long enough such that all the T_2 components in the distribution are fully measured.

Beyond T_2 distributions, the choice of pulse parameters and NMR technique are also important for other NMR measurements. Figure 2 shows an image recorded with an FSE [6] (Figure 2 – left panel) and SPRITE [4] (Figure 2 – right panel) imaging technique. SPRITE is a very good technique for samples that have very short relaxation rate (T_1 and T_2) but not a good technique when otherwise. You can see from the two images that the FSE provides superior detail compared to SPRITE for this sandstone image. However, in Figure 3 images of a shale sample, the SPRITE technique provides a better image (Figure 3 – right hand panel).

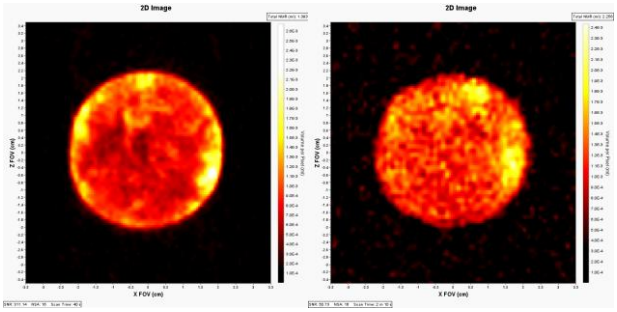

Fig. 2. The left-hand panel shows a 2D image of a sandstone sample recorded with a FSE pulse sequence with a maximum T_2 of 1000 msec. The right-hand panel shows the corresponding image recorded with a 2D SPRITE pulse sequence. Both images have the same number of signal averages (16). The FSE provides superior detail compared to the SPRITE image as the sample has large pores and long relaxation rates (T_1 and T_2). SPRITE is a very good technique for samples that have very short relaxation rate (T_1 and T_2) but not a good technique when otherwise

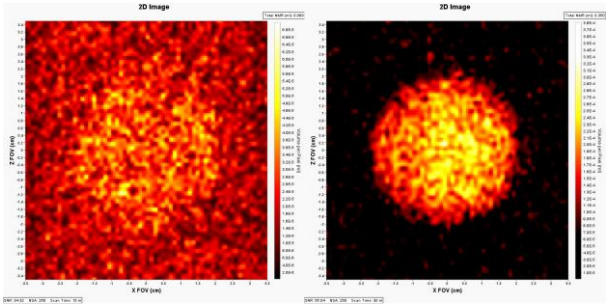

Fig. 3. Images of a shale sample that has a maximum T_2 of 2 msec. The left image is a 2D FSE and the rightl shows the corresponding 2D SPRITE image. Both images have the same number of signal averages (256). In this case the SPRITE image has superior signal-to-noise as the sample has short relaxation times (T_1 and T_2) making it well suited for measurement with the SPRITE NMR pulse sequence.

3 How to Best Set NMR Parameters Correctly

To set the parameters correctly a few assumptions must be made, such as:

1. The goal is to produce good results 90% of the time and require NO user parameter selection. The user would only select what type of scan/information they wanted (i..e 1D profile, 2D image, T_2 distribution, etc). Like any automatic technique, there will always be instances where things go wrong. For example, if the system has very low NMR detectable volume the prescans may not be able to correctly measure the relaxation rates.

2. For prescan data, a SNR of 25 is sufficient to define all the relaxation rates. From our experience, this is usually the case for defining the minimum and maximum relaxation times.

3. For the scan, the signal to noise ratio should be a minimum of 100. This will ensure good separation of relaxation values when performing a continuous fit [8].

4. The tau value should be set to the minimum value allowed by the NMR instrument.

5. The maximum relaxation value max will be taken as the value which incorporates 95% of the observed pore volume (when data is fitted with a continuous fit).

6. The minimum relaxation value should be the value which incorporates 5% of the observed pore volume.

7. The recycle delay should be five times T_1 max. This represents a 99% recovery of all signal (Observed Signal = $\exp(-5/T_{1max})$). For prescan data two times T_1 max will be used to make the scans faster (represents 86% recovery)

8. A maximum expected T_1 and T_2 for the system is required. For example, for hydrogen NMR of fluids we know that water will have the longest T_1 (approximately 3 seconds). This expected maximum value is set by the user in initial preferences and can be easily estimated.

9. It is assumed the system is properly calibrated (pulse length determined, etc) and on resonance.

10. The reported NMR volume should be accurate to 95% of the expected volume. For imaging sequences, we know relaxation weighting can be introduced affecting the overall reported volume. For example, during an FSE sequence the first NMR point is only acquired after the first echo time. This first point is usually not encoded and thus directly relates to the reported imaging volume (it is the center of k-space). If the intensity of this first point will be less than 95% of the expected value due to T_2 decay (Observed Signal = exp(-echo time / Minimum T_2), then a different technique like SPRITE will be used.

These are just a few of the many assumptions or rules of thumb that have been developed over the years from many NMR core analysis measurements. Along with these rules of thumb, users also typically follow work flows to best set the NMR parameters for the measurements of interest. With experience this process gets easier. However, this year we looked to automate in software

these rules of thumb and work flows so that end users do not have to select any (or very few) NMR parameters prior to a NMR core analysis measurement.

4 How to Best Automate Parameter Selection

After identifying the knowledge that needed to be automated, the next step was to determine how to automate this knowledge. Simply hardcoding the rules of thumb was not possible as they are sample dependent and can't be applied globally. For example, a shale sample with very small pores will have a much lower T_2 max then a sandstone sample which has much larger pores. A more robust method was needed to determine the parameters.

It was decided that the best way to implement automated scanning and data processing was to perform a series of "prescans". These "prescans" would be simple NMR measurements done automatically to quickly determine some of the NMR parameters. The values derived from these scans are then used to automatically select scanning and processing parameters. After much testing it was determined that the "prescans" would be run as follows:

1) T_1 – The T_1 value of the sample is important to know first as it is needed to effectively run the subsequent "prescans". A saturation recovery [7] is run with approximately ten steps (see Table 1 for other parameters for this "prescan"). A T_1 max value is chosen as approximately one fifth the expected maximum value for any/all samples (one of the assumptions above). The T_1 value retrieved from this "prescan" data and used in implementation of the other "prescans" (and the final scan) is chosen as the value that has 95% of the signal in the inverted data.

2) T_2 – A CPMG pulse sequence is run where the recycle delay is set to two times the T_1 value derived from the first "prescan". Two times the T_1 value is used rather than five times the T_1 value to speed up the scan and as we are not concerned with determining accurate volume for this prescan measurement (only the T_2 value). Two times T_1 max allows for 86% recovery of all the signal between averages. The value of T_2 max is set to T_1 max as we know that T_2 cannot be longer than T_1. In addition, the tau value is set to the minimum value allowed by the NMR instrument. See Table 1 for the other parameters employed in this "prescan". Again, the T_2 maximum and minimum values are retrieved from this "prescan" data and used in implementation of the final scan.

3) T_2* - A free induction decay (FID) is run. Again, the recycle delay is set to two times the T_1 value derived from the first "prescan". See Table 1 for the other parameters employed in this "prescan". The value of T_2* retrieved from this "prescan" is set as the value of T_2* retrieved from the continuous fit of the FID data.

It should be noted that each of these "prescans" are done to a lower SNR than is normally employed for final data acquisition. This is because the purpose of the "prescans" is not to determine the final values of T_1, T_2 and T_2* but rather to know approximate values to help guide setting the NMR parameters correctly for each scan in order to fully automate it. It is important to keep these "prescans" short to minimize the overall data acquisition time. It is nice to have full automation of these NMR scans but it cannot come at the expense of total data acquisition time. The final values of T_1, T_2 and T_2* can be measured to a higher SNR subsequent to these "prescans" with the preliminary values determined from the "prescans".

Table 1. Prescan Parameters.

T_1 Prescan	
Number of saturation Steps	10
Filter	125kHz
Inversion Start/End	0.01 to 10,000 msec
Number of Inversion points	121
Target SNR	25
Number of points per step	1
T_2 Prescan	
Number of points per echo	1
Filter	125kHz
Inversion Start/End	0.01 to 10,000 msec
Number of Inversion points	121
Target SNR	25
Tau	Minimum allowed
T_2* Prescan	
Number of points	1024
Filter	125kHz
Inversion Start/End	0.001 to 100 msec
Number of Inversion points	121
Target SNR	25

In addition, to help automate T_1, T_2 and T_2* measurements, the values derived from these "prescans" are also employed to help automate other techniques such as imaging sequences. Two primary images sequences are used. SPRITE for short relaxation times and FSE otherwise as we know FSE has superior SNR if it can be used. The FSE technique is used as long as the T2 is long enough to not have more than 5% signal lost. This is computed using the first echo time (which encoded the first k-space point that defines signal intensity) and the minimum T2 found in the prescan. If this condition is not met a SPRITE based technique is used. In the future, additional techniques such as SE-SPI will be incorporated to make this selection more optimal.

To further ensure the efficiency of the automated scan a workflow was developed which ensures that "prescans" are not repeated unnecessarily. The values retrieved from the "prescans" for T_1, T_2 and T_2* are stored with the sample state of the sample. Then anytime a scan is repeated with this same sample in this same sample state the existing T_1, T_2 and T_2* values are employed in the automation of this scan. The "prescans" are not repeated if the values already exist. This ensures maximum efficiency as "prescans" are only repeated as new samples or sample states are added. See Figure 4 for a summary of the workflow employed.

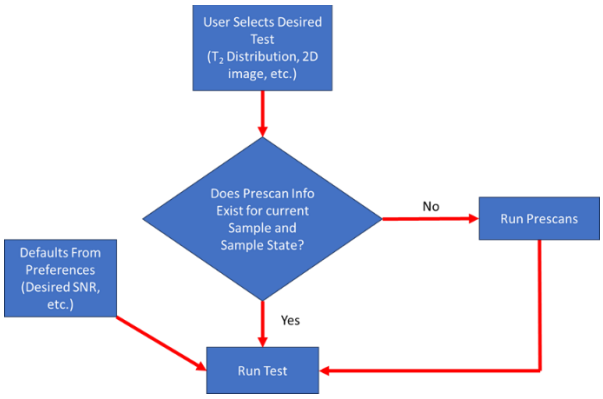

Fig. 4. Workflow defining when prescan is run.

The main draw back of utilizing the prescans is the time the take to acquire, making the whole scanning time longer. For the worst case sample in which the T1 and T2 is actually very long (at the maximum expected), the whole prescan process takes approximately 10 minutes as long as sufficient SNR can be achieved in 16 averages. However, as each successive prescan uses information from the previous prescan, typically prescan times are only approximately 4 minutes.

There will still be instances where the user will want control over parameter selection directly. Most notably when comparisons between results the user may wish the scanning parameters to be identically and when subtracting results from each other. In these cases, it is recommended to run the AI process once, then simply rerun the scan with the same scan parameters.

5 Discussion Of Automated Parameter Selection

The following section will outline the pluses and minuses of determination of the scan parameters via automated prescans. The resulting data will then be compared with T_2 distributions recorded with the same sample where the scan parameters were determined by an experienced user.

For this initial testing a calibration sample was employed. This sample is a container with a dimension similar to a typical core plug (3.5 cm in diameter and 5 cm in length). The container is filled with a mix of H_2O and D_2O. The ratio of H_2O to D_2O in the container is chosen to give the calibration a NMR volume similar to a saturated core plug. In this case approximately 25 ml. In addition, the H_2O/D_2O fluid is doped with $CuSO_4$ to shorten the NMR relaxation times (T_1, T_2 and T_2*) from the values for bulk water to values more akin to those observed in the pores of typical core plugs. In this case, the T_1, T_2 and T_2* values for the calibration sample were <200ms, <100ms and <10 ms respectively. Table 2 summarizes the parameters determined for the T_1, T_2 and T_2* prescans for the calibration sample.

Table 2. Maximum And Minimum values for T_1, T_2 and T_2* As Determined from Prescans For Calibration Sample

	Duration (s)	T_x min (ms)	T_x max (ms)
T_1 Prescan	125	50	400
T_2 Prescan	40	100	200
T_2* Prescan	14	1.58	2.82

Using the maximum and minimum T_1, T_2 and T_2* values determined via prescans, a T_2 distribution of the calibration sample was recorded using the NMR scan parameters as derived from the prescan data. Table 3 summarizes the scan parameters employed for this measurement. Also shown in Table 3, are the same scan parameters as determined by an experienced user.

The tau value (77 µs) selected based on the prescan values is longer than that determined by the user (45 µs). 45 µs is the minimum tau value the NMR system can achieve. Users often run with this minimum value by default so as to not miss any short T_2 relaxation components. This is particularly true for core samples which may have fluid in small pores leading to short T_2 relaxation times. However, having measured the minimum and maximum T_2 values, the prescan data shows that there are no components with T_2 values less than 100 ms. Meaning the tau value can be increased without penalty of missing short relaxation components. Running with the shortest tau available is not always prudent as too many echoes can lead to unwanted sample heating leading to a reduction in the observed NMR volume. We have investigated the effect of unwanted sample heating in a previous paper [9]. By increasing the tau from 45 µs to 77 µs the number of echoes has been reduced from 3333 echoes to 2597 echoes.

Another difference in the scan parameters as determined by the prescans versus those determined by the user is the recycle delay. The recycle delay is how long the CPMG sequence waits between the end of one pulse train and the beginning of the next. The recycle delay should be long enough for all the nuclei to fully relax back to equilibrium so they are ready to be excited again by the next pulse train. Typically, this is five times T_1 max. The length of the recycle delay is the primary factor in determining the total scan time of any CPMG pulse sequence. In this case the user set the recycle delay to be 7.5 times the T_2 max. This is based on the rules of thumb for core samples where T_1 max can be estimated as 1.5 times T_2 max. Therefore,

in this case the recycle delay would be estimated as 5 x 1.5 x 150ms = 7.5 x 150 ms = 1125 ms. The problem with this rule of thumb is that it is only valid for core samples. Yet, as is the case with this calibration sample, the rule of thumb is often applied to non-core samples. This can lead to an underestimated recycle delay which ultimately can lead to a reduction in the measured NMR volume. A more prudent way to set the recycle delay is to measure the T_1 relaxation and determine the T_1 max. Performing prescans allowed the T_1 max to be determined as 400 ms. The recycle delay can then more accurately be set to five times this maximum T_1 value. In this case 5 x 400 ms = 2000 ms. This lead to an overall longer scan time of 49 s as compared to 30s for the parameters employed by the user.

Table 3. Scan Parameters and measured values as determined by both prescans and an experienced user for a calibration sample

Scan Parameters	Prescan	User
Tau (μs)	77	45
T_2 Max (ms)	200	150
Recycle Delay (ms)	2000	1125
# of echoes	2597	3333
# points per echo	10	1
Number of scans	16	16
Scan Time (s)	49	30
Measured Values		
Peak T_2 Value (ms)	141.25	141.25
Log Mean T_2 (ms)	137.16	142.6
NMR Volume (ml)	24.70	24.69
Signal to Noise Ratio	22328	7462

Beyond the scan parameters, Table 3 also shows a comparison between the measured values for the T_2 distribution for the calibration source as derived by prescans and the experienced user. The T_2 peak value, log mean T_2 and NMR volume derived via the prescan parameters agree well with those derived from the user's parameters. The only difference between the measured values derived from the prescan parameters and those derived employing the user-based parameters is the signal to noise ratio (SNR). The SNR derived from the prescan parameters is nearly three times higher than that derived from the user-based parameters. This is because the prescan-based measurement employed ten data points per echo leading to more data and a better SNR. The user chose to employ only one point per echo leading to less data and a lower SNR. Users are hesitant to employ more than one point per echo because if the T_2* value is not known more than one point per echo in a CPMG measurement can introduce T_2* waiting to the measured T_2 distribution. This waiting can lead to a reduction in the observed NMR volume. However, if the T_2* value is known more points can be measured per echo if the decay between the first point measured and the last point measured is not less than 5%. A decrease of less than 5% will not lead to any significant T_2* waiting in the measured T_2 distribution. This is a clear advantage of having measured T_2* prior to the T_2 measurement.

While the measured values derived with the prescan paramters agree well with the values derived by the user set parameters, the obvious downside of employing prescans is the increase in the total data acquisition (DAQ) time. For the user set scans, the total DAQ time is just the scan time required to measure the T_2 distribuiton (30s). For the prescan based data, the total DAQ time includes both the time required to run the prescans (179s) and the scan time required to measure the T_2 distribution (49s). This is a nearly 7.5 times increase in total DAQ time for the prescan based measurement (approximately 4 mins) as compared to the user-based measurement (approximately 0.5 mins).

There can be several arguments made to explain or justify this increase in total DAQ time. Firstly, as explained above while the measured values were similar for the user-based measurement as compared to the prescan-based measurement, one could argue the quality of the data is better for the prescan-based measurement. Knowing the maximum and minimum T_1, T_2 and T_2* values in advance, allowed better scan parameters to be selected. For example, knowing the T_2* value allowed more data points to be measured per echo leading to a better SNR. Secondly, users often inherently employ prescans when they are setting the scan parameters. For example, it is common for a user to run a quick T_2 scan to ensure the T_2 max is selected correctly to measure the full decay. These prescans are not listed in the total DAQ time but if an apples to apples comparison is to be made with the prescan based measurement they should be. Finally, the prescan data needs to only be acquired once per sample state. So if you repeat the same measurement several times on the same sample in the same sample state the same prescan T_1, T_2 and T_2* values can be employed to set the parameters for all scans. In addition, these same prescan values can be employed for other measurements beyond the T_2 distribution. For example, T_1-T_2 maps.

6 Further Examples Of Automated Parameter Selection

Having discussed the advantages and disadvantages of employing the prescan method for scan parameter selection, a few more examples of automated parameter selection will now be discussed.

The next sample chosen for comparison between prescan-based parameter selection and user-based parameter selection was bulk water. Table 4 lists the parameters determined for the T_1, T_2 and T_2* prescans for the bulk water sample. Table 5 compares the scan parameters and measured values as determined by both prescans and an experienced user for the bulk water sample.

Table 4. Maximum And Minimum values for T_1, T_2 and T_2* As Determined From Prescans For A Bulk Water Sample

	Duration (s)	T_x min (ms)	T_x max (ms)
T_1 Prescan	123	1000	4000
T_2 Prescan	393	1995	5011
T_2* Prescan	83	1.12	4.47

Table 5. Scan Parameters And Measured Values As Determined By Both Prescans And An Experienced User For A Bulk Water Sample

Scan Parameters	Prescan	User
Tau (μs)	65	500
T_2 Max (ms)	5011	3000
Recycle Delay (ms)	20000	15000
# of echoes	65000	6000
# points per echo	6	1
Number of scans	16	16
Scan Time (s)	720	470
Measured Values		
Peak T_2 Value (ms)	3548	3162
Log Mean T_2 (ms)	3364	3038
NMR Volume (ml)	14.52	14.26
Signal to Noise Ratio	10770	4607

The obvious shortcoming of this data is that the prescans took a significant amount of time (approximately 600s). This is due to the slow relaxation times of bulk water and lead to an overall DAQ time for the prescan based data of 22 mins. This is significantly longer than the DAQ time for the user-based measurement of approximately 8 mins. Figure 5 shows a comparison of the T_2 distributions recorded with scan parameters defined by the user (Figure 5 – Blue Trace) and scan parameters defined by prescans (Figure 5 – Red Trace).

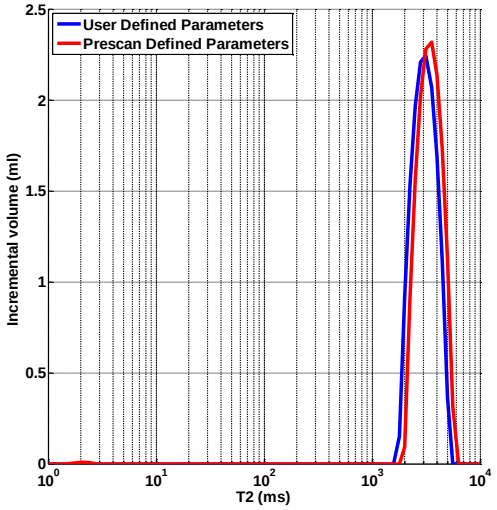

Fig. 5. A comparison of the T_2 distributions recorded with scan parameters defined by the user (Blue Trace) and scan parameters defined by prescans (Red Trace) for a bulk water sample.

Both the T_2 distributions shown in Figure 5 and the measured values reported in Table 5 are within 5% of each other but do show some discrepancy between the data measured with user-defined scan parameters and scan parameters derived from the prescans. This is because the scan parameters selected by the user are not well chosen. Specifically, the T_2 max value of 3000 ms is not long enough. The T_2 relaxation is not fully measured. This leads to reduction in the T_2 peak value. In addition, the recycle delay, which is derived from the T_2 max value, is not long enough. As a result, the sample is not fully relaxed prior to initiation of the next pulse train in the CPMG pulse sequence. This lead to a reduction in the measured NMR volume for the data derived from the user defined parameters (14.26 ml) as compared to those derived from the prescans (14.52 ml). It is not uncommon for users (even experienced ones) to select the incorrect scan parameters. Especially for measurements of species with long relaxation times. Impatience with waiting for results can lead to the choice of shorter relaxation delays.

The next sample chosen for comparison between prescan-based parameter selection and user-based parameter selection was a sandstone sample. Table 6 lists the parameters determined for the T_1, T_2 and T_2* prescans for the sample. Table 7 compares the scan parameters and measured values as determined by both prescans and an experienced user for the sample. Figure 6 shows the T_2 distributions derived from scan parameters defined by the user and those defined by prescan data.

Table 6. Maximum And Minimum values for T_1, T_2 and T_2* As Determined From Prescans For A Sandstone Sample

	Duration (s)	T_x min (ms)	T_x max (ms)
T_1 Prescan	124	8	1584
T_2 Prescan	158	0.32	501
T_2* Prescan	34	0.79	1.58

Table 7. Scan Parameters And Measured Values As Determined By Both Prescans And An Experienced User For A Sandstone Sample

Scan Parameters	Prescan	User
Tau (μs)	57	45
T_2 Max (ms)	501	1000
Recycle Delay (ms)	7900	7500
# of echoes	8790	22222
# points per echo	4	1
Number of scans	16	16
Scan Time (s)	168	197
Measured Values		
Peak T_2 Value (ms)	199.5	199.5
Log Mean T_2 (ms)	37.5	36.96
NMR Volume (ml)	5.41	5.48
Signal to Noise Ratio	3238	1663

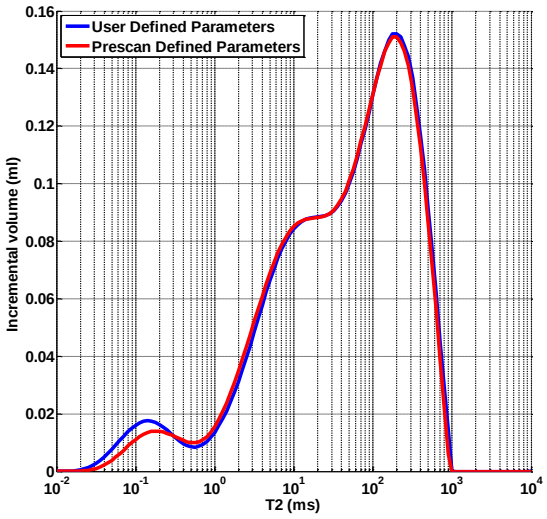

Fig. 6. A comparison of the T_2 distributions recorded with scan parameters defined by the user (Blue Trace) and scan parameters defined by prescans (Red Trace) for a sandstone sample.

First looking at total DAQ time for this data set, the prescan total DAQ time was 484 seconds compared to the user defined DAQ time of 197 seconds. Again, DAQ time is being sacrificed for automation and better-informed selection of scan parameters.

The T_2 distributions and measured values for sandstone sample derived from the user-defined and prescan-defined data agree within 5% with each other. There is a small difference at the shortest T_2 values of the distribution where the prescan-defined distribution underestimates the pore volume as compared to the user-defined data. This is because the automated scan parameters based on the prescan data chose a longer tau (57 µs) as compared to the user-defined tau (45 µs). Once again, this is due to the fact that the scan parameter selection algorithm chose to replace a shorter tau value with a longer value in order accommodate more data points per echo and improve the SNR. In this case, the algorithm may need to be improved to put more emphasis on measuring the shortest T_2 components of a distribution at the expense of SNR.

The final sample chosen for comparison between prescan-based parameter selection and user-based parameter selection was a shale sample. Table 8 lists the parameters determined for the T_1, T_2 and T_2* prescans for the sample. Table 8 compares the scan parameters and measured values as determined by both prescans and an experienced user for the sample. Figure 7 shows the T_2 distributions derived from scan parameters defined by the user and those defined by prescan data.

Table 8. Maximum And Minimum values for T_1, T_2 and T_2* As Determined From Prescans For A Shale Sample

	Duration (s)	T_x min (ms)	T_x max (ms)
T_1 Prescan	124	0.63	398
T_2 Prescan	42	0.11	31.6
T_2* Prescan	10	0.2	0.56

Table 9. Scan Parameters And Measured Values As Determined By Both Prescans And An Experienced User For A Shale Sample

Scan Parameters	Prescan	User
Tau (µs)	45	45
T_2 Max (ms)	30	100
Recycle Delay (ms)	2000	750
# of echoes	667	2222
# points per echo	1	1
Number of scans	16	16
Scan Time (s)	36	20
Measured Values		
Peak T_2 Value (ms)	1.12	1.12
Log Mean T_2 (ms)	1.32	1.24
NMR Volume (ml)	2.95	2.93
Signal to Noise Ratio	758	806

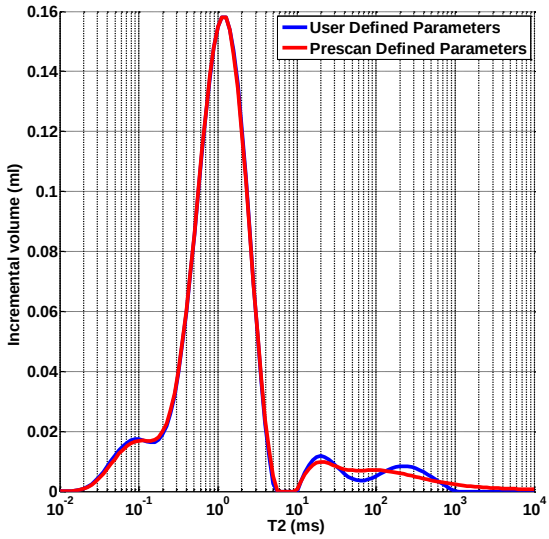

Fig. 7. A comparison of the T_2 distributions recorded with scan parameters defined by the user (Blue Trace) and scan parameters defined by prescans (Red Trace) for a shale sample.

As with the other samples, the total DAQ time for the shale sample was longer for the prescan-derived data as compared to the data derived from the user defined scan parameters. In addition, the measured values and T_2 distributions once again agreed within 5% with each other. This time, the small discrepancy between the T_2 distribution measured by the user-defined scan parameters and the distribution measured by the prescan-defined parameters is found in the pores with the longer T_2 components. The distribution derived from the prescan-

defined parameters underestimates the pore volume as compared to the user-defined data for these longest T_2 components. From the scan parameters, it is obvious that this is due to the difference in the T_2 max selected from the prescan based data as compared to the T_2 max defined by the user. As explained in section four of this paper, the scan parameter selection algorithm chooses the maximum T_2 value as the T_2 value which incorporates 95% of the signal recorded in the prescan. In this case, the maximum T_2 was measured as 31 ms from the prescan data and was set to 30 ms in the final scan parameters. Unfortunately, as shown in Figure 7 this T_2 max value was not quite long enough to fully measure the T_2 decay leading to underestimate of the longest T_2 components of the distribution. This is again another example where accuracy may be sacrificed slightly to benefit automation.

7 Conclusions And Future Work

In this paper, we have presented a new method for automating the selection of NMR scan parameters. This method hinges on prescans performed prior to the full NMR measurement on the sample of interest. These prescans are shorter scans with lower SNR than the full NMR measurement but provide the maximum and minimum T_1, T_2 and T_2* values for the sample. These max and min values are then employed to determine the best scan parameters for the full NMR measurement based on series of assumptions derived from prior knowledge of NMR core analysis. For example, the recycle delay of the final CPMG measurement is taken as five times the T_1 maximum value derived from the prescan. These assumptions were then hard coded into software.

A discussion of the advantages and disadvantages of this method for automating NMR scan parameter selection was also undertaken in this paper. The principal disadvantage of this method is that it increases the overall data acquisition time as compared to when users set the scan parameters independently. This is due to the time it takes for the prescans to run prior to the final NMR measurement of interest. The main advantages of this method are that knowing the maximum and minimum T_1, T_2 and T_2* values prior to the final NMR measurement can lead to a better selection of the scan parameters. For example, knowing T_2* allows more data points per echo to be acquired without T_2* weighting leading to better SNR.

The T_2 distributions for several samples were measured both where the scan parameters were selected by an experienced user and where the scan parameters were set based on the prescan data. In each case, the final T_2 distributions as well as the scan parameters selected for each T_2 distribution were compared. In all cases, the T_2 distributions recorded with each method agreed within 5% of each other. Any small discrepancies between the two measured data set can be attributed to biases in how the user selected the scan parameters as compared to the scan parameter selection algorithm based on the prescan data.

Finally, we have employed the term artificial intelligence (AI) to describe this method of determining scan parameters via prescans. We acknowledge that this method does not employ any machine learning. However, we contend that the term AI is a valid descriptor of the prescan technique as this technique is giving computational systems the ability to perform tasks typically associated with humans. In addition, as our work continues and we automate more complex scanning techniques, like diffusion and flow mapping, machine learning may be implemented into the automation. In fact, this effort has already begun as we have shown how machine learning can be employed to derive a better T_2 cutoff for bound vs free fluid analysis [10].

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