DECOMPOSITION METHOD OF NUCLEAR MAGNETIC RESONANCE T2 SPECTRUM COMPONENTS BASED ON RESIDUAL FULLY CONNECTED NEURAL NETWORK

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The decomposition of nuclear magnetic resonance T2 spectrum components is an important means of fluid identification. Based on the forward simulation, this paper constructs a data set, transforms the problem into a nonlinear regression problem, and proposes a residual fully connected neural network model. By debugging the network structure and hyperparameters, the optimal model is determined. The results show that the model has a better fitting effect than Gaussian decomposition and Transformer model and has good stability and generalization ability. Experimental data verification further illustrates its practical application value in T2 spectrum component decomposition.

Keywords: Deep Learning, Residual Fully Connected Network, Forward Simulation, Nuclear Magnetic Resonance T2 Spectrum, Component Decomposition

1. Introduction

As the production of conventional oil and gas resources continues to decline globally, the direction of oil and gas exploration is gradually changing and innovating. Unconventional oil and gas resources have replaced traditional oil and gas extraction fields, achieving a series of breakthroughs and becoming the forefront of petroleum exploration and a hot research area in various oil fields. However, unconventional reservoirs have complex pore structures and diverse fluid occurrence states, making it difficult for conventional methods to accurately evaluate reservoir fluid properties, posing significant challenges for fluid evaluation in unconventional reservoirs [1,2].

Currently, nuclear magnetic resonance (NMR) logging is an important research method for evaluating reservoir fluids, as it can directly measure the hydrogen nuclear signals in pore fluids without considering the rock matrix. NMR technology is widely used in petroleum logging to evaluate reservoir pore structures.

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Using NMR T2 spectra, it can obtain abundant reservoir fluid information such as porosity, permeability, and fluid saturation [3]. Traditional NMR logging methods include the Twin Wait Time (TW) method and the Twin Echo Time (TE) method. The TW method evaluates reservoir fluids based on the different polarization times of fluids by comparing the measurements of long and short wait times, utilizing techniques such as differential spectrum method and time-domain analysis. The TE method determines reservoir fluid properties by comparing NMR T2 spectra at different echo intervals, based on the differences in fluid diffusion coefficients, using methods like shifted spectrum method, diffusion analysis, and enhanced diffusion method. Among these, the differential spectrum method and time-domain analysis have good theoretical support, but due to the combined effects of pore structure and fluid properties, the fluid identification capability of these methods in unconventional reservoirs is low [4,5].

To expand the application of NMR technology in reservoir evaluation, many scholars have proposed new fluid identification methods based on NMR technology. In 2015, Jiang T.M. [6] and others used the factor analysis method proposed by Jain V. [7] to evaluate the producibility and reservoir quality of shale oil and gas reservoirs, demonstrating the potential of this technology in fluid property identification. In 2020, Zhong [8] and others proposed decomposing NMR T2 spectra into multiple normal distribution curves to identify fluid properties within pores. Previous studies indicate that the decomposition method of NMR T2 spectrum components is significant for exploring the application value of NMR technology.

Machine learning is an interdisciplinary field that uses models developed with deep learning techniques to learn complex concepts using simple concepts. Deep learning, a subclass of machine learning, sets many hidden layers between input and output, with each layer undergoing multiple linear and nonlinear transformations. By extracting multiple levels of features from raw data through sequential or recurrent computational units, deep learning autonomously finds the features that best describe the dataset, making it highly suitable for solving complex nonlinear problems [9,10]. Over the past decade, machine learning has been increasingly combined with NMR logging in various aspects. Zhang [11] and others combined artificial neural networks (ANN) with dimensionality reduction methods for reservoir parameter measurement, significantly improving the accuracy of parameter predictions. Misra [12] and others used variational autoencoder neural networks, generative adversarial networks, variational encoder-generative adversarial networks, and long short-term memory networks to encode, decode, and predict NMR T2 spectra.

Although the component decomposition problem of nuclear magnetic resonance T2 spectra can be achieved through traditional methods such as Gaussian mixture models or Gaussian process regression, the applicability of traditional

methods is significantly limited for the non-ideal characteristics such as spectral peak overlap and non-Gaussian peak shape existing in T2 spectra of unconventional reservoirs. In contrast, deep learning can implicitly learn the complex mapping relationships in the data through hierarchical feature extraction and nonlinear transformation mechanisms. At the same time, it combines the physical constraints in the training data set, thereby taking into account both the decomposition accuracy and robustness of the model. Furthermore, the end-to-end training mechanism of deep neural networks avoids subjective dependencies such as manually presetting the number of components and iterative parameter adjustment in traditional methods, significantly improving the generalization ability and computational efficiency of the method in complex reservoir environments. Therefore, deep learning models show better adaptability in the task of T2 spectrum decomposition.

In this paper, we apply a deep learning model to the problem of decomposing NMR T2 spectrum components and propose a T2 spectrum component decomposition method based on a residual fully connected neural network. This method uses a theoretical dataset generated through forward simulation as input data and the construction parameters corresponding to individual T2 spectra in the dataset as label data. Through model training and hyperparameter optimization, a stable and highly generalized model was obtained, which directly decomposes NMR T2 spectra into component spectra representing different components. The transverse relaxation characteristics of each component spectrum can accurately identify fluid types, providing a new technical means for evaluating unconventional reservoirs.

2. Objectives

This paper aims to solve the problem of NMR T2 spectrum component decomposition with the following main objectives:

1. Based on the traditional residual network, modify the residual block structure to build a residual fully connected neural network. Train the neural network using a sufficiently large dataset constructed through forward simulation to achieve the decomposition of NMR T2 spectrum components.
2. By adjusting the depth and width of the network structure, the model's hyperparameter settings are optimized to improve the model's performance in the theoretical T2 spectrum component decomposition task.
3. The actual measured NMR T2 spectrum was decomposed into components through the final optimal model, and the results were compared with the real results to verify the accuracy and reliability of the model in the actual NMR T2 spectrum component decomposition task.

3. Methods

3.1 Decomposition of NMR T2 Spectrum Components

Nuclear Magnetic Resonance (NMR) logging measures the relaxation signals of hydrogen atoms in reservoir pores using a spin-echo pulse sequence (Carr, Purcell, Meiboom, Gill, CPMG) to represent echo train signals. The transverse relaxation time (T2 time) is determined by the decay process, where the echo amplitude decays exponentially at a rate of 1/T2. Since the storage space within the rock is composed of pores of various sizes, and these pores contain different types of fluid components, the echo signal is often represented by a multi-exponential decay formula:

$$A(t) = \sum_{i=0}^{n} M_i(0) \exp(-\frac{t}{T_{2i}}) \tag{1}$$

where $A(\mathrm{t})$ represents the echo amplitude at time t; T_{2i} represents the T2 time of the i-th fluid component; $M_i(0)$ represents the echo signal magnitude of the i-th fluid component at $t = 0$.

By performing multi-exponential inversion fitting of the hydrogen nucleus spin echo signals using Equation (1), the T2 distribution spectrum of the transverse relaxation time can be obtained. The NMR T2 spectrum is typically considered to be linearly superimposed by multiple Gaussian distribution curves and can thus be accurately fitted with multiple independent Gaussian distribution curves (see Fig. 1). Conversely, decomposing the NMR T2 spectrum into multiple component spectra allocates the corresponding reservoir pore fluid information to these component spectra.

3.2 Residual Fully Connected Neural Network

In recent years, constructing deeper neural networks has become a popular trend in machine learning, known as deep learning. From LeNet, AlexNet, to tens of layers of VGG-Net, and to Google's Inception or hundreds of layers of Residual Neural Network (ResNet), these networks have played key roles in the development of machine learning and its applications [13]. The traditional ResNet introduces the concept of residual learning based on Convolutional Neural Networks (CNN), designing residual blocks with shortcut connections and using multiple such residual blocks end-to-end to construct a residual neural network, as shown in Fig. 2(a). Traditional ResNet algorithms use local convolutional kernels and deep neural networks, with input typically being multi-channel images, performing well in image processing [14-16]. However, the input for nonlinear functions is usually a one-dimensional vector, and convolution is a local operator. This means if the vector is reconstructed into a matrix, the convolutional kernel can only affect part of the sequence, not the entire sequence. Therefore, it is not suitable for complex nonlinear function regression problems like NMR T2 spectrum component

decomposition.

Based on the original structure of ResNet, the convolutional and pooling layers in the residual block were replaced with fully connected layers while retaining the batch normalization layers of the original model. This constructs a nonlinear regression neural network more suited to solving nonlinear regression problems, as shown in Fig. 2(b).

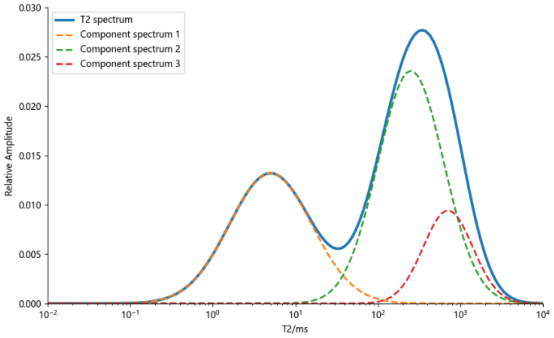
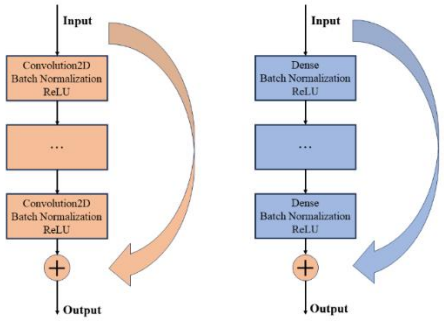


Fig. 1. NMR T2 Spectrum and Component Signals



(a) Traditional ResNet Residual Block Structure (b) Modified Residual Block Structure

Fig. 2. Traditional ResNet Residual Block Structure and Modified ResNet Structure

3.3 Construction of Forward Simulation Dataset

Deep learning can establish the relationship between input data and target output based on a limited sample space by constructing and minimizing the loss function. Deep learning networks can map input data to make predictions. If a high-quality large dataset exists, the universality of deep neural networks can reveal relationships of any complexity. Generating theoretical T2 spectra through forward simulation ensures an accurate correspondence between data and labels.

The forward simulation model is based on Gaussian distribution, where the distribution of each component can be represented by a Gaussian function, including variance (σ_i) , expectation $\mu(\mu_i)$, and the relaxation time corresponding to the spectrum peak (T_{2peak}^{i}). The calculation expression for $\mu_i$is as follows:

$$\mu_i = \frac{T_{2\,peak}^{i} - T_{2\min}}{T_{2\max} - T_{2\min}} (i = 1, 2, ...n) \tag{2}$$

where T_{2min} represents the minimum relaxation time on the T2 spectrum axis, and T_{2max} represents the maximum relaxation time on the T2 spectrum axis. $n = 1,2 \ldots N, N$, where N is the number of discrete relaxation times for T2, i.e., the number of sampling points. The complete T2 spectrum is obtained by linear superposition of each component.

When constructing the T2 spectrum model, the value range of the T2 spectrum's horizontal axis is crucial. The horizontal axis of the T2 spectrum represents the transverse relaxation time, typically set between 0.3 to 3000 ms in actual logging. Bound water and heavy oil are usually distributed in the range of 0.3 to 30 ms, while free water and light oil are distributed in the range greater than 30 ms, generally within hundreds of milliseconds. Gases are located on the far right of the T2 spectrum, in the range of thousands of milliseconds. If the T2 value range is set too small, important information may be missed. In this paper, the minimum relaxation time for T2 is set to 0.01 ms, and the maximum relaxation time is 10,000 ms. A T2 spectrum with 64 discrete relaxation time points is constructed (N=64), and these time points are selected within the preset T2 value range to ensure a detailed description of the T2 spectrum.

During the construction of the dataset, the amplitude values of each component in a single T2 spectrum are first normalized so that the sum of the amplitude values is 1, facilitating subsequent neural network model training. T2 spectra with 2 to 5 components are generated randomly, based on the distribution range of bound water, heavy oil, water, light oil, and gas components in the T2 spectrum. The random generation method helps improve the model's prediction and analysis capabilities for actual NMR data. The amplitude at each sampling point of the T2 spectrum is processed using a summation normalization method to facilitate subsequent model training. The summation normalization formula is as follows:

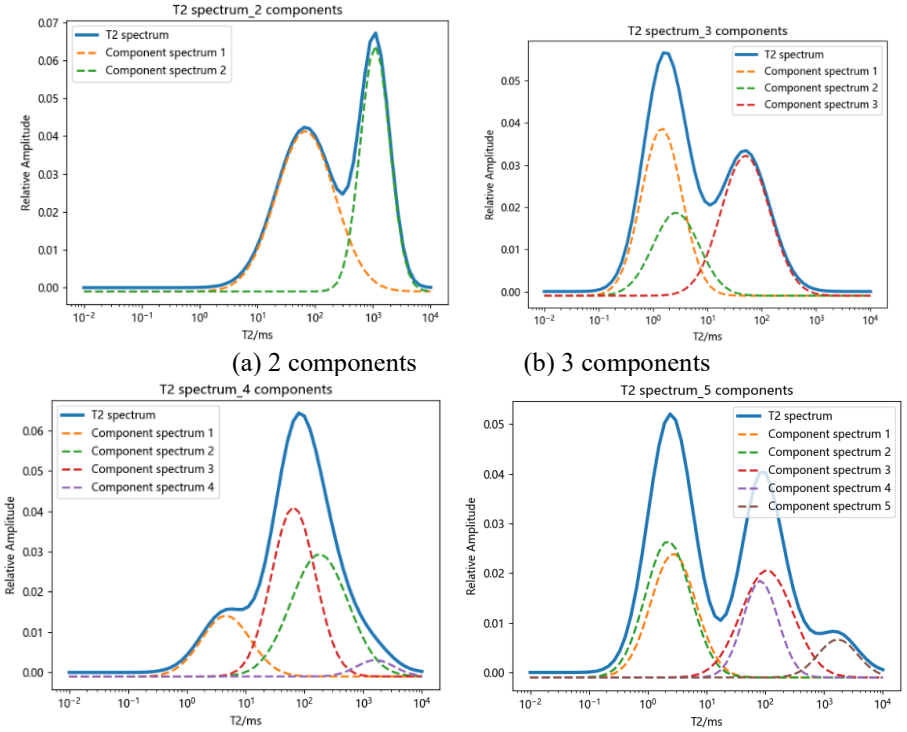
$$g(x) = h \frac{e^{\frac{-(x-c)^2}{2w^2}}}{\sum_{i=1}^{N} e^{\frac{-(x-c)^2}{2w^2}}} \tag{3}$$

where h represents the peak value of each component's T2 spectrum, c represents the peak center of each component's T2 spectrum, w represents the peak width of each component's T2 spectrum, and N represents the number of sampling points on the T2 spectrum.

For T2 spectra with fewer than 5 components, zero values are used to supplement the data, ensuring that regardless of the number of components, the amplitude information of a single T2 spectrum (1×64) corresponds to the one-

dimensional Gaussian parameter information (1×15). The original dataset consists of T2 spectra generated through forward simulation and the Gaussian parameters corresponding to multiple components in a single T2 spectrum.

The original dataset constructed in this paper contains 200,000 theoretical T2 spectrum data, including T2 spectra with 2 to 5 components (see Fig. 3), and it preserves the Gaussian parameters corresponding to multiple components in a single T2 spectrum. The objective of this research is to solve the component decomposition problem of T2 spectra. Whether it is laboratory sample data or actual logging data, the obtained T2 spectra are all the results of the original echo signals processed by the inversion algorithm, and the noise has been preprocessed through techniques such as smooth filtering and regularization constraints during the inversion process. Therefore, no additional noise was introduced in the original dataset constructed in this paper to match the input distribution characteristics of the real data.



(a) 2 components (b) 3 components

(c) 2 components (d) 4 components

Fig. 3. NMR T2 Spectra of Training Set Components

3.4 Construction and Hyperparameter Selection of Residual Fully Connected Neural Network

The residual fully connected neural network is a modified version of the traditional residual network (ResNet), where the convolutional and pooling layers

in the ResNet residual blocks are replaced with fully connected layers, while retaining the batch normalization layers of the original model. This modification makes the residual blocks more suitable for solving complex nonlinear regression problems and alleviates the vanishing gradient problem.

In the model used in this paper, each residual block consists of the following structure: a fully connected layer using Rectified Linear Unit (ReLU) as the activation function, another fully connected layer without an activation function, followed by a shortcut connection that directly adds the input to the output of the second fully connected layer, and finally another fully connected layer using ReLU activation function. After the input layer, the model stacks different numbers of fully connected layers and residual blocks, gradually reducing the number of neurons in each layer to capture the complex features of the input data.

NMR T2 spectrum component decomposition is a regression problem, where the component spectrum generated by the linear superposition of multiple Gaussian parameters fits the T2 spectrum. Therefore, this experiment uses Root Mean Square Error (RMSE) and R-squared (R^2) as evaluation metrics for model prediction results. The smaller the RMSE, the smaller the prediction error and the higher the accuracy; the larger the R^2, the higher the overall accuracy of the results.

ReLU is used as the activation function in this experiment because its gradient is easy to compute and it effectively addresses the problem of getting stuck at saddle points or local minima during training [17]. The ReLU expression is as follows:

$$\mathrm{Re}\,LU(x) = \max(0, x) \tag{4}$$

To minimize the loss function, the Adaptive Moment Estimation (Adam) method is used. The Adam method combines the advantages of the Adaptive Gradient Algorithm (AdaGrad) by calculating individual adaptive learning rates for different parameters, allowing it to perform well even with sparse gradients.

To avoid overfitting, the early stopping strategy is employed. When training large models, it is often observed that the training loss decreases over time while the validation loss starts to increase. The early stopping strategy stops training at the point of lowest validation loss, resulting in a model with better validation performance. This strategy is widely used in deep learning due to its effectiveness and simplicity. The algorithm stops training when no progress is made in the validation loss within a pre-specified number of epochs.

The depth and width of ResNet affect its approximation ability. To evaluate the effect, one factor is fixed while considering the impact of the other. Specifically, when assessing the effect of depth, the width of each hidden layer is fixed, and the depth is varied. Conversely, when considering the impact of width, the depth of ResNet is fixed, and the width is varied.

3.4.1 Selection of the Number of Nodes in the First Layer

In this experiment, the input consists of 64 T2 spectrum amplitude

information, and the output consists of 15 component parameter information. Since the number of input features is greater than the number of output features, each new hidden layer added to the network should have fewer nodes than the previous layer to effectively extract detailed features from the data. Therefore, the width of the first layer is crucial. In this paper, the number of nodes in the first hidden layer (m) is set to 32, 64, 128, and 256, respectively, and a 5-layer network (excluding the input layer) is constructed with the following structure: input layer, one fully connected layer (number of nodes m), one modified residual block mentioned earlier (Fig. 5(a), containing fully connected layer nodes m), and an output layer. Fig. 4 shows the prediction results for different numbers of neurons in the first hidden layer.

In Fig. 4, m represents the number of nodes in the first hidden layer. As shown, as the number of nodes increases, the prediction accuracy gradually improves, peaking at 128 nodes. However, when the number of nodes increases to 256, the prediction accuracy decreases. The input data used in this experiment is the 1×64 T2 spectrum amplitude information, where each point is an amplitude feature, and the entire input data represents the component information of the entire T2 spectrum. Therefore, around 128 neurons can better fit the feature information contained in the amplitude data. When the number of neurons continues to increase, the feature information in the amplitude data is dispersed across more neurons, leading to blurred features and decreased prediction accuracy. Thus, in this experiment, using 128 as the number of nodes in the first hidden layer of the network is the optimal structure.

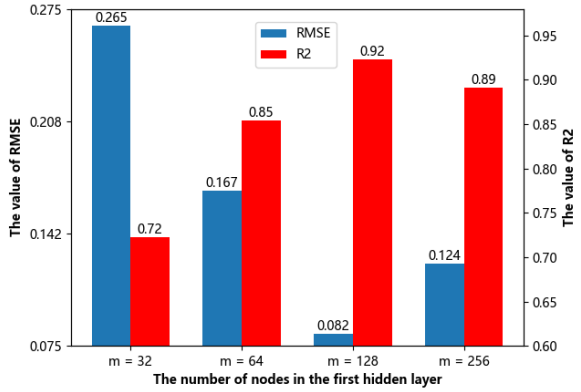


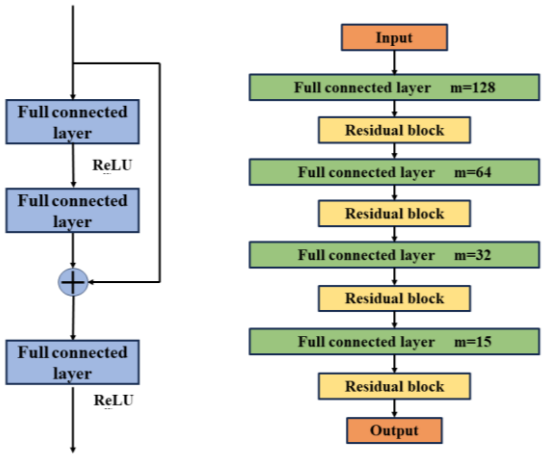
Fig. 4. Training Results with Different Numbers of Neurons in the First Hidden Layer

3.4.2 Selection of Network Layers

The number of hidden layers in a network significantly impacts the component decomposition results. Typically, as network depth increases, the model's predictive performance also improves. However, increasing the number of layers can lead to gradient vanishing and exploding problems. Additionally, deep

networks are prone to overfitting and network degradation. Therefore, finding the appropriate number of network layers is crucial.

In the process of parameter transmission and error backpropagation in neural networks, neurons in the earlier hidden layers can learn more generalized features, while neurons in the higher hidden layers can learn more detailed features. In this experiment, the input consists of 64 T2 spectrum amplitude information, and the output consists of 15 component parameter information. Since the number of input features is greater than the number of output features, each new hidden layer added to the network should have fewer nodes than the previous layer to effectively extract detailed features from the data. The residual structure used in this paper is shown in Fig. 5(a), where each residual block includes: a fully connected layer using ReLU activation function, another fully connected layer without an activation function, a shortcut connection that directly adds the input to the output of the second fully connected layer, and finally, a fully connected layer using ReLU activation function. The number of nodes in the fully connected layers in the residual block is the same as the number of nodes in the fully connected layer of the preceding layer in the residual block.



(a) Residual Block (b) Residual Fully Connected Neural Network

Fig. 5. Residual Block Structure and Residual Fully Connected Neural Network used in this paper

From the experiment in section 3.1.1, it was determined that 128 is the optimal number of nodes for the first hidden layer for this task. Therefore, the number of nodes in the second hidden layer is set to 64, and the third hidden layer is set to 32. Each residual block is considered as a 3-layer network structure. One or two residual blocks are added after each fully connected layer. Table 1 shows the results of the number of nodes in the hidden layers of residual fully connected neural networks with different layers (different numbers of residual blocks).

Table 1 provides the training information for residual regression models of

different depths. As it can be seen, the optimal depth is approximately 17 layers. Fig. 5(b) shows the corresponding network structure diagram. At this depth, the model achieves the minimum loss function, the smallest RMSE value, and the largest R^2 value.

Table 1

Training Metrics of Residual Fully Connected Neural Networks with Different Layers

Depth of ResNet	Stopping Epochs	Training Loss(10^{-4})	Validation Loss(10^{-4})	RMSE	R^2
5	100	14.074	19.865	0.2647	0.6272
9	100	5.765	7.281	0.1241	0.7834
13	76	5.075	5.211	0.0852	0.873
17*	**65**	**4.862**	**4.5221**	**0.0425**	**0.9531**
21	59	4.273	5.376	0.0527	0.9104
25	100	6.683	5.872	0.1311	0.7653
29	78	7.993	10.869	0.1825	0.6977
33	100	36.554	39.897	0.3655	0.5924

3.4.3 Selection of Hyperparameters

Based on the experimental results in Sections 3.4.1 and 3.4.2, the hyperparameters of the model were selected. The key hyperparameters for the model include: Learning Rate, Epochs, and Batch Size. These three parameters have a significant impact on the gradient calculation of the network's backpropagation and the optimization of the total loss function. Improper settings can lead to model overfitting or underfitting. Ultimately, a dynamic adjustment strategy for the learning rate was adopted in this paper: when the model's loss function does not significantly improve over a period of time, the learning rate is actively reduced to help the model converge better in the later stages of training. Additionally, the early stopping strategy is used to ensure the optimal model is obtained in a single training session. After multiple adjustments, the batch size was set to 512. All subsequent network models were trained and predicted using the above strategy and hyperparameters.

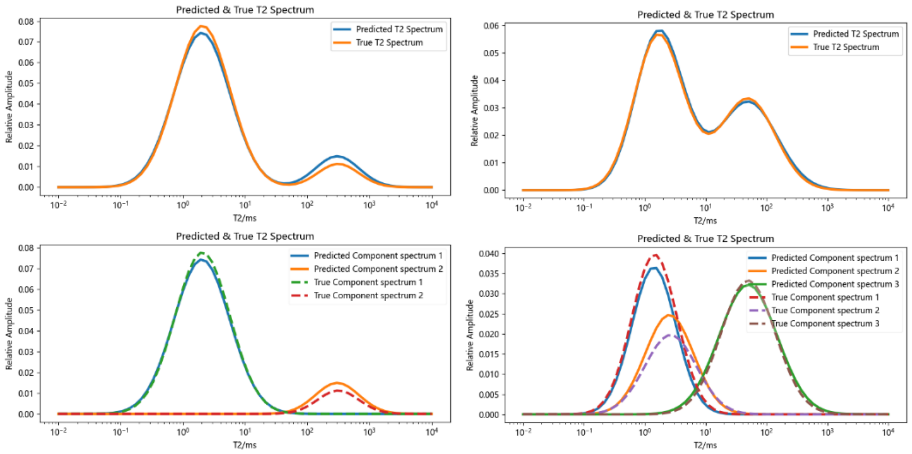
After determining the above parameters, a 17-layer residual fully connected neural network was constructed (as shown in Fig. 5(b)), and the constructed forward simulation dataset was used for training. Out of 200,000 data points, 190,000 were randomly selected as the training set, and 10,000 as the test set, for model training and prediction, resulting in the outcomes shown in Fig. 6.

Fig. 6(a)-(d) respectively shows the comparison between the model's component decomposition results on the NMR T2 spectra of 2 to 5 components and the real component spectra and compares the result of linear superposition of each decomposed component with the real T2 spectrum. It can be seen from the figure that the peak positions and peak amplitudes of different components in the predicted results and the real results are basically consistent, and the similarity in spectral morphology is also very high. The T2 spectrum after linear superposition almost

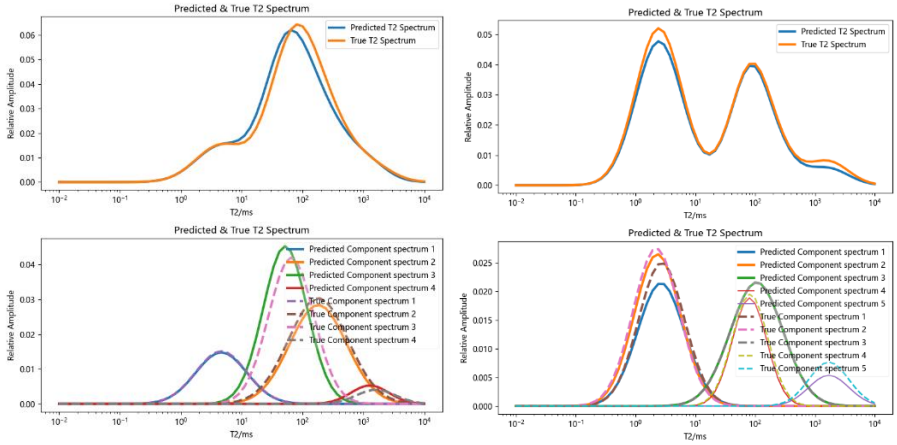
completely overlaps with the real T2 spectrum, and the peak height, peak center and peak width are basically the same. It can be seen that the final model has good prediction effect and high generalization ability.

3.5 Decomposition Results and Comparative Analysis of Other Methods

Based on the experiments in Section 3.4, this section uses two methods to perform the same T2 spectrum component decomposition task, including the Gaussian decomposition method and the Transformer model. The following will introduce these two methods and compare and analyze their decomposition results.



(a) Decomposition Results for 2 Components (b) Decomposition Results for 3 Components



(c) Decomposition Results for 4 Components (d) Decomposition Results for 5 Components

Fig. 6. Decomposition Results of Residual Fully Connected Neural Network Components

3.5.1 Gaussian decomposition method

Gaussian decomposition method is a traditional spectral decomposition technique. The nuclear magnetic resonance T2 spectrum is usually regarded as a

linear superposition of multiple normal distribution curves, and the specific expression is:

$$f(T_2) = \sum_{i=1}^{k} a_i \exp\left(-\frac{(\log T_2 - \mu_i)^2}{2\sigma_i^2}\right) \quad (5)$$

Where $\boldsymbol{a_i, \mu_i, \sigma_i}$represent the amplitude, center position and width of the i-th component, respectively, and k is the number of components. In this experiment, the nonlinear least squares fitting method is used to perform Gaussian fitting on the T2 spectrum, with the goal of minimizing the error between the synthetic T2 spectrum and the actual T2 spectrum. Although this method is highly interpretable and can give a clear spectral decomposition position, it relies on subjective factors such as the number of components preset manually and iterative parameter adjustment. It is easy to fall into a local optimal solution when dealing with non-ideal factors such as spectral peak overlap and non-Gaussian peak shape in the T2 spectrum of unconventional reservoirs.

3.5.2 Transformer Model

The Transformer model is a non-convolutional architecture mainly used to process sequence-to-sequence tasks. The model captures global dependencies through the self-attention mechanism. The Transformer model uses the self-attention mechanism to realize information interaction between any positions in the input sequence. It is suitable for modeling global dependencies and complex nonlinear mapping relationships. Its core idea can also be applied to various sequence data processing tasks, including T2 spectral decomposition. In this experiment, the Transformer architecture used includes: an input layer with a length of 64, an input embedding dimension of 128, and 4 Transformer encoding layers (the number of encoding layers is equal to the number of residual blocks in the residual fully connected neural network). Each encoding layer includes multi-head self-attention, residual connection, layer normalization and feedforward network. The number of multi-head attention heads is 8, the dimension of the feedforward network is 512, and the dimension is 15. The final output layer corresponds to the decomposition of 5 groups of Gaussian function parameters. The Transformer architecture used in this paper is shown in Fig. 7.

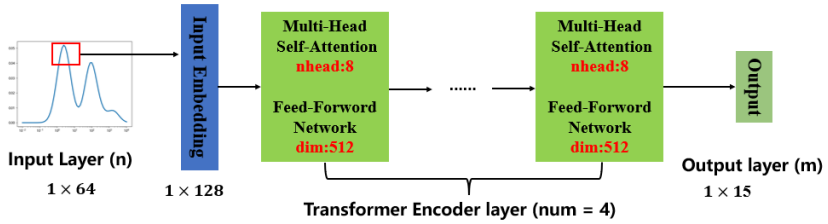


Fig. 7. Tranformer Model Used in this Paper

The Transformer model can effectively handle complex features such as overlapping peaks and non-Gaussian peaks without presetting the number or shape of peaks.

3.5.3 Comparison of decomposition results of each model component

Table 2 compares the results of Gaussian decomposition method, Transformer model and residual fully connected neural network proposed in this paper on the test set. In the prediction results of 10,000 groups of data in the test set, the residual fully connected neural network proposed in this paper has the smallest RMSE value and the largest R2 value, indicating that its prediction error is the smallest and its fitting degree is the highest. In terms of dynamic time warping (DTW), the DTW value of this method is 0.0923, which is significantly lower than that of Gaussian decomposition method and Transformer model. DTW is a method to measure the similarity between two sequences. A lower DTW value indicates that the proposed method can more accurately match the position of the spectral peak. In terms of the peak position (F1-Score, F1), the minimum peak height ratio set during calculation is 5%, and the position matching tolerance is 0.1, that is, the logarithmic difference between the position of the predicted peak and the position of the true peak must be less than or equal to the set 0.1. The proposed method is significantly higher than the Gaussian decomposition method and the Transformer model, indicating that the proposed method has significant advantages in identifying and separating overlapping peaks and hidden peaks, and can more accurately match the number and position of peaks. In terms of spectral overlap coefficient (Spectral Overlap Cofficient, SOC), the SOC value of the proposed method is 0.9573, which is higher than the results of the other two methods. The higher SOC value further proves the superiority of the proposed method in spectral morphology matching, which can be closer to the morphology of the true spectrum. As can be seen from the scores, the Gaussian decomposition method and the Transformer model are lacking in the recognition coefficients of overlapping peaks and hidden peaks and are not as good as the model proposed in this paper. The same is true for the spectral overlap coefficient.

Table 2

Processing results of three methods

Method	RMSE	R^2	DTW	F1	SOC
Gaussian decomposition	0.136	0.85	0.2089	0.86	0.9234
Transformer	0.092	0.89	0.1465	0.93	0.9352
Method of this paper	0.043	0.95	0.0923	0.96	0.9573

In summary, the residual fully connected neural network proposed in this paper performs well in solving the complex nonlinear regression problem of nuclear magnetic resonance T2 spectrum component decomposition, which is better than the traditional Gaussian decomposition method and Transformer model. This further verifies the advantages of the residual fully connected neural network in

processing one-dimensional nonlinear regression tasks.

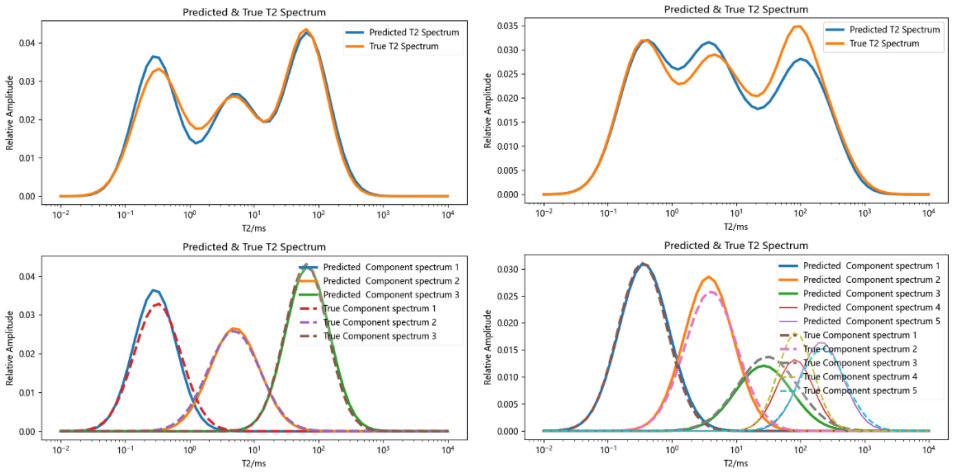
4. Results

After obtaining the NMR T2 spectrum results decomposed from the model trained using the residual fully connected neural network in Section 3, this paper verifies the above experimental results using the actual measured nuclear magnetic resonance logging data. The model was used to test the measured T2 spectra of multiple component manganese chloride samples and cores respectively.

4.1 Sample data of manganese chloride solution

Manganese chloride solution was chosen as the standard sample, and five concentrations of manganese chloride solution were prepared for the experimental data. After preparing the various concentrations of manganese chloride solution, one-dimensional NMR measurements were performed using a 21MHz NMR core analyzer. Additionally, one-dimensional NMR data were measured for the combined three concentrations and all five concentrations of manganese chloride solution. After obtaining the total raw echo train data, inversion was performed to obtain an NMR T2 spectrum with 64 sampling points. The three peak centers of the three concentrations of manganese chloride solutions were 0.292, 5.058, and 67.298 respectively, and the five peak centers of the five concentrations of manganese chloride solutions were 0.369, 3.724, 26.791, 82.605, and 212.814 respectively. Subsequently, the 64 amplitude values of the inverted T2 spectrum were normalized and used as input data for the aforementioned model to obtain the predicted output data. These predicted data were then compared with the component spectra of the various concentrations of manganese chloride solution, as shown in Fig. 8. In the figure, groups a and b respectively represent the true T2 spectra of each component of three and five concentrations of manganese chloride solutions, the predicted T2 spectra of each component by the model, and the total T2 spectrum after the linear superposition of each component. It can be seen from the results in the figure that the peak positions and amplitudes of different components in the predicted results and the true results are basically the same, and the spectral morphology similarity is extremely high. The peak centers of the fitted component spectra of the three concentrations of manganese chloride solutions were 0.318, 4.864, and 64.269, and those of the five concentrations of manganese chloride solutions were 0.350, 3.945, 29.761, 84.140, and 218.829. Although there were slight changes compared with the true peak centers of the spectra, the differences were extremely small.

Moreover, the fitting spectrum errors obtained by superimposing each component spectrum are 1.5% and 3.2% respectively, indicating that the component decomposition accuracy of the T2 spectrum obtained in this paper is relatively high.



(a) Comparison of T2 spectrum decomposition results for 3 concentrations (b) Comparison of T2 spectrum decomposition results for 5 concentrations

Fig. 8. Comparison of True and Predicted T2 Spectrum Decomposition Results for 3 and 5 Concentrations of Manganese Chloride Solution

4.2 Core measurement data

The nuclear magnetic resonance T2 spectra measured under the saturated water experiment of shale rock samples were processed by applying this model. The saturation experiment used distilled water. The main measured parameters were: magnetic field intensity of 21MHz, echo interval of 0.08ms, waiting time of 4000ms, and the number of echoes of 10,000. After performing the addition and normalization operation on the saturated T2 spectra, they were used as the input data of the model obtained above to obtain the predicted output data. Then, these predicted data were compared with the component spectra of manganese chloride solutions of various concentrations, and the results are shown in Fig. 9. Fig. 9 shows the true T2 spectra of each component of the shale rock sample after being saturated with water, the T2 spectra of each component predicted by the model, and the total T2 spectrum after the linear superposition of each component. It can be seen from the results in the figure that the peak positions and amplitudes of different components in the predicted results and the true results are basically the same, and the spectral morphology similarity is extremely high. The three peak centers of the T2 spectrum of the water-saturated rock sample are 0.105, 3.020, and 399.955. The peak centers of each component spectrum after fitting are 0.112, 2.971, and 408.95 respectively. Although there is a slight change compared with the true peak centers of the spectrum, the difference is extremely small. Moreover, the error of the fitting spectrum obtained by superimposing each component spectrum is 1.9%. This indicates that the residual fully connected neural network can accurately decompose each component of the nuclear magnetic resonance T2 spectrum.

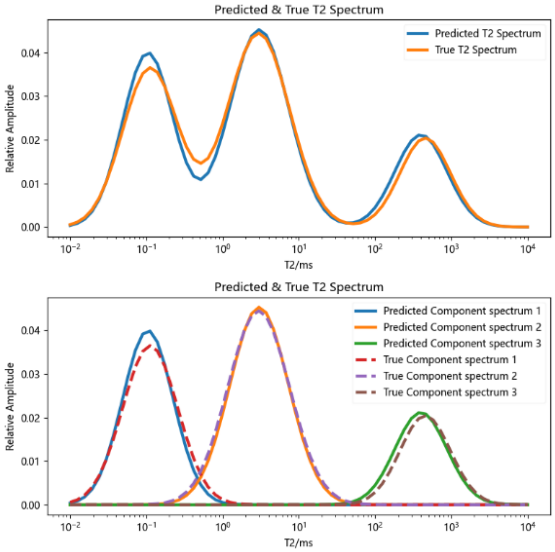


Fig. 9 Comparison of the real and predicted results of the component decomposition in the saturated T2 spectrum of shale rock samples

Therefore, it can be considered that the residual fully connected neural network can be regarded as a component decomposition model of nuclear magnetic resonance T2 spectra, successfully completing the component decomposition task of nuclear magnetic resonance T2 spectra.

5. Conclusions

In this paper, a forward model dataset was first generated, and then a residual fully connected neural network was established to solve the problem of decomposing the components of the nuclear magnetic resonance T2 spectrum. By adjusting the number of neurons in the first hidden layer of the model and the model depth, adjusting the hyperparameter components, and comparing the processing effects with the Gaussian decomposition method and the Transformer model. Through this study, the following conclusions were drawn:

(1) For the complex nonlinear regression problem of NMR T2 spectrum component decomposition, using a residual fully connected neural network yields better results than convolutional neural networks and traditional residual neural networks. The residual fully connected neural network is more suitable for solving nonlinear regression problems.

(2) During the training of deep learning models, the depth and width of the network have varying degrees of impact on the training results. An ultra-deep or ultra-wide network does not necessarily produce better training results. Therefore, it is essential to conduct experiments to determine the optimal network width and depth for the specific problem at hand. The selection of

hyperparameters is also crucial for the model.

(3) The results were verified using actual measured logging data to ensure the accuracy of the experimental results. The findings indicate that the final model obtained in this paper performs well with actual logging data. It can be concluded that integrating deep learning methods with certain problems in the field of NMR logging can also yield excellent results.

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