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Intelligent sequence stratigraphy through a wavelet-based decomposition of well log data

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Abstract

Identification of sequence boundaries is an important task in geological characterization of gas reservoirs. In this study, a continuous wavelet transform (CWT) approach is applied to decompose gamma ray and porosity logs into a set of wavelet coefficients at varying scales. A discrete wavelet transform (DWT) is utilized to decompose well logs into smaller frequency bandwidths called Approximations (A) and Details (D).

The methodology is illustrated by using a case study from the Ilam and upper Sarvak formations in the Dezful embayment, southwestern Iran. Different graphical visualization techniques of the continuous wavelet transform results allowed a better understanding of the main sequence boundaries. Using the DWT, maximum flooding surface was successfully recognised from both highest frequency and low frequency contents of signals. There is a sharp peak in all A&D corresponding to the maximum flooding surface (MFS), which can specifically be seen in fifth Approximation (a5), fifth Detail (d5), fourth Detail (d4) and third Detail (d3) coefficients. Sequence boundaries were best recognised from the low frequency contents of signals, especially the fifth Approximation (a5). Normally, the troughs of the fifth Approximation correspond to sequence boundaries where higher porosities developed in the Ilam and upper Sarvak carbonate rocks. Through hybridizing both CWT and DWT coefficient a more effective discrimination of sequence boundaries was achieved.

The results of this study show that wavelet transform is a successful, fast and easy approach for identification of the main sequence boundaries from well log data. There is a good agreement between core derived system tracts and those derived from decomposition of well logs by using the wavelet transform approach.

Keywords: Sequence stratigraphy, continuous wavelet transform, discrete wavelet transform, wavelet packet decomposition, Ilam and upper Sarvak formations, sequence boundaries.

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