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Harmonic Analysis for Power Systems based on AD-RQEA

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Abstract

High precision harmonic analysis in electric power systems is the precondition to evaluate the power quality of power grids and to control the harmonic of power grids. The fast Fourier transform (FFT) algorithm has shortcomings such as spectrum leakage and the fence effect in harmonic analysis, resulting in lower accuracy. Thus, a power harmonic analysis method based on atomic decomposition combined with the read-coded quantum evolutionary algorithm (AD-RQEA) is proposed. The core of AD-RQEA is to construct an atom library according to the characteristics of harmonic signals and to optimize feature parameters of atoms using AD-RQEA. Finally, optimal matching atoms are adaptively chosen to reconstruct voltage signals. The comparison tests show that the proposed method has high accuracy, and the effectiveness and practicability of this method are verified.

Keywords: harmonic analysis; atomic decomposition; real-coded quantum evolutionary algorithm; FFT

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1. Introduction

The large increase in nonlinear loads of power systems, especially the extensive application of high-power electronic devices, causes many harmonics to appear in the power grid, resulting in serious pollution of power quality. It has a great impact on the power system operation in security and economy [1-2]. The accurate measurement and analysis of harmonics in the power grid is an obstacle for the assessment of power quality, and it is of great significance to improve the power quality and maintain the safe operation of the power grid.

At present, the most common tool for power system harmonic analysis is the FFT algorithm. However, owing to the FFT algorithm having the phenomenon of fence effect and spectrum leakage at the measured signal arising changes and resulting in non-synchronous sampling or non-integer period of the signal truncation, the calculated parameters of the measured signal by FFT such as frequency, amplitude, and phase are not accurate enough. In particular, the phase error is so large that it cannot meet the standard requirements of harmonic measurement [3-4]. At the same time, the larger harmonic calculation error cannot meet the needs of metering relay protection. Aiming at the shortcomings of harmonic analysis using the FFT algorithm, an improved FFT algorithm with window interpolation is proposed. This algorithm uses a window function with excellent performance to reduce the error caused by spectral leakage. Common window functions include rectangular window, triangular window, Hamming window, Blackman window, Nuttall window, rectangular convolution window, and maximum sidelobe attenuation window. It uses interpolation correction to reduce the error caused by the fence effect [5]. Aiming at the shortcomings of the bispectrum interpolation correction algorithm, such as the realization of algorithms, the solution of the correction formula, and the calculation accuracy, an interpolation correction formula based on three spectral lines has been proposed [6]. It further improves the accuracy of the interpolation FFT algorithm. However, window functions and interpolation corrections do not fully eliminate the effects of spectral leakage and fence effects, and they cannot improve the accuracy. At the same time, the interference of the algorithms by the noise is relatively large.

In recent years, atomic decomposition techniques based on the idea of Mallat and Zhang's decomposition of signals over a complete atomic library have been widely used in the field of signal processing [7]. In terms of internal features of

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signals choosing optimal atoms from the atomic library, decomposition of the signal is sparse, and then we can express the signal by less components. The matching pursuit (MP) algorithm is employed in the process of signal decomposition, that is, in each iteration, the most matched atom with the residual component of a signal is selected and then the signal is represented as a linear combination of the most matched atoms [8-9].

This paper presents a method of power harmonic analysis based on AD-RQEA. It applies atomic decomposition to grid harmonic analysis. Considering the shortcomings of the MP algorithm, such as the large amount of computation and the discretization of the search space, it may not find the global optimal solution, so we use a real-coded quantum evolutionary algorithm to optimize the atom parameters in the MP algorithm. Simulation results show that the power harmonic analysis based on AD-RQEA is more accurate than the FFT algorithm and has practical value.

2. Atomic Decomposition

Atomic decomposition belongs to non-orthogonal decomposition. In signal space, a sufficiently dense base is constructed, and a base is called an atom. The library of these atoms is enough complete to select the most matched atoms adaptively to represent arbitrary signals, thus obtaining sparse representation of signals. The selected atoms reflect the characteristics of signals. This paper studies the electric power signal, which can be regarded as a sinusoidal signal. The mathematical expression of the atom is as follows:

$$g_{\gamma(i)}(t) = A_i \sin(2\pi k f_i t + \phi_i) \tag{1}$$

Where A_i is the amplitude of the i^{th} atom, f_i is the frequency of the i^{th} atom, and ϕ_i is the phase of the i^{th} atom. $g_{\gamma(i)}(t)$ is uniquely determined by parameters $\gamma = (A_i, f_i, \phi_i)$.

The matching pursuit algorithm (MP) is usually used in the process of atomic decomposition. The signal to be measured is the inner product with all atoms in the atomic library. The atom with the largest inner product is chosen as the optimum atom, which is a component of the atomic decomposition of the signal to be measured. The mathematical expression is as follows:

$$f(t) = \left\langle f(t), g_{\gamma(0)}(t) \right\rangle g_{\gamma(0)}(t) + R(t) \tag{2}$$

Where $R(t)$ is a signal and $f(t)$ is the residual signal after decomposition.

By continuous iteration, when the accuracy requirements are met, the decomposition will stop. The signal can be expressed as:

$$f(t) = \sum_{k=0}^{m-1} \left\langle R^k(t), g_{\gamma(k)}(t) \right\rangle g_{\gamma(k)}(t) + R^m(t) \tag{3}$$

Where $R^0(t) = f(t) \cdot \left\| R^m(t) \right\|$ is a small constant that describes the error after signal decomposition. Thus, we can use the m atoms that have been selected to approximate the original signal. That is:

$$f(t) = \sum_{k=0}^{m-1} \left\langle R^k(t), g_{\gamma(k)}(t) \right\rangle g_{\gamma(k)}(t) \tag{4}$$

During the process of computation, the inner product can go through the entire atomic library, and there is a huge amount of calculation. The MP algorithm needs to be converted from the continuous time domain space into the discrete time domain space. Discrete space search limits the accuracy of finding the optimal atom. In this paper, RQEA is used to optimize atomic parameters. Continuous search in real space improves accuracy and efficiency.

3. AD-RQEA Algorithm

The atomic characteristics constructed in this paper are determined by parameter γ. A chromosome of RQEA represents an atom. Its allele is composed of the parameter vector γ_{i} of the i^{th} atom and a pair of probability amplitudes $(\alpha_i, \beta_i)^T$. Any chromosome of RQEA can be described as:

$$\begin{pmatrix} A_i & f_i & \phi_i \\ \alpha_1 & \alpha_2 & \alpha_3 \\ \beta_1 & \beta_2 & \beta_3 \end{pmatrix} \tag{5}$$

Where α_i and β_i satisfy the normalization condition, $i = 1, 2, 3$, and $\gamma_{\mathrm{i}} = (A_i, f_i, \phi_i)$.

The fitness function is taken as the inner product of the atom and the signal to be measured. After the second iteration, the fitness function is taken as the inner product of the atom and the residual signal of this iteration. The larger the inner product, the more relevant the selected atom to the signal in this iteration. The mathematical description of the fitness function is as follows:

$$f = \left|\left\langle r^m, g_{\gamma(m)} \right\rangle\right| = \sup_{\gamma\in\Gamma} \left|\left\langle r, g_\gamma \right\rangle\right| \tag{6}$$

Where r^m is the residual signal in the *m* times of iteration and r^0 is the signal to be measured.

Assuming that a single chromosome is c_j^t, the i^{th} allele of the j^{th} chromosome $\left(\gamma_{j,i}^t, \alpha_{j,i}^t, \beta_{j,i}^t\right)^{\mathrm{T}}$ is selected, and the atomic parameters are mutated by Gauss, we can obtain:

$$\gamma_{j,i}^{t+1,n} = \gamma_{j,i}^t + \left(\gamma_{i,\max} - \gamma_{i,\min}\right) N\left(0, \left(\sigma_{j,i}^{t,n}\right)^2\right) \tag{7}$$

Where $k = \alpha, \beta$, $(\sigma_{j,i}^k)^2$ denotes Gaussian distribution variance, and its value is designed as [10]:

$$(\sigma_{j,i}^k)^2 = \begin{cases} \left|\alpha_{j,i}^t\right|^2, & k = \alpha \\ \left|\alpha_{j,i}^t\right|^2 \big/ 5, & k = \beta \end{cases} \tag{8}$$

If the fitness of the new chromosome is better than that of the existing chromosome, the new chromosome will be retained.

Otherwise, it is updated by the quantum revolving gate [11-12], that is:

$$\begin{bmatrix} \alpha_{j,i}^{t+1} \\ \beta_{j,i}^{t+1} \end{bmatrix} = \begin{bmatrix} \cos(\Delta\theta_{j,i}^t) & -\sin(\Delta\theta_{j,i}^t) \\ \sin(\Delta\theta_{j,i}^t) & \cos(\Delta\theta_{j,i}^t) \end{bmatrix} \begin{bmatrix} \alpha_{j,i}^{t+1} \\ \beta_{j,i}^{t+1} \end{bmatrix} \tag{9}$$

Where $\Delta\theta_{j,i}^t$ is the rotation angle, and the value of $\Delta\theta_{j,i}^t$ is designed as:

$$\Delta\theta_{j,i}^t = \mathrm{sgn}(\alpha_{j,i}^t \beta_{j,i}^t)\theta_0 \exp\left(-\frac{\left|\beta_{j,i}^t\right|}{\left|\alpha_{j,i}^t\right| + \gamma}\right) \tag{10}$$

Where $\mathrm{sgn}(\cdot)$ is the sign function and determines the direction of $\Delta\theta_{j,i}^t$, θ_0 is the initial rotation angle, and γ is the evolutionary scale. θ_0, γ, and $(\alpha_{j,i}^t \beta_{j,i}^t)^{\mathrm{T}}$ decide the size of $\Delta\theta_{j,i}^t$ together, and they further control the convergence rate of algorithms [13-15]. In order to improve the diversity of the population and speed up the convergence rate, the crossover strategy is adopted to designate the chromosome and exchange the gene position with another chromosome selected by 0.5 probability. Specific expressions can be described as:

$$\left(\gamma_{c,i}^{t},\alpha_{c,i}^{t},\beta_{c,i}^{t}\right)^{T}=\begin{cases}\left(\gamma_{u,i}^{t},\alpha_{u,i}^{t},\beta_{u,i}^{t}\right)^{\mathrm{T}}, & x<0.5\\ \left(\gamma_{v,i}^{t},\alpha_{v,i}^{t},\beta_{v,i}^{t}\right)^{\mathrm{T}}, & x\geq 0.5\end{cases} \tag{11}$$

4. Simulation Experiment

Assuming the power system signal includes the order of harmonics from 1 to 9, the parameters of signal for the power system are shown in Table 1. In order to verify the effectiveness of the proposed algorithm, we use the MATLAB platform for simulation experiments. Set the sampling frequency to 2400Hz and the sampling length to 0.2s, and then the number of sampling points is 480.

Test 1:

Accurate measurement of the fundamental frequency in power systems is of great significance for relevant relay protection, synchronous switching closing, and so on. We use the proposed method to simulate the fundamental frequency calculation of the power system signal waveform. In the experiment, the fundamental frequency of the signal is changed from 49Hz to 51Hz at 0.1Hz intervals to verify the accuracy of the proposed algorithm at different fundamental frequencies. Due to space limitations, the results of 49.0Hz, 49.5Hz, 50.0Hz, 50.5Hz, and 51.0Hz are shown in Table 2 only.

Table 1. Parameters of signal for power system

Harmonic order	Amplitude/V	Phase/°
1	220	0
2	4	15
3	17	45
4	2	60
5	7	60
6	1	45
7	5	90
8	0.5	90
9	3	45

Table 2. The error of parameters for fundamental frequency signals

Fundamental frequency	Amplitude/V		Frequency/Hz		Phase/°	
	Absolute error/V	Relative Error/%	Absolute error/Hz	Relative Error/%	Absolute error/°	Relative Error/%
49.0	5.23e-3	-3.37 e-3	5.77e-5	1.18e-4	-9.45 e-7	-7.21 e-4
49.5	6.45e-3	2.93e-3	-6.54 e-5	-1.32 e-4	6.45e-7	4.92e-4
50.0	-5.12 e-3	-2.32 e-3	-3.98 e-5	-7.96 e-5	-3.76 e-7	-2.86 e-4
50.5	-7.45 e-3	-3.38 e-3	8.23e-5	1.62e-4	-8.54 e-7	6.52e-4
51.0	3.91e-3	1.77e-3	1.43e-5	2.80e-5	-7.76 e-7	5.92e-4

As can be seen from Table 2, the absolute error of fundamental amplitude is less than 0.01V when using the AD-RQEA algorithm, and the relative error is less than 0.01%. The absolute error of the fundamental frequency measurement is less than 10^{-4} Hz, and the relative error is less than 0.001%. The phase absolute error is less than 10^{-6}, and the relative error is less than 0.001%. We can conclude that the method proposed in this paper can extract the fundamental information accurately and meet the requirements of power systems for frequency and phase.

Test 2:

The harmonic is an important parameter to measure the power quality of power systems, and the accurate measurement of the harmonic is key to evaluating and controlling harmonic pollution. We use the proposed method to analyse harmonic signals in power systems to verify its effectiveness. In the experiment, the fundamental frequency of the signal was changed from 49Hz to 51Hz at a 0.1Hz interval to test the accuracy of harmonic analysis at different fundamental frequencies. Due to space limitations, we give only the results of harmonic analysis at a fundamental frequency of 50Hz. Figure 1 depicts the decomposition of the voltage signal of the power system. The absolute error and relative error of the fundamental wave and harmonic wave's amplitude, frequency, and phase are shown in Table 3. Atom decomposition from the 1st time to the 7th time are shown as follows.

Figures 1-16 indicate the voltage signal decomposition process. The fundamental signal is obtained by the first decomposition, as shown in Figure 2. By subtracting the fundamental signal from the voltage signal, the other frequency components can be obtained as shown in Figure 3. After nine rounds of decomposition, we can get the 1st to 9th harmonic amplitude, frequency, phase, and other related signals. Figure 16 is a reconstructed signal obtained from the decomposition of each harmonic signal. It can be seen that the reconstructed signal can recover the voltage signal well.

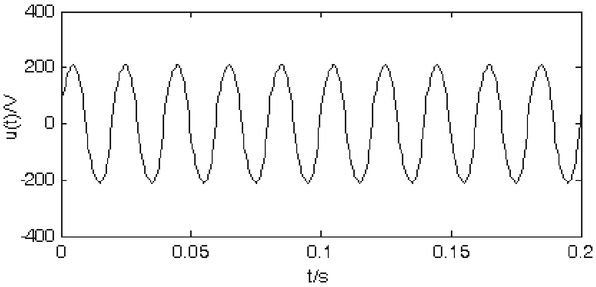

Figure 1. Voltage signals

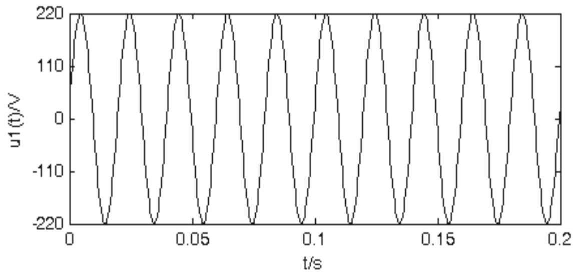

Figure 2. The 1st decomposed atoms

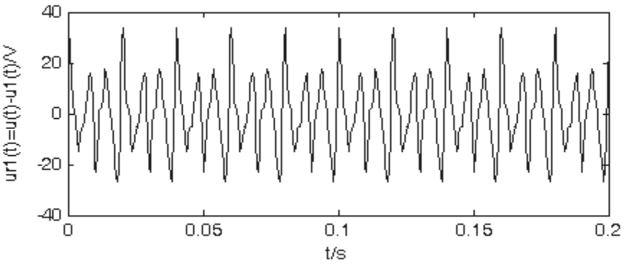

Figure 3. The residual signals of the 1st decomposition

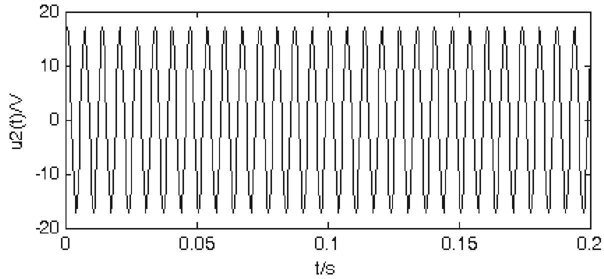

Figure 4. The 2nd decomposed atoms

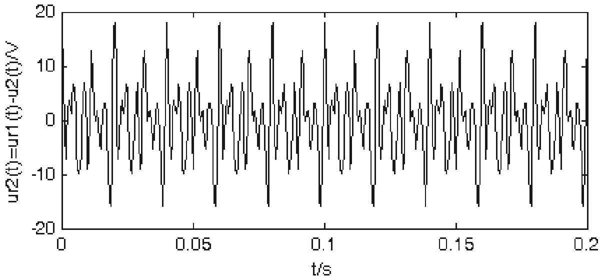

Figure 5. The residual signals of the 2nd decomposition

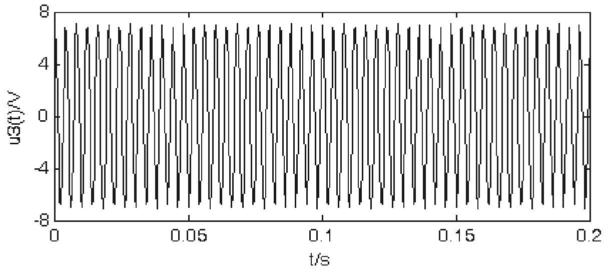

Figure 6. The 3rd decomposed atoms

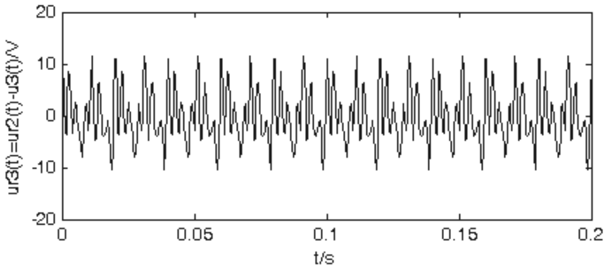

Figure 7. The residual signals of the 3rd decomposition

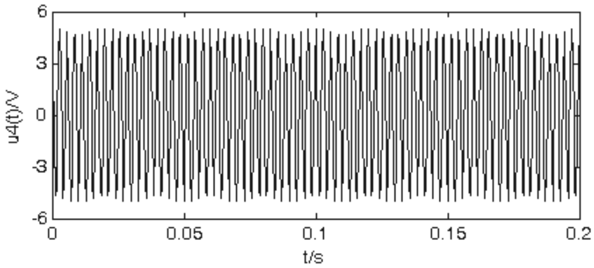

Figure 8. The 4th decomposed atoms

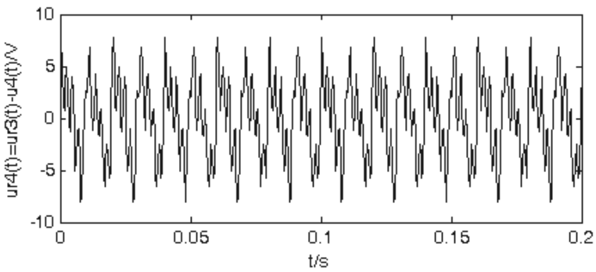

Figure 9. The residual signals of the 4th decomposition

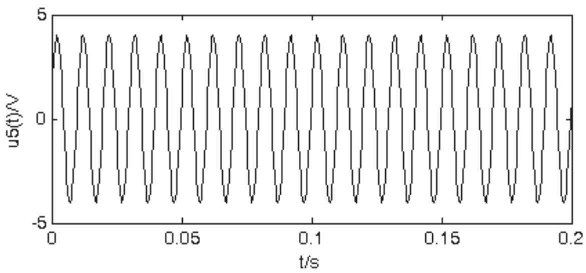

Figure 10. The 5th decomposed atoms

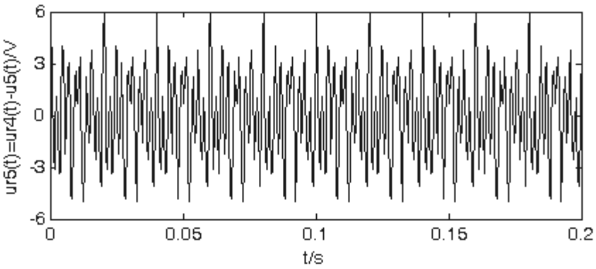

Figure 11. The residual signals of the 5th decomposition

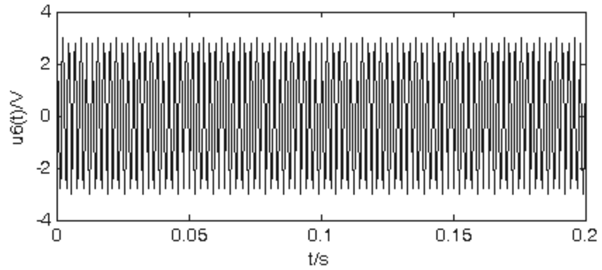

Figure 12. The 6th decomposed atoms

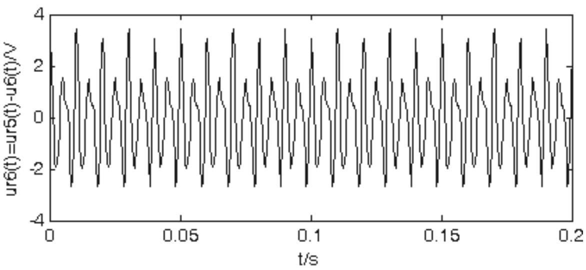

Figure 13. The residual signals of the 6th decomposition

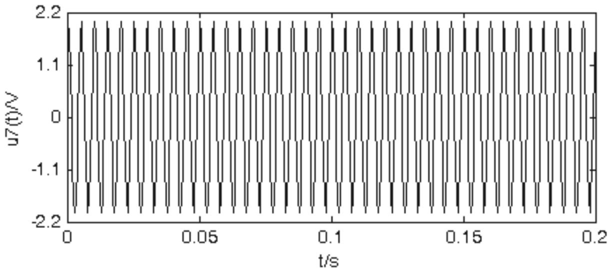

Figure 14. The 7th decomposed atoms

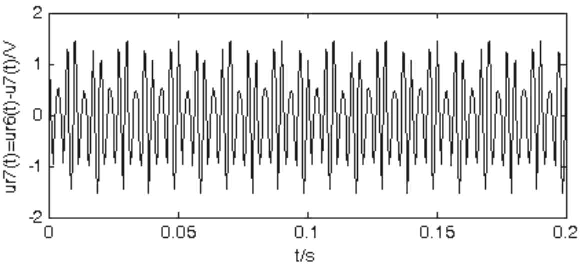

Figure 15. The residual signals of the 7th decomposition

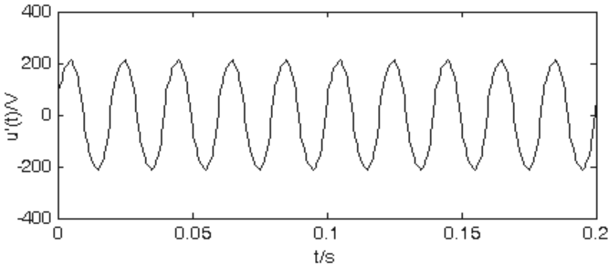

Figure 16. The reconstruction for voltage signals

From the data in Table 3, we can see that when using AD-RQEA to analyse the harmonic of power systems, the parameters of amplitude, frequency, and phase have high precision and can meet the requirements of harmonic analysis. The FFT algorithm has a large error in the harmonic analysis and cannot meet the requirements of power systems.

Table 3. Error comparison of parameters for harmonic signals

Harmonic order	Method	Amplitude/V		Frequency/Hz		Phase/°	
		Absolute error/V	Relative error/%	Absolute error/Hz	Relative error/%	Absolute error/°	Relative error/%
1	FFT	-0.3273	-0.1488	0.1040	0.2083	5.44e-5	0.0416
	AD-RQEA	-0.0051	-0.0023	-3.98e-5	-7.96e-5	-3.76e-7	-2.86e-4
2	FFT	0.4905	12.2625	0.2079	0.2083	4.90e-3	1.8716
	AD-RQEA	0.0052	0.1300	9.56e-4	9.56e-4	-1.71e-3	-0.6531
3	FFT	0.2890	1.7000	0.3119	0.2083	-2.80e-3	-0.3565
	AD-RQEA	0.0512	0.3013	4.76e-5	3.13e-5	2.1e-6	2.67e-4
4	FFT	0.1127	5.6350	0.4158	0.2079	7.39e-3	0.7056
	AD-RQEA	0.0035	0.1790	8.78e-4	4.39 e-4	1.05e-3	0.1002
5	FFT	0.2202	3.1460	0.5197	0.2078	3.55e-4	0.0338
	AD-RQEA	0.0396	0.5663	4.53e-5	1.82e-5	2.83e-6	2.70e-4
6	FFT	0.1634	16.3400	0.6237	0.2079	-2.80e-3	-0.3565
	AD-RQEA	8.00e-4	8.00e-2	7.95 e-4	2.56e-4	8.32e-4	0.10659
7	FFT	0.1842	3.6840	0.7277	0.2079	1.68e-3	0.1069
	AD-RQEA	0.0245	0.4904	-5.36e-5	-1.53e-5	4.33e-6	2.75e-4
8	FFT	0.0579	11.5800	0.8316	0.2079	-3.54e-4	-0.0225
	AD-RQEA	-9.0e-4	-0.1800	8.54e-4	2.13e-4	-1.81e-5	-1.15e-3
9	FFT	0.3179	10.5966	0.9355	0.2078	-3.78e-3	-0.4710
	AD-RQEA	8.60e-3	0.2866	-6.74e-5	-1.49e-6	1.32e-4	0.0168

5. Conclusions

In this paper, a novel method of power system harmonic analysis based on AD-RQEA is proposed. It applies atomic decomposition to reconstructing the voltage signal of the grid and obtains the harmonic information of frequency, amplitude, and phase. Using the read-coded quantum evolutionary algorithm to optimize the parameters of atoms, it prevents the search from being trapped in the local optimal caused by the discrete search space. Thus, the search efficiency and accuracy are improved. The simulation results show that the proposed method has higher accuracy, thereby providing an effective tool for harmonic analysis of power systems.

Acknowledgements

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