

# Study of Algorithm to Ensemble Atomic Time

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*Abstract*- An ensemble atomic time algorithm was developed based on wavelet packet analysis. Ensemble atomic time can be obtained by decomposing the clock difference of atomic clocks, extracting the components of different frequency domain, and then choosing the weight according to the stability of different component denoted with wavelet variance. The optimization characteristic of genetic algorithm was introduced and model of atomic clock signal was constructed. And genetic algorithm was used to optimize this model, then to validate the optimization model with dispersion data of atomic clock measured in laboratory. It can prove that genetic algorithm and wavelet packet algorithm was appropriate.

## I. INTRODUCTION

To maintain time scale exact and consecutive, and time unit can approach SI second as possible, cesium atomic clock were collocated in every time and frequency laboratory. Every atomic clock can maintain a time scale, however, every atomic clock probably have a screw loose. So many atomic clocks were required to keep time in every laboratory, and atomic time algorithm was required to compute ensemble atomic time. The aim of studying atomic time algorithm is to obtain higher stability atomic time.

In this paper, the classical weighted average algorithm developed by BIPM, i.e. ALGOS were investigated. To this algorithm only one weight can be chosen within the whole interval of the sampling time on each atomic clock, and the criterion for weight was the stability  $\sigma_y^2(\tau)$  of each single atomic time. We investigated the wavelet packet analysis and developed an ensemble atomic time algorithm based on this method. Ensemble atomic time can be obtained by decomposing the clock difference of atomic clocks, extracting the components of different frequency domain, and then choosing the weight according to the stability of different component denoted with wavelet variance. The optimization characteristic of genetic

algorithm and developed an ensemble atomic time algorithm based on this method were analyzed. The object function of genetic algorithm was based on the model of ALGOS and the initial weights were random value of 0~1. The maximal characteristic of genetic algorithm is that the frequency stability of each clock is not depended on to choose the weight.

## II. THE CLASSICAL WEIGHTED AVERAGE ALGORITHM

As presented as before, the atomic time (AT) defined by single atomic clock is influenced by five identifiable noise, white-noise PM, flicker-noise PM, white-noise FM, flicker-noise FM, random-walk FM. We can consider these noise sources are independent to different atomic clocks. To reduce the influences of every independent noise sources and obtain a more stable atomic time scale, in analogy with what is done for the ensemble atomic time, the definition of the ensemble atomic time is the weighted average of the atomic time defined by several atomic clocks. TA(t) can be expressed as

$$TA(t) = \sum_{i=1}^N P_i T_i(t) / \sum_{i=1}^N P_i. \quad (1)$$

Where  $P_i$  is the relative weight assigned to atomic clock  $i$ . Weights should be inversely proportional to the instability of each atomic clock for integration times of a few years. If many data sets were available it might be worth estimating the instability by an N-cornered hat technique[1].

## III. WAVELET PACKET ANALYSIS ALGORITHM

For classical weighted average algorithm of ensemble atomic time only one weight can be chosen to the identical atomic clock, and the classical weighted average algorithm of ensemble atomic time can not consider the short-term instability and long-term instability at the same time, so there is some limitation in this algorithm. An ensemble

atomic time algorithm based on wavelet packet analysis is to decompose the signal of single atomic clock in wavelet domain, then to extract the components at different frequency range, after that the instabilities of different residuals component at different frequency range denoted by wavelet square error were used in the weighted average algorithm of ensemble atomic time.

In time-frequency field Fourier Transform is the most frequently used analysis method. However, Fourier Transform is the whole domain transform and it can not supply the correlative information of signal in time domain and frequency domain. Gabor introduced “Window” Fourier Transform to overcome this disadvantage, Window Fourier Transform have localized function in both time domain and frequency domain. The windows’ size of time domain and frequency domain of Window Fourier Transform is changeless, and Window Fourier Transform is not self-adaptively, so this method is not applicable to analyze multi-scale signal and the process with break. Wavelet packet Transform inherits and develops Window Fourier Transform. The wavelet packet basis function is similar to a window function, and wavelet packet shifting is similar to window shifting. Wavelet packet analysis is a perfect time-frequency analysis instrument[2].

#### A. Definition of wavelet packet

Atomic clock timing data can be effectively decomposed in time domain and frequency domain by Wavelet Multiresolution Analysis, but its scales changed in binary system, which result in bad frequency resolution rate of high frequency segment and bad time resolution rate of low frequency segment, That is to say, the frequency range of atomic clock timing data was divided equispacedly in exponential[3]. However, wavelet packet analysis can supply a kind of more elaborate analysis method to atomic clock timing data, it divides the frequency range to more levels, and it can decompose the further high frequency segment that multiresolution analysis can not divide elaborately. Furthermore wavelet packet analysis can choose the relevant frequency range self-adaptively according to the character of analyzed signal and make it match the signal frequency spectrum so that it improves the time-frequency resolution rate.

Figure 1 shows the tree-structure of three levels wavelet packet decomposition[4]. Where A denotes low frequency and D denotes high frequency, the serial number after that is the levels number (scales number) of wavelet

packet decomposition. The decomposition relation is expressed,

$$S = AAA3 + DAA3 + ADA3 + DDA3 + AAD3 + DAD3 + ADD3 + DDD3$$

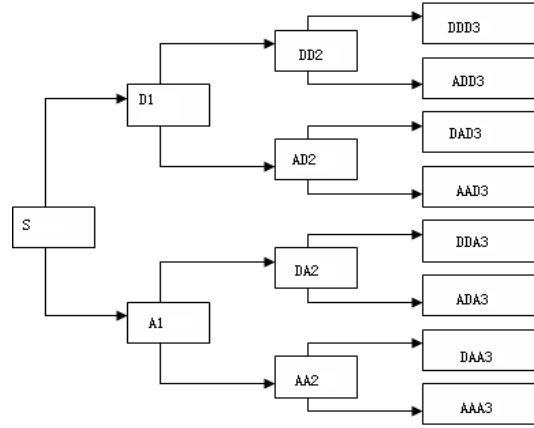


Figure 1 The structure of three levels wavelet packet decomposing tree

There is some difference from the wavelet multiresolution, the wavelet subspace  $W_j$  is divided elaborately according to binary system. Now let's denote the scale subspace  $V_j$  and wavelet subspace  $W_j$  with a space  $U_j^n$  uniformly[3], for

$$\left. \begin{aligned} U_j^0 &= V_j \\ U_j^1 &= W_j \end{aligned} \right\} j \in \mathbb{Z} \quad (2)$$

So the Hilbert space can be uniformed with the decomposition of space  $U_j^n$ ,

$$U_{j+1}^0 = U_j^0 \oplus U_j^1 \quad j \in \mathbb{Z} \quad (3)$$

To define that the subspace  $U_j^n$  is the close packet of function  $u_n(t)$  and the subspace  $U_j^{2n}$  is the close packet of function  $u_{2n}(t)$ , and to make  $u_n(t)$  content the binary scale equation below:

$$\left. \begin{aligned} u_{2n}(t) &= \sqrt{2} \sum_{k \in \mathbb{Z}} h(k) u_n(2t - k) \\ u_{2n+1}(t) &= \sqrt{2} \sum_{k \in \mathbb{Z}} g(k) u_n(2t - k) \end{aligned} \right\} \quad (4)$$

Where,  $g(k) = (-1)^k h(1-k)$ , namely both of the coefficients are orthogonal. When  $n = 0$  both of the two function above become

$$\begin{cases} u_0(t) = \sum_{k \in \mathbb{Z}} h_k u_0(2t - k) \\ u_1(t) = \sum_{k \in \mathbb{Z}} g_k u_0(2t - k) \end{cases} \quad (5)$$

Compared with that in the multiresolution analysis  $\phi(t)$  and  $\psi(t)$  content binary scale equation:

$$\begin{cases} \phi(t) = \sum_{k \in \mathbb{Z}} h_k \phi(2t - k) & \{h_k\}_{k \in \mathbb{Z}} \in l^2 \\ \psi(t) = \sum_{k \in \mathbb{Z}} g_k \phi(2t - k) & \{g_k\}_{k \in \mathbb{Z}} \in l^2 \end{cases} \quad (6)$$

Functions  $u_0(t)$  and  $u_1(t)$  are separately degenerated as scale function  $\phi(t)$  and wavelet function  $\psi(t)$ . Formula (5) is the equivalence of formula (3), now we generalize this equivalence to that instance of  $n \in \mathbb{Z}_+$ , so we can obtain the equivalence of formula (4):

$$U_{j+1}^n = U_j^{2n} \oplus U_j^{2n+1} \quad j \in \mathbb{Z}; \quad n \in \mathbb{Z}_+ \quad (7)$$

The sequence  $\{u_n(t) | n \in \mathbb{Z}_+\}$  constructed by formula (4) become the orthogonal wavelet packet confirmed by the basis function  $u_0(t) = \phi(t)$ . When  $n = 0$ , this orthogonal wavelet packet expressed as formula (5).

Because the function  $\phi(t)$  is confirmed only by  $h_k$ , function group  $\{u_n(t)\}_{n \in \mathbb{Z}}$  are called orthogonal wavelet packet about sequence  $\{h_k\}$ .

#### B. The algorithm of wavelet packet

In the first place we assumed  $g_j^n(t) \in U_j^n$ , then

$g_j^n$  can be expressed as[3]

$$g_j^n(t) = \sum_i d_l^{j,n} u_n(2^j t - l) \quad (8)$$

The decomposition algorithm of wavelet packet is to obtain  $\{d_l^{j,2n}\}$  and  $\{d_l^{j,2n+1}\}$  by  $\{d_l^{j+1,n}\}$ , which is expressed as

$$\begin{cases} d_l^{j,2n} = \sum_k a_{k-2l} d_k^{j+1,n} \\ d_l^{j,2n+1} = \sum_k b_{k-2l} d_k^{j+1,n} \end{cases} \quad (9)$$

The reconstruction of wavelet packet is to obtain  $\{d_l^{j+1,n}\}$  by  $\{d_l^{j,2n}\}$  and  $\{d_l^{j,2n+1}\}$ , which is expressed as

$$d_l^{j+1,n} = \sum_k [h_{l-2k} d_k^{j,2n} + g_{l-2k} d_k^{j,2n+1}] \quad (10)$$

#### C. Compute the ensemble atomic time using wavelet packet analysis algorithm

Because the orthogonal wavelet packet is confirmed only by basis function  $\phi(t)$ , in analogy with what is done for the wavelet analysis algorithm[3], under the scale  $j$  the measured signal  $i$  can be decomposed by the orthogonal wavelet packet function as

$$f^i(x) = \sum_{k=-\infty}^{\infty} d_{j,k}^i \phi_{j,k}^i(x) \quad (11)$$

The energy of atomic clock signal can be denoted as[5]:

$$E_j = \frac{1}{\sum_{k=n1}^{n2} (n2 - n1) d_{j,k}^2} \quad (12)$$

The partial of atomic clock signal have the same dimension as variance of atomic clock signal, so the variance of atomic clock signal can be defined as

$$\sigma_j^2 = \frac{1}{\sum_{k=n1}^{n2} (n2 - n1) d_{j,k}^2} \quad (13)$$

So  $\sigma_j$  is the weight under the wavelet packet scale  $j$ .

The weighted sum of  $l$  atomic clock signal  $f^i(x) (i = 1, \dots, l)$  is denoted as

$$\bar{f}(x) = \sum W_i f^i(x) / \sum W_i \quad (14)$$

Where  $W_i$  denotes the weight of atomic clock signal.

Formula (14) can be written as formula (15) below according to the relation of wavelet packet decomposition and reconstruction

$$\bar{f}(x) = \frac{\sum_{k=-\infty}^{\infty} \sigma_j^i d_{j,k}^i \varphi_{j,k}^i(x)}{\sum_i \sigma_j^i} \quad (15)$$

Where  $\sigma_j^i$  denotes the weight of atomic clock signal

$f^i(x)$  under wavelet packet scale  $j$ .

#### IV. GENETIC ALGORITHM

Genetic Algorithm (GA) which advanced by J.H.Holland from Michigan college America 1975 is a sort of optimization algorithm that simulated genetic theory of natural selection[6]. It is based on Darwinism and Mendelism. According to Darwinism, each species were more and more adaptive to living environment along with evolution, the essential characteristic of each individual of species were inherited by offspring, however, the offspring were not absolutely same. These new varieties would be preserved if they adapted environment, otherwise they would be eliminated. Genetic algorithm simulated genetic and evolution theory of biology, and quoted random statistic theory. Genetic algorithm began with an initial variable population, searched for the best individual generation by generation, till satisfied the convergent criterion or prescriptive iterative degree.

The advantages of genetic algorithm are[7]: 1) Search begins with multi-point not single point. 2) During searching optimization, the fitness value information transformed from object function value is the only need, other assistant information including derivative in not needed. 3) The whole search process would not plunge into partial optimization point generally. At present, genetic algorithm had infiltrated many fields and it is the powerful tool to solve complicated problem of these fields.

##### A. The basal theory of genetic algorithm

In genetic algorithm, decision-variables of problem were coded individuals of genetic space one by one, each individual was genotype data string, meanwhile, the objective function value were transformed to fitness value. Fitness value was used to evaluate best or worst of individual and was the basis of genetic operation. Genetic operation included three operators: selection, crossover, and mutation. Selection operator was used to perform survival of the fittest principle, viz. copied individuals of current population to new population by probability proportional with fitness value, and formed the copulation

pool (the mid population between the current population and new population). Selection operator advanced average fitness value of population. Because selection operator did not bring new individual, the fitness value of best individual of population was not improved by selection operator. Crossover operator could bring new individual, above all it made the individuals of copulation pool copulate randomly, crossed the partial gene of every two copulatory individual by some mode. Mutation operator was to change certain or some gene of individual according to some lesser probability. From the capability of bringing new individual, crossover operator algorithm was the primary method, it decided the global search capability of genetic algorithm. Mutation algorithm was only accessorial method of bringing new individual, however, it was absolutely necessarily, because it decided the partial search capability. It was necessary to combine crossover and mutation algorithms to complete the global and partial search.

The basal process of genetic algorithm is[8]: 1) Initialization. M individuals created randomly were regarded as initial population  $P(0)$ ; 2) Evaluate individual. To compute fitness of each individual of  $P(t)$ ; 3) Individuals which had bigger fitness value were composed of copulation pool according to fitness value of individuals; 4) To perform crossover operator and mutation operator to the individuals of copulation pool and bring new generation; 5) To perform the process from 2~4 till the biggest number of evolution generation.

There were some run-parameters need to be decided when we used genetic algorithm, the length of code string, the number of individual of population, the biggest generation number, crossover probability and mutation probability[9]. The length of code string was decided by precision of the result that optimization problem needed. When the number of individual of population was smaller, the operation speed of genetic algorithm would be improved, however, the multiformity was depressed and the optimization result could not be obtained. When the number of individual of population was bigger, the operation speed of genetic algorithm would be slow. Generally, the number of individual of population was 20~100. The biggest number of evolution generation was a parameter that denoted the term to end genetic algorithm and denoted that genetic algorithm would circulate no longer after achieving the number, and the optimization

result viz. the best individual of current population would be exported. The crossover probability controlled the frequency of crossover operate. Because crossover operator algorithm was the primary method, the value of crossover probability was bigger. However, if the value of crossover probability was too big, the excellent pattern would be destroyed. Generally, it was 0.4~0.99. The mutation probability was also a factor that influenced, if it was smaller, the new individual number would be few, if it was bigger, genetic algorithm would be random search. Generally, the mutation probability value was 0.0001~0.1[10].

### B. The designation of genetic operator[11]

1) *select operator*: The select operation was the regenerative process of population generation by generation. The select strategy was that 1) the best chromosome came into next generation directly, 2) taxis select, viz. to compute the select probability according to fitness value of chromosomes, big fitness value corresponded to big probability, vice versa.

2) *crossover operator*: The crossover operation process was that two individuals of parent generation were exchanged partial genes to bring new individuals. To two individuals of the copulation pool, selecting a locality  $i$  ( $1 \leq i \leq I$ ), the character string left or right of location  $i$  of the two individuals were exchanged each other and bringing two new individuals. These two new individuals combined characteristic of parent generation individuals. Apparently, the aim of crossover was to bring new gene combination and to bring new individuals and not to repeat the same population generation by generation. Fig.1 was the crossover operation sketch map according to exchange the part right of  $i$ .

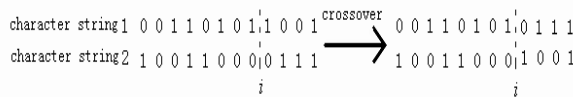


Figure 2 The sketch map of crossover operator

3) *mutation operator*: Mutation operation was to provide new information for population, so it could keep population multiformity and prevent bringing precocity phenomena. Selecting the mutation locality according to mutation probability  $p_m$ , and taking the contrary of the bit at the mutation. point  $i$ . Viz., on the selected point 1 was become to 0 or 0 was become to 1. The changed quantity

minished gradually with increase of number of evolution generation, and at the evolution anaphase the quantity would approach 0. Mutation operation showed at fig.2.

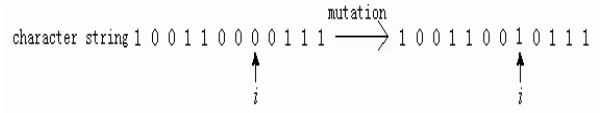


Figure 3 The sketch map of mutation operator

Generally, it's impossible to achieve progress only depended on mutation, because the mutation probability was very small. However, mutation operator can guarantee that the population continued evolving and provide the chance to bring new individuals.

### C. the application of genetic algorithm

genetic algorithm was used to compute the ensemble atomic time and optimize the weight  $P_i$  of function (1), where  $P_i$  just was the decision-variables, and function (1) was the objective function. The optimization object was to make the ensemble atomic time  $TA(t)$  minimal, the fitness function maybe defined as

$$f(P_i) = \frac{1}{[TA(t)]^2} = \frac{1}{[\sum_{i=1}^N P_i T_i(t) / \sum_{i=1}^N P_i]^2} \quad (16)$$

Where  $0 < P_i < 1$ , decision-variables was coded with binary system. The coding string length of each variable was 10, the population size  $M=30$ , the maximal generation  $T=200$ . proportion select, one point crossover and mutation on the basic bit were introduced in genetic operator. The crossover probability  $p_c=0.8$ , the mutation  $p_m=0.05$ .

### V. COMPUTED RESULT AND DISCUSSION

Method described in previous section has been applied to real atomic clock timing residuals from laboratory.

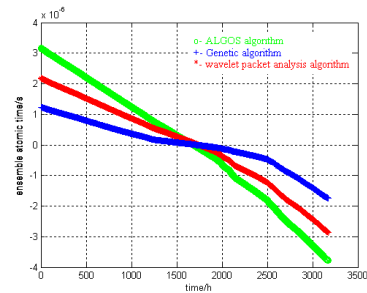


Figure 4 the comparisons of ensemble atomic time computed with three algorithms

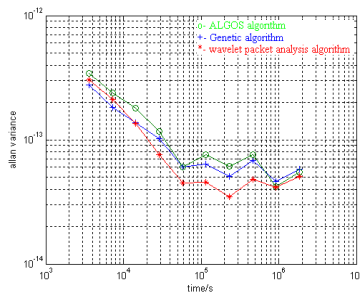


Figure 5 the stability comparisons of ensemble atomic time computed with three algorithms

Figure 4 shows the ensemble atomic time to atomic clock difference of six Hydrogen-clocks and one cesium-clock computed by classical weighted average algorithm, three levels wavelet packet analysis algorithm and genetic algorithm. The result of classical weighted average algorithm is computed by the weight of reciprocal of  $\sigma^2_z(\tau)$  with that  $\tau$  is about  $2.30 \times 10^5$  s. In this figures, we can find that the ensemble atomic time computed by classical weighted average algorithm fluctuate more outstandingly, namely the range of residuals is large. However wavelet packet analysis can respectively weight to the residuals of different frequency range and the computed residuals fluctuate gently. Moreover, the ensemble atomic time computed by genetic algorithm fluctuate more gently. The curve of the ensemble atomic time computed by genetic algorithm is best, wavelet packet analysis algorithm is in the next place and both of the two algorithms are better than classical weighted average algorithm. Figure 5 shows the stability denoted with logarithmic form of the ensemble atomic time computed by genetic algorithm, three levels wavelet packet and classical weighted average algorithm, the abscissa is the average time  $\log \tau$  denoted with logarithmic form. From the figure we can conclude the stability of ensemble atomic time computed by either genetic algorithm or three levels wavelet packet analysis algorithm is better than the stability of ensemble atomic time computed by classical weighted average algorithm. From figure 4 and figure 5 we can conclude that genetic algorithm and three levels wavelet packet are more appropriate than classical weighted average algorithm, and to obtain higher stability atomic time, wavelet packet analysis algorithm is the most appropriate.

## VI. CONCLUSION

Using three algorithms to computer ensemble atomic time of local laboratory that held several clocks were introduced and the results of three algorithms were compared in this paper. The author developed vavelet packet analysis and genetic algorithms defferent from ALGOS. From the compared result we can concluded that both of the two new algorithms were better than ALGOS. Among of these algorighms wavelet packet analysis algorithm was the best algorithm and it can improve the long-term sability of ensemble atomic time more effectively.

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