Selecting the Best Wavelet Packet Pier Inspired by Biological Methods

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ABSTRACT:
In this project, a new method for selecting the best wavelet packet pier is presented. The method of complex organisms from simple gradual chromosomes early to more complex organisms have been inspired by the current. In this algorithm, first, the best pier to the lowest level of analysis based on the shannon entropy measure using Genetic Algorithm (GA) is selected, then the pier to create optimal early population to a higher level is used and the work until the last level of analysis is repeated. The results show that this way, with a gradual increase during chromosomes best wavelet packet pier with higher convergence rate, higher accuracy and less computation than previous methods is selected. In addition, previous methods based on GA, the best possible level of analysis did not exist, but this method, access is provided.

KEYWORDS: wavelet packets, best basis, the best level of analysis, genetic algorithms, variable-length Chromosome, shannon entropy

1. INTRODUCTION

Wavelet transformation today widely different fields, signal processing, such as noise removal, compression, classification, feature extraction, etc. on the wave of sound signals, image and ... Used. Wavelet packets (WPs) is a simple and very powerful expansion and wavelet analysis is multi resuletion.

WPs in each subband not need to be re-analysis, the criteria must stop or there is continuance analysis [7]. If a signal using wavelet transformation to the level n have to be analyzed, then 2n +1-2 subband caused. Therefore, increasing analysis, and best of the best basic level of analysis will be difficult [2]. So it seems that a solution to find the best and the best base-level analysis is the use of GA.

Peng Xu and A.K. Chan [2] to select the best method based on GA have been introduced. In this manner simple method to correct for crossover and mutation chromosomes credit note is created, thus replacing the correct code with invalid chromosomes increase the possibility of calculation error is created. Also, this method calculating the best possible level of analysis does not exist.

T. Schell and A. Uhi [1] to select the best method based on GA have been introduced. This method has been validated chromosomes attention, but using a standard method of GA increased volume and computing time has been. In this method, calculating the best possible level of analysis does not exist.

In this project, a new method for selecting the best wavelet packet pier is presented. This method of gradual chromosomes complex cells to simple basic things more complicated now is inspired by [3]. In this algorithm, first, the best pier to the lowest level of analysis based on the shannon entropy measure using Genetic Algorithm (GA) is selected (a lot of criteria for selecting the best base there that the application can be from each They used this project [6], [5], [4]). First, because analysis of the level is low, chromosome length is small and rapidly is convergent algorithm. This pier to create optimal early population to a higher level is used. And the work to the last level of analysis is repeated. The results show that this way, with a gradual increase during chromosomes can be number generation and a smaller population size and therefore the best wavelet packet pier with higher convergence rate, higher accuracy and less computation than previous methods of selection be. In addition, previous methods based on GA, the best possible level of analysis did not exist, but this method, access is provided.

In Section 2 a summary of the wavelet transformation is given. Algorithm used in Section 3, is explained, also required changes in the crossover and mutation to maintain tree WPs and how to create each level of the early population analysis, are indicated. Simulation conditions and results are listed in Section 4.

2. CONVERSION WAVELET

Wavelet transformation can be continuous (CWT) or discrete (DWT). Today, more applications are DWT and WPs. DWT signal functions based on scale and wavelet functions and frequency shifts when they are extended.

Expanded signal using the DWT is shown in Figure 1 [2].

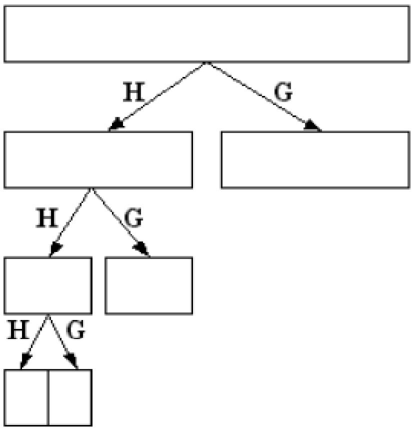


Fig. 1. Expand the signal using DWT

DWT analyzes the signal for all the needs of different applications does not provide, so in many cases, especially in the uplink to the high-frequency narrow-band analysis we need, the WP is used. Expanded signal using WPs in Figure 2 is shown. [8]

Analysis signal using WP to create a tree structure in Figure 3 is shown. WPs in each sub band not need to be re-analysis [8]. Many criteria for stopping or continuance analysis are based on their best and the best base-level analysis is selected. One of these criteria, the shannon entropy in this project it has been used [1].

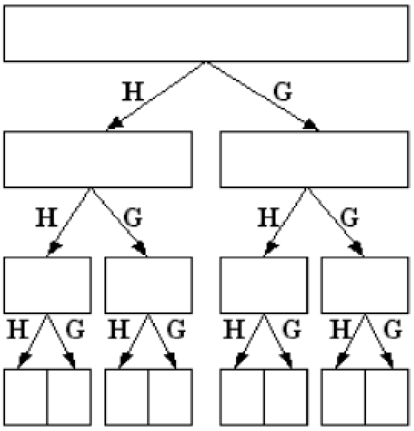


Fig. 2. Expand the signal using WPs.

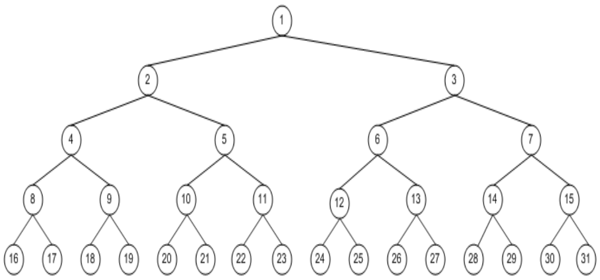


Fig.3. tree

3. GA WITH VARIABLE LENGTH CHROMOSOME

As mentioned in previous methods select the best base [1], [2], length chromosome has been fixed, so the volume and time calculations are sometimes very high compared to previous methods [4] has not been proven. For example, if you want the best basic level we find analyse 5, a 63-bit chromosome is need. Therefore, to achieve public the best answer, should the number of generation and large population size and because we must assess each chromosome WP coefficients corresponding to calculate it, we will be very high volume calculations.

In this project, a new method that the length chromosome gradually be increasing [3], has been used. In this algorithm, first, the best pier to the lowest level of analysis based on the shannon entropy measure using Genetic Algorithm (GA) is selected (other criteria such as energy, orthogonality, and other entropy basis for selecting the best there is, that the applications can be any one of them used in this project.) Maintain tree crossover and mutation WPs should be used in certain sections 2-3 and 3-3 are described.

First, because analysis of the level is low, chromosome length, population size and number of generation is small and the algorithm will converge quickly. This pier to create optimal early population to a higher level is used, Section 4-3 of this technique is explained. This work to the last level of analysis is repeated. The previous example, consider the first level of analysis lies in two equal length chromosome 7-bit would be there only four valid modes, so easily the best basis is selected. This pier optimal population for early production from the third level analysis of chromosome 15-bit is.

Made, we use (size of this population is higher than the previous stage) and again the best base to bring. The same work up to that length chromosomes analysis 5 63-bit is, we repeat. Thus, with a gradual increase during chromosome, population size and generation number can be the best wavelet packet pier with higher convergence rate, higher accuracy and less computation than previous methods selected. In addition, previous methods based on GA, the best possible level of analysis did not exist, but this method is possible.

3.1. To make the code chromosome WPs

For being able to use the GA should WP coefficients as a string of binary code, we become. If a signal using WP to level n have to be analyzed, then 2n +1-2 subband caused, if any band a bit below the original signal and we also as root (the first bit) to consider, in this case, a chromosome length 2n +1 -1 bits need. Therefore, increasing decomposition, the number of bits required can be increased to 2. If k bits that I've corresponding subband k is decomposed, the value of a will. If my analysis in subband k be stopped, and its corresponding bit is zero. Because the first bit is always analysis, is a value.

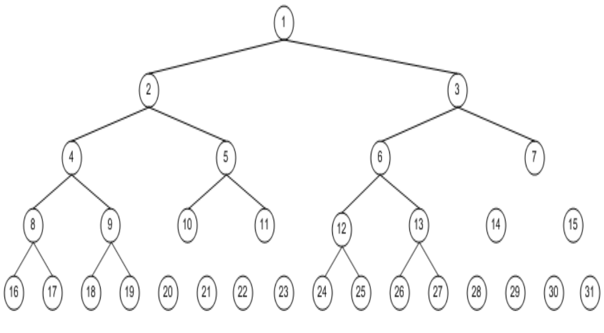


Fig. 4. Crossover tree

3.2. Crossover

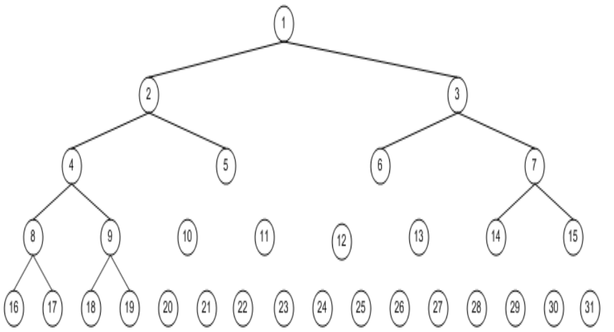
Section 1-3 with an alternative method WPs coefficients described binary field, but the WP structure is a tree structure, so if a single crossover point or two point we use binary field may be obtained, showed absence of pier is not correct (a subband may be selected more than once or collection of subbands selected no cover total signal bandwidth) [1].

Thus, for the problems listed in a tree crossover is used; a bit which is a value, is selected as random. The following bands corresponding to the bit between the two trees that have been selected as a parent, to be moved. Thus, two new tree structure which is caused are valid. This method is shown in Figure 4.

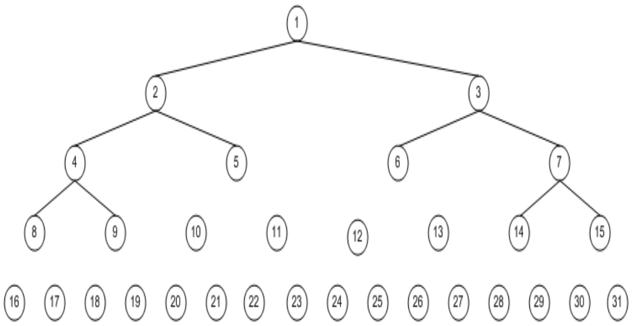
3.3. Mutation

Due to reasons mentioned in Section 4 and the necessity to maintain the structure of WP, routine mutation can not be used. Method used in this project is as follows; a bit random is selected as

A PARENT
PARENT 2



CHILD 1 (CROSSOVER AT POINT



CHILD 2 (CROSSOVER AT POINT 4)

If this bit is a value, this bit and all bits corresponding to zero subcollection this we subband. If the selected bit is zero, the bits must be corresponding subband is higher than one (otherwise, these bits correspond to a subband not selected), in this case in this bit and all bits corresponding subband subcollection this, except the last level of analysis a we.

3.4. Initial population production

To generate initial population the following method is used; difference between the number of bits in two consecutive analysis counts and the number of its bits to zero before the end of stage the best answer is added (last-level coefficients, analysis can not, therefore, corresponding bits They always zero.) The optimum chromosome directly part of the population makes up the primary. Remaining initial population using the mutation operation on optimum chromosome is produced.

4. CONCLUSION

Simulation of this project is as follows; population size for two equal analysis level 4 is considered, then each level analysis, population size and length are doubled chromosome. As explained in section 4-3, the initial population is not fully random selection, but the answer is the best stage before production. Initial population for the first decomposition level (level 2) with regard to mode 4 may be, is created. chromosomes Shannon entropy criteria are evaluated. Each level of analysis, if the integration algorithm 20 times after generation, is hindered. Crossover rate equal to 0.6 is selected. Of elite selection and mutation has also been used. Validated methods for tree mentioned in WPs 2-3 and 3-3 are applied.

Implementation of this algorithm for analysis level 5 and compare it with [1] and [2] shows that time and volume calculations has decreased dramatically. Components such as initial population are close to the optimal answer, very much faster algorithm is convergent and the results show that even if a smaller number generation, we significant error in selecting the best pier WPs is not created. Therefore, this algorithm the confidence coefficient greater than previous methods has.

Also in this algorithm because the best answer every level analysis, obtained separately, there is the possibility to compare different levels of analysis and determine the best level.

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