DNA Computing with Water Strider Based Vector Quantization for Data Storage Systems

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Abstract: The exponential growth of data necessitates an effective data storage scheme, which helps to effectively manage the large quantity of data. To accomplish this, Deoxyribonucleic Acid (DNA) digital data storage process can be employed, which encodes and decodes binary data to and from synthesized strands of DNA. Vector quantization (VQ) is a commonly employed scheme for image compression and the optimal codebook generation is an effective process to reach maximum compression efficiency. This article introduces a new DNA Computing with Water Strider Algorithm based Vector Quantization (DNAC-WSAVQ) technique for Data Storage Systems. The proposed DNAC-WSAVQ technique enables encoding data using DNA computing and then compresses it for effective data storage. Besides, the DNAC-WSAVQ model initially performs DNA encoding on the input images to generate a binary encoded form. In addition, a Water Strider algorithm with Linde-Buzo-Gray (WSA-LBG) model is applied for the compression process and thereby storage area can be considerably minimized. In order to generate optimal codebook for LBG, the WSA is applied to it. The performance validation of the DNAC-WSAVQ model is carried out and the results are inspected under several measures. The comparative study highlighted the improved outcomes of the DNAC-WSAVQ model over the existing methods.

Keywords: DNA computing; data storage; image compression; vector quantization; ws algorithm; space saving

1 Introduction

With the development of digital systems for storage, generation, and broadcast of data, there increases require to ongoing and active maintenance of digital media. With the huge amount of digital information that needs that storing to further utilize, a problem arises from the storage of irresistible number of information [1]. Yearly the storage need is increased by 50% [2]. Nowadays, most of the digital data is storing with a technique that only will last long for a minimum duration. Chips and Memory cards are sustainable for five years from their primary purpose [3]. However solid-state drive operates better when compared to hard drives, when not operated for long duration, they have the tendency of losing data [4]. Thus, researcher dedication has been driven toward the advancement of storage methods that successfully overcome the abovementioned problems. Fig. 1 illustrates the process involved in DNA data storage.
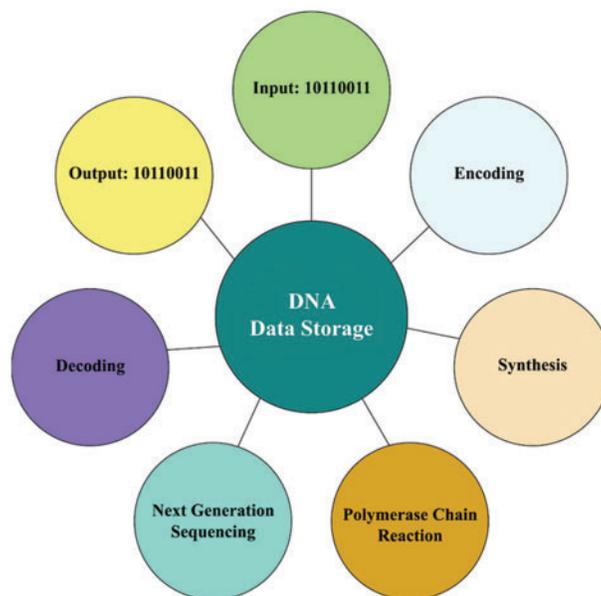
Figure 1: Process in DNA data storage

Furthermore, the environment might be polluted with non-biodegradable and silicon materials that are constrained in resources and will drain someday. File sharing systems are preferred for moving to new technology since the present storage technology is incapable of handling it effectively [5]. Any organism that is composed of 2 stranded spirals of nucleotides has cells named Deoxyribonucleic Acid (DNA) cells. Cytosine, Adenine, Thymine, and Guanine form these nucleotides that comprise one phosphate group, 5 carbon sugar, and 4 nitrogen bases. A massive number of data is stored in DNA to exploit considerable amount of combinatory questions, DNA registering methodology is used. It is possible that some grams of DNA have the opportunity of storing each information across the world. As well, this DNA could be preserved in dark and dry cold environments. Since it come for storage problems, there is several reasons to utlized DNA because of its very small size and ubiquity [6,7].

Currently, development of image compression (IC) technique with regenerated image quality is a challenging and crucial tasks for the researcher [8]. It aims at transmitting the image using lower bits. Detection of redundancy in image, suitable and perfect encoding techniques and conversion technology are the major factor for IC. Quantization consist of: vector and scalar quantization.

Vector quantization (VQ) has been a non-transformed compression system, is an efficient and effective mechanism for lossy IC [9]. The primary objective of VQ is to develop an effective codebook that comprises a collection of codeword where input image vector has been allocated according to the minimal Euclidean distance. The most used and primary VQ method is Linde Buzo Gray (LBG) approach [10].

This article introduces a new DNA Computing with Water Strider Algorithm based Vector Quantization (DNAC-WSAVQ) technique for Data Storage Systems. The proposed DNAC-WSAVQ technique allows data encoding by the use of DNA computing and then compresses it for effective data storage. Moreover, the DNAC-WSAVQ model initially performs DNA encoding on the input images to generate a binary encoded form. Furthermore, a Water Strider algorithm with LBG (WSA-LBG) model is utilized to accomplish effective compression process and thereby storage area can be considerably minimized. For generating an optimum codebook for LBG, the WSA is applied to it. The performance validation of the DNAC-WSAVQ model is carried out and the results are examined under several measures.

2 Related Works

The authors in [11] presented Cuckoo search (CS) metaheuristic optimization method which enhances the LBG codebook through levy flight distribution process which follows the Mantegna algorithm in place of Gaussian distribution. Dimopoulou et al. [12] proposed an end-to-end storage system for effective storage of images to synthetic DNA. This system employs an encoding approach that serves the need for IC while being strong to the biological error that might corrupt the encoding. Kumar et al. [13] proposed a biomedical IC method from the cloud computing (CC) platform with Harris Hawks Optimization (HHO)-based LBG approaches. The presented method accomplishes a smooth transition amongst exploitation and exploration.

Guo et al. [14] designed a bat algorithm based adopted separation search mode to enhance the codebook design with the mean square error (MSE) as the adaptation values. The presented method employs pulse emission rate for switching the loudness and the search mode to define the searching range, however, it continued suffering from a deficiency of searching ability. Thus, adoptive separation rule is presented for enhancing the global exploration ability and for avoiding earlier convergence. Khan [15] examined several executions of IC techniques which utilize approaches like artificial neural networks (ANNs), Residual Learning, Fuzzy Neural Networks (FNN), convolution neural network (CNNs), deep learning (DL), and genetic algorithm (GA). This work also explains an execution of VQ utilizing GA for generating codebook that is utilized for Lossy IC. In [16], a new DNA based fast and secured data access control method was established in the cloud environments. During this presented method, a long 1024-bit DNA based password or confidential key was utilized for encrypting user secret or personal information.

Wu et al. [17] considered DNA computation based image encryption method that executes to cloud CCTV model. In several distinct image encryption studies, the artefact hyperchaotic map is utilized. It is presented an image encryption technique dependent upon DNA coding and hyperchaotic map that employs the chaotic property of hyperchaotic map on maximum of DNA calculating. In [18], VQ was utilized that employs the local binary pattern technique. While a novel purpose, the codebooks were optimized by an enhanced optimized technique. During this method, the database image was primarily divided as to a group of blocks, namely, pixels, and these groups of blocks were mentioned that vectors. Afterward, an appropriate codeword was chosen for all the vectors such that

is neighboring representation of input vectors. To obtain an optimum IC result, the codebook was optimized utilizing the Best Fitness Updated Rider Optimized technique.

3 The Proposed Model

In this objective, a new DNAC-WSAVQ technique has been developed for effective data storage systems. The proposed DNAC-WSAVQ technique mainly intends in data encoding via DNA computing and then compresses it for effective data storage. Moreover, the DNAC-WSAVQ model primarily carried out DNA encoding on the input images for producing binary encoded form. Furthermore, a WSA-LBG model is utilized for the compression process and thereby storage area can be considerably minimized.

3.1 DNA Computing for Data Encoding

A DNA sequence is comprised of 4 nucleic acid bases, such as adenine (A), cytosine(C), guanine (G), and thymine (T), where A and T, and G and C are complements. The researcher uses the binary values 00, 01, 10, and 11 to denote four bases [19]. An overall of 24 kinds of coding could be listed; but based on the complementary relationship among 0 and 1 in binary. Thus, 8 out of 24 coding rules are carefully chosen for satisfying the base complementary condition. The pixel value of image lies among [0, 255], and comprises eight-bit binary numbers. The present image encryption algorithm depends on DNA coding are nearly inseparable in this coding rule or deforming according to the coding rule. Fig. 2 depicts the components in DNA.
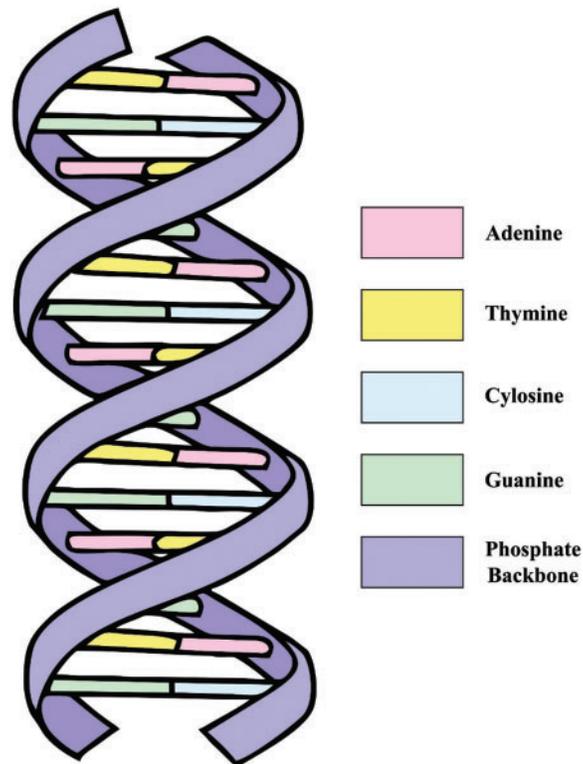
Figure 2: Components in DNA

Two DNA sequence complements are available namely single base direct complement approach and the method that employs the principle of single base and double base complementary pairing in biotechnology to implement the complement process.

$$\begin{cases} T = complement\,(A) \\ A = complement\,(T) \\ G = complement\,(C) \\ C = complement\,(G) \end{cases} \tag{1}$$

where complement $(\cdot)$ denotes the function of complement. The complement rule is determined according to the double helix model; a nucleoside is paired based on the double helix model [19]. Assuming the complementary conversion is D, each nucleoside x_i fulfills the subsequent formula:

$$\begin{cases} x_i \neq D\,(x_i) \neq D\,(D\,(x_i)) \neq D\,(D\,(D\,(x_i))) \\ x_i = D\,(D\,(D\,(D\,(x_i)))) \end{cases} \tag{2}$$

Whereas x_i and $D\,(x_i)$ denotes complementary, that is x_i and $D\,(x_i)$ indicates a pair of base pairs.

3.2 Design of WSA-LBG Model

The compression of input images is implemented utilizing VQ on co-efficient of sub-bands $b \in \{1, 2, \ldots, B\}$, with $B = 3i+1$ created by i-level discrete wavelet transform (DWT) decompositions. The benefit of utilizing VQ rather than scalar quantization is that it gives optimum compression efficiency but is connected to a set length code. During this case, the selection of utilizing a set length code instead of variable length one is simulated as the detail it can be effectual manner that further robust to sequence noise [20].

The drive of VQ is for mapping n dimension vectors from the vector space $\mathbb{R}^n$ as to finite group of vectors Σ (the codebook) whereas $\Sigma = \{V_j \in \mathbb{R}^n | j = 1, 2, \ldots, K\}$. The vector set Σ has the centroid vector which is calculated then clusters a group of trained vectors based on generalization Lloyd technique is projected.

3.2.1 LBG Algorithm

The LBG approach is an iterative method that requires a primary codebook to initiate with. At this point, the generation of codebook was completed utilizing a trained group of images, whereas the set specifies the distinct types of images that are compressed. This codebook (initial) was obtained by "splitting method'" from the LBG method. During this approach, a primary code vector was set as a mean of every trained sequence and is then separated as to two [20]. The compression method is investigated by particular performances such as compression rate, peak signal to noise ratio (PSNR). The set of points at quantize outcome was named as codebook of quantizing and the process of placing this resultant points is named as "codebook design".

LBG approach was demonstrated from the subsequent steps.

1. Start with a primary group of reconstruction values $\{R_i^{(o)}\}_{i=1}^W$. Allocate iteration $p = 0$, $H^{(o)} = 0$. Select a threshold $\in$.
2. Determine regions of quantization as per Eq. (3).

$$V_i^{(p)} = \{U : h\,(U, R_i) < h\,(U, R_j)\,\forall j \neq i\}j = 1, 2..M \tag{3}$$

3. Estimate distortion as per Eq. (4).

$$H^{(p)} = \sum_{i=1}^{W} \int_{V_i^{(p)}} \left\| U - R_i^{(p)} \right\|^2 fx(U)\, dU \tag{4}$$

4. *If* $\frac{(H^{(p)} - H^{(p-1)})}{H^{(p)}} < \epsilon$, terminating or continuing.
5. $p = p + 1$. Determine novel creating values $\{R_i^{(p)}\}_{i=1}^{W}$ that are centroids of $\{V_i^{(p-1)}\}$. Continue step2.

These method procedures are the root of popular VQ techniques. It is generally recognized as the LBG manner. A primary codebook to 2level VQ is obtained by incorporating the resultant point to 1level quantizing and 2nd resultant point was achieved by summing up existing perturbation vector. Moreover, the LBG method is utilized for obtaining the 2 levels VQ. Fig. 3 portrays the process flow of LBG.
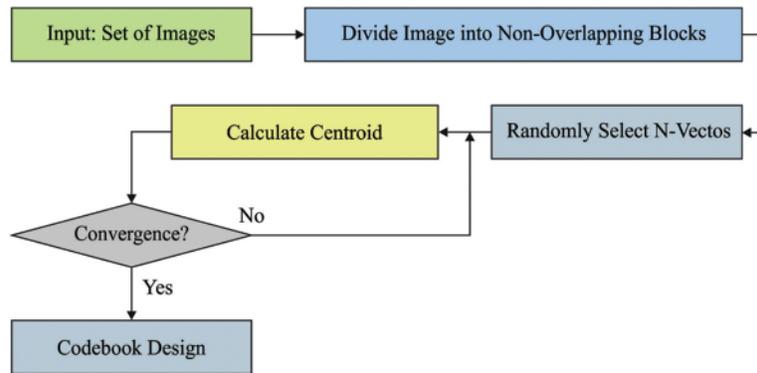
Figure 3: Process in LBG

The 2 codebook vectors were exploited for attaining a primary codebook to 4level VQ if the technique converges. A primary 4level codebook includes 2 codebook vectors in the final codebook of 2 levels VQ and other 2 vectors were obtained by summing up to 2 codebook vectors. The LBG method is utilized still this 4level VQ converges. Thus, the level is doubled still the optimum amount of levels are achieved. This technique was continued still the distortion drives under a particular lesser threshold.

The size of codebook was higher exponentially with rate of VQ that in order improves the quality of reform; but, the encoder time increases because of the increase from the computation essential for discovering the neighboring match. On integrating the preceding codebook of previous stage at all the divisions, it is certain that codebook then separating is an optimum as the codebook earlier to separating.

3.2.2 Optimal Codebook Construction Using WSA

In recent times, a new metaheuristic approach was stimulated from the behavior of Water Strider (WS) bugs [21] that is named WSA. It provides the best solution for complex optimization problems [22–24]. The process starts with initial random generating individual that is named Birth phase. Now, the male WS (keystone) gets mate with female WS for generating a population initialization (eggs). It

can be expressed as follows.

$$X_i(0) = Lb + r \times (Ub - Lb) \tag{5}$$

$i = 1, 2, \ldots, n.$

Whereas, r determines an arbitrary number within $[0, 1]$, $X_i(0)$ defines the first location of *ith* individual, n indicates the candidate number, and Lb and Ub represent the lower and the upper limits, correspondingly. To generate n territories using n WSs, the objective value of WS is sorted and saved according to their cost value. Next, the mating begins with larger attempts, energy utilization, and search of the male WSs to achieve the female WS. Due to the stronger shield of females on their body, the male WS cannot do mating even with force that is

$$\begin{cases} X_i(t+1) = X_i(t) + R \times r, & \textit{if mating happens} \\ X_i(t+1) = X_i(t) + R \times (1+r), & \textit{Otherwise} \end{cases} \tag{6}$$

Whereas, $X_i(t)$ describes the location for ith WS and R defines the distance among the male WS position ($X_i(t)$) and the female territory ($X_F(t)$) endpoint that is expressed by the following:

$$R = X_F(t) - X_i(t) \tag{7}$$

Next, the foraging procedure initiates. Because of consuming a longer time of male WS to search the female WS gets laid, they must reenergize itself to recover their body. It can be performed by searching for new location with high food sources. When the candidate objective values are lesser when compared to the previous position, it moves to the optimal territory using the maximum fitness($X_{BL}(t)$).

$$X_i(t+1) = X_i(t) + 2 \times rand \times (X_{BL}(t) - X_i(t)) \tag{8}$$

Here, the succession and death of individuals are simulated so that the solution would be saved when they are determined in the predetermined boundary and they would be removed when they move beyond the constraint. This implies, when stranger WSs enter new territory, the male WS behaves brutally with him such that killing him or bringing him out. In this method, when the novel population is an appropriate solution when compared to the old one, it would be a substitute and the old one would be eliminated and killed.

$$X_i(t+1) = Lb_j(t) + r \times (Ub_j(t) - Lb_j(t)) \tag{9}$$

Whereas, $Lb(t)$ and $Ub(t)$ describe the minimal and the maximal value of the position of the WS in jth territory. Eventually, the process ends when the ending criteria are satisfied. The objective model of presented WSA based VQ model is for minimizing the rate of compression and consequently, the error variance amongst the decompressed as well as original images have that minimizing as illustrated by Eq. (10). In Eq. (10), E represents error variance among the decompressed and novel images, and CI represents the compression ratio.

$$Min = E + CI \tag{10}$$

$$CI = \frac{Size\ of\ Compressed\ image}{Size\ of\ original\ image} \tag{11}$$

4 Performance Validation

This section inspects the data storage efficiency of the DNAC-WSAVQ model using benchmark test images. The results are inspected under several aspects and measures. Some sample images are illustrated in Fig. 4.

Figure 4: Sample images

Tab. 1 and Fig. 5 reports the compression ratio (CR) examination of the DNAC-WSAVQ model with other methods on distinct test images [25]. The results indicated that the DNAC-WSAVQ model has resulted in effective outcomes with increased CR on all test images. For instance, on test image 1, the DNAC-WSAVQ model has obtainable higher CR of 3.6746 whereas the L2LBG methodology, CSLBG system, FFLBG approach, and JPEG2000 models have obtained lower CR of 2.2456, 2.1274, 1.7819, and 1.5268 respectively. Besides, on test image 4, the DNAC-WSAVQ model has provided increased CR of 3.2269 whereas the L2LBG methodology, CSLBG system, FFLBG approach, and JPEG2000 models have provided reduced CR of 2.5347, 2.2133, 1.7860, and 1.5148 respectively.

Table 1: Compression ratio analysis of DNAC-WSAVQ technique with recent methods on different test images

No. of test images	Compressed ratio (CR)				
	DNAC-WSAVQ	L2LBG	CSLBG	FFLBG	JPEG 2000
Test image-1	3.6746	2.2456	2.1274	1.7819	1.5268
Test image-2	3.0598	2.5347	2.2133	1.7860	1.5148
Test image-3	3.2405	2.2857	1.9200	1.8113	1.3788
Test image-4	3.2269	2.2261	2.1818	1.7902	1.3427
Test image-5	3.6056	2.4151	2.2925	1.7067	1.3863
Test image-6	3.1605	2.6483	1.9492	1.7696	1.4328
Test image-7	3.3684	2.4695	2.1215	1.8641	1.5029
Test image-8	3.0476	2.3133	2.0757	1.8071	1.3665
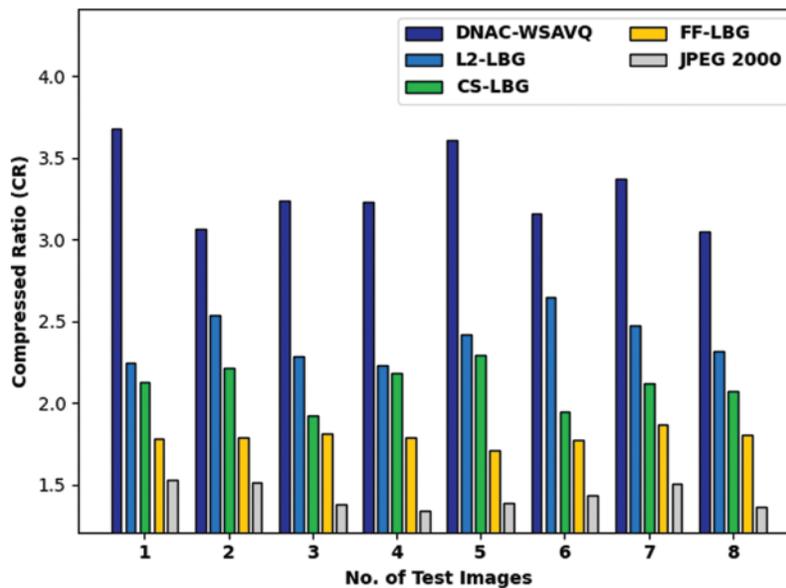
Figure 5: CR analysis of DNAC-WSAVQ technique with recent approaches

A detailed compression factor (CF) assessment of the DNAC-WSAVQ model with recent methods is provided in Tab. 2 and Fig. 6. The experimental results reported that the DNAC-WSAVQ model has resulted in proficient results with least values of CF. For instance, on test image 1, the DNAC-WSAVQ model has attained decreased CF of 0.2721 whereas the L2LBG methodology, CSLBG system, FFLBG approach, and JPEG2000 models have achieved increased CF of 0.4453, 0.4701, 0.5612, and 0.6549 respectively. Concurrently, on test image 5, the DNAC-WSAVQ model has resulted to minimal CF of 0.2773 whereas the L2LBG methodology, CSLBG system, FFLBG approach, and JPEG2000 models have obtained maximum CF of 0.4141, 0.4362, 0.5859, and 0.7214 respectively.

Table 2: Compression factor analysis of DNAC-WSAVQ technique with recent methods on different test images

No. of test images	Compressed factor (CF)				
	DNAC-WSAVQ	L2LBG	CSLBG	FFLBG	JPEG 2000
Test image-1	0.2721	0.4453	0.4701	0.5612	0.6549
Test image-2	0.3268	0.3945	0.4518	0.5599	0.6602
Test image-3	0.3086	0.4375	0.5208	0.5521	0.7253
Test image-4	0.3099	0.4492	0.4583	0.5586	0.7448
Test image-5	0.2773	0.4141	0.4362	0.5859	0.7214
Test image-6	0.3164	0.3776	0.5130	0.5651	0.6979
Test image-7	0.2969	0.4049	0.4714	0.5365	0.6654
Test image-8	0.3281	0.4323	0.4818	0.5534	0.7318
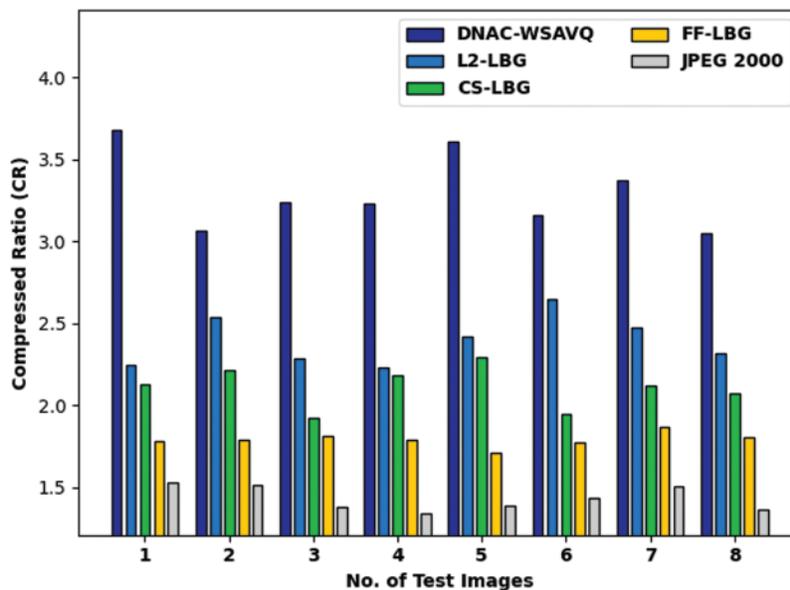
Figure 6: CF analysis of DNAC-WSAVQ technique with recent approaches

A comprehensive bit rate per pixel (BRPP) assessment of DNAC-WSAVQ system with current approaches is shown in Tab. 3 and Fig. 7. The experimental result reports that the DNAC-WSAVQ system has resulted in proficient outcomes with least values of BRPP. For example, on test image 1, the DNAC-WSAVQ approach has accomplished decreased BRPP of 2.177 while the L2LBG methodology, CSLBG system, FFLBG approach, and JPEG2000 methods have accomplished increased BRPP of 13.091, 8.444, 9.551, and 9.336 correspondingly. Simultaneously, on test image 5, the DNAC-WSAVQ technique has resulted in minimal BRPP of 2.219 while the L2LBG methodology, CSLBG system, FFLBG approach, and JPEG2000 methods have attained maximal BRPP of 11.944, 8.428, 10.746, and 9.849 correspondingly.

Table 3: BRPP analysis of DNAC-WSAVQ technique with recent methods on different test images

No. of test images	Bit rate per pixel				
	DNAC-WSAVQ	L2LBG	CSLBG	FFLBG	JPEG 2000
Test image-1	2.177	13.091	8.444	9.551	9.336
Test image-2	2.615	9.657	9.162	9.914	9.433
Test image-3	2.469	11.342	9.524	8.480	10.509
Test image-4	2.479	11.597	8.162	9.750	10.667
Test image-5	2.219	11.944	8.428	10.746	9.849
Test image-6	2.531	9.547	10.869	8.812	9.880
Test image-7	2.375	10.912	9.312	9.105	9.922
Test image-8	2.625	10.540	8.916	9.189	10.579
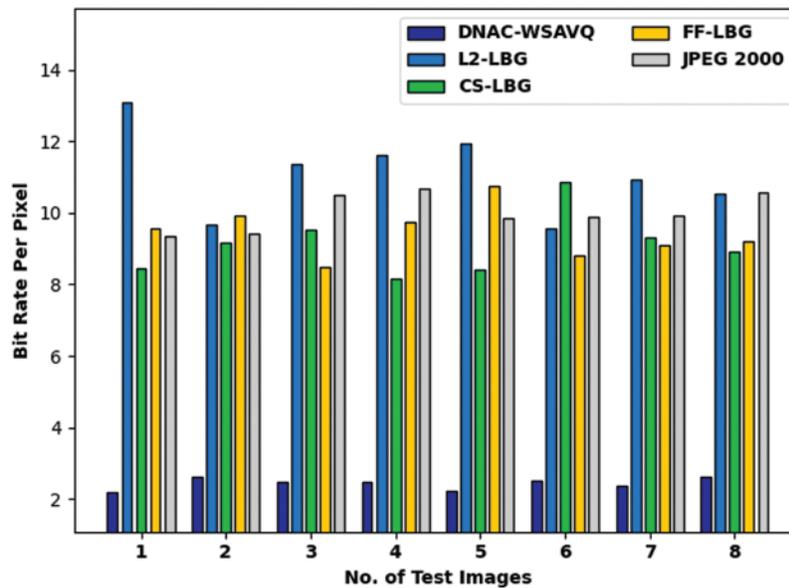
Figure 7: BRPP analysis of DNAC-WSAVQ technique with recent approaches

A detailed MSE assessment of DNAC-WSAVQ approach with current approaches is given in Tab. 4 and Fig. 8. The experimental results show that the DNAC-WSAVQ technique has resulted in proficient outcomes with minimum values of MSE. For example, on test image 1, the DNAC-WSAVQ algorithm has gained reduced MSE of 0.160 while the L2LBG methodology, CSLBG system, FFLBG approach, and JPEG2000 methods have reached improved MSE of 1.370, 1.300, 1.510, and 2.300 correspondingly. Synchronously, on test image 5, the DNAC-WSAVQ method has resulted in least MSE of 0.120 while the L2LBG methodology, CSLBG system, FFLBG approach, and JPEG2000 techniques have attained maximal MSE of 1.360, 1.370, 1.550, and 2.200 correspondingly.

Table 4: MSE analysis of DNAC-WSAVQ technique with recent methods on different test images

No. of test images	MSE				
	DNAC-WSAVQ	L2LBG	CSLBG	FFLBG	JPEG 2000
Test image-1	0.160	1.370	1.300	1.510	2.300
Test image-2	0.130	1.390	1.480	1.600	2.110
Test image-3	0.130	1.170	1.400	1.570	2.090
Test image-4	0.150	1.390	1.500	1.600	2.220
Test image-5	0.120	1.360	1.370	1.550	2.200
Test image-6	0.180	1.220	1.450	1.540	2.160
Test image-7	0.170	1.160	1.320	1.580	2.020
Test image-8	0.130	1.190	1.440	1.600	2.400
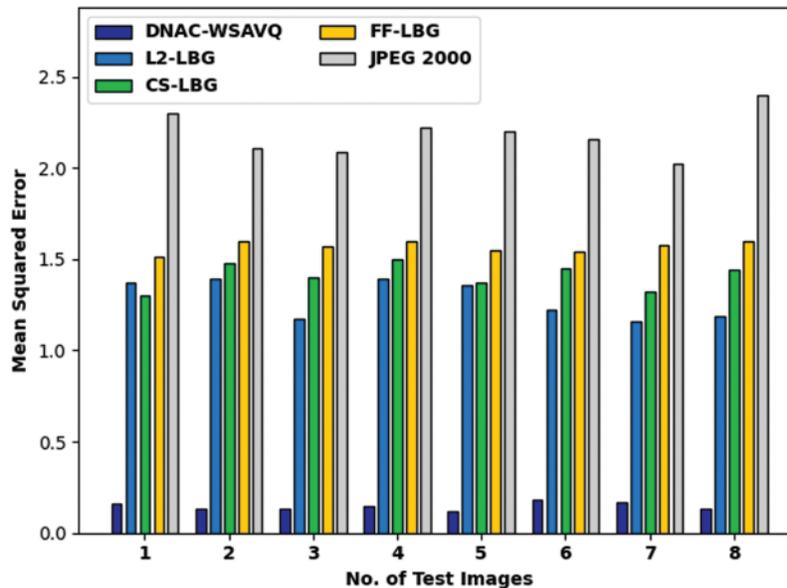
Figure 8: MSE analysis of DNAC-WSAVQ technique with recent approaches

A detailed root mean square error (RMSE) assessment of the DNAC-WSAVQ models with current approaches is given in Tab. 5 and Fig. 9. The experimental results show that the DNAC-WSAVQ technique has resulted in proficient outcomes with minimum values of RMSE. For example, on test image 1, the DNAC-WSAVQ method has accomplished reduced RMSE of 0.400 while the L2LBG methodology, CSLBG system, firefly based LBG (FFLBG) approach, and JPEG2000 techniques have accomplished improved RMSE of 1.170, 1.140, 1.229, and 1.517 correspondingly.

Table 5: RMSE analysis of DNAC-WSAVQ technique with recent methods on different test images

No. of test images	Root mean square error				
	DNAC-WSAVQ	L2LBG	CSLBG	FFLBG	JPEG 2000
Test image-1	0.400	1.170	1.140	1.229	1.517
Test image-2	0.361	1.179	1.217	1.265	1.453
Test image-3	0.361	1.082	1.183	1.253	1.446
Test image-4	0.387	1.179	1.225	1.265	1.490
Test image-5	0.346	1.166	1.170	1.245	1.483
Test image-6	0.424	1.105	1.204	1.241	1.470
Test image-7	0.412	1.077	1.149	1.257	1.421
Test image-8	0.361	1.091	1.200	1.265	1.549
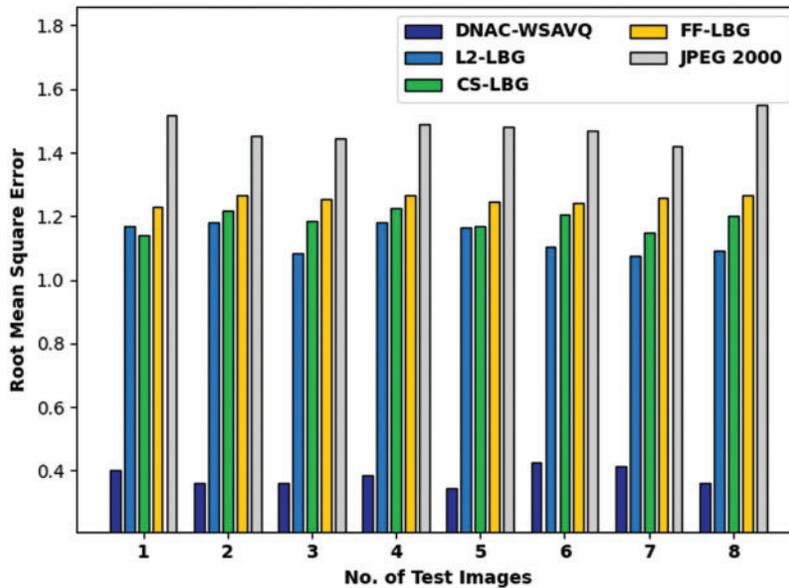
Figure 9: RMSE analysis of DNAC-WSAVQ technique with recent approaches

Simultaneously, on test image 5, the DNAC-WSAVQ method has resulted in least RMSE of 0.346 while the L2LBG methodology, CSLBG system, FFLBG approach, and JPEG2000 systems have attained maximal RMSE of 1.166, 1.170, 1.245, and 1.483 correspondingly.

Tab. 6 and Fig. 10 show the PSNR examination of the DNAC-WSAVQ approach with other approaches on distinct test images. The results show that the DNAC-WSAVQ system has resulted in effective outcomes with improved PSNR on all test images.

Table 6: PSNR analysis of DNAC-WSAVQ technique with recent methods on different test images

No. of test images	Peak signal noise ratio				
	DNAC-WSAVQ	L2LBG	CSLBG	FFLBG	JPEG 2000
Test image-1	56.090	46.764	46.991	46.341	44.514
Test image-2	56.991	46.701	46.428	46.090	44.888
Test image-3	56.991	47.449	46.670	46.172	44.929
Test image-4	56.370	46.701	46.370	46.090	44.667
Test image-5	57.339	46.795	46.764	46.227	44.707
Test image-6	55.578	47.267	46.517	46.256	44.786
Test image-7	55.826	47.486	46.925	46.144	45.077
Test image-8	56.991	47.375	46.547	46.090	44.329
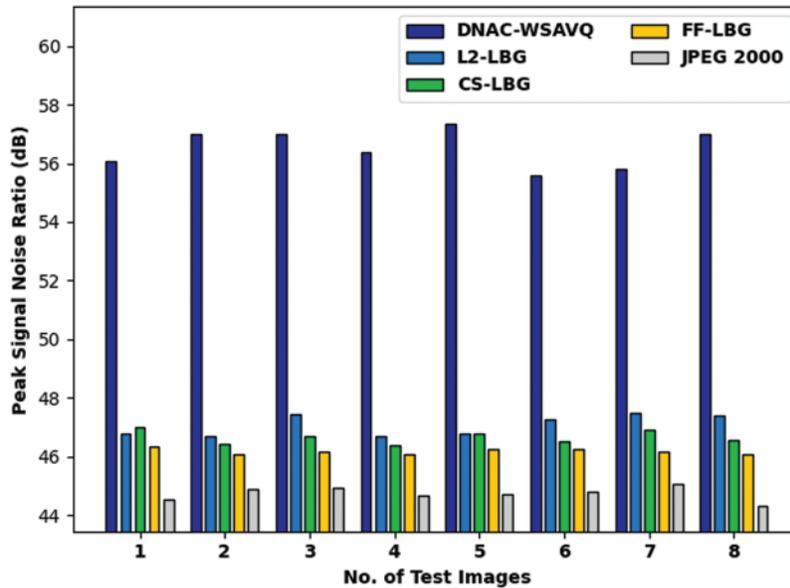
Figure 10: PSNR analysis of DNAC-WSAVQ technique with recent approaches

For example, on test image 1, the DNAC-WSAVQ model has accessible high PSNR of 56.090 dB while the L2LBG methodology, CSLBG system, FFLBG approach, and JPEG2000 models have accomplished lower PSNR of 46.764 dB, 46.991 dB, 46.341 dB, and 44.514 dB correspondingly. As well, on test image 4, the DNAC-WSAVQ approach has provided increased PSNR of 56.370 dB while the L2LBG methodology, CSLBG system, FFLBG approach, and JPEG2000 methods have provided reduced PSNR of 46.701 dB, 46.370 dB, 46.090 dB, and 44.667 dB correspondingly.

5 Conclusion

In this objective, a new DNAC-WSAVQ technique was developed for effective data storage systems. The proposed DNAC-WSAVQ technique mainly intends in data encoding via DNA computing

and then compresses it for effective data storage. Moreover, the DNAC-WSAVQ model primarily carried out DNA encoding on the input images for producing binary encoded form. Furthermore, a WSA-LBG model is utilized for the compression process and thereby storage area can be considerably minimized. For generating an optimum codebook for LBG, the WSA is applied to it. The performance validation of the DNAC-WSAVQ model is applied and the outcomes are examined under several measures. The comparative study highlighted the improved outcomes of the DNAC-WSAVQ model over the existing methods.

Conflicts of Interest: The authors declare that they have no conflicts of interest to report regarding the present study.

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