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# The Haar Wavelet Transform of the DNA Signal Representation

Abdelkader Magdy, Magdy Saeb, A. Baith Mohamed, and Ahmed Khadragi

*Abstract*—The Deoxyribonucleic Acid (DNA) which is a double-stranded helix of nucleotides consists of: Adenine (A), Cytosine (C), Guanine (G) and Thymine (T). In this work, we convert this genetic code into an equivalent digital signal representation. Applying a wavelet transform, such as Haar wavelet, we will be able to extract details that are not so clear in the original genetic code. We compare between different organisms using the results of the Haar wavelet Transform. This is achieved by using the trend part of the signal since the trend part bears the most energy of the digital signal representation. Consequently, we will be able to quantitatively reconstruct different biological families.

*Keywords*—Digital Signal, DNA, Fluctuation part, Haar wavelet, Nucleotides, Trend part.

## I. INTRODUCTION

ALL organisms on this planet are made of the same type of genetic blueprint that is the deciding factor of organism specifications. This is called Deoxyribonucleic Acid (DNA) which is a double-stranded helix of nucleotides that carries the genetic information of a cell. DNA is a combination of 4 nucleotides: Adenine (A), Cytosine (C), Guanine (G) and Thymine (T).

The massive amounts of these combinations allow for the multitude of differences between all living things on the planet from the large scale (mammal versus plant), to the small scale (blue eyes versus green eyes). In this work, we compare between multi species DNA by transferring the data stored in DNA from its biological space to the signal space.

Hence, the proposed approach will take advantage of the techniques of signal processing. The signal representation of DNA sequences will enable us to apply wavelet transforms to the resulting signal [1].

The human is considered a member of the Ape family. There are 193 living species of apes, 192 of them are covered with hair. The exception is a naked ape self-named Homo sapien [2].

The recent publication of the complete chimp genome [3], marked by a celebratory issue of the journal "Nature" recounts

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that humans and chimps share 96 percent of the same genetic material. The number of genetic differences between humans and chimps is ten times smaller than that among mice and rats [4].

In the following sections, we will discuss and explain how we compare between different organisms by extracting information from DNA code not so clear in the original biological space. In Section II, we present the binary and quaternary representation of the DNA sequence and the length of DNA code. In Section III, the Haar wavelet is applied on the resulting signal to enable us to extract information from DNA code. In Section IV, we compare between different species of the same evolutionary space. In Section V, we compare between different species of different evolutionary families.

## II. DNA SIGNAL REPRESENTATIONS

To deal with DNA code we must convert it into signal space. That means taking the advantage of the signal processing and hence can apply known signal processing techniques to analyze genomic information.

### A. DNA Binary and Quaternary Representations

Mapping the DNA sequences to binary representation is a simple and a straight forward procedure. For most tasks, a flat encoding of 2 bits/nucleotide, assigned in an alphabetical order would be a sufficient starting point [5].

$$A = (00)_2 \quad \text{or} \quad A = 0_Q$$
$$C = (01)_2 \quad \text{or} \quad C = 1_Q$$
$$G = (10)_2 \quad \text{or} \quad G = 2_Q$$
$$T = (11)_2 \quad \text{or} \quad T = 3_Q$$

For example the DNA sequence:

ACTGGTTTAAACTC

Will be represented in binary format as:

$(00,01,11,10,10,11,11,11,00,00,00,01,11,01)_2$

It will be represented in quaternary format as:

$(0,1,3,2,2,3,3,3,0,0,0,1,3,1)_q$

### B. DNA Genomic Length

The length of the DNA sequence may reach millions of bases. The DNA sequence of any organism can be downloaded from the gene bank [6].

When the length of the DNA sequence increases, the resulting resolution increases accordingly and vice versa. These results are used to distinguish between different organisms.

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The following examples compare between three different species such as Human, Shaping frog and Eurasian wolf in a small and large DNA sequence.

1) Choose Only 100 DNA Sequences for Each Species

Applying Haar wavelets on the three strands, we get:

Human = 16.5286210102355575202182080802952
Frog = 14.4956890143242311808080805579666
Wolf = 17.2357277914221036496655866999618

2) Choose Only 5000 DNA Sequences for Each Species

Applying Haar wavelets on the three strands, we get:

Human = 131.57710401797817212354857474566
Frog = 127.22397789629849285120144486427
Wolf = 119.2358809775816865794695331715

From the above results, when the number of the DNA sequences decreases the results between Human and the two other species are too close and the resultant resolution is not clear. However, when the DNA sequence increases, the results between Human and two other species are more separate.

The DNA of any organism contains millions of DNA sequences. In our experiments we use only 5000 base pairs of this DNA sequence to increase the resultant resolution and to reduce execution time.

### III. THE HAAR WAVELET

A wavelet is a function with some special properties. Literally, the term "wavelet" means little wave [7]. The Haar wavelet is the simplest type of wavelets [8], [9]. Usually it is used for compressing signals and for removing noise.

The Haar transform decomposes signal into two half sub-signals. The first half is called the "Trend" and the second half is called the "Fluctuations".

#### A. The Haar Trend Part

The first trend sub-signal $a^1 = (a_1, a_2, \ldots, a_{N/2})$,
Where N is the length of the signal.
The signal **f** is computed by the general formula for the values of $a^1$ is

$$a_m = \frac{f_{2m-1}+f_{2m}}{2} * \sqrt{2} \qquad (1)$$

Where m = 1,2,3,……..,N/2.

#### B. The Haar Fluctuation Part

The first fluctuation sub-signal $d^1 = (d_1, d_2, \ldots, d_{N/2})$,
Where N is the length of the signal.
The signal **f** computed by the general formula for the values of $d^1$.

$$d_m = \frac{f_{2m-1}-f_{2m}}{2} * \sqrt{2} \qquad (2)$$

Where m = 1,2,3,……..,N/2.

#### C. Conservation of Energy

The Total energy of the original signal defined by:

$$\varepsilon_f = f_1^2 + f_2^2 + \ldots\ldots + f_N^2 \qquad (3)$$

Where $f_N$, represents the elements of the original signal. Haar transform redistributes the energy in a signal by compressing most of the energy into the trend sub- signal [8]. So we can compute the energy of the original signal by calculating energy of the total trends $n^{th}$ parts.

### IV. METHODOLOGY

In this section, we compare between organisms DNA by comparing the results extracted from DNA sequence; by applying the Haar wavelet on the DNA code. The process is repeated until the trend part becomes one term only. This term has the most focused energy of the original signal. It can be considered as a good approximation to the original signal [8].

#### A. Comparing DNA Results for Mammal's Family

Mammals are warm-blooded vertebrates which, with the exception of a few notable species, nurse their young with milk produced by the female's mammary glands. They give birth to live young, and have bodies insulated by hair [10].

Table I compares between different species of the mammalian family.

TABLE I
THE $N^{TH}$ TREND FOR DIFFERENT TYPES OF MAMMAL FAMILY

| # | Family | Type | $N^{th}$ Trend |
|---|--------|------|----------------|
| 1 | Carnivorous | Spectacled Bear | 124.50603620611269661822007037699 |
| 2 | | Sloth Bear | 122.87085177461878515714488457888 |
| 3 | | Malayan Sun Bear | 122.67197799241004929626797093078 |
| 4 | | Asiatic Lion | 118.78289069588404913702106568962 |
| 5 | | Snow Leopard | 117.58964800263174765859730541706 |
| 6 | | Cheetah | 115.21421115958318637240154203027 |
| 7 | | Amur Tiger | 115.02638592083050639303110074252 |
| 8 | Hoofed | Bactrian Camel | 118.92652176081256243378447834402 |
| 9 | | Eurasian Elk | 116.38535676592341872037650318816 |
| 10 | | American Bison | 119.15854117338940909576194826514 |
| 11 | | Horse | 114.15355098780338494179886765778 |

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| # | | Type | $N^{th}$ Trend |
|---|---|---|---|
| 12 | | Human | 131.57710401797817212354857474566 |
| 13 | Apes | Chimpanzee | 132.206870994972433663386101115495 |
| 14 | | Gorilla | 119.22483243412564490881777601317 |
| 15 | | Western Lowland Gorilla | 121.33510423422924873193551320583 |
| 16 | | Proboscis Monkey | 118.03158974087334343303940157406 |
| 17 | Monkeys | Black Snub-Nosed Monkey | 120.07557028024069722960120998323 |
| 18 | | Grivet Monkey | 114.05411409669900990593305323273 |

In this table, we show the $n^{th}$ trends for some mammal species. Each species are indicated by a family type.

In the carnivorous part, all species of the same type are close to each other like bears and tigers family.

We note that in the hoofed part, camel and bison are much closer to each other, but at the other species they are relatively close.

In the ape family, we found some apes are much closer to each other. Human and chimpanzee DNA results are much closer than any other species.

The last part is the monkey family; some of them are much closer to each other.

### B. Comparing DNA results for Reptiles Family

The Reptile family is a cold-blooded, scaly-skinned vertebrates. Most reptiles reproduce by laying leathery eggs. However, many lizards and snakes give birth to live young [10].

Table II compares between different species of reptiles family.

TABLE II
THE $N^{TH}$ TREND FOR DIFFERENT TYPES OF REPTILES FAMILY

| # | Family | Type | $N^{th}$ Trend |
|---|---|---|---|
| 1 | | Nile Crocodile | 118.17522080580187093801214359701 |
| 2 | Alligators And Crocodiles | American Alligator | 117.14770626439016609765531029552 |
| 3 | | Chinese Alligator | 118.78289069588404913702106568962 |
| 4 | Snakes | Ball Python | 114.83856068207784062451537465677 |
| 5 | | king cobra | 115.58986163708856054199713980779 |
| 6 | | Vietnamese Big-headed Turtle | 117.29133732931866518356400774792 |
| 7 | Tortoises And Turtles | Egyptian Tortoise | 112.02118210078768356652290094644 |
| 8 | | Annam leaf turtle | 113.68951216264969161784392781556 |
| 9 | Chameleon | Parson's | 114.17564807471543986139295157045 |
| 10 | | spiny leaf | 115.98760920150598963118682149798 |

In this table, we present the $n^{th}$ trends for some reptile species. Each species is separated by a family type with a horizontal line.

In the Alligator and Crocodile family, the results are close to each other. The same is true at the snake and chameleon families. However, in the Tortoises and Turtles some results are close as Egyptian Tortoise and the Annam leaf turtle.

### C. Comparing DNA results for Amphibians Category

TABLE III
THE $N^{TH}$ TREND FOR DIFFERENT TYPES OF AMPHIBIAN FAMILY

| # | Family | Type | $N^{th}$ Trend |
|---|---|---|---|
| 1 | | Lake Victoria Clawed Frog | 123.92046340294257333880523219705 |
| 2 | Frogs and Toads | Shaping Frog | 127.22397789629849285120144486427 |
| 3 | | Chusan Island Toad | 129.00279339272088918733061291277 |
| 4 | Newts | Ryukyu Spiny Newt | 118.56191982676325835655006812885 |
| 5 | | Hong Kong Warty Newt | 116.54003637430795946769369577989 |

Amphibians include frogs, toads, newts, salamanders and the curiously worm-like caecilians. Some of amphibians live

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permanently on land, while others, such as the axolotl, never leave the water [10].

Table III compares between different species of amphibian family. In this table, we present the $n^{th}$ trends for some amphibian species. Each species is separated by a family type.

In the frogs and toads family, the results are relatively close like, Shaping Frog and Chusan Island Toad. At Newts family, the results are close to each other.

### D. Comparing DNA Results for Canis Family

Canis family includes dogs, wolves and foxes. Table IV compares between different species of canis family.

TABLE IV
THE $n^{TH}$ TREND FOR DIFFERENT TYPES OF CANIS FAMILY

| # | Type | $N^{th}$ Trend |
|---|---|---|
| 1 | Domestic Dog | 119.50104602052664404254755936563 |
| 2 | Coyote | 120.42912367083400226874800864607 |
| 3 | Eurasian Wolf | 119.23588097758168657946953317 15 |
| 4 | Mongolian Wolf | 119.68887125927932402191800065339 |

In this Table, we present the $n^{th}$ trends for some canis species. The results of this family are relatively the same for different species.

### E. Comparing DNA results for Felines Family

Table V compares between different species of feline family. The feline family includes cats, lions, tigers, and cheetahs.

TABLE V
THE $n^{TH}$ TREND FOR DIFFERENT TYPES OF FELINES FAMILY

| # | Type | $N^{th}$ Trend |
|---|---|---|
| 1 | Asiatic Lion | 118.78289069588404913702106568962 |
| 2 | Leopard | 116.86044413453313950412848498672 |
| 3 | Snow Leopard | 117.58964800263174765859730541706 |
| 4 | Clouded Leopard | 115.86607522348953125401749275625 |
| 5 | Cheetah | 115.21421115958318637240154203027 |

In this table, we present the $n^{th}$ trends for some feline species. The results are relatively close to each other.

### F. Comparing DNA Results for Fish Family

Fish were the earliest vertebrates to appear on Earth, having evolved more than 500 million years ago. Fish typically have fins and are covered in scales, are cold-blooded and breathe using gills [10].

Table VI compares between different species of fish family.

TABLE VI
THE $n^{TH}$ TREND FOR DIFFERENT TYPES OF FISH FAMILY

| # | Family | Type | $N^{th}$ Trend |
|---|---|---|---|
| 1 | Shark | Shark Mullet | 126.55001674548003620657254941761 |
| 2 | | Elephant Shark | 126.27380315907903707284276606515 |
| 3 | | Gummy Shark | 129.49997784824267910153139382601 |
| 4 | Whale | Blue Whale | 117.78852178484048351947421906516 |
| 5 | | Pygmy Right Whale | 112.57360927358968183398246765137 |
| 6 | | Striped Dolphin | 114.09830827052317658854008186609 |
| 7 | | Beluga | 121.21357025621280456562089 96661 |
| 8 | Other | American Angler | 119.69991980273536569256975781173 |
| 9 | | Swordfish | 126.50582257165589794567495118827 |

In this table, we present the $n^{th}$ trends for some fish species. Each species are separated by a family type.

In the shark family, some results are close to each other like, mullet and elephant shark. Swordfish is much closer to shark family than any other families.

## V. VERIFICATION

Table VII compares between different species of different families by the value of the energy concentrated at the trend part, and the ratio calculated between the species and human energy.

This Table gives a ratio between human and different species. Pig is added as a new species.

Amazingly, with 5000 base pairs-based computation, The ratio between human and pig is much closer than the ratio between human and chimpanzee.

Dr. L. Schook and J. Beever at University of Illinois animal geneticists, have created a side-by-side comparison of the human genome and the pig genome that reveals remarkable similarities. Dr. Schook said, we took the human genome, cut it into 173 puzzle pieces and rearranged it to make a pig, everything matches up perfectly. The pig is genetically very close to humans [11].

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TABLE VII
THE RATIO BETWEEN SPECIES AND HUMAN BY TOTAL TREND ENERGY

| # | Type | Total Energy | Ratio |
|---|------|--------------|-------|
| 1 | Homo | 17312.53430175784887978807091713 | |
| 2 | Chimp | 17478.6567382812827418092638825417 | 99.04956978 |
| 3 | Pig | 17210.9223632812900177668780088842 | 99.413073 |
| 4 | Snow Leopard | 13827.3253173828361468622246096134 | 79.86886886 |
| 5 | Nile Crocodile | 13965.3828125000272848410531878847 | 80.66631129 |
| 6 | Cheetah | 13274.3144531250236468622246096134 | 76.67458861 |
| 7 | Python | 13187.8950195312736468622246096134 | 76.17541597 |
| 8 | Shaping Frog | 16185.9405517578470607986673712730 | 93.49261217 |
| 9 | Domestic Dog | 14280.5000000000272848410531878847 | 82.48647917 |
| 10 | Swordfish | 16003.7231445312827418092638825417 | 92.44009494 |
| 11 | Blue Whale | 13874.1358642578416038304567333704 | 79.37758646 |

## VI. SUMMARY AND CONCLUSION

Within the cells of any organism is a substance called Deoxyribonucleic Acid (DNA) acting as the genetic blueprint. DNA sequence consists of A, C, G and T. Applying multi-resolution Haar Transform on the quaternary digital signal equivalent of the DNA, we were able to compare different genetic codes quantitatively. In the appendix, a chart that provides Nth-trend value of different species is shown. In this work we have discussed the following:

- Converting a DNA biological signal into a digital signal.
- The digital representation of DNA sequences will enable us to apply wavelet transforms to the developed signal.

- The wavelet transform has a lot of families but a Haar wavelet is chosen since Haar wavelet is the simplest and fastest type of wavelet families.
- The results are depicted in Tables I-VI to show the numeric relations between the species of the same family.
- Table VII compares between different species of the different families by the value of the energy concentrated in the trend parts.
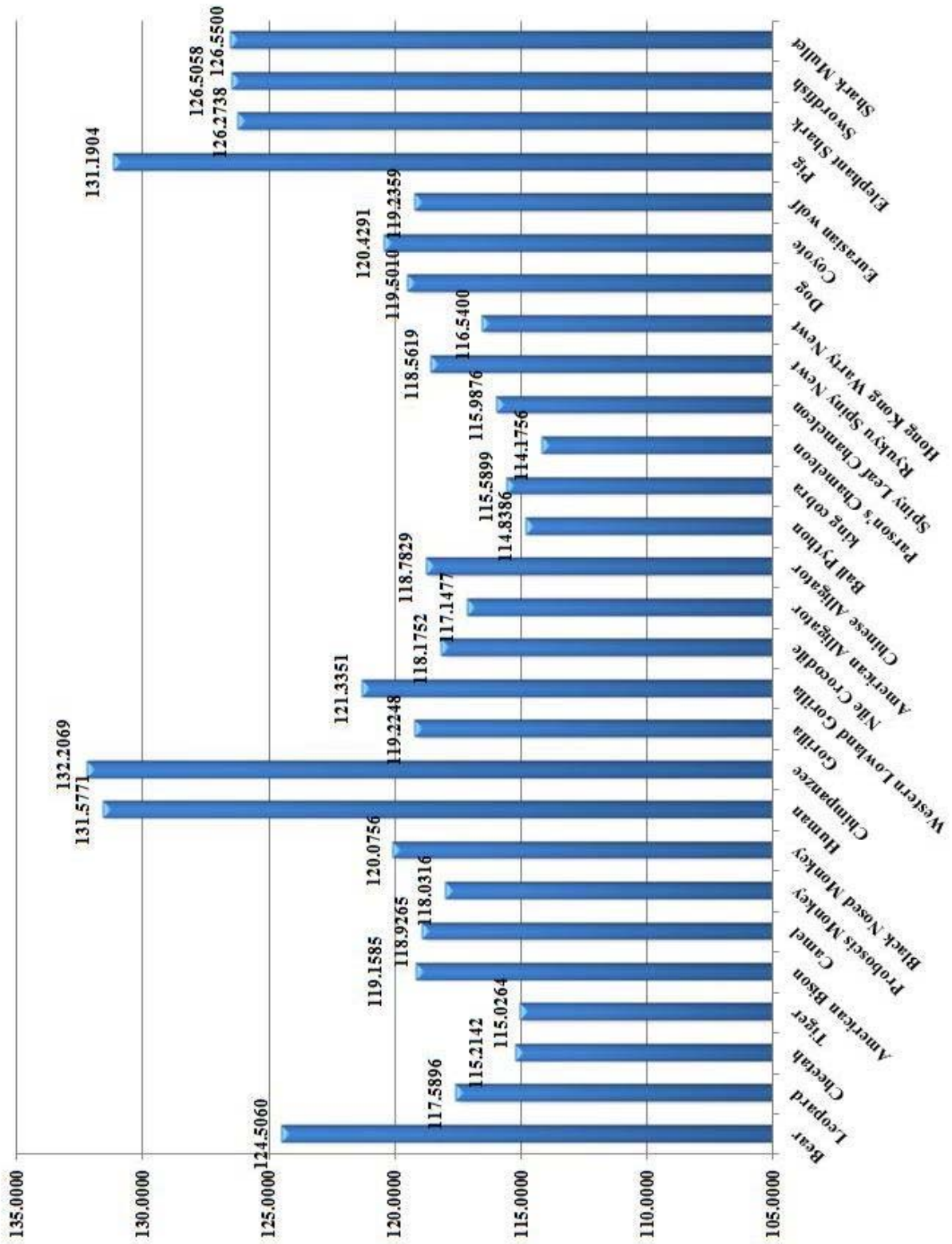
Applying this methodology, different biological families can be quantitatively reconstructed.

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APPENDIX



n<sup>th</sup> Trend Chart of Different Species for Different Families

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