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Automatic Classification of Standard Arabic Phonemes Using Parallel Genetic Algorithms

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Abstract:
The aim of this work is the application of the Parallel Genetic Algorithms (PGAs) to the Automatic Speech Recognition (ASR) domain at the acoustic sequences classification level. Speech recognition was been cast as a pattern classification problem where we would like to classify an input acoustic signal into one of all possible phonemes. Thus, we have looked for recognizing Standard Arabic (SA) phonemes of continuous, naturally spoken, speech by using PGAs whose have several advantages in resolving complicated optimization problems. The phonemes classification duration or problem resolution time is reduced by the number of the Genetic Algorithms (Gas) used in parallel, simultaneously. In SA, there are forty sounds. We have analysed a corpus that contains several sentences composed of the whole SA phonemes types in the initial, medium and final positions, recorded by several male speakers, in low noisy environment. Thus, the acoustic segments classification and the PGAs have been explored. We have used the decision rule Manhattan distance as the fitness functions for the PGAs evaluations whose topology chosen is the isolated island one. The Corpus phonemes were extracted and classified successfully with an overall accuracy of 95, 75% more rapidly than in the classical GAs methods. In addition, the computational cost was greatly reduced, and so the performances of the GAs were improved.

Keywords: *Parallel Genetic Algorithms, distance classifier, standard Arabic phonemes, automatic speech recognition*

1. Introduction

The ASR has been intensively researched for more than four decades. In the last one, significant improvements and successes were achieved. However, there are too few studies about the application of evolutionary algorithms to the automatic speech domain. In this work, we have used parallel GAs as functions optimization problem to evolve structures representing sets of acoustic segments rules [1, 2].

In our case, the ASR deals with mathematical and technical aspects of classifying different acoustic segments through their observable information. The extracted parameters of the speech signal are classified by using a certain type of measures, such as distance, likelihood and Bayesian, over class models. In our case, we have used the Manhattan distance as a criterion measure or a decision rule in the supervised classification of the SA phonemes

The GAs are search methods for good solutions in a large population of candidate solutions. GAs use extensive search of the current candidate space, to find the currently best approximations to the unknown solution. They have several advantages. They work with both continuous and discrete parameters, execute simultaneous searches over several regions of the search space and work with a population instead of a unique point. In addition, they optimize a large number of parameters; have successfully found global minimum even on very complex and complicated objective functions and their computer implementations are portable and modular. Also, they are tolerant to incomplete and noise data [2].

However, computing cost is the main problem of GA, especially in our situation of large size of population. In order to apply the genetic search into large-scale problems, we have used **P**arallel **G**enetic **A**lgorithms (**PGA**s) with an isolated multiple-deme parallel GA topology. It simply consists in evolving all the tasks of a basic genetic algorithm on each deme or subpopulations, in parallel manner. For each phoneme class, we have a subpopulation. The demes individuals or chromosomes are defined as the segmentation acoustic vectors. So, we have forty demes. For each one, we apply a basic GA in parallel with the others, no time will be spent on communication and thus, the algorithm is run much faster and has found more accurate results than the sequential one.

2. Standard Arabic phonemes

The Standard Arabic language is composed of 28 phonetically distinct consonant phonemes and three short vowels, [a, u, i], which contrast phonemically with their long counterparts, [a:, u :, i :]. Throughout the text, phonemic length is indicated by writing the vowel symbol twice. In addition, there are six (06) correspondent variants of the short and the long vowels, in emphatic context.

Generally, consonants have less energy than vowels. The characteristics which form a vowel are relatively more prominent and stable than those of the consonants. The consonants vary individually, making it easier to deal with them in group. All the Arabic

vowels are oral and fully voiced. But, they can be nasalized in nasal consonants context (assimilation). The difference between short and long ones is approximately double duration or more [3].
The 28 consonants of SA are classified physiologically as follow:

- 13 fricatives ; [θ],[ħ], [X], [ð], [s], [ʃ], [$s^{\mp}$],[f], [z], [ð$^{\mp}$],[ʕ], [ʁ], [h]. Fricatives are consonant sounds where the vocal tract is excited by a turbulent airflow, produced when the airflow passes a constriction in the vocal tract. ;
- 08 stops : [ʔ], [k], [q], [t], [d], [b], [$t^{\mp}$], [d$^{\mp}$]. Stop consonants, also called plosives, are produced in two phases. In the first phase, air pressure is built up behind a complete constriction at some point in the vocal tract. In the second phase, there is a sudden release of this air which produces the plosive sound. Stops are transient sounds, generally short in duration. ;
- 02 nasals: [n], [m]. These are all voiced and involve moving air through the nasal cavities by blocking it with the lips, gums, and so on. Nasals are lower in energy than most vowels due to the closure of the oral cavity and the limited ability of the nasal cavity to radiate sound ;
- 02 Semi-Vowels: the two glide [j], [w]. They have vowel-like acoustic characteristics ;
- the trill [r] and the liquid : [l].
- 01 affricate: [dz]. It is a dynamic consonant sound that results from the combination of two sounds: the transition from a plosive to a fricative.

The relative duration of the consonants depends upon whether they occur initially, medially or finally. It also depends on whether they are aspirated or unaspirated, voiced or unvoiced and single or geminated.
The SA is characterized by three phonetic phenomena which are the presence of the emphatic consonants, the geminate ones and by the presence of glottal, pharyngeal, velar and uvular ones called back consonants. The SA possesses eight back phonemes. The phonemes in Arabic that are not found in English include the following: [$t^{\mp}$], [d$^{\mp}$], [ð$^{\mp}$], [$s^{\mp}$], [X], [ʁ], [ħ], [ʕ], and [ʔ].
The emphasis is a complex phenomenon that possesses certain characteristics like the pharyngalization and the velarization. The three emphatic consonants are the fricatives [ð] and the two consonants are stops [$t^{\mp}$], [d$^{\mp}$]. On the neighbouring emphatic consonants, all the Arabic vowels are strongly influenced. So we obtain variants: emphasized vowels in opposition to the not emphasized ones.
The gemination corresponds to the consonant production with intensive energy concentration. In phonetic terms, the distinction between the geminated and ingeminated segments is predicated on the fact that the hold phase in the production of the consonant is lengthened to approximately double the length of the ingeminated one. The entire Arabic consonants can be geminate except the glottal stop consonant [ʔ] [4].

3. Speech Encoding

In speech processing, speech signal is usually a realization of some messages encoded as a sequence of one or more symbols which are represented as a sequence of equally spaced discrete parameter vectors. An observed speech signal is converted to some type of parametric representation for further analysis and processing. It transforms the high-dimensional speech signal space to a relatively low-dimensional features subspace while preserving the speech discriminative information to application. Several speech analysis methods can be used to extract spectral envelope characteristics of the speech signal such as filter bank analysis, Linear Predictive Coding (LPC), and cepstral analysis. Among these techniques, we have used both the lpc and the cepstral analysis because the LPC Coefficients and the Mel Frequency Cepstrum Coefficients (MFCCs) are the best known and most commonly used features for ASR. Just the first coefficients of the predictive coding and the cepstral sequence are interesting for smoothing the spectrum and minimising the pitch influence [5].

3.1. Vowels/Semi-Vowels Short Parametric Vectors

It turns out that the vowel and semi-vowel segments have a great steady-state part. Consequently, the first twelve **C**oefficients of **L**inear **P**rediction **C**oding (**LPCC**) perform a sufficiently high prediction gain. Broadly, the autocorrelation method of linear prediction ensures the stability of the estimated all-pole filter and hence, is used here for analysis (with 20 ms Hamming window). Each 10 ms frame or segment n°m noted S_m is represented by a short time parametric vector noted Vv_{12m} composed of ten predicting coefficients a_{im} . The description of this vector is as follows:

$$Vv_{12m} = (a_{1m}, \dots, a_{im}, \dots, a_{12m}) \tag{01}$$

3.2. Short-Parametric Vectors of Consonants

Temporal changes, in speech spectra, play an important role in perception. This information is captured in the form of velocity and acceleration coefficients (collectively referred to as differential or dynamic features). It is often the dynamic characteristics of the features that provide most information about phonetic properties of speech sounds (related to, for example, formant transitions or the closures and releases of stop consonants). No time evolution information is included in MFCCs. But it is often included in the feature set by cepstral derivatives. The first order derivatives of MFCCs are called Delta coefficients, and their second order derivatives are called Delta-Delta coefficients.
It is common to append an energy coefficient to the cepstrum feature vector. Differences in energy among phonemes show that it is a good feature to distinguish between them. **S**hort **T**ime **E**nergy (**STE**) is simply the mean square power in the frame.

Consequently, the fricative and nasal consonants segments n°m are represented by a features vector noted Vcf_{42m} which contains the thirteen first MFCCs, the STE and their first and second order derivatives. The description of this vector is as follows :

$$Vcf_{42m} = (cf_{1m}, cf_{2m}, ..., cf_{42m}) \quad (02)$$

The **B**urst **F**requency (**BF**) was found to be one of the most important perceptual clues to human classification of stops. The BF is a parameter aimed at finding the frequency where power is concentrated in a stop. Essentially, at each time position of the stop burst, there exists a position of maximum intensity. Each of these positions has a corresponding frequency. The BF is the minimum value of that set. The **V**oicing **O**nset Time (**VOT**), defined as the duration from the release to the start of voicing (burst duration) was used to detect voicing. Unvoiced stops were found to have longer VOTs [6].

To search stop and affricate consonants, each parameter vector noted Vcs_{44m} of the acoustic segment n° m is composed of the first twelve MFCCs, the STE and their first and second time derivatives. Also, we add to this set of parameters the VOT and the BF ones. The description of this vector is as follows:

$$Vcs_{44m} = (cs_{1m}, cs_{2m}, ..., cs_{44m}) \quad (03)$$

4. Genetic Classification

The **G**enetic **A**lgorithms (**GA**s) are global optimization procedures those use analogies with the genetic evolution of biological organisms. It is a heuristic search procedure that modifies function values of individuals coded as binary (or real or symbol) strings, through the application of predefined reproduction operators in a stochastic manner. The string, referred to as a chromosome, is divided into individual sections called genes. GA has been shown to be a robust and effective search method requiring very little information about the problem to explore a large search space.

In our case, the GAs consist on looking for, among the various acoustic segments of a vocal sequence, structures which correspond to those of the representative reference vectors of every class. To associate entities to be recognized in classes, it is enough to find an analytical correspondence between the two groups of the acoustic vectors respectively vocal sequences and entities to be recognized of reference. The vectors of the initial population represent the search space for potential solutions. The GA will have for task to make on these initial vectors some modifications, reorganizations, to produce the best vector as the potential solution [7].

Each individual of the population represents a potential solution by encoding it into a data structure called chromosome. Each individual is evaluated and given a measure of how good it is to solve the problem at hand. This measure is named fitness. The next steps produce, in successive generations, new populations. Three basic operations are used to transform a current population into a new one: selection, crossover and mutation. The selection operator selects a sample of individuals favouring the high-fitness individuals. The crossover takes two selected individuals called parents and combines its parts creating new ones called offspring. Mutation takes an offspring and creates a transformed individual by modifying its parts randomly. The transformed ones will compose the new generation of individuals. That procedure is repeated until a satisfactory solution is found.

4.1. Reference Acoustic Data

The choice of the type of the discriminative acoustic parameters of phonemes to be recognized is very important. These last ones, as acoustic vectors form, constitute the set of reference data for the AG. Each SA phoneme of class k is represented by a mean parameters vector noted μ_{km} :

$$\mu_{km} = (\mu_{k1}, \mu_{k2}, ..., \mu_{km}) \quad (04)$$

k is the number of SA phonemes. The SA alphabet is composed of 28 consonants, 06 vowels and their 06 vocalic variants in emphatic context.

These reference acoustic vectors are obtained during the learning phase. Each of the forty phonemes is represented by an acoustic reference vector of a specific order. The mean vectors of the forty phonemes classes are computed from the data in the training set by using the following relations:

$$\mu_{km} = \frac{1}{N_k} \sum_{z=1}^{N_k} v_{kz} \qquad 1 \leq k \leq 40 \quad (05)$$

Where N_k is the number of preclassified vectors in the class k and v_{kz} the vector z of the class k.

4.2. Problem Encoding

In GAs, each potential solution is represented in the form of a bit string which is dubbed a chromosome or an individual. A pool of strings forms a population. We use a fixed length chromosome for the GA, where each chromosome contains, as genes, the coefficients of several segments noted S_m of the vocalic continuum of the chosen corpus. The bit string length depends on the required numerical precision. The precision of the solutions is bounded by the precision of the data type used in the implementation of the genetic algorithm. We have used a double precision data type of 64 bits following the specification IEEE Standard for Binary Floating-Point Arithmetic. This data type has a precision of 15 - 17 digits [8, 9].

The individuals are elaborated relatively to the phoneme to be classified. For example, if we want to classify the vowel [u], we proceed to the segmentation of the vocalic continuum into a set of acoustic vectors according to the corresponding individual that will be definite as the chromosome. This acoustic vector noted $V_{vo_k\ m}$ is composed of the coefficients of a certain number of successive concatenated acoustic segments and it's size is equal to the order noted vo_K of the phoneme reference vector and it is expressed as follows:

- stop and affricate consonants :

$$V_{vo_k\ m} = (cs_{1m},..., cs_{44m},..., cs_{1(m+1)},..., cs_{44(m+1)},..., c_{vo_k}), \qquad vo_k = r \times 44 \qquad (06)$$

r : number of acoustic segments concatenated to form the individual vector.

- b- fricative and nasal consonants:

$$V_{vo_k\ m} = (cf_{1m},..., cf_{42m},..., cf_{1(m+1)},..., cf_{42(m+1)},..., cf_{vo_k}), \qquad vo_k = r \times 42 \qquad (07)$$

- c- vowels and semivowels :

$$A_{vo_k\ m} = \left(a_{1m},..., a_{im},..., a_{12m},... a_{1(m+1)},..., a_{vo_k}\right), \qquad vo_k = r \times 12 \qquad (08)$$

It results that the initial population noted pop will be composed of all possible acoustic vectors $V_{m\ vo_K}$ when we vary the values of *m* and vo_K. The different values of m are as follow:

$$m = 1, \ . \ . \ . \ , M, \qquad M = T/10, \qquad (09)$$

T: vocalic continuum duration.

Therefore, each individual is made up of vo_K genes.

4.3. Fitness Function

Acoustic classification is the elaboration of a decision rule that assigns acoustic feature vectors of phonemes to one of the existent classes. The classification criterion is also called decision rule. The most widely used classification criteria are distances, Bayesian and likelihood ones. The first criterion is the simplest and most direct one. The basic idea of distance classification criterion is that a data is classified to a class that is closest to it. A variety of distance functions are available for such uses, including the Minkowsky, Mahalanobis and others. Distances are often normalized by dividing the distance for each attribute by the standard deviation, noted σ instead of by range.

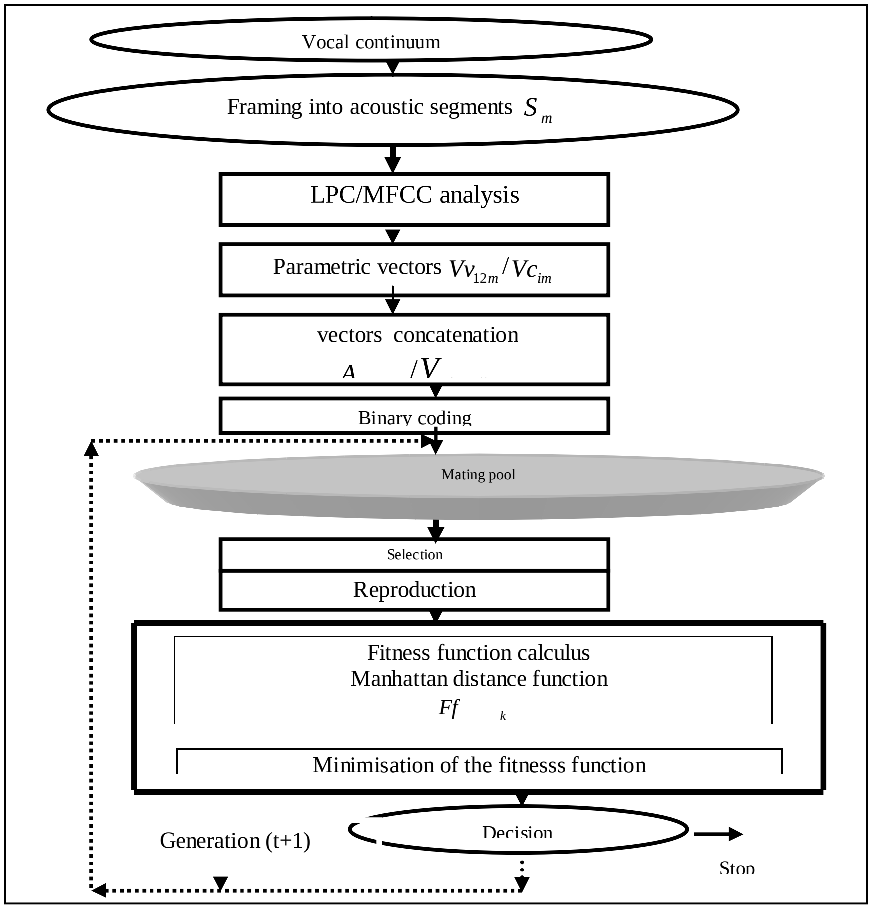


Figure 1: Flowchart of phonemes Classification Genetic Algorithm (GA)

To evolve good solutions and to implement natural selection, we need a measure for distinguishing good solutions from bad ones. The measure could be an objective function that is a mathematical model or a subjective function where humans choose better solutions over worse ones. In essence, the fitness measure must determine a candidate solution's relative fitness, which will subsequently be used by the GA to guide the evolution of good solutions. Once the problem is encoded in a chromosomal manner and a fitness measure for discriminating good solutions from bad ones has been chosen, we can start to *evolve* solutions to the search problem [10, 11].

The **F**itness **f**unction (**Ff**) can be represented rigorously by the Manhattan distance between the vectors of the acoustic segments and the vectors of reference of every class of phonemes. It can be expressed as follows (Fig. 1).

- Vowels and semivowels :

$$Ff_k = \sum_{m=1}^{n} \frac{\left| A_{vok\ m} - \mu_{mk} \right|}{\sigma} \tag{10}$$

b- Consonants :

$$Ff_k = \sum_{m=1}^{n} \frac{\left| V_{vok\ m} - \mu_{mk} \right|}{\sigma} \tag{11}$$

To estimate potential solutions of our problem, we minimize the Ff to decide of the type of membership classes of the acoustic segment or the sets of these segments. So, we maximize the inverse function of Ff, and looking for the extrema which can give two types of results: the global maximum means the existence of the phoneme we are looking for. In that case, we continue the search of the same type of sound for the rest of the vocal continuum witch is somme sentences of ten minutes duration. Otherwise, the end of the vocal continuum means that there is no phoneme of class k in the vocal continuum, so we repeat the research for the other phonemes of the same type (Fig.2a, 2b, 2c).

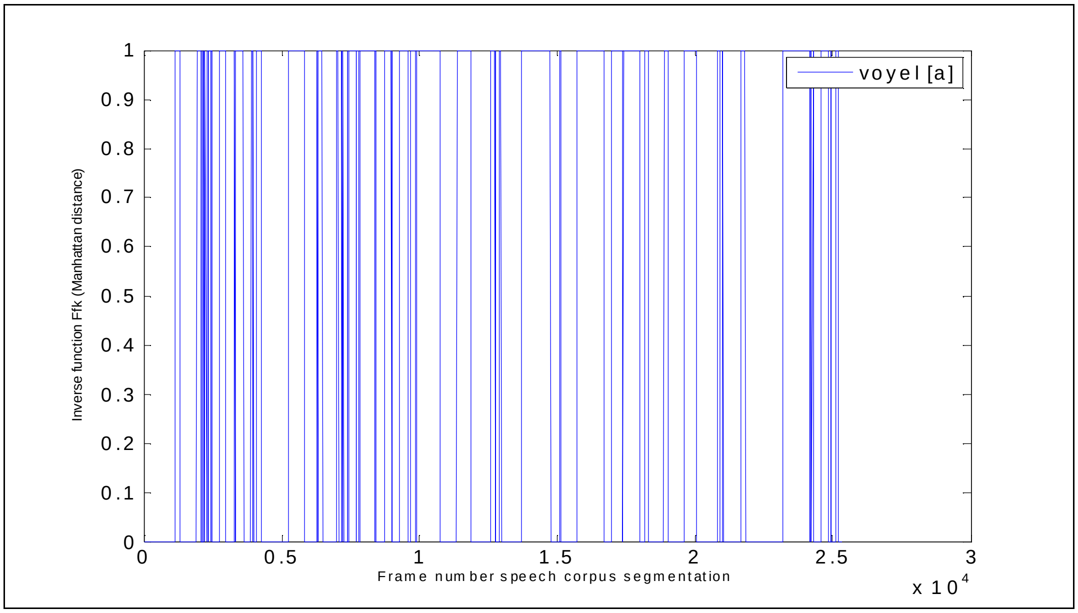


Figure 2.a: Localisation of existing vowels [a] in the vocalic continuum.

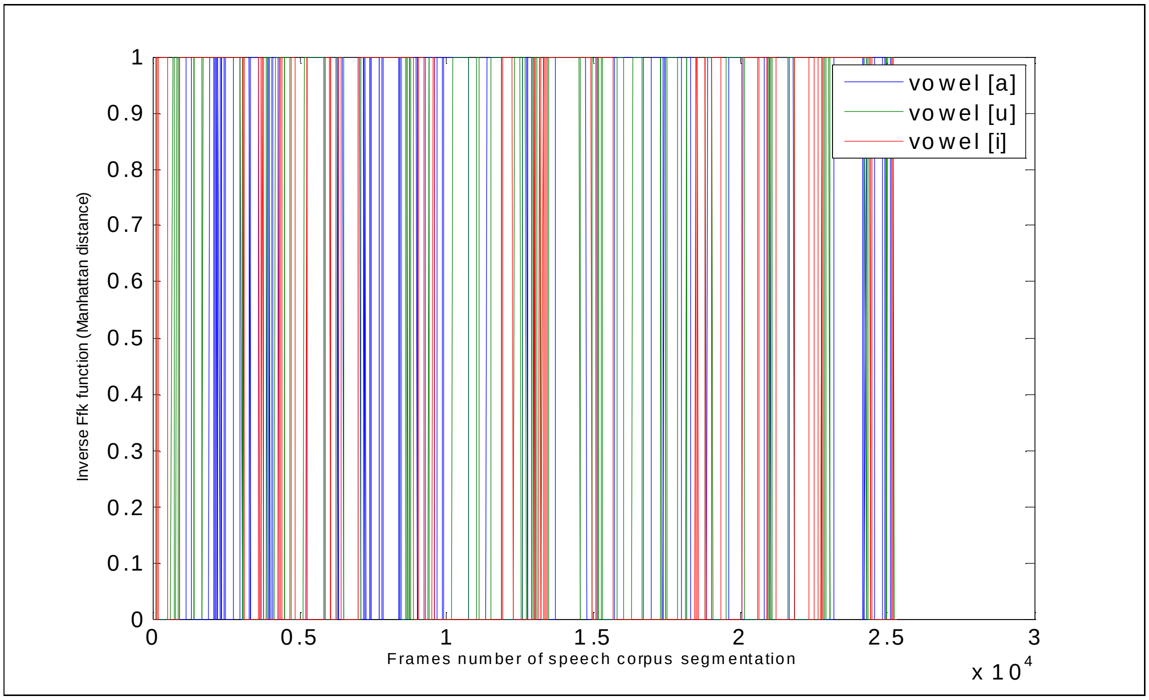


Figure 2.b: Localisation of existing short vowels [a], [u] and [i] in the vocalic continuum.

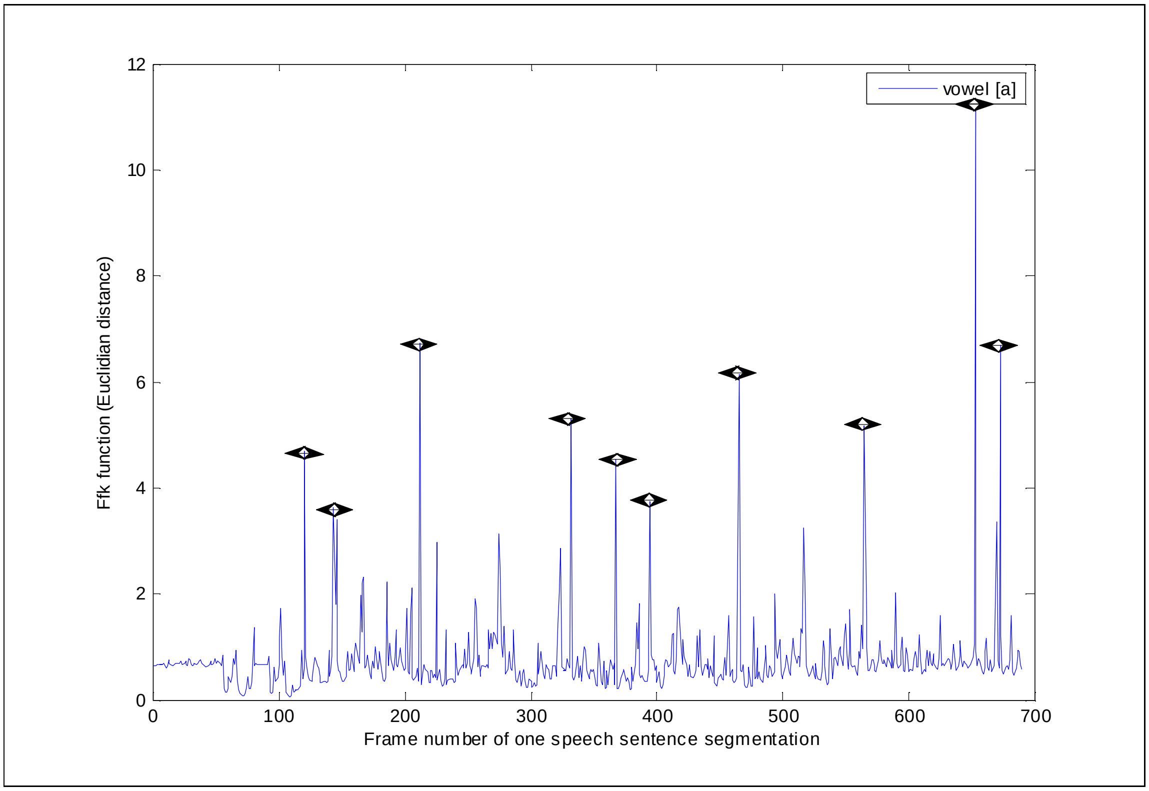


Figure 2.c: Localisation of existing short vowel [a] in one vocalic sentence

4.4. Parallel Genetic Algorithms

It has been established that GA efficiency to find optimal solution is largely determined by the population size. With a larger population size, the genetic diversity increases, and so the algorithm is more likely to find a global optimum. A large population requires more memory to be stored; it has also been proved that it takes a longer time to converge. The use of new parallel computation methods not only provide more storage space but also allow the use of several processors to produce and evaluate more solutions in a smaller amount of time.

There are several ways to parallelize the GA such as the Master Slave Parallel GAs also called Global Parallelisation and the Multiple-demes parallel GAs also called "coarse_grained". For the first one, the basic idea is that different processors can create new individuals and compute their fitness in parallel almost without any communication between each other when the algorithm still manipulates a single population. For the second one, we divide the population into subpopulations or demes, run a conventional GA in each subpopulation and allow the periodic communication of information between subpopulations that helps in the search for the solution. Most studies of parallel GAs are empirical investigations that concentrate on the choices of topology, migration rates and the population sizing [7,12].

4.5. Multiple-Deme PGAs

Multiple-deme parallel GAs are also called "distributed" GAs, because the communication to computation ratio is low, and they are often implemented on distributed memory computers. They are also known as "island model" GAs, because they are like a model which is used to describe natural populations isolated by the distance between them (as in islands). Both in the model and in the GAs individuals may migrate occasionally to any population. The population is divided into a few subpopulations or demes, and each of these relatively large demes evolves separately on different processors. Exchange between subpopulations is possible via a migration operator. On each deme or island the population is free to converge toward different optima. Technically, there are three important features in the coarse grained PGA: the topology that defines connections between subpopulations, migration rate that controls how many individuals migrate, migration intervals that affect how often the migration occurs [12].

4.6. Isolated Demes

This bounding case of PGAs considers that the demes evolve in complete isolation. Without communication, the migration rate is zero, and this is clearly a lower bound. Also, no connections between the demes represent a lower bound in the connectivity of the topology. Since the demes are completely isolated, the parallel speedup is simply the ratio of the time used to evaluate individuals in the serial and parallel cases [13].

This is the topology we have chosen to our PGA. For each phoneme class, we have a subpopulation or deme. The deme individuals or chromosomes are defined as the segmentation acoustic vectors. We devise our population into three main groups of subpopulations according to the nature of their individuals.

The first subpopulations group is noted VST. It contains as individuals, the acoustic vectors $A_{vo_k\ m}$ (08). This group is divided into sixteen demes according to the number of vowels, correspondent variants in emphatic context and the semivowels including the trill and the liquid ones. Each deme which corresponds to one phoneme constitutes the initial population of the basic GA.

The second subpopulations group is noted SA. It contains as individuals, the acoustic vectors $V_{vo_k\ m}$ (07). This group is divided into nine demes according to the number of stops and the affricate consonants.

The third group is noted FN and contains as individuals, the acoustic vectors $V_{vo_k\ m}$ (06). This group is divided into fifteen demes according to the number of fricative and nasal consonants.

For each deme, basic GA evolves in parallel and without communication with the other GAs (Fig.3).

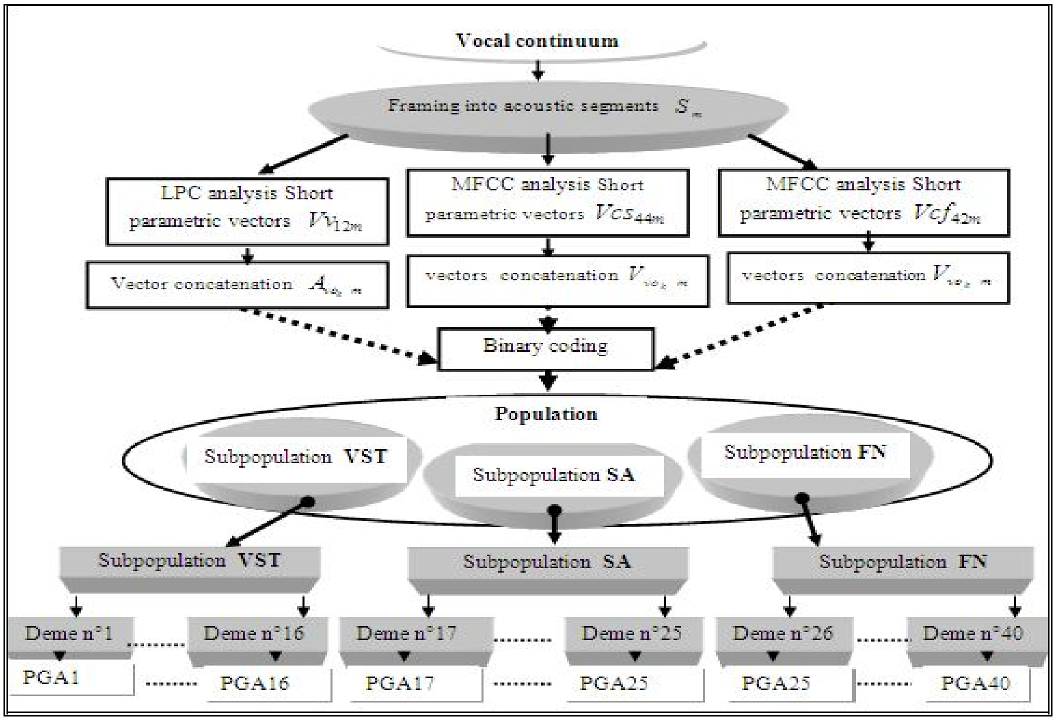


Figure 3: Flowchart of phonemes classification Parallel Genetic Algorithms.

5. Results and Discussions

The GAs are very advantageous compared to the deterministic algorithms, in the sense that further improvements can be made in various ways. Also, they are more suitable for large-sized problems. We have developed a Parallel Genetic Algorithm for speech units' classification task. To design fast and reliable parallel Gas; we must decide on a configuration among the many choices of topologies, migration rates, number and size of demes. Each parameter affects the quality of the search and the efficiency of the algorithm in non-linear ways.

Our PGA is a multiple-deme parallel GAs. The population is divided into a few subpopulations or demes, and each of these relatively large demes evolves separately on different processors in complete isolation. Without communication, the migration rate is zero. This is the topology we have chosen to our PGA. For each phoneme class, we have a subpopulation or deme. For each deme, basic GA evolves in parallel and without communication with the other GAs. We have chosen uniform crossover operator because it combines any material of the parents and the ordering of genes is irrelevant. Its probability noted p_c is equal to 0.8. The probability uniform mutation noted p_m was fixed to zero. This means that too poor attribute values were modified in each recombination. These values are chosen empirically to improve each deme GA by performing multiple executions to choose the best solution [14].

For each GA, we have used tournament selection and an elitist generational population model without any overlap of the populations. Fixed length chromosomes were used relatively to the order of reference vector of each phoneme sound.

The experiment was conducted using a medium-sized corpus composed of 100 naturally spoken sentences of Standard Arabic continuous speech from Arabic normalized database. This corpus is spoken by several male Jordanian speakers in low noisy environment. It contains hundreds of consonants (stops, fricatives, semivowels) which occurred in the three possible positions: initially, medially and finally. Speakers were asked to read a list of meaningful and grammatically correct sentences. The sentences were selected so that the number of consonants with the two voicing properties is fairly well balanced.

The results analysis shows that the PGAs application to the speech classification domain is very interesting, since we have obtained good results. This evaluation was conducted in terms of two criteria: classification accuracy and computation time. The Corpus phonemes were extracted and classified successfully with an overall accuracy of 95.75% in different contexts. Approximately, there is similar classification accuracy between the same types of consonants. It means that we have used a good front-end signal processing used in our system to characterize, acoustically, the consonants.

The results show that the classification accuracy of vowels and semivowels which is equal to 97,50% is higher than the accuracy of the other phonemes. It can be explained by the steady character of their acoustic characteristics. Also, they show that the classification accuracy of stops which is equal to 93,1%, is the worse one because of their dynamic acoustic character (Fig. 4).

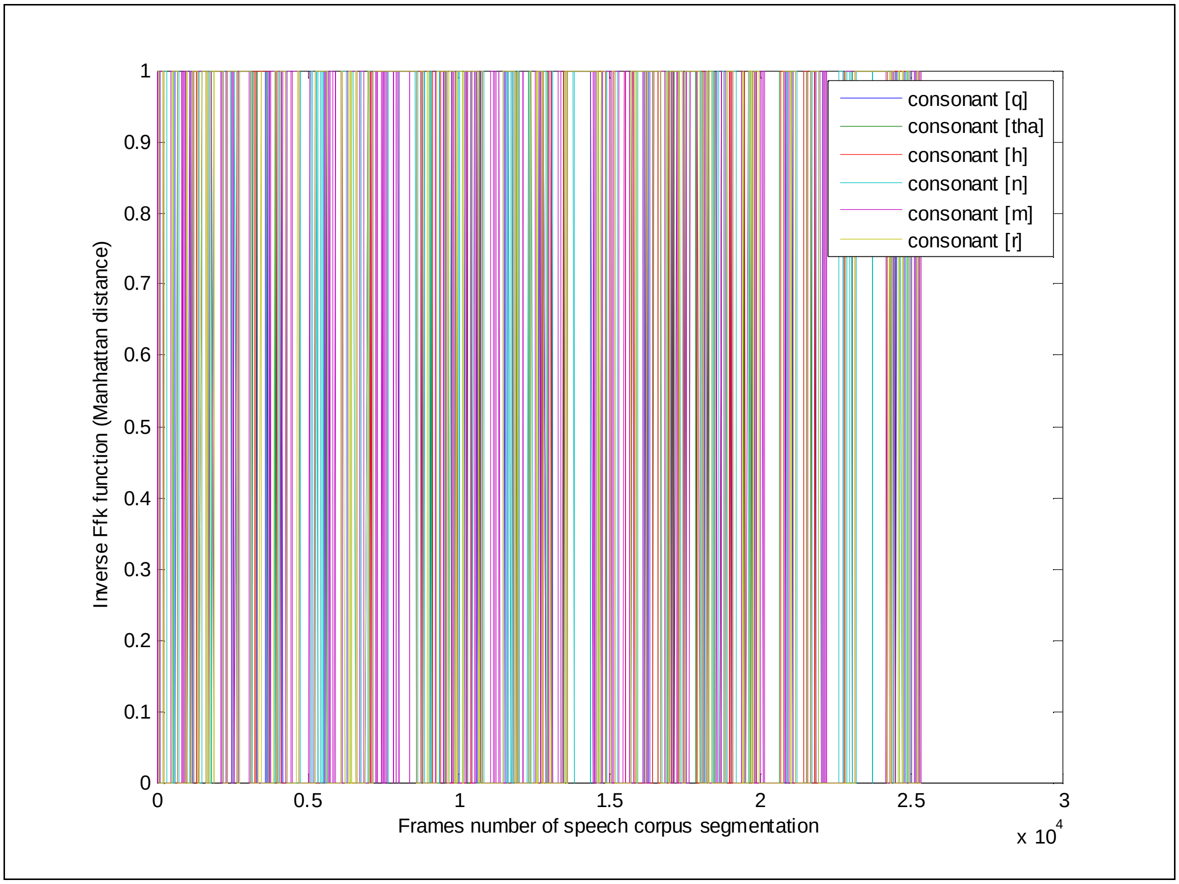


Figure 4: Localisation of existing consonants [q], [n], [m], [r], [h] and [ʃ] in the vocalic continuum.

The unclassified phonemes are essentially due to the segmentation difficulties and to the coarticulation phenomenon problems. In natural speech, there are no marked boundaries between acoustic data segments. Word and phoneme boundaries are non-existent. Even with expert labelling of the acoustic data, it is very difficult to establish a hard boundary between the phonemes and words that form an utterance. Speech is a stream of phonemes that sounds very smooth. This smoothness results from the coordination of the articulators' movements by the brain. The movements of these articulators - lips, tongue, jaw, velum, and larynx- are coordinated so that movements needed for adjacent phonemes are simultaneous and overlapping.

In addition, we can say that the unclassified phonemes accuracy is due to the fact that the GA has many inherent variations and parameters that need to be handled properly in the implementation stage, in order for reasonable or good performance to be obtained.

In most cases the convergence of the algorithm was rapid (forty evaluations in parallel). This is too prompt compared to the sequential GAs. All the GA tasks are parallelized. The number of evaluations in our PGA is at least equals to the number of a similar sequential GA divided by forty.

6. Conclusions

In this paper, we use speech segments classification method based on the Parallel Genetic Algorithms in order to recognize, automatically Standard Arabic phonemes. Though they have been studied since the birth of speech recognition, even modern automatic speech recognition systems are unreliable at classifying them because of their context dependence. We have used a corpus composed of 100 naturally spoken sentences of continuous speech from Arabic corpus recorded by several Jordanian male speakers in low noisy environment.

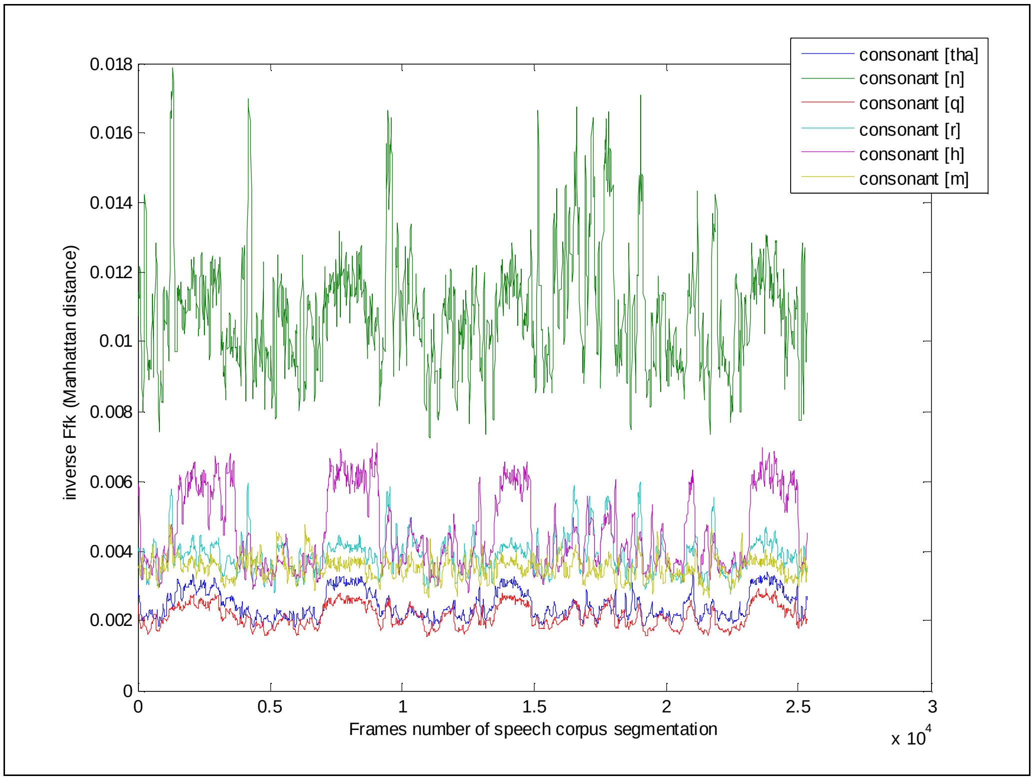
We have formulated the classification model as a function optimization problem using an isolated multiple-deme parallel GA. For each phoneme class, there is an isolated subpopulation or deme. For each one, basic GA evolves in parallel with the decision rule distance as the GA evaluation or fitness function. Also, we have used three structure modification operators: uniform crossover, uniform mutation and tournament selection. The first difficult task is how to set up the GAs parameters. Unfortunately, there is no unified guidance for this. Empirically, we set the crossover probability 0.8 and the mutation probability zero. In order to maximize the reproducibility and minimize the ambiguity in the GA implementation, the deme population size was chosen to be dependant on the size chosen corpus. The binary tournament selection was used to increase the selection pressure which allowed us to measure whether each crossover was able to keep the population diversity [15].

Our promising results show that the PGA is capable to precisely classify almost all instances. Despite its simplicity, it may give competitive performance compared to many other methods. By parallelising the algorithm, we have increased population size, reduced the computational cost, and so have improved the performance of the GAs. We have compared these results with those of other promising machine learning sequential approaches and we have found that our classification model PGA is most performing than the other known approaches in low noisy environment.

7. References

1 Hansohm,J.(2000). Two-mode Clustering with Genetic Algorithms, Classification, Automation, and New Media. 24th Annual Conference of the Gesellschaft Fur Klassifikation, 87-94.
2 GUO, Q.(2007). Parallel genetic algorithms for the solution of inverse heat conduction problems. International Journal of Computer Mathematics, 84(2), 241-249.
3 Al Ani, S. h. (1970). Arabic Phonology an acoustical and physiological investigation. Edition Mouton.
4 Bonnot, J.F. (1979).Etude expérimentale de certains aspects de la gémination et de l'emphase en Arabe., Actes du 9éme ICPS Copenhague, 1,45-79.
5 Vergin,R & all.(1999), september).Generalized Mel frequency cepstral coefficients for large-vocabulary speaker-independent continuous-speech recognition, IEEE Transactions on Speech and Audio Processing, 525–532.
6 Ali, A.M. A. & all.(1999). Acoustic-phonetic Features for the Automatic Classification of Stop Consonants, IEEE Transaction on Speech and Audio Processing, in press.
7 HE, H., SYKORA, O., SALAGEAN, A., & MAKINEN, E. (2007). Parallelisation of genetic algorithms for the 2-page crossing number problem. Journal of Parallel and Distributed Computing, 67(2), 229-241.
8 Goldberg,D.E.(1994). Algorithme génétique Exploration, optimisation et apprentissage automatique, Edition Addison-Wesley, France.
9 Goldberg, D.E. (1989). Genetic Algorithms in Search, optimisation and Machine Learning. T. Reading, Addison-Wesley.
10 De Jong, K. A. & Spears, W. M. (1991) . Learning concept classification rules using genetic algorithms. International Joint Conference on Artificial Intelligence, 651-656.
11 Goldberg, D.E. (2002). Design of Innovation: Lessons From and For Competent Genetic Algorithm. Kluwer, Boston, MA.
12 Cantu_Paz, E. (1998). A survey of parallel genetic algorithms. Calculateurs Paralléles. Reseaux et Systems Repartis, 10(2), 141-171.
13 Cantu.Paz.E. & Goldberg, D.E. (1997). Predicting speedups of idealized bounding cases of parallel genetic algorithms. T. BÄck. Editor, Proceedings of the Seventh International Conference on Genetic Algorithms, 113-121. San Francisco.
14 Banzhaf,w. Harding, S. Langdon, W.B. & Wilson,G. (2009). Accelerating genetic programming through graphics processing units. In Genetic Programming Theory and Practice VI, 1–19. Springer.
15 Herrera.F, & all. (2003). Taxonomy for the crossover operator for real-coded genetic algorithms: An experimental study. International Journal of Intelligent Systems, 18, 309–338.

ANNEXURE


consonant [tha]
consonant [n]
consonant [q]
consonant [r]
consonant [h]
consonant [m]
inverse Ffk (Manhattan distance)
0.018
0.016
0.014
0.012
0.01
0.008
0.006
0.004
0.002
0
0
0.5
1
1.5
2
2.5
3
Frames number of speech corpus segmentation
x 10^4