

A Template Matching Approach to Classification of QAM Modulation using Genetic Algorithm

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Abstract

The automatic recognition of the modulation format of a detected signal, the intermediate step between signal detection and demodulation, is a major task of an intelligent receiver, with various civilian and military applications. Obviously, with no knowledge of the transmitted data and many unknown parameters at the receiver, such as the signal power, carrier frequency and phase offsets, timing information, etc., blind identification of the modulation is a difficult task. This becomes even more challenging in real-world.

In this paper modulation classification for QAM is performed by Genetic Algorithm followed by Template matching, considering the constellation of the received signal. In addition this classification finds the decision boundary of the signal which is critical information for bit detection. I have proposed and implemented a technique that casts modulation recognition into shape recognition. Constellation diagram is a traditional and powerful tool for design and evaluation of digital modulations. The simulation results show the capability of this method for modulation classification with high accuracy and appropriate convergence in the presence of noise.

Keywords: Automatic Modulation Recognition, Genetic Algorithm, Constellation Diagram, Template Matching.

1. INTRODUCTION

Recognition of the modulation type of an unknown signal provides valuable insight into its structure, origin and properties. Automatic modulation classification is used for spectrum surveillance and management, interference identification, military threat evaluation, electronic counter measures, source identification and many others. For example, if the modulation type of an intercepted signal is extracted, jamming can be carried out more efficiently by focusing all resources into vital signal parameters. Other applications may include signal source

identification. This is particularly applicable to wireless communications where different services follow well known modulation standards.

There is another usage for both urban and military applications and recently has attracted many attention that is making possible to build Intelligent receivers which can recognize the modulation type without having any prior information from the transmitting signal. Thus intelligent transmitters-receivers appears that can select the most appropriate modulation type to transmit the information due to the environmental condition and communicative channel, and also the receiver can recognize the changes of the modulation types immediately. Therefore, in the subject of the communication, transparency is developed due to the modulation type [1, 2, and 3].

Modulation is the process of varying a periodic waveform, i.e. a tone, in order to use that signal to convey a message. The most fundamental digital modulation techniques are: Amplitude Shift Keying (ASK), Frequency Shift Keying (FSK), Phase Shift Keying (PSK) and Quadrature - Amplitude Modulation (QAM). The QAM modulation is more useful and efficient than the others and is almost applicable for all the progressive modems.

Modulation recognition is an intermediate step on the path to full message recovery. As such, it lies somewhere between low level energy detection and a full fledged demodulation. Therefore, correct recovery of the message per se is not an objective, or even a requirement [4, 5]. The existing methods for modulation classification span four main approaches. Statistical pattern recognition, decision theoretic (Maximum Likelihood), M-th law non-linearity and filtering and ad hoc [6, 7].

Early on it was recognized that modulation classification is, first and foremost, a classification problem well suited to pattern recognition algorithms. A successful statistical classification requires the right set of features extracted from the unknown signal. There have been many attempts to extract such optimal feature. Histograms derived from functions like amplitude, instantaneous phase, frequency or combinations of the above have been used as feature vectors for classification, Jondral [8], Dominguez et al. [9], Liedtke [10]. Also of interest is the work of Aisbett [11] which considers cases with very poor SNR.

The current state of the art in modulation classification is the decision theoretic approach using appropriate likelihood functional or approximations thereof. Polydoros and Kim [12] derive a quasi-log-likelihood functional for classification between BPSK and QPSK modulations. In a later publication, Huang and Polydoros [13] introduce a more general likelihood functional to classify among arbitrary MPSK signals. They point out that the S-classifier of Liedtke, based on an ad hoc phase-difference histogram, can be realized as a noncoherent, synchronous version of their *qLLR*. Statistical Moment-Based Classifier (SMBC) of Solimon and Hsue [14] are also identified as special coherent version of *qLLR*. Wei and Mendel [15] formulate another likelihood-based approach to modulation classification that is not limited to any particular modulation class. Their approach is the closest to a constellation-based modulation classification advocated here although they have not made it the central thesis of their work. Carrier phase and clock recovery issues are also not addressed. Chugg et al [16] use an approximation of log-ALF to handle more than two modulations and apply it to classification between OQPSK/BPSK/QPSK. Lin and Kuo [17] propose a sequential probability ratio test in the context of hypothesis testing to classify among several QAM signals. Their approach is novel in the sense that new data continuously updates the evidence.

There have been other approaches to modulation classification. A method has been proposed by Ta [18] which uses the energy vectors derived from wavelet packet decomposition as feature vectors to distinguish between ASK, PSK and FSK modulation types.

Past work on modulation recognition has primarily used signal properties in time and/or frequency domain to identify the underlying modulation. One of the typical analysis methods for the modulated signal is the extraction of In-Phase (I) and Quad-Phase (Q) components.

According to these components, we can see the signal as a vector in the $I-Q$ plane which is referred to as the constellation diagram. With the use of modulated signal constellation, modulation classification can be investigated as pattern recognition problem and well known pattern recognition algorithms can be used.

2. SIGNAL TRAJECTORY AND CONSTELLATION

One of the best methods for classification of signal modulation is the use of signal trajectory and its constellation. Since each type of modulations has a unique constellation and signal trajectory recognition of modulation could be performed accurately.

This approach to the analysis of modulated signals is based on the extraction of the *in-phase* (I) and *quadrature* (Q) components of the signal, which are obtained through a suitable demodulator. This allows seeing the modulating signal as a vector in the $I-Q$ plane, whose measured trajectory is presented in a two-dimensional diagram. The two most common diagram types are:

Constellation: presents the values obtained by sampling the (I) and (Q) components at the time instants given by the receiver clock. A constellation diagram thus presents the actual received symbol values (Fig. 1.a);

Vector diagram: presents in the $I-Q$ plane the whole trajectory of the vector associated with the demodulated signal. To obtain a vector diagram the (I) and (Q) components must be sampled at a higher rate than the receiver clock rate (Fig. 1 .b).

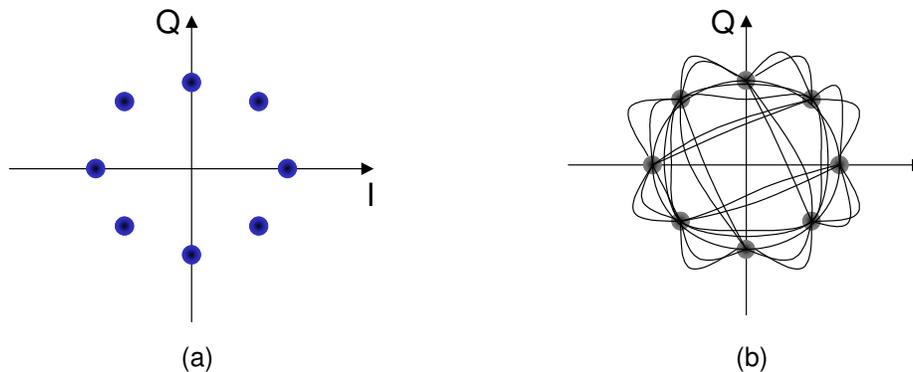


FIGURE 1: $I-Q$ diagrams: a) constellation; b) vector diagram.

From a measurement point of view, the main difference between the two diagrams lies in the different way of sampling the signal. To obtain a constellation diagram, the receiver clock must be available and determines the sampling instants. This may be provided by the system under test as an external clock input, or may be recovered by the measuring instrument from the analysed signal itself. In this way, by obtaining the number of clusters created in $I-Q$ plane, levels and type of modulation could be identified.

To the knowledge of author, one work on constellation diagram is reported by [6, 7], which is worked on fuzzy system. In [6, 7], fuzzy c-means clustering is used for initial processing but for final decision, it used a kind of template matching which uses a maximum likelihood approach.

In This paper proposes a Genetic Algorithm based approach to recognize QAM and PSK modulation schemes from their symbols. It classifies the symbols using the Genetic Algorithm and

hierarchical clustering to find the natural clusters which are equal to the modulation levels. The main advantage of this approach is that the decision boundaries can be accurately identified. The simulation results show that the proposed method has a high success rate at the presence of noise and can be easily applied over the single dimensional modulation schemes such as FSK.

3. CLASSIFICATION OF QAM AND PSK MODULATION USING GENETIC ALGORITHM (GA)

Genetic algorithm is a special kind of evolution algorithms that populations of chromosomes which are nominees to solve the problem are finally led to a better solution. The hypothesis beings with a complete random population and continues in generations. In each generation, all the members are evaluated. Several chromosomes are selected from the current generation based on the worthiness and modified to form the new generation and in the next repeat of algorithm, will be the current generation. In every problem to find the genetic algorithm to obtain an answer, we need two elements: first a method to represent an answer in such a way that genetic algorithm can apply that. Second a method that can calculate the proposed answer by using the fitness functions.

Modifiers selection is the most important part of the genetic algorithm. In fact, genetic algorithm searches the answer to find new answers by the genetic modifiers. This process is repeats for every member and then calls for genetic algorithms modifiers such as selection, cross over, reproduction and mutation forms the next generation. Producing of new generation will be continued to get the best solution. Generally, a genetic algorithm has a main five parts:

1. member presentation in genetic algorithm
2. a method of creation a first population
3. evaluation function to determine the fitness rate of each member
4. genetic modifiers which causes to combine the genetic structure of offspring during reproduction
5. numbers related to the genetic algorithm parameters.

As mentioned, constellation diagram, which consists of In-phase and Quad-phase components, can be used for modulation classification. Since the constellation is symmetric with respect to its axes, in order to reduce complexity, we can map all the received symbols into the first quadrant in the constellation diagram. After obtaining number and location of clusters in first quadrant, centroids of clusters could be extended to the whole constellation, symmetrically. The proposed technique has been designed so that it would be capable of recognizing MPSK and MQAM, so the initial number of clusters has been set to 16 in the first quadrant. Therefore, the initial centroids can be defined as a vector of 16 elements in which each element is a point in the first constellation quadrant. In order to reduce processing, calculation is done in the first quadrant, absolute value of signal's $I-Q$ components are calculated and stored in a 2D matrix and used in future processing.

This method proposes a Genetic Algorithm based approach to recognize QAM and PSK modulation schemes from their symbols. It classifies the symbols using the Genetic Algorithm and hierarchical clustering to find the natural clusters which are equal to the modulation levels. The main advantage of this approach is that the decision boundaries can be accurately identified. The simulation results show that the proposed method has a high success rate at the presence of noise and can be easily applied over the single dimensional modulation schemes such as FSK.

4. REGULATION OF GENETIC ALGORITHM PARAMETERS

In this step, the following parameters are regulated as the essential genetic algorithm parameters:

- Max-Gen parameter that determines the maximum time of reproducing and its number is selected 80 in this algorithm.
- Pop-Size parameter that represent the population size and number of chromosomes in members and is considered 300 here.
- P_c parameter that introduces the probability of two chromosomes crosses over and is considered 0.7 here.
- P_m parameter which shows the probability of mutation in genes of a chromosome and here is 0.15.

In this algorithm is tried to select the related points of a chromosome purposely with all page scattering and some random numbers are increased or decreased to the selected pointed of the first chromosome to select other points in the other chromosomes. By this method, we achieved the speed rise to the algorithm convergence.

To put a problem through GA, we should have a representation for solution of the problem. So, in our case, in order to provide a set of chromosomes which each one presents a solution to the problem, we let each chromosome to be a set of 16 centroids (the centers of clusters). In this way, each chromosome consists of an array of 16 pair values which are I and Q components of the centroids. In order to improve the convergence, the scattering of the initial centroids, as initial chromosomes, was chosen similar to ideal constellation, although relatively, with the PSK and QAM constellations.

In the next step, the fitness of each chromosome is evaluated by comparing with signal symbols and then computing the objective function through HCM (hard C-means) and then ascending sort these values. Fitness function is defined as inverse of the objective function. Therefore, a chromosome with the highest fitness value will have the rank one in the population. In this manner, the rank of each chromosome is defined proportionally. Chromosomes with the high fitness will have a higher chance to be present at the next population. In this step, also the cumulative probabilities are computed to be utilized at the selection step. The pseudo code of this step is shown in figure (2).

```

For  $j = 1$  to Pop-Size do
    Compute the objectives  $Z_j$  for  $U_j$ ;
End for
For  $j = 1$  to Pop-Size do
    Compute the fitness evaluation ( $U_j$ );
End for
For  $j = 1$  to Pop-Size do
    Compute the cumulative probabilities ( $q_j$ );
End for

```

FIGURE 2: The pseudo code of fitness evaluation.

Selection operator uses the fitness of chromosomes in the preceding step and selects some chromosomes within the population, to be employed at the next step. Chromosomes with high fitness values will have a higher chance to be selected. Hence, increasing the probability of selection and propagation leads to that a higher number of duplicates and children, which resulted from chromosomes with high fitness, may be existed at the next generation. Selection of chromosomes to product the next generation is performed by rotating the Roulette Wheel for times equal to the number of members of population, so that in each rotation exactly one chromosome is selected to contribute in the production of the next generation. The pseudo code of selection step is shown in figure (3).

```

For  $j = 1$  to Pop-Size do

    Generate a random real number  $r_s$  in the interval of  $[0, 1]$ 

    If  $(q_j - 1 < r_s < q_j)$  then

        Select  $U_j$  ;

    end if

End for

```

FIGURE 3: The pseudo code of selection step.

Then, the crossover operator operates on the chromosomes of the intermediate population and combines those together. This modifier combines the chromosomes with the hope of reproducing a better chromosome of the offspring than the parent. After the two chromosomes were selected to cross over, they can be combined with different method of crossing over. In the present plan, we use the single point crossing over. For this, we selected two chromosomes among the middle population of chromosomes. Then we select a point of the chromosome randomly and exchange all the gens of these two chromosomes after this point. To improve the algorithm efficiency, we select the random number among 3 and 14 and then with a crisscross way we exchange all the gens after that point and reproduce two offspring chromosome from the two parent chromosomes. After that, offspring chromosomes replace for its parents chromosome. The pseudo code of crossover step is shown in figure (4).

```

For  $j = 1$  to Pop-Size / 2 do

    Generate a random real number  $r_c$  in the interval of  $[0, 1]$  ;

    If  $r_c \leq P_c$ 

        Perform the Crossover on randomly selected the  $l^{th}$  and  $m^{th}$  chromosomes;

    end if

End for

```

FIGURE 4: The pseudo code of crossover step.

Then, it is time to apply the mutation operator that randomly varies one or more elements of a chromosome. When a mutation modifier is implemented on a chromosome, mutation will be created in that chromosome. A current method to implement mutation is to change a one or more gens from a chromosome randomly. In other words, this modifier is defined as a change in one or more bits of a vector of answers. Therefore, in the present problem, mutation modifier is done with changes on the elements of one or more rows of matrixes of answers. Finally, after implementation of mutation modifier, the middle population replace for the initial population so that during the next repeat all the processes of evaluation, crossing over, mutation and

replacement are done on the new generation and lead to the next generation. The pseudo code of mutation step is shown in figure (5). Termination condition of the algorithm is satisfied when the objective function value hasn't considerable variation through the recent iterations. After termination, the chromosome (i.e. set of centroids) with the highest fitness within the final population is presented in the output [19].

```

For  $j = 1$  to Pop-Size do
    For  $k = 1$  to  $n$  do
        Generate a random real number  $r_m$  in the interval of  $[0, 1]$  ;
        If ( $r_m \leq P_m$ ) then
            Generate new elements in the  $k^{th}$  row of the  $j^{th}$  Chromosome ;
        End if
    End for
End for

```

FIGURE 5: The pseudo code of mutation step.

5. MODULATION CLASSIFICATION USING TEMPLATE MATCHING

In template matching method by eliminating of the used post processing step in previous methods, the possibility of error marking was decreased and also this method can recognize 256QAM modulation with high accuracy.

The main idea in this method is assessment and investigating of input signals based on relative similarity that exist between different kind of standard QAM modulations with predefined levels. In fact we suppose that the signal modulation kind is according to 4QAM, 16QAM and 256QAM, so at last our purpose is the recognition of modulation between all different kinds.

In this method the standard models of constellation diagram of QAM modulation signals when they are not on the influence of noises and deviation and etc, are the parameters in decision making and choosing the modulation kind. It is done by analyzing the resulted similarity of constellation of input signals with standards constellations and then the modulation that has the greatest similarity would be chosen. For this purpose, the genetic algorithm had been used that the details of used algorithms are given below.

5.1 Definition of Ideal Cluster Centriods

In the beginning for, every kind of QAM modulation family, the ideal centriods would be defined, so after we can compare them with resulted centriods from signals. We define the template forms of 256QAM, 64QAM, 16QAM and 4QAM modulation constellations in $I-Q$ quarter page. For 4QAM modulation, an ideal cluster centriod in quarter page and for 16QAM modulation, 4 ideal cluster centriods and for 64QAM modulation, 16 cluster centriods and for 256QAM, 64 cluster centriods can be defined. All centriods are defined in $I-Q$ quarter page and in $[0, 1]$ interval. So here because we would have the possibility of comparing of centriods of input signals with ideal centriods, the absolute value of receiving samples from input are calculated and then normalized.

5.2 Recognition of QAM Family

The first kind of modulation that is assessed is 256QAM. First, preliminary centriod for using genetic algorithm is defined and then these preliminary centriods are applies in genetic

program. The centroids that are given by genetic program are compared by 256QAM ideal centroids. This comparison is done by calculating of Euclidean distance of centroids.

The given value is compared with defined corresponding threshold for 256QAM and in a case that the given value would be less than threshold, this kind of modulation is introduced as the detection modulation and the program would be end. But if this case is not full filled, the next kind of modulation that is 64QAM would be assessed in a similar way and in a case the requirement for similarity of modulation is full filled, it will be introduced as the input detection modulation, otherwise the assessment is done for the next modulation, 16QAM. If none of the modulation kinds did not full filled, the requirement for similarity at last the 4QAM is supposed as the input signal and would be introduced in the outputs.

So the assessment of different kinds of modulations is started from 256QAM and would be end with 4QAM. The reason is when the correctness of similarity is full filled for 256QAM, this be full filled for lower levels too. Also if the similarity requirement is full filled for 64QAM, it would be right for 16QAM and 4QAM, but the reverse would not be right. It means that if the requirement for similarity for 16QAM is full filled, it would not be full filled for modulations with higher levels (64QAM and 256QAM), so the assessment is standard from high levels of 256QAM and will be end in 4QAM.

From below threshold value for comparing the similarities are used for recognition of different modulations of QAM families in this program. The 290 threshold was used for 256QAM modulation recognition. Threshold is used for differentiate of 64QAM modulation is set to 320 and at last threshold for recognition of 16QAM modulation is set to 350. Figure (6) shows the flowchart of the proposed method for recognition of modulation.

6. PERFORMANCE EVALUATION AND SIMULATION RESULTS

In order to evaluate the performance of the proposed method, simulation has been performed for various SNR values and various types of QAM modulations. Channel model, applied in this work, has been assumed to be an AWGN channel, and it is also assumed that there is no time and/or frequency synchronization error. Simulation results show that this method has an efficient performance and high accuracy for the recognition of modulation. Figures (7), (8) and (9) show the centroids of the clusters which are obtained from Genetic algorithm and ideal constellation points of related modulation for 16-QAM, 64-QAM and 256-QAM, respectively.

The main program finds a template (ideal constellation points) with matches more to the detected centroids. This judgment is done based on the threshold related to each type of modulation. Finally, the detected centroids in $I-Q$ plane and the recognized modulation type and the fitness value are considered as output. Figure (10), (11), (12) and (13) depict the detected centroids and data symbols in the whole constellation diagram, for types of 4-QAM, 16-QAM, 64-QAM and 256-QAM, respectively.

For recognition of these types of modulation with various SNR, different numbers of samples are used which are presented in table (1). Figure (14) presents the accuracy percentage of the modulation recognition versus SNR, for various types. The accuracy percentages have been obtained by executing algorithm enough times and calculating the ratio between correct recognition and total number of execution.

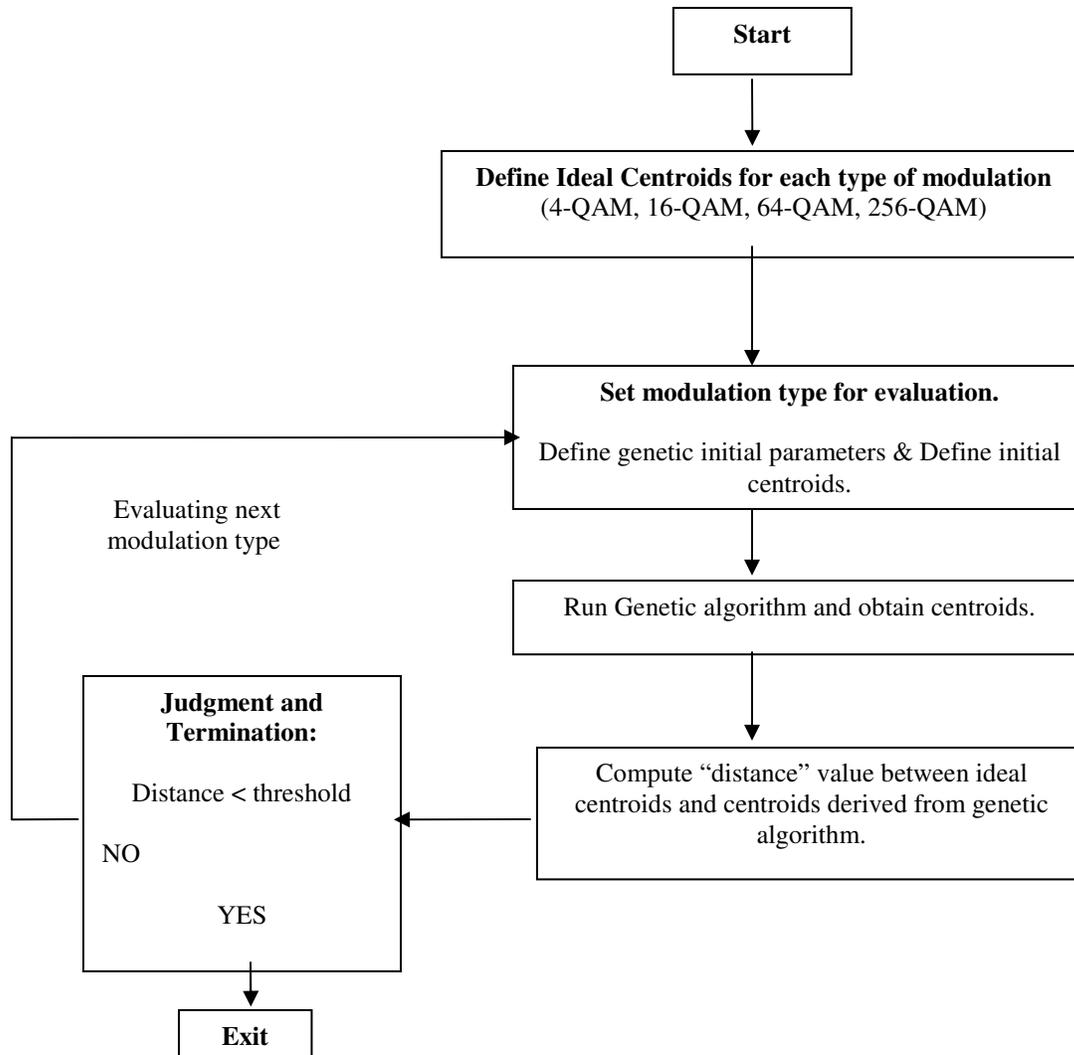


FIGURE 6: The flowchart of propose method.

7. CONCLUSION

In this paper Genetic algorithm and template matching was used to classify different modulation types of QAM, using the constellation diagram of the received signal. The proposed method shows a good performance for recognition even in extremely low SNR condition. Of course, it must be mentioned that the performance could be increased with higher number of data symbols. Another advantage of this method is calculating final centroids of clusters and determining the location of these centroids in constellation diagram.

Using Template matching technique would increase the accuracy of recognition of modulation in low SNR and because of that; we succeed in recognition of 256QAM modulation with SNR equal to 17 with 100% accuracy and acceptable accuracy for lower values. As a result the

capability of proposed method in recognition of 64QAM modulation for SNR equal to 10 and more than that was 100% and for lower values was in acceptable levels. This method is also capable for recognition of 16QAM modulation with SNR equal to 2.5 and values more than that and for lower SNR values was in acceptable accuracy levels. This method can recognize all 4QAM modulations with any signal to noise values with 100% accuracy. At last simultaneously with decreasing of the value of SNR, with increment of the number of input samples, the accuracy of modulation recognition can be increased.

The method that have been used can be expanded and use them for modulation recognition of any PAM signals. These signals have one dimensional constellation while in this research we study the signals with two dimensional constellations which are more complicated. Thus with a little change we can use them for recognition of PAM signals. From these signals the MFSK and MASK modulations can be referred.

With little changes in proposed method it can be used in recognition of modulations which have non standard one dimensional or two dimensional constellations. By rotating the constellation diagram of PAM signals for 45° in $I-Q$ plane, without any change in proposed method, it can recognize modulations.

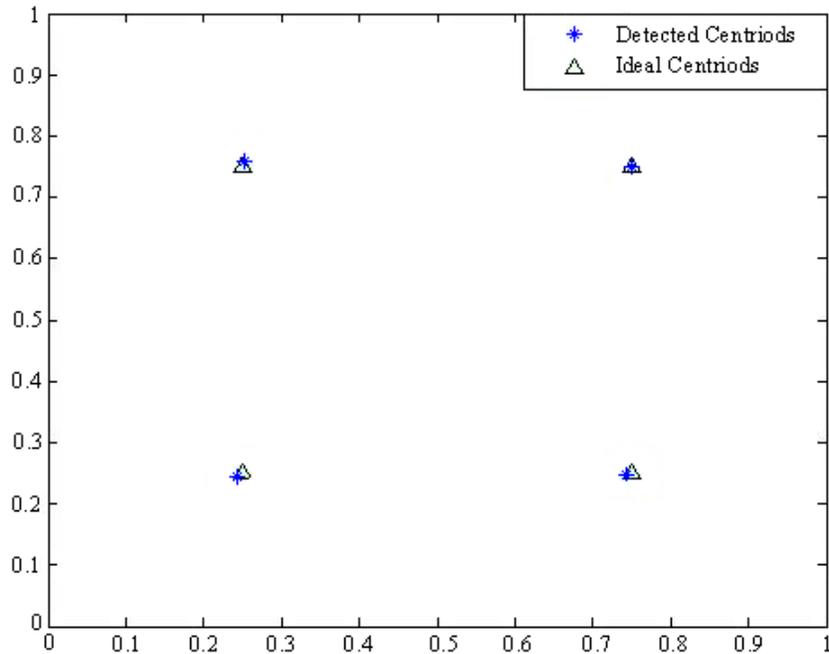


FIGURE 7: Centroids resulted from FCM algorithm in first quadrant for 16-QAM with SNR=5dB, and comparison with the 16-QAM template.

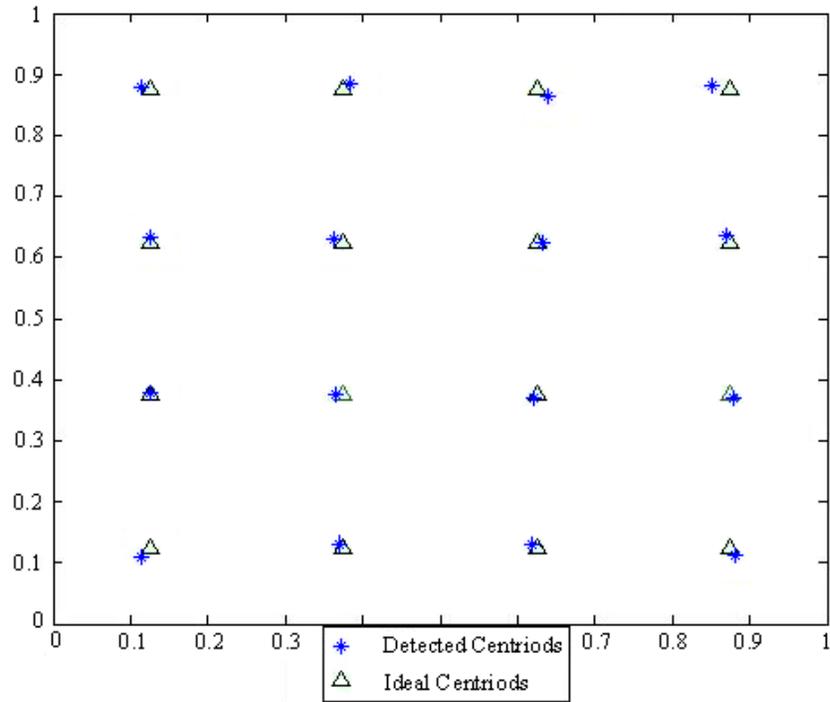


FIGURE 8: Centroids resulted from FCM algorithm in first quadrant for 64-QAM with SNR=12dB, and comparison with 64-QAM template.

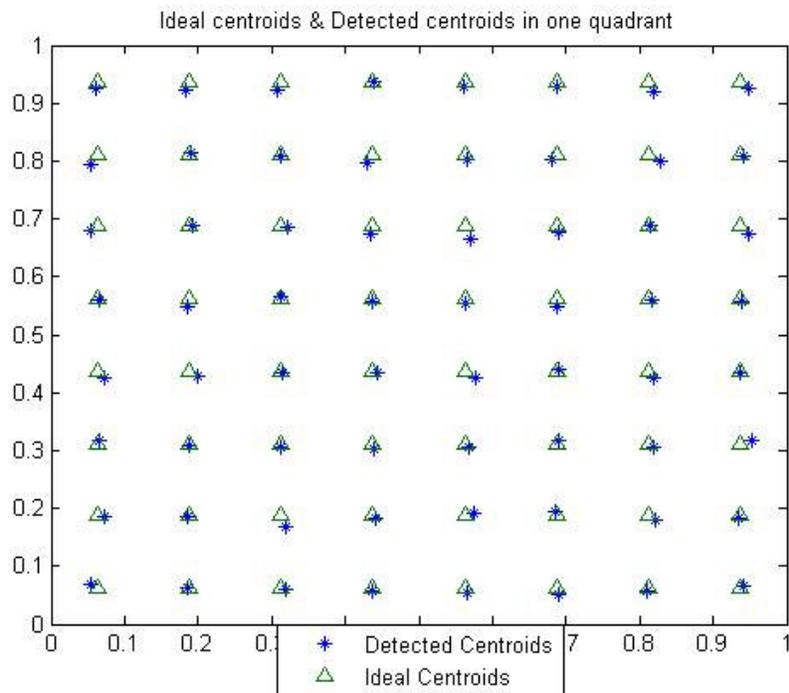


FIGURE 9: Centroids resulted from FCM algorithm in first quadrant for 256-QAM with SNR=23dB, and comparison with 256-QAM template.

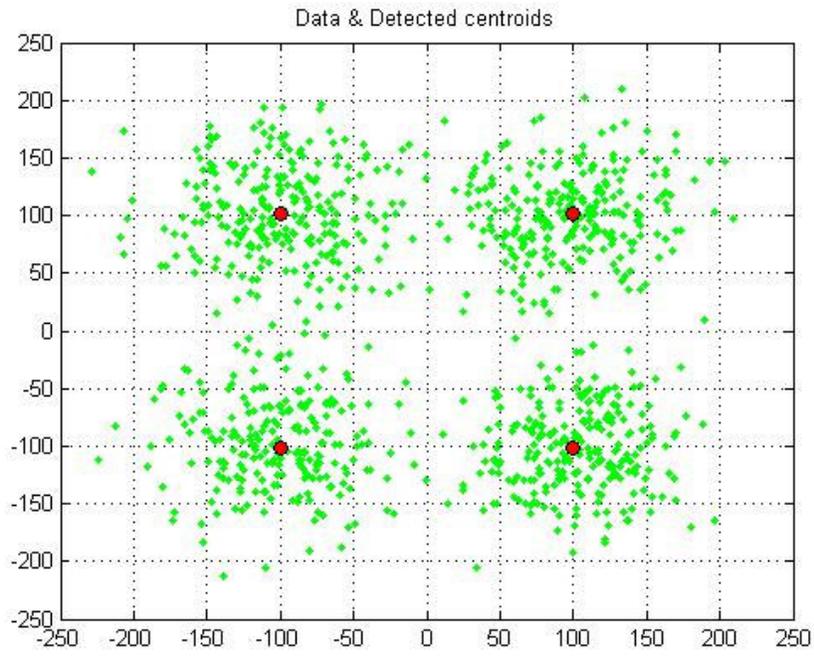


FIGURE 10: Data symbols and resulted centroids after recognition of 4-QAM.

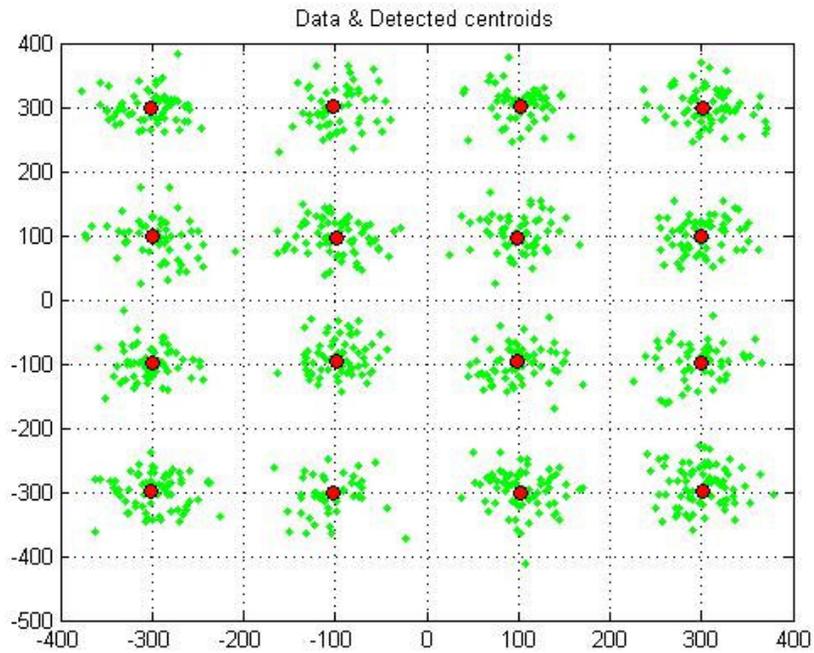


FIGURE 11: Data symbols and resulted centroids after recognition of 16-QAM.

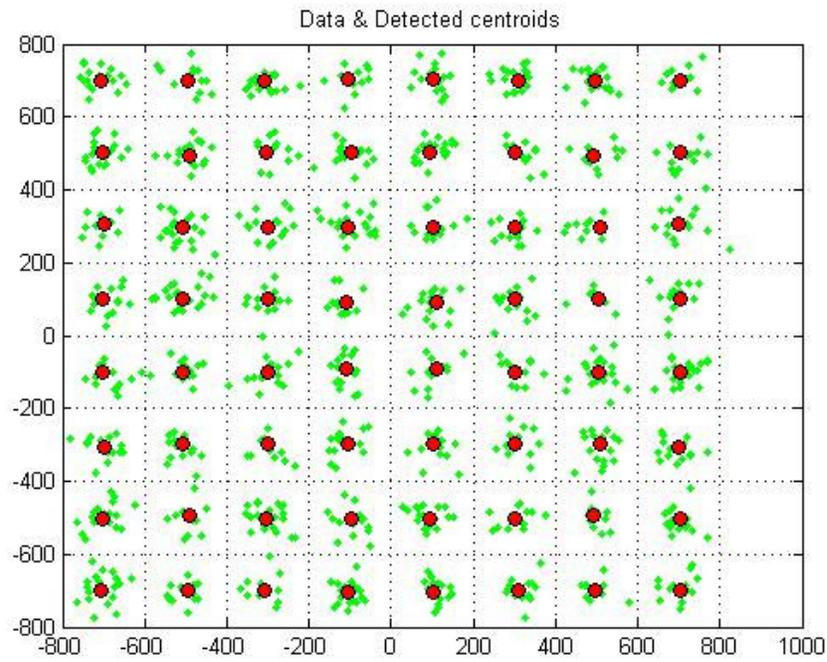


FIGURE 12: Data symbols and resulted centroids after recognition of 64-QAM.

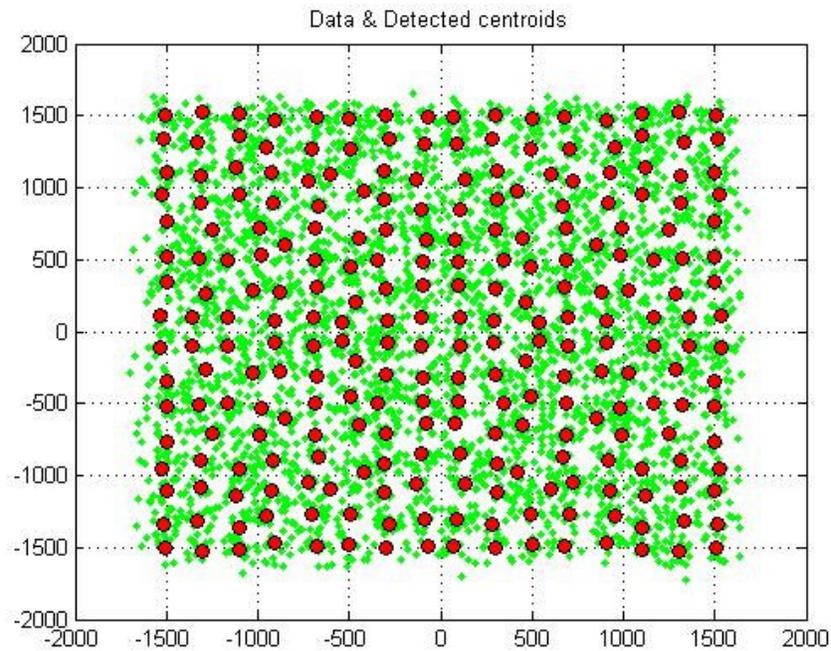


FIGURE 13: Data symbols and resulted centroids after recognition of 256-QAM.

256-QAM	SNR	30dB	25dB	20dB	19dB	18dB	17dB
	Number of Samples	1000	1500	3000	4000	9000	22000
64-QAM	SNR	25dB	20dB	17dB	15dB	12dB	10dB
	Number of Samples	1000	1000	1000	1000	3000	10000
16-QAM	SNR	15dB	10dB	8dB	5dB	3dB	2.5dB
	Number of Samples	1000	1000	1000	1000	3500	10000
4-QAM	SNR	10dB	5dB	3dB	1dB	0dB	-2dB
	Number of Samples	1000	1000	1000	1000	1000	1000

TABLE 1: Number of samples for modulation recognition with various SNR.

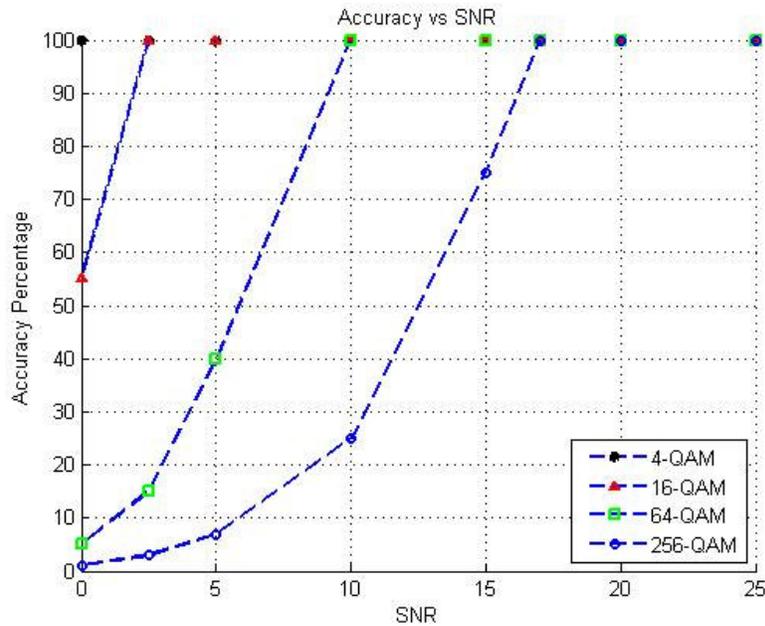


FIGURE 14: Accuracy percentage of recognition versus SNR.

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