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## IN-AIS-MACA: Integrated Artificial Immune System based Multiple Attractor Cellular Automata for Human Protein Coding and Promoter Prediction of 252bp Length DNA Sequence

By Pokkuluri Kiran Sree, Inampudi Ramesh Babu & SSSN Usha Devi N

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Abstract - Gene prediction involves protein coding and promoter predictions. There is a need of integrated algorithms which can predict both these regions at a faster rate. Till date, we have individual algorithms for addressing these problems. We have developed a novel classifier IN-AIS-MACA, which can predict both these regions in genomic DNA sequences of length 252bp with 93.5% accuracy and total prediction time of 1031ms. This classifier will certainly create intuition to develop more classifiers like this.

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## IN-AIS-MACA: Integrated Artificial Immune System based Multiple Attractor Cellular Automata for Human Protein Coding and Promoter Prediction of 252bp Length DNA Sequence

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#### I. Introduction

NA contains lots of information. For DNA sequence to transcript and form RNA which copies the required information, we need a promoter. So promoter plays a vital role in DNA transcription. It is defined as "the sequence in the region of the upstream of the transcriptional start site (TSS)". Identifying a new promoter in a DNA sequence will lead to find a new protein. If we identify the promoter region we can extract information regarding gene expression patterns, cell specificity and development. Promoters will regulate a gene expression. Some of the genetic diseases which are associated with variations in promoters are asthma, beta thalassemia and rubinsteintaybi syndrome. Promoter sequence can be used to control the speed of translation from DNA into protein. It is also used in genetically modified foods.

In vertebrates only five percentage of the gene is made up of exons. Genes mostly will have seven to eight exons with 145 bp length at an average. Introns have 3365 bp length at an average. Promoter comprises a small percentage of entire genome. The features of promoters are different from other functional regions like exons, introns and 3'UTRs. These facts make protein coding and promoter region predictions as very difficult tasks.

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#### II. LITERATURE REVIEW

Steven Salzberg [7] has used a decision tree algorithm for locating protein coding region. This algorithm is adoptable and can handle DNA sequences of length 54,108 and 162. P.Maji [8] et al. has developed neural network tree classifier for prediction of splice junction and coding regions in genomic DNA. A decision tree named as NNTree (Neural Network Tree) is constructed by dividing the training set with their corresponding labels to recursively generates a tree. Ying Xu [9] et al. has developed an improved system GRAIL II which is a hybrid AI system which can predict the number of exons in a human DNA sequence and also supports gene modeling. This process combines edge signal like accepter, donor, translation start site detection and coding feature analysis.

Eric E Snyder [10] et al. has applied dynamic programming and neural networks for predicting protein coding regions from a genomic DNA. They have developed a program Gene Parser which first scores the DNA sequences based on exon-intron specific measures like local compositional complexity, codon usage, length distribution, 6-tuple frequency and periodic asymmetry. Edward C Uberbacher [11] et al. has proposed a method which combines some set of sensor algorithms and neural network to predict the protein coding regions in eukaryotes. The programs developed will calculate the values of seven sensors that were considered by the authors. The measures are frame bias matrix. Fickett(three periodicity), dinucleotide fractal dimension, coding six tuple word preferences, coding six tuple in frame preferences, commonality and repetitive six tuple word preferences.

J. Pinho [12] et al. has proposed a three state model for protein coding region prediction. Authors have considered three base periodicity property. M.Q. Zhang [13] has used quadratic discriminant analysis method named as MZEF for identifying protein coding regions in genomic human DNA. David J. States [14] at el. proposed a computer program named BLASTC which

uses sequence similarity and codon utilization for predicting the protein coding regions.

Method [8] takes more time to construct a tree for sequences of length 162. The height of the trees is also a major concern for using this algorithm with DNA sequences of more length. Method [9] suffers with less accuracy due to more error rate at classifier nodes. Methods [10], [11], [12] depends more on the statistical information. After this literature survey the concern of a new classifier is to achieve a good classifier accuracy and develop a classifier which can handle DNA sequences of length more than 162 with a fewer nodes. Jia Zeng [15] et al. has proposed a hierarchical promoter prediction system named as SCS where they have used signal, structure and context features .Xiomeng Li [16] et al. has proposed a method PCA-HPR (Principal Component Analysis-Human Promoter Recognition) to predict the promoters and transcription sites (TSS). Sridgar Hannenhalli [17] et al. tried to enhance the accuracy of promoter prediction by combining CpG island feature with information of independent signals which are biologically motivated and these cover most of the knowledge to predict the promoter in human genome.

Shuanhu Wu et al. have proposed a method [18] for enhancing the performance of human promoter region identification by selecting most important features of DNA sequence for each different functional region. Uwe Ohler et al. have proposed a model [19] which integrates physical properties of DNA into a probabilistic eukaryotic promoter prediction system. Goni J Ramon et al. has proposed a system ProStar[20] which uses structural parameters for promoter region identification. Authors only used descriptors derived from physical first principles.

Vladimir B. Bajic [21] et al. has developed new software for identifying promoters in a DNA sequence of vertebrates. This program takes input as DNA sequence and generates a list of predicted TSS (Transcription Stating Site). Michael Q. Zhang [22] has proposed a new program for predicting a core promoter in human gene named as CorePromoter. After the literature survey on promoter prediction, the main goal of proposed classifier is to reduce the false prediction rates and improve specificity and sensitivity values.

#### III. DESIGN OF IN-AIS-MACA

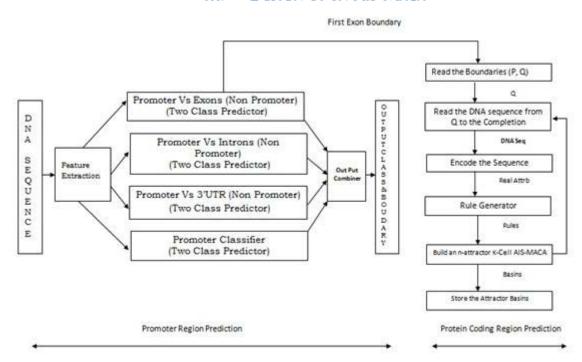


Figure 1: IN-AIS-MACA design

IN-AIS-MACA partial design is shown in Fig: 1. IN-AIS-MACA takes a DNA sequence as input and extracts the features. Initially IN-AIS-MACA checks whether the given sequence belongs to an exon or not. If it belongs to an exon, the exact boundaries with non-promoter class will be displayed. These boundaries will be used to trace the protein coding region starting from that boundary. Since the first exon boundary is already

predicted say (P, Q), this algorithm reads the encoded DNA sequence starting with Q to the end of the string say R. The IN-AIS-MACA tree is built only for a length R-Q for PCR prediction. If the input does not belong to exons then it is checked whether it is an intron or 3'UTR or a promoter. The corresponding class and boundary is displayed.

#### IV. Data Sets and Methods

Human promoter data sets are collected from DBTSS database consist of 30,966 of length 251. We have used 7,741 for constructing an IN-AIS-MACA tree and 7,741 for checking the accuracy of the tree. Rest of the 15,483 promoter sequences are used for testing the proposed classifier.

Human non-promoter data sets are collected from EID and UTRdb databases. We have extracted 75,438 exons from EID database, where 18,859 are used for constructing an IN-AIS-MACA tree and 18,860 data components are used for checking the accuracy of the constructed tree. Rest of 37,719 data components are used for testing the classifier. We have extracted 53,684 introns from EID database, where 13,421 are used for constructing the tree and 13,421 are used for checking the accuracy of the constructed tree, rest of the 26,842 are used for testing the classifier. We have extracted 80,538 3'UTRs from UTR dB. In that 21,134 are used for constructing the tree and 21,135 data components are used for checking the accuracy of the tree. The rest of 40,269 components are used for testing the classifier. IN-AIS-MACA allows 1bp error tolerance.

Data components for identifying the protein coding regions in human are taken from MMCRI database for length 252bp; 2,489 coding sequence examples are extracted for training. This training set is divided into 1229,1230 sets, where 1229 data components are used for building the IN-AIS-MACA tree and 1230 data components are used for testing the accuracy of the tree, 1895 data component are used for testing the coding regions.

20,002 non-coding sequence examples are extracted for training. This training set is divided into 10,000 , 10,002 sets, where 10,000 data components are used for building the IN-AIS-MACA tree and 10,002 data components are used for testing the accuracy of the tree; 15,456 data components are used for testing the non-coding regions.

DNA sequences of lengths 252 are taken from chromosome7, chromosome11 and GenBank. A total of 15,456 are extracted from the above data sets. We have extracted 1,300 examples of RSCS, where 650 examples are used for testing the classifier, 325 examples are used for constructing the tree and 325 examples are used for checking the accuracy of the constructed tree in training. We have extracted 16,456 data components from where 10,200 are used for testing the classifier, 3128 data components are used for constructing the tree and 3218 data components are used for checking the accuracy of the constructed tree in training.

No information regarding the reading frame is used in our study. We are going to predict both regions where nothing is known. Each window should belong to a single class (promoter/non-promoter, coding /non-

coding). IN-AIS-MACA has created 4 best trees for predicting PCR and 8 best trees for predicting PR.

#### V. Learning of In-Ais-Maca

IN-AIS-MACA consists of five p state, 3 neighborhood AIS-MACA classifiers. Four classifiers are used for the predicting promoter regions and one for predicting protein coding regions. A total of 1, 43,158(1, 20,667 for promoters and 22,491 for protein coding regions) components are trained for predicting promoter and protein coding regions. IN-AIS-MACA algorithm will create five different set of trees and thirty attractor basins. This algorithm executes for five times (Exon, Intron, 3'UTR, Promoter, Protein Coding).

#### Algorithm:

Input: DNA Sequence

Output: Attractor Basins

Step 1: Read the DNA sequence in the multiples of

three

Step 2: Encode the sequence in the multiples of three

Step 3: Extract the features

Step 4: Construct a 3-cell, 6-attractor IN-AIS-MACA tree with 2 classes to be predicted.

Step 5: Save all the best IN-AIS-MACA trees. (Use Fitness Function)

Step 6: Store the basins (Be, Bi, Bu, Bp, Bpr).

Step 7: Repeat the steps 1 to 6 till the completion of input or individual attractor basins count is 6.

Step 8: Stop

Where Be represents the exon basins, Bi represents the intron basins, Bu represents the 3'UTR basins, Bp represents the promoter basins and Bpr represents the protein coding region basins.

#### VI. Testing of In-Ais-Maca

The accuracy of protein coding region prediction with IN-AIS-MACA depends on the accuracy of exon prediction. As the promoter prediction module has reported 96.5% accuracy, the protein coding region prediction accuracy gets improved. The main aim of this algorithm is to process the DNA sequence based on the features and distribute it into any one of the basin.

#### Algorithm:

*Input:* DNA Sequence

Output: Class of the sequence

Step 1: Read the DNA sequence in the multiples of three.

Step 2: Encode the sequence in the multiples of three

Step 3: Extract the features

Step 4: Check whether the input belongs to EXON class, if not, go to step 6. If it is found as EXON report the corresponding class and boundary.

Step 5: (a) Read the encoded DNA sequence starting with the upper bound to the end of the string.

- (b) Choose best fitness rule to direct the sequence to the attractor basins of Bpr
- (c) Report the respective class.

Step 6: Check whether the sequence belongs to intron, 3'UTR or promoter.

- 6a) Choose the best fitness rule to direct the sequence to the attractor basins of Bi,Bu,Bp
- 6c) Report the boundaries and respective class.

Step 7: Stop.

#### Output 1:

**DNA Sequence** 

CAATGGACGTGACTGTCGTTTGCCAGATCAGCAGAAGCCGAAAGGAATCCTTTCGGCTTCTGCTGATCTGGCAAAC GACAGTCACGTCCATTGCTGAATAACACTCACTGGAATAATTCACTTGGAATATCCCCGAACTTCATTGAGCCCAATT CCTTCTCAACAAGAATTC

# Sequence Kiran 63jntuh Length = 252 bp

Sequence Kiran_63jntuh,			Human Promoter Prediction
Start	End	Score	Non Promoter Sequence/Exon
3.0	64	0 61	ATGAAGTTCGGGGATATTCCAAGTGAATTATTCC

Sequence Name	Program	Type of Exon	Boundary		Strand
Kiran 63jntuh	IN-AIS-MACA	First	82	189	+
Kiran 63jntuh	IN-AIS-MACA	First	82	207	+
Kiran 63jntuh	IN-AIS-MACA	First	82	222	+
Kiran 63jntuh	IN-AIS-MACA	First	198	207	+
Kiran_63jntuh	IN-AIS-MACA	First	198	214	+
Kiran_63jntuh	IN-AIS-MACA	First	198	222	+
Kiran_63jntuh	IN-AIS-MACA	First	198	226	+
Kiran_63jntuh	IN-AIS-MACA	First	198	232	+
Kiran_63jntuh	IN-AIS-MACA	First	198	207	+
Kiran_63jntuh	IN-AIS-MACA	Internal	53	222	+
Kiran_63jntuh	IN-AIS-MACA	Internal	66	87	+
Kiran_63jntuh	IN-AIS-MACA	Internal	80	199	+
Kiran_63jntuh	IN-AIS-MACA	Internal	80	207	+
Kiran_63jntuh	IN-AIS-MACA	Internal	80	222	+
Kiran_63jntuh	IN-AIS-MACA	Internal	106	132	+
Kiran_63jntuh	IN-AIS-MACA	Internal	106	207	+
Kiran_63jntuh	IN-AIS-MACA	Terminal	106	136	+
Kiran_63jntuh	IN-AIS-MACA	Terminal	106	197	+
Kiran_63jntuh	IN-AIS-MACA	Terminal	111	136	+
Kiran_63jntuh	IN-AIS-MACA	Terminal	111	197	+
Kiran_63jntuh	IN-AIS-MACA	Terminal	167	193	+
Kiran_63jntuh	IN-AIS-MACA	Terminal	167	197	+
Kiran_63jntuh	IN-AIS-MACA	Internal	151	249	_
Kiran_63jntuh	IN-AIS-MACA	Internal	151	249	_
Kiran_63jntuh	IN-AIS-MACA	Internal	130	249	_
Kiran_63jntuh	IN-AIS-MACA	Terminal	194	249	_



The output1 shown below is a DNA sequence of length 252bp. The output of promoter prediction has indicated initial exon at 30 to 64. So the protein coding interface starts its processing from 64 to 251. The next internal and terminal exons are reported in both the strands.

Kiran_63jntuh	IN-AIS-MACA	Terminal	76	249	_
Kiran_63jntuh	IN-AIS-MACA	Terminal	72	249	

## VIII. Comparison of the Performance of In-Ais-Maca

IN-AIS-MACA uses the strength of existing AIS-PRMACA design to predict both PR & PCR regions. The accuracy, Se, Sp and execution time of PR prediction with IN-AIS-MACA is same as of AIS-PRMACA reported in chapter 6. So we report the accuracy, Se and Sp of predicting PCR using this IN-AIS-MACA. The important challenge of IN-AIS-MACA is to reduce the total prediction time (TPT) of both PCR and PR which will be discussed in this section.

The performance of IN-AIS-MACA is measured with Se,Sp and accuracy as shown in table 1. We have extended the DT and NNtree to accommodate 252 length DNA sequences and compared the results with them. IN-AIS-MACA reports a high sensitivity, specificity, accuracy of 0.934, 0.925 and 0.93 respectively. This improved performance, when compared with AIS-MACA prediction for 252bp length DNA sequence is due to the classifier accuracy of AI-PRMACA.

Table 1: IN-AIS-MACA Performance in PCR prediction

Method	Se	Sp	Se+Sp	Accuracy
IN-AIS-MACA	0.934	0.925	1.859	0.93
Decision Tree	0.851	0.879	1.73	0.865
Neural Network	0.876	0.87	1.746	0.873
Tree				

If the accuracy of AIS-PRMACA to predict the first exon is more, then the accuracy of predicting the PCR with IN-AIS-MACA is more. The accuracy of AIS-PRMACA prediction of exon is 94.5%, so there is a considerable improvement of PCR prediction with IN-AIS-MACA particularly in the 252bp length DNA sequences. IN-AIS-MACA maintains good balance

between Se and Sp, Se+Sp ie 1.859. The performance of a decision tree in processing lengths of 252bp is poor due to the height of the tree build for predicting the PCR is more. Decision tree reports an accuracy of 86.5%. NNtree performs better compared with DT reports 87.3% accuracy. Performance of both classifiers suffers when processing a DNA sequence of length more than 162.

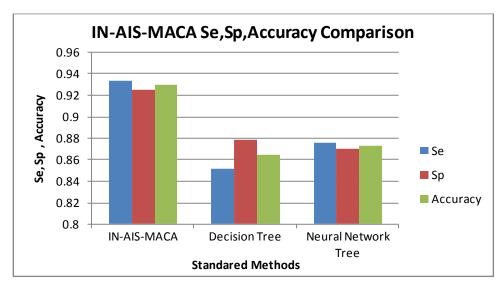


Figure 2: IN-AIS-MACA Performance in PCR prediction VS Standard Methods

### IX. Execution Time Comparisons with In-Ais-Maca

The aim of IN-AIS-MACA is to predict both PCR and PR in human DNA sequence of length 252bp. Since

this is the first algorithm to handle predictions of both regions, we have chosen better algorithms in combination, to report the corresponding execution times of individual predictions and total predictions. In the first combination we have used classifiers AIS-MACA

and AIS-PRMACA which reports the total prediction time of 1827ms. In the second combination we have used classifiers AIS-MACA and SCS which reports the total

prediction time of 1917 ms. In the third combination we have used classifiers AIS-MACA and McPromoter which reports the total prediction time of 1821 ms.

Table 2: IN-AIS-MACA total prediction time comparison

Method	Execution time to predict PCR (ms)	Execution time to predict PR (ms)	Total Prediction Time(TPT) (ms)
IN-AIS-MACA	1031	1031	1031
AIS-MACA & AIS+PRMACA	796	1031	1827
AIS-MACA & SCS	796	1121	1917
AIS-MACA & McPromoter	796	1025	1821
DT & AIS-PRMACA	899	1031	1930
NNTree & AIS-PRMACA	866	1031	1897
Dicodon Usage & AIS- PRMACA	956	1031	1987

In the fourth combination we have used classifiers decision tree and AIS-PRMACA which reports the total prediction time of 1930 ms. In the fifth combination we have used classifiers NNtree and AIS-PRMACA which reports the total prediction time of 1897 ms. In the sixth combination we have used classifiers dicodon usage and AIS-PRMACA which reports the total

prediction time of 1897 ms. The proposed classifier IN-AIS-MACA reports a total prediction time of 1031ms which is best among all the reported classifiers in table 2 and figure 3. Identifying both PCR and PR with a minimum execution time leads to a faster gene prediction.

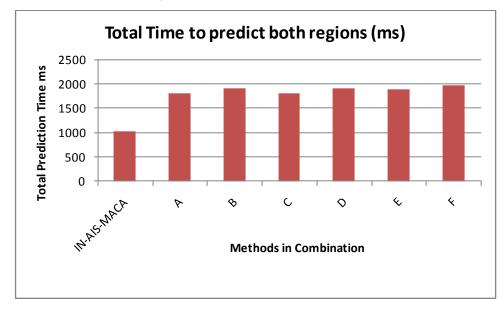


Figure 3: IN-AIS-MACA total execution time Prediction Comparisons

A: AIS-MACA & AIS+PRMACA B: AIS MACA & SGS C: AIS-MACA & McPromoter D: DT & AIS-PRMACA

E: NNTree & AIS-PRMACA F: Dicodon Usage & AIS PRMACA

## X. Parameters Manipulation for Higher Accuracies of In-Ais-Maca

For achieving higher accuracies with IN-AIS-MACA to predict protein coding regions and promoter regions, we have to analyze three important parameters. The first parameter is the number of generations. We have to extract higher accuracies with lesser

generations. Figure 4 shows that the minimum number of generations that required to achieve a higher accuracy for PCR prediction is 75.

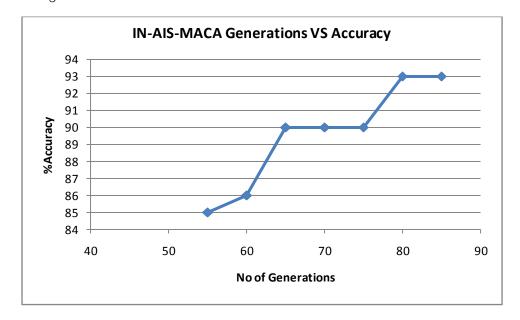


Figure 4: IN-AIS-MACA Accuracy VS No of generations

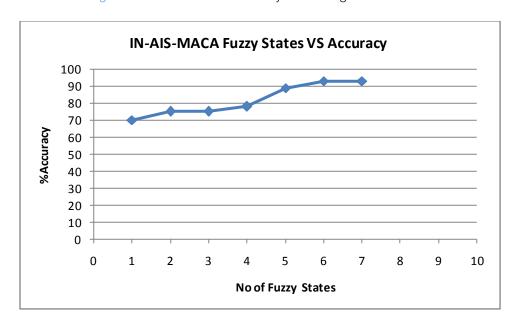


Figure 5: IN-AIS-MACA Accuracy VS Fuzzy States

The second parameter is the number of fuzzy states. Depending on the fuzzy states also the performance of the classifier varies considerably. IN-AIS-MACA attains good accuracy with six fuzzy states as shown in figure 5. The third parameter to be

considered is the clonal factor ( $\beta$ ). The clonal factor plays an important role in attaining a higher accuracy. IN-AIS-MACA attains higher accuracy when clonal factor ( $\beta$ ) is 0.5 as shown in fig 6.

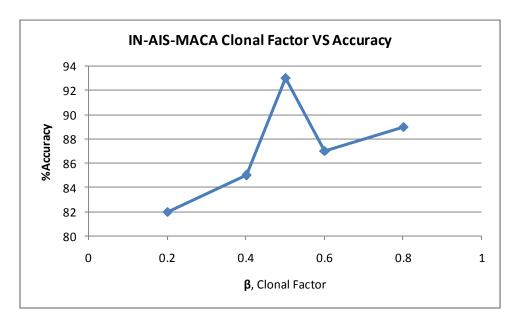


Figure 6: IN-AIS-MACA Accuracy VS Clonal Factor

#### XI. Conclusion

We have successfully developed an integrated classifier which can predict both protein coding and promoter regions in human DNA of length 252bp. IN-AIS-MACA reports a Sensitivity (Se) of 0.934 ,Specificity(Sp) of 0.925 and accuracy of 93% which makes this as the best algorithm for predicting both PCR and PR. The important contribution of this classifier lies in predicting both these regions with an execution time of 1031ms, which will faster the gene perdition rate.

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# Analysis of Distance Measures in Content Based Image Retrieval By Dr. Meenakshi Sharma & Anjali Batra

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Abstract - Content predicated image retrieval (CBIR) provides an efficacious way to probe the images from the databases. The feature extraction and homogeneous attribute measures are the two key parameters for retrieval performance. A homogeneous attribute measure plays a paramount role in image retrieval. This paper compares six different distance metrics such as Euclidean, Manhattan, Canberra, Bray-Curtis, Square chord, Square chi-squared distances to find the best kindred attribute measure for image retrieval. Utilizing pyramid structured wavelet decomposition, energy levels are calculated. These energy levels are compared by calculating distance between query image and database images utilizing above mentioned seven different kindred attribute metrics. A sizably voluminous image database from Brodatz album is utilized for retrieval purport. Experimental results shows the preponderating of Canberra, Bray-Curtis, Square chord, and Square Chi-squared distances over the conventional Euclidean and Manhattan distances.

Keywords: CBIR, distance metrics, euclidean distance, manhattan distance, confusion matrix, mahalanobis distance, cityblock distance, chebychev distance.

GJCST-G Classification: 1.4.10



Strictly as per the compliance and regulations of:



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## Analysis of Distance Measures in Content based Image Retrieval

Dr. Meenakshi Sharma a & Aniali Batra o

Abstract- Content predicated image retrieval (CBIR) provides an efficacious way to probe the images from the databases. The feature extraction and homogeneous attribute measures are the two key parameters for retrieval performance. A homogeneous attribute measure plays a paramount role in image retrieval. This paper compares six different distance metrics such as Euclidean, Manhattan, Canberra, Bray-Curtis, Square chord. Square chi-squared distances to find the best kindred attribute measure for image retrieval. Utilizing pyramid structured wavelet decomposition, energy levels are calculated. These energy levels are compared by calculating distance between query image and database images utilizing above mentioned seven different kindred attribute metrics. A sizably voluminous image database from Brodatz album is utilized for retrieval purport. Experimental results shows the preponderating of Canberra, Bray-Curtis, Square chord, and Square Chi-squared distances over the conventional Euclidean and Manhattan distances.

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#### Introduction

ontent-based image retrieval (CBIR), additionally kenned as query by image content (QBIC) and content-based visual information retrieval (CBVIR) is the application of computer vision techniques to the image retrieval quandary, that is, the quandary of probing for digital images in immensely colossal databases (optically discern this survey for a recent scientific overview of the CBIR field). Content-predicated image retrieval is opposed to traditional conceptpredicated approaches (optically discern Concept predicated image indexing).

"Content-based" designates that the search analyzes the contents of the image rather than the metadata such as keywords, tags, or descriptions associated with the image. The term "content" in this context might refer to colors, shapes, textures, or any other information that can be derived from the image itself. CBIR is desirable because searches that rely pristinely on metadata are dependent on annotation quality and broadness. Having humans manually annotate images by entering keywords or metadata in an astronomically immense database can be time consuming and may not capture the keywords desired to describe the image. The evaluation of the efficacy of

keyword image search is subjective and has not been well-defined. In the same regard, CBIR systems have homogeneous challenges in defining success.

#### Related Literature II.

Due to exponential increase of size of soi-disant multimedia files in recent years because of the substantial increase of affordable recollection storage on one hand and the wide spread of World Wide Web (www) on the other hand, the desideratum for the efficient implement to retrieve the images from the immensely colossal data base becomes crucial. This motivates the extensive research into image retrieval systems. From the historical perspective, the earlier image retrieval systems are rather text-predicated with the thrust from database management community since the images are required to be annotated and indexed accordingly. However with the substantial increase of the size of images as well as size of image database, the task of utilizer-predicated annotation becomes very cumbersome and at some extent subjective and thereby, incomplete as the text often fails to convey the affluent structure of images. In the early 1990s, to surmount these difficulties this motivates the research into what is referred as content based image retrieval (CBIR) where retrieval is predicated on the automating matching of feature of query image with that of image database through some image-image kindred attribute evaluation. Therefore images will be indexed according to their own visual content such as color, texture, shape or any other feature or a coalescence of set of visual features. The advances in this research direction are mainly contributed by the computer vision community.

#### PROPOSED WORK III.

We apply different distance metrics and input a query image based on similarity features of which we can retrieve the output images. These distance measures or metrics have been illustrated as follows:

#### a) Euclidean distance

It is also called the  $L_2$  distance. If u=(x1, y1) and v=(x2, y2) are two points, then the Euclidean Distance between u and v is given by

EU (u, v) = 
$$\sqrt{(x_1-x_2)^2 + (y_1-y_2)^2}$$
 (1)

Instead of two dimensions, if the points have ndimensions, such as a=(x1, x2, ...,xn) and b =(y1,y2,...,yn) then, eq. 1 can be generalized by defining the Euclidean distance between a and

b as EU (a, b) = 
$$\sqrt{(x_1-y_1)^2 + (x_2-y_2)^2 + \dots + (x_n-y_n)^2}$$

#### b) Manhattan distance

It is also called the  $L_1$  distance. If u=(x1, y1) and v=(x2, y2) are two points, then the Manhattan Distance between u and v is given by

$$MH (u, v) = |x1-x2| + |y1-y2|$$
 (2)

Instead of two dimensions, if the points have n-dimensions, such as a=(x1,x2,.....,xn) and b=(y1,y2,....,yn) then, eq. 2 can be generalized by defining the Manhattan distance between a and b as MH(a,b)=|x1-y1|+|x2-y2|+......|xn-yn|=

$$\Sigma$$
 |xi-yi| for i = 1, 2..., n.

The distance between two points in a grid based on a strictly horizontal and/or vertical path (that is, along the grid lines), as opposed to the diagonal or "as the crow flies" distance. The Manhattan distance is the simple sum of the horizontal and vertical components, whereas the diagonal distance might be computed by applying the Pythagorean Theorem.

#### c) Standard Euclidean distance

Standardized Euclidean distance means Euclidean distance is calculated on standardized data. Standardized value = (Original value - mean)/Standard Deviation

$$d = \sqrt{\sum (1/si^2) (xi-yi)^2}$$

Distance measures such as the Euclidean, Manhattan and Standard Euclidean distance have been used to determine the similarity of feature vectors. In this CBIR system Euclidean distance, Standard Euclidean distance and also Manhattan distance is used to commonly to compare the similarity between the images. Distance between two images is used to find the similarities between query image and the images in the database.

#### d) Mahalanobis distance

The Mahalanobis distance is a measure of the distance between a point P and a distribution D, introduced by P. Mahalanobis in 1936. [1] It is a multi-dimensional generalization of the idea of measuring how many standard deviations away P is from the mean of D. This distance is zero if P is at the mean of D, and grows as P moves away from the mean: Along each principal component axis, it measures the number of standard deviations from P to the mean of D. If each of these axes is rescaled to have unit variance, then Mahalanobis distance corresponds to standard Euclidean distance in the transformed space. Mahalanobis distance is thus unit less and scale-invariant, and takes into account the correlations of the data set. The Mahalanobis distance

of an observation  $x=(x_1,x_2,x_3,\ldots,x_N)^T$  from a group of observations with mean  $\mu=(\mu_1,\mu_2,\mu_3,\ldots,\mu_N)^T$  and covariance matrix Sis defined as:

$$D_M(x) = \sqrt{(x-\mu)^T S^{-1}(x-\mu)}.$$

Mahalanobis distance (or "generalized squared inter point distance" for its squared value (3) can also be defined as a dissimilarity measure between two random vectors  $\vec{x}$  and  $\vec{y}$  of the same distribution with the covariance matrix S:

$$d(\vec{x}, \vec{y}) = \sqrt{(\vec{x} - \vec{y})^T S^{-1} (\vec{x} - \vec{y})}.$$

If the covariance matrix is the identity matrix, the Mahalanobis distance reduces to the Euclidean distance. If the covariance matrix is diagonal, then the resulting distance measure is called a normalized Euclidean distance:

$$d(\vec{x}, \vec{y}) = \sqrt{\sum_{i=1}^{N} \frac{(x_i - y_i)^2}{s_i^2}},$$

where  $s_i$  is the standard deviation of the  $x_i$  and  $y_i$  over the sample set.

Mahalanobis distance is preserved under full-rank linear transformations of the space spanned by the data. This means that if the data has a nontrivial null space, Mahalanobis distance can be computed after projecting the data (non-degenerately) down onto any space of the appropriate dimension for the data.

#### e) Chebyshev distance

The Chebyshev distance between two vectors or points p and q, with standard coordinates  $p_i$  and  $q_i$ , respectively, is

$$D_{\text{Chebyshev}}(p,q) := \max_{i} (|p_i - q_i|).$$

This equals the limit of the L<sub>o</sub> metrics:

$$\lim_{k \to \infty} \left( \sum_{i=1}^{n} |p_i - q_i|^k \right)^{1/k},$$

hence it is also known as the L $_{\infty}$  metric. Mathematically, the Chebyshev distance is a metric induced by the supremum norm or uniform norm. It is an example of an injective metric. In two dimensions, i.e. plane geometry, if the points p and q have Cartesian coordinates  $(x_1,y_1)$  and  $(x_2,y_2)$ , their Chebyshev distance is

$$D_{\text{Chess}} = \max(|x_2 - x_1|, |y_2 - y_1|).$$

Under this metric, a circle of radius r, which is the set of points with Chebyshev distance r from a center point, is a square whose sides have the length 2r and are parallel to the coordinate axes. On a chess board, where one is using a discrete Chebyshev distance, rather than a continuous one, the circle of radius r is a square of side lengths 2r, measuring from the centers of squares, and thus each side contains 2r+1 squares; for example, the circle of radius 1 on a chess board is a  $3\times3$  square.

In one dimension, all Lp metrics are equal they are just the absolute value of the difference. The two dimensional Manhattan distance also has circles in the form of squares, with sides of length  $\sqrt{2}r$ , oriented at an angle of t/4 (45°) to the coordinate axes, so the planar Chebyshev distance can be viewed as equivalent by rotation and scaling to the planar Manhattan distance. However, this equivalence between  $L_1$  and  $L_{\infty}$ metrics does not generalize to higher dimensions. A sphere formed using the Chebyshev distance as a metric is a cube with each face perpendicular to one of the coordinate axes, but a sphere formed using Manhattan distance is an octahedron: these are dual polyhedra, but among cubes, only the square (and 1dimensional line segment) are self-dual polytopes. The Chebyshev distance is sometimes used in warehouse logistics, [4] as it effectively measures the time an overhead crane takes to move an object (as the crane can move on the x and y axes at the same time).

On a grid (such as a chessboard), the points at a Chebyshev distance of 1 of a point are the Moore neighborhood of that point.

#### IV. Experiments on Matlab

L1 (numOfReturnedImages, queryImageFeatureVector, dataset)

function L1(numOfReturnedImages, queryImageFeatureVector, dataset)

% input: % numOfReturnedImages: num of images returned by query

% queryImageFeatureVector: query image in the form of a feature vector

% dataset: the whole dataset of images transformed in a matrix of

% features

%

% output:

% plot: plot images returned by query

% extract image fname from queryImage and dataset query\_image\_name = queryImageFeatureVector (:, end);

```
dataset_image_names = dataset (:, end);
queryImageFeatureVector (:, end) = [];
```

```
dataset (:, end) = [];
% compute Manhattan distance
manhattan = zeros(size(dataset, 1), 1);
for k = 1:size(dataset, 1)
%manhattan(k)
                  =
                               abs(dataset(k,
                       sum(
                                                 :)
queryImageFeatureVector));
% ralative manhattan distance
manhattan(k)
                =
                      sum(
                              abs(dataset(k,
queryImageFeatureVector) ./ ( 1 + dataset(k, :)
queryImageFeatureVector ) );
% add image fnames to Manhattan
manhattan = [manhattan dataset image names];
% sort them according to smallest distance
[sortedDist indx] = sortrows(manhattan);
sortedImgs = sortedDist(:, 2);
% clear axes
arrayfun(@cla, findall(0, 'type', 'axes'));
% display query image
str name = int2str(query image name);
querylmage = imread(strcat('images\', str name, '.ipg')
);
subplot(3, 7, 1);
imshow(querylmage, []);
title('Query Image', 'Color', [1 0 0]);
% dispaly images returned by query
for m = 1:numOfReturnedImages
img name = sortedImgs(m);
img name = int2str(img name);
str name = strcat('images\', img name, '.jpg');
returnedImage = imread(str name);
subplot(3, 7, m+1);
imshow(returnedImage, []);
end
```

#### a) Confusion Matrix

Confusion matrix is used to compare the performance of the CBIR system using different distance metrics. To evaluate the overall performance of the CBIR system and compare the different distance metrics for retrieval accuracy, confusion matrix is calculated. A confusion matrix represents the actual classifications compared with the number of correct and incorrect prediction. The confusion matrix is n-by-n matrix, where n is the number of classes from the dataset. Each row represents the number of instances in actual class. Each column represents the number of instances in predicted class. Table 1 shows a confusion matrix for a 3 classes classification model. In this confusion matrix, of the actual 5 A instances, the system predicted that

the 5 instances were A, and of the 5 B instances, it predicted that 1 was A, 3 were B and 1 was C. All correct predictions are located in the diagonal of the table, so the other positions except the diagonal are errors. Accuracy (AC) is the most intuitive assessment from the confusion matrix. It is the correct classifications divided by all classifications. In the confusion matrix, the overall accuracy is calculated as the sum of the diagonal numbers divided by the sum of all the numbers in the matrix. For example, the accuracy of the example in Table 1 is:

$$(5+3+1)/(5+0+0+1+3+1+2+2+1) = 0.6$$

Table 1: Confusion Matrix

Predicted	Δ	R	C
Actual	(	ם	O
А	5	0	0
В	1	3	1
С	2	2	1

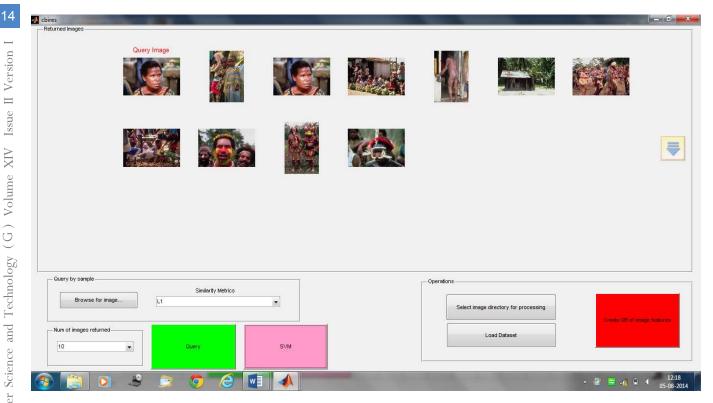


Figure 1: Content Based Image Retrieval based on Query Image and L1 Distance Metric

#### b) Feature Extraction

When the input data to an algorithm is too sizably voluminous to be processed and it is suspected to be notoriously redundant (much data, but not much information) then the input data will be transformed into a reduced representation set of features Transferring the input data into the set of features is called feature extraction. The features provide the characteristics of the input type to the classifier by considering the description of the pertinent properties of the image into a feature space. If the extracted features are meticulously culled, it is expected that they will extract the pertinent information from the input data in order to perform the desired task utilizing this reduced representation in lieu of the full size input. Feature extraction is simplifying the amount of data required to describe an immensely

colossal set of data accurately. When performing analysis of hard data one of the major quandaries stems from the number of data's involved. Analysis with an astronomically immense number of data's generally requires a substantial amount of recollection and computation power or a relegation algorithm which over fit's the training sample and generalizes poorly to incipient samples. Feature extraction can be utilized in the area of image processing which involves utilizing algorithms to detect and isolate sundry desired portions or shapes (features) of a digitized image or video stream. Another paramount feature processing stage is feature cull. However, when immensely colossal and perplexed feature sets are acclimated to train on more diminutive training sets, classifiers can over fit' the learned model, since it is likely that spurious patterns can be found that can accurately relegate the training data, but do not pertain to unseen test data. Feature cull is partially up to the designer to cull a felicitous feature set, but automatic methods can withal be utilized. In culling features, it is consequential to consider whether features will avail in discriminating unseen data, and how perplexed the interactions between the features are liable to be in order for them to be utilized in discrimination.

#### c) GLCM (Gray level Co-occurrence matrix)

A gray level co-occurrence matrix (GLCM) contains information about the positions of pixels having similar gray level values. A co-occurrence matrix is a two-dimensional array, P in which both the rows and the columns represent a set of possible image values. A GLCM Pd [i, i] is defined by first specifying a displacement vector d = (dx, dy) and counting all pairs of pixels separated by d having gray levels i and j. The GLCM is defined by Where nij is the number of occurrences of the pixel values (i, j) lying at distance d in the image. The co-occurrence matrix Pd has dimension  $n \times n$ , where n is the number of gray levels in the image. For example, if d = (1, 1).

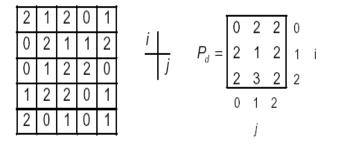


Figure 2: Extraction by GLCM

CBIR performance is analyzed by computing the values of precision and recall. Precision = Number of relevant images retrieved / Total number of images retrieved.

The efficacy of the image retrieval is predicated on the performance of the feature extraction and kindred attribute quantification. In this section we describe the performance metrics which have been adopted not only to evaluate the efficacy of image retrieval but withal to ascertain of the stability of the results. In order to evaluate the retrieval performance of CBIR, three quantifications are utilized: precision, and F-Score.

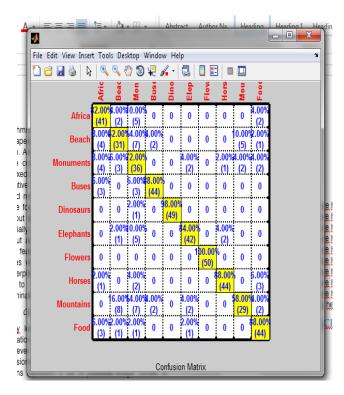


Figure 3: Confusion Matrix

The precision in image retrieval can be defined as: precision is the measurement of the retrieved relevant images to the query of the total retrieved images. The recall in image retrieval can be defined as: Recall is the measurement of the retrieved relevant images to the total database images.

#### Conclusion

Query image is given as input and using different similarity metrics, we can retrieve the required number of output images. The similarity metrics have been used based on distances like Euclidean distance, Manhattan distance. Mahalanobis distance Chebyshev distance. Different features of the image like color, shape and text are used to extract the number of images based on the query image as input.

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## Transforming IT Management

### By Richard Scroggins

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Introduction- Weill and Ross (2008) describe IT governance as a messy process, "IT governance can be messy, but good governance arrangements enable individuals representing an enterprises conflicting goals to reconcile their views to the enterprise's benefit." (p. 1). This is a process that must involve the CIO or highest ranking IT manager. This is one area where the role of the CIO has changed over time, to share a role in governance with others in upper management. On the issue of true IT governance and best practices, the CIO plays the principle role. The CIO must understand the expectations of the management team and also know the limitations of the IT resources and how best to meet the management teams needs within existing or available limitations or capabilities. I see IT governance as a function of structure or procedure that is related to organizational structure. Following a set of best practices would help Alcon. (Dube, Bernier, & Roy, 2009) Best practices is a term that has a wide availability of interpretations. Best practices are usually a set of configuration guidelines from a manufacturer or high level users group. It is also common to find different sets of best practices from different sources. IT governance is a critical factor in establishing the right IT-business alignment and for meeting the needs of high level stakeholders. This has an effect on the performance of an organization and is critical to that organization meeting its mission or goals.

GJCST-G Classification: K.6.3



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## Transforming IT Management

#### Richard Scroggins

#### I. Introduction

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when drafting or contributing to policies and this is an issue that can get very deep. Overall, I thing that the position of CIO is one that is far more improved and respected than it once was, to spite the complications that come with the job. I also believe that this trend will continue in the same direction in the future as the CIO role will take on more and more strategic importance in the company and corporation of tomorrow. I am currently at the IT Manager level, but once I am finished with my doctoral degree, the position of CIO is a reasonable goal for my future. I am looking forward to the challenges and opportunities that I may face if fate and determination lead me in that direction.

Informal or undocumented governance is acceptable in an IT organization for many functions that are not directly related to high level project components or management tasks. Such informal governance can include tasks that the CIO or IT Manager may perform as part of the unspoken portions of the job. One role that I think that it important of any CIO or IT Manager is that of leading and inspiring the IT department. This may providing leadership and direction, maintaining a high level of moral. One way to keep moral high may be by providing newer equipment; most IT employees like to use and play with the latest toys and have good equipment for everyday use. Another way might be in providing occasional team building activities, like a weekly lunch or monthly activities that the department does together. Communications to the group and keeping everyone in the loop to company changes is also important. Treating everyone with respect and letting them know that they are doing a good job and contributing. Also, the CIO has to function as a buffer between upper management and IT employees for many programming or support issues, or corporate policies that effect the IT department. Basically, the CIO is in a position to look out, so to speak, for the people in their department, and their interests. (Weill & Ross, 2009) This also includes managing the expectations of the upper management group. I am not necessarily suggesting that the IT department is exempt from IT policies, but there is room for stretching policies within the IT department and the CIO should understand that.

My company has an established a governance format that applies to all sections and departments of the company. The governance format or archetype that we use is a Business Monarchy backed up by the ISO 9001 standard. This standard is defined by Wikipedia (n.d) as "The ISO 9000 family of standards is related to

quality management systems and designed to help organizations ensure that they meet the needs of customers and other stakeholders while meeting statutory and regulatory requirements related to the product. The standards are published by ISO, the International Organization for Standardization, and available through National standards bodies. ISO 9000 deals with the fundamentals of quality management systems, including the eight management principles on which the family of standards is based. ISO 9001 deals with the requirements that organizations wishing to meet the standard have to fulfill. Third party certification provide independent confirmation organizations meet the requirements of ISO 9001. Over a million organizations worldwide are independently certified, making ISO 9001 one of the most widely used management tools in the world today." (p. 01). Sandford (2006) details the value of the ISO 9000 family, "ISO 9001 describes a basic, effective quality management system (QMS). Compliance to its requirements is the starting point toward achieving excellence in an organization. ISO 9001 compliant QMS can act as the first steps toward excellence." (p. 01). The ISO 9000 family of standards is the world leader in standardization of processes and value chain management. On the reasons behind the widespread use, Wikipedia (n.d) says, "The global adoption of ISO 9001 may be attributable to a number of factors. A number of major purchasers require their suppliers to hold ISO 9001 certification. In addition to several stakeholders' benefits, a number of studies have identified significant financial benefits for organizations certified to ISO 9001." (p.01). A 2011 survey from the British Assessment Bureau showed that 44% of certified clients had won new business since gaining certification. (ISO 9001 proven to help win new business, 2001) This is used to establish competitive advantage in our industry and the structure of our company is molded around this standard. Organizational structure is definitely influenced by the economy and industry trends. My current company used to have a standard departmental structure, but now we refer to everything at that level as a process and groups have been reorganized along process lines. As such, we have process owners and process champions instead of managers and supervisors; however individuals may be part of multiple processes within the organization. We call the IT department "Managing Information Services" for instance. These choices affected our organizational structure and in turn the global organization because we are a worldwide company. Trends set in the western culture, where most businesses are based effect businesses in those countries and then it ripples around the world. These two structure, what I consider the traditional model and then the process model each have their own pros and cons. The traditional model is more common and can

make it easier when dealing with new people, whether

new employees or within a relationship with another company. This is a real concern, because we make a lot of acquisitions and the process based structure has a steep learning curve. The process based model appears more complex to the outsider, but in reality is more streamlined and efficient. Economic challenges are a partial driver for us in adapting to the process based structure initially and the ISO 9001 standard, and they affect virtually all businesses. This is because even in a good economy, every business must seek optimum efficiency and profit. This is even more critical in lean time like the global economy is currently experiencing.

I think that the alignment between business and IT is identified by the performance of the business and the commitment to IT. I also see the position of CIO or IT Manager as the central figure in measuring this. One reason to measure this is to see where the business is headed and if you will be able to respond to future change and be successful in the future. The role of the CIO has changed dramatically over the last few decades. (Chun & Mooney, 2009) This is something that I have seen first hand over the course of my own career, in fact. I my company, the CIO role actually manages the technology and strategic use of IT for two sister companies. I have seen the business or functional groups grow more and more dependent on the IT department and the CIO for not just technology, but also strategic business direction and process design. The modern IT department seems to be seen as a corporate brain trust. I see that businesses rely on IT and the CIO role far more than they used to, and that is fine as long as proper boundaries are maintained. The IT department and IT resources represent a large part of any modern business and are justified by large savings for the business in money and manpower. I know that this was not always the case. A few decades ago the IT department was seen as not needed at all, then as a necessary evil. I worked in company just a decade ago that still had older executives that saw the IT department as just that, a marginally necessary evil. Today, it is a foregone conclusion for any executive or business student that the IT department will play a large role in any company at least of medium size. So this is progress for sure, that allows the modern IT department and CIO to have a place of honor, purpose, and great responsibility. Also, the CIO has to function as a buffer between upper management and IT department employees for many things, like programming or support issues, or corporate policies that effect the IT department. Basically, the CIO is in a position to look out, so to speak, for the people in their department, and their interests. This also includes managing the expectations of the upper management group. Another major aspect of the CIO role that has changed over time due to legal and cultural changes is the contribution to IT and corporate policies. These policies can cover a broad range of topics, from the use of thumb drives and

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## Development of a Portable GSM SMS-Based Patient Monitoring System for Healthcare Applications

By Md. Maruf Hossain Shuvo, Krishna Chandra Roy & Md. Rokibul Hasan Robin

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Abstract- Although health care is a vital problem, in recent years mobile communication has become a widespread part and parcel of everyday life even in the rural areas of developing countries. This paper proposed a model to include the mobile communication for monitoring vital signs of health such as blood pressure, heart rate, body temperature; blood glucose level and sends result as Short Message Service (SMS) for the physician so as to monitor their patients continuously. Cuffless pressure sensing transducer is taken into consideration to measure pressure pulse and then combined with oscillometric method to measure Blood Pressure (BP). Availability of different sensors and measurement techniques to determine heart rate is presented. Conventional glucometry in low cost electronics and body temperature measurement using electronic thermistor is also described here. Sensed parameters are processed and stored into an array in ARM7 processor and sent via GSM SIM300 Modem. This portable vital sensing system is useful to analyze daily health condition; can be used both in home and hospital to prevent Hypertension, Heart Attack and to control Diabetes.

Keywords: health monitoring, GSM sim300, ARM7 microprocessor, cuffless BP measurement, glucometry.

GJCST-G Classification: J.3, C.2.2



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## Development of a Portable GSM SMS-based Patient Monitoring System for Healthcare Applications

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Abstract- Although health care is a vital problem, in recent years mobile communication has become a widespread part and parcel of everyday life even in the rural areas of developing countries. This paper proposed a model to include the mobile communication for monitoring vital signs of health such as blood pressure, heart rate, body temperature; blood alucose level and sends result as Short Message Service (SMS) for the physician so as to monitor their patients continuously. Cuffless pressure sensing transducer is taken into consideration to measure pressure pulse and then combined with oscillometric method to measure Blood Pressure (BP). Availability of different sensors measurement techniques to determine heart rate is presented. Conventional glucometry in low cost electronics and body temperature measurement using electronic thermistor is also described here. Sensed parameters are processed and stored into an array in ARM7 processor and sent via GSM SIM300 Modem. This portable vital sensing system is useful to analyze daily health condition; can be used both in home and hospital to prevent Hypertension, Heart Attack and to control Diabetes. Keywords: health monitoring, GSM sim300, ARM7 microprocessor, cuffless BP measurement, glucometry.

#### I. INTRODUCTION

he use of mobile phones has grown exponentially over the last few years in the developing countries [1]. But healthcare issue remains a vital problem and health monitoring in home is not possible without visiting a physician. The heart, cardiovascular and hypertension diseases are the Top 10 Causes of Death [2]. The blood pressure can be an early evaluation index of cardiovascular disorders. Another most common chronic disease among the elderly is the Diabetes. Regular monitoring of vital signs such as blood pressure, heart rate, body temperature, breathing rate and glucose measurement for diabetic patient is essential as they are primary indicators of an individual's physical well-being. One of the advantages for both patients and physicians is that there are many devices available in the market today that allow patients to monitor their own health on a regular basis from the comfort of their home.

A home medical care system to monitor vital signs consisting of a computer and requires internet

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connection [3]. This system can provide a number of healthcare services for those living in remote areas. Real time health monitoring for ICU patients has also been designed [4]. This system is mainly based on continuous monitoring aspect of ICU patients which enables the doctors to monitor patient's parameters (temp, heartbeat, ECG) in real time using http protocol. Wireless blood pressure measuring system with a Zigbee wireless transmission module and a PC based management unit requires complex graphic user interface and database [5]. These systems are costly and computer based, also not easily portable and uses internet for data transfer; which is not available in rural areas and requires expert to operate. So the objectives of this paper is to design a model of a portable health monitoring system that investigates users blood pressure, heart rate, body temperature an blood glucose level; which is low cost, consume low power, easy to operate and transfer data using SMS of mobile phone communication.

#### II. PROPOSED SYSTEM

The proposed system consists of several blocks that perform the sensing of different health parameters. These measured data received by a 32 bit processor ARM7; where different signal conditioning and processing task performed. The complete system block is shown in Figure.1.

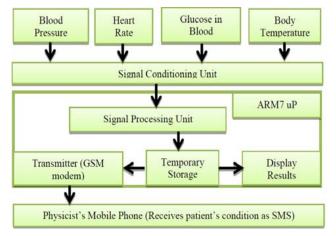


Figure 1: Complete block diagram of the proposed system

Using the built-in ADC of ARM7 microprocessor analog results are converted and displayed using an appropriate display and also sent to the GSM modem through which an SMS is sent to the previously entered physician's mobile phone.

#### III. HARDWARE DESIGN

#### a) Blood Pressure Measurement

Traditionally air cuff is used to measure blood pressure. But recently certain technology has been developed to measure the blood pressure accurately and automatically without cuff. Cuffless BP measurement techniques based on pulse transit time (PTT) and wavelet transform have been studied [6]. PTT refers to the duration for a pressure pulse to travel between two measuring sites in the arterial system. In order to predict Blood Pressure (BP), these techniques have to measure multi-points of the body and therefore patients may feel uncomfortable. Also, they need both the electrocardiogram (ECG) photoplethysmography (PPG) and introduce problems in accuracy. Applied pressure (APm) which has the maximum pulse pressure, was proposed as an alternative to PTT for predicting BP, especially mean arterial pressure (MAP) without cuff. To make the model user friendly and easily portable this model takes one such method developed using silicon rubber constructed over the pressure transducer (MPS-3117, Metrodyne, Taiwan) [7].

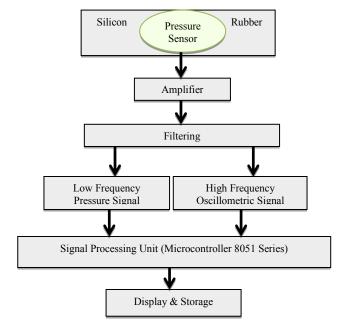


Figure 2: Cuffless Blood Pressure Measuring System

The cuffless pressure sensing module was constructed by enclosing a blood pressure transducer into a silicon rubber doom. As the silicon rubber is airtight and elastic, the pressure signal can conducted into the pressure transducer with little distortion. The

signal obtained from the pressure sensor is amplified and filtered by the signal conditioning circuits. Fig.2 presents the schematic diagram of the cuffless blood pressure measuring system. The signal conditioning hardware separates the pressure signal into two components, the low frequency pressure signal and the high frequency oscillometric signal, before passing them to the signal processing unit. In signal processing unit after the essential digital low pass filtering, the digital signal unit detects the maxima and minima in each and every heart beats, from the oscillometric signal, in order to determine the magnitude of pulse pressure. The corresponding pressure readings are collected and sorted. At the same time the pulse pressures are rearranged according to their pressure reading values. Out of the rearranged pressure waveform (oscillometric waveform), systolic and diastolic pressures are deducted through a mathematical algorithm which is firm dependent. The mathematical algorithm consists roughly of two parts: a preprocessing part to smooth the signal and an optimization part to compute the systolic and diastolic pressures [8]. During the measurement, the user holds the cuffless sensing module in one hand and place the silicon doom on top of the radial artery on the other hand [7]. To maintain the applied pressure onto the radial artery increasing as linear as possible is necessary; which is one of the disadvantages of this system. For slowly applied pressure, the applied pressure did not reach the systolic pressure and the determination of systolic pressure was not possible. On the other hand, when the pressure was applied too fast, the number of heart cycle in the measurement period was inadequate. Although this process is not accurate but this eliminates the use of cuff in which a trained physicist would needed to measure. Some advance signal processing technique may eliminate the inaccuracy. To obtain improved blood pressure estimates [9] the breathing signal is extracted from the oscillometric (OMW) signal and validated. When the OMW is strongly influenced by the breathing signal, a homomorphic filter is applied. Then an adaptive scheme is used to suppress the effects of the breathing signal and the output of this signal is used to obtain the blood pressure estimates.

#### b) Heart Rate Monitoring

Heart attack has become the number one killer in many countries. However, if help is given within 10 minutes of an attack occurring, there is a chance that heart attack will not cause death [10]. In detecting a heart attack, one of the early symptoms is irregular heartbeat. The heart rate or pulse rate is the number of heart cycles that occur every minute [11].

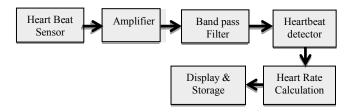


Figure 3: Generalized block diagram for heart rate monitoring

A heart beat monitor has to take readings of the systole and the diastole which occur every 0.30 and 0.55 seconds [12], respectively in order to determine a heartbeat pattern. A sensor that can [13] detect the small displacements associated with the arterial pulse can be used in this application. A piezoelectric sensor pressed against the wrist over the radial artery will detect the arterial pulse or a strain gauge in a mechanical structure that would convert the pulse to a varying strain in the sensor can be used here. A tissue that has a high capillary density will have a significant change in volume over the cardiac cycle: its volume will be greater during systole and less during diastole. Therefore, any sensor that can detect change in volume in biologic tissue could be used to detect the peripheral pulse. Now a signal containing information about the peripheral pulse or heartbeat is detected, the next step is to recognize each heartbeat and to determine the heart rate. This is done by the signal processing block of the instrument shown in Fig.3. The first step of the signal processing is to amplify the signal to a level where it can be processed. The signal is then filtered by a band pass filter that helps to minimize noise and interference that could lead to errors in heartbeat detection. After the heartbeat detector, the next step in the signal processing is to determine heart rate, counting the detected beats and display and/or store the results. Since physician measures heart rate in beats per minute, the interval between beats is often converted to heart rate using the formula,

Heart rate in beats per minute  $=\frac{60,000}{\text{beat interval in miliseconds}}$ 

Average heart rate can be displayed as an analog or digital quantity which has its corresponding advantage and disadvantages.

#### c) Blood Glucose Level Measurement

Diabetes mellitus is a common health problem throughout the world. It prevents the body from producing enough insulin (hormone produced in the pancreas). According to the World Health Organization statics, the global prevalence of diabetes mellitus is approximately 155 million people and expected to increase to 300 million[14] in the year 2025. Glucometry is a technique that obtains the value of glucose concentration in peripheral or central blood to determine

metabolic disorders such as diabetes mellitus, denutrition, and other consequences like hyperosmolar coma, malabsorption syndrome, and mostcritical hypoglycemia. A glucometer and proper pharmaceutical treatment is fundamental for glycemic control of diabetic patients [14].

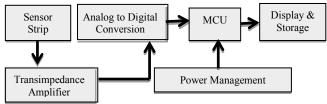


Figure 4: Connection diagram of glucometer

To measure the glucose in the blood firstly the glucose concentration is converted into a voltage or current signal, this is possible with special sensor strips for amperometry. The sensor uses a platinum and silver electrode to form part of an electric circuit where hydrogen peroxide is electrolyzed.

Glucose+Oxygen→Gluconoic Acid+Hydrogen PerOxide

The hydrogen peroxide is produced as a result of the oxidation of glucose on a glucose oxide membrane. The current through the circuit provides a measurement of the concentration of hydrogen peroxide, giving the glucose concentration. Current produced must be changed to voltage for processing by the microcontroller (MCU) in Fig.4. This action is performed by the transimpedance amplifier. Finally, the MCU detects and processes this signal with the ADC module and displays the glucose concentration in blood.

#### d) Body Temperature Measurement

Body temperature is one of the vital signs that are the indicators of human being's overall physiological states [15]. Human body temperature varies within a narrow range of values. Variation of temperature depends on many things, including level of activity, time of day, and psychological factors. One of the most accurate types of body temperature measurement incorporates the measurement from ear [11]. As the temperature sensor a non-linear thermistor with tolerance of  $\pm 0.2^{\circ}\text{C}$  can measure temperatures ranging from 0°C to 50°C and has a fast response time and low power dissipation, which makes it ideal for such medical application. Thermistor based body temperature measurement depicts in Fig.5.

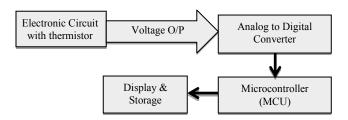


Figure 5 : Connection diagram of thermistor based body temperature sensor

The output voltage can range from +2.5 V to -2.5 V. Change in temperature causes the thermistor's resistance to change accordingly. The relationship between this thermistor's resistance and temperature is non-linear. When the thermistor's resistance changes due to change in temperature, the output voltage will change. Wheatstone bridge can be used that accurately measures small changes in resistances and produces a voltage output. This voltage output is sent through an ADC into the microcontroller. Inside the microcontroller, there is a table stored in EEPROM that has temperature values corresponding to voltage values. From this

lookup table, the body temperature in degrees Celsius is determined.

# IV. Communication between GSM Modem & Mobile Phone

## a) ARM7 Microprocessor

The ARM7TDMI-S is a general purpose 32-bit Reduced Instruction Set (RISC) microprocessor, offers high performance and very low power consumption [4]. The programming of ARM7 can be done using various programming software like Keil uVision4.

## b) GSM Modem

A GSM modem is a specialized type of modem, which accepts a SIM card, and operates like a mobile phone; could also be a standard GSM mobile phone with the appropriate cable and software driver to connect to a serial port or USB port on computer. Any phone that supports the "extended AT command set" for sending/receiving SMS messages can be supported by the SMS/MMS Gateway.

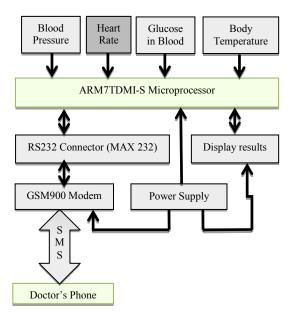


Figure 7: Implementation of the complete system of patient monitoring system

This model proposed using SIMCOM SIM300 GSM module [1]. SIM 300 Modem [4] is built with tri Band GSM/GPRS engine, works on 900/ 1800/ 1900 MHz Frequency band can be set by AT commands. The Modem has RS232 interface which allows connecting microcontroller with MAX232. The MAX232 converter converts from RS232 voltage levels to TTL voltage levels and vice versa [1]. RS-232 connector circuit [4] is a serial port connector used to send the sensed parameters from patient to the modem, which then transmits all the parameters to the mobile phone of the physicist via SMS. To communicate and send results

from GSM modem to desired mobile phone, Fig.7 presents necessary steps. Modem having internal TCP/IP stack suitable for SMS, Voice as well as DATA transfer application in M2M interface.

### c) Algorithm for Coding

Programming the ARM7 processor to implement the proposed model of patient monitor system needs the steps for as shown in Fig.8. The ARM7 microprocessor was chosen because of its faster speed. When the overall system is accumulated in a single chip such RISC microprocessor is necessary. The

coding was done using C programming language and then converted to hex and loaded into microprocessor.

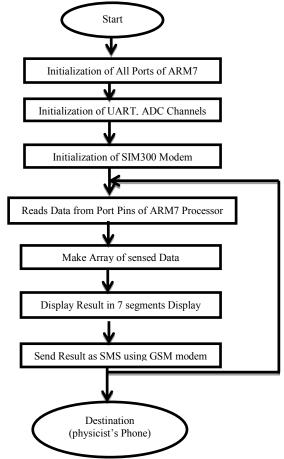


Figure 8: Algorithm for coding

#### Implementation & Future V. **IMPROVEMENTS**

This model will further modified to include Global Positioning System (GPS) tracking to make it more appropriate for hospital application. Sometimes age-old patient may fall in lift or washroom and serious hamper may occur. Incorporating GPS system the position of the patient will be monitored continuously and send via SMS. As internet facilities growing day by day online monitoring system will also tried to include. This will enable to send the observed data from the server computer to the monitoring computer via HTTP protocol which ameliorates the worldwide prescribtion for the patient. The measurement technique will also include some major signs like oxygen saturation, water level of saline bottle, pulse oximetry etc. so that this model can be used in both home healthcare and in hospital for general and ICU patient monitoring. Another modification will include visualizing the patient's condition using a webcam. In this model these facilities are avoided because of cost and to make it widespread applicable.

#### Conclusion VI.

This model of patient monitoring system includes several subsystems which are reliable, cost effective, and accurate, user friendly and includes latest improvements. Using the system observing the data received experts can easily prescribe drug for that situation of patient via SMS. So implementation of these systems will be a great advancement in biomedical engineering and will provide healthcare facilities for the deprived mass people as well as for everyone.

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Result	Well organized, Clear and specific, Correct units with precision, correct data, well structuring of paragraph, no grammar and spelling mistake	Complete and embarrassed text, difficult to comprehend	Irregular format with wrong facts and figures
Discussion	Well organized, meaningful specification, sound conclusion, logical and concise explanation, highly structured paragraph reference cited	Wordy, unclear conclusion, spurious	Conclusion is not cited, unorganized, difficult to comprehend
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