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Highlights

Generalized Invexity

Verification of Bangla Sentence

Discovering Thoughts, Inventing Future

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Contents of the Volume

i. Copyright Notice
ii. Editorial Board Members
iii. Chief Author and Dean
iv. Table of Contents
v. From the Chief Editor's Desk
vi. Research and Review Papers

1. Verification of Bangla Sentence Structure using N-Gram. *1-5*
2. Distributed Bioinformatics Computing System for DNA Sequence Analysis. *7-12*
3. A Review on Non-Linear Programming and Generalized Invexity. *13-15*

vii. Auxiliary Memberships
viii. Process of Submission of Research Paper
ix. Preferred Author Guidelines
x. Index

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Verification of Bangla Sentence Structure using N-Gram

By Nur Hossain Khan, Md. Farukuzzaman Khan, Md. Mojahidul Islam,
Md. Habibur Rahman & Bappa Sarker
Islamic University, Bangladesh

Abstract- Statistical N-gram language modeling is used in many domains like spelling and syntactic verification, speech recognition, machine translation, character recognition and like others. This paper describes a system for sentence structure verification based on Ngram modeling of Bangla. An experimental corpus containing one million word tokens was used to train the system. The corpus was a part of the BdNC01 corpus, created in the SIPL lab. of Islamic university. Collecting several sample text from different newspapers, the system was tested by 1000 correct and another 1000 incorrect sentences. The system has successfully identified the structural validity of test sentences at a rate of 93%. This paper also describes the limitations of our system with possible solutions.

Keywords: *N-gram, sentence structure, corpus, witten-bell smoothing, word error.*

GJCST-A Classification: *D.3.2*

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Verification of Bangla Sentence Structure using N-Gram

Nur Hossain Khan [α], Md. Farukuzzaman Khan [σ], Md. Mojahidul Islam [ρ], Md. Habibur Rahman [ω] & Bappa Sarker [¥]

Abstract- Statistical N-gram language modeling is used in many domains like spelling and syntactic verification, speech recognition, machine translation, character recognition and like others. This paper describes a system for sentence structure verification based on N-gram modeling of Bangla. An experimental corpus containing one million word tokens was used to train the system. The corpus was a part of the BdNC01 corpus, created in the SIPL lab. of Islamic university. Collecting several sample text from different newspapers, the system was tested by 1000 correct and another 1000 incorrect sentences. The system has successfully identified the structural validity of test sentences at a rate of 93%. This paper also describes the limitations of our system with possible solutions.

Keywords: N-gram, sentence structure, corpus, witten-bell smoothing, word error.

I. Introduction

The goal of Statistical Language Modeling is to build a statistical language model that can estimate the distribution of natural language as accurate as possible. A statistical language model (SLM) is a probability distribution P(s) over strings S that attempts to reflect how frequently a string S occurs as a sentence. By expressing various language phenomena in terms of simple parameters in a statistical model, SLMs provide an easy way to deal with complex natural language in computer. Therefore N-gram based modeling finds extensive acceptance to the researchers working with structural processing of natural language. An n-gram model is a type of probabilistic model for predicting the next item in such a sequence. More concisely, an n-gram model predicts x_i based on $X_{i-1}, X_{i-2}, X_{i-3}, \ldots\ldots\ldots, X_{i-n}$.

In Probability terms, this is nothing but $P(X_i \mid X_{i-1}, X_{i-2}, \ldots\ldots\ldots, X_{i-n})$. An n-gram of size 1 is referred to as a "unigram"; size 2 is a "bigram", size 3 is a "trigram"; and size 4 or more is simply called an "n-gram". For a sequence of words, for example "the dog smelled like a skunk", the trigrams would be: "# the dog", "the dog smelled", "dog smelled like", "smelled like a", "like a skunk" and "a skunk #". N-Grams are typically constructed from statistics obtained from a large corpus of text using the co-occurrences of words in the corpus to determine word sequence probabilities. N-Grams have the advantage of be able to cover a much larger language than would normally be derived directly from a corpus. Open vocabulary applications are easily supported with N-Gram grammars [1]. Within the much application areas, an important application is to assess the probability of a given word sequence appearing in text of a language of interest in pattern recognition systems, speech recognition, OCR Intelligent Character Recognition (ICR), machine translation and similar applications [2]. By converting a sequence of items to a set of n-grams, it can be embedded in a vector space, thus allowing the sequence to be compared to other sequences in an efficient manner. The idea of n-gram based sentence structure verification has come from these opportunities provided by n-grams. Sentence structure verification is the task of testing the syntactical correctness of a sentence. It is mostly used in word processors and compilers. For applications like compiler, it is easier to implement because the vocabulary is finite for programming languages but for a natural language it is challenging because of infinite vocabulary. Three methods are widely used for grammar checking in a language; syntax-based checking, statistics-based checking and rule-based checking. In syntax based grammar checking [3], each sentence is completely parsed to check the grammatical correctness of it. The text is considered incorrect if the parsing does not succeed. In statistics-based approach [4], a corpus is used to train a model. Some sequence will be very common others will probably not occur at all. Uncommon sequences in the training corpus can be considered incorrect in this approach. In rule-based approach [5], a set of hand crafted rules is matched against a text which has at least been POS tagged. This approach is very similar to statistics-based approach, but the rules are developed manually. However, one of the most widely used grammar checkers for English, Microsoft Office Suite grammar checker, is also not above controversy [6]. It demonstrates that work on

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grammar checker in real time is not very easy task; so starting the implementation for language like Bangla structural verification of a sentence is a major feat. In our work, an effort has been made to develop system to verify Bangla sentence structure using statistical or more specifically n-gram based method. This is because, this approach does not need language resources like handcrafted grammatical rules, except for a corpus to train the language model (LM). Given the scarcity of language resources for Bangla, proposed approach may be the only reasonable one for the foreseeable future.

II. Techniques Adopted in the Proposed System

In statistical approach we can simply measure the probability of a sentence using n-gram analysis. For example, using bigram probability of the sentence "রহিম ফুটবল খেলে।" is,

P ("রহিম ফুটবল খেলে।") = P (রহিম | <s>) * P (ফুটবল | রহিম) * P (খেলে | ফুটবল)

To estimate the structural correctness of a sentence, we calculate the probability of a sentence using the formula above. If the value of the probability is above some threshold then we consider the sentence to be structurally correct. Now if any of these three words (রহিম,ফুটবল,খেলে) are not in the corpus then the probability of the sentence will become zero because of multiplication. To solve this problem, Witten-Bell smoothing [7] was used to calculate the probability of a sentence in our work. A sample corpus was used in this work that is a part of another corpus under construction in the speech and image processing lab of Islamic University, Bangladesh. We have developed necessary programs to assemble sequences of N tokens into N-grams. Typically N-grams are formed of contiguous tokens that occur one after another in the input corpus. If we consider a bangla sentence "আমরা যে দেশে বাস করি তার নাম বাংলাদেশ", the possible bigrams (N-grams with N=2) are: আমরা যে, যে দেশে, দেশে বাস, বাস করি, করি তার, তার নাম, নাম বাংলাদেশ

Bigram probability, P(আমরা যে দেশে বাস করি তার নাম বাংলাদেশ) = P(আমরা | <s>) * P(যে | আমরা) * P(দেশে | যে) * P(বাস | দেশে) * P(করি | বাস) * P(তার | করি) * P(নাম | তার) *P(বাংলাদেশ | নাম)

and possible trigrams (Ngrams with N=3) are:
আমরা যে দেশে, যে দেশে বাস, দেশে বাস করি, বাস করি তার, করি তার নাম, তার নাম বাংলাদেশ

Trigram probability, P(আমরা যে দেশে বাস করি তার নাম বাংলাদেশ) = P(আমরা | <s1><s2>) * P(যে | <s1> আমরা) * P(দেশে | আমরা যে) * P(বাস | যে দেশে) * P(করি | দেশে বাস) * P(তার | বাস করি) * P(নাম | করি তার) *P(বাংলাদেশ | তার নাম)

Similarly, the possible quad-grams (N-grams with N=4) are:
আমরা যে দেশে বাস, যে দেশে বাস করি, দেশে বাস করি তার, বাস করি তার নাম, করি তার নাম বাংলাদেশ

Quad-gram probability, P(আমরা যে দেশে বাস করি তার নাম বাংলাদেশ) = P(আমরা | <s1><s2><s3) * P(যে | <s1> <s2> আমরা) * P(দেশে | <s1> আমরা যে) * P(বাস | আমরা যে দেশে) * P(করি | যে দেশে বাস) * P(তার | দেশে বাস করি) * P(নাম | বাস করি তার) *P(বাংলাদেশ | করি তার নাম)

After training a model using above concept it was used to design a test system. For the purpose of testing whether a sentence is correct or not, the number of N-grams (2, 3, or 4) in the sentence was counted first. Using all the N-grams of the sentence, we have generated a score for the sentence. If the score is greater than a predefined threshold, the sentence is syntactically correct. On the other hand, if the score is not greater than the threshold, the sentence is syntactically incorrect.

III. Training the N-gram Model

The first step to compute N-grams is counting unigrams. The unigram count and necessary software tools was ready in the laboratory and the work was started from bigram count. After updating the existing software tools bigrams, trigrams and quad-grams were identified, counted and stored in separated disk files. In all cases input to the software was the sample corpus contained in file corpus.txt. The outputs are shown in figure-1(a) & 1(b)

আবার জমজমাট রাজনীতি।
দীর্ঘদিনের জড়তা কাটিয়ে
ফের সরগরম রাজপথ।
আবার জমজমাট রাজনীতি।

Unigram	Frequency
আবার	২
জমজমাট	২
রাজনীতি	২
দীর্ঘদিনের	১
জড়তা	১
কাটিয়ে	৩
ফের	১
সরগরম	১
রাজপথ	১

Figure 1(a) : Samples of first step computation

Bigram	Frequency
আবার জমজমাট	২
জমজমাট রাজনীতি	১
দীর্ঘদিনের জড়তা	২
জড়তা কাটিয়ে	১
কাটিয়ে ফের	১
ফের সরগরম	১
সরগরম রাজপথ	১

Trigram	Frequency
আবার জমজমাট রাজনীতি	২
দীর্ঘদিনের জড়তা কাটিয়ে	১
জড়তা কাটিয়ে ফের	২
ফের সরগরম রাজপথ	১

Quadrigram	Frequency
দীর্ঘদিনের জড়তা কাটিয়ে ফের	১
জড়তা কাটিয়ে ফের সরগরম	২
কাটিয়ে ফের সরগরম রাজপথ	১

Figure 1(b) : Samples of first step computation

Bigram	Probability
আবার জমজমাট	০.০০০৬
জমজমাট রাজনীতি	০.০০০৩
দীর্ঘদিনের জড়তা	০.০০০৬
জড়তা কাটিয়ে	০.০০০৩
কাটিয়ে ফের	০.০০০৩
ফের সরগরম	০.০০০৩
সরগরম রাজপথ	০ ০০০৩

Trigram	Probability
আবার জমজমাট রাজনীতি	০.০০০৪
দীর্ঘদিনের জড়তা কাটিয়ে	০.০০০২
জড়তা কাটিয়ে ফের	০.০০০৪
ফের সরগরম রাজপথ	০.০০০২

Quadrigram	Probability
দীর্ঘদিনের জড়তা কাটিয়ে ফের	০.০০০২৬
জড়তা কাটিয়ে ফের সরগরম	০.০০০১৩
কাটিয়ে ফের সরগরম রাজপথ	০.০০০২৬

Figure 2 : Sample results of second step computation

In the second step of computation, outputs of the first step were used as inputs. A set of program modules were developed to compute bigram, trigram and quad-gram probabilities using N and N-1 gram count. For example, bigram probabilities were calculated by using unigram and bigram counts. The intermediate results of the system as the outputs of the second step are shown in figure-2.

IV. The Test System

For the purpose of testing whether a sentence is correct or not, at first, all the number of bigrams of the sentence was counted. Getting probabilities from the respective models, Witten-Bell smoothing was applied to compute a set of probabilities contained all nonzero values. Multiplying all the bigrams of the sentence, a score for the sentence was generated. If the score is greater than a predefined threshold, the sentence is syntactically correct. The functional block diagram of the system is shown in figure 3. For the trigram or quad-gram models, the same algorithm was followed by replacing only the bigrams with trigrams or quad-grams respectively.

V. Experimental Results and Discussion

In our experiment, 1000 sentences collected from the web edition of a daily newspaper to form a test set. The test set was disjoint from the training corpus. All of these 1000 sentences were structurally correct. Taking these correct sentences as input, the result generated by the test system is shown in table–1. For another experiment, All of these 1000 sentences were modified to make structurally incorrect and presented again as input to the test system. The result generated by second experiment is also shown in table-1.

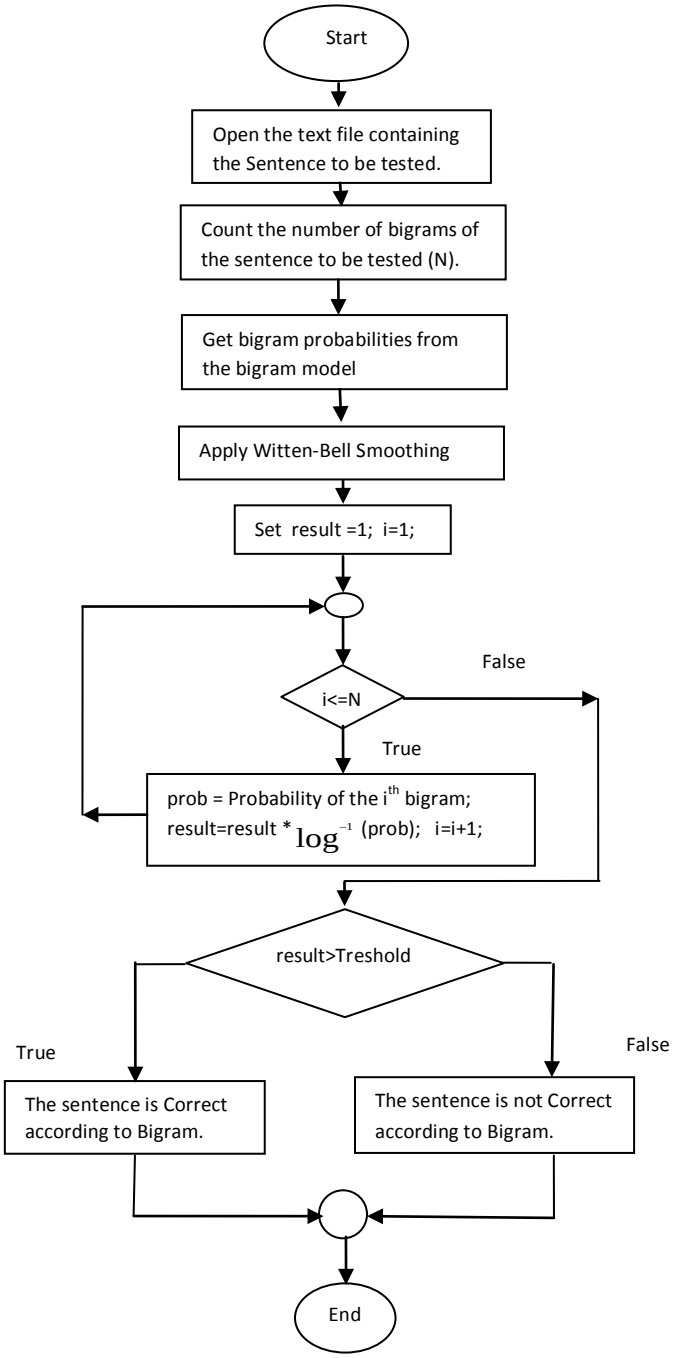

Figure 3 : Block Diagram of the Bigram Model of the System.

Table 1 : The test result with correct and incorrect sentences.

Results with correct sentences			
Models	No. of Sentences	No. of success	Performance
Bigram	1000	900	90%
Trigram	1000	905	90.5%
Quadrigram	1000	907	90.7%
Results with incorrect sentences			
Bigram	1000	950	95%
Trigram	1000	961	96.1%
Quadrigram	1000	963	96.3%
		Average	93.1%

VI. Discussion

The word-error in Bangla can belong to one of the two distinct categories, namely, non-word error and real-word error. A string of characters separated by spaces without a meaning is a non-word. By real-word error we mean a valid but not the intended word in the sentence, thus making the sentence syntactically or semantically ill-formed or incorrect. The developed system can identify both types of errors with an failure rate of 6.9% on average. The major cause of this error is the volume of training corpus. As large as the volume of training corpus so will be success rate.

VII. Conclusion

We have developed a statistical Sentence structure verifier for Bangla, which has a reasonably good performance as a rudiment Sentence verifier. By increasing the volume of training data the performance of the system can be improved and a hybrid system combining both statistical and rule based system can be developed.

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Distributed Bioinformatics Computing System for DNA Sequence Analysis

By Mohammad Ibrahim Khan, Kaushik Deb & Chotan Sheel
Chittagong University of Engineering & Technology, Bangladesh

Abstract- This paper provides an effective design of computing technique of a distributed bioinformatics computing system for analysis of DNA sequences using OPTSDNA algorithm. This system could be used for disease detection, criminal forensic analysis, gene prediction, genetic system and protein analysis. Different types of distributed algorithms for the search and identification for DNA segments and repeat pattern in a given DNA sequence are developed. The search algorithm was developed to compute the number of DNA sequence which contains the same consecutive types of DNA segments. A distributed subsequence identifications algorithm was designed and implemented to detect the segment containing DNA sequences. Sequential and distributed implementation of these algorithms was executed with different length of search segments patterns and genetic sequences. OPTSDNA algorithm is used for storing various sizes of DNA sequence into database. DNA sequences of different lengths were tested by using this algorithm. These input DNA sequences varied in size from very small to very large. The performance of search technique distributed system is compared with sequential approach.

Keywords: distributed bioinformatics system, DNA sequence, search segments, identify DNA sequences, reported gene sequences.

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Distributed Bioinformatics Computing System for DNA Sequence Analysis

Mohammad Ibrahim Khan [α], Kaushik Deb [σ] & Chotan Sheel [ρ]

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Keywords: distributed bioinformatics system, DNA sequence, search segments, identify DNA sequences, reported gene sequences.

I. Introduction

Distributed Computing (DC) provides a cost effective frame work with efficient execution of a solution on multiple computers connected by a network. For distributed Computing (DC), large tasks are divided into smaller problems which can then be executed on multiple computers at the same time independent of each other. The task must be broken up into independent problems to minimize inter-computers communication; otherwise distributed computing will not be effective. Over the past few years, the intermixing of computer science and the complexity of biology has lead to the prosperous field of bioinformatics [1-2] Advances in molecular biology and technology for research have facilitated the process of sequencing of large portions of genomes in various species. Today computers have made medical research more efficient and accurate, by using parallel and distributed computers and complex biological modeling. Bioinformatics, is one of the newer areas, and has opened our eyes to a whole new world of biology [1].

The fusion of computers and biology has helped scientists learn more about species, especially humans [3-5]. With the aid of the computers, we have learned a great deal about genetics, but there still stand many unanswered questions, that are being researched today. DNA sequence analysis can be a lengthy process ranging from several hours to many days. This paper builds a distributed system that provides the solution for many bioinformatics related applications.

The overall goal of this paper is to build a Distributed Bioinformatics Computing System for genetic sequence analysis of DNA. This system is capable of searching and identifying gene patterns in a given DNA sequence. For the purpose of computing we stored a large no. of DNA sequence using OPTSDNA algorithm [13] and segments is divided two to six consecutive nucleotide [13]. The system was tested for its correctness and efficiency. Different lengths of DNA sequences were used for the consecutive and non-consecutive pattern search to compare the system's response time obtained using single and multiple computers [6]. In addition, different lengths of DNA sequences were also used for the pattern identification to compare its response time observed using a single computer and multiple computers. Several different distributed implementations of search algorithms have been reported in the literature. The characteristics of some of those distributed algorithms are listed in Table 1.

It can be observed that the most of the existing approaches require high performance parallel processors and are not implemented on loosely coupled distributed network. Moreover, most of them require specialized programming language for their implementation on these parallel processors.

The specific objective of the proposed distributed algorithm for analysis of DNA sequences are:

1. Develop an effective distributed DNA sequence analysis algorithms for pattern matching of DNA Gene sequence and sub-sequences identification.
2. Implement them on loosely coupled distributed network such as regular local area network and

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wide area network using standard programming language.

This paper is organized in four sections. Section 2 discusses the material and method of algorithm. Section 3 discusses the results and discussion and conclusions included in section 4.

Table 1 : Comparative Study with Existing Approaches

Reference	Algorithm Complexity	Special Purpose Computer Required	No. of Computers Required	Special Language Required	Useful on General Network
[2]	O(n)	Yes	Flexible	Yes	No
[9]	O(n)	Yes	Not Flexible	Yes	No
[10]	O(n)	Yes	Not Flexible	Yes	No
[11]	$O(n^2)$	Yes	Not Flexible	Yes	No
[12]	O(n)	Yes	Not Flexible	Yes	No

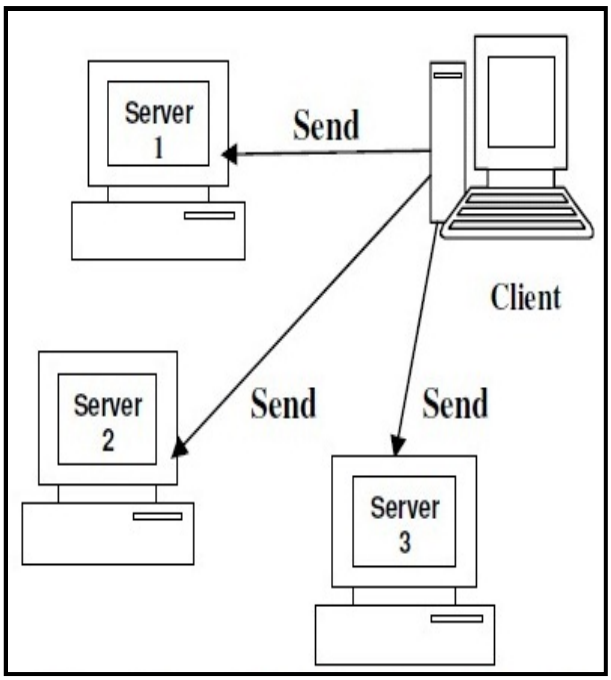

Figure 1 : Layout of the System (Sending of Data)

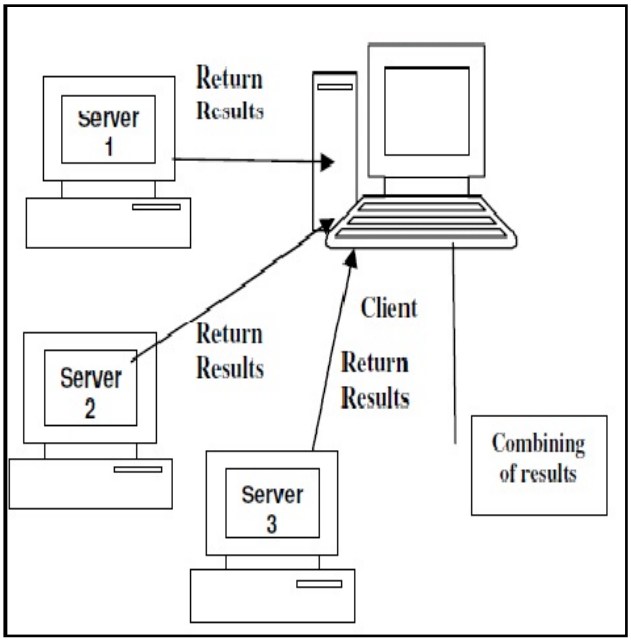

Figure 2 : Layout of System (Returning Results)

a) Application of the Proposed Distributed Algorithm

This distributed Bioinformatics system developed in this paper could be used for disease detection, criminal forensics analysis, genetics systems and protein analysis. Di-let, Triplet, Tetra-let, Pentad-let, Hexed-let repeats formally known as a Di-nucleotide, Tri-nucleotide, Tetra-nucleotide, Pent nucleotide, Hex nucleotide. Repeat occurs when two, three, four, five and six consecutive nucleotides are repeated within a specific region of DNA sequence. These repeats can occur within or between genes. These consecutive repeats are frequently located in genes that encode transcription factors and which are active in the organism development process. Extensive Di-let, Triplet, Tetra-let, Pant-lets, Hex-let repeats are found when a mutation occurs in a gene. This mutation increases the number of occurrences of a particular nucleotide which can lead to a number of neurodegenerative diseases. These diseases include, Huntington's Disease (HD), Fragile X Syndrome, Kennedy's Disease, Myotonic Dystrophy, Spinocerebellar Ataxia Type 1 (SCA1), Dentatorubral Pallidoluysian atrophy (DRPLA),and Fragile X E mental retardation (FRAXE). In Kennedy's Disease, Huntington's disease, Spinocerebellar Ataxia Type 1, and Dentatorubral Pallidoluysian atrophy, the number of triplet repeats is quite small, in contrast to Fragile X Syndrome, Myotonic Dystrophy, and FRAXE, where the number of consecutive repeats may be very large, producing alleles that consist of thousands of repeats. These algorithms can help to detect Di-let, Triplet, Tetra-let, Patna-led and Hex-let repeats in gene sequence, and can also search through DNA sequences to identify most frequently occurring repeats.

The proposed distributed algorithms will be able to first identify a DNA sequence Gene pattern in the DNA obtained from the crime scene and then it can search for those patterns in suspects DNA, which will be helpful for criminal investigation, Disease analysis, Gene Sequence Prediction, Human Identification etc. Criminal investigation can now be facilitated by the DNA forensic analysis. Forensic analysis is a process by which two organism's DNA is compared with each other. DNA analysis is effective in finding criminals, because two different individuals will have different DNA sequence. In DNA analysis one can look for matching gene patterns at different locations of the suspect's DNA and the DNA obtained at the crime scene. Gene pattern matching at one, two or three locations in DNA usually aren't enough to associate a suspect with a crime, but gene pattern matches at 5 or more locations in DNA are usually good enough to identify a criminal. Experts believe that DNA forensic technology is more reliable than eyewitnesses, where the odds are fifty-fifty. In DNA analysis one can look for matches based on number of repeating patterns at different locations of the suspect's genome.

II. Materials and Method

The proposed distributed algorithm is based on client server model. For distributed search and identification algorithms on DNA sequence, the proposed framework avoids duplicates computations on server machines. The two input items are provided by the user for pattern search and identification:

1. The DNA sequence which is stored by OPTSDNA algorithm with extend two to six consecutive nucleotides division.
2. Search string DNA subsequences or identification DNA segments (Di-nucleotides to Hex-Nucleotides Segment pattern).

Using OPTSDNA algorithm, the DNA sequence is broken up in X segments where X = m * p. Here m = number of storage DNA and p = length of storage nucleotide base. Number of storage DNA is also used as number of servers used in distributed algorithm implementation and length of storage nucleotide base represents the length of pattern for search or identification. In the first step each server gets one segment of data and the required search or identification pattern for carrying out its computation as shown in Figure 1. In addition, an offset value is sent to the server as well to make sure that no two servers are performing the same computation for search or identification. The individual results from each server are sent back to the clients where partial results are combined as shown in Figure 2. The complete details of client and server side interaction are shown in Figure 3. The actual pattern search for a DNA sequence with three servers is shown in Figure 4, where each server starts the match at different Gene chromosome. Different starting point at various servers guarantees that no comparison for pattern search and identification is performed more than once on any server. The worst case complexity of this distributed search or identification algorithm is O (L/X), where L is the length of DNA sequence and X = m/p. In case of Figure 4 value of X = 1 because m = 3 and p = 3. That implies that complete DNA sequence is end to all three servers and the offset for starting the search or identification.

a) Implementation of Distributed Algorithms

A Dot net based client server system was developed for this project[7-8] shown in figure A and figure B. The client and server side logic implementation is given in Figure 3 and figure 4. This framework can distribute the workload across multiple servers as specified by the user. In this paper, a client provides the user input from Graphical User Interface (GUI) and then send this input to one or more server computers as directed by the user (shown figure A and B). The processing option is developed in GUI. When a client selects a processing option such as pattern identification, appropriate input for carrying out a search or identification in a DNA sequence displayed (shown in figure A and B). The client program then sends the input data to multiple servers (as specified by the user). The code at the server executes the desired algorithm and returns its results to the client. The client then receives the results from all the servers and combines to individual results to generate a final output of the processing a shown in figure A and figure B.

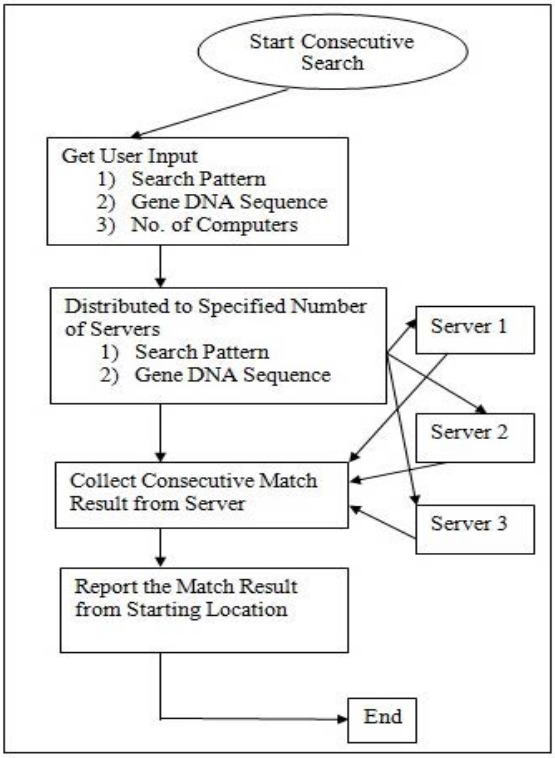

Figure 3 : Flow Diagram for Clint Side Implementation

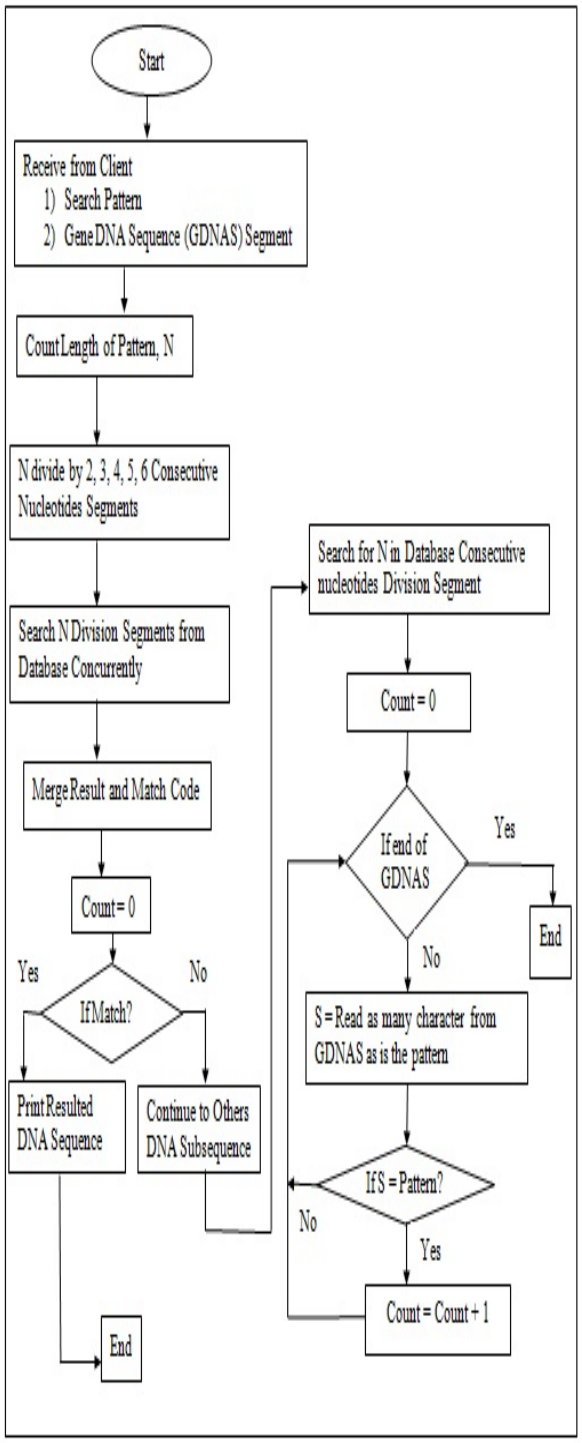

Figure 4 : Flow Diagram for Consecutive Search Pattern from Server

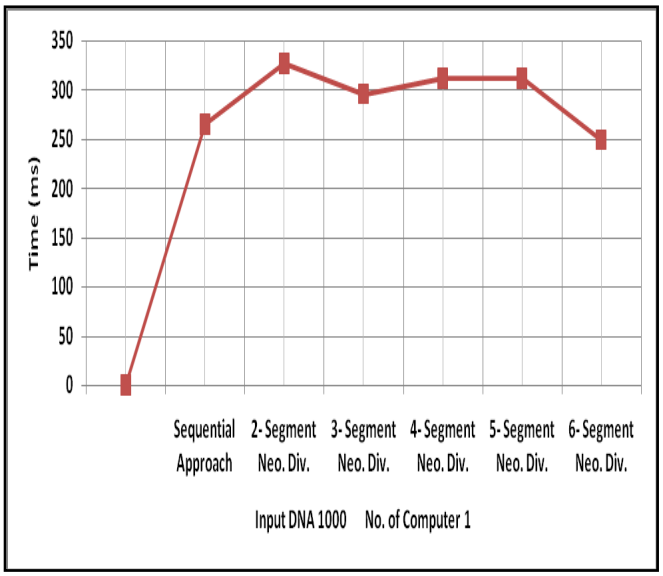

Figure 5 : Effect of Data size on using Single Computer

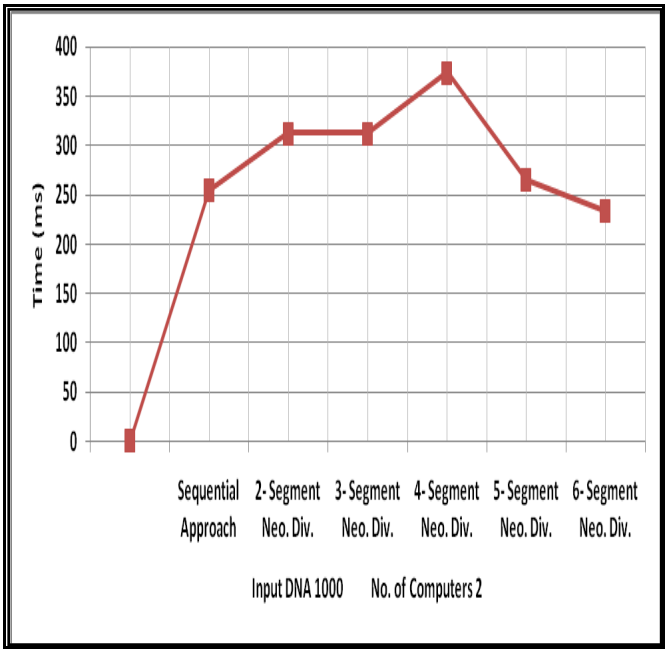

Figure 6 : Effect of Data size on using Two Computers

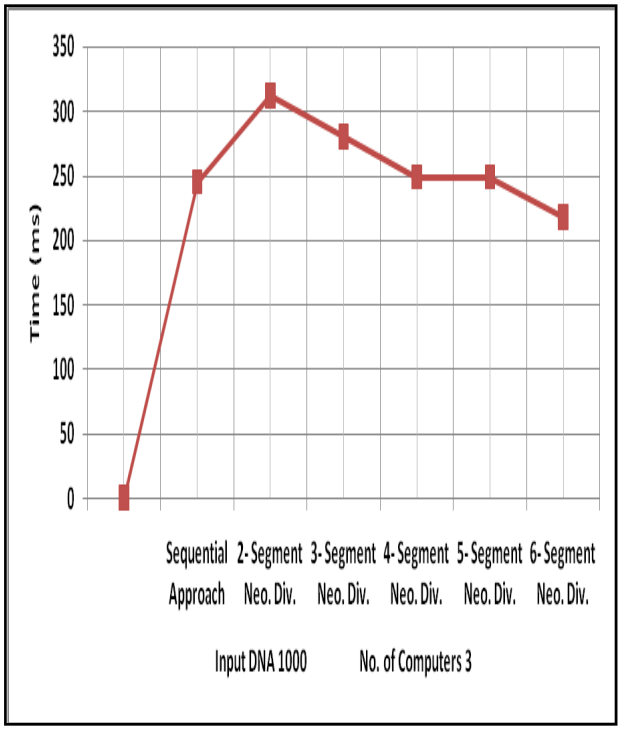

Figure 7 : Effect of Data size on using Three Computers

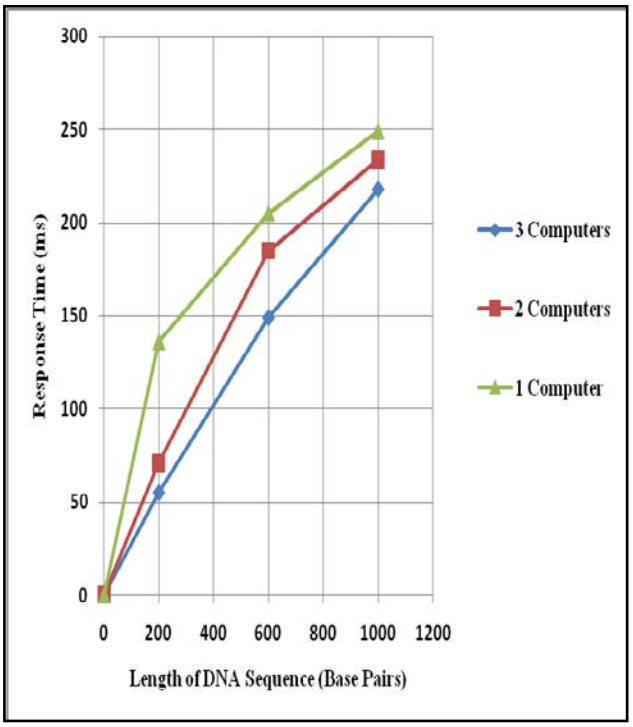

Figure 8 : Effect of Data Size on Computation Time

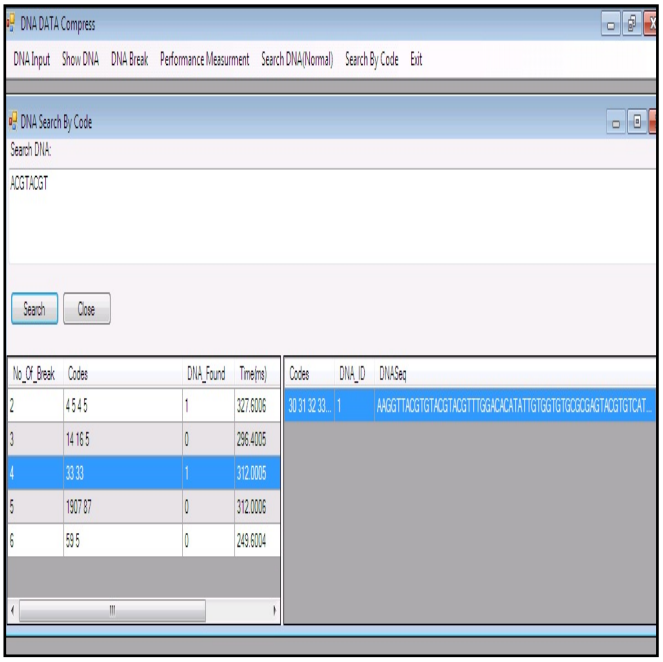

Figure A : Screen Shot for the Search Process by Generating Code

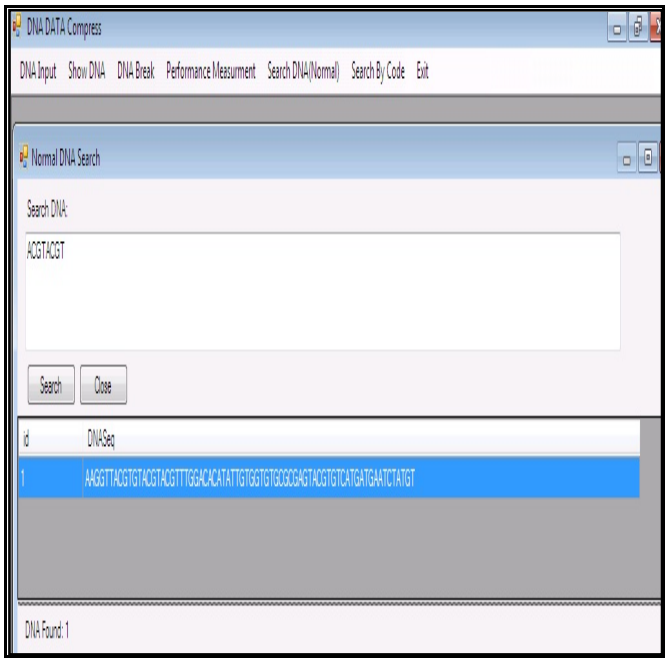

Figure B : Screen Shot for the Search Process by Sequential Approach

III. Results and Discussion

Sequential and Distributed versions of the algorithms were executed with different patterns of genetic sequences. These sequences were of different sizes ranging from very small to very large. The response times for sequential and distributed versions of the programs were plotted to demonstrate the effectiveness of distributed DNA sequence analysis algorithms. Figure 5, 6, and 7 shows the response time

of consecutive pattern search execution on single machine and multiple machines. The execution time was calculated for DNA sequences of sizes 1 to 1000 sequences. It can be observed that execution time reduces significantly as number of servers increased. Moreover, the improvement in execution time is significant when DNA sequence size is 600 with 3 servers. Figure 5, 6 and 7 shows the response time of consecutive pattern identification execution on single machine and multiple machines. It can be observed that the execution time reduces significantly as number of servers increased.

Similar observation was made for sequential approach consecutive pattern identification algorithm execution shown in Figure 5, 6, and 7. Figure 8 demonstrates how the data size affected the computation time. With a single computer the response time of each gene sequence was significantly more than that of the distributed execution using two and three servers. In addition, rate of growth of execution time is almost linear with three servers as the size of DNA sequence increases.

IV. Conclusions

As shown in the previous figures, it is clear that as complexity of the algorithm increases the response time also increases. The algorithm for the Pattern Identification was the most complex one and the algorithm for the pattern search was the least complex. It can be seen in Figure 5 the response times for the Pattern Identification were much lower compared to the other two studies shown in Figures 5 and 6. This is due to the fact that more complex algorithms usually involve more steps, which increases the response time. To help get a better understanding of the effects of Distributed Systems on DNA sequences, more DNA sequences of various lengths should be tested. This would provide more data for a larger analysis. It is also recommended that the computers used in the investigation should not exceed the length of the repeat pattern that is being searched or identified, because this will not improve the response time. The complexity of our algorithm is O(n). For computing DNA sequences special purpose of computer is required. Using this algorithm no. of computer required is flexible and special language is required. Our algorithm is useful on general network. So our algorithm is more efficient then previous all. In addition, this system could be interfaced with the Internet, so that all these feature of DNA analysis are accessible to everyone via Web.

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A Review on Non-Linear Programming and Generalized Invexity

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Abstract- Over past few years, the concept of NLPP and their related results based on generalized invexity has become one of the prominent and important areas of classical optimization. This paper presents a brief review on such problems and their respective results in game theory, continuous time programming, multivariable optimization, composite programming etc.

Keywords: *non-linear programming, invexity, optimality, duality.*

GJCST-A Classification: *G.1.3*

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A Review on Non-Linear Programming and Generalized Invexity

L. V. Reddy [α], B. Satyanarayana [σ] & D. Devanandam [ρ]

Abstract- Over past few years, the concept of NLPP and their related results based on generalized invexity has become one of the prominent and important areas of classical optimization. This paper presents a brief review on such problems and their respective results in game theory, continuous time programming, multivariable optimization, composite programming etc.

Keywords: non-linear programming, invexity, optimality, duality.

I. Introduction

Optimization theory plays an important role in Science and Engineering. The concept of convexity and their generalizations have great significance in nonlinear programming. We deal with constrained optimization problems in which the essential constraints are defined by some parametric variational inequalities or parametric auxiliary systems. It has many important applications in many fields, such as engineering design, economic equilibria, transportation science, multilevel game, and mathematical programming itself. However, this kind of problems is generally difficult to deal with because its constraints fail to satisfy the standard Mangasarian, Mangasarian – Fromovitz constraint qualification (MFCQ) at any feasible point [20].

Since last two decades a lot of research has been done to study the first-order optimality conditions for NLPP ,such as Clarke (C), Mordukhovich (M), Strong(S), Bouligrand (B) stationarity conditions; see, e.g., [1–5,19-20]. And also various algorithms were studied for solving those NLP problems and have been proposed for enumerating various results by using different approaches, such as sequential quadratic programming approach, penalty function approach, relaxation approach, active set identification approach, composite multi-objective programming, continuous time programming, etc.; see, e.g., [9–11].

In this paper, we unify various results on first order and second-order optimality conditions for NLP by using generalized invexity and their classifications. In general, first order optimality conditions tell us how the first derivatives of the functions involved are related to each other at locally optimal solutions. However, for some feasible directions in the tangent cone such as the so-called critical directions, we cannot determine from the first derivative information alone whether the objective function increases or decreases in this direction. Therefore second-order optimality conditions examine the second derivative terms in the Taylor series expansions of the functions involved to see whether this extra information resolves the issue of increase or decrease in the objective function as well as a set of lagrange multipliers. Also, the second-order optimality conditions are concerned with the curvature of the so-called NLPP Lagrangian function in the critical directions. Moreover, second-order optimality conditions play important roles in convergence analysis for numerical algorithms, saddle points for game theoretic problems and the stability analysis for MPEC; see, e.g., [12–18].In recent times, many research observed and compared with the first-order optimality conditions, there is very little research done with the second-order optimality conditions for MPEC. Recently, Scheel and Scholtes [1] showed that S-stationary points satisfying the refined second-order sufficient optimality conditions are strictly and locally optimal and they derived a strong second-order necessary optimality condition under the MPEC strict MFCQ. Also, Izmailov[19] investigated second-order optimality conditions under the MPEC linear by using dependence constraint qualification (MPEC-LICQ).Further, Lei Guo and others studied second order conditions for equilibrium of saddle points. These results are further studied to scalar valued games to multiple objectives by using invexity coeffiecients.

In this paper, we unify various first and second order optimality conditions for MPEC in a similar manner. Note that, recently, several new constraint qualifications weaker than the LICQ and MFCQ have been introduced for standard nonlinear programming problems. We use these new constraint qualifications to derive some second-order optimality conditions for standard nonlinear programming problems and apply the obtained results to MPEC. We further study some MPEC variants of these new constraint qualifications, which are weaker than the MPEC-LICQ, and derive some second-order optimality conditions for MPEC in terms of S- and C-multipliers under these new MPEC

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constraint qualifications. Moreover, we identify some relationships between various second-order optimality conditions for MPEC in terms of the classical NLPP multipliers and multipliers respectively. It is interesting to see that not all second-order optimality conditions in terms of the classical NLPP multipliers and S-multipliers are equivalent.

In addition, unlike the first-order conditions, the second-order conditions in terms of singular multipliers provide a solution but the significance may be different. This significance is observed in equilibrium of saddle points for multi objective NLPP and composite multi objective NLPP problems. To unify these generalizations, we can use generalized invexity and their related properties. These results further generate different optimality and duality results by using the various conditions of univexity with the help of Mangasarian Constraint Qualification. This new set up has numerous applications in game theory, decision theory, cloud computing environment in generating first and second order optimality conditions for NLPP.

We consider a general NLPP for multi variable optimization as follows:

$$\text{minimize } f_i(x),\ i=1,2,\ldots\ldots,m$$
$$\text{subject to: } g_j(x)>0,\ j=1,2,\ldots,n$$
$$h_k(x)=0,\ k=1,2,\ldots\ldots,p.$$

Then the corresponding auxiliary function for the above NLPP is

$$L(x) = \sum r\, f_i(x) + \sum \lambda_j\, g_j(x) + \sum \mu_k h_k(x)$$

Where the langrange multipliers λ and μ have their usual meanings. These multipliers play a complementary role in most of NLPP problems. For instance, Clarke sub-differentials, Mangasarian constraint qualifications hold for such case. For this problem, the various generalized invexity concepts were studied and observed that the well known first and second order optimality conditions and duality results satisfied under this setting. These results have many important applications in game theory, decision making, cloud computing and so on. The Clarke sub-differentials are also hold for sufficient conditions[10]. And also, the constraint qualifications in[20,21] were studied for NLPP under this new setting.

II. Conclusion

This survey is very use full for generating various results on mathematical programming and its related results. We develop many second order optimality and duality results for NLPP using generalized invexity and their unifications. The same results are further studied to equilibria of saddle points. Further , we explore different formulations for continuous time programming.

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3. Submission of Manuscripts,

4. Manuscript's Category,

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16. Use proper verb tense: Use proper verb tenses in your paper. Use past tense, to present those events that happened. Use present tense to indicate events that are going on. Use future tense to indicate future happening events. Use of improper and wrong tenses will confuse the evaluator. Avoid the sentences that are incomplete.

17. Never use online paper: If you are getting any paper on Internet, then never use it as your research paper because it might be possible that evaluator has already seen it or maybe it is outdated version.

18. Pick a good study spot: To do your research studies always try to pick a spot, which is quiet. Every spot is not for studies. Spot that suits you choose it and proceed further.

19. Know what you know: Always try to know, what you know by making objectives. Else, you will be confused and cannot achieve your target.

20. Use good quality grammar: Always use a good quality grammar and use words that will throw positive impact on evaluator. Use of good quality grammar does not mean to use tough words, that for each word the evaluator has to go through dictionary. Do not start sentence with a conjunction. Do not fragment sentences. Eliminate one-word sentences. Ignore passive voice. Do not ever use a big word when a diminutive one would suffice. Verbs have to be in agreement with their subjects. Prepositions are not expressions to finish sentences with. It is incorrect to ever divide an infinitive. Avoid clichés like the disease. Also, always shun irritating alliteration. Use language that is simple and straight forward. put together a neat summary.

21. Arrangement of information: Each section of the main body should start with an opening sentence and there should be a changeover at the end of the section. Give only valid and powerful arguments to your topic. You may also maintain your arguments with records.

22. Never start in last minute: Always start at right time and give enough time to research work. Leaving everything to the last minute will degrade your paper and spoil your work.

23. Multitasking in research is not good: Doing several things at the same time proves bad habit in case of research activity. Research is an area, where everything has a particular time slot. Divide your research work in parts and do particular part in particular time slot.

24. Never copy others' work: Never copy others' work and give it your name because if evaluator has seen it anywhere you will be in trouble.

25. Take proper rest and food: No matter how many hours you spend for your research activity, if you are not taking care of your health then all your efforts will be in vain. For a quality research, study is must, and this can be done by taking proper rest and food.

26. Go for seminars: Attend seminars if the topic is relevant to your research area. Utilize all your resources.

27. Refresh your mind after intervals: Try to give rest to your mind by listening to soft music or by sleeping in intervals. This will also improve your memory.

28. Make colleagues: Always try to make colleagues. No matter how sharper or intelligent you are, if you make colleagues you can have several ideas, which will be helpful for your research.

29. Think technically: Always think technically. If anything happens, then search its reasons, its benefits, and demerits.

30. Think and then print: When you will go to print your paper, notice that tables are not be split, headings are not detached from their descriptions, and page sequence is maintained.

31. Adding unnecessary information: Do not add unnecessary information, like, I have used MS Excel to draw graph. Do not add irrelevant and inappropriate material. These all will create superfluous. Foreign terminology and phrases are not apropos. One should NEVER take a broad view. Analogy in script is like feathers on a snake. Not at all use a large word when a very small one would be sufficient. Use words properly, regardless of how others use them. Remove quotations. Puns are for kids, not grunt readers. Amplification is a billion times of inferior quality than sarcasm.

32. Never oversimplify everything: To add material in your research paper, never go for oversimplification. This will definitely irritate the evaluator. Be more or less specific. Also too, by no means, ever use rhythmic redundancies. Contractions aren't essential and shouldn't be there used. Comparisons are as terrible as clichés. Give up ampersands and abbreviations, and so on. Remove commas, that are, not necessary. Parenthetical words however should be together with this in commas. Understatement is all the time the complete best way to put onward earth-shaking thoughts. Give a detailed literary review.

33. Report concluded results: Use concluded results. From raw data, filter the results and then conclude your studies based on measurements and observations taken. Significant figures and appropriate number of decimal places should be used. Parenthetical remarks are prohibitive. Proofread carefully at final stage. In the end give outline to your arguments. Spot out perspectives of further study of this subject. Justify your conclusion by at the bottom of them with sufficient justifications and examples.

34. After conclusion: Once you have concluded your research, the next most important step is to present your findings. Presentation is extremely important as it is the definite medium though which your research is going to be in print to the rest of the crowd. Care should be taken to categorize your thoughts well and present them in a logical and neat manner. A good quality research paper format is essential because it serves to highlight your research paper and bring to light all necessary aspects in your research.

Informal Guidelines of Research Paper Writing

Key points to remember:

- Submit all work in its final form.
- Write your paper in the form, which is presented in the guidelines using the template.
- Please note the criterion for grading the final paper by peer-reviewers.

Final Points:

A purpose of organizing a research paper is to let people to interpret your effort selectively. The journal requires the following sections, submitted in the order listed, each section to start on a new page.

The introduction will be compiled from reference matter and will reflect the design processes or outline of basis that direct you to make study. As you will carry out the process of study, the method and process section will be constructed as like that. The result segment will show related statistics in nearly sequential order and will direct the reviewers next to the similar intellectual paths throughout the data that you took to carry out your study. The discussion section will provide understanding of the data and projections as to the implication of the results. The use of good quality references all through the paper will give the effort trustworthiness by representing an alertness of prior workings.

Writing a research paper is not an easy job no matter how trouble-free the actual research or concept. Practice, excellent preparation, and controlled record keeping are the only means to make straightforward the progression.

General style:

Specific editorial column necessities for compliance of a manuscript will always take over from directions in these general guidelines.

To make a paper clear

· Adhere to recommended page limits

Mistakes to evade

- Insertion a title at the foot of a page with the subsequent text on the next page
- Separating a table/chart or figure - impound each figure/table to a single page
- Submitting a manuscript with pages out of sequence

In every sections of your document

· Use standard writing style including articles ("a", "the," etc.)

· Keep on paying attention on the research topic of the paper

· Use paragraphs to split each significant point (excluding for the abstract)

· Align the primary line of each section

· Present your points in sound order

· Use present tense to report well accepted

· Use past tense to describe specific results

· Shun familiar wording, don't address the reviewer directly, and don't use slang, slang language, or superlatives

· Shun use of extra pictures - include only those figures essential to presenting results

Title Page:

Choose a revealing title. It should be short. It should not have non-standard acronyms or abbreviations. It should not exceed two printed lines. It should include the name(s) and address (es) of all authors.

Abstract:

The summary should be two hundred words or less. It should briefly and clearly explain the key findings reported in the manuscript--must have precise statistics. It should not have abnormal acronyms or abbreviations. It should be logical in itself. Shun citing references at this point.

An abstract is a brief distinct paragraph summary of finished work or work in development. In a minute or less a reviewer can be taught the foundation behind the study, common approach to the problem, relevant results, and significant conclusions or new questions.

Write your summary when your paper is completed because how can you write the summary of anything which is not yet written? Wealth of terminology is very essential in abstract. Yet, use comprehensive sentences and do not let go readability for briefness. You can maintain it succinct by phrasing sentences so that they provide more than lone rationale. The author can at this moment go straight to shortening the outcome. Sum up the study, with the subsequent elements in any summary. Try to maintain the initial two items to no more than one ruling each.

- Reason of the study - theory, overall issue, purpose
- Fundamental goal
- To the point depiction of the research
- Consequences, including definite statistics - if the consequences are quantitative in nature, account quantitative data; results of any numerical analysis should be reported
- Significant conclusions or questions that track from the research(es)

Approach:

- Single section, and succinct
- As a outline of job done, it is always written in past tense
- A conceptual should situate on its own, and not submit to any other part of the paper such as a form or table
- Center on shortening results - bound background information to a verdict or two, if completely necessary
- What you account in an conceptual must be regular with what you reported in the manuscript
- Exact spelling, clearness of sentences and phrases, and appropriate reporting of quantities (proper units, important statistics) are just as significant in an abstract as they are anywhere else

Introduction:

The **Introduction** should "introduce" the manuscript. The reviewer should be presented with sufficient background information to be capable to comprehend and calculate the purpose of your study without having to submit to other works. The basis for the study should be offered. Give most important references but shun difficult to make a comprehensive appraisal of the topic. In the introduction, describe the problem visibly. If the problem is not acknowledged in a logical, reasonable way, the reviewer will have no attention in your result. Speak in common terms about techniques used to explain the problem, if needed, but do not present any particulars about the protocols here. Following approach can create a valuable beginning:

- Explain the value (significance) of the study
- Shield the model - why did you employ this particular system or method? What is its compensation? You strength remark on its appropriateness from a abstract point of vision as well as point out sensible reasons for using it.
- Present a justification. Status your particular theory (es) or aim(s), and describe the logic that led you to choose them.
- Very for a short time explain the tentative propose and how it skilled the declared objectives.

Approach:

- Use past tense except for when referring to recognized facts. After all, the manuscript will be submitted after the entire job is done.
- Sort out your thoughts; manufacture one key point with every section. If you make the four points listed above, you will need a least of four paragraphs.

- Present surroundings information only as desirable in order hold up a situation. The reviewer does not desire to read the whole thing you know about a topic.
- Shape the theory/purpose specifically - do not take a broad view.
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Procedures (Methods and Materials):

This part is supposed to be the easiest to carve if you have good skills. A sound written Procedures segment allows a capable scientist to replacement your results. Present precise information about your supplies. The suppliers and clarity of reagents can be helpful bits of information. Present methods in sequential order but linked methodologies can be grouped as a segment. Be concise when relating the protocols. Attempt for the least amount of information that would permit another capable scientist to spare your outcome but be cautious that vital information is integrated. The use of subheadings is suggested and ought to be synchronized with the results section. When a technique is used that has been well described in another object, mention the specific item describing a way but draw the basic principle while stating the situation. The purpose is to text all particular resources and broad procedures, so that another person may use some or all of the methods in one more study or referee the scientific value of your work. It is not to be a step by step report of the whole thing you did, nor is a methods section a set of orders.

Materials:

- Explain materials individually only if the study is so complex that it saves liberty this way.
- Embrace particular materials, and any tools or provisions that are not frequently found in laboratories.
- Do not take in frequently found.
- If use of a definite type of tools.
- Materials may be reported in a part section or else they may be recognized along with your measures.

Methods:

- Report the method (not particulars of each process that engaged the same methodology)
- Describe the method entirely
- To be succinct, present methods under headings dedicated to specific dealings or groups of measures
- Simplify - details how procedures were completed not how they were exclusively performed on a particular day.
- If well known procedures were used, account the procedure by name, possibly with reference, and that's all.

Approach:

- It is embarrassed or not possible to use vigorous voice when documenting methods with no using first person, which would focus the reviewer's interest on the researcher rather than the job. As a result when script up the methods most authors use third person passive voice.
- Use standard style in this and in every other part of the paper - avoid familiar lists, and use full sentences.

What to keep away from

- Resources and methods are not a set of information.
- Skip all descriptive information and surroundings - save it for the argument.
- Leave out information that is immaterial to a third party.

Results:

The principle of a results segment is to present and demonstrate your conclusion. Create this part a entirely objective details of the outcome, and save all understanding for the discussion.

The page length of this segment is set by the sum and types of data to be reported. Carry on to be to the point, by means of statistics and tables, if suitable, to present consequences most efficiently.You must obviously differentiate material that would usually be incorporated in a study editorial from any unprocessed data or additional appendix matter that would not be available. In fact, such matter should not be submitted at all except requested by the instructor.

Content

- Sum up your conclusion in text and demonstrate them, if suitable, with figures and tables.
- In manuscript, explain each of your consequences, point the reader to remarks that are most appropriate.
- Present a background, such as by describing the question that was addressed by creation an exacting study.
- Explain results of control experiments and comprise remarks that are not accessible in a prescribed figure or table, if appropriate.
- Examine your data, then prepare the analyzed (transformed) data in the form of a figure (graph), table, or in manuscript form.

What to stay away from

- Do not discuss or infer your outcome, report surroundings information, or try to explain anything.
- Not at all, take in raw data or intermediate calculations in a research manuscript.
- Do not present the similar data more than once.
- Manuscript should complement any figures or tables, not duplicate the identical information.
- Never confuse figures with tables - there is a difference.

Approach

- As forever, use past tense when you submit to your results, and put the whole thing in a reasonable order.
- Put figures and tables, appropriately numbered, in order at the end of the report
- If you desire, you may place your figures and tables properly within the text of your results part.

Figures and tables

- If you put figures and tables at the end of the details, make certain that they are visibly distinguished from any attach appendix materials, such as raw facts
- Despite of position, each figure must be numbered one after the other and complete with subtitle
- In spite of position, each table must be titled, numbered one after the other and complete with heading
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Discussion:

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- Make a decision if each premise is supported, discarded, or if you cannot make a conclusion with assurance. Do not just dismiss a study or part of a study as "uncertain."
- Research papers are not acknowledged if the work is imperfect. Draw what conclusions you can based upon the results that you have, and take care of the study as a finished work
- You may propose future guidelines, such as how the experiment might be personalized to accomplish a new idea.
- Give details all of your remarks as much as possible, focus on mechanisms.
- Make a decision if the tentative design sufficiently addressed the theory, and whether or not it was correctly restricted.
- Try to present substitute explanations if sensible alternatives be present.
- One research will not counter an overall question, so maintain the large picture in mind, where do you go next? The best studies unlock new avenues of study. What questions remain?
- Recommendations for detailed papers will offer supplementary suggestions.

Approach:

- When you refer to information, differentiate data generated by your own studies from available information
- Submit to work done by specific persons (including you) in past tense.
- Submit to generally acknowledged facts and main beliefs in present tense.

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- To guard yourself and others from possible illegal use please do not permit anyone right to use to your paper and files.

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	A-B	**C-D**	**E-F**
Abstract	Clear and concise with appropriate content, Correct format. 200 words or below	Unclear summary and no specific data, Incorrect form Above 200 words	No specific data with ambiguous information Above 250 words
Introduction	Containing all background details with clear goal and appropriate details, flow specification, no grammar and spelling mistake, well organized sentence and paragraph, reference cited	Unclear and confusing data, appropriate format, grammar and spelling errors with unorganized matter	Out of place depth and content, hazy format
Methods and Procedures	Clear and to the point with well arranged paragraph, precision and accuracy of facts and figures, well organized subheads	Difficult to comprehend with embarrassed text, too much explanation but completed	Incorrect and unorganized structure with hazy meaning
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
References	Complete and correct format, well organized	Beside the point, Incomplete	Wrong format and structuring

INDEX

A

Annealing · 20, 24

F

Fromovitz · 14

G

Genomes · 8

M

Mangasarian · 14, 16, 17
Mordukhovich · 14
Myotonic · 9

N

Neurodegenerative · 9
Nucleotide · 8, 9, 10

P

Pallidoluysian · 9

S

Spinocerebellar · 9

U

Univexity · 16

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