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Discovering Thoughts, Inventing Future

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String Matching Problems with Parallel Approaches - An Evaluation for the Most Recent Studies

By Chinta Someswara Rao, K. Butchi Raju & Dr. S. Viswanadha Raju

Andhra University, India

Abstract - In recent years string matching plays a functional role in many application like information retrieval, gene analysis, pattern recognition, linguistics, bioinformatics etc. For understanding the functional requirements of string matching algorithms, we surveyed the real time parallel string matching patterns to handle the current trends. Primarily, in this paper, we focus on present developments of parallel string matching, and the central ideas of the algorithms and their complexities. We present the performance of the different algorithms and their effectiveness. Finally this analysis helps the researchers to develop the better techniques.

Keywords : *text processing, irs, string matching, parallel algorithms.*

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STRING MATCHING PROBLEMS WITH PARALLEL APPROACHES AN EVALUATION FOR THE MOST RECENT STUDIES

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String Matching Problems with Parallel Approaches – An Evaluation for the Most Recent Studies

Chinta Someswara Rao ^α, K. Butchi Raju ^σ & Dr. S. Viswanadha Raju ^ρ

Abstract - In recent years string matching plays a functional role in many application like information retrieval, gene analysis, pattern recognition, linguistics, bioinformatics etc. For understanding the functional requirements of string matching algorithms, we surveyed the real time parallel string matching patterns to handle the current trends. Primarily, in this paper, we focus on present developments of parallel string matching, and the central ideas of the algorithms and their complexities. We present the performance of the different algorithms and their effectiveness. Finally this analysis helps the researchers to develop the better techniques.

Keywords : text processing, irls, string matching, parallel algorithms.

I. INTRODUCTION

The problem of string matching has been studied from several decades. String matching problem is all about searching a given pattern of interesting length in a large text. The problem is very practical in its nature: it occurs in many real-worlds applications such as web search engines, linguistics, bioinformatics etc. This is the reason why algorithms should be efficient even if the speed and capacity of storage of computers increase regularly. String matching performs important tasks in many applications including information retrieval; library systems, artificial intelligence, pattern recognition, molecular biology, and text search and edit systems. The challenge is that for the string matching to be accurate, it needs to be able to search every byte of every input data streaming for a potential match from a large set of strings [1-7].

The main contributions of this work are summarized as follows. This work offers a comprehensive study as well as the results of typical parallel string matching algorithms at various aspects and their application on computing models. This work suggests the most efficient algorithmic models and demonstrates the performance gain for both synthetic and real data. The rest of this work is organized as, review typical algorithms, algorithmic models and finally conclude the study.

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II. OUR CONTRIBUTION

Thousands of papers, literally, have been published about string matching, exploring the multitude of theoretical and practical facets of this fascinating fundamental problem. For example let us consider text(T) length of n and pattern(P) length of m. suppose there is an occurrence of P in T, it means the text string $t_i, t_{i+1}..t_{i+m-1}$ equal to P, so that $H(t_i, t_{i+1}..t_{i+m-1}, P) = 0$. Many other algorithms have been published; some are faster on the average, use only constant auxiliary space, operate in real-time, or have other interesting benefits. This work categorizes the algorithms into some categories to emphasize the data structure that drives the matching. These categories are discussed here.

a) Intrusion Detection Systems (Ids)

Yongin-si et.al [8] proposed an algorithm that maps target patterns onto parallel string matching architectures in intrusion detection systems(IDS). In this iterative pattern mapping, the sets of patterns that are mapped onto string matchers are stored in ascending order of the average pattern length in each turn. By mapping a set of patterns for a string matcher onto the string matchers repeatedly, the required number of string matchers is reduced. Therefore, the proposed iterative pattern mapping minimizes the total memory requirement for parallel string matching architecture.

i. DFA Based Approaches

Issues in accelerating DFA-based multi-pattern matching have received much attention in recent years by several researchers. Here we discuss some of them. Hongbin Lu et al.,[9] propose a memory-efficient multiple-character-approaching architecture consisting of multiple parallel deterministic finite automata (DFAs), called TDP-DFA. By employing efficient representations for the transition rules in each DFA, TDP-DFA significantly reduces the complexity. They also present a novel scheme to share the storage of transition rules among multiple DFAs, substantially decreasing the total storage cost, and avoiding the cost increase being proportional to the number of DFAs. They evaluate this design through theoretical analysis and comprehensive experiments.

Results show that TDP-DFA is able to meet the critical requirement of OC-768 wire speed processing, as well as constituting a promising way for scaling up to cope with throughput over 100 Gb/s in the future.

Experimental Results: Using the pattern set from Snort, they extract 2234 distinct substrings containing 33 793 characters from the signature

database. In their prototype, the space for each state field in a CDLE entry is 2 bytes, allowing the maximum number of states up to 65 536. This is large enough considering the maximum number they measured in real cases is less than 6000. Similarly, the "Action ID" field in an entry of the associated RAM also occupies 2 bytes. It is shown in the Fig.1.

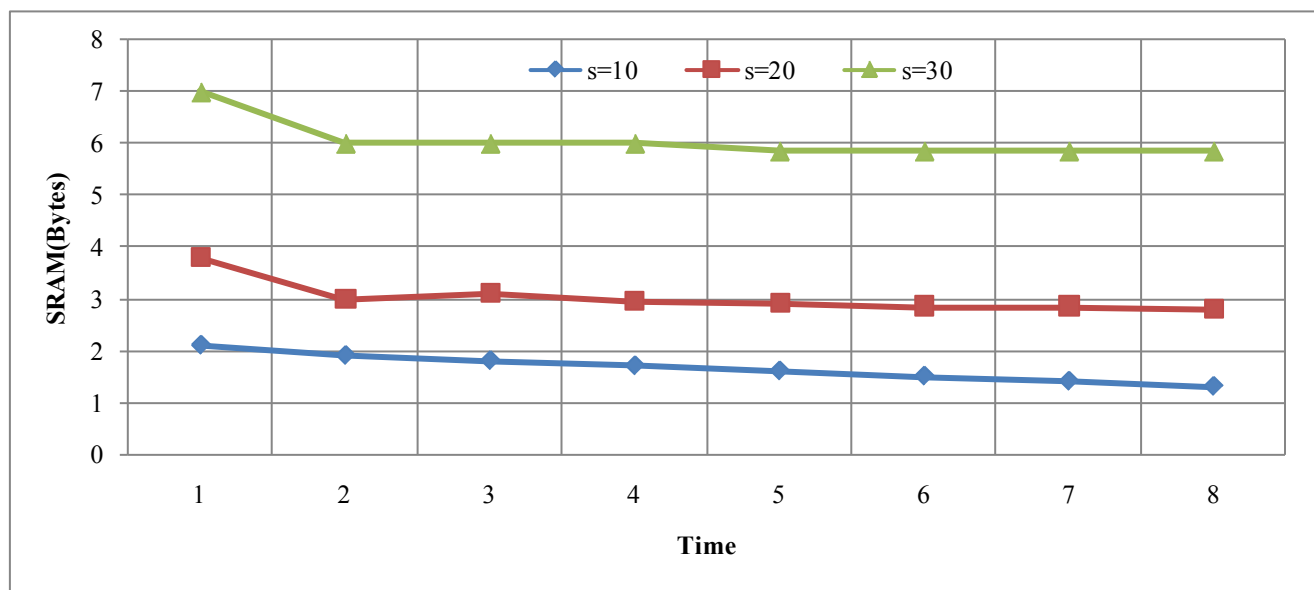


Figure 1 : Trade off for t

Yi-Hua E. Yang et al.,[10] proposed a novel partitioning algorithm which converts an AC-DFA into a "head" and a "body" parts. The head part behaves as a traditional AC DFA that matches the pattern prefixes up to a predefined length; the body part extends any head match to the full pattern length in parallel body-tree traversals. Taking advantage of the SIMD instructions in modern x86-64 multi-core processors, they design compact and efficient data structures packing multi-path and multi-stride pattern segments in the body-tree. Compared with an optimized AC-DFA solution, their head-body matching (HBM) implementation achieves 1.2x to 3x throughput performance when the input match (attack) ratio varies from 2% to 32%, respectively. Their HBM data structure is over 20x smaller than a fully-populated AC-DFA for both Snort and ClamAV dictionaries. The aggregated throughput of their HBM approach scales almost 7x with 8 threads to over 10 Gbps in a dual-socket quad-core Opteron (Shanghai) server.

b) Parallel Processing based Approaches

K.L. Chung et al.,[11] presents an $O(n)$ time parallel algorithm for finding all initial palindromes and periods of the string matching on an $n \times n$ reconfigurable mesh(RM) where n is the length of the string. They provide a partitionable strategy when the RM doesn't offer sufficient processors under the same

strategy. This overcomes the hardware limitation and is very suitable for VLSI implementation.

Heikki Hyyro and Gonzalo Navarro [12] presented a new bit-parallel technique for approximate string matching. They build on two previous techniques. The first one, BPM (Myers, 1999), searches for a pattern of length m in a text of length n permitting k differences in $O(\lceil m/w \rceil n)$ time, where w is the width of the computer word. The second one, ABNDM (Navarro and Raffinot, 2000), extends a sublinear-time exact algorithm to approximate searching. ABNDM relies on another algorithm, BPA (Wu and Manber, 1992), which makes use of an $O(k \lceil m/w \rceil n)$ time algorithm for its internal workings. BPA is slow but flexible enough to support all operations required by ABNDM. They improve previous ABNDM analyses, showing that it is average-optimal in number of inspected characters, although the overall complexity is higher because of the $O(k \lceil m/w \rceil)$ work done per inspected character. They then show that the faster BPM can be adapted to support all the operations required by ABNDM. This involves extending it to compute edit distance, to search for any pattern suffix, and to detect in advance the impossibility of a later match. The solution to those challenges is based on the concept of a witness, which permits sampling some dynamic programming matrix values to bound, deduce

or compute others fast. The resulting algorithm is average-optimal for $m \leq w$, assuming the alphabet size is constant. In practice, it performs better than the original ABNDM and is the fastest algorithm for several combinations of m , k and alphabet sizes that are useful, for example, in natural language searching and computational biology. To show that the concept of witnesses can be used in further scenarios, they also improve a recent variant of BPM. The use of witnesses greatly improves the running time of this algorithm too.

M. Oguzhan Külekci [13] proposed a new bit-parallel algorithm, given name *BLIM* (bit-parallel length independent matching), and for exact pattern matching that does not restrict the input pattern to be shorter than the word size. The multiple pattern case is also addressed, and it is shown that up to computer word size number of patterns, whatever their lengths are, can be searched simultaneously in a single bit-parallel framework. Similar to other algorithms of this genre, BLIM is also capable of handling fixed-length gaps and character classes in the input strings as well. The proposed algorithm is compared with the other alternatives of its class, mainly the shift-or and BNDM variants. Experimental results indicate that BLIM is compatible with the previous bit-parallel algorithms with an additional gain of overcoming the word size

limitation. The main contribution of this study is not a new faster string matching algorithm, but a new approach identifying the use of bits in a different manner. Each bit in the proposed scheme represents an event, and the observations performed during the investigation alter these events according to the pre computed masks. In the exact pattern matching problem examined in this study, the events correspond to the alignments of the patterns in a window, and the observations are actually the characters accessed.

Jorg Nolte And Paul Horton [14] discuss an experimental application that exploits TACO's distributed object groups and collective operations for computing the similarity between groups of molecular sequences, a computationally intensive core problem in molecular biology research. In particular they show how TACO's distributed collections can be conveniently combined with well known concepts found in the C++ standard template library (STL) to solve matching and sorting problems effectively on distributed hardware platforms. Figure 2 shows the results of the measurements using both a binary tree (par. red-2) and a 4-ary tree (par. red-4) topology. TACO's implementation is by all means in the competitive range and the reduction on the 4-ary tree topology even outperforms the MPI-based implementation.

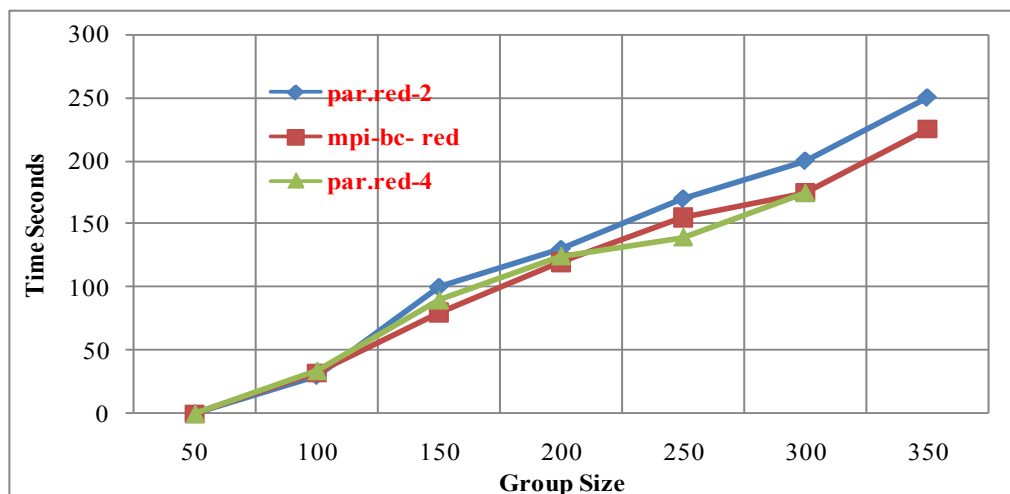


Figure 2 : TACO VS.MPI

c) Aho Corasick based Approaches

Many researchers propose the different hardware architectures based on the Aho-Corasick algorithm for accelerating string matching. Here we discuss one of them.

Kuo-Kun Tseng et al.,[15] propose a new Parallel Automaton string matching approach and its hardware architecture for content filtering coprocessor. This new approach can improve the average matching time of the Parallel Automaton with Pre-Hashing and Root-Indexing techniques. The Pre-Hashing technique uses a hashing function to verify quickly the text against the partial patterns in the Automaton, and the Root-

Indexing technique matches multiple bytes for the root state in one single matching. A popular Automaton algorithm, Aho-Corasick (AC) is chosen to be implemented by adding the two techniques; they employ these two techniques in a memory efficient version of AC namely Bitmap AC. For the average-case time, their approach improves Bitmap AC by 494% and 224% speedup for URL and Virus patterns, respectively. Since Pre-Hashing and Root-Indexing techniques can be concurrently executed with Bitmap AC in the hardware, their proposed approach has the same worst-case time as Bitmap AC.

Yunho Oh, Doohwan Oh and Won W. Ro [16] proposed a new parallel genome matching algorithm using graphics processing units (GPUs). Their proposed approach is based on the Aho–Corasick algorithm and it was developed based on a consideration of the architectural features of existing GPUs with a hundred or more cores. Thus, they provide an appropriate task partitioning method that runs on multiple threads and they fully utilize the cache memory and the shared memory structures available in GPUs. Especially, they propose a tiled access method for rapid data transfer from the global memory to the shared memory. They also provide new models for cache-friendly state transition table to improve performance of pattern matching operations on GPUs. The maximum throughput they achieved in various experiments was 15.3Gbps.

For the performance evaluation, they selected five genome sequences and used the EST database provided by the UC Santa Cruz Genome Browser as the pattern set. The details of the input sequences are described in Table 2(a). In order to analyze the performance of modern GPU architectures, all experiments were performed using an NVIDIA GTX 285 (GT200 architecture) and a GTX 480 (Fermi architecture).

J. J. ASTRAIN et al.,[17] apply a genetic algorithm to adjust the automaton parameters for selecting the ones best fit to a particular application. They have introduced a genetic algorithm to adjust the parameters of a deformed fuzzy automaton. They propose the use of genetic algorithms for the automatic parameter tuning of a deformed fuzzy automaton and they validate it for the approximate string matching problem. This genetic approach overcomes the difficulty of using common optimizing techniques like gradient descent, due to the presence of non derivable functions in the calculus of the automaton transitions. Experimental results, obtained in a text recognition experience, validate the proposed methodology.

Yoginder S Dandass et al.,[18] describes techniques for accelerating the performance of the string set matching problem with particular emphasis on applications in computational proteomics. The process of matching peptide sequences against a genome translated in six reading frames is part of a proteogenomic mapping pipeline that is used as a case-study. The Aho-Corasick algorithm is adapted for execution in field programmable gate array (FPGA) devices in a manner that optimizes space and performance. In this approach, the traditional Aho-Corasick finite state machine (FSM) is split into smaller FSMs, operating in parallel, each of which matches up to 20 peptides in the input translated genome. Each of the smaller FSMs is further divided into five simpler FSMs such that each simple FSM operates on a single bit position in the input (five bits are sufficient for

representing all amino acids and special symbols in protein sequences). This bit-split organization of the Aho-Corasick implementation enables efficient utilization of the limited random access memory (RAM) resources available in typical FPGAs. The use of onchip RAM as opposed to FPGA logic resources for FSM implementation also enables rapid reconfiguration of the FPGA without the place and routing delays associated with complex digital designs. Experimental results show storage efficiencies of over 80% for several data sets. Furthermore, the FPGA implementation executing at 100 MHz is nearly 20 times faster than an implementation of the traditional Aho Corasick algorithm executing on a 2.67 GHz workstation.

d) *Finite Automata Based Approaches*

Gerald Tripp [19] describes a finite state machine approach to string matching for an intrusion detection system. To obtain high performance, they typically need to be able to operate on input data that is several bytes wide. However, finite state machine designs become more complex when operating on large input data words, partly because of needing to match the starts and ends of a string that may occur part way through an input data word. Here they use finite state machines that each operates on only a single byte wide data input. They then provide a separate finite state machine for each byte wide data path from a multi-byte wide input data word. By splitting the search strings into multiple interleaved substrings and by combining the outputs from the individual finite state machines in an appropriate way they can perform string matching in parallel across multiple finite state machines. A hardware design for a parallel string matching engine has been generated, built for implementation in a Xilinx Field Programmable Gate Array and tested by simulation. The design is capable of operating at a search rate of 4.7 Gbps with a 32-bit input word size.

Panagiotis D. Michailidis and Konstantinos G.Margaritis[20] proposed a linear processor architecture for flexible string matching. This architecture is a bit-parallel realization of the non-deterministic finite automation, which minimizes the amount of data flow between adjacent cells. Initially a bit-level algorithm is discussed which consists of two phases, i.e. preprocessing and searching. Then, starting from the data dependence graph of the searching phase processor array architecture is derived. Further, the preprocessing phase is also accommodated onto the same processor array design.

Junchen Jiang et al.,[21] proposed a multi-string matching acceleration scheme named Synergic Parallel Compact Finite Automata (SPC-FA) Matching System together with its conflict-free dispatching algorithm and the corresponding memory optimization mechanisms. Their scheme can be understood as consisting of k SPC-FAs, each of which processes one

of every k characters from the input stream and can achieve a speed up factor of $\frac{10}{13^k}$ with low memory occupation.

e) Prefix based Approaches

Abdelghani Bellaachia and lehab Al Rassan [22] proposed a Tagged Sub-optimal code (TSC), a new coding technique to speed up string matching over compressed databases on personal digital assistants (PDA). TSC is a variable-length sub-optimal code that supports minimal prefix property. It always determines its codeword boundary without traversing a tree or lookup table. TSC technique may be beneficial in many types of applications: speeding up string matching over compressed text, and speeding decoding process. This paper also presents two algorithms for string matching over compressed text using TSC (SCTT) and the Byte Pair Encoding (BPE) technique (SCTB). Several experiments were conducted to compare the performance of TSC, Byte Pair Encoding (BPE), and Huffman code. Several PDA databases with different record sizes were used: the well-known Calgary dataset and a set of small-sized PDA databases. Experimental results show that SCTT is almost twice as fast as the Huffman-based algorithm. SCTT has also the same performance in search time as the search in uncompressed databases and is faster than the SCTB

algorithm. For frequently updated PDA databases such as phone books, to-do list, and memos, SCTT is the recommended method regardless of the size of the average record length, since the time required to compress the updated records using BPE poses significant delays compared to TSC.

Experimental Results: The experimental results for Searching over Compressed Text using BPE (SCTB) and Searching over Compressed Text using TSC (SCTT) solutions are presented, which was shown in the figure 3. A library application was developed on a Palm OS handheld device. The application supports basic functions such as adding, deleting, or modifying an article entry, where each entry is a record consisting of author, title, and subject fields. Different sized database records and different record numbers in each database were loaded and implemented for testing purposes. Both searching techniques were implemented in the library application to allow searching while databases were in compressed form. C language with CodeWarrior compiler version 4.01 was the development environment used for designing and implementing the library application. Figure 3 shows the searching time using the SCTT, SCTB, and Huffman-based methods. Results show that SCTT is 88% faster than Huffman-based and 92% slower than SCTB-SO. Moreover, SCTT is 22% slower than the SCTB-Linear solution.

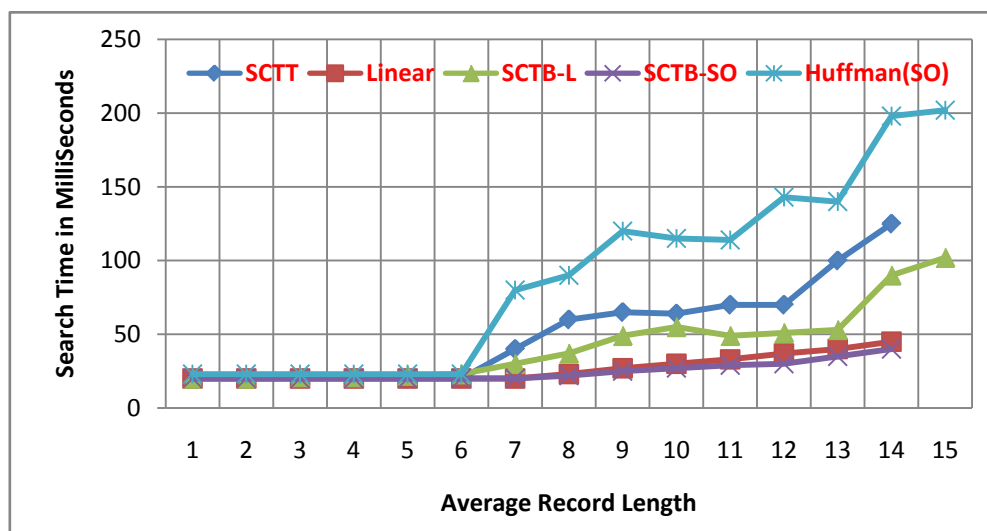


Figure 3: Searching Time on PDA

Figure 4 shows the searching time using the SCTT, SCTB, and Huffman-based methods compared to a linear search over uncompressed databases for small-sized records. Results show that SCTT is 85% faster than Huffman-based and 6% faster than SCTB-SO. In addition, SCTT is 15% faster than the SCTB-Linear solution for small-sized records.

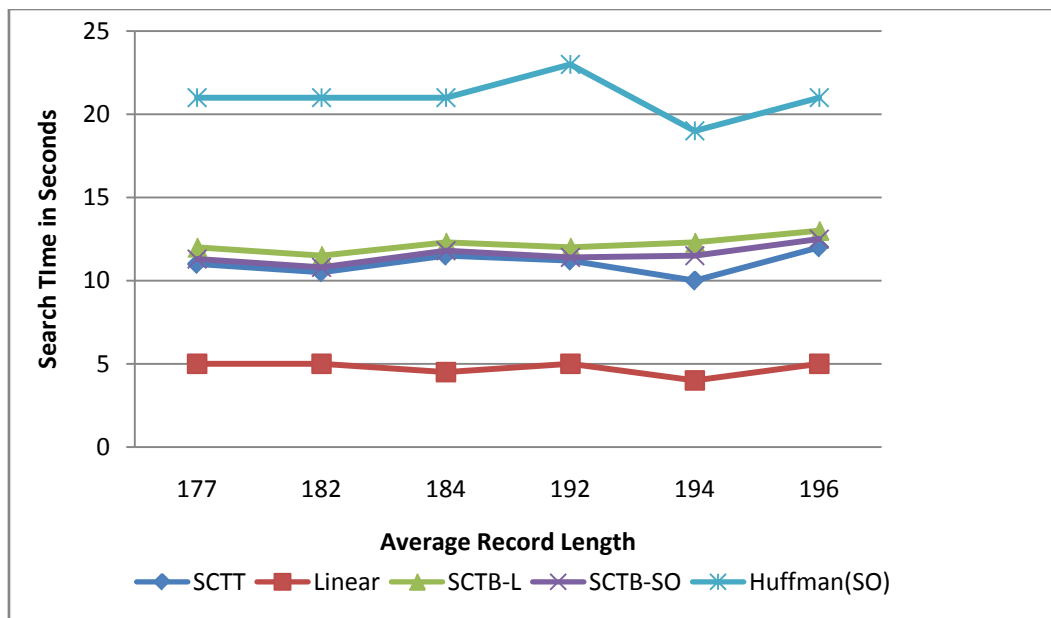


Figure 4 : Searching time on PDA for small-sized records

f) Hardware Related based Approaches

Leena Salmela, Jorma Tarhio and Petri Kalsi [23] proposed the improvements for FAST algorithm, a variation of Boyer-Moore string matching problem for k -mismatches. FAST is specifically tuned for small alphabets. They further improve FAST algorithm gaining speedups in both preprocessing and searching. They also present three variations of the algorithm for the k -difference problem. They show that the searching time of the algorithms is average-optimal and the preprocessing also has a lower time complexity than FAST. Their experiments show that their algorithm for the k -mismatch problem is about 30% faster than FAST and the new algorithms compare well against other state-of-the-art algorithms for approximate string matching.

Mihai Oltean[24] proposed a solution for finding a pattern P of length m in text T of length n . They describe a special device which can do string matching by performing $n-m + 1$ text-to-pattern comparisons. The proposed device uses light and optical filters for performing computations. Two physical implementations are proposed. One of them uses colored glass and the other one uses polarizing filters. They have made an in-depth analysis of the strengths and of the weaknesses of each method. At first sight they can infer that polarizing filters are more stable than colored glass for the string matching problem. The physical implementation of the proposed devices might be time consuming, so these methods might not bring such a great benefit unless they find some real-world cases where there are no other options for implementation but the ones they have proposed. However, the greatest benefit is that they have shown

that string matching can be efficiently done by using the massive parallelism of the light.

Guang-Ming Tan et al.,[25] proposed an attempt to design efficient multiple pattern searching algorithms on multi-core architectures. They observe an important feature which indicates that the multiple pattern matching time mainly depends on the number and minimal length of patterns. The multi-core algorithm proposed in this paper leverages this feature to decompose pattern set so that the parallel execution time is minimized. They formulate the problem as an optimal decomposition and scheduling of a pattern set, and then propose a heuristic algorithm, which takes advantage of dynamic programming and greedy algorithmic techniques, to solve the optimization problem. Experimental results suggest that their decomposition approach can increase the searching speed by more than 200% on a 4-core AMD Barcelona system.

Experimental Results: The input text and patterns are randomly generated. The length of the input text is 10 million bytes; the lengths of patterns follow a random distribution in a range [2; 200]. The number of patterns is set to be {10 000; 20 000; 40 000}. They examine the parallel algorithms on a commercial multi-core processor, AMD Barcelona. It is a quad-core processor which features a highly integrated design with all four cores on a single die with shared resources. Each core has its own private 128KB L1 cache and 512KB L2 cache. All four cores share a common L3 cache that is at least 2MB in size. The full system provides an aggregate memory bandwidth of 21.4 GB/s and 54.4 GFlops/s peak performances. The compiler used in the experiment is GCC 4.1. Fig.5 shows a

comparison of the parallel searching time. The comparison suggests that their proposed parallel optimization can increase the searching speed by more

than 200% and the performance advantage is higher when the pattern number increases.

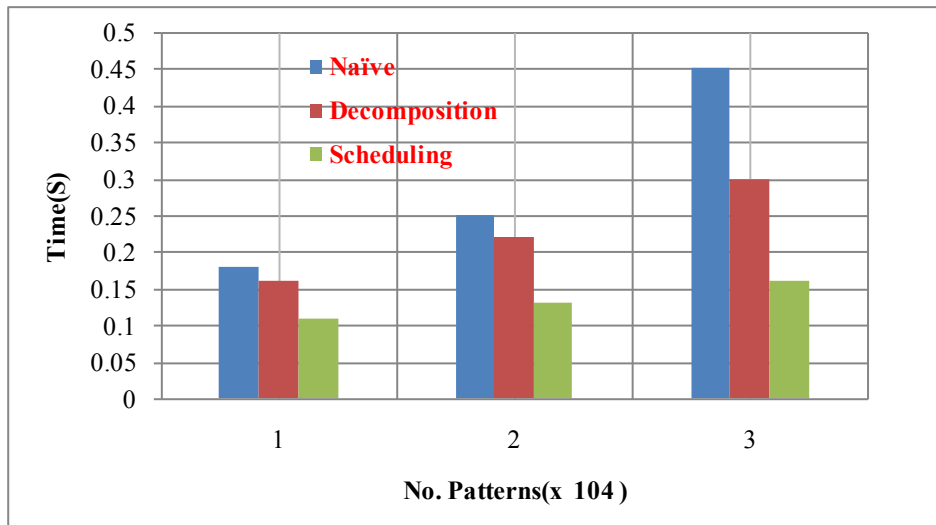


Figure 5 : Comparison of execution time. X-axis is the number of patterns

Fig.6 plots the scalability of the final parallel program with an increasing number of cores. The result

shows that the parallel program achieves sub-linear speed up from 1 core to 4 cores.

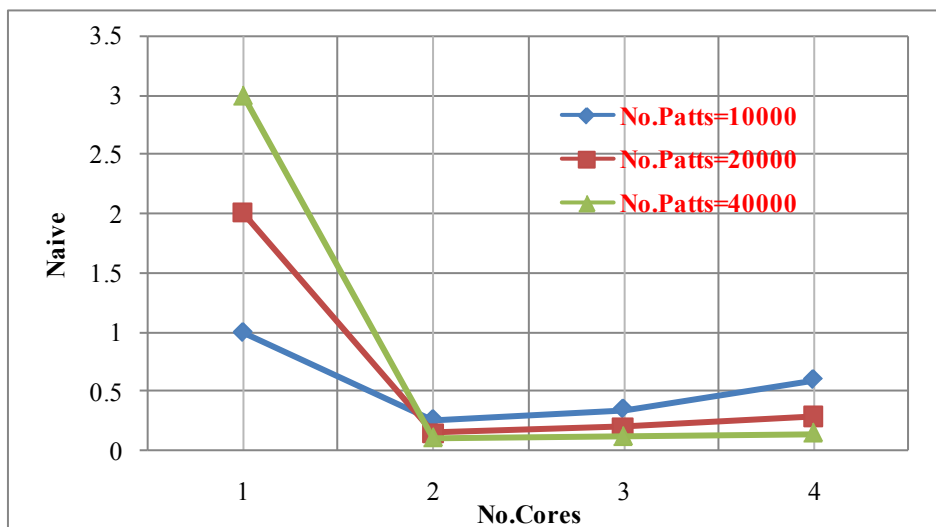


Figure 6 : Scalability of the parallel programs for different problem sizes, x-axis is the number of cores

g) Other Approaches

Hung-Che Shen, and, Chungnan Lee [26] proposed a “Whistle for Music” system which enables users to retrieve MIDI format music by whistling a melodic fragment. Three essential components are query processing, MIDI preprocessing and an approximate search engine. For query processing, they have achieved a real-time and robust whistle-to-MIDI converter. For feature extraction, the proposed MIDI preprocessing can extract individual, local and global melodic descriptions from MIDI files. In order to match query with target, they extend an existing search engine into a fast approximate melodic matching engine. Based

on the integration of those three components, the system can return a list of MIDI files that are ranked by how closely they match the whistling. The systematic evaluation for the query-by-whistling system is finally performed. Although the content is focused on MIDI data, the unified algorithmic framework is suitable for a wide range of applications in music information retrieval. They have demonstrated three essential components: a melody transcription (a query processing), a MIDI preprocessing (feature extraction) and melodic AGREP (a search engine). One major feature in their system implementation is that “Whistle for music” is fast enough for “searching while whistling.” The other feature is that

they provide detailed description of extracting multi-level melodic descriptions from a MIDI database. In order to provide a more sophisticated MIR system, they explore the query representation by individual, local and global descriptions. In addition, they have provided a helpful sight whistling tutor for derive a high-quality query. Finally, they have shown that the issue of scaling with database size can be studied by simulation. Given error distances between queries and targets, they can plot the expected number of queries whose correct targets will be ranked over a specific database size. The results show that careful measurement and objective comparisons can lead us to know the scaling trend about query and target. One encouraging aspect is that the performance can be predicted based on the evaluation methods.

HU Yue et al.,[27] proposed a complete automaton and its high-speed construction algorithm for large-scale U-, V-, and U-V-uncertain multiple strings, including two or more uncertain strings interlaced with one another. The maximum number of parallel complete automation of the V-uncertain string is also given. This paper reveals that there are two kinds of prepermissions, i.e., similarly-connected and interlaced string prepermissions, and that mistake may appear in the matching of the regular expressions, or states in the automaton may increase in number, if the intersection of the U-uncertain strings sets and the homologous subsequent special point in the U-uncertain strings sets are not eliminated from the whole system.

B. N. Araabi et al.,[28] presents a syntactic/semantic string representation scheme as well as a string matching method as part of a computer-

assisted system to identify dolphins from photographs of their dorsal fins. A low-level string representation is constructed from the curvature function of a dolphin's fin trailing edge, consisting of positive and negative curvature primitives. A high-level string representation is then built over the low-level string via merging appropriate groupings of primitives in order to have a less sensitive representation to curvature fluctuations or noise. A family of syntactic/semantic distance measures between two strings is introduced. A composite distance measure is then defined and used as a dissimilarity measure for database search, highlighting both the syntax (structure or sequence) and semantic (attribute or feature) differences. The syntax consists of an ordered sequence of significant protrusions and intrusions on the edge, while the semantics consist of seven attributes extracted from the edge and its curvature function. The matching results are reported for a database of 624 images corresponding to 164 individual dolphins. The identification results indicate that the developed string matching method performs better than the previous matching methods including dorsal ratio, curvature, and curve matching. The developed computer-assisted system can help marine mammalogists in their identification of dolphins, since it allows them to examine only a handful of candidate images instead of the currently used manual searching of the entire database. The figure 7 describes the percentage of test images with first correct match VS number of database individuals examined before catching the correct match.

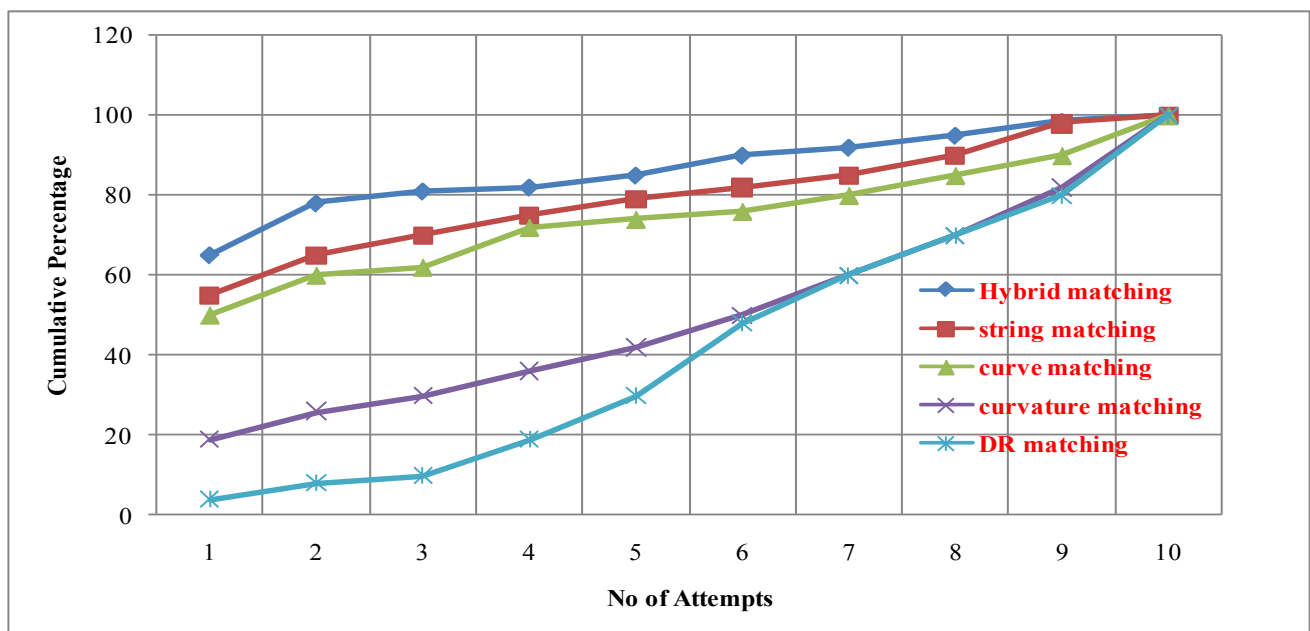


Figure 7 : Dolphin photo identification

III. CONCLUSIONS

In this study, we widely investigate the problem of sequential and parallel approaches in the context of string matching. An outline of string corresponding is made, in which the special forms of parallel string matching problem are also distinguished, and the classifications of parallel string matching problem are discussed. We importantly review different classifications of parallel string matching algorithms. Based on this study, a number of positive suggestions are made which will be cooperative to the researchers for developing better techniques.

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Achieving Flexible Multipath Routing through Dag's

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Abstract - With a specific end goal to realize versatile multipath steering, we present the notion of free regulated non-cyclic charts (IDAG's) in this paper. Join autonomous (hub free) DAG's fulfil the property that any way from a source to the root on one DAG's is connection disjoint (hub disjoint) with any way from the source to the root on the other DAG. Given a system, we advance polynomial time calculations to process join free and hub autonomous DAG's. The calculation advanced in this paper furnishes multipath tracking, uses all conceivable edges, ensures recuperation from single connection inadequacy and accomplishes all these with at most one touch for every bundle as overhead when steering is dependent upon terminus address and approaching edge. We indicate the viability of the proposed IDAG's approach by contrasting key execution lists with that of the autonomous trees and various combines of free trees strategies through broad recreations.

Keywords : *multipath, cyclic graph, connections, dag.*

GJCST-C Classification : *C.2.2*



Strictly as per the compliance and regulations of:



Achieving Flexible Multipath Routing through Dag's

Macha Prasanth ^α & L. Naresh Babu ^σ

Abstract - With a specific end goal to realize versatile multipath steering, we present the notion of free regulated non-cyclic charts (IDAG's) in this paper. Join autonomous (hub free) DAG's fulfil the property that any way from a source to the root on one DAG's is connection disjoint (hub disjoint) with any way from the source to the root on the other DAG. Given a system, we advance polynomial time calculations to process join free and hub autonomous DAG's. The calculation advanced in this paper furnishes multipath tracking, uses all conceivable edges, ensures recuperation from single connection inadequacy and accomplishes all these with at most one touch for every bundle as overhead when steering is dependent upon terminus address and approaching edge. We indicate the viability of the proposed IDAG's approach by contrasting key execution lists with that of the autonomous trees and various combines of free trees strategies through broad recreations.

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I. INTRODUCTION

Web furnishes stage for a mixture of requisitions and all these provisions have the need for strength and transmission capacity. Different systems have been produced for attaining better vigor of the system. Multipath tracking is a system in which the parcels are steered along various ways between the source and the goal. This plan guarantees security and burden equalizing. Recuperation methods dependent upon multipath steering utilize more than one track to the end and utilize various traversing trees or DAG's. The point when there is a flop in one of the tracks, the parcels is steered through the substitute tracks. In, each hub has reinforcement sending edges. The point when the default sending edge falls flat, exchange edge is browsed the reinforcement sending edges. In, the creators present a skeleton for IP quick reroute itemizing three applicant answers for IP quick reroute that have all picked up impressive consideration. These are numerous tracking setups (Mrcs), inadequacy heartless steering (FIR) and tunnelling utilizing not through locations (Not by means of).

The normal characteristic of all these methodologies is that they utilize numerous steering tables. Shaded trees approach for multipath steering is investigated in. In this approach, two colored trees are

developed that are connection or hub disjoint with every other. This approach is comparable to utilizing numerous tracking tables aside from those just two tables are needed hence. The Independent DAG's, acquainted in, are comparative with the shaded trees. The trees can use a most extreme of $2(|n|-1)$ administered edges for tracking from a source to a terminus, where $|n|$ is the amount of hubs in the system. The IDAG's defeat this characteristic limit of the trees by using all conceivable edges accessible in the system with the exception of the aforementioned radiating from the goal what's more those constrained by the underlying system topology. The IDAG tracking sureties single connection washout recuperation.

What is not recognized is the productivity of the interchange track picked. There are numerous Quality of Service (Qos) based procedures accessible to pick the slightest cost way around the accessible tracks. We think about here the Dijkstra's calculation to perform the slightest expense way calculation. We present the idea Weighted Independent Directed Non-cyclic Graphs (WIDAG's), to incorporate the connection cost relating to the system qualities to the IDAG's. In this paper, we advance a productive tracking system over the versatile steering method IDAG. We present the notion of WIDAG's, a broadening of IDAG's. The system attributes of deferral, data transmission, transforming power and the like are merged and spoke to as an expense for every connection of the system. IDAG's are developed utilizing direct time calculations and washout tracking is attached with effective minimum cost way calculation calculations. The calculations for development of IDAG's are demonstrated to use most extreme conceivable edges of the system. The Dijkstra's calculation picks the most proficient way heuristically.

II. EXISTING SYSTEM

Fig. 1 shows a case system where red and blue trees, established at hub are built. This tree development empowers recuperation from a solitary connect inadequacy by exchanging starting with one tree then onto the next. For instance, think about a parcel that is sent from hub F to hub An on the blue tree. The point when there are no washouts, the parcel might take the way F-c-b-a. In the event that connection C-b fizzles, then hub C might reroute the bundle on the red tree, in this way the parcel will take after the way F-c-f-i-h-g-d-a. Accept that a second connection

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inadequacy happens on connection I-h. As just two autonomous trees were developed and recuperation from subjective two connection washouts can't be ensured, the parcel will be dropped when the second connection disappointment is experienced. One approach to improve the strength is to permit the bundle to be exchanged various times between the trees. Such a methodology will fall flat in the case acknowledged previously.

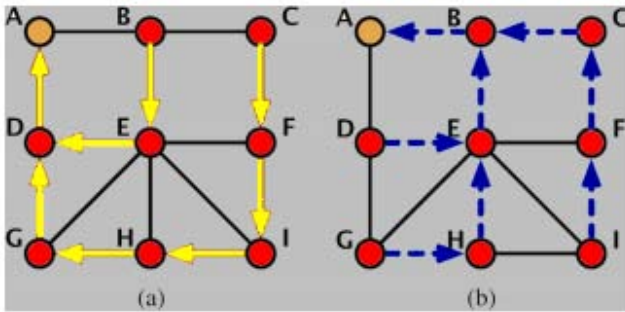


Figure 1 : Illustration of node-independent trees for the example network. (a) Red tree. (b) Blue tree. Node A is the root (destination) node

The bundle will be rerouted here and there and then here again on the way I-f-c. We may break down when exchanging once more to a tree might ensure not experiencing a past washout again [18] by watching the lands of the autonomous tree development prepare. Then again, the characteristic restriction of the tree-based methodology is that it uses just $2(|n| - 1)$ directed edges to track to a goal, where $|n|$ signifies the amount of hubs in the system. Our objective is in this way to use the extra joins accessible in the system to enhance strength. To this end, we look to develop free administered non-cyclic diagrams established at every hub.

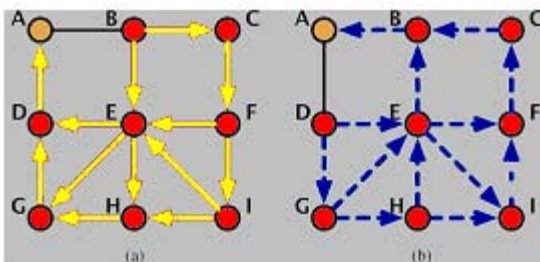


Figure 2 : Illustration of node-independent trees for the example network. (a) Red tree. (b) Blue tree. Node A is the root (destination) node

Fig. 2(a) and (b) shows two autonomous administered Non-cyclic charts established at hub A. Watch that hub I has two red sending edges accessible. In this way, in the prior illustration, provided that connection I-h comes up short, the parcel may be sent on connection I-e to achieve the goal. Most extreme Alternative Routing Algorithm (MARA) builds a DAG that uses all edges in the system to increment the amount of

ways significantly. Then again, the calculation does not furnish an instrument for reinforcement sending the point when experiencing a solitary join or hub washout. An alternate approach is to utilize different matches of shaded (autonomous) trees, however such a system will require the parcel to convey data on which match is, no doubt utilized for tracking. Our objective in this paper is to improve a classy answer for accomplish multipath steering, use all conceivable edges, ensure recuperation from single connection flops and decrease the amount of overhead bits needed in the parcel header. Besides, the utilization of different non disjoint ways is invaluable in burden adjusting furthermore forestalling snooping on information, not in addition to improving resiliency to multiple link failures. Disseminated duplicate. In the event that that duplicate is later run across in the hands of an unapproved gathering, the leaker might be identified. Watermarks could be extremely convenient in a few cases, yet once more, include some modification of the first ever information. Besides, watermarks can here and there be obliterated if the information beneficiary is spiteful. In this paper we improve a model for evaluating the "blame" of operators. We likewise introduce calculations for distributing protests executors, in a manner that enhances our shots of distinguishing a leaker. At last, we additionally think about the choice of including "fake" questions the appropriated set. Such objects don't relate to genuine substances however seem practical to the executors. It could be said, the fake protests goes about as a sort of watermark for the whole set, without altering any distinctive parts. Provided that it makes executor was given one or more fake articles that were spilled, then the merchant might be more confident that operator was blameworthy. And let us consider another example E.g. A hospital may give patient records to researchers who will devise new treatments. Similarly, a company may have partnerships with other companies that require sharing customer data. Another enterprise may outsource its data processing, so data must be given to various other companies. We call the owner of the data the distributor and the supposedly trusted third parties the agents.

III. ANALYSIS FOR INDEPENDENT WEIGHTED DAG

Think about a system with a set of hubs and connections signified by N and L, individually. Expect that the connections are bidirectional in nature, which may be acknowledged by utilizing two unidirectional connections. A bidirectional connection between hubs i and j is signified by $i - j$, while the guided connection from i to j is indicated by $i \rightarrow j$. The point when a connection comes up short, it is accepted that both administered edges $i \rightarrow j$ and $j \rightarrow i$ have fizzled. DAG is established at d if d is the main hub in the DAG that has no friendly edges. Each other hub has anyhow one friendly edge. Provided that the arrangement of edges

beginning from any hub is crossed, the way will end at hub d and will be circle free. Think about two regulated non-cyclic charts that are established at d . The two DAG's are said to be connection free if for each hub $s \in N$, $s \neq d$, any way from s to d on one DAG is connection disjoint with any way from s to d on the other DAG. So also, the two DAG's are said to be hub autonomous if for each hub $s \in N$, $s \neq d$, any way from s to d on one DAG is hub disjoint with any way from s to d on the other DAG. The system is accepted to utilize connection state convention; thus each hub has the perspective of the whole system topology. Each hub registers two DAG's, to be specific red and blue, for every goal and keeps up one or all the more sending entrances for every terminus for every DAG. Think about a system $G(n;l)$ made out of a set of hubs N and a set of connections L . The connections are thought to be bi-directional. A circular segment $i \rightarrow j$ speaks to a steered connection between hubs i to j . Let W_{ij} indicate the expense of connection $i-j$, for example postpone on a connection. Given a terminus hub, we build and look after two trees R and B (alluded to as the red and blue trees, individually) that are hub (join) autonomous and established at d such that the normal way length from a hub to the channel is minimized. A system must be two hub associated (two edge joined).

Also, the system must remain two associated with remake the shaded trees after a flop. In the event that an answer for the connection disjoint (hub disjoint) issue is needed after k self-assertive hub (join) washouts, then the system must be $k + 2$ hubs (edge-) associated. While there exists a set of m hubs (joins), where $m > k$, whose evacuation might bring about a less than 2 hub (edge) joined system, not all mixes of m hub (join) evacuation will bring about an absence of two connectivity. Figure 1 shows the move from IDAG to WIDAG for a case network. The productive re tracking requires the connection lands like deferral, movement, transmission capacity and the like to be acknowledged. These parameters are amassed and every connection in the system is given a weight. In this way the IDAG's shaped from such systems are Weighted Independent Directed Acyclic Graphs. Accordingly, the Weighted Independent Directed Acyclic Graphs (WIDAG's) are as well as weights for the connections of the relating autonomous guided non-cyclic chart.

Likewise, when there is a connection $i-j$ with weight w_{ij} in the system, both the regulated connections $i \leftarrow j$ and $i \rightarrow j$ are allotted the same weight w_{ij} , for straightforwardness. This is additionally since the vast majority of the static parameters will not shift between both bearings of the link of the original network.

IV. WIDAG DESIGNING

We build the IDAG's utilizing the method talked about. In like manner, two vertex connectivity is the need

and the sufficient condition for development of two hub autonomous IDAG's. We first register the base autonomous trees by utilizing way enlargement strategies. We then include the edges that are not introducing in either of the Dags and keep up priority connection around the hubs in both the trees. From, A hub x goes before y , indicated by, on a DAG if hub y utilizes hub x in no less than one of its ways to d . The fractional request on a DAG may be seen basically as reach ability on the DAG that seems to be, infers that x is reachable on the DAG by y . This relationship is the key to the development as it escapes any cycle framing, henceforth the Dags. The system for building WIDAG. We expand this method with the minimum way calculation calculation. Thusly, on any hub washout, the quest for an elective way will be consolidated with Dijkstra's calculation to make the most optimal choice.

Widag Algorithm

Consider a network of N nodes and E links.

- Get the network layout in the form of adjacency matrix.
- The adjacency matrix has entries as $\{W$ when edge present 0 when edge absent $\}$ where w is the weight of the edge.
- Check if the entered network is two-vertex connected.
- Get the source node s and the destination node d in the network.
- For the given source and destination node, we construct a DAGR from the underlying undirected graph, utilizing all its edges.
- We construct the corresponding IDAG B of the DAG R using N -IDAG construction method.
- For a given failure node in R , we find an alternate shortest Route from the source to the destination in R .
- We switch to B in case an alternate route is unavailable in R .

V. RESULTS

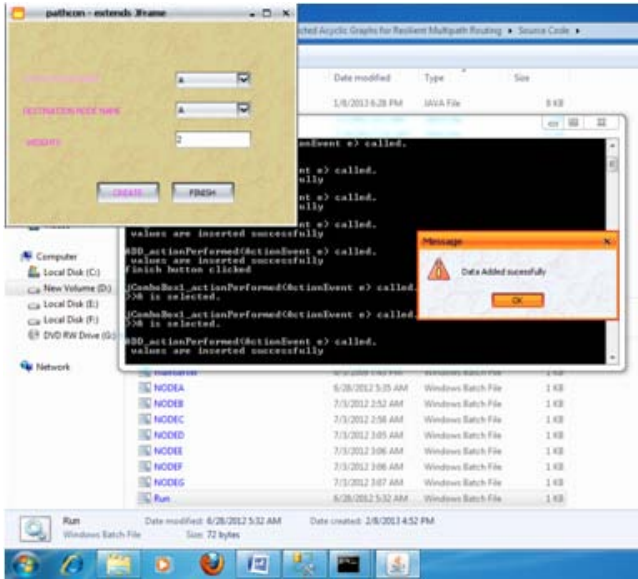


Figure 3 : Adding nodes & Assign weights

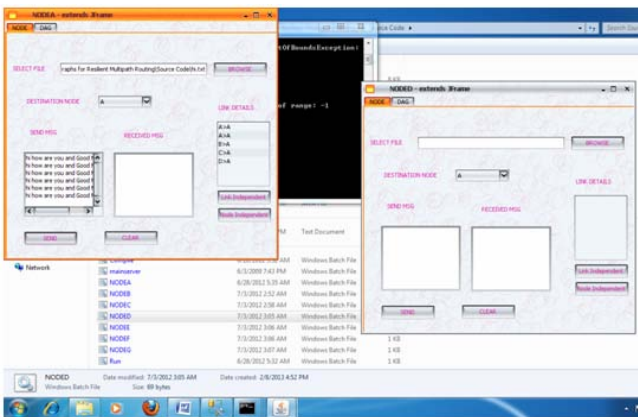


Figure 4 : Sending data from source to destination

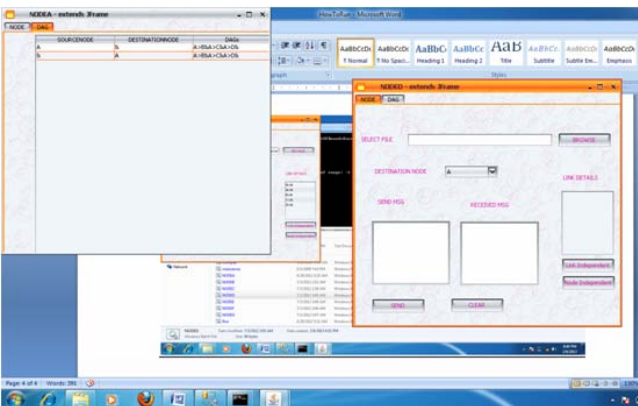


Figure 5 : Independent directed acyclic graph

VI. CONCLUSION

We presented the thought of free administered non-cyclic diagrams (IDAG's) and improved an approach for strong multipath tracking utilizing two

IDAG's. We advanced polynomial time calculations to build hub autonomous and join autonomous DAG's utilizing all conceivable edges as a part of the system.

The IDAG's methodology was assessed on four genuine system topologies and contrasted with ITREE's and different combines of colored trees methodologies to demonstrate the legitimacy of the calculation. Through re-enactments, we indicated that the IDAG's approach performs significantly superior to the autonomous trees approach as far as expanding number of ways offered, lessening the likelihood of a two-connection disappointment disengaging a hubs from the terminus, and normal connection stack. Likewise, the trees dependent upon the most brief ways on the IDAG's have preferred execution over that of the ITREE's approach since the normal most brief way length on the IDAG's is shorter than the normal way length on the ITREE's. Various matches of coloured trees methodology are better as far as the result of the amount of basic connections and normal connection load contrasted with the ITREE's and IDAG's approaches. None the less, the technique is illogical since it needs numerous overhead bits in the parcel header.

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Performance Analysis of Improved Component Based Software Reliability Model

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Abstract - Software reliability engineering techniques focus on development and maintenance of software systems. This paper presents a improved component model. The model is used to estimate the reliability of software systems and the usage ration of each component. A component impact analysis which helps in focusing of testing is presented .The proposed method exhibits considerable improvement when compared against conventional methods.

Keywords : *software reliability, component ratio, reliability estimation model.*

GJCST-C Classification : *D.2.4*



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K. Venkata Subba Reddy ^α & Dr. B. Raveendra Babu ^ο

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I. INTRODUCTION

There is probably no other human made material which is more Omni present than software in our modern technical worlds. New applications softwares are coming into the market day by day to meet the human requirements. Software has become one of the key parts of many aspects of society like banking, telecommunications, automobiles, aviation, shopping, auditing, web teaching, personal entertainment, and so on. Today, science and technology demand high quality software for making improvements and breakthroughs [1].

SRE is mainly focused on key properties like reliability that can be defined as probability of a failure free operation over a period of time under specified environment [2]. Among many other properties like functionality, flexibility, capability and so on reliability has got its own importance and accepted as the major factor in quality assessment of software. This assessment quantifies failures that make the powerful systems to inoperative. SRE is defined as the qualitative study of the operational behavior of software based systems with respect to user requirements concerning reliability. As a proven technique, SRE has become a standard and currently practiced by more than 50 organizations in their software projects and reports including AT&T, Lucent, IBM, NASA, Microsoft, and many others in Europe, Asia, and North America. However, this number is still relatively small compared to the large amount of software producers in the world.

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Reliability measurements are useful in supporting management of the software development process. For instance, obtaining reliability estimates early in the development process can help determine if the software system is on track to meet its reliability goals and therefore increase management effectiveness. Because research in software reliability is both necessary and beneficial, this paper proposes further work in this field of software engineering. In particular, efforts are focused towards structure based software reliability models.

This paper is organized as; section II discuss about the history of SR and the structural model, Section III explains about the proposed component model for SR estimations ending with section IV and V about the results and discussions.

II. BACKGROUND

a) Software Structure Model

Software structure model can be defined by the components from which the software system is built and by establishing the relationships between these components. Many methods are available for the designing of software systems, and these methods provide a framework for decomposing the problem of software design into smaller pieces that are related to one another. Because the design process ultimately provides a blueprint for implementation, software design methods can be used to describe how software is physically decomposed. The two most popular categories of software design methods are Structured Design (SD) and Object-Oriented Design (OOD). Previous work on structural reliability models assumes that software is designed according to SD principles [3, 4, and 5]. The proposed model assumes that software is designed according to OOD principles.

Relationships are the basis of methods for calculating a total software system reliability figure from the reliability of the components. Current structural models follow one of two trends: execution path based [6, 7]. The practicality of the execution path approach is questionable; execution paths are preferred to the transition probability models because of the Markov process which does not reflect reality. In this paper, execution paths are used; however, execution paths are considered as series of component executions and reliability of a path will be obtained from the reliability of the path components.

Although the problems associated with execution paths can now potentially arise, the mathematical formulas derived for the software system reliability estimation will be simplified in a way that prior knowledge of the set of all execution paths is not necessary. Also, it is important to note that the combination of relationships and components that form the software structure model is extremely simplified. As software systems scale up, it might be necessary, for practicality purposes, to provide other components to group sub-components and other relationships.

b) *Component Model*

As stated in [7] shooman's model provides an equation to estimate the expected number of software failures (n_f)

$$n_f = Nf_1q_1 + Nf_2q_2 + \dots + Nf_nq_n \tag{1}$$

Where n is the number of software tests, f_i is the execution path usage ratio and q_i is the probability of failure of the path and n is the number of execution paths. Using the above equation (1) the software system probability of failure Q_s can be defined as

$$Q_s = \frac{n_f}{N} = \sum_{i=1}^{n_1} f_i q_i \tag{2}$$

The above equation describes the system unreliability is equal to the sum of the likelihood of failure over every execution path weighted by its corresponding execution path usage ratio. The software reliability R_s is defined as

$$R_s = 1 - Q_s \tag{3}$$

III. METHODOLOGY

The probability of a successful path represents that all components in the path execute successfully. In terms of conventional reliability theory, execution paths are equivalent to series reliability models. Series models require that all components work properly for system success. For independent component failures, the probability of failure along a given execution path is solely a function of the probability of failure of each component along the path.

$$p_i = p(C_{i1}) \cdot p(C_{i2}) \dots \cdot P(C_{in}) \tag{4}$$

Where n_i is the number of components on the respective path

$$p_i = \prod_{j=1}^n C_{ij} = \prod_{j=1}^n (1 - d_{ij}) \tag{5}$$

Unreliability can be written as

$$q_i = 1 - \prod_{j=1}^n (1 - d_{ij}) \tag{6}$$

If the components have a high reliability then the above equations can be rewritten as

$$p_i = 1 - \sum_{j=1}^n d_{ij} \tag{7}$$

$$q_i = \sum_{j=1}^n d_{ij} \tag{8}$$

Therefore software reliability can be defined as

$$R_s = 1 - Q_s = 1 - \sum_{k=1}^m \varphi_k D_k \tag{9}$$

Where D_k represents the probability of failure of component.

The component usage ratio parameter represents the ratio of total component execution time over the total software system execution time. The value of the component usage ratio is . The total of all components usage ratios is equal to 1. The component usage ratio weights the component reliability impact of the component reliabilities on the overall software system reliability. As a general the calculation of software reliability based rule, the reliability of a component frequently on component testing and/or inspection does not executed is expected to have more impact on the produce an accurate estimate of the reliability of overall system reliability than a component rarely the software system. When components are executed

$$\varphi_k = \frac{t_k}{T_s} \tag{10}$$

Calculation of component execution time is more difficult because it is necessary to track when each component is executed. The total component execution time describes the time spent executing instructions inside a component.

IV. RESULTS AND DISCUSSIONS

Table 1 : Example Data

K	C _k	D _k	φ _k
1	0.96	0.04	0.2
2	0.96	0.04	0.02
3	0.96	0.04	0.001
4	0.98	0.02	0.05
5	0.98	0.02	0.05
6	0.98	0.02	0.05
7	0.99	0.01	0.05
8	0.99	0.01	0.02
9	0.99	0.01	0.006
10	0.99	0.01	0.006
11	0.99	0.01	0.2
12	0.99	0.001	0.07
13	0.99	0.001	0.02
14	0.99	0.001	0.001
15	0.99	0.001	0.001

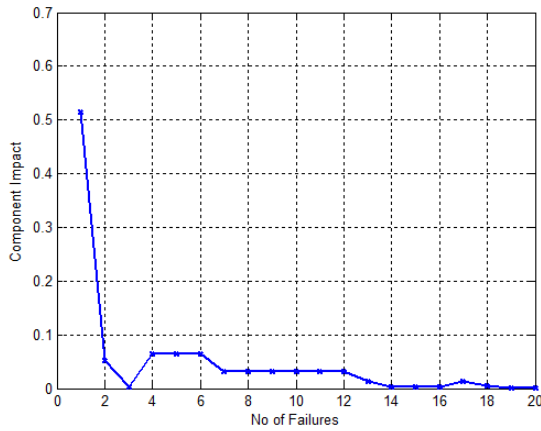


Figure 1 : Performance analysis of component Impact

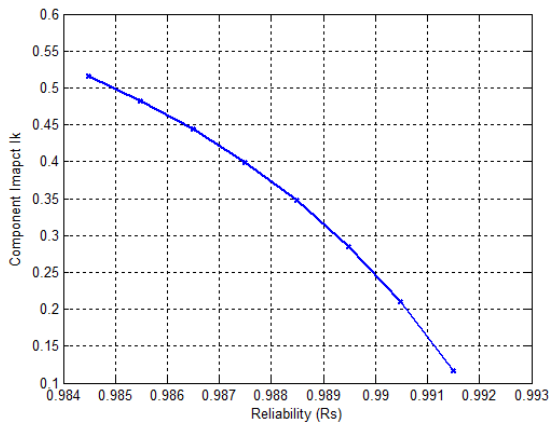


Figure 2 : performance analysis of component impact with respect to reliability

In this experiment we have considered a data as shown in the table 1. The above figure shows the impact of components with respect to the failures and the reliability. It is clear that the components reliability plays a prominent role in deciding the quality of the software. Numbers of failures are very low at a higher component impact and decreases gradually when it comes for the reliability.

V. CONCLUSIONS

A new mathematical model of software reliability is proposed in this paper. This focuses mainly on the impact of components when the reliability of software is estimated. It is proved that the malfunctioning of components have a great impact on the estimated reliability of software and the number failures are not optimal for calculations.

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Enhanced Novel Sorting Algorithm

By R. Srinivas

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Abstract - In computer science and mathematics; we can formulate a procedure for sorting unordered array or a file. Such procedure is always governed by an algorithm; which is called as Sorting Algorithm. Sorting is generally understood to be the process of rearranging a given set of objects in a specific order. The purpose of sorting is to facilitate the later search for members of the sorted set.

GJCST-C Classification : E.5



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Enhanced Novel Sorting Algorithm

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Abstract - In computer science and mathematics; we can formulate a procedure for sorting unordered array or a file. Such procedure is always governed by an algorithm; which is called as Sorting Algorithm. Sorting is generally understood to be the process of rearranging a given set of objects in a specific order. The purpose of sorting is to facilitate the later search for members of the sorted set.

I. INTRODUCTION

The intelligent and most intuitive way to do this is to analyze the items in the array or list with each other and adapt them according to their relative order, moving an element forward or backward in the list depending on whether items next to it are greater or smaller. This is called a comparison sort.

Bubble sort algorithm[13], which is a simple sorting algorithm, works by repeatedly stepping through the list to be sorted, comparing each pair of adjacent items and swapping them if they are in the wrong order.

We considered three elements and move one element towards left or right and while moving this element other element moved one or two position towards opposite direction.

The main drawback of the proposed algorithm is that if smallest element is at last location then it requires $n/2$ iterations to move to first location. To overcome this draw back we proposed a modification to the sorting algorithm, in this for each iteration in first half the largest in the first half moved to first location of second half and in the second half, iteration start from the last element and in this iteration smallest in second half moved to the last location of first half of the elements. This procedure is repeated for $n/2$ times to arrange the elements in sorted order.

II. PROPOSED MODIFICATION

In each iteration in first half the largest in the first half moved to first location of second half and in the second half iteration start from the last element and in this second half iteration smallest in second half moved to the last location of first half of the elements. In successive iterations the smallest element moved to first half may be moved towards left if it is smaller than other elements in the first half same is true for the element moved to second half of the element. This procedure is repeated to arrange the elements in sorted order.

For example consider set of elements 9 4 6 7 8 3 9 5 2
Novel sorting algorithm

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First iteration

Pass One

Element 4 compared with 9 and 6 arrange these elements in order. The order of elements after arrangement 4 6 9 7 8 3 9 5 2

Element 7 compared with 9 and 8 arrange the elements. The order of elements after arrangement 4 6 7 8 9 3 9 5 2

Element 3 compared with 9 and 9 arrange the elements. The order of elements after arrangement 4 6 7 8 3 9 9 5 2

Element 5 compared with 9 and 2 arrange the elements. The order of elements after arrangement 4 6 7 8 3 9 2 5 9

Pass Two

4 6 7 8 3 9 2 5 9

4 6 3 7 8 9 2 5 9

4 6 3 7 2 8 9 5 9

4 6 3 7 2 8 9 5 9

4 6 3 7 2 8 5 9 9

Pass Three

3 4 6 7 2 8 5 9 9

3 4 2 6 7 8 5 9 9

3 4 2 6 5 7 8 9 9

Pass Four

2 3 4 6 5 7 8 9 9

2 3 4 5 6 7 8 9 9

Using proposed modification

Consider same set of elements 9 4 6 7 8 3 9 5 2

Pass One

for first half

4 6 9 7 8 3 9 5 2

4 6 7 8 9 3 9 5 2

Second half

4 6 7 8 9 3 2 5 9

4 6 7 8 2 3 9 5 9

Pass Two

for first half

4 6 7 8 2 3 9 5 9

4 6 2 7 8 3 9 5 9

Second half

4 6 2 7 8 3 5 9 9

4 6 2 7 3 5 8 9 9

Pass three

for first half

2 4 6 7 3 5 8 9 9

2 4 3 6 7 5 8 9 9

Second half

2 4 3 6 7 5 8 9 9
2 4 3 6 5 7 8 9 9

Pass Four
for first half

2 3 4 6 5 7 8 9 9
2 3 4 5 6 7 8 9 9

III. ALGORITHM

Input: List of elements a[0..n-1] where n is number of elements.

- Step 1: swap=0
- Step 2: repeat step 3 to 6 for j=0 to n/2 where step size=1
- Step 3: repeat step 4 for i=1 to n/2 where step size=2
- Step 4: compare elements a[i-1],a[i] and a[i+1]. If they are not in order arrange them in order. Set swap=1;
- Step 5: repeat step 6 for k=n-1 to n/2 where step size=-2
- Step 6: compare elements a[k-1], a[k] and a[k+1]. If they are not in order arrange them in order. Set swap=1;
- Step 7: If swap=0 then given elements are in order break the outer loop else set swap=0.

a) Algorithm Analysis

The time for most sorting algorithms depends on the amount of data or size of the problem.[4]

Worst Case

The outer loop repeats for n/2 times.

In first pass of outer loop, the first inner loop repeats for (n/4) times and performs 3n/4 comparison operations and second inner loop repeats for (n/4) times and perform 3n/4 comparisons. The number of assignments performed depends on the order of elements. The maximum number of assignments performed is 2n.

In the second pass (n/2) in third pass (n/2).....
Inner loop repeats n/2+n/2+n/2 terms.
=n²/4

Therefore the worst time complexity is O(n²)

IV. RESULTS

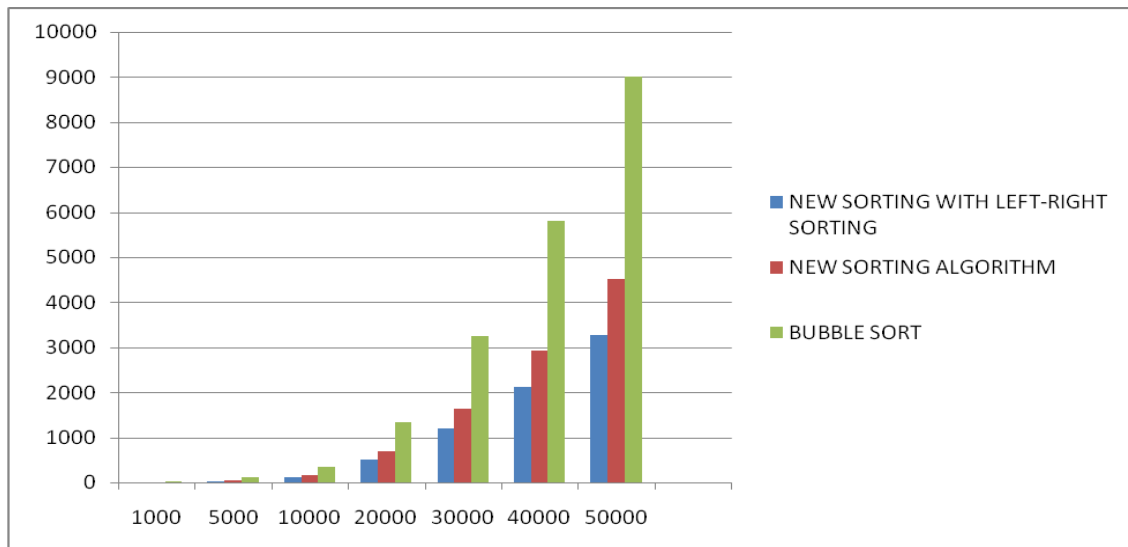
The time complexity of this algorithm in in worst case O(n²) same as bubble sort but their actual run time differ. For better understanding the actual performance we conducted some experiments.

The run times are measured on a PC, (AMD athlaon 220xd) processor and1G.B. RAM under Microsoft XP operating system. These algorithms are compiled using the sun java platform compiler and run under the java interpreter. The run time shown is CPU execution time measured using object of Date class. The class Date available in java util package. The elements are generated using nextInt method of Random class. The same set of elements is used for algorithms.

Table 1 : For average execution times

	1000	5000	10000	20000	30000	40000	50000
New Sorting With Left-Right Sorting	1.58	32.2	118.22	502.52	1206.58	2114.72	3279.4
New Sorting Algorithm	2.84	45.74	167.76	692.56	1635.94	2918.8	4513.8
Bubble Sort	21.9	103.66	342.2	1345.84	3240.56	5814.6	9010.04

Graph 1 : Graph drawn for execution times



V. CONCLUSION

We have proposed modification to a novel sorting algorithm to sort given elements. The Proposed method uses three elements at a time to compare based on the result it arranges the elements. The proposed algorithm is easy to understand and easy to implement. We also proposed a modification of considering iterations to increase the speed of execution. The proposed novel algorithm has similarity like bubble sort that is in every phase one element moved to its correct location.

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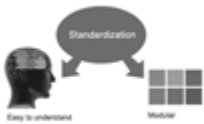




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30. Think and then print: When you will go to print your paper, notice that tables are not be split, headings are not detached from their descriptions, and page sequence is maintained.

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 through 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 an 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 an 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.
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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:

The Discussion is expected the trickiest segment to write and describe. A lot of papers submitted for journal are discarded based on problems with the Discussion. There is no head of state for how long a argument should be. Position your understanding of the outcome visibly to lead the reviewer through your conclusions, and then finish the paper with a summing up of the implication of the study. The purpose here is to offer an understanding of your results and hold up for all of your conclusions, using facts from your research and generally accepted information, if suitable. The implication of result should be visibly described. Infer your data in the conversation in suitable depth. This means that when you clarify an observable fact you must explain mechanisms that may account for the observation. If your results vary from your prospect, make clear why that may have happened. If your results agree, then explain the theory that the proof supported. It is never suitable to just state that the data approved with prospect, and let it drop at that.

- 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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<i>Introduction</i>	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
<i>Methods and Procedures</i>	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
<i>Result</i>	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
<i>Discussion</i>	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
<i>References</i>	Complete and correct format, well organized	Beside the point, Incomplete	Wrong format and structuring



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