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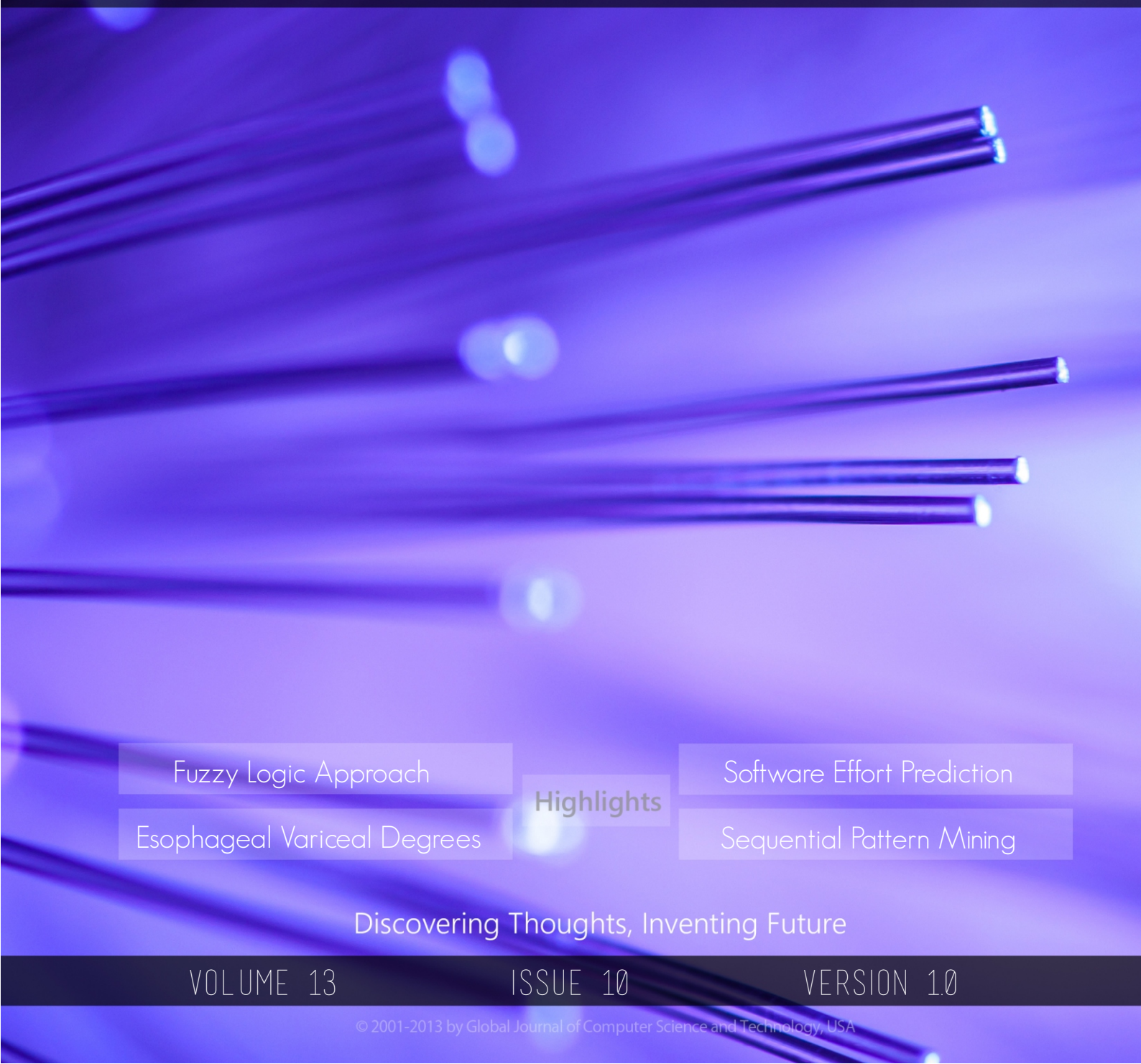

Highlights

- Fuzzy Logic Approach
- Esophageal Variceal Degrees
- Software Effort Prediction
- Sequential Pattern Mining

Discovering Thoughts, Inventing Future

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Prediction Analysis of Esophageal Variceal Degrees using Data Mining: Is Validated in Clinical Medicine?

By Abd Elrazek Mohammad Aly Abd Elrazek & Hamdy Mahfouz
Al-Azhar University, Egypt

Abstract - The objective of this study is to assess the feasibility of a data mining association analysis technique in early prediction of esophageal varices in cirrhotic patients and prediction of risky groups candidates for urgent interventional procedure. A manuscript titled "Detection of Risky Esophageal varices using 2D U/S: when to perform Endoscopy", published in The American Journal of The Medical Science on 21Th of December 2012, to our knowledge it was the first prospective study to assess the degree of esophageal varices by 2D ultrasound using the data mining statistical computed analysis in 673 patients. A descriptive model was generated using a decision tree algorithm (Rapid Miner, version 4.6, Berlin, Germany), the over all accuracy was 95%. Following another 59 patients using statistical analysis to determine the association between esophageal variceal degrees detected by Ultrasound in comparable to Upper Endoscopy, was done.

Categorical data were compared using the x^2 test, where as continuous variables were compared using Student's *t* test.

The comparative results accuracy of both two studies was 97.9%.

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I. Introduction

Although the rate of mortality from GI bleeding episodes has decreased with improved endoscopic and radiologic techniques together with new pharmacologic therapies, the 13% to 20% mortality implies the clinical importance, whatever most of mortalities due vaiceal rupture or leakage [1]. Concern has been raised about the prediction of Esophageal varices for those expected to develop gastrointestinal bleeding in the future, analyzing data by Data mining programs discovered the significant important leading mortality factors; risky Esophageal varices [2]. Thus the major challenge of biomedical data mining over the next 5-10 years is to make these systems useful to biomedical researchers [3]. This paper discuss the utility usefulness of data mining as a predictor statistical tool used to predict esophageal variceal degrees in cirrhotic patients, through measuring the intra-abdominal esophageal wall thickness, by non invasive ultrasound technique.

II. Clinical View

a) Causes of Upper GI bleeding

The most common causes of upper gastrointestinal bleeding are: Gastric and/or duodenal ulcers, Esophagogastric varices with or without portal hypertensive gastropathy, Esophagitis, Erosive gastritis/duodenitis, Mallory-Weiss syndrome, Angiodysplasia, Mass lesions (polyps/cancers), Dieulafoy's lesion. [4].

Helicobacter pylori infection, Non Steroidal anti-inflammatory drugs (NSAIDs), physiologic stress, and excess gastric acid are major risk factors for bleeding peptic ulcers. Reduction or elimination of these risk factors reduces ulcer recurrence and rebleeding rates, whatever Esophagogastric varices develop as a consequence of portal hypertension Less common causes of upper gastrointestinal bleeding include Hemobilia, Hemosuccus pancreaticus, Aortoenteric fistula and Cameron lesions.[5,6].

b) Causes of Esophageal Varices

Esophageal varices are swollen blood vessels in the esophagus, which is the tube that connects the mouth to the stomach. Esophageal varices often happen in people with serious liver disease, called "cirrhosis." As a result of portal hypertension [Figure1], Cirrhosis is a medical term, usually used to describe a diseased liver that has been severely scarred injury. There are numerous causes of liver cirrhosis, the two most common causes of cirrhosis worldwide are alcoholic liver disease and viral hepatitis C, which together accounted for approximately one-half of patients on the liver transplantation wait list worldwide whatever portal hypertension can also be present in the absence of cirrhosis, a condition referred to as "noncirrhotic portal hypertension". The causes of non-cirrhotic portal hypertension can be divided into prehepatic, intrahepatic and post hepatic (presinusoidal, sinusoidal and post sinusoidal causes).

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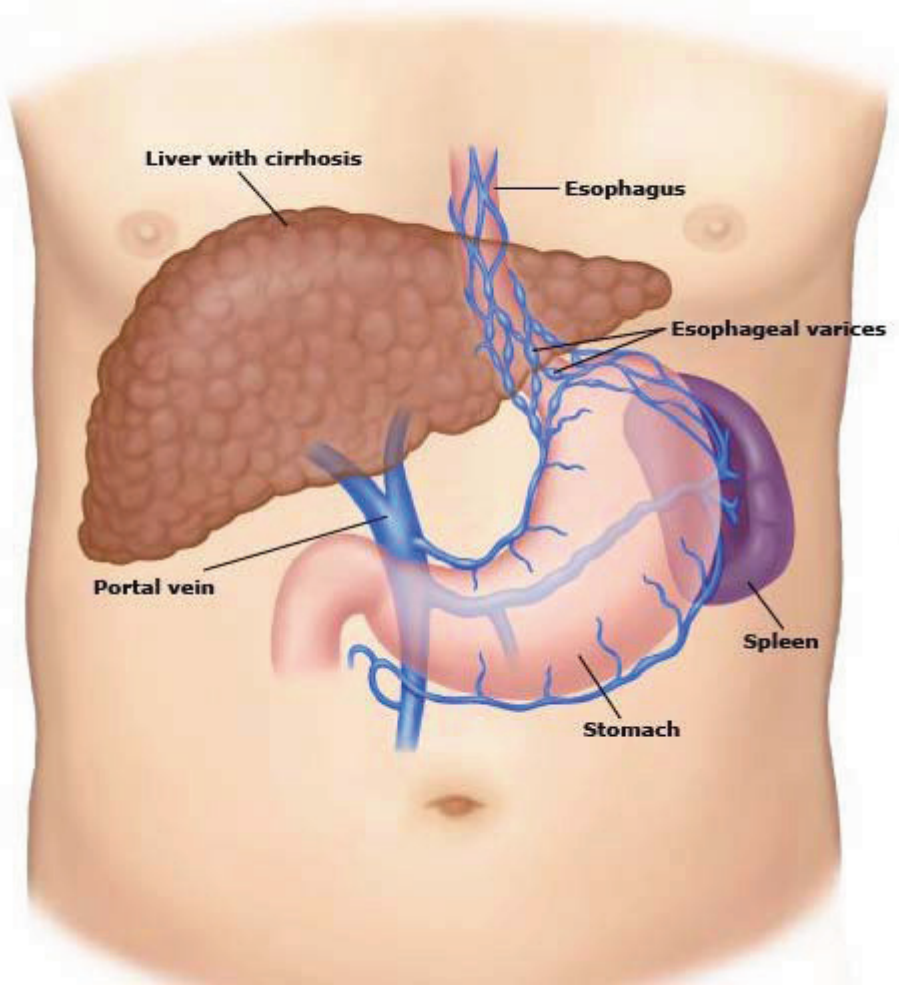

Figure 1 : Showing the esophageal varices interlacing the Esophagus and Upper part of the stomach, these varices can burst and cause internal bleeding, leading to death in many institutions.
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c) Diagnostic Techniques

Upper gastrointestinal endoscopy remains the gold standard for the diagnosis of esophagogastroduodenal lesions, despite its limitations. Early endoscopy (within 24 hours) is recommended for most patients with acute UGI bleeding, though whether early endoscopy affects outcomes and resource utilization is unsettled [7].

d) Non- Invasive Diagnoses

The identification of Cirrhotic patients with esophageal varices using non-invasive means has been attempted using different clinical, laboratory and radiological approaches, unfortunately many of these approaches still controversial ,recently non-invasive 2 D U/S can detect esophageal variceal degrees in cirrhotic patients with high accuracy, through measuring the intra-abdominal wall thickness of the esophagus, there were proportional relations between esophageal wall thicknesses detected by ultrasound and the esophageal variceal degrees diagnosed by Upper Endoscopy.

III. Analysis by Data Mining

The basic classification is based on supervised algorithm, whatever algorithms are applicable for the input data, the accuracy of each algorithm could be changed according to data nature. In clinical medicine, there are different laboratory, clinical and radiological factors determine the progress of each disease. Identification of important and risky factors is of great importance to predict out come in each disease stage. Analyzing of our data by data mining computed program shed light on the significant important factors for each disease condition. Thus the major challenge of biomedical data mining is to make these systems useful to biomedical researchers. The decision tree analysis was performed using Intelligent Miner software (Rapid Miner, Berlin, ver.4.6, Germany), which can automatically search a data set to find the optimal classification variables leading to the building of a decision tree algorithm . Briefly, all items derived from the patients were evaluated to determine which variables and cutoff points might produce the most

significant division into two subgroups; group with risky esophageal varices when esophageal wall thickness >6.5 mm and not risky group when esophageal wall thickness ≤ 6.5 mm.

IV. Validation Accuracy

In our previous study the algorithm was selected by evaluating each supervised machine learning algorithms by using supervised learning assessment (10-folds-cross validation) on the training set, we chose the best test applicable to our clinical data, accordingly we used Naïve-base test, and the overall accuracy we obtained was 95%.

We followed 59 patients presented with portal hypertension as a result of End stage-liver cirrhosis; the thicknesses of esophageal walls were measured using 2D U/S. All patients underwent diagnostic Esophag-ogastrodudonoscopy to estimate corresponding degrees of varices. According to the decision tree algorithm we obtained from the previous study, the esophageal wall thickness > 4.2 mm with inner wall irregularities, should be Esophageal varices with variable degrees, esophageal wall thickness <4.2mm measured by U/S without inner wall irregularities, indicating no varices, if the esophageal wall thickness > 6.5mm it should be risky esophageal varices (Grade III or IV varices), accordingly upper endoscopy should be performed early as a prophylactic intervention before further bleeding.

V. Results

(out of 59 patients presented with Liver cirrhosis and portal hypertension , only 53 patients had varices when esophageal wall thicknesses were > 4.2 and 6 patients had not varices when esophageal wall thicknesses were <4.2mm, all measured by U/S and diagnosed by upper Endoscopy; (100 % Comparative validation result for detection of Esophageal varices), whatever 48 patients had esophageal wall thicknesses > 6.5mm; risky esophageal varices, only 45 patients had risky esophageal varices diagnosed with Upper endoscopy; (93.75% Comparative validation result for detection of risky Esophageal varices).

Categorical data were compared using the χ^2 test, where as continuous variables were compared using Student's *t* test.

The overall comparative validation accuracy was 97.9 %. Table [1].

Esophageal wall Thickness	Cases	Result	Comparative
< 4.2 mm ; No varices	6	6	100%
>4.2 mm*; Varices	53	53	100%
>6.5 mm; Risky varices	48	45	93.75%
Over All Accuracy			97.9%

Table 1 : Describing the Comparative results between Analyses obtained by Data mining Computed Software; Rapid Miner ver.4.6 Berlin, Germany and results obtained from the current study

* Inner esophageal wall irregularies are confirmatory leading signs for esophageal varices with variable degrees.

VI. Conclusion

Based on the available evidence, prediction identification of esophageal variceal degrees in cirrhotic patients presented with manifestations of portal hypertension using non-invasive 2D ultrasound could be a very helpful tool saving time and money. Data mining shed light on the most significant predictors-related esophageal wall thicknesses in 673 patients with very high accuracy; identification high risky groups needed urgent interventional Endoscopy; less complication, better out come and decrease mortality.

Data mining would be the coming statistical evolution in clinical medical data statistical analysis with reasonable limitation.

VII. Limitation of the Study

Given the small sample size of 59 patients (8.7%) in comparable to 673 reported in the pervious study, the validation accuracy might be changed if we apply more patients in the future, whatever our clinical experience played a major role in assessing the information mentioned above, in our point of view our results should be confirmed with more evidence-based criteria using independent laboratory and clinical factors all together.

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A Novel Approach for Scalability - Two Way Sequential Pattern Mining using UDDAG

By Dr. P. Raguraman, Mr. S. Hariharan & Dr. J. Jaya A Celin
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Abstract - Traditional pattern growth-based approaches for sequential pattern mining derive length- (k + 1) patterns based on the projected databases of length-k patterns recursively. At each level of recursion, they unidirectionally grow the length of detected patterns by one along the suffix of detected patterns, which needs k levels of recursion to find a length-k pattern. In this paper, a novel data structure, UpDown Directed Acyclic Graph (UDDAG), is invented for efficient sequential pattern mining. UDDAG allows bidirectional pattern growth along both ends of detected patterns. Thus, a length-k pattern can be detected in $\lfloor \log_2 k + 1 \rfloor$ levels of recursion at best, which results in fewer levels of recursion and faster pattern growth. When minSup is large such that the average pattern length is close to 1, UDDAG and PrefixSpan have similar performance because the problem degrades into frequent item counting problem. However, UDDAG scales up much better. It often outperforms PrefixSpan by almost one order of magnitude in scalability tests. UDDAG is also considerably faster than Spade and LapinSpam. Except for extreme cases, UDDAG uses comparable memory to that of PrefixSpan and less memory than Spade and LapinSpam. Additionally, the special feature of UDDAG enables its extension toward applications involving searching in large spaces.

Indexterms : *data mining algorithm, directed acyclic graph, performance analysis, sequential pattern, transaction database.*

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Indexterms : data mining algorithm, directed acyclic graph, performance analysis, sequential pattern, transaction database.

I. Introduction

SEQUENTIAL pattern mining is an important data mining problem, which detects frequent subsequences in a sequence database. A major technique for sequential pattern mining is pattern growth. Traditional pattern growth-based approaches (e.g., PrefixSpan) derive length-(k + 1) patterns based on the projected databases of a length-k pattern recursively. At each level of recursion, the length of detected patterns is grown by 1, and patterns are grown unidirectionally along the suffix direction. Consequently, we need k levels of recursion to mine a length-k pattern, which is expensive due to the large number of recursive database projections. In this paper, a new approach based on UpDown Directed Acyclic Graph (UDDAG) is proposed for fast pattern growth. UDDAG is a novel data structure, which supports bidirectional pattern growth from both ends of detected patterns. With UDDAG, at level i recursion, wemay grow the length of patterns by 2i_1 at most. Thus, a length-k pattern can be detected in $\lceil \log_2 k + 1 \rceil$ levels of recursion at minimum, which results in better scale-up property for UDDAG compared to PrefixSpan. Our extensive experiments clearly demonstrated the strength of UDDAG with its bidirectional pattern growth strategy. When minSup is very large such that the average length of patterns is very small (close to 1), UDDAG and PrefixSpan have similar performance because in this case, the problem degrades into a basic frequent item counting problem. However, UDDAG scales up much better compared to PrefixSpan. It often outperforms PrefixSpan by one order of magnitude in our scalability tests. UDDAG is also considerably faster than two other representative algorithms, Spade and LapinSpam. Except for some extreme cases, the memory usage of UDDAG is comparable to that of PrefixSpan. UDDAG generally uses less memory than Spade and LapinSpam. UDDAG may be extended to other areas where efficient searching in large searching spaces is necessary.

II. Related Work

The problem of sequential pattern mining was introduced by Agrawal and Srikant [1]. Among the many algorithms proposed to solve the problem, GSP [17] and PrefixSpan[13], [14] represent two major types of approaches: a prioribased and pattern growth-based. A priori principle states that any supersequence of a nonfrequent sequence must not be frequent. A priori based approaches can be considered as breadth-first traversal algorithms because they construct all length-k patterns before constructing length-(k+1) patterns. The AprioriAll algorithm [1] is one of the earliest a prioribased approaches. It first finds all frequent item sets, transforms the database so that each transaction is replaced by all frequent item sets it contains, and then finds patterns. The GSP algorithm [16] is an improvement over AprioriAll. To reduce candidates, GSP only creates a new length-k candidate when there are two frequent length-(k _ 1) sequences with the prefix of one equal to the suffix of the other. To test whether a candidate is a frequent length-k pattern, the support of each length-k candidate is counted by examining all the sequences. The PSP algorithm [12] is similar to GSP except that the placement of candidates is improved through a prefix tree arrangement to speed up pattern

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discovery. The SPIRIT algorithm [9] uses regular expressions as constraints and developed a family of algorithms for pattern mining under constraints based on a priori rule. The SPaRSe algorithm [3] improves GSP by using both candidate generation and projected databases to achieve higher efficiency for high pattern density conditions.

III. Problem Definition

a) Updown Directed Acyclic Graph-Based Sequential Pattern Mining

UDDAG-based pattern mining approach, which first transforms a database based on frequent item sets, then partitions the problem, and finally, detects each subset using UDDAG. The absolute support for an item set in a sequence database is the number of tuples whose sequences contain the item set. An item set with a support larger than minSup is called a frequent item (FI) set. Based on frequent item sets, we transform each sequence in a database D into an alternative representation.

i. *Transformed Database Definition*

Let D be a database and P be the complete set of sequential patterns in D, D' be its transformed database, substituting the ids of each item pattern contained in D' with the corresponding item sets, and denoting the resulted pattern set by P', we have P = P'.

Based on frequent item sets, we transform each sequence in a database D into an alternative representation. Steps involved in Database Transformation:

1. Find the set of frequent items in D.
2. Assign a unique id to each FI in D and then replace each item set in each sequence with the ids of all the FIs contained in the item set.

Seq. Id	Sequence
1	<1 (1,2,3) (1,3) 4 (3,6)>
2	<(1,4) 3 (2,3) (1,5)>
3	<(5,6) (1,2) (4,6) 3 2>
4	<5 7 (1,6) 3 2 3>

Table 1 : Sequence Database

Seq. Id	Sequence
1	<1 (1,2,3,4,5) (1,5) 6 (5,8)>
2	<(1,6) 5 (3,4,5) (1,7)>
3	<(7,8) (1,2,3) (6,8) 5 3>
4	<7 (1,8) 5 3 5>

Table 2 : Transformed Database

For the database in Table 1, **the FIs are: (1),(2), (3), (4), (5), (6), (1,2), (2,3).**

By assigning a unique id to each FI, e.g., (1)-1, (1,2)-2, (2)-3, (2,3)-4, (3)-5, (4)-6, (5)-7, (6)-8, we can transform the database as shown in Table 2 (infrequent items are eliminated).

ii. *Problem Partitioning Definition*

Let {x1, x2, . . . , xt} be the frequent item sets in a database D, x1 < x2 <. . . . < xt, the complete set of patterns (P) in D can be divided into t disjoint subsets. The ith subset (denoted by $P_{xi,}$ 1 < = i <= t) is the set of patterns that contains xi and FIs smaller than xi.

iii. *Definition (Projected database)*

The collection of all the tuples whose sequences contain an item set x in a database D is called x-projected database, denoted by ^{x}D.

The total number of different Frequent Items FIs in the Sequential Database are found by Database Transformation module. For a database with n different frequent items, its patterns can be divided into n disjoint subsets. The ith subset (1 < i < n) is the set of patterns that contain i (the root item of the subset) and items smaller than i.Each subset i of the problem is mapped into a projected database denoted by (^{i}D).

P is partitioned into eight subsets as there are 8 FIs in table-2, the one contains 1 (P1), the one contains 2 and smaller ids (P2), . . . ,and the one contains 8 and smaller ids (P8).

Given the following database (P8) alone is found as given by ^{8}D:

1. <9 4 5 8 3 6>
2. <3 9 4 5 8 3 1 5>
3. <3 8 2 4 6 3 9>
4. <2 8 4 3 6>
5. <9 6 3>

^{8}D is,

1. <4 5 8 3 6>
2. <3 4 5 8 3 1 5>
3. <3 8 2 4 6 3>
4. <2 8 4 3 6>

b) UpDown Directed Acyclic Graph

i. *Definition*

Directed acyclic graph (UDDAG) is a graphical approach that represents patterns as vertices and contain relationships as directed edges in between vertices.

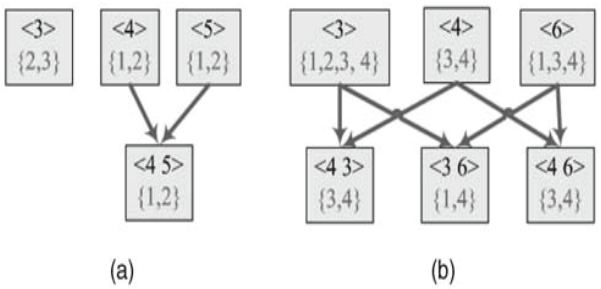
Given an FI x and ^{x}D, an UpDown Directed Acyclic Graph based on P_x, denoted by x-UDDAG, is constructed as follows:

1. Each pattern in P_x corresponds to a vertex in x-UDDAG. <x> corresponds to the root vertex, denoted by V_x

2. Let P_U be the set of length-2 patterns ending with x in P_x . Add a directed edge from V_x to U_v called up root child of V_x. This represents the common prefix set to root X.
3. Let P_D be the set of length-2 patterns starting with x in P_x, add a directed edge from V_x to V_D called a down root child of V_x. This represents the common suffix set to root X.

Such a DAG can be recursively constructed in an efficient way to derive the contain relationship of patterns

Example of UDDAG Construction



By concatenating the patterns {<3>,<4>,<5>,<4 5>} of Pre(^{8}D) with 8, we derive patterns {<3 8>, <4 8>, <5 8>, <4 5 8>} in figure-a.

By concatenating patterns {<3>, <4>, <6>, <3 6>, <4 3>, <4 6>} of Suf(^{8}D) with 8,we derive patterns {<8 3>, <8 4>, <8 6>, <8 3 6>, <8 4 3>, <8 4 6>} in figure-b.

iii. *UDDAG based Pattern Mining*

In the ith subset, each pattern in the projected database (^{x}D) can be divided into two parts, prefix and suffix of i.

The collection of all the prefix/suffix tuples of a frequent item set X in ^{x}D is called the prefix/suffix-projected database of x, denoted by Pre(^{x}D) / Suf(^{x}D).

To detect the sequential pattern in projected database (^{x}D) P_x,

- Detect patterns in Pre(^{x}D) called pattern prefix (PP).
- Detect pattern in Suf(^{x}D) called pattern suffix (PS)
- The above steps are repeated recursively until no frequent items are found in the pre(^{x} D) / suf(^{x} D).
- Combine the patterns of all the iterations to derive P_x.

The complete set of patterns is the union of patterns of the all subsets or projected database (^{x}D) detected above.

The Apriori property is used to reduce the number of candidate sets to be considered

Example for Pattern Mining

Assuming ^{8}D is,

1. <4 5 8 3 6>
2. <3 4 5 8 3 1 5>
3. <3 8 2 4 6 3>
4. <2 8 4 3 6>.

The prefix subsequences of 8 in ^{8}D, or Pre(^{8}D) is :**{<3 8>, <4 8>, <5 8>, <4 5 8>}** the patterns with 8 at the end.

The suffix subsequences of 8 in ^{8}D, or Suf(^{8}D) is : **{<8 3>, <8 4>,<8 6>, <8 3 6>, <8 4 3>, <8 4 6>}** the patterns with 8 at the beginning.

The patterns with 8 in between the beginning and end of each pattern is: **{<3 8 3>,<4 8 3>, <5 8 3>, <4 5 8 3>}**

Example: UDDAG based Pattern Mining

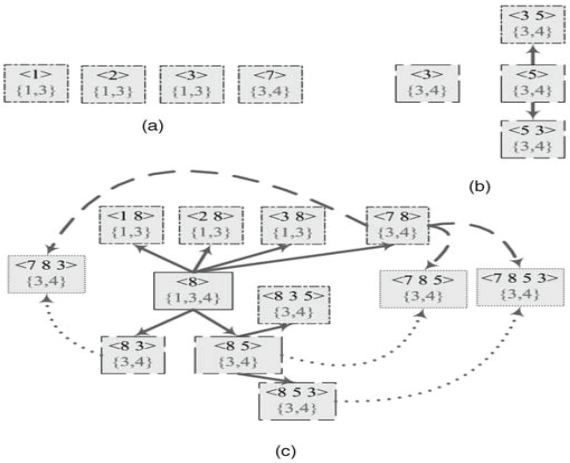


Figure : (a) UP DAG, (b) DOWN DAG & (c) UPDOWN DAG

Algorithm 1 : UDDAG based pattern Mining.
Input : A database D and the minimum support
Output : P, the complete set of patterns in D
Method : findP (D, minSup){
P = Φ
FISet=D:getAllFI(minSup);
D.transform( );
for each FI x in FISet{
UDVertexrootVT = newUDVertex(x)
findP(D.getPreD(x), rootVT, up, minSup)
findP(D.getSurD(x),rootVT,down,minSup)
findPUDDAG(rootVT)
P = P U rootVT.getAllPatterns( )
}
}

Subroutine
findP(PD,rootVT,type, minSup){
FISet=PD.getAllFI(minSup);
for each FI x in FISet{
UDVertexcurVT=new DVertex(x, rootVT)
if(type==up) rooVT.addUpChild(curVT)
else rootVT.addDownChild(curVT)
findP(PD. getPreD(x), curVT, up, minSup)
findP(PD.getSufD(x),curVT,down,minSup)
findPUDDAG(curVT)
}
}

Subroutine

```
findPUDDAG(rootVT){
upQueue.enQueue (rootVT.upChildren)
while(!upQueue.isEmpty()){
UDVertex upVT=upQueue.deQueue()
if(upVT.upParent==rootVT)
downQueue.enQueue(rootVT.downChildren)
else if (upVT.downParent==null)
downQueue.enQueue(upVT.upParent.VDVS)
else downQueue.enQueue(upVT.upParent.VDVS n
upVT.downParent.VDVS)
while(!downQueue.isEmpty()){
UDVertexdownVT=downQueue.deQueue()
if(isValid(upVT, downVT){
UDVertexcurVT=new UDVertex (upVT, downVT)
upVT.addVDVS(downVT)
if(upVT.upParent==rootVT)
downQueue.enQueue(downVT.children)
}
}
if(upVT.VDVS.size>0)upQueue.enQueue(upVT.children)
}
}
```

IV. Performance Evaluation

We conducted an extensive set of experiments to compare our approach with other representative algorithms. All the experiments were performed on a windows Server 2003 with 3.0 GHz Quad Core Intel Xeon Server and 16 GB memory. The algorithms we compared are PrefixSpan, Spade, and LapinSpam, which were all implemented in C++ by their authors (Minor changes have been made to adapt Spade to Windows). Two versions of UDDAG were tested. UDDAG-bv uses bit vector to verify candidates and UDDAG-co uses co-occurrences to verify candidates whenever possible. We perform two studies using the same data generator as in [14]: 1) Comparative study, which uses similar data sets as that in [14]; 2) Scalability study. The data sets were generated by maintaining all except one of the parameters as shown in Table 4 fixed, and exploring different values for the remaining ones.

V. Conclusion

In this paper, a novel data structure UDDAG is invented for efficient pattern mining. The new approach grows patterns from both ends (prefixes and suffixes) of detected patterns, which results in faster pattern growth because of less levels of database projection compared to traditional approaches. Extensive experiments on both comparative and scalability studies have been performed to evaluate the proposed algorithm.

One major feature of UDDAG is that it supports efficient pruning of invalid candidates. This represents a promising approach for applications involving searching in large spaces. Thus, it has great potential to related areas of data mining and artificial intelligence. In the future, we expect to further improve UDDAG-based pattern mining algorithm as follows: 1) Currently, FI detection is independent from pattern mining. Practically, the knowledge gained from FI detection may be useful for pattern mining. In the future, we will integrate the solutions of the two so that they can benefit from each other. 2) Different candidate verification strategies may have different impacts to the efficiency of the algorithm. In the future, we will study more efficient verification strategy. 3) UDDAG has big impact to the memory usage when the number of patterns in a subset is extremely large. In the future, we will find an efficient way to store UDDAG.

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Software Effort Prediction - A Fuzzy Logic Approach

By Sanjay Kumar, Jaya Pal & Vandana Bhattacherjee
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GJCST-C Classification : *D.2.8*

Strictly as per the compliance and regulations of:

Software Effort Prediction - A Fuzzy Logic Approach

Sanjay Kumar [α], Jaya Pal [σ] & Vandana Bhattacherjee [ρ]

Abstract - **Accuracy in the estimation of software Effort/Cost is one of the desirable criteria for any software cost estimation model. The estimation of effort or cost before the actual development of any software is the most crucial task of the present day software development project managers. Software project attributes are often measured in terms of linguistic values such as very low, low, Average, high and very high. The imprecise nature of such attributes constitutes uncertainty and vagueness in their subsequent interpretation. In this paper we propose a Fuzzy logic based model for software effort prediction. We feel that fuzzy Software cost estimation Model should be able to deal with imprecision and uncertainty associated with various parameter values. Fuzzy analogy model has been developed and validated upon student data.**

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I. Introduction

Accurate and timely prediction of the development effort and schedule required to develop a software system is one of the most critical activities in managing software projects. In addition software estimation has been identified as one of the three great challenges for half-century-old computer science. [19] In the last 30 years many different studies have been done in the area of Software Cost Estimation to improve the estimation accuracy and so many models are introduced. The rest of the paper contains the following sections as follows: section II represents Research Method, section III represents Experimental Results, and section IV represents Conclusion and Future Scope.

a) Fuzzy Logic

Intelligent Systems provide alternative paradigms aimed at facilitating the representation and manipulation of uncertain, incomplete, imprecise or noisy data. Fuzzy logic is a form of many-valued logic or probabilistic logic; it deals with reasoning that is approximate rather than fixed and exact.

The traditional approach to building system controllers requires a prior model of the system. The quality of the model, that is, loss of precision from linearization and/or uncertainties in the system's parameters negatively influences the quality of the resulting control. It is well known that the fuzzy theory not only provides natural tool for describing quantitative data but also generally produces good performance in many applications. In addition, fuzzy rules allow us to effectively classify data having non-axis-parallel decision boundaries, which is difficult for the conventional attribute-based methods. However, one of the difficulties with fuzzy decision trees is determining an appropriate set of membership functions representing fuzzy linguistic terms. Usually membership func-tions are given manually, however, it is difficult for even an expert to determine an appropriate set of membership functions when the volume and dimensionality of data are large.

At the same time, methods of soft computing such as fuzzy logic possess non-linear mapping capabilities, do not require an analytical model and can deal with uncertainties in the system's parameters. Although fuzzy logic deals with imprecise information, the information is processed in sound mathematical theory [40]. Based on the nature of fuzzy human thinking, Lofti Zadeh originated the "fuzzy logic" or "fuzzy set theory", in 1965. Fuzzy logic deals with the problems that have fuzziness or vagueness. In fuzzy set theory based on fuzzy logic a particular object has a degree of membership in a given set that may be anywhere in the range of 0 (completely not in the set) to 1 (completely in the set) [41].

For this reason fuzzy logic is often defined as multi-valued logic (0 to 1), compared to bi-valued Boolean logic [42]. Specifically, Fuzzy Logic offers a particularly convenient way to generate a keen mapping between input and output spaces thanks to fuzzy rules' natural expression [2]. Fuzzy logic has been used in[36][37][38][39]. Fuzzy set theory and fuzzy logic are a highly suitable and applicable basis for developing knowledge-based systems This paper presents a fuzzy rule based system having two fuzzy inputs, namely Line of code (LOC) and Adjusted difficulty level (Adj.diff.level) and one output Development time (Devtime) as shown in Figure 1.

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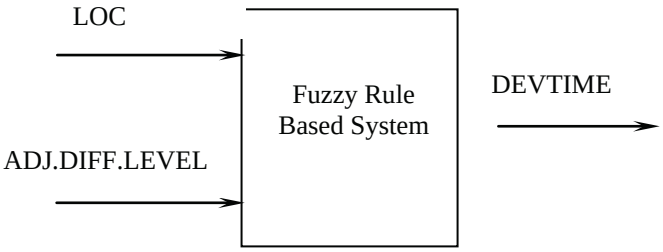
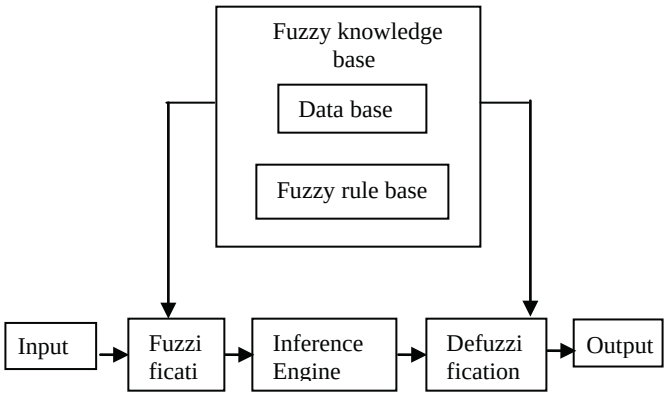


Figure 1 : Fuzzy Rule Based System

b) Fuzzy Rule Based System

A typical fuzzy logic system consists of four main components as shown in Figure.



i. *Fuzzification*

That contains predefined set of linguistic values. It converts non-fuzzy (Deterministic) inputs of fuzzy system into fuzzy inputs for inference mechanism.

ii. *Knowledge Base*

That consists of two parts: database that defines linguistic variables conditional statements (Fuzzy sets, and rule base that represents the mapping of fuzzy input set into a fuzzy output set. Rules are fuzzy implications). Fuzzy sets, and rule base that represents the mapping of fuzzy input set into a fuzzy output set. Rules are fuzzy conditional statements (implications).

iii. *Decision Logic*

That simulates human decision making based on fuzzy concepts. Conclusion of certain condition is derived by decision making logic.

iv. *Defuzzification*

That converts rule base fuzzy outputs into non-fuzzy (.numerical) values.

Central mechanism of knowledge base and decision making logic considers the fuzzy extension of conventional rule inferencing concept to fuzzy rules inferencing. Premises and conclusions of rules now contain fuzzy values. These facts by definition describe practically continual input set of characteristics. In this manner, one rule can replace more conventional rules. Fuzzy inferencing rules generally connect m conditional variables X1,..., Xm to n consequent variables Y1,..., Yn in form of:

IF (X1 is A1 and ……..Xm is Am) THEN (Y1 is B1 and ... Yn is Bn).

Where *A1,..., Am* and *B1,..., Bn* are linguistic terms of linguistic variables *X1,...,Xm* and *Y1,..., Yn,* respectively.

The IF part is called the "antecedent" and the THEN part is called the "consequent". To make a decision based on a set of rules, a rules-based system follows these steps:

1. All the rules that apply are invoked, using the membership functions and truth values obtained from the inputs (by a process called fuzzification), to determine the result of the antecedent.
2. This result in turn will be mapped into a membership function and truth value controlling the output variable. This process is known as implication. Two of the more common implication functions are: clipping (the fuzzy set is clipped to a value given by the level of activation of the input variables) and scaling (the fuzzy set is multiplied by a value given by the level of activation of the input variables).
3. These results are combined by a process called aggregation. One common approach for the aggregation involves using the "maximum" of the implicated sets.
4. Finally, a process known as defuzzification is used to compute a single value that is representative of the aggregated fuzzy set.

c) Multiple Regressions

A linear equation with three independent variables (multiple regressions) may be expressed as:

$$y = b_0 + b_1x_1 + b_2x_2 \quad (1)$$

Where b_0, b_1, and b_2 are constants; x_1, and x_2 are the independent variables, and y is the dependent variable. The values of b_0, b_1, and b_2 of the multiple regression. Equation may be obtained solving the following system of linear equations

$$\Sigma y = nb_0 + b_1(\Sigma x_1) + b_2(\Sigma x_2) \quad (2)$$

$$\Sigma x1y = b_0(\Sigma x_1) + b_1(\Sigma_{x1}{}^2) + b_2(\Sigma x_1x_2) \quad (3)$$

$$\Sigma x_2y = b_0(\Sigma x_2) + b_1(\Sigma x_1x_2) + b_2(\Sigma x_2{}^2) \quad (4)$$

d) Evaluation Criteria

A common criterion for the evaluation of software effort models is the Magnitude of Relative Error (MRE) which is defined as follows:

$$MRE = \left| \frac{\text{Actual devtime–Predicted devtime}}{\text{Actual devtime}} \right|$$

The MRE value is calculated for each observation whose devtime is predicted. The

aggregation of MRE over multiple observations (N) can be achieved through the Mean MRE (MMRE) as follows:

$$MMRE = \frac{1}{N} \sum_{i}^{N} MRE$$

A complementary criterion is the prediction at level *l*, Pred *(l)* = k/N, where *k* is the number of observations where MRE is less than or equal to *l,* and *N* is the total number of observations. Thus, Pred (25) gives the percentage of development time of software which were predicted with a MRE less or equal than 0.25.

II. Research Method

a) Metrics Used

The following metrics have been used Line of Code (LOC), and Adjusted Difficulty Level (ADJ.DIFF.LEVEL) which is served as input to the Fuzzy Logic System. And one output Development Time (DEVTIME).

Description of Metrics

1. *Line of Code (LOC):* Loc is the total number of lines of code used to develop the software excluding the comment lines. This metric was measured on the scale of 0-60.
2. *Adjusted Difficulty Level (ADJ.DIFF.LEVEL):* This is the difficulty level of the programmers to develop the software which is further adjusted with the help of expert judgments. This metric was measured on the scale of 0-6.
3. *Development Time (Devtime):* It is the time taken to develop the software. This metric was measured on the scale of 0-24.

b) Data Gathered

The proposed model was validated by a data set collected from the BIT, students of MCA. This data set consists of 10 project data. The data set is applied to the proposed fuzzy model is shown in the Table 1.

Table 1

PROG_ID	LOC	ADJ.DFF.LEVEL	DEVTIME(ACT)
1	16	1.5	3
2	32	1.8	4
3	23	2.3	10
4	18	2.8	15
5	16	1.5	3
6	32	1.3	4
7	16	1.3	4
8	18	1.4	4
9	19	1.8	7
10	22	1.9	5

c) Fuzzy Rules

The term fuzzy identification usually refers to the techniques and algorithms for constructing fuzzy models from data. The expert knowledge in a verbal form is translated into a set of if–then rules. A certain model structure can be created, and parameters of this structure, such as membership functions and weights of rules, can be tuned using input and output data.

This paper is based on five fuzzy rules as follows:

1. If ADJ.DIFF.LEVEL is (Very Low) then (DEVTIME (Very Low). (1).
2. If (loc is Low) and (ADJ.DIFF.LEVEL is (Average)) then (DEVTIME is (Low)) (1).
3. If (loc is Average) and (ADJ.DIFF.LEVEL is (Average)) then (DEVTIME is (Average)) (1).
4. If (loc is High) and (ADJ.DIFF.LEVEL is (Average)) then (DEVTIME is (High)) (1).
5. If (loc is Very High) and (ADJ.DIFF.LEVEL is (High)) then (DEVTIME is (Very High)) (1).

The weight of all the rule is 1.

Input and output Membership Functions (MF) are depicted in Table 2. All are triangular and their scalar parameters (a, b, c) are defined as follows:

Table 2 : Membership Function Characteristics

Variable Name	Range	MF	Parameters		
			a	b	c
LOC	0-60	VL	0	10	20
		L	10	20	30
		AV	20	30	40
		H	30	40	50
		VH	40	50	60
ADJ.DIFF.LEVEL	0-6	VL	0	1	2
		L	1	2	3
		AV	2	3	4
		H	3	4	5
		VH	4	5	6

Output

Variable Name	Range	MF	Parameters		
			a	b	c
DEVTIME	0-24	VL	0	4	8
		L	4	8	12
		AV	8	12	16
		H	12	16	20
		VH	16	20	24

Where MF is membership function.

The membership function plots corresponding to Table 2 are shown in figures2 (a), 2(b) and 2(c).

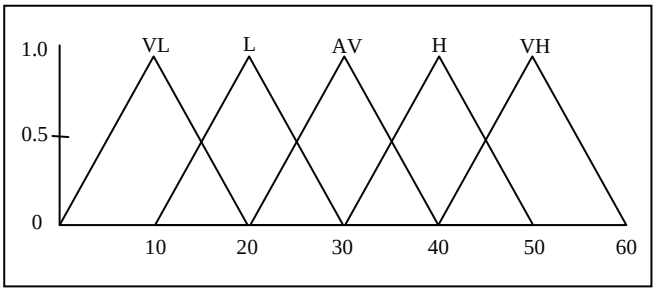


Figure 2(a) : LOC *(Input)*

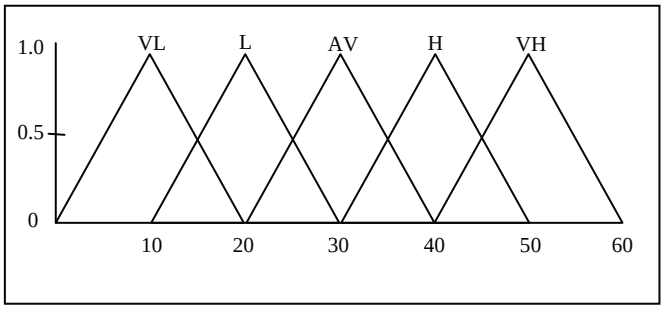


Figure 2(b) : ADJ.DIFF.LEVEL *(input)*

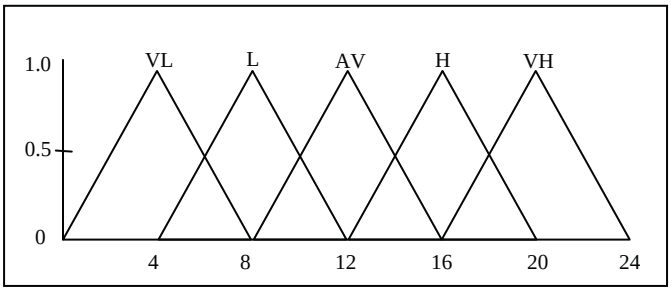


Figure 2(c) : DEVTIME *(output)*

d) Multiple Regressions

The same dataset has been used in Multiple Regression model to estimate the development time, which is to be used to develop a software. The estimated value of development time is compared with the actual value of development time, and with the help of this, using the evaluation criterion the MRE, MMRE and the Pred(25) value is also calculated.

e) Evaluation criteria

For this model the same evaluation criterion is used. The criterion which is used to evaluate the fuzzy model.

III. Experimental Results

The results show more accuracy in case of effort estimation by the proposed fuzzy model. The result is shown in the Table 3, Table 4 and Table 5.

Table 3

PROG_ID	DEVTIME (ACT)	DEVTIME (PRED) CALCULATED USING FUZZY LOGIG	MRE
1	3	4	0.3333
2	4	4	0.0000
3	10	10	0.0000
4	15	8	0.4667
5	3	4	0.3333
6	4	4	0.0000
7	4	4	0.0000
8	4	4	0.0000
9	7	4	0.4285
10	4	4	0.0000

Table 4

PROG_ID	DEVTIME (ACT)	DEVTIME (PRED) CALCULATED USING LINEAR REGRESSION	MRE
1	3	4.2048	0.4016
2	4	5.7181	0.4295
3	10	9.8191	0.1808
4	15	13.7431	0.0838
5	3	4.2048	0.4016
6	4	2.0155	0.4961
7	4	2.7237	0.3191
8	4	3.3757	1.5606
9	7	6.2935	1.0092
10	4	6.9013	0.4753

Table 5 : Prediction Results

	Multiple Regression	Fuzzy Logic
Min(MRE)	0.0838	0.0000
Max(MRE)	1.5606	0.4667
MMRE	0.5358	0.1762
Pred(25)	0.3	0.6

We have compared the actual development time with the predicted development time given by the model for each data set and found that difference between the actual devtime and predicted devtime. Then we calculated the MRE of each project and MMRE =0.1762 and pred(0.25%) which is 0.6. The same dataset has been tested using multiple regression model and the calculated MMR was used to further find out the MMRE=0.5358 and Pred(0.25%)=0.3. after going through the results we conclude that the proposed fuzzy model gives the better accuracy.

IV. Conclusion and Future Scope

The main benefit of this model is its good interpretability by using fuzzy rules and another great advantage of this research is that it can put together expert knowledge (Fuzzy rules) and project data into one general framework that may have a wide range of applicability in software estimation.

Further the comparison with multiple regression model to fuzzy logic model, and the results support the fuzzy logic model.

In our future work we will test this model upon different real-time datasets. Datasets have been collected from the software engineering data repository [34]. These datasets have been used by various researchers in their work [4] [34] [35].

V. Acknowledgment

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An On-Chip Delay Measurement Technique for Small-Delay Defect Detection using Signature Registers

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GJCST-C Classification : *D.2.5*

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Rajeshwari Soma [α], Zulekha Tabassum [σ] & S. Prathap [ρ]

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I. Introduction

With the scaling of semiconductor process technology, performance of modern VLSI chips will improve significantly. However, as the scaling increases, small-delay defects which are caused by resistive-short, resistive-open, or resistive-via become serious problems. If small-delay defects cannot be detected in LSI screening, the chips will behave abnormally under particular operations in certain applications, and their lifetime may become very short due to the vulnerability to the transistor aging. Therefore to keep the reliability after shipping, Enhancing the quality of the testing for the smalldelay defect detection is an urgent need. The delay measurement of paths inside the circuits is useful for detection and debugging of small-delay defects.

However, it is impossible to measure the small circuit path delays using an external tester, even if the resolution is high. Therefore development of the embedded delay measurement technique is required. Some embedded delay measurement techniques have been proposed. The scan-based delay measurement technique with the variable clock generator is one of these on-chip delay measurements techniques. In this technique, the delay of a path is measured by continuous sensitization of the path under measurement with the test clock width reduced gradually by the resolution. The main good point of the scan-based delay measurement technique is its high accuracy. The reason of the high accuracy is that the technique measures just the period between the time when a transition is launched to the measured path and the time when the transition is captured by the flip flop connected to the path, directly. The variation of the measured value just depends on the variation of the clock frequency of the clock generator. Therefore, if the clock generator is compensated the influence of the process variation, the measured value does not depend on the process variation. However, it has a drawback. The measurement time of the technique depends on the time for the scan operation. These days, the gap between the functional clock and scan clock frequency increases. Therefore the measurement time becomes too long to make it practical. Noguchi *et al.* proposed the self testing scan-FF. The flip flop reduces the required number of scan operations, which makes the measurement time practical. They also proposed the area reduction technique of the self testing scan-FF. However, the area overhead of these methods is still expensive compared with the conventional scan designs. This paper presents a scan-based delay measurement technique using signature registers for small-delay defect detection.

The proposed method does not require the expected test vector because the test responses are analyzed by the signature registers. The overall area cost is of the order of conventional scan designs for design for test (DFT). The measurement time of the proposed technique is smaller than conventional scan-based delay measurement. The extra signature registers can be reused for testing, diagnosis, and silicon debugging. The rest of this paper is organized as follows. In section II, preliminaries are discussed. Section III explains the proposed method. Section IV

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shows the experimental results. Finally, Section V concludes this paper.

II. Preliminaries

a) Related Works

These days, various methods for small-delay defect detection have been proposed. The path delay fault testing with a normal clock width is the most popular and is widely used. In this method, we choose the longer paths to detect the smaller cumulative delay due to the small delay distributed on the paths. The larger the cumulative delays, the higher the probability of the detection of the distributed small delay. However, the coverage of the small delay defect detection largely depends on the normal clock width, which is a problem of this method. On the other hand, to solve the problem, methods with delay fault testing using a variable clock generator have been proposed. The delay fault testing with a smaller test clock reduces the slack of the paths. Therefore the smaller delay defects which cannot be captured with the normal clock width can be captured with the appropriate smaller test clock width. Lieu*et al.* proposed a small-delay defect detection method consisting of two test phases using both a tighter test clock and a normal clock. In this method, the transition delay fault testing with a tighter test clock width which is calculated basedon the characterized delay distribution is applied in the first phase. After that, path or transition delay fault testing is applied with a normal clock width in the second phase. The quality of the method is higher than the conventional one phase test with normal clock width. Yan. proposed a delay testing scheme that identifies small-delay defects in the slack interval by comparing switching delays of a neighboring die on a wafer. In this method, a fault site is sensitized multiple times continuously with reducing the test clock width by the slack interval. The abnormal switching delays are detected by comparison with the test results in the neighboring die. Another work detects small-delay defects by analyzing the failing frequency, which is the minimum frequency that the delay fault testing fails when the path is sensitized multiple times continuously with increasing the test clock frequency. Generally, the variable clock testing requires a variable on-chip clock generator. Various variable on-chip clock generators have been proposed. In variable clock testing, the test clock frequency should be optimized to each test vector. To improve the test quality, various optimization methods of the test clock and test set have been proposed. These days, small-delay defect detection methods using on-chip delay measurement techniques have been proposed. The direct measurement of the real delay of each path of each chip screens outlier chips robustly even in the presence of process variation or the gap between real and simulation environment. It realizes higher fault coverage of small-delay defects than the simulation based ones. In addition, it can be used not only for the detection of small delay defects, but also for the debugging. Because modern chips are too huge and complex, LSI CAD tools cannot optimize the design enough. Hence, the manufactured first silicon chip usually does not meet the specification in spite of the tighter release to production (RTP) schedule.

Therefore silicon debugging and design for debugging (DFD) become much more important in modern chips. Various silicon debugging technologies and DFD methods have been proposed. On-chip delay measurement provides accurate information of the delay of inside paths for the debugging of small-delay defects. Most of the conventional works of on-chip delay measurement are classified to either a proposal of an embedded delay Fig.1.On-chip variable clock generator measurement circuit or that of a scan architecture for scan-basedon-chip delay measurement with a variable clock generator. Some works proposed embedded delay measurement circuits of modified vernier delay line (VDL). Datta *et al.* proposed the embedded delay measurement circuit with high resolution. It is the first work of an embedded measurement circuit of modified VDL to the best of our knowledge. Tsai *et al.* proposed the area efficient and noise-insensitive modified VDL with coarse and fine parts namely BIDM. Pei *et al.* also proposed the area efficient modified VDL. The feature of this method is delay range of each stage of VDL .The delay ranges increase bya factor of two gradually, which reduces the required stages. Therefore the area is smaller than Data's work. The modified VDLs achieve high resolution. However they require redundant lines to feed the input and output signals of the measured paths, which needs the compensation of the delay effect of the redundant lines. Tanabe *et al.* solved the problem by removing the delay of the redundant lines from the measured delay using some additional embedded circuits. The proposed technique is categorized to the scan-based one.

b) Variable Clock Generator

In the proposed method, the clock width should be reduced continuously by a constant interval as explained later. It is difficult for an external tester to control this clock operation. Therefore an on-chip variable clock generator is indispensable for the proposed method. In this paper, we use the on-chip variable clock generator proposed by Noguchi. Fig. 1 illustrates the circuit.

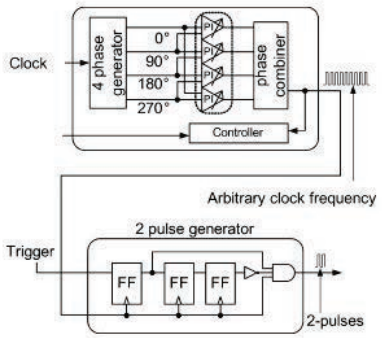

Figure 1 : On-chip Variable Clock Generator [2]

The circuit consists of the phase interpolator-based clock generator and the 2-pulse generator. The phase interpolator-based clock generator generates an arbitrary clock width. The 2-pulse generator generates 2-pulsetest clocks with arbitrary timing in response to a trigger signal.

Some of the specification and the evaluation results are shown in Table I.

Table 1 : Specification and Measurement Result

Process	90nm CMOS
Occupied area	300 [μm] × 128 [μm]
Input clock	1.5GHz 4phase
Output clock	1GHz to 2GHz 4phase
Functions	· Frequency control · Jitter generation · Duty ratio control · Phase control
Timing (Phase) Step resolution	5.2ps (2.8°)
Step error (5 chip measured)	±1.3ps ~ ±2.4ps (±0.7° ~ ±1.3°)
Cumulative timing error (5 chip measured)	Best chip Worst chip ±5.4ps ~ ±11.2ps (±2.9° ~ ±6.3°)

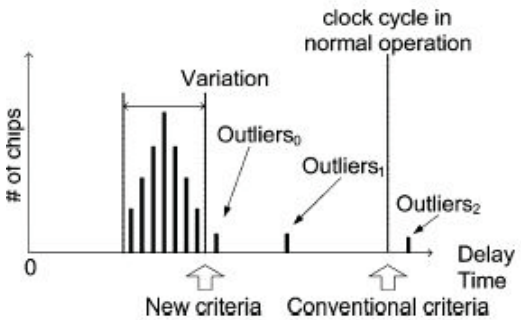

Figure 2 : Decision of test clock width based on path delay distribution obtained by chip measurement

c) Small-Delay Defect Detection with Delay Measurement of Chips

The proposed method uses the Noguchi's small-delay defect detection technique. In this technique, the test clock width for delay fault testing of each path is determined with the normal path delay distribution of each path. This strategy has already been applied to various small-delay detection techniques. But its originality is to obtain the path delay distribution with the delay measurement of the paths of the fabricated chips. Fig. 2 shows the path delay distribution of a path obtained by the delay measurement of the fabricated sample chips. The horizontal axis is measured delay. The vertical axis is the number of chips. The chips which have delay inside the range Variation are normal chips. The chips which have delay outside the range Variation, namely, are abnormal chips. The delay is the outside of the clock cycle in normal operation. Therefore it will be detected by conventional delay fault testing with the clock cycle in normal clock operation which is Conventional criteria. The delay and are within the clock cycle in normal operation. The conventional delay fault testing regards them as good chips. However because the delay is outside Variation, it will cause improper operations under particular operation in certain applications and may cause improper operations after shipping due to the effect of aging. In Noguchi's technique, the test clock cycle is set to the upper limit of the distribution of normal chips, which are new criteria. Then all the outlier chips are detected by the delay fault testing. In small technology, the path-delay distribution calculated by simulation is different from that of the fabricated chips. Therefore the quality of its strategy is higher than that of simulation based ones. Because the Noguchi's technique requires the measurement of the explicit paths, the paths should be single-path sensitizable. The aim of the technique is to screen the chips.

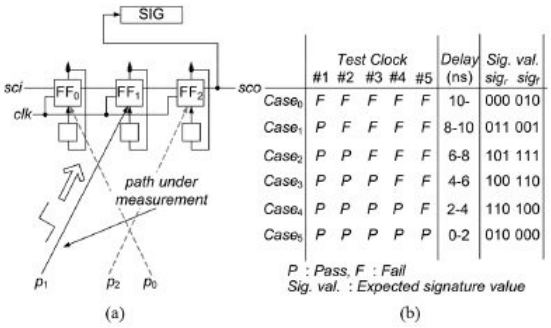

Figure 3 : Concept of proposed delay measurement. (a) Basics of proposed measurement, (b) Signature Table

Which have abnormal delay in gates or wires Therefore the test Set for the measurement should detect all the transition faults which are sensitized through single-path sensitizable paths. The proposed method is a new delay measurement technique for the small-delay defect detection technique.

III. Delay Measurement Technique using Signature Registers

This section explains the proposed measurement method. Section III-A presents the

concepts of the proposed method. Section III-B explains the implementation of the proposed method. Section III-C describes the measurement sequence. The data volume and area overhead should be realistic compared with the conventional scan designs for DFT. Section III-D explains the reduction method of the tester channel. Section III-E describes the scheme for the decision of the number of the required extra latches to keep the cost realistic. To apply the proposed method and realize short measurement time, some constraints should be put on ATPG. Section III-F explains the ATPG constraints. Section III-G describes the measurement time and data volume. Finally, Section III-H describes the test response tracing mode for finding lowest failing frequency or diagnosis with transition fault test vectors.

a) Basics

This section explains the concept of the proposed delay measurement. The target paths of the proposed method are single path sensitizable. Basically, the proposed method is scan-based delay measurement. The difference from the basic one is the usage of the signature registers and the additional latches for the acceleration of the delay measurement. Fig. 3(a) shows the basics of the proposed method. This example has three flip flops, and each flip flop has the input line (bottom), the output line (upper), and the clock line. Each flip flop is connected to an extra latch. At first, we assume that each flip flop has its own extra latch. The value of each flip flop is stored in the correspondent latch, and the value of each latch can be loaded to the correspondent flip flops in arbitrary timing. In the proposed measurement, the test vector is stored in these latches after scan-in operation. Once the test vector is stored in the latches, the test vector can be loaded from these latches in a clock without scan-in operation. It reduces the time for multiple sensitization of a path drastically. The horizontal line through these flip flops represents the scan path. The symbols and represent the scan input and output, respectively. The rectangle SIG represents the signature register using the linear feedback shift register as its basic component. The input of SIG is connected to the output of the last flip flop. More detail structures of the flip fops and the signature register are shown in Figs. 4 and 5, respectively.

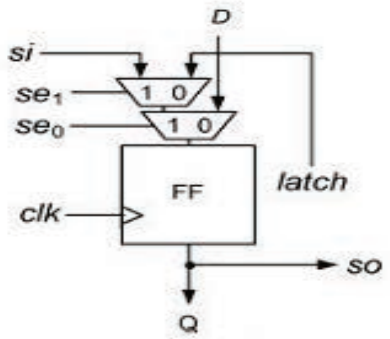

Figure 4 : Scan Flip Flops for Proposed Measurement

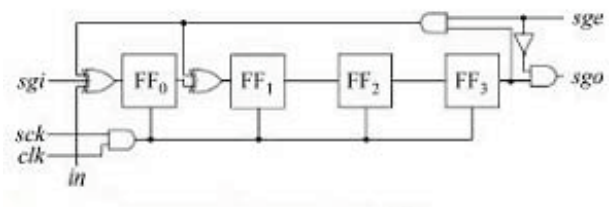

Figure 5 : Four Bit Reconfigurable Signature Register

Here, we measure the delay of. In this example, we assume that the clock width of normal operation is 10 ns, and the resolution of the delay measurement is 2 ns. First, SIG is initialized with reset operation. Second, the target path is tested continuously 5 times with the test clock reduced gradually by the resolution. The multiple clock width testing is realized by the variable clock generator explained in Section II-B. The test clock of the 1st testing (#1) is 10 ns. After the test, the test response is sent to SIG through the scan path with two clock shift out operation. The test clock of the second testing (#2) is 8 ns. Similarly, the test clock width of the third, fourth, and fifth testing's (#3, #4, #5) are the difference between 2 ns and the previous test clock width. Each test response is sent to SIG with two clocks. After the above 5 times of delay fault testing's, the signature value of SIG is retrieved. To estimate the delay, the retrieved signature value is compared with the expected signature values of the signature table. Fig. 3(b) shows the signature table in this example. The table has four columns. The first column is the cases of the measurement. The second column is the sequences of the test responses of #1–#5. The third column is the path delay value. The fourth column is the signature values of each case.

Here, and are the signature values for rising and falling transition testing's, respectively. The delay of each path is decided as more than 10, 8–10, 6–8, 4–6, 2–4, or 0–2ns, with 2ns resolution. The sequences of the test responses of the 5 times measurement are shown in Fig. 3(b). The symbols indicate the cases with path delays, more than 10, 8–10, 6–8, 4–6, 2–4, 0–2 ns, respectively. The symbols and represent the pass and fail of a testing, respectively. In case of rising transition testing, and, and in case of falling transition testing, and. The retrieved signature value is compared with the expected signature values on the table, and decides the delay value. When the number of flip flops is, clock width is, the measurement resolution is, and the continuous testing time is, the delay measurement sequence of a target path is as follows. Here, we assume that the test vector is already stored in the latches. The end point of the measured path is.

Step 1: Initializing SIG.
Step 2: Test vector is loaded from the latches.
Step 3: Test clock width is set to normal clock width.
Step 4: Test clock is applied.
Step 5: The test response is sent to SIG which is connected to the output of with clocks.
Step 6: If testing time is equal to, go to Step 7 after the signature value of SIG is retrieved, otherwise go back to Step 2 after the test clock width is updated to
Step 7: The delay value is estimated by comparing the retrieved signature value and the signature table.

b) Implementation

In this subsection, we explain the implementation of the proposed measurement system. First we explain the important components to understand the whole system. After that, the whole system is presented.

i. *Scan Flip Flop for Measurement*

Fig. 4 is the gate level description of the scan flip flop for the proposed measurement. The lines, and are the input, output, and clock lines, respectively. The line is connected to an extra latch which provides the test bit to the flip flop. The lines and are the input and output for constructing the scan path. The input is connected to of an adjacent scan flip flop or the scan input. The output is connected to of an adjacent scan flip flop or the scan output. The flip flop has two multiplexers. The lines and are the inputs of the upper multiplexer controlled by the output of the upper multiplexer and are the inputs of the bottom multiplexer controlled by When, the flip flop is in normal operation mode. When and, the flip flop is in scan operation mode. When the flip flop loads the value stored in the latch connected to the latch line.

ii. *Reconfigurable Signature Register*

The signature register for the proposed measurement requires the following functions to meet the demand of the proposed measurement.

- Capturing the test response in arbitrary timing.
- Shifting out the signature data in arbitrary timing.

Fig. 5 shows the architecture of the signature register for the proposed measurement. The length of the signature register in this example is four bit. Therefore it has four flip flops. The signature register can be configured to a shift register. The line controls the configuration. When, it works as a signature register. When, it works as a shift register.

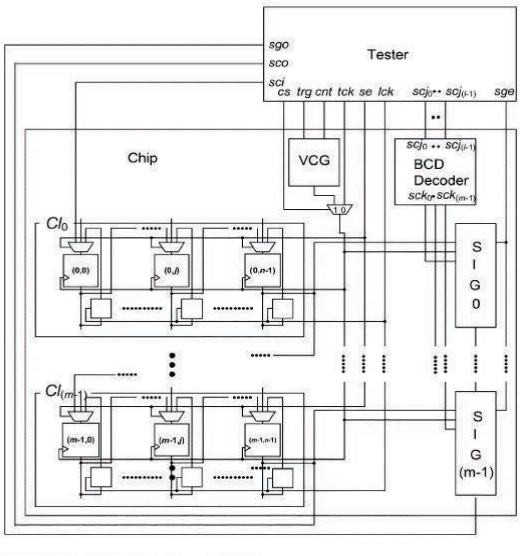

Figure 6 : Proposed Measurement System

The line is the input of the signature register. During measurement, test responses are sent to. The line is clock line. The clock line is controlled by. When, the signature register does not capture the input value. When, the signature register captures the input value synchronizing with the positive edge of. By controlling, the signature registers capture only the target test response. When, this circuit is configuring to the shift register. The input is. The output is. As explained later, the measurement system requires multiple signature registers generally. The input and output are connected to the output and the input of adjacent signature registers to construct a long shift register for sending all the signature values to the external tester.

iii. *Whole System*

Fig. 6 shows the proposed measurement system. The proposed system consists of the low cost tester and the chip with the variable clock generator (VCG) explained in Section II-B and a BCD decoder. The chip is assumed to have single functional clock in the proposed method, and the chip has two reset lines for initializing the flip flops and the signature registers independently. The reset operations are controlled by the tester. The low cost tester controls the whole measurement sequence. The clock frequency is slower than the functional clock. The line retrieves the signature data from the signature registers to estimate the measured delay. The line sends the test vectors to the scan input of the chip. The line gets the data of the flip flops from the scan output of the chip. In the proposed measurement sequence, is not used. However, it is used to check the flip flops or the additional latches before the measurement. The line is the clock control line. The proposed measurement uses both the slow tester clock and the fast double pulse generated by on-chip VCG. The lines elect the slow and fast clock. If is 1,

the fast clock is sent to the clock line of the components. Otherwise the slow tester clock is sent. The lines and are the input lines for VCG. The fast double pulse is launched synchronizing with the positive edge of. The line controls the width of the double pulse. The line controls the scan flip flops. The line controls the latches for storing test vectors. The lines are the inputs for the encoded data to control the capture operation of the signature registers. The BCD decoder decodes the encoded input data to the control data of the signature registers. As explained later, the decoder is used to reduce the input lines for the control data of the signature registers. The is the enable signal for the signature registers. The flip flops in the chip are classified to the clusters. Here, we assume that each cluster has flip flops, and thus the number of the flip flops is. In general, the number of the flip flops of the last cluster is, where is the number of flip flops, or. The coordinate written in the flip flops indicates the location. The number is the cluster id. The number is the order in the cluster. The output of the flip flop of which is the tail flip flop of each cluster is connected to the flip flop of which is the head flip flop of. These lines construct the scan chain. The output of the tail flip flop of each cluster is connected to the input of the corresponding signature register. The path whose test response is captured by the flip flops included in is measured by. The control lines of the signature registers are connected to the BCD decoder.

c) Measurement Sequence

Here, we explain the measurement sequence. First, the measurement sequence of the paths simultaneously sensitized in a test vector is explained in Section III-C1. After that, the whole measurement sequence is explained in Section III-C2.

i. *Measurement Sequence per a Test Vector*

When the measurement system has signature registers, Paths can be measured in parallel maximally. To reduce the measurement time, we measure multiple paths simultaneously. We explain the measurement strategy using the example depicted in Fig. 7. In this example, the proposed method is applied to the circuit with six flip flops. These flip flops are classified to the two clusters and. The cluster includes, and includes. The cluster has the signature register. The cluster has the signature register. The clock line controls these flip flops. The control lines controls the capture operation of, and controls the capture operation of. The paths are sensitized simultaneously by the test vector. The test response of is captured by The expected test response is The paths and are measured by. The paths and are measured by. The combination of the two paths, one of which is selected from and, the other of which is selected from and, can be measured simultaneously.

IV. Experimental Result

In this section, we present the experimental results. The proposed method is compared with the conventional methods. The clock frequencies are the same as that of Noguchi's methods that is, the normal clock frequency is 100 MHz, and the scan clock frequency is 10 MHz the length of the signature register is 8 bit. The test set consists of test vectors which detects all single-path sensitizable transition faults. The paths sensitized by these test vectors are measured. In this evaluation, the average delay of signal propagation of the measured paths is assumed to be the half of the clock width. Usually the length of the sensitized paths for transition delay defect detection is relatively short because ATPG seeks the paths whose length is as short as possible for the cost of test generation. From this point of view, we believe that this assumption is valid. In this evaluation, the test set for the measurement is generated by podem-based ATPG algorithm, which is implemented by C++. The back track limit is 200. For the evaluation, relatively larger ISCAS'89 benchmark circuits are used. The measurement time using the proposed scan design and standard scan design is calculated by the (1) and (3), respectively. The results of area are obtained by synthesis with Synopsys design compiler using Rohm 0.18 m process. The data volume of these methods is calculated by the (4) and (5), respectively. In this evaluation, area overhead, area overhead including the area of VCG, and the routing overhead are defined as follows. , where the area of the circuits is implemented the evaluated method except VCG, and is the area of the non-scan circuit except clock generator. Where the area of the circuits is implemented the evaluated method including VCG. The area of VCG is obtained from the paper. Note that, and include the area of the wires. , where and are the routing area of the evaluated circuit and non-scan circuit, respectively. The reduction ratio of measurement time is defined as, where and is the measurement time of the evaluated method and that of standard scan, respectively. The increase ratio of the data volume is defined as, where and is the data volume of the evaluated method and that of standard scan, respectively.

a) Comparison with Conventional Scan-Based Measurement

Tsig=time required for {whole scan-in + double pulse + SIG data

Table 1 : Measurement Time

Circuit	EMB	T_{sig}	R_1
S5378	635.4	181.2	71.5
S9234	703.1	135.5	80.7
S38584	4025	1011.5	72.6
Ave			74

Table 2 : Comparison with Delay Measurement using Embedded Delay Measurement Circuit

Circuit	EMB	SIG	R
S5378	46.7	181.2	3.9
S9234	164.5	135.5	0.8
Ave			2.3

The result of the measurement time is shown in Table III. Here, we show the result when and, respectively. The sub columns (ms) and (ms) are the measurement time of standard scan design and the proposed method, respectively. According to the result, when and are 67.8% and 71.9%, respectively. The reduction ratio when is 4.1% higher than when. It is because the impact of the time for scan-in operation of each test vector on the measurement time decreases as increases.

V. Conclusion

The proposals of this paper are as follows:

- The proposal of the delay measurement method using signature analysis and variable clock generator.
- The proposal of a scan design for the delay measurement of internal paths of SoC.

The first proposal can be applied not only SoC but also field programmable gate array (FPGA). Because the process of FPGA is getting extraordinary smaller these days, the small delay defect becomes serious problem in FPGA, too. In this meaning, the application of the proposed method to FPGA is also useful. A future work is the low cost application of the proposed measurement to FPGA. When we measure short paths the measurement error can increase for the IR drop induced by higher test clock frequency. It can reduce the test quality. Another future work is the reduction and the avoidance of the measurement error caused by the IR drop.

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On the $M/M/c/N$ Call Center Queue Modeling and Analysis

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Abstract – The $M/M/c/c$ model is the most widely applied queueing model in the mathematical analysis of call centers. The $M/M/c/c$ model is also referred to as the Erlang Loss System. The Erlang loss model does not take into consideration system attributes such as blocking and busy signals, balking and reneging, retrials and returns. Although, the Erlang loss model is analytically tractable, it is not easy to obtain insight from its results.

The need to develop a more accurate call center model has necessitated the modification of the Erlang loss model. In this research, we model and analyze a call center using $M/M/c/N$ the model. The goal of this paper is to extend existing results and prove new results with regards to the monotonicity and limiting behaviour of the $M/M/c/N$ model with respect to the system capacity N.

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I. Introduction

The call center industry has grown explosively in the recent past and that has aroused the interest of researchers from different disciplines. Mandelbaum [11] have provided a comprehensive research bibliography with abstracts in diverse disciplines such as Operations research, Statistics, Engineering, and so on. Call Center research has been reviewed in the tutorial and survey paper by Gans et al. [6]. In this paper, our focus is on the computational rigor of the call center performance metrics using the $M/M/c/N$ model.

a) *Description of a Call Center*

A call center is a department of an establishment that attends to customers via telephone conversation often for the purpose of sales and product support, or that makes outgoing telephone calls to customers usually for the purpose of advertisement or telemarketing. Suppose the department also attends to e-mails, faxes, letters, and other similar written correspondence, then, it is called a contact center.

Inbound call center only handle incoming telephone calls initiated by customers while out bound call centers only make outgoing telephone calls to customers. There are call centers that deal with both types of calls. In majority of the call centers, inbound calls form the bulk of contacts with customers. In addition, inbound calls are more time consuming compared to other types of contacting options (e.g. e-mails, faxes, or letters) in terms of waiting times in the telequeue or sojourn times. Hence, we will only focus on inbound call centers. In an inbound call center, there is a group of agents (Customer Sales Representatives, CSRs) who provide the needed service through talking to customers on phones. In this paper, we shall use the terms "agents" and "CSRs" interchangeably. Agents are equipped with equipment, such as a Private Automatic Branch Exchange (PABX or PBX), an Interactive Voice Response Unit (IVRU or VRU), an Automatic Call Distributor (ACD), and computers [16]. See Figure 1.1 for details on the operational process and components of an inbound call center.

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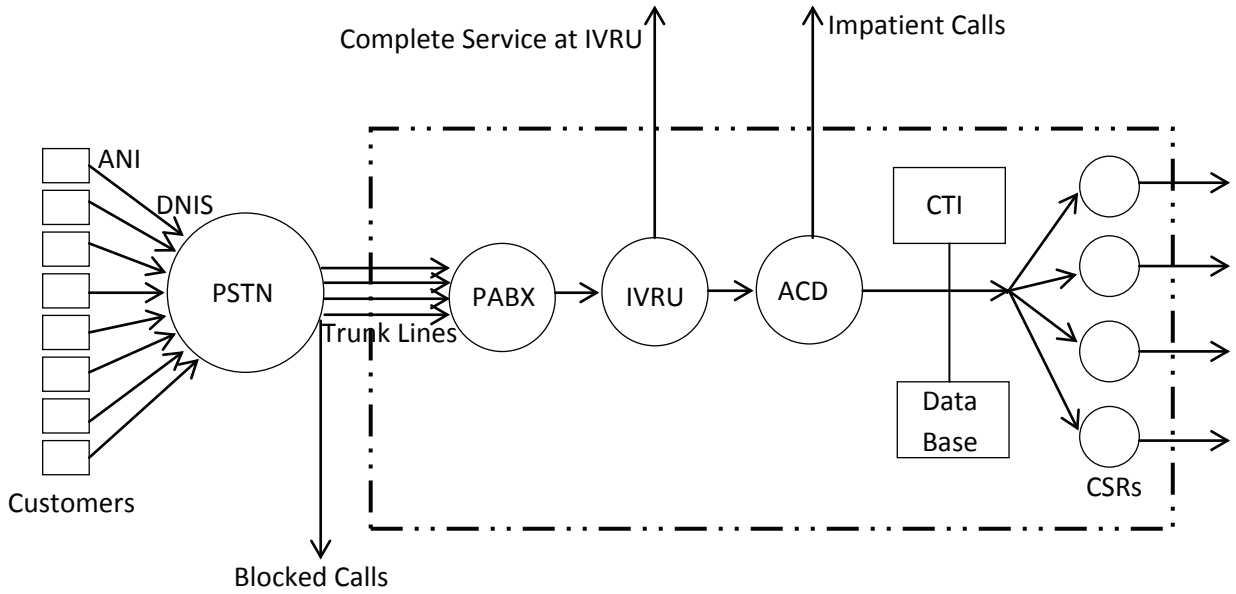

Figure 1.1 : Operational process of an inbound call center

b) The Operational Process of an Inbound Call Center

At some point in our lives, we have all called a call center. We will describe the operational process and components of an inbound call center in line with the description in [6, 17]. The process is depicted in Figure 1.1. Customers wanting to receive service from a call center, dial a special number provided by the call center. The Public Service Telephone Network (PSTN) company then uses the Automatic Number Identification (ANI) number (the phone number from which the customer dials) and the customer's Dialed Number Identification Service (DNIS) number (the special number being dialed) to connect the customer to the PABX privately-owned by the call center. The telephone lines (usually called trunk lines) connect the PABX to PSTN. If a trunk line is available, the customer seizes it; else the customer receives a busy signal and will be rejected. Hence, this customer is said to be blocked. Once the call is accepted, the customer will be connected through the PABX to the IVRU. The IVRU provides some automatic service for customers as well as several options for customers to choose from. Upon service completion at the IVRU, some customers leave the system and release the trunk lines. If the customer requires the service of an agent, the call will be passed from the IVRU to the ACD. The ACD is a sophisticated instrument designed to route calls to agents based on the specific needs of calls. If no appropriate CSRs are available, the customer is informed to wait and join a queue at the ACD. The customer is said to be delayed. The ACD decides the next customer to get service according to some preprogrammed queueing discipline (usually First Come First Served, FCFS). Delayed customers may decide to hang up and abandon (or renege) before they are served if they perceive that the service is not worth the wait. Such customers are said to be impatient. Patient customers (who do not abandon service) will eventually be connected to an agent. In serving a customer, the CSR works with a PC furnished with Computer-Telephony Integration (CTI), which is the technology that allows interactions on a telephone and a computer to be integrated. CTI will help ACD to route the call, help the CSR to get the caller's information from the database and hence facilitate the service process. At the completion of service and exit of the customer, the CSR still needs some wrap-up time to finish the whole service process and then may be available for the next customer. The service time is the sum of talk time and wrap-up time. Customers who abandoned and were blocked may try to call again after some random amount of time and these calls are referred to as retrials. Customers who finished talking with anagent may also need further assistance and therefore call back. Hence they become return customers or feedback customers. Notice that these two types of customers are not shown in Figure 1.1.

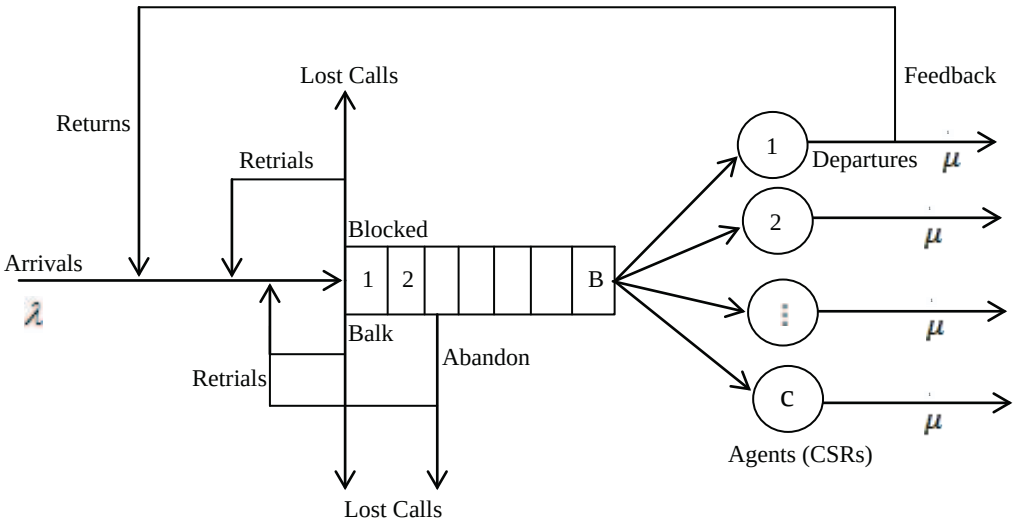

Figure 1.2 : Call Center as a Queueing System

c) The Call Center as a Queueing System

Figure 1.2 depicts the call center as a queueing system [7]. The number of agents (CSRs) and waiting spaces are denoted respectively by c and B. Hence there are $N = B + c$ trunk lines at the call center with B waiting spaces. If an arriving call finds all N trunk lines occupied, it gets a busy signal and as such is blocked and cannot access the system. If there is an available truck line, the call is either connected to the system and seizes one of the free trunk lines or it balks. Suppose there is an available trunk line and at least a free agent, then the call is immediately serviced. Otherwise the call experiences delay and has to wait in a queue at the ACD for a CSR to become available. Calls at the ACD may become impatient and abandon (renege) the system before being served and thus release the trunk line. The ACD usually implements the FCFS queueing discipline. Upon service completion by a CSR, the call leaves the system and then releases both the trunk line and the CSR and these resources become available to other arriving calls. Return (or feedback) calls are calls that return after been served by an agent. Some of those calls who do not get served (blocked, abandon or balk) may call again and they become retrials. The remaining calls become lost calls.

Suppose that the call arrivals follow a Poisson process with mean rate λ and that the service times of the calls are independent and identically distributed $(i.i.d)$ exponential random variables with mean $1/\mu$. Then we can model the system as a $M/M/c/N$ queueing system with features such as balking, abandonment, retrial, and feedback.

d) Performance Evaluation of the Call Center Queueing Model

In this paper, we will ignore features such as balking, abandonment, retrial, and feedback. Following the above assumptions, we will apply the $M/M/c/N$ model in analyzing the call center performance. The $M/M/c/N$ queueing system has a closed-form solution for the system state (number of calls in the system), the queue length (number of calls in the queue) distribution and waiting time distribution. Then we can obtain system performance metrics such as average waiting time, average queue length, and probability of blocking. We will apply the performance analysis of the $M/M/c/N$ queueing system to call center modeling and in turn show new results. The call center performance measures (metrics or indicators) provide useful information in the design and management of call centers. Performance measures are used in determining the service levels (or quality of service) in call centers.

Not all queueing models can be analyzed exactly to obtain performance measures as $M/M/c/N$ model. For instance, if we include additional features such as Non-Poisson time varying arrival process, balking, abandonment, retrial, feedback, and non-exponential service times, the model may become insolvable using traditional queueing techniques and other techniques have to be used to analyze the model such as simulation modeling.

II. Modeling Call Centers as Single-Node Exponential Queueing Models

In this section, we provide a detailed review of relevant single-node multiserver Markovian queueing models of call centers. Table 2.1 provides a list some main Markovian queueing models and their

performance indicators. Our emphasis is on the computational rigor of the exact performance measures of these well-known models as well deriving new results.

Table 2.1 : Some Multiserver Markovian Queueing Models

Notation	Models	Performance Indicators
$M/M/c$	Delay Model (Erlang C)	$P(delay) = P(W_q > 0)$ (Erlang C formula) *TSF ; ASA*
$M/M/c/c$	Blocking/Loss Model (Erlang B)	$P(blocking) = p_c$ (Erlang B formula)
$M/M/c/N$	Blocking and Delay Model	$P(delay) = P(W_q > 0); P(blocking) = p_N$ *TSF ; ASA*

TSF : Telephone Service Factor ; ASA: Average Speed to Answer; AWT: Acceptable Waiting Time

a) Model Assumptions

The $M/M/c/N$ is a generalization of the $M/M/c$ and $M/M/c/c$ models. In order to analyze a call center using the $M/M/c/N$ Markovian queueing model, we assume that the inter arrival and service times are exponentially distributed random variables.

Calls arriving at the call center are of a single type following a homogeneous Poisson process with rate λ. Callers are assumed to be patient and there is no form of impatience (balking or reneging). All agents (CSRs) are assumed to be statistically identical (i.e., equally skilled and provide service at the same rate). The service times are assumed to follow the exponential distribution with mean $1/\mu$. Services are rendered according to the First-Come-First-Serve queueing discipline. There are $N - c$ waiting spaces in the $M/M/c/N$ queueing system.

Let $L(t)$ be the number of calls in the system and $L_q(t)$ be the number of calls waiting in queue at time t. Let $W(t)$and $W_q(t)$ be the steady-steady sojourn time and waiting time in queue respectively. Since the models are Markovian, $L(t), L_q(t), W(t), and\ W_q(t)$ can be obtained using the birth-death processes. Our focus is on steady-state distribution of $L(t), L_q(t), W(t),$ and $W_q(t)$ with corresponding variables $L, L_q, W, and\ W_q$, respectively.

Let $p_n = P(L = n),\ n = 0,1,2, \ldots$ denote the steady-state probability (if it exits) of the system being in state n (i.e. having n calls in the system). Applying the modeling techniques of the birth-death processes, we can obtain some interesting system performance measures such as $E(L), E(L_q), E(W), and\ E(W_q)$.

Due to the PASTA property, we have for the $M/M/c$ model, $P(waiting) = \sum_{n=c}^{\infty} p_n$ and in the cases of the $M/M/c/N$ and $M/M/c/c$, we have $P(blocking) = p_N$ and $P(blocking) = p_c$ respectively.

b) Review of the M/M/c/c Model and the Erlang B Formula

In this section of the paper we will review the $M/M/c/c$ Erlang B model paying attention to the aspects that are relevant to call center modeling. The $M/M/c/c$ queue models a single-node system with c truck lines and no waiting spaces. Figure 2.1 depicts the $M/M/c/c$ queue and figure 3.2, its state transition.

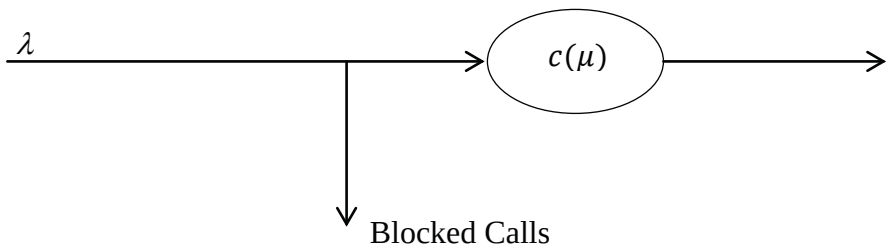

Figure 2.1 : Description of the $M/M/c/c$ Model and its parameters

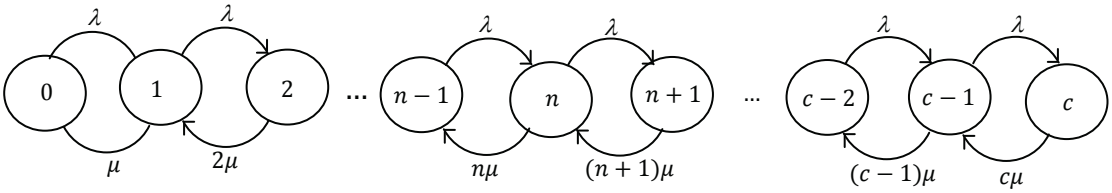

Figure 2.2 : $M/M/c/c$ Flow Rate [Multiple-Server Case($c \geq 2$)]

Considering figures 2.1 and 2.2, it is obvious that $L(t)$ is a finite birth-death process with birth rate

$$\lambda_n = \begin{cases} \lambda, & if\ n < c \\ 0, & if\ n \geq c \end{cases}$$

and state-dependent death rate $\mu_n = n\mu, n = 0,1,2, \ldots, c$.

By the application of the fundamental equation in queueing theory, the steady-state solution of the $M/M/c/c$ model using birth-death process is given by

$$p_n = p_0 \prod_{i=1}^{n} \frac{\lambda_{i-1}}{\mu_i}$$

where p_0 is computed from $\sum_{n=0}^{N} p_n = 1$. The solution is given by

$$p_n = \frac{(\lambda/\mu)^n/n!}{\sum_{i=0}^{c}(\lambda/\mu)^i/i!} = \frac{a^n/n!}{\sum_{i=0}^{c} a^i/i!}, \qquad 0 \leq n \leq c$$

where $a := \lambda/\mu$ is called the offered load which describes the demand made on the system.

i. *PASTA: Poisson Arrivals See Time Averages*

An important feature of the Markovian queueing models is that the arrival process follows a Poisson process. Considering the Poisson arrival process, the distribution of customers seen by an arrival to a queueing facility is, stochastically the same as the limiting distribution of customers at that facility. In other words, once the queueing system has reached steady state, each arrival from a Poisson process finds the system at equilibrium. If p_n is the probability that the system contains n customers at equilibrium and a_n denotes the probability that an arriving customer finds $n$customers already present, then PASTA states that $a_n = p_n$. This implies that the Poisson process sees the same distribution as a random observer, i.e., at equilibrium, Poisson arrivals take a random look at the system. This result is a direct consequence of the memoryless property of the interarrival time distribution of customers to a queueing system fed by a Poisson process. In particular, it does not depend on the service time distribution. To prove the PASTA property, we proceed as follows.

Let

$L(t)$ = Number of customers in the system at time t

$p_n(t) = P(System\ is\ in\ state\ n\ at\ time\ t) = P(L(t) = n)$

$a_n(t) = P(Arrival\ at\ time\ t\ finds\ system\ in\ state\ n)$

$A(t, t + \delta t]$ = The event of an arrival in $(t, t + \delta t]$

Then

$$a_n(t) = \lim_{\delta t \to 0} P(L(t) = n | A(t, t + \delta t])$$

$$= \lim_{\delta t \to 0} \frac{P(L(t) = n\ and\ A(t, t + \delta t])}{P(A(t, t + \delta t])}$$

$$= \lim_{\delta t \to 0} \frac{P(A(t, t + \delta t] | L(t) = n) P(L(t) = n)}{P(A(t, t + \delta t])}$$

$$= \lim_{\delta t \to 0} \frac{P(A(t, t + \delta t]) P(L(t) = n)}{P(A(t, t + \delta t])}$$

$$= P(L(t) = n) = p_n(t)$$

The crucial step in the above argument is

$$P(A(t,t+\delta t]|L(t)=n)=P(A(t,t+\delta t])$$

This results from the fact that, since interarrival times possess the memoryless property, $P(A(t,t+\delta t])$ is independent of the past history of the arrival process and hence independent of the current state of the queueing system. With the Poisson arrival process having a constant rate λ, the probability of having an arrival in $(t,t+\delta t]$ is equal to $\lambda\delta t+o(\delta t)$ which does not depend on $L(t)$. Note that the PASTA property only holds for Poisson arrival processes.

The formula for p_c is called "Erlang Loss Formula" and is the fraction of time that all c servers are busy. It denotes the probability that an arrival call finds all the truck line busy, (i.e. the blocking probability, p_c). It is written as $B(c,\lambda/\mu)$s and is called "Erlang B formula":

$$p_c=a_c=P(blocking)=B(c,\lambda/\mu)=B(c,a)=\frac{(\lambda/\mu)^n/n!}{\sum_{n=0}^{c}(\lambda/\mu)^n/n!}=\frac{a^c/c!}{\sum_{n=0}^{c}a^n/n!} \quad (2.1)$$

Notice that the probability that an arrival is lost is equal to the probability that all channels are busy. Erlang loss formula is also valid for the $M/G/c/c$ queue. In other words, the steady-state probabilities are a function only of the mean service time, and not of the complete underlying cumulative distribution function. An efficient recursive algorithm for computing $B(c,a)$ is given by

$$B(0,a)=1,\quad B(c,a)=\frac{aB(c-1,a)}{c+aB(c-1,a)} \quad (2.2)$$

Recall that $a=\lambda/\mu$ is the offered load, we define $a'\coloneqq E(L_b)=a[1-B(c,a)]$ as the carried load, where we obtain the last equality by Little's law applying to number of busy servers and L_b is a random variable representing the number of busy servers in steady-state.

The utilization

$$v\coloneqq\frac{a'}{c}=\frac{a[1-B(c,a)]}{c}=\rho[1-B(c,a)]<1$$

is the fraction of time that a server is busy, where $\rho\coloneqq\frac{a}{c}$ is called the traffic intensity.

Hence we have that

$$1-\frac{1}{\rho}<B(c,a) \quad (2.3)$$

which defines a lower bound for $B(c,a)$

Next, we show the monotonicity property of the $B(c,a)$ with respect to c.

$$B(c,a)=\frac{aB(c-1,a)}{c+aB(c-1,a)}<\frac{aB(c-1,a)}{a[1-B(c-1,a)]+aB(c-1,a)}=B(c-1,a) \quad (2.4)$$

since

$$a[1-B(c-1,a)]<c-1<c$$

We do not consider performance measures relating to waiting time and queue length since there is no waiting space in the $M/M/c/c$ model.

c) Review of the $M/M/c$ Model and the Erlang C Formula

The $M/M/c$ queue can be used to model multiprocessor systems or devices that have several identical servers (or agents) and all jobs (or calls) waiting for these servers are kept in one queue. It is assumed that there are c agents each with a service rate of μ jobs per unit time. The arrival rate is λ calls per unit time. If any of the c agents are idle, the arriving call is serviced immediately. If all c agents are busy, the arriving calls wait in a queue. The state of the system is represented by the number of calls n in the system. The state transition diagram is shown in figure 2.4. It is easy to see that the number of jobs in the system is a birth-death process with the following correspondence:

$$\lambda_n = \lambda, \qquad n \geq 0$$

$$\mu_n = \begin{cases} n\mu, & if\ 1 \leq n \leq c-1 \\ c\mu, & if\ n \geq c \end{cases}$$

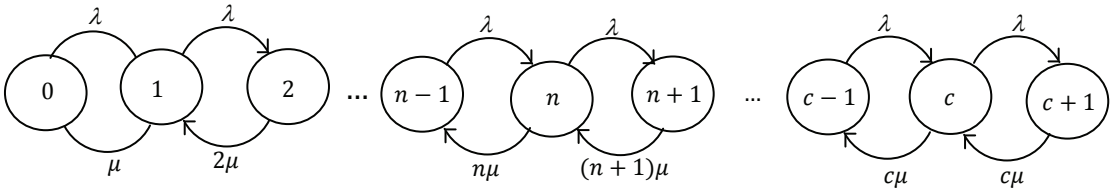

Figure 2.4 : $M/M/c$ Flow Rate [Multiple-ServerCase($c > 1$)]

Owning to the fact that the system is of infinite capacity, the carried load is equal to the offered load, i.e., $a' = a$ so that the utilization $v = \rho$ and as such, we require the stability condition

$$\rho = \frac{\lambda}{c\mu} = \frac{a}{c} < 1$$

Given that the system is stable, the solution to the balance equations obtained from figure 2.4 is

$$p_n = \begin{cases} \frac{a^n}{n!} p_0, & if\ 0 \leq n \leq c \\ \frac{a^n}{c!\, c^{n-c}} p_0, & if\ n \geq c \end{cases} \tag{2.5}$$

with

$$p_0 = \left(\sum_{n=0}^{c-1} \frac{a^n}{n!} + \frac{a^c}{c!} \frac{1}{1-\rho} \right)^{-1} \tag{2.6}$$

Since the arrival process follows the Poisson process, the PASTA property holds so that $a_n = p_n$ for $n \geq 0$. The steady-state probability of waiting of an arriving call is given by the Erlang C formula:

$$P(waiting) = \sum_{n=c}^{\infty} a_n = \sum_{n=c}^{\infty} p_n = C(c,a) = \frac{\frac{a^c}{c!(1-\rho)}}{\sum_{n=0}^{c-1} \frac{a^n}{n!} + \frac{a^c}{c!(1-\rho)}} = \frac{a^c}{c!\,(1-\rho)} p_0 \tag{2.7}$$

So that

$$p_0 = \frac{C(c,a)c!\,(1-\rho)}{a^c} \tag{2.8}$$

The relationship between $C(c,a)$ and $B(c,a)$ is given by

$$C(c,a) = \frac{B(c,a)}{B(c,a)\rho + 1 - \rho}$$

Further simplification using (2.2) yields

$$C(c,a) = \frac{\rho}{\rho + (1-\rho)/B(c-1,a)}$$

From equation 2.5, we it is obvious that $p_c = \frac{a^c}{c!} p_0$, hence by the application of equation 2.8, we obtain $p_c = C(c,a)(1-\rho)$. Using $p_c = \frac{a^c}{c!} p_0$ in equation 2.5 we obtain a new expression for p_n in terms of p_c as follows:

$$p_n = \begin{cases} \frac{c!}{n!\, a^{c-n}} p_c, & if\ 0 \leq n \leq c \\ \rho^{n-c} p_c, & if\ n \geq c \end{cases} \tag{2.9}$$

The new expression for p_c and the above formula for p_n is computationally more efficient, especially for calculating $p_n, n \geq c$ because it does not involve factorials.

i. *The Waiting Time Distribution of the M/M/c Model*

To compute the Telephone Service Factor $TSF = P(W_q \leq AWT)$, we need to compute $P(W_q \leq t)$ which is the steady-state probability of waiting time in queue less than or equal to $t \geq 0$.

Using the concept of total probability, we have that

$$P(W_q > t) = \sum_{n=c}^{\infty} P(W_q > t \mid system\ in\ state\ n\ upon\ arrival) P(system\ in\ state\ n\ upon\ arrival)$$

$$= \sum_{n=c}^{\infty} P(service\ completion\ time\ of\ n-c+1\ calls > t) a_n$$

Using the PASTA property, we can write $P(system\ in\ state\ n\ upon\ arrival) = p_n = a_n$ which is the steady-state probability of an arriving call meeting n calls in the system. Since the service times are exponentially distributed and $n \geq c$, the completion time of $n-c+1$ calls (denoted by) Y_i has an Erlang distribution $Er(n-c+1, c\mu)$ with survival function given by

$$R(t) = P(Y_i > t) = P(service\ completion\ time\ of\ n-c+1\ calls > t) = \sum_{i=0}^{n-c} \frac{(c\mu t)^i e^{-c\mu t}}{i!}$$

Then we have that

$$P(W_q > t) = \sum_{n=c}^{\infty} \sum_{i=0}^{n-c} \frac{(c\mu t)^i e^{-c\mu t}}{i!} p_n = \frac{a^c}{c!\,(1-\rho)} p_0\, e^{-(c\mu-\lambda)t} \tag{2.10}$$

$$E(W_q) = \int_0^{\infty} P(W_q > t)dt = \frac{C(c,a)}{c\mu - \lambda} \tag{2.11}$$

Note that $P(W_q = 0) = 1 - C(c,a)$. By the application of Little's law, we have

$$E(L_q) = \lambda E(W_q) = \frac{\rho C(c,a)}{1-\rho}$$

Because of the closed-form solutions of most the performance indicators of the $M/M/c$ model, it is commonly used in performance modeling and analysis of call centers. In the application of $M/M/c$ model in call center analysis, it is usually assumed that the arrival and service rate are piece-wise constant and time-independent. Using the parameters of each interval, the $M/M/c$ is applied to each time interval. The $M/M/c$ model is not a realistic tool for modeling call centers due to the following reasons:

- It assumes there is no blocking since it has infinite buffer capacity.
- It does not consider the impatience (balking and reneging) attributes of customers.

d) Review of the M/M/c/N Model

When the waiting room in a queueing system has a capacity limit we get a finite queue. In most situations, a finite queue occurs more naturally than a queue with a waiting room of infinite size. However, as the capacity limit gets larger, the behavior of the system approximates that of an infinite-capacity system, and in such cases we are justified in ignoring the size limit. A call center with a finite buffer and several agents is a good example of a finite queueing system. In this section we will review the $M/M/c/N$ model and prove new monotonicity properties of performance measures with respect to N.

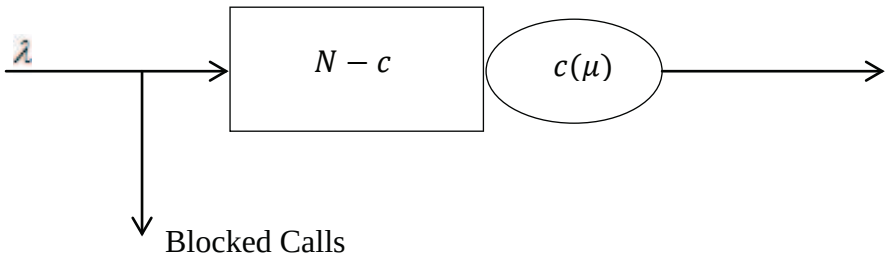

Figure 2.5 : Description of the $M/M/c/N$ Model and its parameters

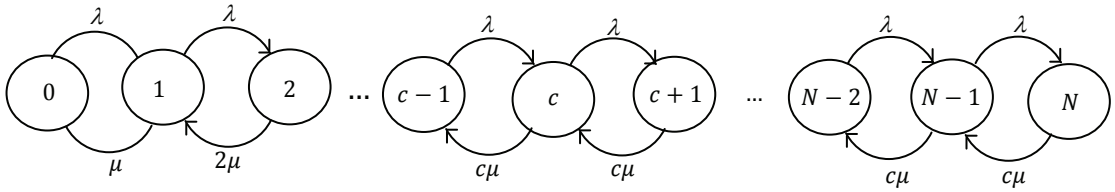

Figure 2.6 : $M/M/c/N$ Flow Rate [Multiple-ServerCase($c > 1$)]

The $M/M/c/N$ queue is similar to the $M/M/c$ queue except that the number of buffers is finite. After $B = N - c$ buffers are full, all arrivals are lost. We assume that B is greater than or equal to c; otherwise, some servers will never be able to operate due to a lack of buffers and the system will effectively operate as a $M/M/B/B$ queue.

The state transition diagram for a $M/M/c/N$ queue is shown in Figure 2.6. The system can be modeled as a birth-death process using the following respective arrival and service rates:

$$\lambda_n = \lambda, \qquad if\ 0 \le n \le N-1$$

$$\mu_n = \begin{cases} n\mu, if\ 0 \le n \le c \\ c\mu, if\ c \le n \le N \end{cases}$$

Solving the balance equations derived from the state diagram, we obtain the following state probabilities.

$$p_n = \begin{cases} \dfrac{a^n}{n!} p_0, & if\ 0 \le n \le c \\ \dfrac{a^n}{c!\, c^{n-c}} p_0, & if\ c \le n \le N \end{cases} \tag{2.12}$$

with

$$p_0 = \begin{cases} \left(\sum_{n=0}^{c-1} \dfrac{a^n}{n!} + \dfrac{a^c}{c!} \dfrac{1-\rho^{N-c+1}}{1-\rho} \right)^{-1}, & if\ \rho \ne 1 \\ \left(\sum_{n=0}^{c-1} \dfrac{a^n}{n!} + \dfrac{a^c}{c!} (N-c+1) \right)^{-1}, & if \rho = 1 \end{cases}$$

and

$$P(waiting) = \sum_{n=c}^{N-1} p_n \,;\ P(blocking) = p_N;\ and\ \ P(no-waiting) = 1 - P(waiting) - P(blocking)$$

i. *The M/M/c/N Waiting Time Distribution*

In this section, we shall provide a mathematical derivation of the waiting time distribution of the $M/M/c/N$ model. Due to the finiteness of the capacity of the $M/M/c/N$ system, deriving the waiting time distribution of the $M/M/c/N$ model is complicated because it results to finite series and also the arrival process is truncated by the system size N. The arrival process no longer follows the Poisson process and has necessitated the need to derive the arrival point probabilities, q_n since $p_n \ne q_n$. In this derivation of q_n, we shall apply the well-known Bayes' theorem.

$$q_n = P(system\ is\ in\ state\ n\ |an\ arrival\ in\ (t, t+\delta t])$$

$$= P(L(t) = n\ |A(t, t+\delta t]) = \frac{P(L(t) = n;\ A(t, t+\delta t])}{P(A(t, t+\delta t])}$$

$$= \frac{P(A(t, t+\delta t]\ |L(t) = n) P(L(t) = n)}{\sum_{n=0}^{N} P(A(t, t+\delta t]|L(t) = n) P(L(t) = n)} = \frac{P(A(t, t+\delta t]\ |L(t) = n) p_n}{\sum_{n=0}^{N} P(A(t, t+\delta t]|L(t) = n) p_n}$$

Taking limits of both sides and using the fact that the probability of an arrival in $(t, t+\delta t]$ is $\lambda\delta t + o(\delta t)$ we have that

$$\lim_{\delta t\to 0} q_n = q_n = \frac{P(A(t,t+\delta t])p_n}{\sum_{n=0}^{N} P(A(t,t+\delta t])p_n} = \lim_{\delta t\to 0}\left(\frac{(\lambda\delta t + o(\delta t))p_n}{\sum_{n=0}^{N-1}(\lambda\Delta t + o(\delta t))\,p_n}\right)$$

$$= \lim_{\delta t\to 0}\left(\frac{\left(\lambda + \frac{o(\delta t)}{\delta t}\right)p_n}{\sum_{n=0}^{N-1}\left(\lambda + \frac{o(\delta t)}{\delta t}\right)p_n}\right) = \frac{\lambda p_n}{1-p_N}, \qquad for\ 0 \le n \le N-1$$

which defines the probability of a call meeting n calls in the system upon arrival given that it is not blocked. Here we have used the fact that

$$\lim_{\delta t\to 0}\frac{o(\delta t)}{\delta t} = 0$$

Using equation (2.12), we can write $p_c = \frac{a^c}{c!}p_0$ which implies that $p_0 = \frac{c!}{a^c}p_c$. Then we can express p_n in terms of p_c as follows:

$$p_n = \begin{cases} \frac{c!}{n!\,a^{c-n}}p_c, & if\ 0 \le n \le c \\ p_c\rho^{n-c}, & if\ c \le n \le N \end{cases}$$

Then for $\rho \neq 1$,

$$1 = \sum_{n=0}^{c}\frac{c!}{n!\,a^{c-n}}p_c + \sum_{n=c+1}^{N} p_c\rho^{n-c}$$

$$p_c = \left(\sum_{n=0}^{c}\frac{c!}{n!\,a^{c-n}} + \sum_{n=c+1}^{N}\rho^{n-c}\right)^{-1} = \left(\frac{1}{B(c,a)} + \frac{\rho(1-\rho^{N-c})}{1-\rho}\right)^{-1}$$

$$p_c = \frac{(1-\rho)B(c,a)}{1-\rho+\rho B(c,a)(1-\rho^{N-c})}$$

For $\rho \neq 1$,

$$P(blocking) = p_N = p_c\rho^{N-c} = \frac{(1-\rho)B(c,a)\rho^{N-c}}{1-\rho+\rho B(c,a)(1-\rho^{N-c})}$$

In same way, for $\rho \neq 1$,

$$P(waiting) = \sum_{n=c}^{N-1} p_n = \sum_{n=c}^{N-1} p_c\rho^{n-c} = \frac{1-\rho^{N-c}}{1-\rho}p_c = \frac{1-\rho^{N-c}}{1-\rho}\frac{(1-\rho)B(c,a)}{1-\rho+\rho B(c,a)(1-\rho^{N-c})}$$

$$P(waiting) = \frac{(1-\rho^{N-c})B(c,a)}{1-\rho+\rho B(c,a)(1-\rho^{N-c})}$$

and

$$P(no-waiting) = 1 - P(waiting) - P(blocking) = \frac{(1-B(c,a))(1-\rho)}{1-\rho+\rho B(c,a)(1-\rho^{N-c})}$$

Now, let us consider computing $P(blocking)$, $P(waiting)$ and $P(no-waiting)$ in the case where $\rho = 1$.

For $\rho = 1$, implies that $a = c$ so that we have

$$p_c = \left(\sum_{n=0}^{c} \frac{c!}{n!\, a^{c-n}} + \sum_{n=c+1}^{N} \rho^{n-c}\right)^{-1} = \left(\frac{1}{B(c,a)} + N - c\right)^{-1} = \frac{B(c,c)}{1 + (N-c)B(c,c)}$$

$$P(blocking) = p_N = p_c \rho^{N-c} = p_c = \frac{B(c,c)}{1 + (N-c)B(c,c)}$$

$$P(waiting) = \sum_{n=c}^{N-1} p_n = \sum_{n=c}^{N-1} p_c \rho^{n-c} = \sum_{n=c}^{N-1} p_c = (N-c)p_c = \frac{(N-c)B(c,c)}{1 + (N-c)B(c,c)}$$

$$P(no - waiting) = 1 - P(waiting) - P(blocking) = \frac{1 - B(c,c)}{1 + (N-c)B(c,c)}$$

Theorem 2.1

Suppose $N = c$ then the $M/M/c/N$ model reduces to the $M/M/c/c$ model with

$$P(blocking) = B(c,a),\ P(waiting) = 0 \text{ and } P(no - waiting) = 1 - B(c,a).$$

Proof

If $N = c$,

$$P(blocking) = p_c = p_N = p_c \rho^{N-c} = \frac{B(c,a)\rho^{N-c}}{1 + (N-c)B(c,a)} = \frac{B(c,a)(1)}{1 + (0)B(c,a)} = B(c,a)$$

$$P(waiting) = \frac{(1 - \rho^{N-c})B(c,a)}{1 - \rho + \rho B(c,a)(1 - \rho^{N-c})} = \frac{(0)B(c,a)}{1 - \rho + \rho B(c,a)(0)} = 0$$

$$P(no - waiting) = 1 - P(waiting) - P(blocking) = 1 - 0 - B(c,a) = 1 - B(c,a)$$

Theorem 2.2

In the limit, as $N \to \infty$, we have the following results:

1. $$\lim_{N\to\infty} P(waiting) = \begin{cases} \frac{1}{\rho}, & if\ \rho > 1 \\ 1, & if\ \rho = 1 \\ C(c,a), & if 0 < \rho < 1 \end{cases}$$

2. $$\lim_{N\to\infty} P(blocking) = \begin{cases} 1 - \frac{1}{\rho}, & if\ \rho \geq 1 \\ 0, & if 0 < \rho \leq 1 \end{cases}$$

3. $$\lim_{N\to\infty} P(no - waiting) = \begin{cases} 0, & if\ \rho \geq 1 \\ 1 - C(c,a), & if 0 < \rho \leq 1 \end{cases}$$

Proof

1. For $0 < \rho < 1$,

$$P(waiting) = \frac{(1-\rho^{N-c})B(c,a)}{1-\rho+\rho B(c,a)(1-\rho^{N-c})} \xrightarrow{as\ N\to\infty} \frac{B(c,a)}{1-\rho+\rho B(c,a)} = C(c,a)$$

For $\rho = 1$,

$$P(waiting) = \frac{(N-c)B(c,c)}{1+(N-c)B(c,c)} = \frac{B(c,c)}{\frac{1}{(N-c)}+B(c,c)} \xrightarrow{as\ N\to\infty} 1$$

For $\rho > 1$,

$$P(waiting) = \frac{(\rho^{N-c}-1)B(c,a)}{\rho+\rho B(c,a)(\rho^{N-c}-1)-1} = \frac{\frac{(\rho^{N-c}-1)B(c,a)}{\rho^{N-c}-1}}{\frac{\rho-1}{\rho^{N-c}-1}+\frac{\rho B(c,a)(\rho^{N-c}-1)}{\rho^{N-c}-1}} = \frac{1}{\rho}$$

So that

$$\lim_{N\to\infty} P(waiting) = \frac{1}{\rho}, \qquad if\ \ \rho > 1$$

2. For $0 < \rho < 1$,

$$P(blocking) = p_N = p_c\rho^{N-c} = \frac{(1-\rho)B(c,a)\rho^{N-c}}{1-\rho+\rho B(c,a)(1-\rho^{N-c})} \xrightarrow{as\ N\to\infty} 0$$

Since $\rho^{N-c} \to 0\ as\ N \to \infty, for\ \ 0 < \rho < 1.$

For $\rho = 1$,

$$P(blocking) = p_N = \frac{B(c,c)}{1+(N-c)B(c,c)} \xrightarrow{as\ N\to\infty} 0$$

For $\rho > 1$,

$$P(blocking) = p_N = \frac{(\rho-1)B(c,a)\rho^{N-c}}{\rho+\rho B(c,a)(\rho^{N-c}-1)-1} = \frac{\frac{(\rho-1)B(c,a)\rho^{N-c}}{\rho^{N-c}}}{\frac{\rho-1}{\rho^{N-c}}+\frac{\rho B(c,a)(\rho^{N-c}-1)}{\rho^{N-c}}}$$

$$= \frac{(\rho-1)B(c,a)}{\frac{\rho-1}{\rho^{N-c}}+\frac{\rho B(c,a)(\rho^{N-c}-1)}{\rho^{N-c}}} \xrightarrow{as\ N\to\infty} \frac{(\rho-1)B(c,a)}{\rho B(c,a)} = 1-\frac{1}{\rho}$$

3. For $\rho > 1$,

$$P(no-waiting) = \frac{\big(1-B(c,a)\big)(\rho-1)}{1-\rho+\rho B(c,a)(1-\rho^{N-c})} = \frac{\frac{\big(1-B(c,a)\big)(\rho-1)}{\rho^{N-c}}}{\frac{\rho+\rho B(c,a)(\rho^{N-c}-1)-1}{\rho^{N-c}}}$$

$$= \frac{\frac{(1-B(c,a))(\rho-1)}{\rho^{N-c}}}{\frac{\rho-1}{\rho^{N-c}}-\frac{\rho B(c,a)}{\rho^{N-c}}+\frac{\rho B(c,a)(\rho^{N-c})}{\rho^{N-c}}} \xrightarrow{as\ N\to\infty} 0$$

For $0 < \rho < 1$,

$$(no - waiting) = \frac{\big(1 - B(c,a)\big)(1-\rho)}{1 - \rho + \rho B(c,a)(1-\rho^{N-c})} \xrightarrow{as\ N\to\infty} \frac{\big(1 - B(c,a)\big)(1-\rho)}{1 - \rho + \rho B(c,a)(1-\rho^{N-c})}$$

$$= 1 - C(c,a)$$

For $\rho = 1$,

$$P(no - waiting) = \frac{1 - B(c,c)}{1 + (N-c)B(c,c)} \xrightarrow{as\ N\to\infty} 0$$

Before we proceed to derive the formula for computing an important performance measure $E(W_q)$, we shall prove some new results that will be useful in the course of our derivations and computations.

For $\rho \neq 1$,

$$P(waiting|no - blocking) = P(W_q > 0) = \sum_{n=c}^{N-1} q_n = \sum_{n=c}^{N-1} \frac{p_n}{1-p_N} = \frac{1}{1-p_N}\sum_{n=c}^{N-1} p_n$$

$$= \frac{1}{1-p_N} P(waiting) = \frac{P(waiting)}{1 - P(blocking)}$$

$$= \frac{1 - \rho + \rho B(c,a)(1-\rho^{N-c})}{1 - \rho + \rho B(c,a)(1-\rho^{N-c-1})} \frac{B(c,a)(1-\rho^{N-c})}{1 - \rho + \rho B(c,a)(1-\rho^{N-c})}$$

$$P(waiting|no - blocking) = P(W_q > 0) = \frac{B(c,a)(1-\rho^{N-c})}{1 - \rho + \rho B(c,a)(1-\rho^{N-c-1})}$$

But

$$P(no - waiting|no - blocking) = P(W_q = 0) = \sum_{n=0}^{c-1} q_n = 1 - P(waiting|no - blocking)$$

$$= \frac{(1-\rho)[1 - B(c,a)]}{1 - \rho + \rho B(c,a)(1-\rho^{N-c-1})}$$

For $\rho = 1$,

$$P(waiting|no - blocking) = \frac{P(waiting)}{1 - P(blocking)} = \frac{\frac{(N-c)B(c,c)}{1+(N-c)B(c,c)}}{1 - \frac{B(c,c)}{1+(N-c)B(c,c)}}$$

$$= \frac{(N-c)B(c,c)}{1 + B(c,c)[N-c-1]}$$

Now, using the principles of conditional probability, we can write

$$P(W_q > t | W_q > 0) = \frac{P(W_q > t;\ W_q > 0)}{P(W_q > 0)} = \frac{P(W_q > t)}{P(W_q > 0)}$$

$$P(W_q > t) = P(W_q > t | W_q > 0) P(W_q > 0)$$

$$P(W_q > t) = P(W_q > t | W_q > 0) P(waiting | no - blocking)$$

For $\rho \neq 1$,

$$P(W_q > t | W_q > 0) = P(W_q > t | c \leq Q \leq N-1)$$

$$= \sum_{n=0}^{N-c+1} P(W_q > t | L = c+n;\ c \leq L \leq N-1) P(L = c+n | c \leq L \leq N-1)$$

$$= \sum_{n=0}^{N-c-1} \left(\sum_{k=0}^{n} \frac{(c\mu t)^k e^{-c\mu t}}{k!} \right) \frac{\rho^n}{1 + \rho + \cdots + \rho^{N-c-1}}$$

$$= \sum_{k=0}^{N-c-1} \frac{(c\mu t)^k e^{-c\mu t}}{k!} \sum_{n=k}^{N-c-1} \frac{\rho^n}{1 + \rho + \cdots + \rho^{N-c-1}}$$

$$P(W_q > t | W_q > 0) = \sum_{k=0}^{N-c-1} \frac{(c\mu t)^k e^{-c\mu t}}{k!} \frac{\rho^k - \rho^{N-c}}{1 - \rho^{N-c}} = \sum_{k=0}^{N-c-1} \frac{(\lambda t)^k e^{-c\mu t}}{k!} \frac{1 - \rho^{N-c-k}}{1 - \rho^{N-c}}$$

Then for $\rho \neq 1$, we have that

$$P(W_q > t) = P(waiting | no - blocking) \sum_{k=0}^{N-c-1} \frac{(\lambda t)^k e^{-c\mu t}}{k!} \frac{1 - \rho^{N-c-k}}{1 - \rho^{N-c}}, t \geq 0 \quad (2.13)$$

Where we have used the fact that[15]

$$P(L = c+n | c \leq L \leq N-1) = \frac{\rho^n}{1 + \rho + \cdots + \rho^{N-c-1}}, \qquad for\ 0 \leq n \leq N-c-1 \quad (2.14)$$

For $\rho = 1$, we also have that

$$P(W_q > t) = P(waiting | no - blocking) \sum_{k=0}^{N-c-1} \frac{(\lambda t)^k e^{-c\mu t}}{k!} \left(1 - \frac{k}{N-c}\right) \quad (2.15)$$

In same line of reasoning, we derive the mathematical formula for computing the Average Speed to Answer (ASA) as follows:

$$ASA = E(W_q) = \int_0^{\infty} P(W_q > t)dt$$

$$= P(waiting|no - blocking) \sum_{k=0}^{N-c-1} \frac{\rho^k - \rho^{N-c}}{1-\rho^{N-c}} \int_0^{\infty} \frac{(c\mu t)^k e^{-c\mu t}}{k!} dt$$

$$= P(waiting|no - blocking) \sum_{k=0}^{N-c-1} \frac{\rho^k - \rho^{N-c}}{(1-\rho^{N-c})c\mu}$$

$$= P(waiting|no - blocking) \frac{1-\rho^{N-c}(1+(1-\rho)(N-c))}{(1-\rho)(1-\rho^{N-c})c\mu}$$

$$= \frac{B(c,a)(1-\rho^{N-c})}{1-\rho+\rho B(c,a)(1-\rho^{N-c-1})} \frac{1-\rho^{N-c}\left(1+(1-\rho)(N-c)\right)}{(1-\rho)(1-\rho^{N-c})c\mu}$$

$$E(W_q) = \frac{(1-\rho^{N-c}(1+(1-\rho)(N-c))B(c,a)}{(1-\rho+\rho B(c,a)(1-\rho^{N-c-1}))(1-\rho)c\mu}$$

By the application of Little's law, we have that

$$E(L_q) = \lambda E(W_q)(1 - P(blocking))$$

III. Limiting Behaviour of the M/M/c/N Model Performance Indicators

In this section of the paper we shall prove some limiting properties of the $M/M/c/$ model with respect to N.

Theorem 3.1

Given that c and other model parameters remain constant, $P(W_q > t)$ is an increasing function of N.

For $0 < \rho < 1$,

Proof

First, we need to show that $P(waiting|no - blocking)$ is an increasing function of N:

$$P(waiting|no - blocking) = \frac{B(c,a)(1-\rho^{N-c})}{1-\rho+\rho B(c,a)(1-\rho^{N-c-1})} = \frac{B(c,a)}{\frac{1-\rho}{(1-\rho^{N-c-1})}+\rho B(c,a)}$$

$$< \frac{B(c,a)}{1-\rho+\rho B(c,a)}, \qquad \text{Since } 1-\rho+\rho B(c,a) > \frac{1-\rho}{(1-\rho^{N-c-1})}+\rho B(c,a)$$

For $\rho = 1$,

$$P(waiting|no-blocking) = \frac{(N-c)B(c,c)}{1+B(c,c)[N-c-1]} = \frac{B(c,c)}{\frac{1}{N-c}+\frac{B(c,c)[N-c-1]}{N-c}}$$

$$\cong \frac{B(c,c)}{\frac{1}{N-c}+B(c,c)} < 1, \qquad \text{since } \frac{1}{N-c}+B(c,c) > B(c,c)$$

Now that we have established the fact that $P(waiting|no-blocking)$ is an increasing function of N, we will proceed to show that $P(W_q > t)$ is an increasing function of N, given that c and other model parameters remain constant.

Recall from equation 2.13; for $0 < \rho < 1$

$$P(W_q > t) = P(waiting|no-blocking)\sum_{k=0}^{N-c-1}\frac{(\lambda t)^k e^{-c\mu t}}{k!}\frac{1-\rho^{N-c-k}}{1-\rho^{N-c}}, t \geq 0$$

and from equation 2.15; for $\rho = 1$, we have

$$P(W_q > t) = P(waiting|no-blocking)\sum_{k=0}^{N-c-1}\frac{(\lambda t)^k e^{-c\mu t}}{k!}\left(1-\frac{k}{N-c}\right)$$

We are only left to show that

$$\gamma(N) := \sum_{k=0}^{N-c-1}\frac{(\lambda t)^k e^{-c\mu t}}{k!}\frac{1-\rho^{N-c-k}}{1-\rho^{N-c}} \quad and \quad \varphi(N) := \sum_{k=0}^{N-c-1}\frac{(\lambda t)^k e^{-c\mu t}}{k!}\left(1-\frac{k}{N-c}\right)$$

are increasing functions of N.

$$\text{For } i \in \mathbb{N}, \qquad \gamma(N+i) := \sum_{k=0}^{N+i-c-1}\frac{(\lambda t)^k e^{-c\mu t}}{k!}\frac{1-\rho^{N+i-c-k}}{1-\rho^{N+i-c}}$$

$$\gamma(N+i) = \sum_{k=0}^{N-c-1}\frac{(\lambda t)^k e^{-c\mu t}}{k!}\frac{1-\rho^{N+i-c-k}}{1-\rho^{N+i+c}} + \sum_{k=N-c}^{N+i-c-1}\frac{(\lambda t)^k e^{-c\mu t}}{k!}\frac{1-\rho^{N+i-c-k}}{1-\rho^{N+i-c}}$$

$$> \sum_{k=0}^{N-c-1}\frac{(\lambda t)^k e^{-c\mu t}}{k!}\frac{1-\rho^{N-c-k}}{1-\rho^{N-c}} = \gamma(N)$$

since

$$\sum_{k=N-c}^{N+i-c-1}\frac{(\lambda t)^k e^{-c\mu t}}{k!}\frac{1-\rho^{N+i-c-k}}{1-\rho^{N+i-c}} > 0 \quad and \quad \frac{1-\rho^{N+i-c-k}}{1-\rho^{N+i+c}} \geq \frac{1-\rho^{N-c-k}}{1-\rho^{N-c}}$$

In same way,

$$\text{For } i \in \mathbb{N}, \qquad \varphi(N+i) := \sum_{k=0}^{N+i-c-1} \frac{(\lambda t)^k e^{-c\mu t}}{k!}\left(1 - \frac{k}{N+i-c}\right)$$

$$\varphi(N+i) = \sum_{k=0}^{N-c-1} \frac{(\lambda t)^k e^{-c\mu t}}{k!}\left(1 - \frac{k}{N+i-c}\right) + \sum_{k=N-c}^{N+i-c-1} \frac{(\lambda t)^k e^{-c\mu t}}{k!}\left(1 - \frac{k}{N+i-c}\right)$$

$$> \sum_{k=0}^{N-c-1} \frac{(\lambda t)^k e^{-c\mu t}}{k!}\left(1 - \frac{k}{N-c}\right) = \varphi(N)$$

since

$$\sum_{k=N-c}^{N+i-c-1} \frac{(\lambda t)^k e^{-c\mu t}}{k!}\left(1 - \frac{k}{N+i-c}\right) > 0 \; and \; 1 - \frac{k}{N+i-c} \geq 1 - \frac{k}{N-c}, 0 \leq k \leq N-c-1$$

IV. Conclusions

In this paper, we have discussed in detail the modeling of a call center as single-node using the Markovian queueing techniques. We considered the $M/M/c/c$ Erlang B Loss model and the $M/M/c/c$ Erlang C model as well as the more general $M/M/c/N$ model. Our emphasis is on the derivation of the exact performance measures of these well-known models. Considering the $M/M/c/N$ model, we expressed the system performance measures in terms of Erlang B formula, which facilitates the computation as well as the analysis. Using the results emanating from the analysis, we showed the monotonicity properties for performance measures with respect to N and c.

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Feature Selection Algorithm for High Dimensional Data using Fuzzy Logic

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Abstract - Feature subset selection is an effective way for reducing dimensionality, removing irrelevant data, increasing learning accuracy and improving results comprehensibility. This process improved by cluster based FAST Algorithm and Fuzzy Logic. FAST Algorithm can be used to Identify and removing the irrelevant data set. This algorithm process implements using two different steps that is graph theoretic clustering methods and representative feature cluster is selected. Feature subset selection research has focused on searching for relevant features. The proposed fuzzy logic has focused on minimized redundant data set and improves the feature subset accuracy.

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Feature Selection Algorithm for High Dimensional Data using Fuzzy Logic

T. Jaga Priya Vathana [α], C. Saravanabhavan [σ] & Dr. J. Vellingiri [ρ]

Abstract - **Feature subset selection is an effective way for reducing dimensionality, removing irrelevant data, increasing learning accuracy and improving results comprehensibility. This process improved by cluster based FAST Algorithm and Fuzzy Logic. FAST Algorithm can be used to Identify and removing the irrelevant data set. This algorithm process implements using two different steps that is graph theoretic clustering methods and representative feature cluster is selected. Feature subset selection research has focused on searching for relevant features. The proposed fuzzy logic has focused on minimized redundant data set and improves the feature subset accuracy.**

I. Introduction

The performance, robustness, and usefulness of classification algorithms are improved when relatively few features are involved in the classification. Thus, selecting relevant features for the construction of classifiers has received a great deal of attention.

With the aim of choosing a subset of good features with respect to the target concepts, feature subset selection is an effective way for reducing dimensionality, removing irrelevant data, increasing learning accuracy, and improving result compre-hensibility. Many feature subset selection methods have been proposed and studied for machine learning applications. They can be divided into four broad categories: the Embedded, Wrapper, Filter, and Hybrid approaches. The embedded methods incorporate feature selection as a part of the training process and are usually specific to given learning algorithms, and therefore may be more efficient than the other three categories. Traditional machine learning algorithms like decision trees or artificial neural networks are examples of embedded approaches. The wrapper methods use the predictive accuracy of a predetermined learning algorithm to determine the goodness of the selected sub-sets, the accuracy of the learning algorithms is usually high. However, the generality of the selected features is limited and the computational complexity is large. The filter methods are independent of learning algorithms, with good generality.

With respect to the filter feature selection methods, the application of cluster analysis has been demonstrated to be more effective than traditional feature selection algorithms. Pereira et al., Baker et al., and Dillon et al. employed the distributional clustering of words to reduce the dimensionality of text data. In cluster analysis, graph-theoretic methods have been well studied and used in many applications. Their results have, sometimes, the best agreement with human performance. The general graph-theoretic clustering is simple: Compute a neighborhood graph of in-stances, then delete any edge in the graph that is much longer/shorter (according to some criterion) than its neighbors. The result is a forest and each tree in the forest represents a cluster. In our study, we apply graph-theoretic clustering methods to features. In particular, we adopt the minimum spanning tree (MST) based clustering algorithms, because they do not assume that data points are grouped around centers or separated by a regular geometric curve and have been widely used in practice. Based on the MST method, we propose a FAST clustering-Based feature Selection algorithm (FAST).The FAST algorithm works in two steps. In the first step, features are divided into clusters by using graph-theoretic clustering methods. In the second step, the most representative feature that is strongly related to target classes is selected from each cluster to form the final subset of features. Features in different clusters are relatively independent; the clustering-based strategy of FAST has a high probability of producing a subset of useful and independent features. The proposed feature subset se-lection algorithm FAST was tested upon 35 publicly available image, microarray, and text data sets. The Experimental results show that, compared with other five different types of feature subset selection algorithms, the proposed algorithm not only reduces the number of features, but also improves the performances of the four well-known different types of classifiers.

II. Literature Review

a) Statistical Comparisons of Classifiers over Multiple Data Sets

In this method introduce some new pre- or post processing step has been proposed, and the implicit hypothesis is made that such an enhancement yields an improved performance over the existing classification

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algorithm. Alternatively, various solutions to a problem are proposed and the goal is to tell the successful from the failed. A number of test data sets is selected for testing, the algorithms are run and the quality of the resulting models is evaluated using an appropriate measure, most commonly classification accuracy. The remaining step, and the topic of this paper, is to statistically verify the hypothesis of improved performance. Various re-searchers have addressed the problem of comparing two classifiers on a single data set and proposed several solutions. The core of the paper is the study of the statistical tests that could be (or already are) used for comparing two or more classifiers on multiple data sets. Learning algorithms is used for the Classification purpose. The main disadvantage of this process is the problems with the multiple data set tests are quite different, even in a sense complementary.

b) A Features Set Measure Based on Relief

It used six real world dataset from the UCI repository have been used. Three of them have classification Problem with discrete features, the next two classifications with discrete and continuous features, and the last one is approximation problem. The learning algorithm is used to check the quality of feature selected are a classification and regression tree layer with pruning. This process and algorithms is implemented by the orange data mining System. Overall, the non-parametric tests, namely the Wilcox on and Friedman test are suitable for our problems. They are appropriate since they assume some, but limited commensurability. They are safer than parametric tests since they do not assume normal distributions or homogeneity of variance. There is an alternative opinion among statisticians that significance tests should not be per-formed at all since they are often misused, either due to misinterpretation or by putting too much stress on their results. The main disadvantage of the system is it measure to low accuracy of the search process.

c) Feature Clustering and Mutual Information for the Selection of Variables In Spectral Data

It face many problems in spectrometry require predicting a quantitative value from measured spectra. The major issue with spectrometric data is their functional nature; they are functions discredited with a high resolution. This leads to a large number of highly-correlated features; many of which are irrelevant for the prediction. The approach for the features is to describe the spectra in a functional basis whose basis functions are local in the sense that they correspond to well-defined portions of the spectra. This process has clustering algorithm that algorithm recursively merges at each step the two most similar consecutive clusters. This algorithm return the output value associated with each cluster, its representative, is chosen to be the mean of the spectra over the range of features defined by the cluster. The main disadvantage of the problem is low number of clusters identified by the method allows the interpretation of the selected variables: several of the selected clusters include the spectral variables identified on these benchmarks as meaningful in the literature.

d) On Feature Selection through Clustering

This paper introduce an algorithm for feature selection that clusters attributes using a special metric and, then uses a hierarchical clustering for feature selection. Hierarchical algorithms generate clusters that are placed in a cluster tree, which is commonly known as a dendrogram. Clustering's are obtained by extracting those clusters that are situated at a given height in this tree. It use several data sets from the UCI dataset repository and, due to space limitations we discuss only the results obtained with the votes and zoo datasets, Bayes algorithms of the WEKA package were used for constructing classifiers on data sets obtained by projecting the initial data sets on the sets of representative attributes. Approach to attribute selection is the possibility of the supervision of the process allowing the user to opt between quasi-equivalent attributes It face classification problems that involve thousands of features and relatively few examples came to the fore. We intend to apply our techniques to this type of data.

III. Fuzzy based Feature Subset Selection Algorithms

Irrelevant features, along with redundant features, severely affect the accuracy of the learning machines. Thus, feature subset selection should be able to identify and remove as much of the irrelevant and redundant information as possible. The cluster indexing and document assignments are repeated periodically to compensate churn and to maintain an up-to-date clustering solution. The k-means clustering technique and SPSS Tool to develop a real time and online system for a particular supermarket to predict sales in various annual seasonal cycles. The classification was based on nearest mean.

In order to more precisely introduce the algorithm, and because our proposed feature subset selection framework involves irrelevant feature removal and redundant feature elimination.

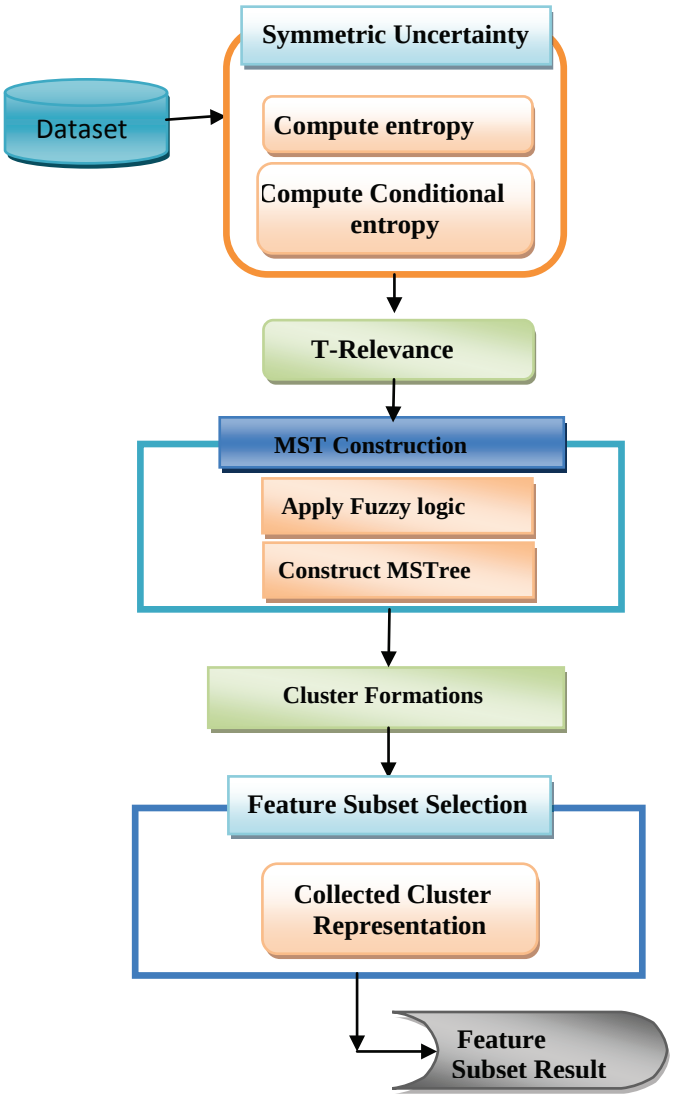

Figure 1 : Framework of the Fuzzy Based

Feature subset selection algorithm Irrelevant features, along with redundant features, severely affect the accuracy of the learning machines, Thus, feature subset selection should be able to identify and Remove as much of the irrelevant and redundant information as possible. Moreover, "good feature subsets contain features highly correlated with (predictive of) the class, yet uncorrelated with (not predictive of) each other. Keeping these in mind, we develop a novel algorithm which can efficiently and effectively deal with both irrelevant and redundant features, and obtain a good feature subset. We achieve this through a new feature selection framework which composed of the two connected components of irrelevant feature removal and redundant feature elimination. The former obtains features relevant to the target concept by eliminating irrelevant ones, and the latter removes redundant features from relevant ones via choosing representatives from different feature clusters, and thus produces the final subset.

The irrelevant feature removal is straightforward once the right relevance measure is defined or selected, while the redundant feature elimination is a bit of sophisticated. In our proposed FAST algorithm, it involves (a) the construction of the minimum spanning tree (MST) from a weighted complete graph; (b) the partitioning of the MST into a forest with each tree representing a cluster; and (c) the selection of representative features from the clusters.

In order to more precisely introduce the algorithm, and because our proposed feature subset selection framework involves irrelevant feature removal and redundant feature elimination, we firstly present the traditional definitions of relevant and redundant features, then provide our definitions based on variable correlation as follows.

John et al. presented a definition of relevant features. Suppose F to be the full set of features, $i \in F$ be a feature, $Si = F - \{Fi\}$ and $S'i \subseteq Si$. Let $s'i$ be a value-assignment of all features in $S'i$, fi a value-assignment of feature Fi, and c a value-assignment of the target concept C. The definition can be formalized as follows.

Definition: (Relevant feature) Fi is relevant to the target concept C if and only if there exists some $s'i$, fi and c, such that, for probability $(S'i = s'i, Fi = fi) > 0$, $p(C = c \mid S'i = s'i, Fi = fi) \neq p(C = c \mid S'i = si)$. Otherwise, feature Fi is an irrelevant feature. Definition 1 indicates that there are two kinds of relevant features due to different $S'i$: (i) when $S'i = Si$, from the definition we can know that Fi is directly relevant to the target concept; (ii) when $S'i \subsetneq Si$, from the definition we may obtain that $p(C \mid Si, Fi) = p(C \mid Si)$. It seems that Fi is irrelevant to the target concept. However, the definition shows that feature Fi is relevant when using $S'i \cup \{Fi\}$ to describe the target concept. The reason behind is that either Fi is interactive with $S'i$ or Fi is redundant with $Si - S'i$. In this case, we say Fi is indirectly relevant to the target concept. Most of the information contained in redundant features is already present in other features. As a result, redundant features do not contribute to getting better interpreting ability to the target concept. It is formally defined by Yu and Liu based on Markov blanket. The definitions of Markov blanket and redundant feature are introduced as follows, respectively.

Let $Mi \subset F (Fi \notin Mi)$, Mi is said to be a Markov blanket for Fi if and only if $p(F - Mi - \{Fi\}, C \mid Fi, Mi) = p(F - Mi - \{Fi\}, C \mid Mi)$. Definition: (Redundant feature). Let S be a set of features, a feature in S is redundant if and only if it has a Markov Blanket within S. Relevant features have strong correlation with target concept so are always necessary for a best subset, while redundant features are not because their values are completely correlated with each other. Thus, notions of feature redundancy and feature relevance are normally in terms of feature correlation and feature-target concept correlation.

Mutual information measures how much the distribution of the feature values and target classes differ from statistical independence. This is a nonlinear estimation of correlation between feature values or feature values and target classes. The symmetric uncertainty (SU) is derived from the mutual information by normalizing it to the entropies of feature values or feature values and target classes, and has been used to evaluate the goodness of features for classification by a number of researchers (e.g., Hall], Hall and Smith, Yu and Liu,, Zhao and Liu,). Therefore, we choose symmetric uncertainty as the measure of correlation between either two features or a feature and the target concept.

The symmetric uncertainty is defined as follows $S(X, Y)=2\times Gain(X|Y)\ H(X)+H(Y)$.

Where,

1. (X)is the entropy of a discrete random variable X. Suppose (x) is the prior probabilities for all values of$X$, $H(X)$is defined by $H(X)=-\sum x\in X\ p(x)\log 2p(x)$.
2. Gain ($X|Y$) is the amount by which the entropy of Y decreases. It reflects the additional information about$Y$provided by$X$and is called the information gain which is given by $Gai(X|Y)=H(X)-H(X|Y)\ =\ H(Y)-H(Y|X)$.

Where ($X|Y$) is the conditional entropy which Quantifies the remaining entropy (i.e. uncertainty) of a random variable X given that the value of another random variable Y is known. Suppose$p(x)$ is the prior probabilities for all values of $X$and $p(x|y)$is the posterior probabilities of Xgiven the values of Y, $H(X|Y)$is defined by $H(X|Y)=-\sum y\in Y\ p(y)\sum x\in X\ p(x|y)\log 2p(x|y)$. (4) Information gain is a symmetrical measure. That is the amount of information gained about Xafter observing$Y$is equal to the amount of information gained about$Y$ after observing X. This ensures that the order of two variables (e.g., (X, Y) or (Y,X)) will not affect the value of the measure.

Symmetric uncertainty treats a pair of variables sym-metrically, it compensates for information gain's bias toward variables with more values and normalizes its value to the range [0,1]. A value 1 of $S(X,\ Y)$ indicates. That knowledge of the value of either one completely predicts the value of the other and the value 0 reveals that $X$and$Y$ are independent. Although the entropy-based measure handles nominal or discrete variables, they can deal with continuous features as well, if the values are discredited properly in advance. Given $SU(X,\ Y)$ the symmetric uncertainty of variables $X$and Y, the relevance T-Relevance between a feature and the target concept C, the correlation F-Correlation between a pair of features, the feature Redundancy F-Redundancy and the representative feature R-Feature of a feature cluster can be defined as follows.

Definition: (T-Relevance) The relevance between the feature $Fi\in F$ and the target concept C is referred to as The T-Relevance of Fi and$C$, and denoted by $S(Fi,C)$. If $S(Fi,C)$ is greater than a predetermined threshold θ, we say that Fi is a strong T-Relevance feature.

Definition: (F-Correlation) The correlation between any pair of features Fi and Fj ($Fi,\ j\in F\wedge i\neq j$) is called the F-Correlation of Fi andFj, and denoted by $SU(Fi,Fj)$.

$Fk<|F|\}$ be a cluster of features. if $\exists Fj\ \in\ S$, $SU(Fj,C)\ \geq\ \ SU(Fi,C)\wedge SU(Fi,Fj)\ >\ SU(Fi,C)$ is always corrected for each $Fi\in S(i\neq j)$, then Fi are redundant features with respect to the givenFj (i.e. each Fi is a F-Redundancy).

Definition: (R-Feature) A feature $Fi\in S=\{F1,2,\ldots,Fk\}(k<|F|)$ is a representative feature of the cluster S(i.e. Fi is a R-Feature) if and only if, $Fi\ =$ argmax $Fj\in SSU(Fj,C)$. This means the feature, which has the strongest T-Relevance, can act as a R-Feature for all the features in the cluster. According to the above definitions, feature subset selection can be the process that identifies and retains the strong T-Relevance features and selects R-Features from feature clusters. The behind heuristics are that

1. Irrelevant features have no/weak correlation with Target concept;
2. Redundant features are assembled in a cluster and a representative feature can be taken out of the Cluster.

IV. Algorithm and Analysis

The proposed FAST algorithm logically consists of three steps:

1. removing irrelevant features,
2. constructing a MST from relative ones,
3. Partitioning the MST and selecting Representative features.

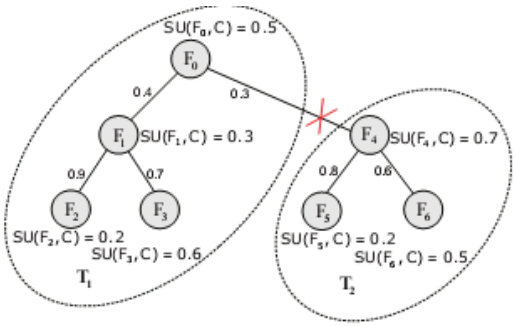

Figure 2 : Example of Clustering Step

After removing all the unnecessary edges, a forest is obtained. Each tree Forest represents a cluster hat is denoted as which is the vertex set of as well. As illustrated above, the features in each cluster are redundant.

The details of the FAST algorithm is shown in Algorithm 1.

Algorithm 1: FAST

```
inputs: D(F1, F2, ..., Fm, C) - the given data set
        θ - the T-Relevance threshold.
output: S - selected feature subset .
//==== Part 1 : Irrelevant Feature Removal ====
for i = 1 to m do
    T-Relevance = SU (Fi, C)
    if T-Relevance > θ then
        S = S ∪ {Fi};
//==== Part 2 : Minimum Spanning Tree Construction ====
G = NULL; //G is a complete graph
for each pair of features {F'i, F'j} ⊂ S do
    F-Correlation = SU (F'i, F'j)
    Add F'i and/or F'j to G with F-Correlation as the weight of
    the corresponding edge;
minSpanTree = Prim (G); //Using Prim Algorithm to generate the
    minimum spanning tree
//==== Part 3 : Tree Partition and Representative Feature Selection ====
Forest = minSpanTree
for each edge Eij ∈ Forest do
    if SU(F'i, F'j) < SU(F'i, C) ∧ SU(F'i, F'j) < SU(F'j, C) then
        Forest = Forest − Eij
S = ϕ
for each tree Ti ∈ Forest do
    F^j_R = argmax_{F'k ∈ Ti} SU(F'k, C)
    S = S ∪ {F^j_R};
return S
```

Time complexity analysis. The major amount of work for Algorithm 1 involves the computation of SU values for T-Relevance and F-Correlation, which has linear complexity in terms of the number of instances in a given data set. The first part of the algorithm has a linear time complexity (m) in terms of the number of features m. Assuming ($1 \leq k \leq m$) features are selected as relevant ones in the first part, when k =1, only one feature is selected. Thus, there is no need to continue the rest parts of the algorithm, and the complexity is(m). When $1<k\leq m$, the second part of the algorithm firstly constructs a complete graph from relevant features and the complexity is (k 2), and then generates a MST from the graph using Prim algorithm whose time complexity. The third part partitions the MST and chooses the representative features with the complexity. Thus when the complexity of the algorithm. This means when FAST has linear complexity while obtains the worst complexity when. However is heuristically set to be in the implementation of FAST. So the complexity, which is typically less than since. This can be explained as follows.

V. Data Source

For the purposes of evaluating the performance and effectiveness of our proposed FAST algorithm, verifying whether or not the method is potentially useful in practice, and allowing other researchers to confirm our results, 35 publicly available data sets were used. The numbers of features of the 35 data sets vary from 37 to 49152 with a mean of 7874. The dimensionality of the 54.3% data sets exceed 5000, of which 28.6% data sets have more than 10000 features. The 35 data sets cover a range of application domains such as text, image and bio microarray data classification.

VI. Experiment Setup

To evaluate the performance of our proposed FAST algorithm and compare it with other feature selection. Algorithms in a fair and reasonable way, we set up our experimental study as follows. 1) The proposed algorithm is compared with five different types of representative feature selection algorithms. They are (i) FCBF, (ii) Relief, (iii) CFS, (iv) Consist and (v) FOCUS SF [2], respectively. FCBF and Relief evaluate features individually. Relief searches for nearest neighbors of instances of different classes and weights features according to how well they differentiate instances of different classes. The other three feature selection algorithms are based on subset evaluation. CFS exploits best-first search based on the evaluation of a subset that contains features highly correlated with the tar-get concept, yet uncorrelated with each other. The Consist method searches for the minimal subset that separates classes as consistently as the full set can under best-first search strategy. FOCUS-SF is a variation of FOCUS [2]. FOCUS has the same evaluation strategy as Consist, but it examines all subsets of features. Considering the time efficiency, FOUCS-SF replaces exhaustive search in FOCUS with sequential forward selection.

Four different types of classification algorithms are employed to classify data sets before and after feature selection. They are (i) the probability-based Naive Bayes (NB), (ii) the tree-based C4.5, (iii) the instance-based lazy learning algorithm IB1, and (iv) the rule-based RIPPER, respectively. Naive Bayes utilizes a probabilistic method for classification by multiplying the individual probabilities of every feature-value pair. This algorithm assumes independence among the features and even then provides excellent classification results. Decision tree learning algorithm C4.5 is an extension of ID3 that accounts for unavailable values, continuous attribute value ranges, pruning of decision trees, rule derivation, and so on. The tree comprises of nodes (features) that are selected by information entropy. Instance-based learner IB1 is a single-nearest-neighbor algorithm, and it classifies entities taking the class of the closest associated vectors in the training set via

distance metrics. It is the simplest among the algorithms used in our study. Inductive rule learner RIPPER (Repeated Incremental Pruning to Produce Error Reduction) is a propositional rule learner that defines a rule based detection model and seeks to improve it iteratively by using different heuristic techniques. The constructed rule set is then used to classify new instances.

3) When evaluating the performance of the feature subset selection algorithms, four metrics, (i) the proportion of selected features (ii) the time to obtain the feature subset, (iii) the classification accuracy, and (iv) the Win/Draw/Loss record, are used. The proportion of selected features is the ratio of the number of features selected by a feature selection algorithm to the original number of features of a data set. The Win/Draw/Loss record presents three values on a given measure, i.e. the numbers of data sets for which our proposed algorithm FAST obtains better, equal, and worse performance than other five feature selection algorithms, respectively. The measure can be the proportion of selected features, the runtime to obtain a feature subset, and the classification accuracy, respectively.

VII. Results and Analysis

In this paper present the experimental results in terms of the proportion of selected features, the time to obtain the feature subset, the classification accuracy, and the Win/Draw/Loss record. For the purpose of exploring the statistical significance of the results, we performed a nonparametric Friedman test followed by Nemenyi post-hoc test, as advised by Demsar and Garcia and Herrerato to statistically compare algorithms on multiple data sets. Thus the Friedman and the Nemenyi test results are reported as well

a) Proportion of selected features

Records the proportion of selected features of the six feature selection algorithms for each data set. From it we observe that) generally all the six algorithms achieve significant reduction of dimensionality by selecting only a small portion of the original features. FAST on average obtains the best proportion of selected features of 1.82%. The Win/Draw/Loss records show FAST wins other algorithms as well. 2) For image data, the proportion of selected features of each algorithm has an increment compared with the corresponding average proportion of selected features on the given data sets except Consist has an improvement. This reveals that the five algorithms are not very suitable to choose features for image data compared with for microarray and text data. FAST ranks 3 with the proportion of selected features of 3.59% that has a tiny margin of 0.11% to the first and second best proportion of selected features 3.48% of Consist and FOCUS-SF, and a margin of 76.59% to the worst proportion of selected features 79.85% of Relief. 3) For microarray data, the proportion of selected features has been improved by each of the six algorithms compared with that on the given data sets. This indicates that the six algorithms work well with microarray data. FAST ranks 1 again with the proportion of selected features of 0.71%. Of the six algorithms, only CFS cannot choose features for two data sets whose dimensionalities are 19994 and 49152, respectively. 4) For text data, FAST ranks 1 again with a margin of 0.48% to the second best algorithm FOCUS-SF. TABLE 2: Proportion of selected features of the six feature selection algorithms.

The Friedman test can be used to compare k algorithms over Ndata sets by ranking each algorithm on each data set separately. The algorithm obtained the best performance gets the rank of 1, the second best ranks 2, and so on. In case of ties, average ranks are assigned. Then the average ranks of all algorithms on all data sets are calculated and compared. If the null hypothesis, which is all algorithms are performing equivalently, is rejected under the Friedman test statistic, post-hoc tests such as the Nemenyi test can be used to determine which algorithms perform statistically different. The Nemenyi test compares classifiers in a pairwise manner. In order to further explore whether the reduction rates are significantly different we performed a Friedman test followed by a Nemenyi post-hoc test. The null hypothesis of the Friedman test is that all the feature selection algorithms are equivalent in terms of proportion of selected features. The test result isp=0. This means that at α= 0.1, there is evidence to reject the null hypothesis and all the six feature selection algorithms are different in terms of proportion of selected features

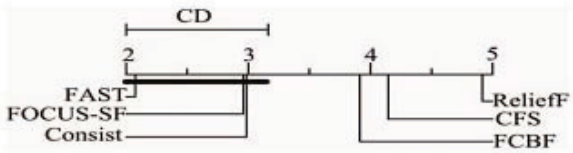

Figure 3 : Proportion of selected features

Comparison of all feature selection algorithms against each other with the Nemenyi test.

In order to further explore feature selection algorithms whose reduction rates have statistically significant differences, we performed a Nemenyi test. Fig. 3 shows the results with α= 0.1 on the 35 data sets. The results indicate that the proportion of selected features of FAST is statistically smaller than those of Relief, CFS and FCBF, and there is no consistent evidence to indicate statistical differences between FAST, Consist, and FOCUS-SF, respectively.

The 10-fold cross-validation accuracies of the four different types of classifiers on the 35 data sets before and after each feature selection algorithm is performed, respectively. The classification accuracy of Naïve Bayes. From it we observe that:

1. Compared with original data, the classification accuracy of Naive Bayes has been improved by FAST, CFS, and FCBF by 12.86%, 6.62%, and 4.32%, respectively. Unfortunately, Relief, Consist, and FOCUS-SF have decreased the classification accuracy by 0.32%, 1.35%, and 0.86%, respectively. FAST ranks 1 with a margin of 6.24% to the second best accuracy 80.60% of CFS. At the same time, the Win/Draw/Loss records show that FAST outer forms all other five algorithms.
2. For image data, the classification accuracy of Naïve Bayes has been improved by FCBF, CFS, FAST, and Relief by 6.13%, 5.39%, 4.29%, and 3.78%, respectively. However, Consist and FOCUS-SF have decreased the classification accuracy by 4.69% and 4.69%, respectively. This time FAST ranks 3 with a margin of 1.83% to the best accuracy 87.32% of FCBF.
3. For microarray data, the classification accuracy of Naive Bayes has been improved by all the six algorithms FAST, CFS, FCBF, ReliefF, Consist, and FOCUS-SF by 16.24%, 12.09%, 9.16%, 4.08%, 4.45%, and 4.45%, respectively. FAST ranks 1 with a mar-gin of 4.16% to the second best accuracy 87.22% of CFS. This indicates that FAST is more effective than others when using Naive Bayes to classify microarray data.
4. For text data, FAST and CFS have improved the classification accuracy of Naive Bayes by 13.83% and 1.33%, respectively. Other four algorithms ReliefF, Consist, FOCUS-SF, and FCBF have decreased the accuracy by 7.36%, 5.87%, 4.57%, and 1.96%, respectively. FAST ranks 1 with a margin of 12.50% to the second best accuracy 70.12% of CFS.

Selection algorithms FAST, FCBF, CFS, Relief, Consist, and FOCUS-SF by 5.31%, 4.54%, 7.20%, 0.73%, 0.60%, and 0.60%, respectively. This time FAST ranks 2 with a margin of 1.89% to the best accuracy 83.6% of CFS and a margin of 4.71% to the worst accuracy 76.99% of Consist and FOCUS-SF. 3) For microarray data, the classification accuracy of C4.5 has been improved by all the six algorithms FAST, FCBF, CFS, Relief, Consist, and FOCUS-SF by 11.42%, 7.14%, 7.51%, 2.00%, 6.34%, and 6.34%, respectively. FAST ranks 1 with a margin of 3.92% to the second best accuracy 79.85% of CFS. 4) For text data, the classification accuracy of C4.5 has been decreased by algorithms FAST, FCBF, CFS, ReliefF, Consist and FOCUS-SF by 4.46%, 2.70%, 19.68%, 13.25%, 16.75%, and 1.90% respectively. FAST ranks 3 with a margin of 2.56% to the best accuracy 83.94% of FOCUS-SF and a margin of 15.22% to the worst accuracy 66.16% of CFS.

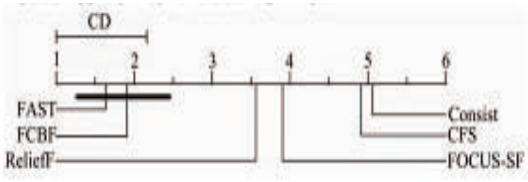

Figure 4 : Runtime comparison of all feature selection algorithms against each other with the Nemenyi test

The classification accuracy of RIPPER. From it we observe that

1. Compared with original data, the classification accuracy of RIPPER has been improved by the five feature selection algorithms FAST, FCBF, CFS, Consist, and FOCUS-SF by 7.64%, 4.51%, 4.08%, 5.48%, and 5.32%, respectively; and has been decreased by Relief by 2.04%. FAST ranks 1 with a margin of 2.16% to the second best accuracy 78.46% of Consist. The Win/Draw/Loss records show that FAST outperforms all other algorithms.
2. For image data, the classification accuracy of RIPPER has been improved by all the six feature selection algorithms FAST, FCBF, CFS, Relief, Consist, and FOCUS-SF by 12.35%, 8.23 %, 4.67%, 3.86%, 4.90%, and 4.90%, respectively. FAST ranks 1 with a margin of 4.13% to the second best accuracy 76.52% of FCBF.
3. For microarray data, the classification accuracy of RIPPER has been improved by all the six algorithms FAST, FCBF, CFS, Relief, Consist, and FOCUS-SF by 13.35%, 6.13%,

This means that at α= 0.1, there are evidences to reject the null hypotheses and the accuracies are different further differences exist in the six feature selection algorithms.

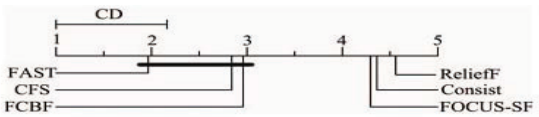

Figure 5 : Accuracy comparison of Naive Bayes with the six feature selection algorithms against each other with the Nemenyi test

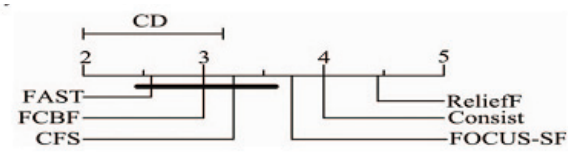

Figure 6 : Accuracy comparison of C4.5 with the six feature selection algorithms against each other with the Nemenyi test

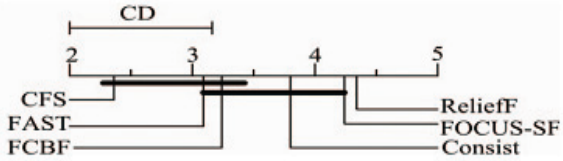

Figure 7 : Accuracy comparison of IB1 with the six feature selection algorithms against each other with the Nemenyi test

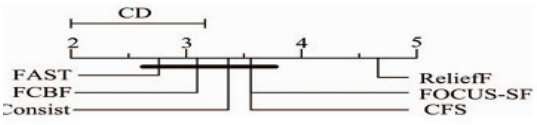

Figure 8 : Accuracy comparison of RIPPER with the six feature selection algorithms against each other with the Nemenyi test

From Fig. 5 we observe that the accuracy of Naïve Bayes with FAST is statistically better than those with Relief, Consist, and FOCUS-SF. But there is no consistent evidence to indicate statistical accuracy differences between Naive Bayes with FAST and with CFS, which also holds for Naive Bayes with FAST and with FCBF. From Fig. 6 we observe that the accuracy of C4.5 with FAST is statistically better than those with Relief, Con-sist, and FOCUS-SF. But there is no consistent evidence to indicate statistical accuracy differences between C4.5 with FAST and with FCBF, which also holds for C4.5 with FAST and with CFS. From Fig. 7 we observe that the accuracy of IB1 with FAST is statistically better than those with Relief. But there is no consistent evidence to indicate statistical accuracy differences between IB1 with FAST and with FCBF, Consist, and FOCUS-SF, respectively, which also holds for IB1 with FAST and with CFS. From Fig. 8 we observe that the accuracy of RIPPER with FAST is statistically better than those with Relief. But there is no consistent evidence to indicate statistical accuracy differences between RIPPER with FAST and with FCBF, CFS, Consist, and FOCUS-SF, respectively. For the purpose of exploring the relationship between feature selection algorithms and data types, i.e. which algorithms are more suitable for which types of data, we rank the six feature selection algorithms according to the classification accuracy of a given classifier on a specific type of data after the feature selection algorithms are performed. Then we summarize the ranks of the feature selection algorithms under the four different classifiers, and give the final ranks of the feature selection algorithms on different types of data. Table 8 shows the results. From Table 8 we observe that (i) for image data, CFS obtains the rank of 1, and FAST ranks 3; (ii) for microarray data, FAST ranks 1 and should be the undisputed first choice, and CFS is a good alternative; (iii) for text data, CFS obtains the rank of 1, and FAST and FCBF are alternatives; and (iv) for all data, FAST ranks 1 and should be the undisputed first choice, and FCBF, CFS are good alternatives.

VIII. Sensitivity Analysis

Like many other feature selection algorithms, our pro-posed FAST also requires a parameter that is the threshold of feature relevance. Different values might end with different classification results. In order to explore which parameter value results in the best classification accuracy for a specific classification problem with a given classifier, a 10 fold cross-validation strategy was employed to reveal how the classification accuracy is changing with value of the parameter.

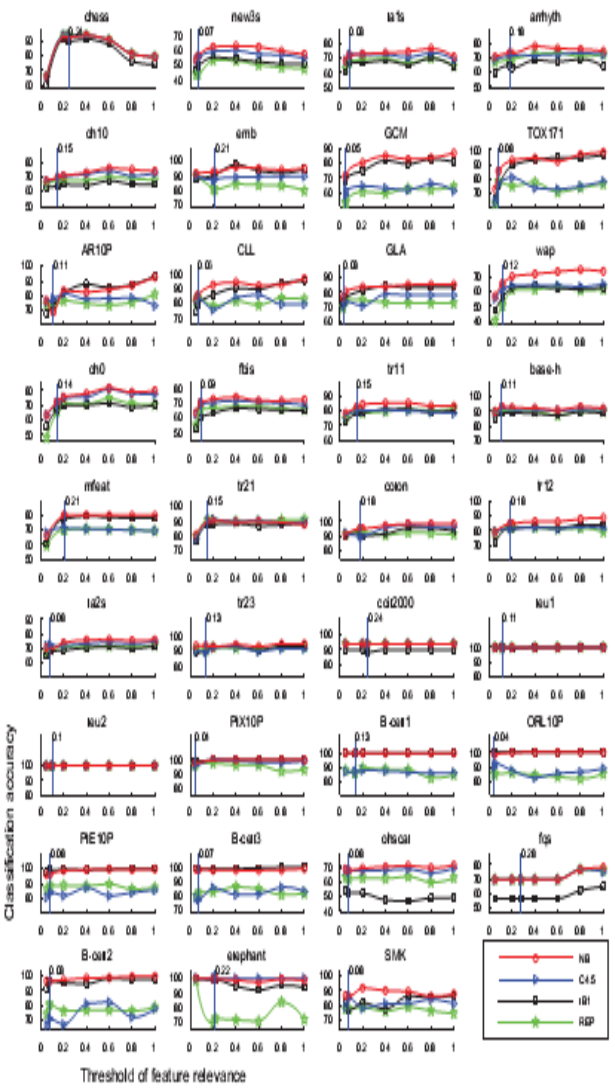

Figure 9 : Accuracies of the four classification algorithms with different θ values

The cross points of the vertical line with the horizontal axis represent the default values of the parameter θ recommended by FAST, and the cross points of the vertical line with the four curves are the

classification accuracies of the corresponding classifiers with the θ values. From it we observe that:

Classification accuracies; (ii) there is a θ value where the corresponding classification accuracy is the best; and (iii) the θ values, in which the best classification accuracies are obtained, are different for both the different data sets and the different classification algorithms. Therefore, an appropriate θ value is desired for a specific classification problem and a given classification algorithm. 2) In most cases, the default θ values recommended by FAST are not the optimal. Especially, in a few cases (e. g., data sets GCM, CLL-SUB-11, and TOX-171), the corresponding classification accuracies are very small. This means the results presented in Section 4.4.3 are not the best, and the performance could be better. 3) For each of the four classification algorithms, al-though the θ values where the best classification accuracies are obtained are different for different data sets.The value of 0.2 is commonly accepted because the corresponding classification accuracies are among the best or nearly the best ones. When determining the value of θ, besides classification accuracy.

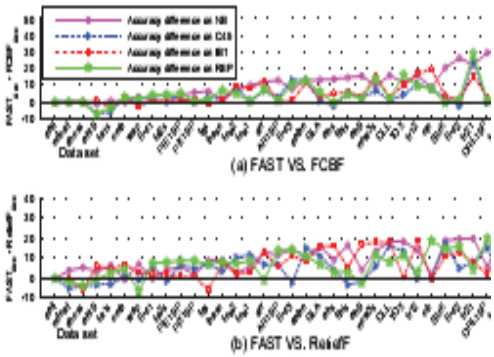

Figure 10 : Accuracy differences between FAST and the comparing algorithms

Just like the default θ values used for FAST in the experiments are often not the optimal in terms of classification accuracy, the default threshold values used for FCBF and Relief (CFS, Consist, and FOCUS-SF do not require any input parameter) could be so. In order to explore whether or not FAST still outperforms when optimal threshold values are used for the comparing algorithms, 10-fold cross-validation methods were firstly used to determine the optimal threshold values and then were employed to conduct classification for each of the four classification methods with the different feature subset selection algorithms upon the 35 data sets. The results reveal that FAST still outperforms both FCBF and Relief for all the four classification methods, Fig. 10 shows the full details. signed ranks tests with $\alpha = 0.05$ were performed to confirm the results as advised by Demsar. All the p values are smaller than 0.05, this indicates that the FAST is significantly better than both FCBF and Relief.

IX. Conclusion

In this paper, we have presented a novel clustering-based feature subset selection algorithm for high dimensional data. The algorithm involves (i) removing irrelevant features, (ii) constructing a minimum spanning tree from relative ones, and (iii) partitioning the MST and selecting representative features. In the proposed algorithm, a cluster consists of features. Each cluster is treated as a single feature and thus dimensionality is drastically reduced. We have compared the performance of the proposed algorithm with those of the five well-known feature selection algorithms FCBF, Relief, CFS, Consist, and FOCUS-SF on the 35 publicly available image, microar-ray, and text data from the four different aspects of the proportion of selected features, runtime, classification accuracy of a given classifier, and the Win/Draw/Loss record. Generally, the proposed algorithm obtained the best proportion of selected features, the best runtime, and the best classification accuracy for Naive Bayes, C4.5, and RIPPER, and the second best classification accuracy for IB1. The Win/Draw/Loss records confirmed the conclusions. We also found that FAST obtains the rank of 1 for microarray data, the rank of 2 for text data, and the rank of 3 for image data in terms of classification accuracy of the four different types of classifiers, and CFS is a good alternative. At the same time, FCBF is a good alternative for image and text data. Moreover, Consist and FOCUS-SF are alternatives for text data. For the future work, we plan to explore different types of correlation measures, and study some formal properties of feature space.

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- Main Text: Font size 10 with justified two columns section
- Two Column with Equal Column with of 3.38 and Gaping of .2
- First Character must be three lines Drop capped.
- Paragraph before Spacing of 1 pt and After of 0 pt.
- Line Spacing of 1 pt
- Large Images must be in One Column
- Numbering of First Main Headings (Heading 1) must be in Roman Letters, Capital Letter, and Font Size of 10.
- Numbering of Second Main Headings (Heading 2) must be in Alphabets, Italic, and Font Size of 10.

You can use your own standard format also.
Author Guidelines:

1. General,

2. Ethical Guidelines,

3. Submission of Manuscripts,

4. Manuscript's Category,

5. Structure and Format of Manuscript,

6. After Acceptance.

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The recommended size of original research paper is less than seven thousand words, review papers fewer than seven thousands words also.Preparation of research paper or how to write research paper, are major hurdle, while writing manuscript. The research articles and research letters should be fewer than three thousand words, the structure original research paper; sometime review paper should be as follows:

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(b) A brief Summary, "Abstract" (less than 150 words) containing the major results and conclusions.

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(e) Resources and techniques with sufficient complete experimental details (wherever possible by reference) to permit repetition; sources of information must be given and numerical methods must be specified by reference, unless non-standard.

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(h) Brief Acknowledgements.

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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.

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Key points to remember:

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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.

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· Use present tense to report well accepted

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- To the point depiction of the research
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- Significant conclusions or questions that track from the research(es)

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- What you account in an conceptual must be regular with what you reported in the manuscript
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- Present a justification. Status your particular theory (es) or aim(s), and describe the logic that led you to choose them.
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- Shape the theory/purpose specifically - do not take a broad view.
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- 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.

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- 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
- All figure and table must be adequately complete that it could situate on its own, divide from text

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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	A-B	**C-D**	**E-F**
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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

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