

AN EVOLUTION OF TCP PERFORMANCE OF REAL TIME IP NETWORK USING BIO- COMPUTING TECHNIQUES

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ABSTRACT

The measurement of performance of Internet Protocol IP network can be done by Transmission Control Protocol TCP because it guarantees send data from one end of the connection actually gets to the other end and in the same order it was send, otherwise an error is reported. There are several methods to measure the performance of TCP among these methods genetic algorithms, neural network, data mining etc, all these methods have weakness and can't reach to correct measure of TCP performance.

This paper proposed a new method of measuring TCP performance for real time IP network using Bio-computing, especially molecular calculation because it provides wisdom results and it can exploit all facilities of phylogenetic analysis. Applying the new method at real time on Biological Kurdish Messenger BIOKM model designed to measure the TCP performance in two types of protocols File Transfer Protocol FTP and Internet Relay Chat Daemon IRC. This application gives very close result of TCP performance comparing with TCP performance which obtains from Little's law using same model (BIOKM), i.e. the different percentage of utilization (Busy or traffic industry) and the idle time which are obtained from a new method base on Bio-computing comparing with Little's law was @0.13%.

KEYWORDS

Bio-computing, TCP performance, Phylogenetic tree, Hybridized Model (Normalized), FTP, IRC

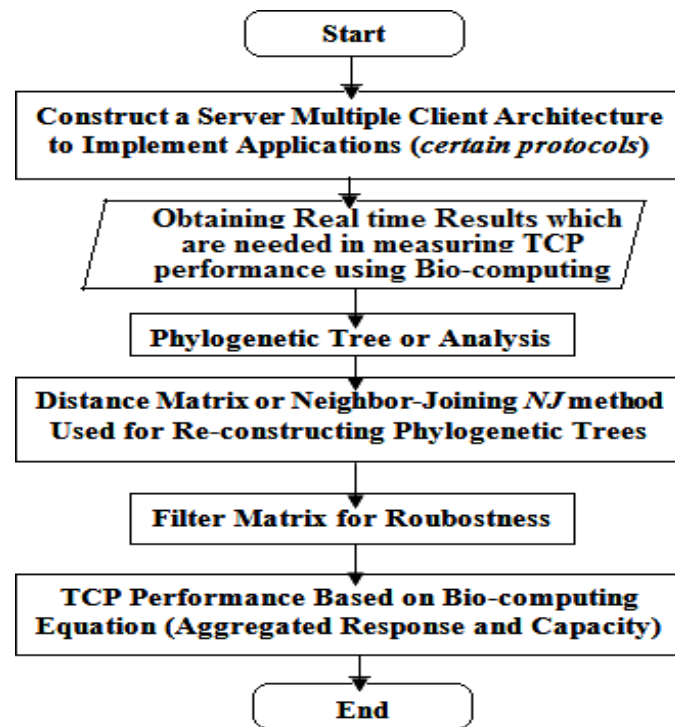
INTRODUCTION

The TCP and the User Datagram Protocol UDP are both IP transport-layer protocols, but TCP can provide a reliable point-to-point communication channel that clients and servers can use to communicate with one another. There are multipurpose focus on modifying TCP performance,

e.g. there is study aims to reduce the idle time before transmission at TCP by preventing timeout occurrences [14], while the others focus on maximising the utilization so the TCP can used as performance measuring because it guarantees send data from one end of the connection actually gets to the other end and in the same order it was send. The Hypertext Transfer Protocol HTTP, FTP, IRC [7], and Telnet are all examples of applications that require TCP There are multiple methods to measure the performance of the TCP, the important of them Genetic Algorithms Gas, Neural Network NN, Data Mining DM, the problem of all these methods which are common in use for measuring the performance of TCP on IP networks they have weakness, limitation, disadvantages, so the thinking about a new method to overcome on drawbacks of these methods is an important issue.

The architecture of measuring TCP performance using bio-computing

The architecture of the new method which is used to measure TCP performance of IP network via Bio-computing summarize at the flowchart shown in Figure

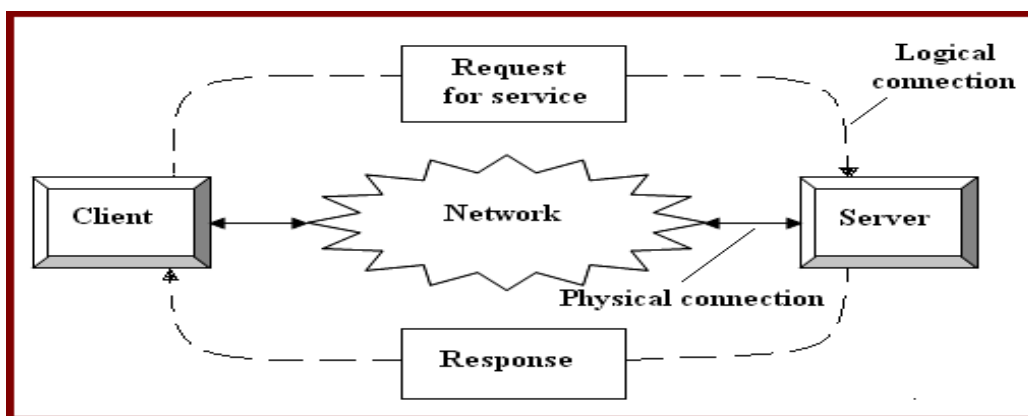


Flowchart of new method for measuring TCP performance using Bio-computing.

Server-client architecture

That means the new method will need server-client model and its applications to obtain the factors for measuring TCP performance using the new method, so the server and clients were implemented as node connected by node; it is possible to consider each path to be a tree therefore this tree is known as phylogenetic tree. Neighbor joining method was used for reconstructing phylogenetic tree, and then this can be taken as filter matrix which is relationship between links and paths. This filter matrix is able to select the links that are used or not. Filter matrix used for robustness which is routing algorithm property, robustness (Adaptation) with respect to failures and changing conditions (failure, congestion), then there are mathematical equations (which are explain later), like aggregate response and capacity to measure system performance.

The client sends messages to the server requesting service of any kind. The server responds with messages containing the desired information or takes other appropriate action. The message containing the client request is encapsulated inside a network packet and transmitted over a physical connection to the server. Conceptually, a logical connection also exists between the client and server.



Phylogenetic Tree

Also called an evolutionary tree or Phylogenetic analysis is a graphical representation of the evolutionary relationship between taxonomic groups, there are many phylogenetic analysis methods as shown in Table 1. NJ method was selected for this purpose because the NJ constructs the tree by sequentially finding pairs of neighbours, which are the pairs of Operational Taxonomy Unit OTUs connected by a single interior node.

Computational phylogenetic methods [1]

Methods	Exhaustive search	Stepwise clustering
Character State	Maximum parsimony MP	
	Maximum likelihood ML	
Distance Matrix	Fitch-Margoliash	UPGMA
		Neighbour-joining NJ

The term phylogeny refers to the evolution or historical development of a plant or animal species, or even a human tribe or similar group. **Taxonomy** is the system of classifying plants and animals by grouping them into categories according to their similarities [3]. External (terminal) nodes are called OTUs and internal nodes are called **Hypothetical Taxonomic Unit HTUs**. A group of taxonomy is called a cluster; as shown in Figure 5; a, the taxonomy A, B, C forms a cluster, having a common ancestor. The branching pattern that is the order of the nodes is called topology of the tree.

A rooted phylogenetic tree is a directed tree with a unique node corresponding to the most recent common ancestor of all the entities at the leaves of the tree. The most common method for rooting trees is the uses of an uncontroversial outgroup. Unrooted trees illustrate the relatedness of the leaf nodes without making assumptions about common ancestry. While un-rooted trees can always be generated from rooted one by simply omitting the root, a root cannot be inferred from an un-rooted tree without some means of identifying ancestry; this is normally done by including an outgroup in the input data or introducing additional assumptions about the relative rates of evolution on each branch. In Figure 5; b, A to E is

called leaves. F to H is inferred nodes corresponding to ancestral species or molecules, branches are also called edges

The new method of TCP performance using Bio-computing

BIOKM package design and implement in java which is used as application for server-client model, it works with Kurdish fonts to satisfy a real time IP network with two applications Kurd messenger for IRCD and Kurd messenger for FTP, these two protocols are connect to Kurd Messenger Database Connectivity KMDBC.

After installing the two main parts of BIOKM, the KMSS and KMCS, then implement (real time) their applications IRCD, FTP, as well as IRCD & FTP together (at the same time). These factors later will be use to determine TCP performance using new method(Bio-computing).

Conclusion

The real-time implementation for BIOKM (server-client model) and its applications to measure the TCP performance using a new method (Bio-computing) give the following conclusions:

- A.** Comparing the results of new method (Bio-computing) with Little's law is very close with difference @ *0.13%*, i.e. dependence the Bio-computing as new method for measuring the real-time TCP performance of IPnetwork.
- B.** Implementing BIOKM application appears obtaining a phylogenetic tree using the NJ method produce a unique tree because the new method base on wisdom results under the principle of minimum evolution.
- C.** Measuring TCP performance using Bio-computing technique especially molecular calculation provides wisdom results and it is possible to exploit all facilities of phylogenetic analysis to obtain better performance and throughput.
- D.** There are many factors affecting on BIOKM and that will reflect on the TCP performance such as:
 - i.** The dynamic parameters of network, e.g. data rate, speed, etc.
 - ii.** Constant factors such as antivirus and memory size which make the system to be slower.
 - iii.** Hub structure (hub only or hub plus firewall), where the firewall doesn't allow KMCS to connect with KMSS.
 - iv.** The Central Processor Unit **CPU** temperature makes the system to be slower.

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