

A SERVICE QUALITY ASSESSMENT INSTRUMENT FOR THE  
BIOINFORMATICS INFORMATION SOURCES

NURSYARAFINA BINTI ABD AZIZ

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## **ABSTRACT**

In today's era, management is confronted with new methodologies to provide competitive solutions. It cannot be denied that the Information Technology sector is developing quickly. This means that the computerization technology is more effective than using manually. The purpose of this research is to capture and understand the process of protein structure prediction by using website. The context of service in this study is about the service of information that been provided by the bioinformatics websites. The service refers to the process of how the website provides data and computational tools to the customer or in this context known as biologists. The biologists use the website as a service in helping them to search for a matching protein structure which is in step by step order. An interview has been conducted to create understanding about the work process by using website. An interview question also has been designed in order to collect primary data for further investigation. A conceptual framework is created for the purpose of understand in details the flow of the study. In the end, this research will provide recommendations for improving the websites.

## ABSTRAK

Dalam era ini, bidang pengurusan berhadapan dengan pelbagai metodologi untuk menghasilkan penyelesaian bagi pelbagai saingan di luar sana. Tidak dapat dinafikan bahawa bidang Teknologi Maklumat kian berkembang pesat. Ini bermakna teknologi pengkomputeran lebih efektif berbanding penggunaan manual. Tujuan kajian ini adalah untuk mengetahui dan memahami proses pencarian struktur protein. Konteks servis dalam kajian ini merujuk kepada servis yang diberi oleh laman web bioinformatik. Servis ini merujuk kepada proses bagaimana laman web menyediakan pelbagai data dan alatan pengkomputeran kepada pelanggan atau dalam konteks ini disebut 'biologist'. 'Biologist' menggunakan laman web ini sebagai servis untuk membantu mereka dalam mencari pasangan protein struktur protein mengikut turutan. Satu sesi temuramah telah diadakan untuk memahami dengan lebih mendalam proses tersebut menggunakan laman web. Soalan temuramah juga telah dihasilkan bagi mengumpul data awalan bagi kajian seterusnya. Juga, rangkakerja konseptual telah dihasilkan yang bertujuan memahami dengan lebih mendalam aliran proses kajian ini. Akhir sekali, kajian ini akan menyenaraikan beberapa cadangan bagi memperbaiki laman web tersebut.

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## **CHAPTER 1**

### **INTRODUCTION**

#### **1.1 Introduction**

In today's era, customers have become the important assets in building up an organization, company or even a service. Some of us have heard of this kind of statement which stated that "care for your customer and they will return but care for your merchandise, they won't return". Another statement is "customers are always right". The key here is no matter how interactive or high tech the product, but without a good service to the customer, you won't gain any profit.

In creating a customer satisfaction, there are indeed many steps. A proper analysis of the process is indeed needed for knowing what should be and not be done for further planning of customer satisfaction. In creating the satisfaction of the customer, a quality of the service should be first identified. Quality is obviously meeting the needs of the customer. It means that quality provides customer with innovative

products or services characteristics or attributes and defect free which provide fitness for use. Quality today is a moving target because we ask for new requirements when something goes wrong. What is not part of the product or service should be taken into consideration when quality is defined.

IT is emerging fast nowadays. Today, a great number of advances in the ITs are being used in all companies. By having ITs, employees may work from home or other locations but still connected to the office. And, customers still can keep in touch with the companies with the help of IT. IT has a good relationship in satisfying the customers. By using new IT, it allows companies to gain important advantages such as cost savings and improving the accuracy of exchanging information. Besides that, it can improve the organizational efficiency and effectiveness by eliminating day, redundant processing steps and by providing better access to information.

Besides that, IT has also created a relationship with the bioinformatics. Bioinformatics can be explained as the application of Information Technology to store, organize and analyze the enormous amount of biological data which is available in the form of sequences and structures of proteins. Bioinformatics derives knowledge from computer analysis of biological data. These can consist of the information stored in the genetic code, but also experimental results from various sources, patient statistics, and scientific literature (bioinformatics resource portal, Bioinformatics Definition, 4<sup>th</sup> April 2009). By using the bioinformatics which refers to the websites, the biologists can get information to support their experimental process. For example, the biological information of nucleic acids is available as sequence while the data of proteins is available as sequence and structures. Sequences are represented in single dimension whereby the structures contains the three dimensional data of sequences. Biologists also use websites that provides literatures, journal, and etc in order to get information.

## 1.2 Problem Background

Many biologists use websites to obtain biological data and tools for predicting protein structures. The use of website has helped the biologists in getting and using data of any protein that they are interested with. The nature of scientists or biologists in determining the protein structure contains several steps. Generally, the process starts with the biologists searching for a matching sequence. This sequence data are in a form of alphabets. When the sequence has been inserted, the website will display the searching results. The next step is searching the secondary structure of the protein. A list of results about the specific sequence will be displayed. The results generally will display their chains, author, id, compound, classification and characteristics. Next, in viewing the visualization of protein structure, the user can click on a link that will result the visualization. Some of the site does not view the specific details of the structure. Until they had to find other alternatives by viewing the visualization separately from the site such as PYMOL, DEEP VIEW, YASARA, and JMOL. Then, the user has to understand the relationship between the sequence and the structure of the protein. Each sequence of activities requires them to view in different sites in order to get the information.

Of course each bioinformatics websites that been used offers specific advantages in terms of their ability to analyze the protein structure. However, there are also problem in using those websites.

As more bioinformatics websites come online, they provides massive amount of data regarding the protein that the biologists are interested with. But there are some problems that can be identified which are:

**i. Choosing which website to use for a certain step.**

Although the websites provides many computational tools, each of them provides tools that require different method of execution. Therefore, biologists have to choose the right website to do certain step. For example, let say the biologists want to search for a sequence protein from a website such as MOTIF Search (<http://motif.genome.jp/MOTIF.html>) and the result displayed is zero. So, the biologists should refer or find other websites in order to find matching sequence. This will give some difficulties for the biologists. And some of the websites provides certain constraint. For example, biologists cannot query sequence shorter than 12 amino acids. NCBI Blast (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) is one of the examples of this kind.

**ii. Running the data through number of functions or querying from various websites.**

The process of protein structure prediction does not only refer to one website only. For example, in the annotation of a gene sequence work process (T. Luca and R. Friedrich, 2005) a literature has been made. The paper stated that actually the data consist of a million EST (expressed sequence tags) which assembled into half a million or so assemblies, as described by Stodola, Tobin and Wiliams, 1997. They selected assemblies to annotate by a procedure that is called “seed selection”. First, they select an organism by using GENBANK with the annotated information where a homology-based functional transfer to humans could be envisaged. Then, by using BLAST X, they daily screened the DNA sequences available for those organisms against a database of human proteins built by redundantly collecting all protein sequences stemming from human sources such as SWISS\_PROT and SP-TREMBL.

By referring to the literature, it is indeed gives difficulties for the biologists in gathering all the data and information from several of websites.



**iii. There might be possibility of data loss.**

Just because the problem that arose from running the data through number of functions from various websites and difficulties of gathering all the data and information, for example, the sequence and structure of protein are not displayed. This will result in inaccurate experimental results.

After identifying the problem background which is choosing the right website to use in certain steps in dry experiments, querying data from various and multiple websites and there might be a possibility of data loss, the researcher found that it is better to do a study about the service quality regarding the existing bioinformatics websites. Mostly the service qualities are based on e-commerce, e-service, online retailing and so on. From the researcher's reading from other journals, researches and etc about service quality, the researcher found that till now there are still no studies that have been made regarding the biology domain. Beginning from that, the researcher tends to assume that it is indeed difficult for the system developer to improve the bioinformatics websites which regards to the customer satisfaction. Therefore, in this study the researcher tries to adapt based on an instrument that can examine the quality of bioinformatics websites regarding the process of predicting protein structure.

In this study, the service refers to the information and services. According to Mc Alexander et. al, 1994, they had examined performance measure, a performance measure weighted by importance and SERVQUAL weighted by importance. And this examination has been done by using the service quality models. Their analysis suggests that service quality is an antecedent of customer satisfaction and that satisfaction has a stronger influence than does service quality on purchase intentions. Different kinds of dimensions from the SERVQUAL instrument can be studied from different kinds of contexts which can best suit for improving the existing bioinformatics websites.

By reading and understanding some of the literature, the service quality is very useful for improving the services and in this study it refers to the bioinformatics websites. The benefits of using this service quality are:

- Would improve customer satisfaction.
- Achieving higher levels of performance.
- Eliminating “extra processing”.
- Understand and improve operational processes.
- Identify problems quickly and systematically.
- Establish valid and reliable service performance measures.
- Measure customer satisfaction and other performance outcomes.

In order to measure the service quality, an instrument which is called SERVQUAL, will be used in this study. Till now, many researchers have used this instrument to measure service quality in different kind of areas such as in airline service, hospital service, library service and etc. It is said as the best application of the service quality model. By identifying five major sources of possible service quality breakdowns or gaps, managers for example may better understand precisely why service quality does or does not meet customer expectation. This is quite important because each gap requires a fundamentally different strategy to eliminate it. (Parasuraman et al., 1985). The five major dimensions that will be used in SERVQUAL are tangibles, reliability, responsiveness, assurance and empathy which will help in examining the service quality of the website.

### 1.3 Problem Statement

According to the problem background that have been discussed earlier, there are several problems that been identified regarding the bioinformatics websites. These problems are choosing the right website to use in certain step in dry experiments, querying data from various and multiple websites and the use of accurate data throughout the experiments. All these problems relates with biologist perception and expectation when using bioinformatics websites. In this context, biologists are the customers who are using the service given by bioinformatics websites. Therefore, the main issue that should be emphasized is:

*“How does customer perception and expectation help in investigating the quality of bioinformatics websites?”*

To answer this main issue, a number of additional questions are needed in supporting the main issue. Some of the questions that arose are:

1. Does existing websites used by biologists to predict protein structure satisfy them?
2. What are the steps in identifying the service quality of the bioinformatics websites?
3. What are the suggestions for the improvement that can benefit the process of protein structure prediction using variety of websites?

## 1.4 Project Objectives

The aim of this study is to identify what is the service quality and customer satisfaction attributes. The reason for identifying these attributes is to understand what are the characteristics that make a bioinformatics websites quality enough to provide data and computational tools to the biologists. In order to achieve this aim, the objectives of this study are:

1. To study the work processes and the websites used in protein structure prediction.
2. To study the biologists' expectation and perception in using variety of websites that supports their work process.
3. To propose a portal design that investigates biologists' perception and expectation in order to detect service quality and customer satisfaction attributes.
4. To propose organizational strategy in order to recommend and improvement a portal with service quality and customer satisfaction attributes.

## **1.5 Project Scope**

The study will focus on bioinformatics aspects which covers two main scopes which are:

- i. The subject domain is restricted to Faculty of Biosciences and Bioengineering, University Technology of Malaysia.
- ii. The components focuses on this study are processes, websites, people which refer to biologists and information.
- iii. The focus process is the work process of protein secondary structure prediction.

## **1.6 The Project Importance**

It is hope that this study recommend appropriate solutions for the problems arises in using variety of data and current tools by the biologists. This study will also propose a framework which will include customer satisfaction and service quality components, followed by proposed elements and features for the portal development as ICT solution.

## **1.7 Conclusion**

This chapter discussed the overview of this study where a brief introduction was explained. The problem statement has been explained in an understandable way that should be answered after the completion of this project. There are three main objectives which explain the process of this study that should be achieved successfully. The importance of the project also been stated in explaining the need of this project. Hopefully, this project will contribute some knowledge in the field of study.

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