

# Robotic Analysis of Breast Cancer Genes

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**Abstract:** Breast cancer database is used to analyse the most commonly diagnosed cancer among women in the world. Substantial progress has been made in diagnosing and treating breast cancer. Germline or familial mutations in the genes BRCA1 and BRCA2 account for only a proportion of hereditary breast cancer. A heterozygous variant in the ataxia-telangiectasia has a substantial breast cancer risk. The completion of the Human Genome Project gives us knowledge of the genetic variations that presumably underlie the fact that a family history of cancer is a risk factor for most cancer types. It has been observed that there are more families with multiple cases and increased risk of breast cancer among women with a family history of the disease. The main aim is to find out the genes that are most significant and non-significant among all the genes present in the breast cancer tissue using microarray data analysis embedded in a chip. It tells that some of the genes that are most expressed in the breast cancer tissue. This paper presents the real time streaming of an indoor environment using a wireless sensor network and a set of self-navigating robots. Mobile robots with mounted sensors and automated programmed chip will autonomously navigate through an indoor area with unknown obstacles to find out the significant and non-significant genes causing breast cancer. The robots will be able to avoid obstacles and move around the region. The robots sense the environmental parameters of the region, and send that data to the remote monitoring terminals using an underlying wireless sensor network. This design is applicable to networks where some of the sensors may not have sufficient range to sense data more accurately and closer monitoring is required. Effective path planning for the mobile robot is achieved by combining a map of the area, the sensor readings and the radio strength of the sensor network.

**Keywords:** Breast Cancer database, Architecture, Programmed chip, Mutations, Oncology, Embedded chip, Microarray, Robotics

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## 1. INTRODUCTION

Key to the definition of cloud computing is the “cloud” itself. For our purposes, the cloud is a large group of interconnected computers. These computers can be personal computers or network servers; they can be public or private. For example, Google hosts a cloud that consists of both smallish PCs and larger servers. Google’s cloud is a private one (that is, Google owns it) that is publicly accessible (by Google’s users). This cloud of computers extends beyond a single company or enterprise. The applications and data served by the cloud are available to broad group of users, cross-enterprise and cross-platform. Access is via the Internet. Any authorized user can access these docs and apps from any computer over any Internet connection. And, to the user, the technology and infrastructure behind the cloud is invisible. It isn’t apparent (and, in most cases doesn’t matter) whether cloud services are based on HTTP, HTML, XML, JavaScript, or other specific technologies. It might help to examine how one of the pioneers of cloud computing, Google, perceives the topic. From Google’s perspective, there are six key properties of cloud computing as below

### 1.1) Cloud computing is user-centric.

Once you as a user are connected to the cloud, whatever is stored there documents, messages, images, applications, whatever becomes yours. In addition, not only is the data yours, but you can also share it with others. In effect, any device that accesses your data in the cloud also becomes yours.

### 1.2) Cloud computing is task-centric.

Instead of focusing on the application and what it can do, the focus is on what you need done and how the application can do it for you., Traditional applications word processing, spread- sheets, email, and so on are becoming less important than the documents they create.

### 1.3) Cloud computing is powerful

Connecting hundreds or thousands of computers together in a cloud creates a wealth of computing power impossible with a single desktop PC. Cloud computing is accessible. Because data is stored in the cloud, users can instantly retrieve more information from multiple repositories. You’re not limited to a single source of data, as you are with a desktop PC.

### 1.4) Cloud Computing is intelligent.

With all the various data stored on the computers in a cloud, data mining and analysis are necessary to access that information in an intelligent manner.

### 1.5) Cloud Computing is Programmable.

Many of the tasks necessary with cloud computing must be automated. For example, to protect the integrity of the data, information stored on a single computer in the cloud must be replicated on other computers in the cloud. If that one computer goes offline, the cloud’s programming automatically redistributes that computer’s data to a new computer in the cloud. Cloud architecture extends to the client, where web browsers and/or software applications access cloud applications.

Cloud storage architecture is loosely coupled, often assiduously avoiding the use of centralized metadata servers which can become bottlenecks. This enables the data nodes to scale into the hundreds, each independently delivering data to applications or users.

### 1.6 Cancer

Cancer (medical term: malignant neoplasm) is a class of diseases in which a group of cells display uncontrolled growth (division beyond the normal limits), invasion (intrusion on and destruction of adjacent tissues), and sometimes metastasis (spread to other locations in the body via lymph or blood). These three malignant properties of cancers differentiate them from benign tumors, which are self-limited, and do not invade or metastasize. Most cancers form a tumor but some, like leukemia, do not. The branch of medicine concerned with the study, diagnosis, treatment, and prevention of cancer is oncology.

### 1.7 Classification of Cancer

Cancers are classified by the type of cell that resembles the tumor and, therefore, the tissue presumed to be the origin of the tumor. These are the histology and the location, respectively. Examples of general categories include:

- 1 Carcinoma: Malignant tumors derived from epithelial cells. This group represents the most common cancers, including the common forms of breast, prostate, lung and colon cancer.
- 2 Sarcoma: Malignant tumors derived from connective tissue, or mesenchymal cells.
- 3 Lymphoma and leukemia: Malignancies derived from hematopoietic (blood-forming) cells
- 4 Germ cell tumor: Tumors derived from totipotent cells. In adults most often found in the testicle and ovary; in fetuses, babies, and young children most often found on the body midline, particularly at the tip of the tailbone; in horses most often found at the poll (base of the skull).
- 5 Blastic tumor or blastoma: A tumor (usually malignant) which resembles an immature or embryonic tissue. Many of these tumors are most common in children.

### 1.8 Breast Cancer

Breast cancer is a disease in which certain cells in the breast become abnormal and multiply without control or order to form a tumor. The most common form of breast cancer begins in cells lining the ducts that carry milk to the nipple (ductal cancer). Other forms of breast cancer begin in the glands that produce milk (lobular cancer) or in other parts of the breast. Early breast cancer usually does not cause pain and may exhibit no noticeable symptoms. As the cancer progresses, signs and symptoms can include a lump or thickening in or near the breast; a change in the size or shape of the breast; nipple discharge, tenderness, or retraction (turning inward); and skin irritation, dimpling, or scaliness. These changes can occur as part of many different conditions, however. Having one or more of these symptoms does not mean that a person definitely has breast cancer. In some cases, cancerous tumors can invade surrounding tissue and spread to other parts of the body. If breast cancer spreads, cancerous cells most often appear in the bones, liver, lungs, or brain. Tumors that begin at one site and then spread to other areas of the body are called metastatic cancers. A small percentage of all breast cancers cluster in families. Hereditary cancers are those associated with inherited gene mutations. Hereditary breast cancers tend to occur earlier in life than noninherited (sporadic) cases and are more likely to involve both breasts.

### 1.9 Oncology

Variations of the BRCA1, BRCA2, CDH1, PTEN, STK11, and TP53 genes increase the risk of developing breast cancer. The AR, ATM, BARD1, BRIP1, CHEK2, DIRAS3, ERBB2, NBN, PALB2, RAD50, and RAD51 genes are associated with breast cancer. Cancers occur when a buildup of genetic mutations in critical genes—those that control cell growth and division or the repair of damaged DNA—allow cells to grow and divide uncontrollably to form a tumor. In most cases, these genetic changes are acquired during a person's lifetime and are present only in certain cells. These changes, which are called somatic mutations, are not inherited. Less commonly, gene mutations inherited from a parent increase the risk of developing cancer. Cancers originating from ducts are known as ductal carcinomas; those originating from lobules are known as lobular carcinomas. There are many different types of breast cancer, with different stages (spread), aggressiveness, and genetic makeup; survival varies greatly depending on those factors.<sup>[1]</sup> Computerized models are available to predict survival. With best treatment and dependent on staging, 10-year disease-free survival varies from 98% to 10%. Treatment includes surgery, drugs (hormonal therapy and chemotherapy), and radiation.

### 1.10 Gene Expression Profiling

Gene expression profiling of lung cancer may provide one method to increase our understanding of this very heterogeneous disease and potentially identify new approaches for early diagnosis, prognosis or treatment. This brief review examines some of the issues that are associated with the clinical presentation of this disease and some important questions that might be addressed using gene expression profiling experiments when applied to human lung cancer. Gene expression profiling allows the examination of thousands of genes in a cell or tumor sample. The analysis of the patterns of gene expression and the identification of specific genes and pathways has the potential to help uncover biologically meaningful information.

## 2.0. SYSTEM MODEL

The proposed system is a multi robot platform, within a wireless sensor network, to monitor the presence of explosives in an indoor area. Figure 1 shows the design of the system, which includes static wireless sensor nodes and mobile nodes. There is a central server, which will collect all the data, analyze it and take appropriate decisions. Static nodes also act as path guides to the

mobile robots. The robot will be able to communicate with the wireless sensor network and to other robots in the network through a zigbee communication module. Embedding sensors into mobile robots allows for the sensors to perform closer monitoring of the environment at shorter ranges.

### 2.1 DESIGN & IMPLEMENTATION

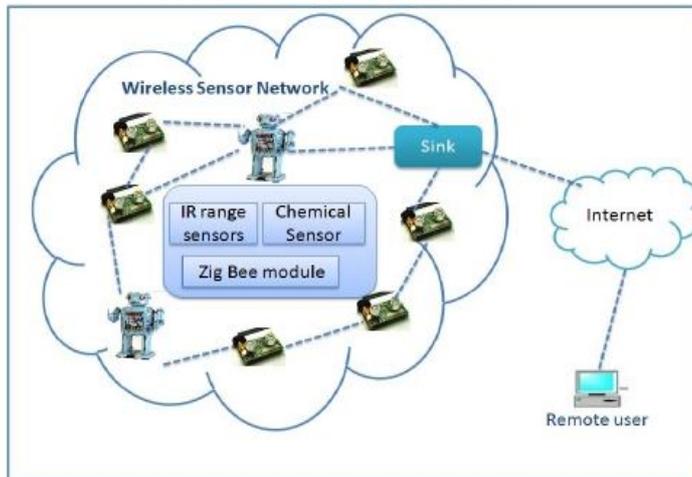


FIG 2.1 OVERVIEW

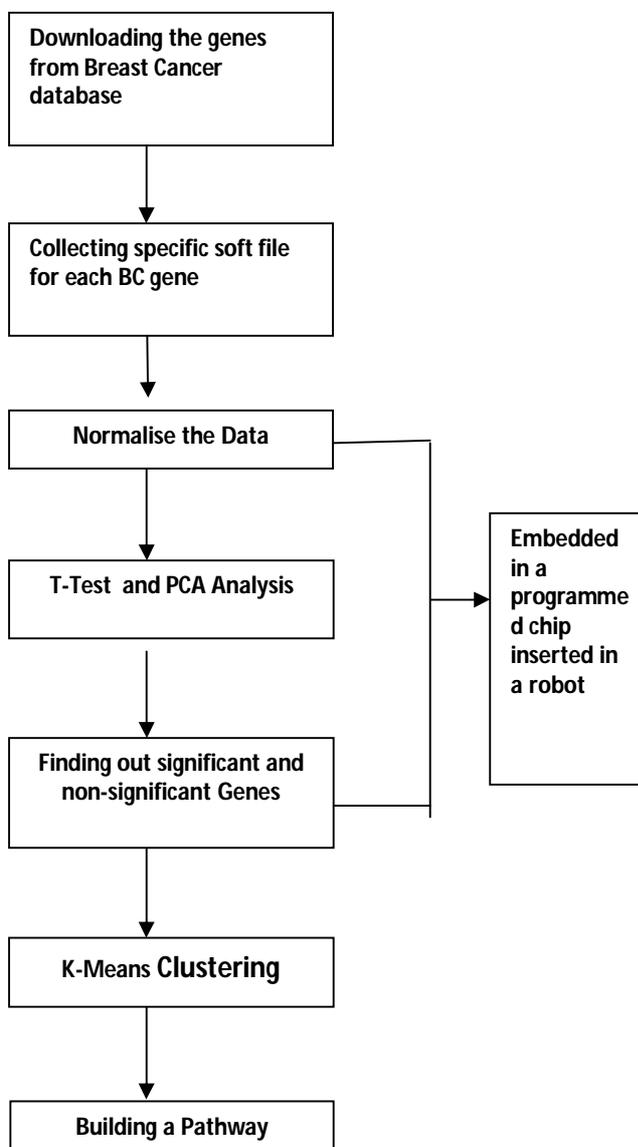


FIGURE 2.0 SYSTEM MODEL

## 2.2 R for Microarray analysis

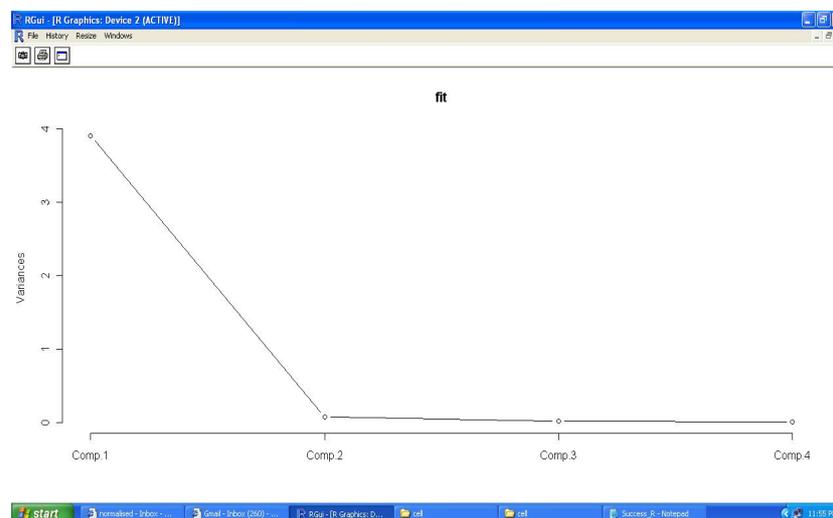
R is an integrated suite of software facilities for data manipulation, calculation and graphical display. Among other things it has - an effective data handling and storage facility a suite of operators for calculations on arrays, in particular matrices, a large, coherent, integrated collection of intermediate tools for data analysis, graphical facilities for data analysis and display either directly at the computer or on hardcopy, and a well developed, simple and effective programming language (called 'S') which includes conditionals, loops, user defined recursive functions and input and output facilities. Indeed most of the system supplied functions are themselves written in the S language.

## 2.3 Normalization

Data normalization means removing certain systematic variation that is introduced during different steps in a microarray experiment from microarray fabrication and biological sample preparation, to data acquisition. It is an intermediate step that has been routinely carried out after image analysis, and before data analysis, in a typical gene expression microarray experiment. One accepted method for minimising errors in the quantification of mRNA transcripts and correction for sample-to-sample variation is to amplify, simultaneously with the target, a cellular RNA that serves as an internal reference against which other RNA values can be normalised. The potential of clustering to reveal biologically meaningful patterns in microarray data was quickly realised and demonstrated in an early paper by Eisen et al. , who used hierarchical clustering to identify functional groups of genes hierarchical clustering is one of many conventional clustering methods that could be applied to microarray data and details of such methods may be found elsewhere for a general introduction to cluster analysis.

## 3.0 RESULTS

FIG 3.0.1  
plotfit()



Biplot(fit)  
FIG 3.0.2

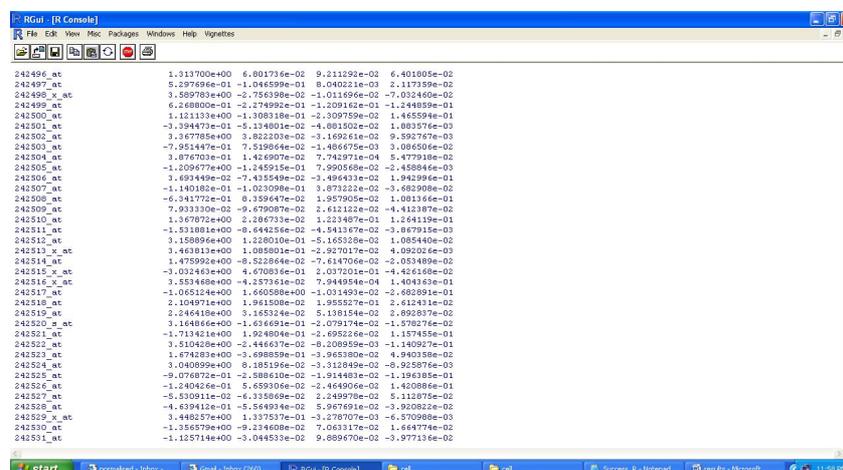


FIG 3.0.3

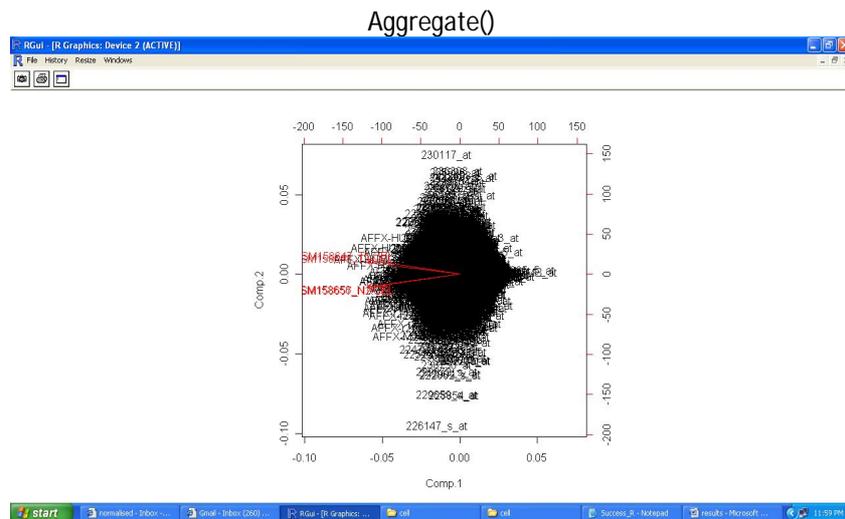


FIG 3.0.4  
Clusplot()

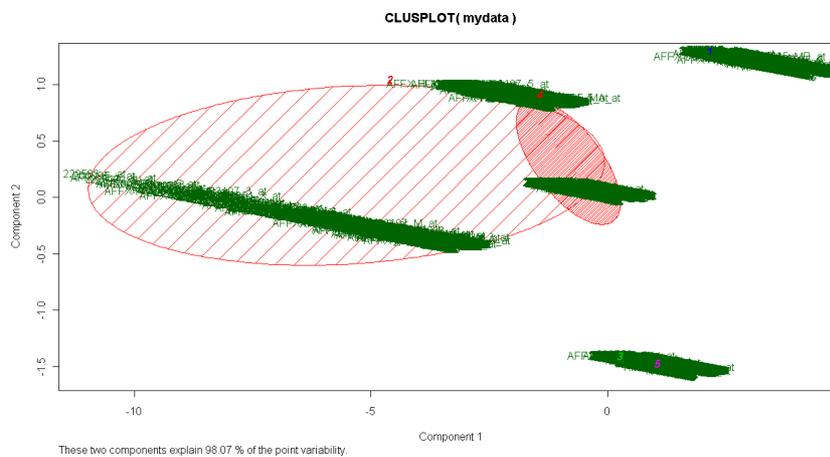


FIG 3.0.5  
Plot(fit)

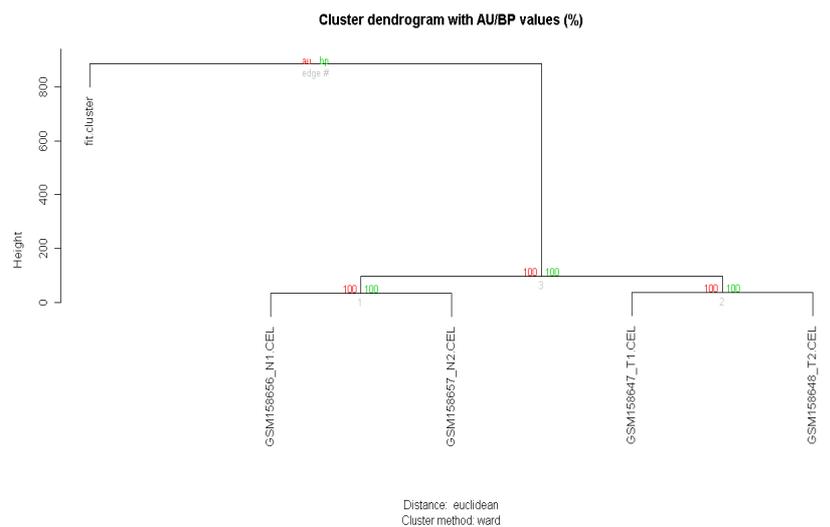


FIG 3.0.6  
Pvrect()

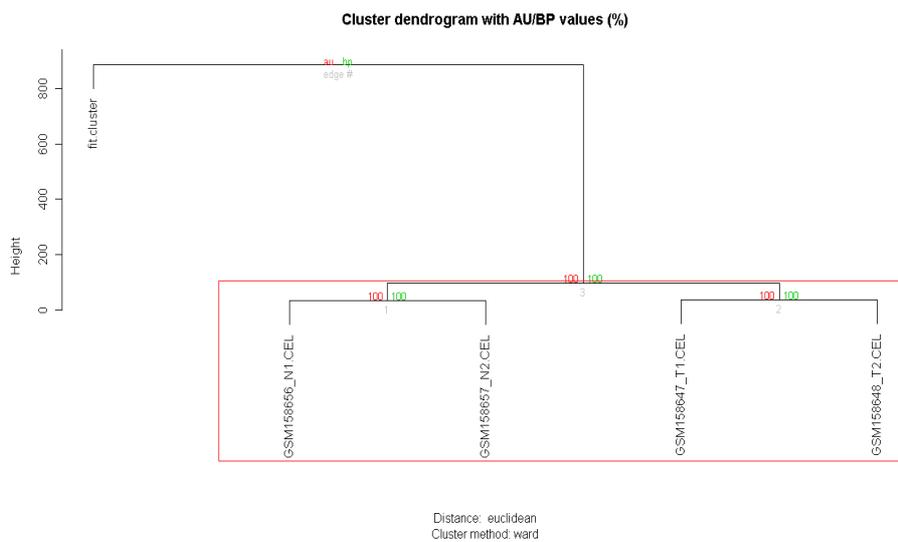
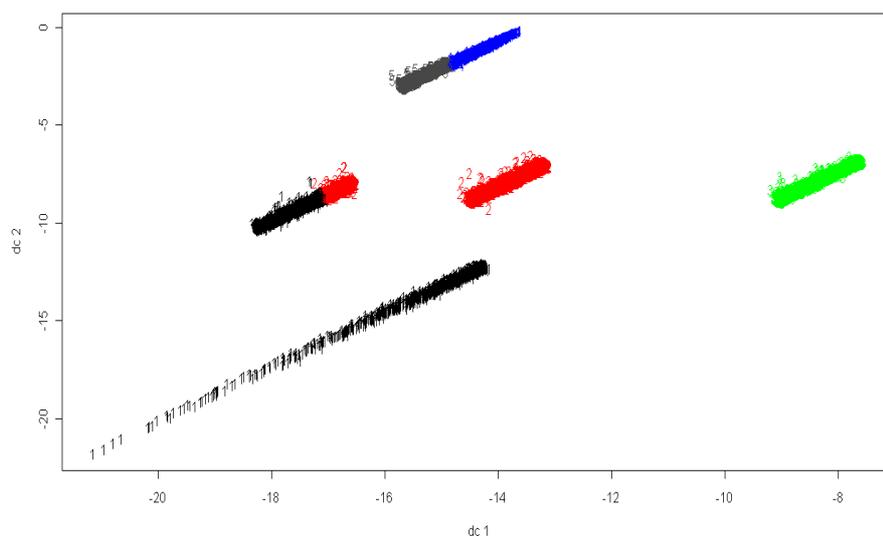


FIG 3.0.7  
Plotcluster()



#### 4.0. CONCLUSION

Cloud computing has been defined as "everything that we currently do". Many technologies that have been branded as "cloud computing" have existed for a long time before the "cloud" label came into existence. Examples include databases, load balanced on-demand web hosting services, network storage, real time online services, hosted services in general. The application of gene expression profiling to breast cancer has begun to provide large amounts of information that when properly interpreted may provide new insights into this disease that continues to represent a significant health problem.

The types of questions that are being asked should influence the design of the studies. Because early detection may actually be one of the most effective mechanisms to increase the survival of patients with breast cancer, gene expression profiling studies that are focused on identifying highly expressed genes or those unique to specific breast subtypes are appropriate.

#### 5.0 REFERENCES

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