DESIGN OF WIRELESS SENSOR NETWORK FOR DEVELOPMENT OF CANCER MONITORING SYSTEM WITH BIOMEDICAL INFORMATICS

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Abstract:

Background*: When a patient goes to hospital, first thing in traditional system of Hospital, patients has to wait for a long time, to get appointment, but in this old system, manual register entry of patients name-age-time- and token was used, the token number was called by Doctor, till then the patients has to wait. But in case of emergency also the patients were the sufferer. Many times rural India suffers a lot due to lack of such modern technology and wireless network. So the demand of ZIGBEE technology is very alarming. To arrive at Zigbee stage at first the frequency of wireless system of hospital is specified, though. We need to know the category of patient, their clinical history, either Genetic disease which is inherited disorders, and then we can compile the patients convert into data-profile of each patient coming to Hospital. The data profile of patient is converted into into paper and Files documentation this file is feeded into system to make it more flexible, and then the patient is given an I.D from the registration Counter where he or she stands in a Queue. The patient is assigned a Digital card, to track his/her status that I.D card of Hospital becomes the personal information of the Patient via which the communication is done to the respective diagnosis lab/Doctors/Nurse/Medicine to get the required facilities the patient need for the treatment. Here we design a Biomedical sensor network with the help of low-power ZIGBEE technology, this can transfer Data of cancer patients from Server – Modem – system sitting at home to hospital- Doctor thus early screening of patient is alerted and important treatment can be taken. Specifically for cancer monitoring system, which will be easily accessible by sitting at home, with the help of medical base station, set-up will be at cancer hospital the data of the patient will be documented in system and transmitted to Doctor, Nurse of hospital, for appropriate care. Bioinformatics web-server will be used, to develop health care monitor server. Collection of Patient I.D – documentation- uploaded to health base station – server – system. Components of the Zigbee network are microcontroller (8051).*

Keywords: *Wireless sensor network, Data Profile, Zigbeetechnology, Biomedical sensor.*
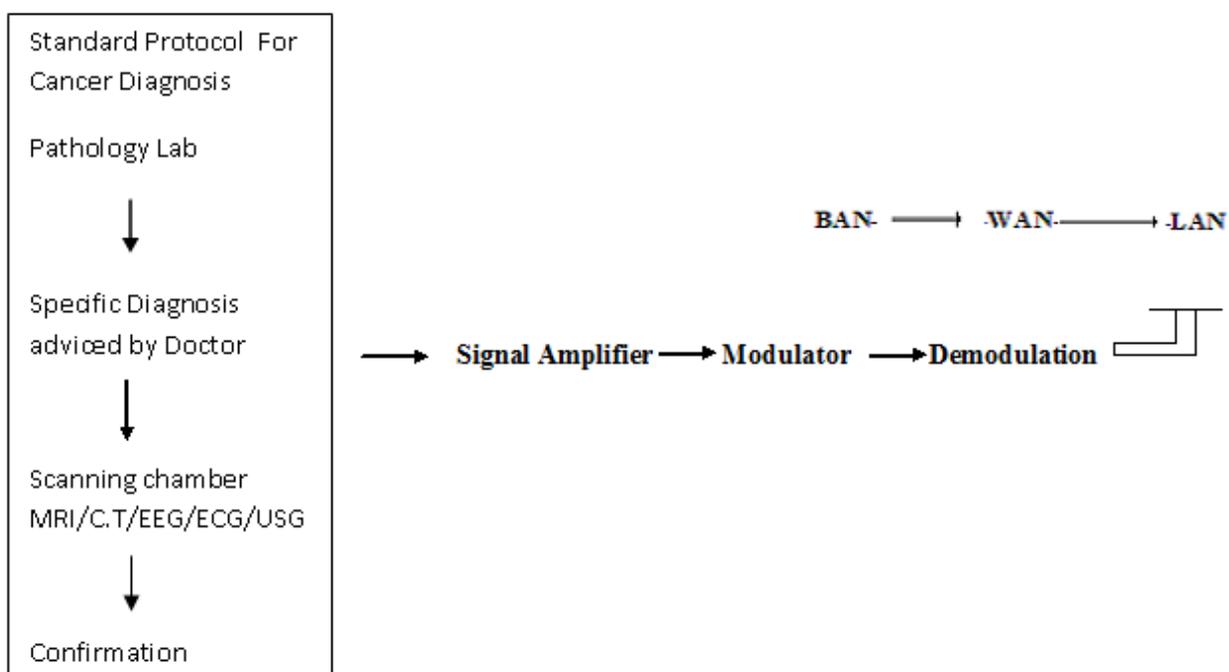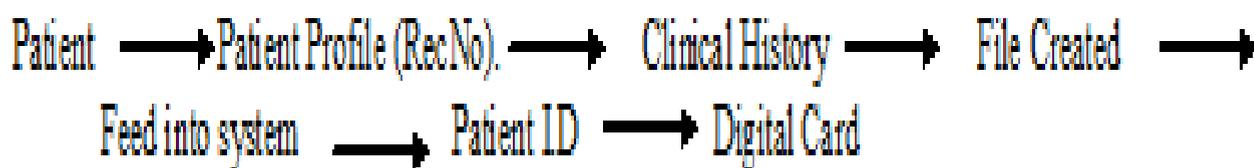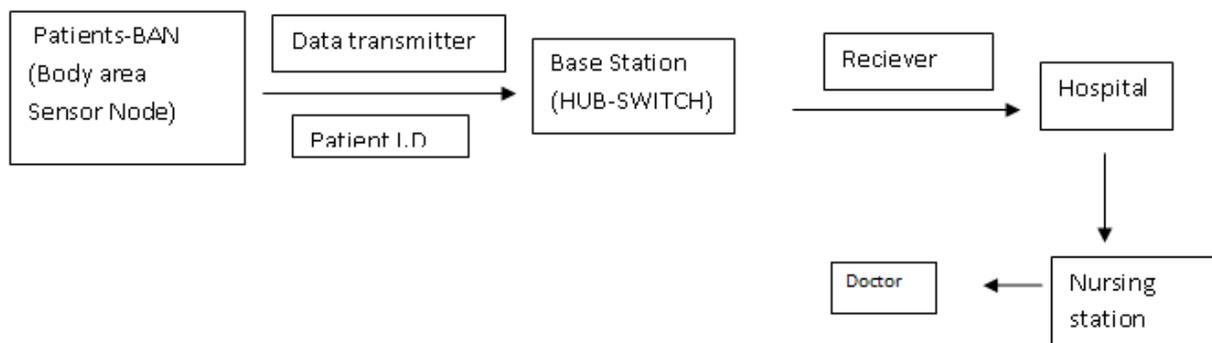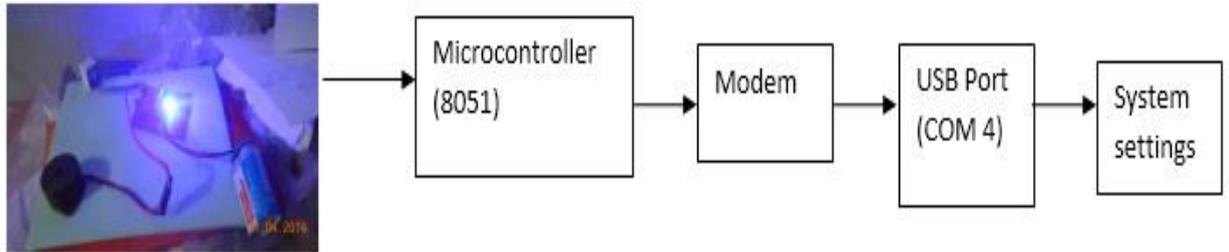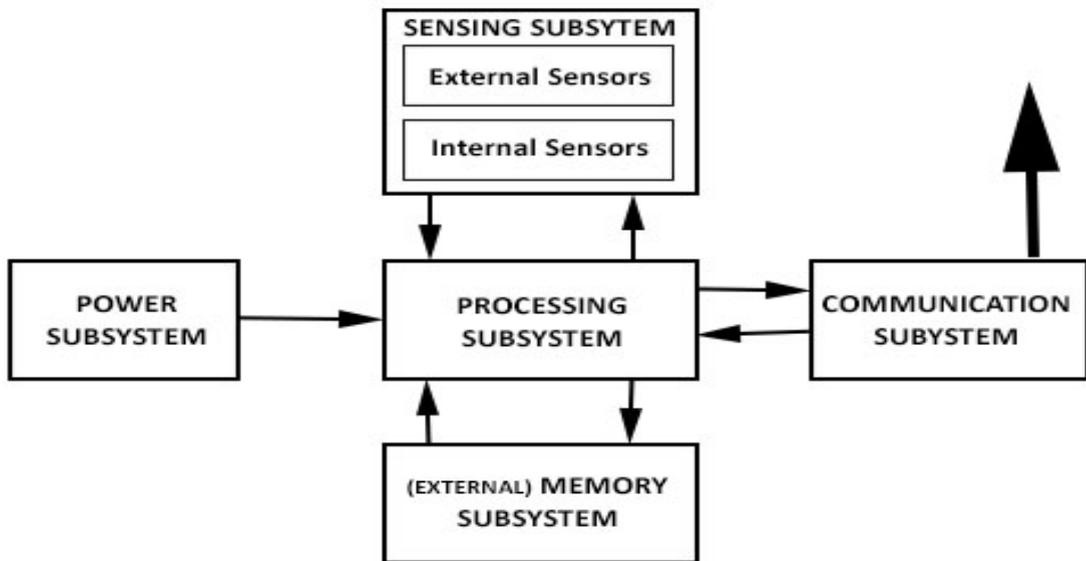
Methodology

Screening and observatory method of symptoms in patient at cancer hospital the most common symptoms of cancer observed in patients: a) Changes in Bowel or bladder habits b) sore that does not heal c) Increase in the size of a mole or change in color of the skin d) Unexpected bleeding or discharge in urine e) Any small lump or swelling on the body f) Indigestion or difficulty in swallowing g) hoarseness h) Weight gain or loss Swelling of one limb.
Human cancer network design

P^H EEG, CMOS Image sensor, Acoustic sensor, Glucometer, Hospital imaging system
Uploaded to Health care server ⟶ medicalbase station.

Architectural design of biomedical informatics sensor network

RIMSHospital ⟶ Oncology block ⟶ Oncologist ⟶ Patient care
(Nursing station)

Patient — Patient ↑ Manual Registration — Doctor

Medical Education Unit (MEU) & Medical Education Technologies → Zigbee wireless server Base station → Patient Data Profile

Diagnosis room
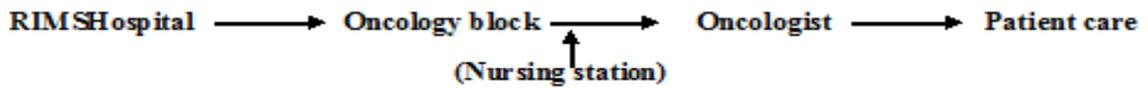
The rural hospital of India are not connected with wireless server base station because the so the need of superspeciality hospital of rural India is the need of the hour where no patient I.D. is created. So the Patient I.D is very important information to know about the patients profile, clinical history for improved healthcare technologies and treatment.

Zigbee Network for Biomedical Cancer Detection System
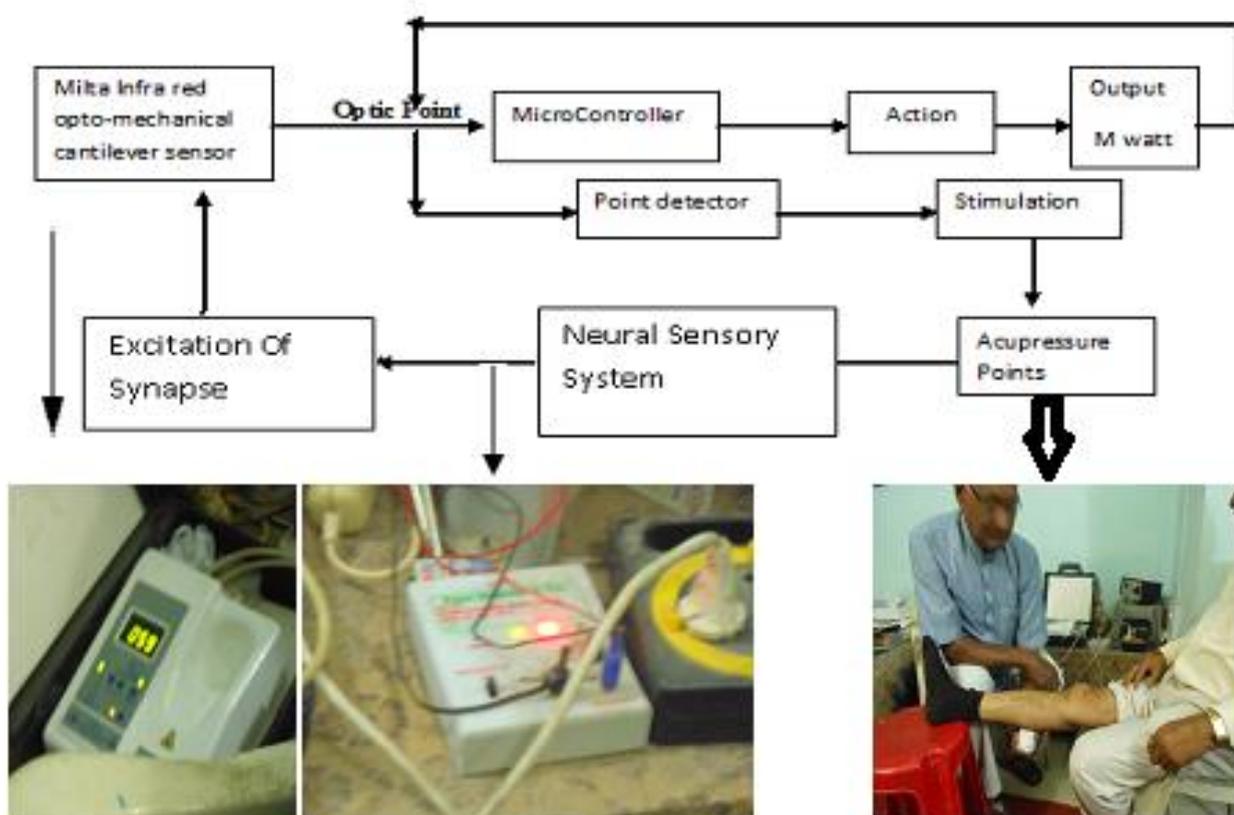
Flow Chart Bio-mimicking architecture with prediction of Homologous animal
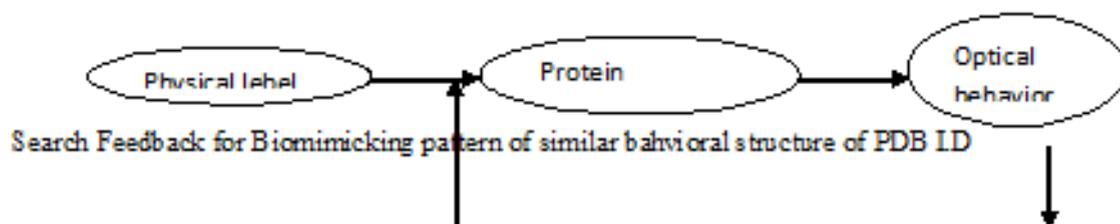
Search Feedback for Biomimicking pattern of similar bahvioral structure of PDB I.D

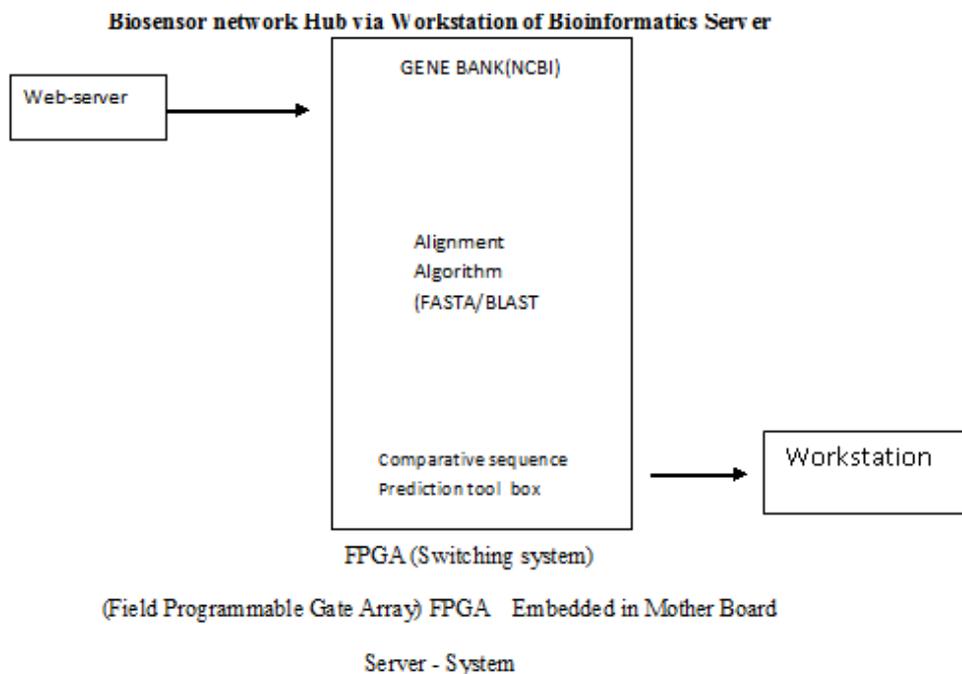## Biosensor network Hub via Workstation of Bioinformatics Server

Biosensor network Hub via Workstation of Bioinformatics Server

Web-server → GENE BANK(NCBI)

Alignment
Algorithm
(FASTA/BLAST

Comparative sequence
Prediction tool box → Workstation

FPGA (Switching system)

(Field Programmable Gate Array) FPGA   Embedded in Mother Board

Server - System

FPGA (Switching system)
(Field Programmable Gate Array) FPGA   Embedded in Mother Board
Server ⟶ System

Reactome Server Data analysis search engine – on Submit Complete: WARNING - Server side error - cannot display expression data (results == null).

Results and Discussion

The data transfer in workstation of Bioinformatics System at BTIS SUBDIC Centre in the department of Biotechnology, from Server to System, within some speed of KBPS range -MBPS range.This all depends on the data load, we want to transfer, volume of data, it may be sequences in FASTA, BLAST Algortihm, Prediction toolbox to match the query sequences.

$$\text{Rate of DataTransfer} = \frac{Bandwidth}{1/2}$$

The data transfer in workstation of Bioinformatics System at BTIS SUBDIC Centre in the department of Biotechnology, from Server to System, within some speed of KBPS range -MBPS range.This all depends on the data load, we wan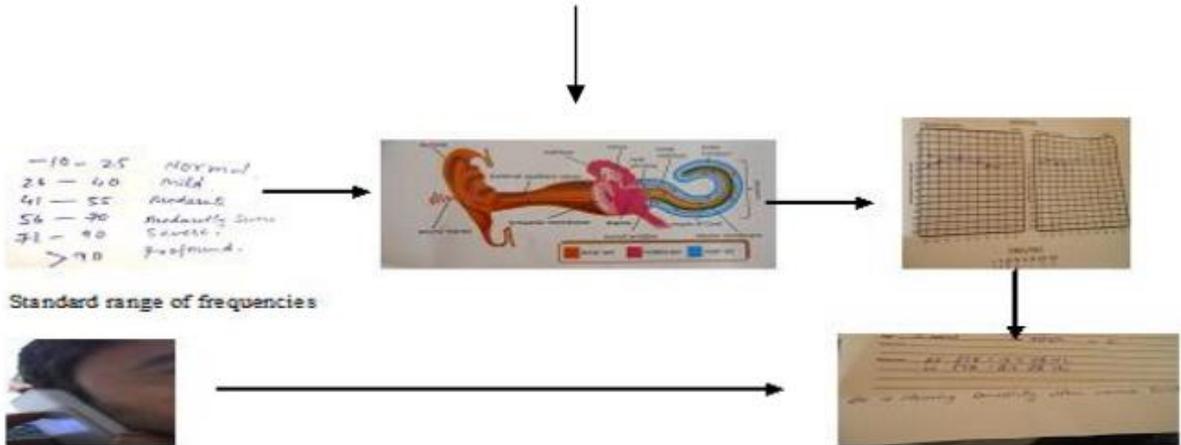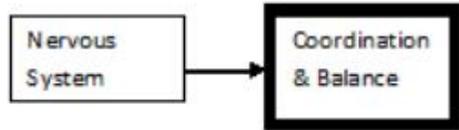t to transfer, volume of data, it may be sequences in FASTA, BLAST Algortihm,Prediction toolbox to match the query sequences.

Neural balancing depends on

1. Cochlear – 8th main vestibule Cochlear nerve
2. Cerebellum
3. Eye

Standard range of frequencies

Hearing analysis with Audiogram input signal is the different hearing frequencies which the person can recognize on the basis of which the deafness is detected from the readout signal frequencies in Decibel. The person talking with cellphone on exposure to music or vehicle horn may disturb the frequency range and the graph gets deviated from the normal (as monitored above). But no such cases is identified, but this is the risk of accident cause.

CMOS Biological clock system monitors the Neurological Clock, here the time gives the signals to every part of our organs system and hypothalamus and neurons to take control of our body, and memory thus time failure is the memory failure which detects the Brain disorder.
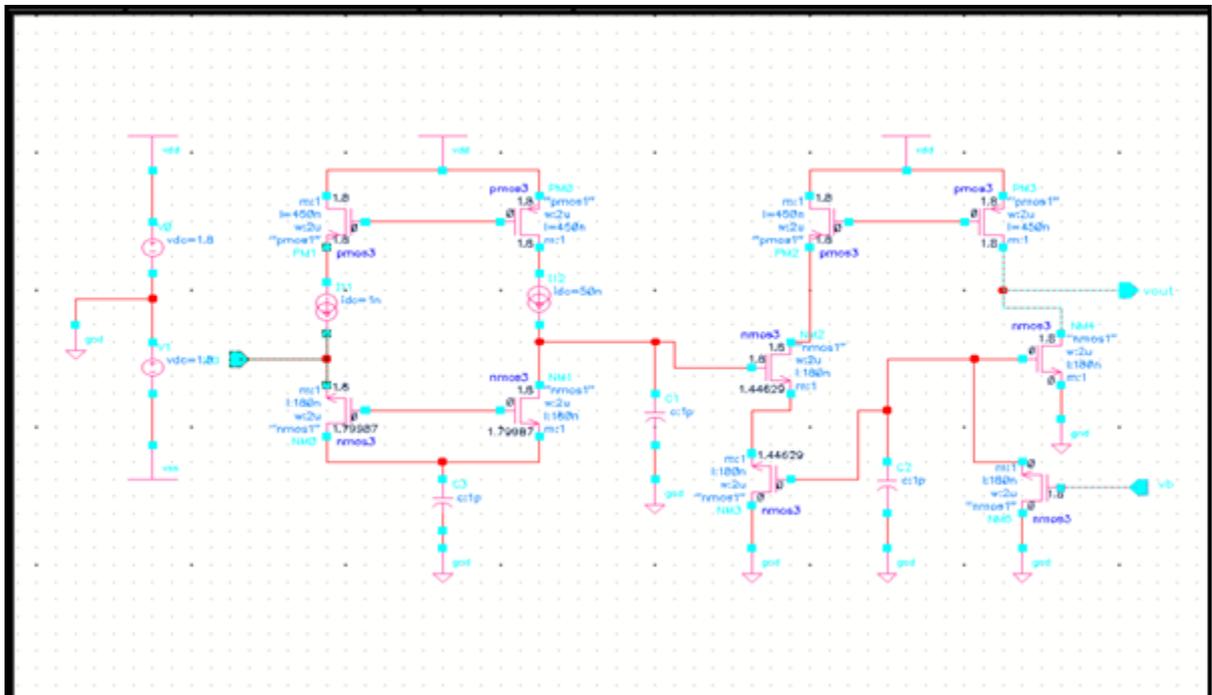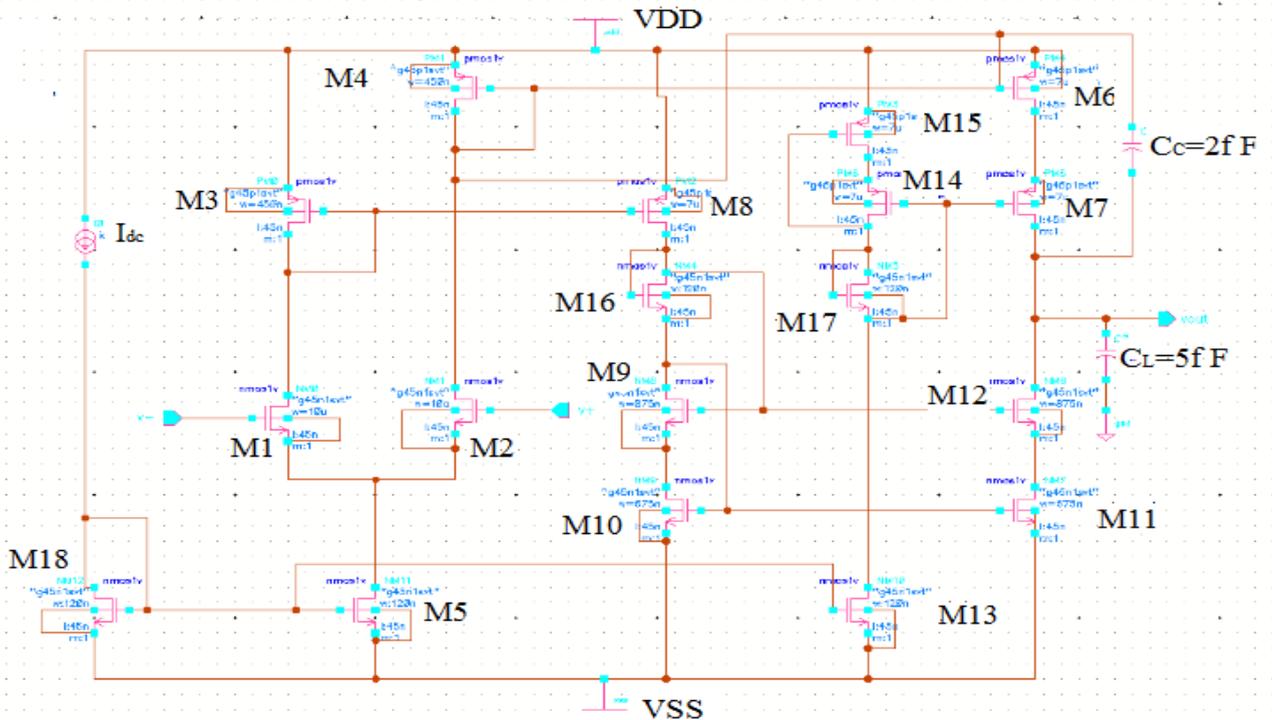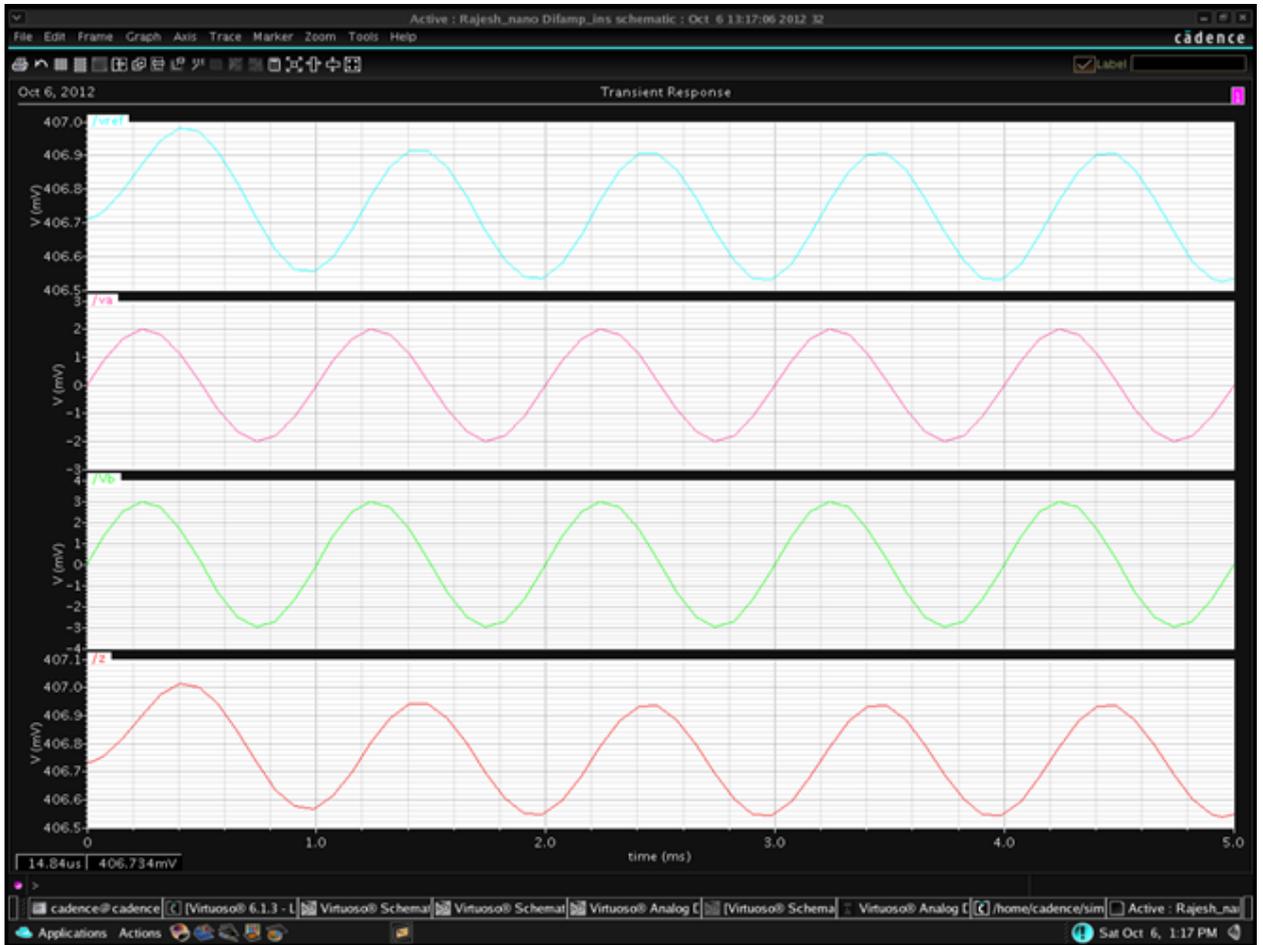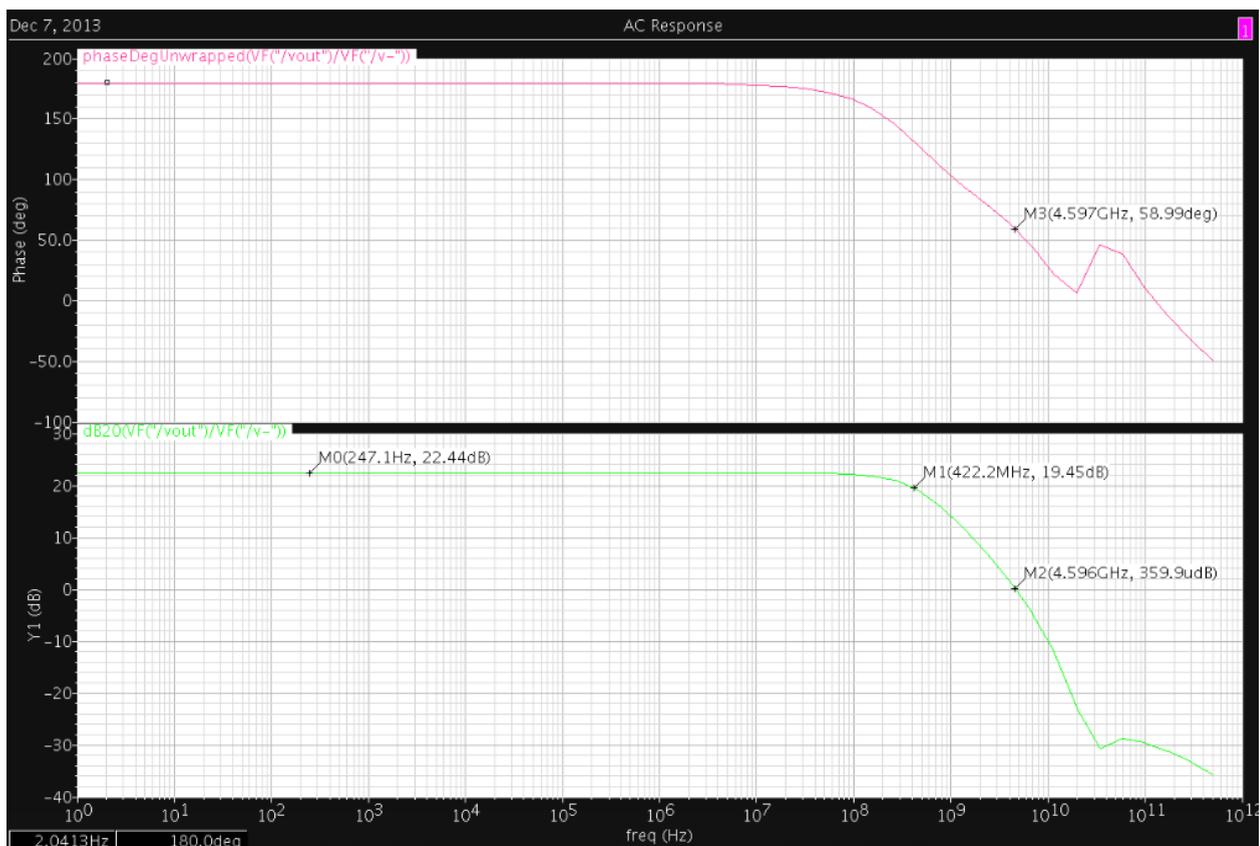
        CMOS SCC (Signal conditioning OPAMP Circuit) this circuit is very universal feature the Gain of the OPAMP decides, where the circuit is to require to connect with Biosensor, becoz it is used an every Type Of Biosensor System to convert weak signal – strong signal in this circuit we achieved the High bandwidth Of 4.55 GHz, is simulated at VLSI Lab, is the optimum value, is the virtual design, can be configured in more improved manner. In this paper Zig-bee network is being established to Bioinformatics nodal network, where the data exchange of Biological sequences, their information about the Bio-system, Database search algorithm (VIA NCBI national centre for Biotechnology information),RCSB (Protein data base search engine. in the format Of FASTA & BLAST. This development of Bio-information sensor network is possible only with Internet connection, it may be through various nodal network like LAN (Local area Network)/ Wifi (Wireless sensor network)/ Mobile Sim (VIA 3-G speed) with the help of Dongle. This are the types of Network via which data transfer can take place, but to be more specific, the speed is the important factor for Data rate of Biological sequences like here in this paper we used Cancer data base is collected using WEBSERVER, the following table format gives detailed of data collection of specific Protein/Protein I.D/ USER mail I.D/ Internet protocol address I.P address via which the internet connection network is extablished.status.in this way this is a promising innovation towards design and development of health care monitoring system with Bioinformation model .Thus the Network is created to transfer the data to Doctor sitting in Hospital, therefore the mass awareness of the patient about cancer is known.

ToolBox for Pairwise search alignment
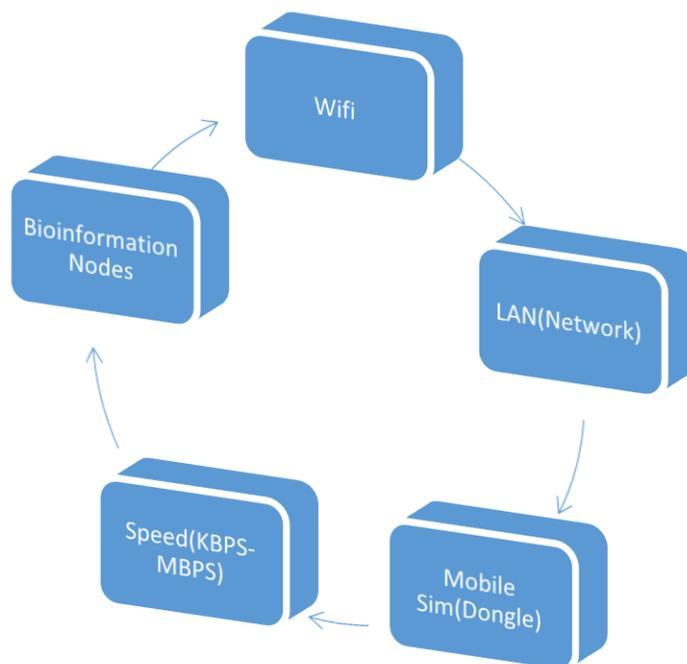
Block diagram representing the Biosensor network Hub via Workstation of Bioinformatics Server

Bioinformation Hub for Biomedical sensor network

Microarray Gene Chip

ID	Protein Name	Length	Submission date	User's email address	User's IP	Status
CF003206	306b	470	2013-10-23	xxx@gmail.com	70.50.130.xxx	The job is pending in queue.
CF003205	225	497	2013-10-23	xxx@gmail.com	70.50.130.xxx	The job is pending in queue.
CF003204	r.l_Glioma	193	2013-10-23	xxx@gmail.com	117.211.90.xxx	Completed
CF003203	Rl	246	2013-10-23	xxx@gmail.com	117.211.90.xxx	Completed
CF003202	Ales	386	2013-10-23	xxx@gmail.com	14.139.155.xxx	Expected time for completion: 10hrs
CF003201	kctc	386	2013-10-23	xxx@gmail.com	14.139.155.xxx	Expected time for completion: 10hrs
CF003200	your_protein	286	2013-10-22	xxx@yyy.zzz	130.102.158.xxx	Expected time for completion: 10hrs
CF003199	lpMIP	204	2013-10-22	xxx@hku.hk	147.8.33.xxx	Completed
CF003198	173	495	2013-10-22	xxx@gmail.com	184.144.17.xxx	Completed
CF003197	34b	536	2013-10-22	xxx@gmail.com	184.144.17.xxx	Completed
CF003196	your_protein	246	2013-10-22	xxx@yyy.zzz	203.64.84.xxx	Completed
CF003195	q849s1	386	2013-10-22	xxx@gmail.com	14.139.155.xxx	Completed
CF003194	upp	379	2013-10-22	xxx@gmail.com	118.151.209.xxx	Completed
CF003193	28	471	2013-10-21	xxx@gmail.com	184.144.17.xxx	Completed
CF003192	8a	475	2013-10-21	xxx@gmail.com	184.144.17.xxx	Completed
CF003191	rosetta_thre	445	2013-10-21	xxx@eden.rutgers.edu	204.52.215.xxx	Completed
CF003190	your_protein	315	2013-10-21	xxx@yyy.zzz	137.132.3.xxx	Completed
CF003189	your_protein	606	2013-10-21	xxx@upm.es	138.4.138.xxx	Completed
CF003188	BRIL	106	2013-10-18	xxx@vivabiotech.com	58.246.38.xxx	Completed
CF003187	ego	412	2013-10-17	xxx@comsats.edu.pk	39.47.206.xxx	Completed
CF003186	ego	412	2013-10-17	xxx@comsats.edu.pk	39.47.206.xxx	Completed
CF003185	LECSA	408	2013-10-17	xxx@webmail.hzau.edu.	220.249.99.xxx	Completed
CF003184	Bovine_ggtas	377	2013-10-17	xxx@mails.bicpu.edu.i	210.212.230.xxx	Completed
CF003183	your_protein	359	2013-10-17	xxx@yyy.zzz	2.188.32.xxx	Completed
CF003182	NirF	371	2013-10-16	xxx@tu-bs.de	134.169.104.xxx	Completed
CF003181	ache_1ea5	531	2013-10-16	xxx@mahidol.ac.th	158.108.103.xxx	Completed
CF003180	ache_1eea	531	2013-10-16	xxx@mahidol.ac.th	158.108.103.xxx	Completed
CF003179	your_protein	407	2013-10-16	xxx@bgsu.edu	107.10.182.xxx	Completed
CF003178	Agde4	149	2013-10-15	xxx@gmail.com	128.219.49.xxx	Completed
CF003177	your_protein	1237	2013-10-15	xxx@topper.wku.edu	161.6.84.xxx	Completed

25 unique tumor instances (of 25212 total) representing 41581 tumor frequency records returned.	Tumor Name Organ Affected Treatment Type *Agents* Strain Name *Strain Types* Tumor Frequency Range Metastasizes To	FM Mixed Un.
Abdominal cavity sarcoma Abdominal cavity Chemical/Drug *corn oil* FVB/N-Tg(Hba-x-v-Ha-ras)TG.ACLed Trp53tm1Brd/+ *transgenic targeted mutation (knockout)*	Abdominal cavity sarcoma Abdominal cavity Chemical / Drug *N-acetyl-L-cysteine (NAC) corn oil* FVB/N-Tg(Hba-x-v-Ha-ras)TG.ACLed Trp53tm1Brd/+ *transgenic targeted mutation (knockout)*	Abdominal cavity sarcoma Abdominal cavity Chemical / Drug *benzo[a]pyrene (BP) (BaP) (B[a]P) corn oil* FVB/N-Tg(Hba-x-v-Ha-ras)TG.ACLed Trp53tm1Brd/+ *transgenic targeted mutation (knockout)* 7.14 8.33
Abdominal cavity sarcoma Abdominal cavity Chemical/Drug *benzo[a]pyrene (BP) (BaP) (B[a]P) N-acetyl-L-cysteine (NAC) corn oil* FVB/N-Tg(Hba-x-v-Ha-ras)TG.ACLed Trp53tm1Brd/+ *transgenic targeted mutation (knockout)* 6.67 8.33	Abdominal cavity sarcoma - undifferentiatedAbdominal cavity None (spontaneous) 129S1-Actbtm1(Tag)Arge/? *targeted mutation (knock-in)* observed	Abdominal cavity sarcoma – undifferentiated Abdominal cavity None (spontaneous) [not specified]-Actbtm1(Tag)Arge/+ Tg(Hsp70-1-cre)1Arge *transgenic targeted mutation (knock-in)* 16.67
Abdominal cavity tumor Abdominal cavity None (spontaneous) [not specified]-Actbtm1(Tag)Arge/+ Tg(Hsp70-1-cre)1Arge *transgenic targeted mutation (knock-in)* 100 91.67 95.83	Abdominal cavity tumor – histiocytic Abdominal cavity None (spontaneous) CD-1 *outbred* 10 - 12.5	Adipose tissue - Abdominal cavity lesion Adipose tissue - Abdominal cavity Hormone, Virus *pregnant mare serum gonadotropin (PMSG) Adenovirus carrying cre recombinase human chorionic gonadotropin (hCG)* [not specified]-Krastm4Tyj/+ *targeted mutation (knock-in)* Observed
Adipose tissue - Abdominal cavity lipoma Peritoneum - Mesentery - Adipose tissue None (spontaneous) B6;129 Tnk1tm1Sksuf *targeted mutation (knockout)* 3.57	Adipose tissue - Brown hibernoma Adipose tissue – Brown None (spontaneous) B6;CB-Tg(Ggamma-T)21Cps *transgenic* 75	Adipose tissue – Brown hibernoma Adrenal gland None (spontaneous) B6;CB-Tg(Ggamma-T)21Cps *transgenic* 40
Adipose tissue - Brown hibernoma Heart None (spontaneous) B6;CB-Tg(Ggamma-T)21Cps *transgenic* 40	Adipose tissue – Brown hibernoma Adipose tissue – Brown None (spontaneous) B6;CB-Tg(Ggamma-T)20Cps *transgenic* 100	Adipose tissue - Brown hibernoma Adrenal gland – Cortex None (spontaneous) B6;CB-Tg(Ggamma-T)2Cps *transgenic* 5
Adipose tissue – Brown hibernoma Heart None (spontaneous) B6;CB-Tg(Ggamma-T)2Cps *transgenic* 5	Adipose tissue – Brown hibernoma Adipose tissue – Brown None (spontaneous) B6;CB-Tg(Ggamma-T)15Cps *transgenic* observed	Adipose tissue – Brown hibernoma Adipose tissue – Brown None (spontaneous) B6;CB-Tg(Ggamma-T)15Cps *transgenic* 25
Adipose tissue - Brown hibernoma Adipose tissue – Brown None (spontaneous) [not specified]-Rb1tm3Tyj Tg(Sp7-tTA,tetO EGFP/cre)1Amc *targeted mutation (conditional) transgenic* 0	Adipose tissue – Brown hibernoma Adipose tissue – Brown None (spontaneous) [not specified]-Tg(Sp7-tTA,tetO-EGFP/cre)1Amc Trp53tm1Brn *targeted mutation (conditional) transgenic* 0	Adipose tissue - Brown hibernoma Adipose tissue – Brown None (spontaneous) [not specified]-Rb1tm3Tyj/+ Tg(Sp7-tTA,tetO-EGFP/cre)1Amc Trp53tm1Brn/+ *targeted mutation (conditional) transgenic* 0

|		
Adipose tissue - Brown hibernoma Adipose tissue – Brown None (spontaneous) [not specified]-Rb1[tm3Tyj] Tg(Sp7-tTA,tetO EGFP/cre)1Amc Trp53[tm1Brn]/+ *targeted mutation (conditional) transgenic* 0	Adipose tissue – Brown hibernoma Adipose tissue – Brown None (spontaneous) [not specified]-Rb1[tm3Tyj]/+ Tg(Sp7-tTA,tetO-EGFP/cre)1Amc Trp53[tm1Brn] *targeted mutation (conditional) transgenic* 0	Adipose tissue – Brown hibernoma Adipose tissue – Brown None (spontaneous) [not specified]-Rb1[tm3Tyj] Tg(Sp7-tTA,tetOEGFP/cre) 1Amc Trp53[tm1Brn] *targeted mutation (conditional) transgenic* 34 – 44 Bone marrow Kidney Liver Lung
Adipose tissue – White choristoma Adipose tissue – White None (spontaneous) (C57BL/6J x SJL/J)F1/J *hybrid* observed		
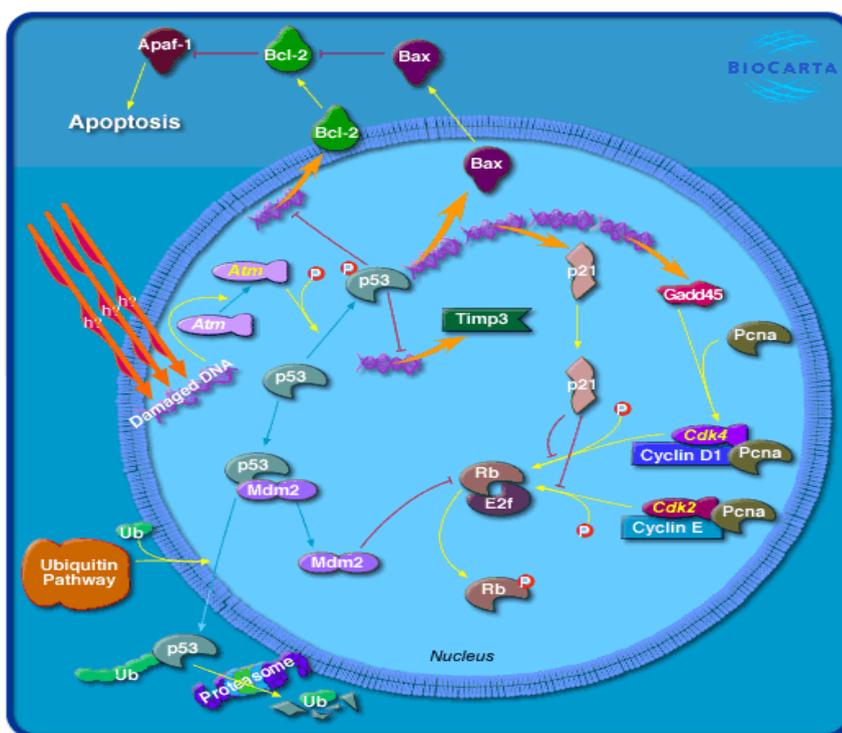
P-53 Cancer Pathways

This pathway is important cellular Circuit system which monitors the cancer genetic switch the apoptotic factor, how the regulations of P[53]gene occurs is shown here cdk4 phosphorylation occurs this is signaling Rb Protein passage in cell cycle. This is a very significant pathway for cancer monitoring its progression to advanced stage of cancer, specially for Blood cancer patients leukemia, Diabetes is the early stage Of Cancer, when the energy meter of our cells system ATP /AMP ratio is monitored. The important Enzyme action like Pyruvate kinase involved with this pathway of cancer is monitored.

The patients symptoms like Hemoglobin affinity for Oxygen increases due to the mutation of this P[53]. Hemolytic Anaemia.

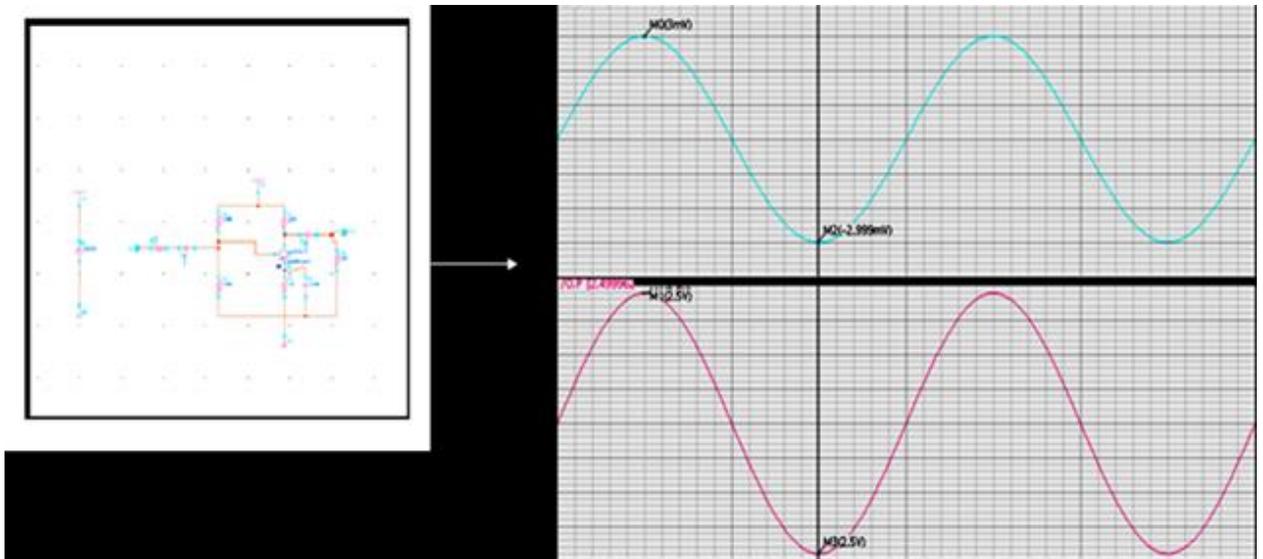| Organism	Symbol	Protein	Homolog					Similarity (% aa unchanged)
			Organism	Symbol	Entrez Gene	Gene Info	Protein	
M.musculus	Ccnd1	NP_031657	R.norvegicus	Ccnd1	58919		NP_741989	99
			H.sapiens	CCND1	595	Gene Info	NP_444284	94
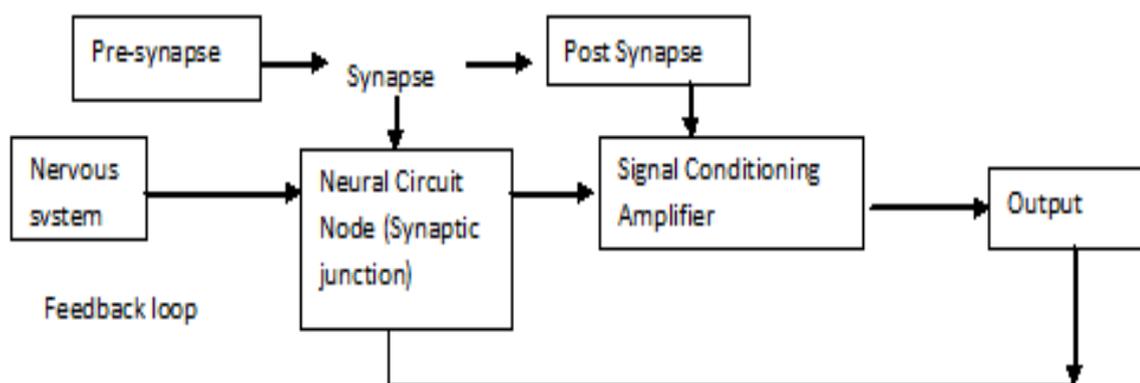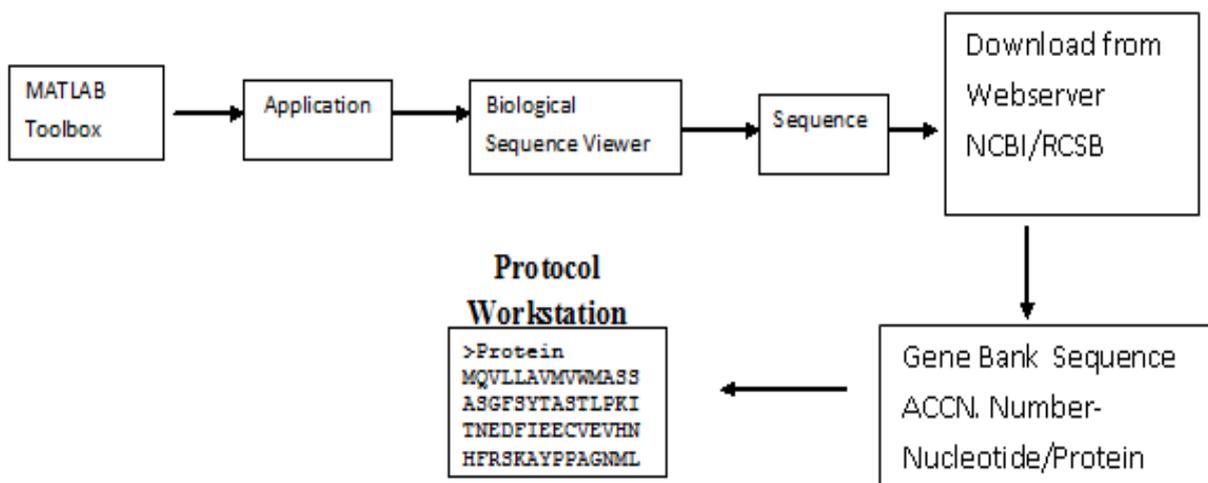
Figure 1: Neural Ear processor Circuit simulation of the Common Emitter amplifier, this circuit mimicks the auditory system behaves as acoustic sensor, so the audio-system, neural recorder here behaves as the transducer converts the electric signal of the voice, in music system into Electrochemical cells of the auditory region of the brain.

This monitors the Brain system and the equilibrium state of the body to check the balance and imbalance system of cerebellum for Parkinsons desease, Ataxia patient.

Data Processing Block Diagram
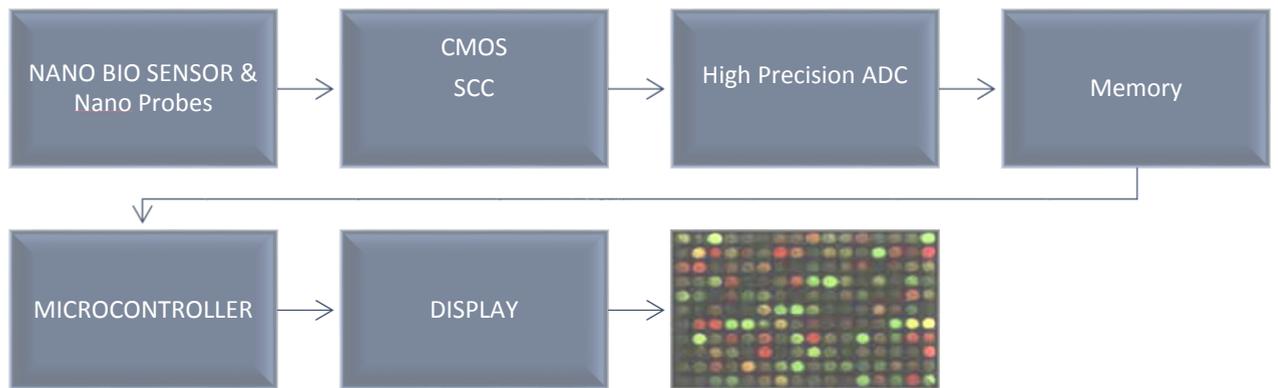
FLUORESCENT LABELLED ARE USED TO LABELAND VISUALIZE DETECTION OF GENE ACTIVITY IN EARLY STAGE CANCER CELLS. IN THIS MICROARRAY EACH DOT REPERESENTS A CANCER GENE

SMART EMBEDDED SYSTEM FOR DETECTION OF CANCER
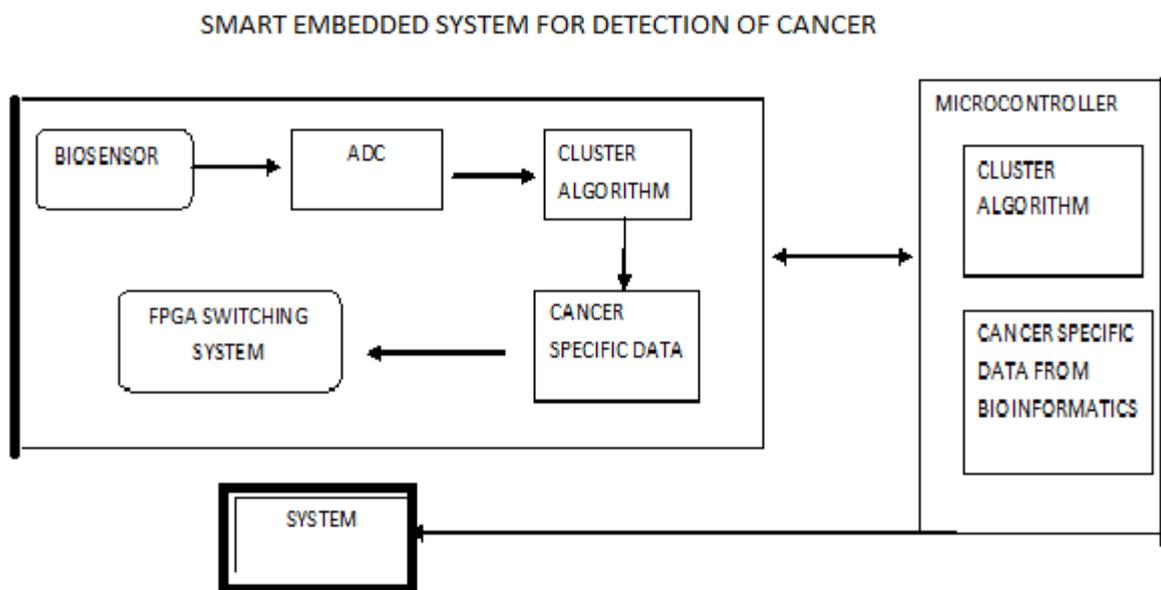
Bioinformatics tool Kit studies[1] has shown the genetic and protein data expression associated with the aetiologies mentioned, This paper give the interpretation and analysis with results in

the form of different comparative algorithm, structural analysis detail downloaded with JAVA Link, and JMOL installation in the system. The comparative tools is used in RCSB DATABANK search engine. Image of the homologous animals taken compared for their structure with behavioral expression and physical being .Computational data flow protocol to monitor the gene expression, the homology detection, computational algorithm gives details about the behavioral similarities & differences in sequence patterns of PDB I.D of cancer protein[12] like GLIPR1[6],Betacell Leukemia [8]factor, Eye degenerative neural disorder causing retinal detachment, Colaboma functionality[10] bio-mimicking with the real nervous system, of our body, comparative structure of the Glioma protein, with its equivalent PDB i.d 3q2u,2CUE gives information about the Ligand molecule and receptor to the Protein. Bioinformatics[7] studies has shown the

formation of tumor at spinal chord. In this fashion we try to identify the correlation of the Colabomatic disorder of human Eye and the other organelle like B-cell Leukemia factor coded by PUFD homology pattern of the colabomatic nucleotide was done with NCBI to know the identity of Human genetic behavior with other animals Cow/Dog/Cat, The computation of the comparative algorithm of PDB ID of 6PAX vs 2CUE vs 1 PUFD is analysed with the help of FATCAT algorithm[2] with external server,with the help of this algorithm[3] pattern.

Table Cancer Specific pathway & Homology detection microarray data analysis chart showing the Homologous relationship within the source organism in their Protein & Gene Expression system table shows the Gene locus number,GeneAccession code, Source Organism, Protein, Gene Expression in speific organ like Brain cerebellum, Retina, mouse gene encoding eye lens – specific structural, Breast cancer significant detection system to show the predicted gene expression of Twilight Eyes, in Horse (Equus- Caballus) for Glioma cancer.

Correlation Of Gene & its structure with pattern of facial expression when mutation occurred in this genes PAX 6 of Eye colaboma, is similarly identified with other homologous species, when performed with Blast algorithm.

BEHAVIORAL EXPRESSION OF CANCER WITH GENETIC ALGORITHM

Physical ⟶ Structural ⟶ Genetics

Physiological features

Protein structure
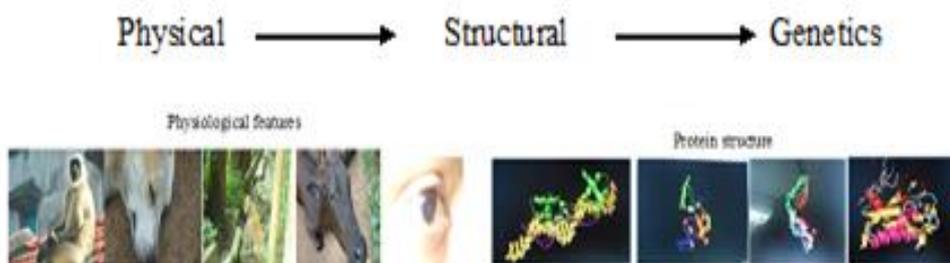
Expression of Eye of homologous animals with similar genetic makeup of PAX-6 gene including human, Iris mutation has appeared in human coded by 2CUE and 6 PAX DNA-Protein interaction, is expressed by the behavior and tested with human for this particular degenerative desease of EYE.

Figure 2: Comparative Structure analysis of PDB I.D Input Interaction of DNA Protein interaction is in the Motif region where DNA Binds to the protein, and the folding takes place, this is the monomer
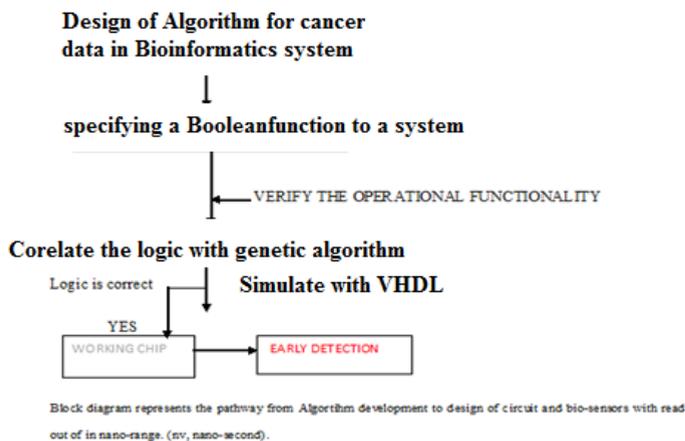
From the above citation we can predict the similarity b/t the structure of Homologous animal and the Human Eye colaboma,Glioma this also detect Genotype and Phenotype behavior b/t the animals Human, in their looking pattern we can see PIG,DOG, same behavior in looking at object when Human Eye has such mutation in Eyes and Glioma this particular behavior in human is noticed can be predicted with the following algorithms discussed in this paper. Its very interesting to study such behavioral significance with nature inhabiting such beautiful creatures. These can also give us the reference to study the and do Bio-mimicking behavior of Human to predict relationship and do monitoring of several detection of disease like Cancer, Tuberculosis and other genetic disease with help of Human Genetic Pedigree analysis. Homologs of the GLIPR1 gene: The GLIPR1 gene is conserved in chimpanzee, Rhesus monkey, dog, cow, mouse, rat, chicken, and zebrafish.
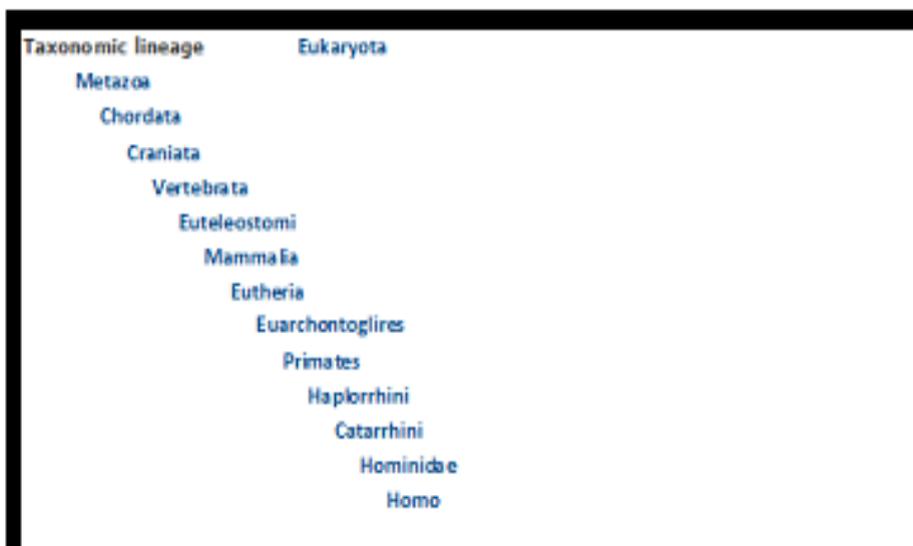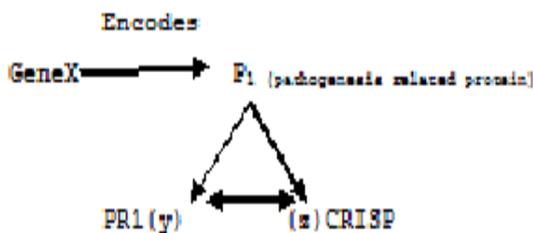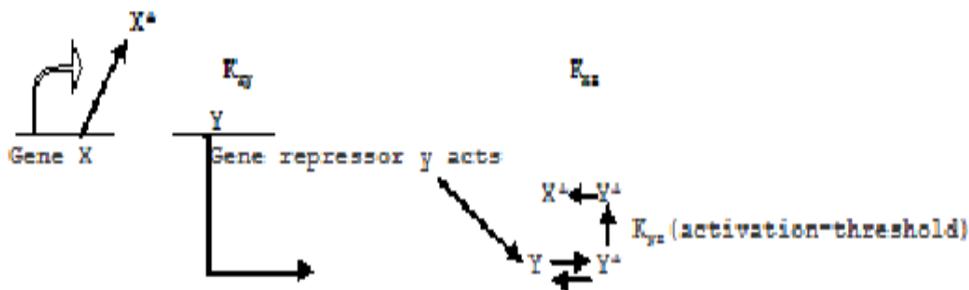
Phylogenetic relationship b/t human and other ancestors in Gentic behavior and homology detection

1. Genetic Algorithm approach

Block diagram represents the pathway from Algorithm development to design of circuit and bio-sensors with read out of in nano-range. (nv, nano-second).

Missense-mutation has changed the sequence code consequently the of SNP thus the amino-acid transformation has occured GeneView via analysis of contig annotation: *PATE1 prostate and testis expressed 1.***GeneModel(s).**

Allele change	Accession	Position	Residue change
GCC ? GGC	NP_612151.1	74	A [Ala] ? G (Gly)
ATA ? GTA	NP_612151.1	66	I [Ile] ? V [Val]
AGG ? ACG	NP_612151.1	88	R [Arg] ? T [Thr]

X^A

K_{xy} K_{xz}

Y

Gene X
Gene repressor y acts

$X^A \leftarrow Y^A$

$\uparrow K_{yz}$ (activation-threshold)

$Y \rightleftarrows Y^A$

Encodes

GeneX ⟶ P1 (pathogenesis related protein)

PR1(y)   (z)CRISP

PR1 protein and Crisp governed by genex and its activation. But when the gene repressor acts hypo-methylation gives rise to Prostate cancer.

The diagram represents the Coherent Feed forward loop, The gene X encodes the pathogenesis related protein, and its similarities between the PR1 and CRISP. When the gene x is activated to X^A and the activation threshold concentration is higher then the expression of X gene occurs, OR else the repressor gene y comes into function suppress Y, and causes prostate cancer and bladder cancer cells.

Gene is switched on/Off in the feed forward loop

Table shows from Bioinformatics data mining search engine the types of cancer, their Specific Pathway code from which we can extract information about the cancer data and their signaling pathway with common Biomarker receptor (Epidermal growth factor receptor).This gives information about the Pancreatic cancer is a part of Diabetes, Glioma is Brain cancer, Bladder cancer, Prostate cancer, Endometrial cancer (Gynecological cancer), Non-small cell lung cancer, Colon cancer (Stomach cancer).
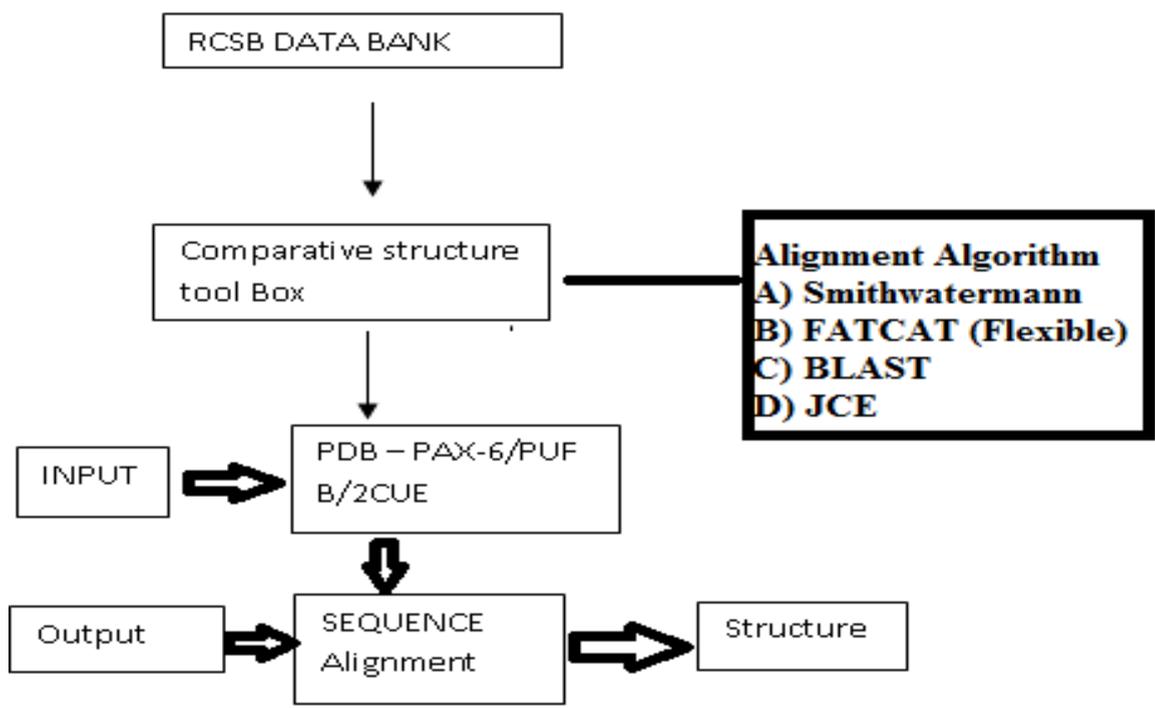
Figure - Algorithm design to compute the comparative protein Model /structure/ Sequence to detect the mutation with different comparative algorithm and to identify the best and Flexible.
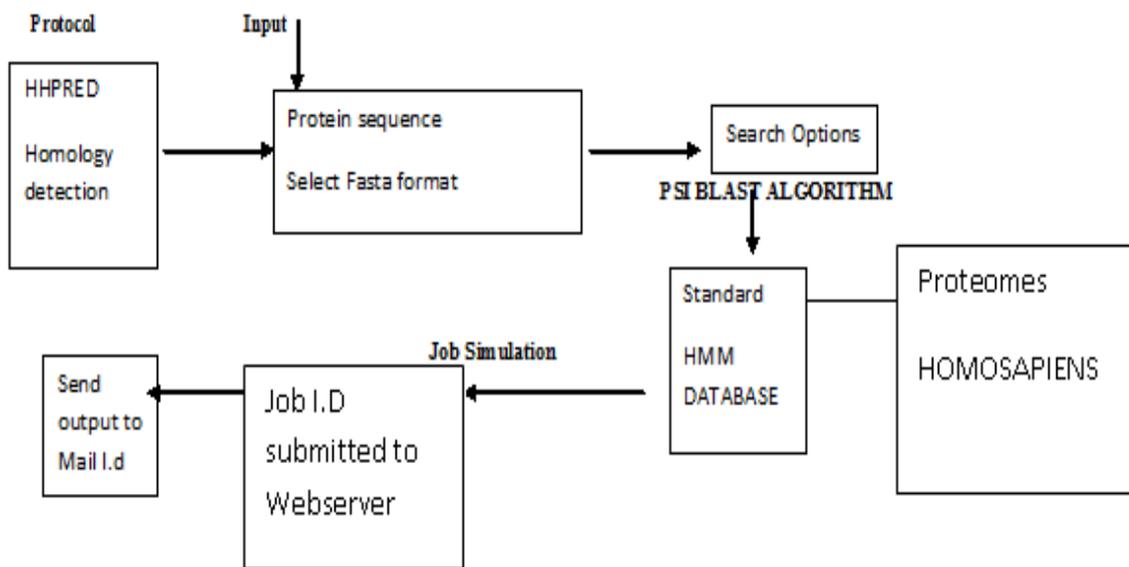
Protocol

Figure - Block diagram showing the algorithm design protocol for detection of structural prediction of Proteome with Homosapiens & other homologous species.
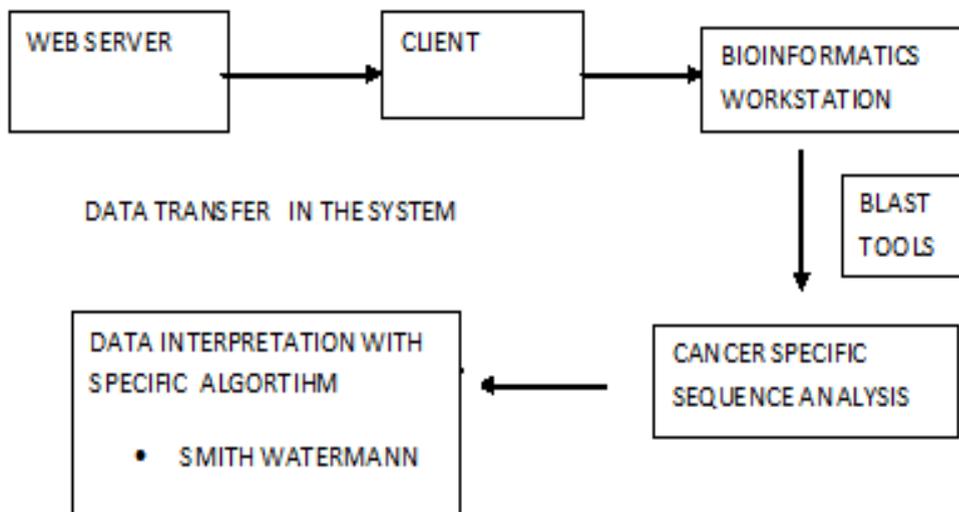
DATA PROCESSING IN SYSTEM

Figure 3:

Conclusions

Bioinformatics data information and extraction with NCBI as a data resource manager helps in mining the biomarkers of cancer and with the help of sequence search database engine and smith waterman algorithm, we have matched the query sequence with the main sequence, identified the different homology of the various animals and correlated with human for the genetic sequences and their probability, in the functioning and hence detection of genetic marker is possible, with specific behavior of the organism. This represents the signal pathway with Gene ID code, and the receptor factor, with specific types of cancer, from this data one can interpret the cancer pathway and their details into molecular level and will be useful to detect the genes of cancer in wet lab, from this information the system can be defined particularly for cancer pathways , when we will click on the codes of the corresponding system, the symptoms and the pathways of each cancer will be monitored and hence we can distinguish the cancer from non-cancer. Comparative studies identifies that the MRI is the best option for brain tumor imaging, as it gives the more clarified picture of the tumor cells. Gadolinium is generally used as the bio-imaging agent with MRI, Bioinformatics gives the detailed analysis of the tumor at protein and genetic level. Laser monitors the different points of the body in details about the functioning of the organ after magnetic induction at that point with point detector and electric impulse it gives the correction. Most Glioma are Malignant, if contrast enhancement does not appear, it is more suggestive of Glioma. Behavioral indications of Brain tumor: like imbalances in the body movement controlled by cerebellar region. Frontal lobe is more concerned with behavior Irritable, Ternatus, hearing loss, Facial nerve palsy are the major behavioral symptoms are the behavioral screenings of Brain tumor. The physical observation of the persons walking nature, behavior way of speech mechanism, headache, difficulty in breathing while sleeping, mechanism of doing Exercise by giving stress to Muscle, way of sitting near the system this all action suggests or give indication to the disorder of the spinal cord, and in the brain, because any defect in the mechanism designs the logic of inverter (NOT), and also exhibit the function of XOR. Ultimately we can find that the logic gates are linked to this

biomechanics.The expression shows the correlation of the homology b/t the Eye of the domestic animals and the structure. In the structure we can see the the DNA protein interaction of at various point of mutation in Colaboma patient in human, Glioma, the picture shows the secondary protein structure. Its structural disorder & nucleotide disorder is expressed in the sequences. The algorithm pattern gives the physical behavior to genetic behavior of the mutation in the cancer of Brain & Eye. With the behavioral pattern the detection of disorder is predicted, the behavioral pattern includes the expression of character, of the animals, their eating habbit, looking pattern to a light, feeling irritation when we put light onto the eye of the Dog,COW, response to human master, supervised method of behavior and unsupervised way of response from Dog, Cat, Cow.can be easily monitored, thus these bahvioral expression is matches with Human for particular disease in Brain cancer and Eye colaboma.

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