CODE OF LIFE: THE INTERSECTION OF MOLECULAR COMPUTING AND BIG DATA ANALYTICS IN PRECISION MEDICINE FOR ONCOLOGY AND e-HEALTH

Salutations/Courtesies

The Vice Chancellor,
Deputy Vice Chancellor,
Members of the Governing Council,
Principal Officers of the University,
Distinguished Members of the University Senate,
My fellow Erudite Academics
Members of Non-Teaching Staff,
My Lords Spiritual and Temporal,
Friends of the University,
All Invited Guests,
Family Members
Gentle Men of the Press,
Great Ladokites
Ladies and Gentlemen.

I give all praises and honor to God for the esteemed privilege to stand before this scholarly gathering of crème de la crème to deliver my inaugural lecture this 14th day of March, 2019 being the 26th in the series of inaugural lectures in the University, the 6th in the faculty of Engineering & Technology and the very first from the Department of Computer Science and Engineering.

PREAMBLE

Mr. Vice chancellor, permit me to begin this lecture by quoting two portions of the Holy Scripture in order to put this inaugural lecture in proper perspective.

"Beloved I wish above all things that thou mayest prosper and be in good health, even as your soul prospers" III John vs 2

I am standing here to give my inaugural lecture today because the Almighty God has prospered the academic endeavor I chose to undertake in life and He also gave me good health all through life's journey to come this far.

Man is a tripartite being, comprising: Spirit, soul and body, with the body as the packaging container or vehicle that carries the other two. The ability for man to work, make profit and prosper depends on the wellness of the body and the mind. "Good health". W.H.O reports of 1948 defined health as a state of complete physical, mental and social well-being, No wonder, even a major aspect of the ministry of Jesus Christ is healing the sick. Health, they say, is wealth; in fact "the richest wealth is Health". From the foregoing, it suffices to say that any positive effort or academic research endeavor towards contributing to the wellbeing and longevity of mankind is worthwhile and commendable.

Mr. Vice Chancellor Sir, my interest in the research niche of e-health and telemedicine is therefore not farfetched. I seek to contribute to, and assist in facilitating quality healthcare service delivery for better quality of life (QoL) particularly for people with chronic health challenges. It is worthy to note that every human being is a patient or will be a patient at one time or the other.

There are many chronic diseases in the world today, one of the most dreaded and seemingly incurable disease which is the core of this inaugural lecture is the canker called cancer or malignant tumor. Cancer is a genetic disease, caused by changes in DNA that control the way cells function, especially how they grow and divide. Cancer has remained a major cause of death all over the world. No particular cure has been found for cancer, available cancer treatments or therapies are

very pocket unfriendly, psychologically devastating and excruciating. Cancer does not only leave its victims crying,

"Why is my pain perpetual and my wounds incurable, which refuseth to be healed? . . . ." Jer. 15:18

It does not only leave them crying, but eventually ends up claiming their lives in most cases. In this lecture, I shall be presenting precision medicine for oncology using next generation sequencing of the whole human genome analyses, utilizing in-memory database technology; a very promising technology for identifying and isolating cancer cells at the DNA (molecular) level. This presentation is part of my ongoing research works in oncology locally over the years, and majorly part of my multi-disciplinary international collaborative research efforts at the Life Science research group of the e-Health Chair at the Hasso Plattner Institut Potsdam, Germany and the Fraunhofer-Institut for Cell Therapy and Immunology, Department of Bioanalytics and Biosensorics, Gohm, Potsdam, Germany. In the course of this lecture, I will talk more about this.

Inaugural lecture is a tradition in Universities where newly appointed Professors are invited to give a lecture. An inaugural lecture is used to justify the promotion of the inaugural lecturer to the exalted post of a Professor. It is also used to solicit support for the discipline or the department to which the lecturer belongs. The lecture represents the official recognition of their promotion to the Professorial chair, and the lecture itself provides an opportunity to showcase their previous or current research work to the wider public. It is also a celebratory occasion when the Professor(s) can share their achievements with colleagues, family and friends. Hence, inaugural lectures are a valued tradition within universities. The inaugural lecturer may choose to focus on his/her research work and his/her area of specialization or, he/she may decide to discuss broad issues of his/her profession. Mr. Vice-Chancellor Sir, today, I intend to combine the two.

HOW IT ALL BEGAN (From Chemical Engineering to Computer Science)

The ardent love and insatiable appetite I had for Chemistry during my secondary school days, coupled with the admiration of an uncle working in NNPC made me determine to pursue a career in chemical engineering. Along the line again, while rounding up my secondary education, I met one Mr. Kunle, a Biochemist but taught chemistry with great passion and enthusiasm, whom we soon nick named ***Kekule*** after Friedrich August Kekulé the great German Organic chemist who discovered Benzene structure (Kekule structure, 1865). In 1990, I got admitted into the Chemical Engineering Department of the Federal University of Technology, Minna to pursue my dream course of becoming a Chemical Engineer.

However, before the end of the 1st semester of 100 level the story changed. I changed from Chemical Engineering Department to Computer Science and Mathematics. When I told my friends about the decision and the change, they felt pity for me, while others laughed me to scorn, that I was abandoning Engineering to become an ***"Advanced Typist"***; because to them at that time, they saw the computer only as an advance typewriter. Today, they have been proved totally wrong by the tremendous impact of the revolutionizing and transformational power of computers globally. I thank God for his leading and direction for making that change then. I made the right choice of course. No regrets. Like the first biological (human) computer created in Eden's garden, the digital computer today has subdued the whole world and is having dominion in all works of life. (Gen. 1.28) ". . . ***And God said . . . let him subdue the earth and have dominion over all the creatures . . ."***

FUT Minna was a good training ground, the B.Tech. combined honors programme in Maths/Computer Science was a very comprehensive and balanced blend. It was a six year, three semesters per- session programme, though later changed to a five year programme. During my undergraduate programme, I met Prof. S. A. Reju (then Dr. S. A. Reju)

a very hardworking, intelligent, disciplined and admirable scholar who later became my mentor. I got inspired to become an academic by the way Dr. Reju wrote his name and degrees on his complimentary card and letterhead. Dr. S. A Reju (B.Sc, M.Sc, PhD, FMAN etc), then I decided I will also like to have behind my name those appellations. So after my B.Tech programme, I proceeded for masters and doctoral degrees.

Going through my academic performance and transcript in the undergraduate, CPT 515 Expert Systems happened to be the course I had the highest score; hence in my M.Tech and Ph.D research, I decided to specialize in Neural Computing/Computational Intelligence and Optimization.

SETTING THE AGENDA FOR PROCEDURAL AND COMPUTATIONAL INTELLIGENCE COMPUTING PARADIGMS

Mr. Vice Chancellor sir, may I remind us that we are living in the so called computer age or information technology era. This era is so labeled because of the profound impact of computer in the world as a whole. It is no news that computer is now a universal language today and has been found indispensable in all works of life; in fact literacy in computer has become the password into the labor market.

Computing is a problem solving discipline. Irrespective of the field, any problem that can be expressed in a procedural manner is a candidate of computer solution. It is interesting to know that computers have gone beyond solving only procedural problems to fuzzy and un-procedural problems.

The ultimate in computer science is to adopt and adapt scientific theories, natural phenomena and engineering principles in identifying complex human problems, designing solution models and providing soft solutions implemented on hardware in various fields to solve human

problems. Procedural problem-solving paradigm is an age long concept that can be dated as far back as the beginning of creation. Hence, we can say that the fundamental concept underlying computing and programming principles started as far back as in the Beginning. In setting the agenda for procedural and intelligent computing-problem solving paradigms, permit me to invoke citation from the undisputable holy antique book.

I do not intend to make this lecture a religious lecture. However, I sincerely wish to acknowledge the One I think in my opinion is the Author of procedural and intelligent computing paradigms. It suffices to say that the problem solving and procedural computing agenda was established in the Beginning. Gen 1.1 The first algorithmic procedure and flowchart is profiled in the sequence of the creative act and later followed by the natural intelligent parallel processing paradigm exhibited in the neurons in the human brain.

The Algorithm:
:

i.	Vs. 1 " In the beginning God. . ."	**(Begin/Start)**
ii.	Vs. 2 The earth was without form and void. . .	(The Problem)
iii.	Vs 3-5. And God said let there be light . . .	(Creation of Day 1)
iv.	Vs 6-8 Let there be firmament	(Creation of firmament, Day 2)
v.	Vs. 9-13 Creation of water bodies, land and vegetation	(Day 3)
vi.	Vs 14-19 Creation of galaxies , Times and seasons	(Day 4)
vii.	Vs. 20-23 Creation of aquatic and terrestrial creatures	(Day 5)
viii.	Vs. 24-28 "Let us make man, . . . let him have Dominion .. .."	(Day 6)
ix.	Gen 2:1 Creation Finished	**END/STOP**

Figure 1. A Basic Procedural Problem Solving Algorithm for Creation

Procedural programming uses a list of instructions to tell the computer what to do step-by-step. A logical step-by-step method to solve a problem is called **algorithm**, in other words, an algorithm is a procedure for solving problems. Algorithms can be presented by natural

languages, pseudo code, and flowcharts, etc. A **flowchart** is the graphical or pictorial representation of an algorithm with the help of different symbols, shapes and arrows in order to demonstrate a process or a program. Figure 2 shows the flowchart representation of the algorithm of creation listed in Figure 1.
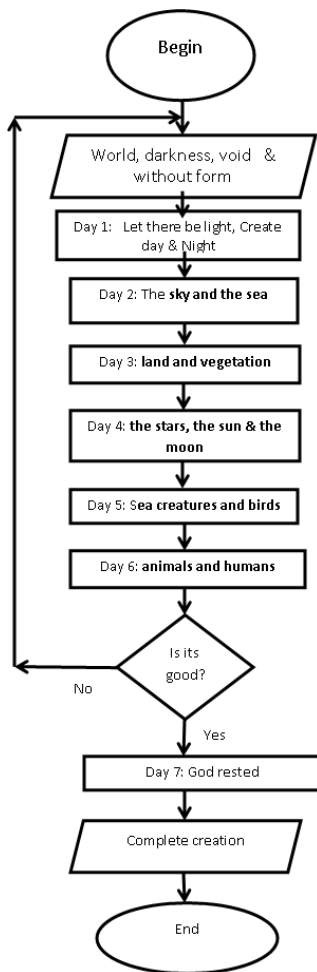

Figure 2. The Flowchart of Creation.

Procedural programming relies on - procedures, also known as routines or subroutines A procedure contains a series of computational steps to be carried out. Procedural programming is also referred to as imperative programming. Procedural programming languages are also known as top-down languages.

Procedural programming is intuitive in the sense that it is very similar to how you would expect a program to work. Procedural language is one of the most common types of programming languages in use, with notable languages such as C/C++, Java, Basic, COBOL, ColdFusion and PASCAL. Mr. Vice Chancellor sir, I wish to draw your attention to the fact that over the years, computer technologies and programming paradigms have however evolved. Today, there are many programming paradigms such as Structured programming, Declarative programming**,** Functional programming**,** Object oriented programming**,** Symbolic programming, Knowledge based programming and Intelligent Computing Programming e.t.c.

COMPUTATIONAL INTELLIGENCE COMPUTING PARADIGMS

It is a known fact that the brain is the most incredible organ in the human body. It dictates the way we perceive every sight, sound, smell, taste, and touch. It enables us to store memories, experience emotions, and even dream. Without it, we would be primitive organisms, incapable of anything other than the simplest of reflexes. The brain is, inherently, what makes us intelligent (Buduma, & Locascio, 2017). It is also an indisputable truism that the Human brain outperforms the fastest digital computer when it comes to intelligent information processing like; Image processing, parttern recognition, speech recognition and comprehension, vision, combinatorial optimization problems solving etc (Garry, 1987).

The computational richness of the brain comes from its large number of living neurons, which are highly connected to each other by a complex

network of synapses forming a neural network of computationally intelligent system. The smartest and most innovative algorithms currently in use today in artificial intelligence (A.I) are inspired by biological systems, hence computer scientists have been compelled to look into biological and natural computing systems from which several intelligent and innovative algorithms have emerged, such as; artificial neural networks, deep neural networks, neuro-fuzzy systems, many versions of evolutionary algorithms (e.g. evolution strategies, genetic algorithm, genetic programming, differential evolution), as well as ant colony optimization, artificial immune systems, multi-agent systems, particle swarm optimization and the hybridization versions of these etc.

The synergy of these algorithms used in innovative ways for solving very complex problems is now referred to as computational intelligence (CI). Xing and Gao, (2014) offer us a brand new perspective in the field of CI research through their book entitled Innovative Computational Intelligence: A Rough Guide to 134 Clever Algorithms. They identified novel CI algorithms and grouped them into four large classes, namely, biology-based C.I algorithms, physics-based C.I algorithms, chemistry-based C.I algorithms and mathematics-based CI algorithms. Computational intelligence has become a popular term being currently used to refer to the synergy of emerging computational techniques in soft computing and natural computing.

Soft computing is an innovative approach to constructing computationally intelligent systems for solving complex real world problems that requires humanlike expertise. Natural computing refers to computing going on in nature and computing inspired by nature. Evolutionary computing and genetic algorithms use the concepts of mutation, recombination and natural selection. Neural computing (artificial Neural Networks) are inspired by the highly interconnected neural structures in the brain and nervous system.

It is believed by many researchers in the field that neural network models offer the most promising unified approach to building truly

intelligent computer systems; and that the use of distributed, parallel computations as performed in ANNs is the best way to overcome the combinatorial explosion associated with symbolic serial computations when using Von Neuman Computer Architecture.

The successful implementation of the application of Artificial Neural Networks (ANNs) have been reported in areas such as Control [Balakrishnan and Weil, (1996)], telecommunications [Cooper, (1994)], Biomedical [Alvager *et al*.,(1994), Hasnain (2001), Muhammad (2001), Emuoyibofarhe **,** Sobayo, Oloke and James (2005) ECG Wave Analysis and Diagnosis], Remote Sensing [Goïta, *et al*., (1994)], Pattern Recognition [Smetanin, (1995)], RF/Microwave design [Zhang, Gupta, and Devabhaktuni, (2003)], Microstrip Circuit design [Horng, *et al*, (1993)], Microwave Circuit analysis and optimization [Zaabab *et al*., (1994)], Application of ANNs to biological systems (stem cells) [Szu and Hwang (2003), Szu (2003), Groβ-Hardt and Laux (2003)].

Emuoyibofarhe and Reju (2008) implemented an hybrid Neural Network for the optimum solution of a process control problem (C.S.T.R) continuous stirred tank reactor problem.
Araromi, Sonibare and Emuoyibofarhe (2014) implemented a Neuro-fuzzy identification for Reactive Distillation for Acetic Acid recovery from waste Water.
Emuoyibofarhe and Taiwo (2012) implemented a Neuro-fuzzy based system for determining the severity level of knee Osteoarthritis. Obanijesu and Emuoyibofarhe (2012) Developed a Neuro-fuzzy System for Early Prediction of Heart Attack. Figure 3 is a conceptual representation of computational intelligence, depicting mapping of the power of the human brain through artificial neural model into the digital computer.

Figure 3. Conceptualization of Computational Intelligence (Emuoyibofarhe, 2008)

Codes and Coding

In programming, code (noun) is a term used for both the statements written in a particular programming language - the source code , and a term for the source code after it has been processed by a compiler and made ready to run in the computer - the object code . To code (verb) is to write programming statements - that is, to write the source code for a program. In cryptography, code has both a specific technical meaning and a general meaning. In the technical sense, code is the substitution of one word or phrase by another word, number, or symbol for the purpose of concealing the original word or phrase. In industry, a developing product is sometimes given a code name to conceal its probable marketing name.

Historically, military operations have often had a code name while in the preparation stage. In World War II, Germany's invasion of the Soviet Union was given the code name of Barbarossa. Code in this

sense is sometimes confused with a cipher, which is substitution of symbols at the letter level. Modern cryptography is much more concerned with ciphers than with code in its limited technical meaning. Code is often used generally to mean any kind of concealed writing, including ciphers. "Breaking the code" usually means the discovery of a way to read one or a series of encrypted messages without being given the key to decrypt them.

Computer programming is the process of designing and building an executable computer program for accomplishing a specific computing task, Emuoyibofarhe, Sunday and Fasaya (2003). Programming involves tasks such as analysis, generating algorithms, profiling algorithms' accuracy and resource consumption and the implementation of algorithms in a chosen programming language (commonly referred to as **coding**). The source code of a program is written in one or more programming languages. The purpose of programming is to find a sequence of instructions that will automate the performance of a task for solving a given problem. The process of programming thus often requires expertise in several different subjects, including knowledge of the application domain, specialized algorithms and formal logic.

Machine code is a computer program written in **machine language** instructions that can be executed directly by a computer's central processing unit (CPU). Each instruction causes the CPU to perform a very specific task, such as a load, a jump or an ALU operation on a unit of data in a CPU register or memory.

Machine code is also known as machine language (ML). Each CPU has its own specific machine language. The processor reads and handles instructions, which tell the CPU to perform a simple task. Instructions are comprised of a certain number of bits. If instructions for a particular processor are 8 bits, for example, the first 4 bits part (the opcode) tells the computer what to do and the second 4 bits (the operand) tells the computer what data to use.

01001000 01100101 01101100 01101100 01101111 00100001
Depending upon the processor, a computer's instruction sets may all be the same length, or they may vary, depending upon the specific instruction. The architecture of the particular processor determines how instructions are patterned. The execution of instructions is controlled by firmware or the CPU's internal wiring.

CODE OF LIFE

Cells are the basic building blocks of all living things. The human body is composed of trillions of cells. They provide structure for the body, take in nutrients from food, convert those nutrients into energy, and carry out specialized functions. Cells also contain the body's hereditary material and can make copies of themselves. Cells have many parts, each with a different function. Some of these parts, called organelles, are specialized structures that perform certain tasks within the cell.

Life is computation. Every single living cell reads information from a memory, re-writes it, receives data input (information about the state of its environment), processes the data and acts according to the results of all this computation (Emuoyibofarhe, 2009). Globally, the zillions of cells populating the biosphere certainly perform more computation steps per unit of time than all man-made computers put together.

The blue print (codes) of life is embedded in the cells {DNA}, Cell contains many biochemical molecules, An important class of molecules are proteins (Zvelebil and Baum, 2007). They are responsible for the cellular structure, catalyzing chemical reactions and regulating gene activities. Understanding the changes in genes (mutation) can aid in finding the cause of disease (genetic) and thus support treatment decision.

DNA, or deoxyribonucleic acid, is the hereditary material in humans and almost all other organisms. Nearly every cell in a person's body has the same DNA. Most DNA is located in the cell nucleus (where it is

called nuclear DNA), but a small amount of DNA can also be found in the mitochondria (where it is called mitochondrial DNA or mtDNA).

The information in DNA is stored as a code made up of four chemical bases: adenine (A), guanine (G), cytosine (C), and thymine (T) referred to as the DNA language code and alphabets (Figure 4). Human DNA consists of about 3 billion bases, and more than 99 percent of those bases are the same in all people. The order, or sequence of these bases determines the information available for building and maintaining an organism, similar to the way in which letters of the alphabet appear in a certain order to form words and sentences. DNA bases pair up with each other, A with T and C with G, to form units called base pairs. Each base is also attached to a sugar molecule and a phosphate molecule.
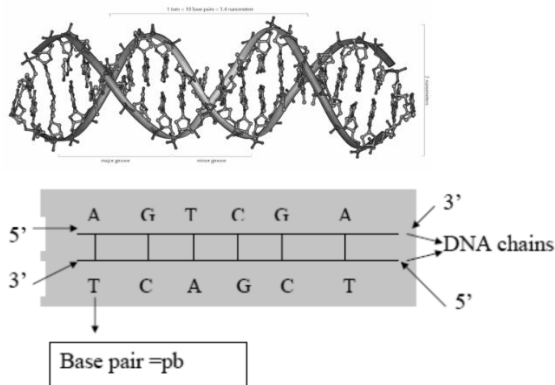
GTCGAATTGGAATTGGGTCGAATTGGAATTGGGTCGAATTGG AATTGG

Figure 4. DNA language code and alphabets

Architecture: Components of Eukaryotic Cells (Organelles)

In 1665, Robert Hook discovered and gave name to cells. Robert Hook published in "Micrographia" that Human cells contain the following major parts with specialized structures that perform certain tasks. Figures 5a and 5b show the organelles of cell and component of the

nucleus. In Table 1 a comparative analogy of the cell components and the digital computer is presented.
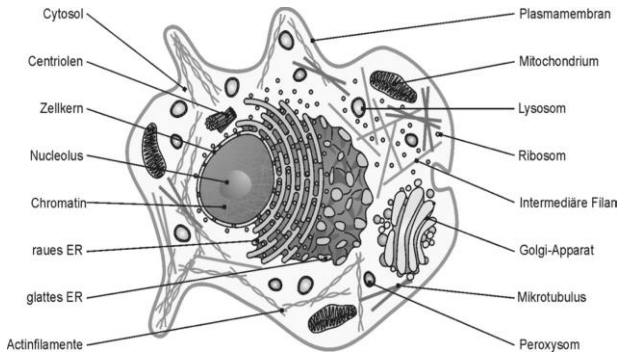

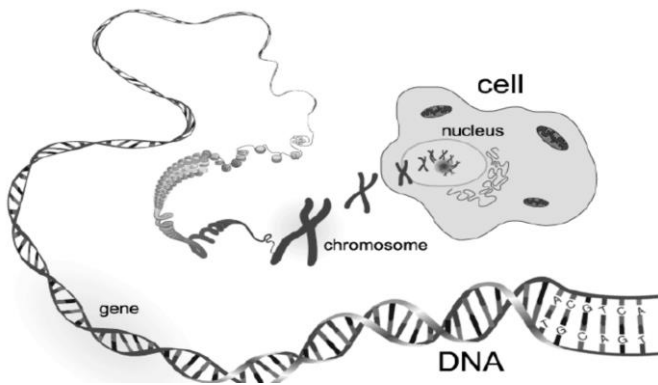Figure 5a: **Components of Eukaryotic Cells (Organelles)**

Figure 5b. Cell nucleus showing chromosomes, gene and DNA

Table 1. Analogy of molecular computer and the digital computer

Mitochondria	Responsible for energy/Power supply and management for the cell
Cell Nucleolus	Contains **Source Code** i.e Condensed DNA in form of chromosomes
Endoplasmic Reticulum (ER)	Provides Transport Network
Ribosomes	**Compiler** i.e translation of messenger RNA (mRNA) to Amino Acid (AA) sequences
Golgi Apparatus	Processes and packages macromolecules similar to **software packaging functions**
Lysosomes and peroxisomes	destroy toxic substances and recycle worn-out cell: **Recycle Bin or Gabbage collector** (Initialization and cleanup)
Transfer (tRNAs) and Ribosomal RNAs (rRNAs)	Help assemble protein building blocks (amino acids) : **Assembler**

Discovery of the DNA

The discovery in 1953 by Francis H. C. Crick and James D. Watson marks the official scientific discovery of the DNA (Watson et al, 1953). Their discovery was based on early research works of Maurice H. Wilkins and Rosaland Franklin. This discovery led to the award of Nobel Prize in Medicine in 1962 to Crick, Wilkins and Watson. However, it is noteworthy to mention that the discovery of the DNA can be traced to a 200 years' research time line beginning from the works of Swiss physiological chemist Friedrich Miescher in 1869 and Russian biochemist Phoebus Levene in 1919.

The DNA which was only officially discovered in 1953 has been embedded in the cell nucleus which was created by God almighty since the creation of the world. "And God said let us make man in our own image . . ." Gen 1:26.

DNA is known to be the key molecule in every living organism as it carries the genetic information concerning each individual. DNA stands for Deoxyribonucleic Acid. DNA molecules are formed by two strands that form a double-helix. Those strands are composed of nucleotides. Each nucleotide contains a sugar (deoxyribose), a phosphate group and one nitrogenous base. There are four bases that can be present on DNA: Cytosine, Adenine, Guanine and Thymine.

RNA stands for Ribonucleic Acid and is a molecule responsible for the coding, decoding, regulation and expression of genes (Clancy, 2008). RNA and DNA have a similar structure, however, RNA only has a single strand that fold onto itself and its sugar is Ribose. It is composed of four types of ribonucleotide bases: Adenine, Cytosine, Guanine and Uracil.

DNA determines the structure of a cell, meaning whether it is meant to be an eye cell, a skin cell and so forth (Ralston and Shaw, 2008). DNA contains genes and those genes are used to produce RNA (the transcription process) that has the information needed to synthesize a protein in a process called gene expression, according to Geoffrey and Robert (2016). The process of transforming DNA into proteins is divided in two stages: transcription, where RNA is produced using DNA templates and translation, where proteins are synthesized using RNA templates.

Components of Deoxyribonucleic Acid (DNA) and Ribonucleic Acid (RNA)
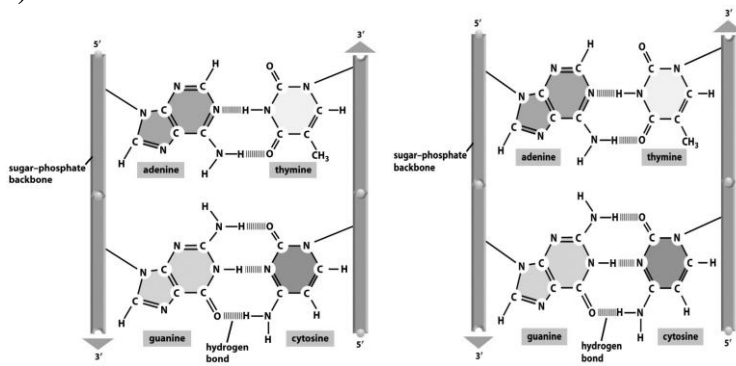

Figure. 6a & 6b Components of Deoxyribonucleic Acid (DNA) and Ribonucleic Acid (RNA)

Why study Analysis of DNA?

Understanding the changes in genes (mutation) can aid in finding the cause of disease (genetic) and thus support treatment decision.
It helps to understand mutations
It helps to identify marker for diseases
It helps to take personalized treatment decisions
It helps to ascertain the percentage of the patient population for which a particular drug in a class is ineffective on average.

MOLECULAR COMPUTING

Molecular computing can be defined as computations going on in life or living systems using molecules as data and/or processing units. Supramolecular chemistry which studies complex systems composed of synthetic molecules associated by weak interactions, has already began to produce some devices such as molecular switches, which have proven useful for future developments in computation (Emuoyibofarhe, 2009).

However, living cells do not use any devices which (1990s computer users) would expect to be necessary for computation. No semiconductor chips, nor quantum dots or mechanical Babbage-type machinery. Rather than mechanics, quantum mechanics or electronics, molecular computers or cell use chemistry, they compute by using molecules, mostly heteropolymeric macromolecules such as proteins and nucleic acids. Protein can, for instance, act as signal receptors, logical gates, or signal transducers between different forms of signaling including light, electricity and chemical messenger systems. Nucleic acids mainly act as memory, both for permanent and short term applications, although the self-splicing activity of setting RNA molecules means that they can perform information processing as well. While the genetic role of nucleic acids has been known for several decades, the roles of proteins for molecular computation in the cell are only just beginning to be explored.

Molecular computing is closer to reality today with the creation of molecular switches that can be turned on and off hundreds of times and could replace silicon-based computing. A molecular switch is a logic gate which can represent the binary language of a digital computer. Molecular switches would be many times cheaper than traditional solid state devices and would allow for continued miniaturization and increase in the power that silicon-based components would never be able to reach (Emuoyibofarhe, 2009).

BIO-INFORMATICS (COMPUTATIONAL BIOLOGY)

BIO	+	INFO	+	MATICS
BIOLOGY		INFORMATION		DATA/COMPUTATION

Bioinformatics refers to the computational manipulation of biological data to facilitate the discovery of new biological insights and discern unifying principles in biology (Oluniyi, 2018). It is the use of computational techniques to analyze biological problems or making sense of biological data using computational and statistical tools. Bioinformatics is a field that applies statistical and computer science

knowledge and technique in solving biological problems. It is an interdisciplinary field that overlaps with many other fields such as biostatistics and computational biology (U2R workshop, 2018).
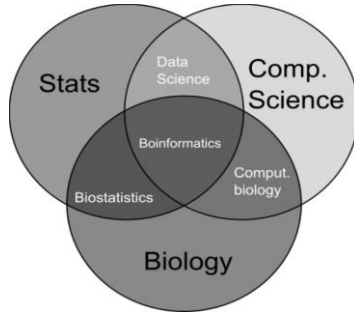

Figure 7. Bioinformatics Defined diagrammatically (U2R workshop, 2018)

Bioinformatics can be used to answer various types of biological problems such as;
•What is the role of a gene?
•Could a particular gene cause a specific disease?
•How does a chemical/drug affect a cell?
•How do genetic variances among people result in different disease susceptibility?
•Is it possible to create trans-genic strains of crop for resisting certain diseases or pests?
•Can we design a drug to treat a particular disease?

The above sets of questions can be answered through development of statistical approaches for assessing relationships among members of large data using;

•Sequence alignment
•Gene detection
•Genome annotation

•Gene expression profiling
•Genome annotation and comparison

BIG DATA and BIG DATA ANALYTICS

What is Big Data?
Collection of data so large and complex that it becomes difficult to process using traditional database management tools and processing framework.

Figure 8. A representation of Big Data

SEVEN V's of Big Data
Three basic V's are commonly used to characterize big data:

Volume – Refers to the **vast amount** of data
Velocity– Refers to the **speed** at which new data is generated and moved
Variety– Refers to the **heterogeneity** of data

Four additional V's, which vary with different purposes:

Veracity – The uncertainty due to correctness and consistency of data
Variability – The variance **in the meaning** of the data
Visualization – Presentation of results in a human readable way

Value – The benefit of insights from Big Data analytics

Where Big Data Comes From? Big Data Facts

Closer Look to Every minute on the Internet reveals the following;
350 Thousand new Tweets generated!
400 Hours of Youtube Videos added!
2.5 Million Instagram Likes & Posts generated!
150 Million Emails sent!
Every day 2.5 exabytes of data are produced

BIG DATA ANALYTICS

Big Data analytics is the process of exploring huge data sets that may contain a variety of data types to reveal hidden patterns, unknown correlations, market trends, customer preferences and other useful business information. Big data analytics has emerged from two distinct concepts: big data and analytics. Big Data analytics in Healthcare is fundamentally a set of methodologies, procedures, frameworks and technologies which are used to transform raw data into meaningful as well as useful information. These set of information are used to make decision making tasks more effective whether they are strategic, tactical or operational.

BIG DATA AND SOURCE OF BIG DATA IN HEALTH CARE

Big data in health-care refers to the patient care data such as physician notes, Lab reports, X-Ray reports, case history, diet regime, list of doctors and nurses in a particular hospital, national health register data, medicine and surgical instruments expiry date identification based on RFID data. Healthcare organizations are depending on big data technology to capture all of these information about a patient to get a

more complete view for insight into care coordination and outcomes-based reimbursement models, health management and patient engagement.

Source and Techniques for Big Data in Healthcare
- Structured EHR Data
- Unstructured Clinical Notes
- Medical Imaging Data
- Genetic Data
- Other Data (Epidemiology and Behavioral)
- Fitness Machines
- Wearable Biosensors
- Pharmaceutical Database and Dictionaries
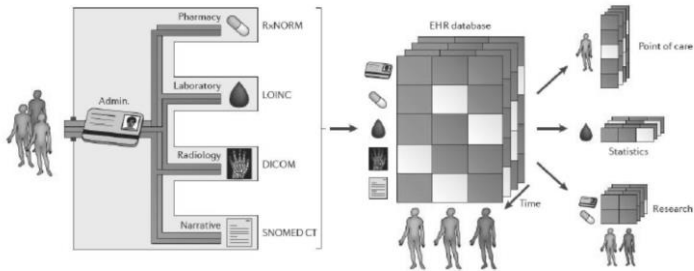- Medical Research and Trials (PubMed)

Figure 9. Data Collection and Analysis Framework

Need for Big Data Analytics in Healthcare

To improve the quality of healthcare by considering the following:

Providing patient centric services: To provide faster relief to the patients by providing evidence based medicine-detecting diseases at the earlier stages based on the clinical data available, minimizing drug doses to avoid side effect and providing efficient medicine based on

genetic makeups. This helps in reducing readmission rates thereby reducing cost for the patients.

Detecting spreading diseases earlier: Predicting the viral diseases earlier before spreading based on the live analysis. This can be identified by analyzing the social logs of the patients suffering from a disease in a particular geo-location. This helps the healthcare professionals to advise the victims by taking necessary preventive measures.

Monitoring the hospital's quality: Monitoring whether the hospitals are setup according to the norms setup by the relevant medical council. This periodical check-up helps government in taking necessary measures against disqualifying hospitals.

Improving the treatment methods: Customized patient treatment-monitoring the effect of medication continuously and based on the analysis dosages of medications can be changed for faster relief. Monitoring patient vital signs to provide proactive care to patients. Making an analysis on the data generated by the patients who already suffered from the same symptoms, helps doctors to provide effective medicines to new patients.

Data mining

Data mining can be seen as the process of extracting knowledge and discovering important patterns from data (Han, Pei, and Kamber, (2011). Data mining algorithms have played an important role in the overall knowledge discovery process. (Bergeron, 2003):

Two of the main goals in data mining are considered to be prediction and description (Fayyad, Piatetsky-Shapiro, and Smyth, 1996), Kantardzic, (2011). Prediction is when the learning algorithm uses the current data to make future predictions whilst description tries to

characterize the properties of the data in a given dataset (Han, Pei, and Kamber, (2011).

Different data mining algorithms like unsupervised learning (clustering), supervised learning (classification), regression, and machine learning techniques etc., can be employed to extract or mine meaningful patterns from the data (Bergeron, 2003). The way data mining achieves these goals and extracts useful information from data includes but not limited to the following:

Classification: Classification algorithm tries to classify data into finite number of predefined labels (class values) by learning a function that maps objects to the labels.

Regression: Regression tries to build a predicting learning function that maps an element to the real-value predicted by the function.

Summarization: Summarization is a descriptive task that tries to represent data in a more concise way while maintaining the main features of the dataset.

Clustering: Clustering is a descriptive task that tries to identify a set of clusters or categories to define similar data. There is a clustering subfield called conceptual clustering that aims to not only cluster the data but also discover and explain the meaning behind each cluster.

Anomaly Detection: Anomaly detection tries to find unusual values, that is, values that deviate from what is normal in the dataset. These values are considered outliers and can be either considered errors or interesting values that should be further investigated.

The general procedure to data mining problem solving involves the following five steps

Figure 10 Data-mining Process (Mehmed. 2012)

IN-MEMORY DATABASE MANAGEMENT

In early computer systems, the frequency of the CPU was the same as the frequency of the memory bus and register access was only slightly faster than memory access. However, CPU frequencies have tremendously increased in the last years following Moore's law (Moore, 1965). Computer hardware is continuously changing and improving. In recent years, multi-core architecture and larger main memory has been the most important trends.

Major requirements for a modern enterprise database management system should be able to handle data coming from several different source types such as:

- Transactional data
- Event processing and Stream data from sensors

- Real-time Analytics and
- Text analytics

A main driver for real-time analysis of large amounts of data is the development of In-Memory Databases (IMDBs) that are capable of processing large volumes of data in a very fast response time. Initial concepts of in-memory database were created in the 1980s, but memory prices were too high and memory capacities too small for those systems to be viable for large applications (Garcia-Molina and Salem, 1992).

In-Memory Database Management technology is a lightweight compressed, combined row and column oriented storage, dictionary encoded, multi-core and parallelization oriented database that enable processing of enterprise data in real time in the main memory. This includes the processing of hundreds of thousands of queries in a multi-user system in sub second response time. In-Memory technology enables decision taking in an interactive way without keeping redundant or pre-aggregate data.

Connection between Processor and Main memory

In 2005, chip manufacturers such as Intel and AMD introduced multi-core processors into the consumer market. With the development of multi-core processors, the Front Side Bus (FSB) became the bottleneck of computers not being able to provide data from main memory as fast as multi-core processor could process the data. To overcome this problem, Intel and AMD developed new technologies that integrate a direct connection from processor cores to main memory. With Intel's Quick Path Interconnect (QPI) and AMD's Hyper Transport Protocol, each processor core has local memory, that is adjacent to its own slot and remote memory that is adjacent to other cores (Advance Micro Devices I, 2001). Computer architecture built on these technologies are called Non-Uniform Memory Access (NUMA) architecture. Data access to remote memory is up to 25 percent slower than access to local memory (Fujitsu Technology Solutions, 2010)

PRECISION MEDICINCE

Stratified Medicine: is based on the identification of subgroups of patients that differ in their mechanisms of disease, their susceptibility to a particular disease, or in their response to a medicine.
A Cohort is defined as a group of people who share a characteristic over a certain period of time (Glenn 2005)
Personalized medicine
The recent trend now is, instead of treating patients based on their symptoms, patients get treated based on the mutations in their genome if the origin of the disease can be found therein. This idea, to treat patient according to the individual conditions and the cause of a disease, and not based on how other patients with similar symptoms were treated before, is the main concept behind personalized medicine (Jain, 2009).

Precision Medicine is "an emerging approach for disease treatment and prevention that takes into account individual variability in genes, environment, and lifestyle for each person." (U.S. National Institute of Health, 2015).

President Obama speaks on the Precision Medicine Initiative, Jan 30, 2015

Figure 11. President Obama unveils the Precision Medicine Initiative on Jan.30, 2015

ONCOLOGY

Oncology is the study and the treatment of cancer or malignant tumors. Cancer is the name given to a group of related diseases, that involve an uncontrolled growth, abnormal cell multiplication and spreading into surrounding tissues and is known to be responsible for the death of millions every year (www.cancerresearchuk.org) and continues to attract more and more researchers in the medical field due to the resulting number of deaths due to the disease. Oncology research focus on prevention, detection and treatment for the disease and it focuses more on some types of cancer that are considered to be more fatal. Cancer is a group of diseases.

Cancer is a genetic disease, that is, it is caused by changes in DNA that control the way cells function, especially how they grow and divide. These changes can be inherited, but most arise randomly during a person's lifetime either as a result of errors that occur as cells divide or from exposure to DNA-damaging carcinogens.

Cancer genome sequencing is the whole genome sequencing of a single, homogeneous or heterogeneous group of cancer cells. It is a biochemical laboratory method for the characterization and identification of the DNA or RNA sequences of cancer cell(s).
Cancer genome sequencing is not limited to WG sequencing and can also include exome, transcriptome, micronome sequencing as well as end-sequence profiling. These methods can be used to quantify gene expression, miRNA expression and identify alternative splicing events in addition to sequence data.

What is Cancer Genomics?

The Genetic Basis of Cancer
All the DNA contained in your cells makes up your genome. In most cells, the genome is packaged into two sets of chromosomes: one set

from your mother and one set from your father. These chromosomes are composed of six billion individual DNA letters. In the English alphabet there are 26 letters: A through Z. In the alphabet of our genes there are four letters: A, C, G and T. Just like the letters in a book make words to tell a story, so do the letters in our genomes. Genomics is the study of the sequence of these letters in your DNA and how each string of letters passes information to help each cell in your body work properly.

In cancer cells, small changes in the genetic letters can change what a genomic word or sentence means. A changed letter can cause the cell to make a protein that doesn't allow the cell to work as it should. These proteins can make cells grow quickly and cause damage to neighboring cells. By studying the cancer genome, scientists can discover what letter changes are causing a cell to become a cancer. The genome of a cancer cell can also be used to tell one type of cancer from another

DNA Sequencing in Cancer Therapy

Cancer therapy is increasingly aimed at the fundamental abnormalities within cancer cells – the genes and proteins that normally keep cell division under control, but are damaged or faulty in tumor cells. To understand which genes are abnormal, where they're located within the genome, and how they affect cell growth, doctors and scientists use a procedure called DNA sequencing.

Sequencing can be defined as figuring out the order of the nucleotides in an organism's DNA.

Sequencing DNA involves determining the precise order of the four chemical building blocks, or "bases," that make up the DNA molecule. The bases – designated A, C, T, and G for the first letters of their chemical names – spell out the genetic code for each cell and each organism. *Human cells have about six billion bases in all, arranged in pairs along the entire length of DNA*. That figure is roughly equal to six gigabytes of data, or the number of letters in a book with three million pages.

Knowing the sequence of bases – also called nucleotides – helps scientists understand how different segments of DNA function. Some segments contain genes, which are blueprints for proteins produced by the cell. Other segments – more numerous and occupying vastly more space than genes – control whether genes are switched on or off. That is, they determine whether genes are actively being "read" by the cell to produce proteins, or are merely "on file" in the nucleus. Other regions of DNA have no known function and may be holdovers from evolutionary wrong turns and detours.

Next-generation sequencing (NGS), otherwise known as deep or massively parallel sequencing refers to the technological advances in sequence techniques that enable a huge number of sequence reads per run (Metzker, 2010).

BUGS (GENETIC CHANGES) and Debugging

Variants and Mutation

Bug in computer programming is an error or error code that hinders the proper function or inhibits the compilation and execution of a program. While debugging on the other hand is the process of locating and correcting errors in a computer program, Emuoyibofarhe, Sunday and Fasanya (2003). There are different types of errors (bugs) in computer programming, namely (i) syntax error (ii) semantic error (iii) logic error (iv) compile time error (v) run time error (vi) resource error and (vii) interfacing error.

DNA sequencing explores the fundamental abnormalities within cancer cells. Since DNA constitutes the "operating manual" of cells, errors in the arrangement of bases can cause a cell to malfunction in a variety of ways. Nowhere is that more evident than in cancer, the disease mostly associated with wayward genes. The kind of sequencing errors that crop up in cancer cells can take several forms. These include mutations, in which one base is incorrectly swapped for another; copy number alterations, in which a gene or section of gene is repeated over and over

or is missing altogether and translocations, in which a stretch of DNA becomes stranded in the wrong part of the genome.

Causes of Error or (dis)similarity in sequences

Mutation: a nucleotide at a certain location is replaced by *another* nucleotide (e.g.: ATA → AGA)
Mutagen: Component that changes genetic material, e.g. radiation, chemicals, temperature, pressure, etc

Insertion: at a certain location one new nucleotide is inserted in between two existing nucleotides (e.g.: AA → AGA)

Deletion: at a certain location one existing nucleotide is deleted (e.g.: ACTG → AC-G)
Indel: an insertion or a deletion
Locations for mutations
□ Gene, i.e. within a specific range on a chromosome
□ Chromosome, i.e. the structure of the chromosome is affected
□ Genome, i.e. the complete genome is affected, e.g. number of chromosomes
Mutation in the genome are often a root cause for diseases (Welcome Trust Sanger Institute, 2013), however, there are abundant of different mutations that can indicate the same superficial results e.g the same disease (Greenman, et al. 2007).
Not every genetic misspelling or abnormality results in cancer. Many have no discernible effect on a cell's function. But certain abnormalities are hallmarks of certain kinds of cancer. Doctors know, for example, that many non-small cell lung cancers (NSCLCs) have mutations in the gene *EGFR*. Targeted drugs are available that counter the effect of some of those mutations. By sequencing tumor cells from patients with NSCLC, therefore, doctors can often identify patients who are likely to benefit from those drugs.

Real-world Use Case: Oncology

Assuming Patient: Jane, 48 years, female, non-smoker, living in a smoke-free environment was diagnosed with Non-Small Cell Lung Cancer (NSCLC), stage IV with the following Markers: KRAS, EGFR, BRAF, NRAS, (ERBB2). The radiological image of the lungs is given in figure 12.

Figure 12. Radiological Image of the patient's lungs

Actors in Oncology

The major actors in the oncology process (Schapranow 2016) are :

i.   Patients: Patients suffering from an actual chronic disease e.g Cancer. Who want to recover in the most efficient way.

ii.   Clinicians: Clinicians have direct contact with patients in the course of treatment or therapy decisions to find optimal treatment decision for each individual patient.

iii.   Researchers: Researchers work in clinical and pharmaceutical environments to acquire new knowledge about therapies and pharmaceuticals.

iv.   Interdisciplinary Teams
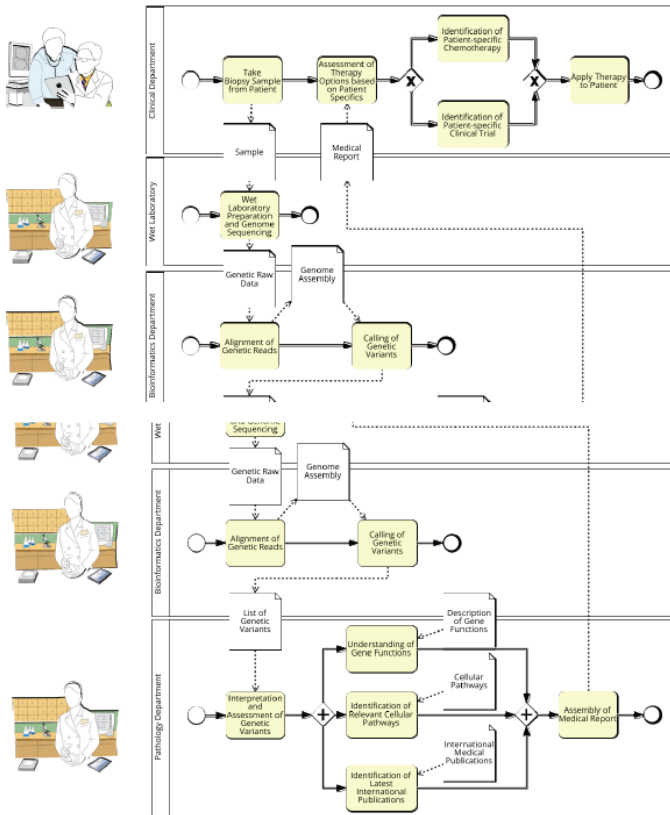
Figure 13 Simplified Clinical Oncology Process

Interdisciplinary Tumor Board

Cancers are often managed through discussion on multi-disciplinary cancer conferences where medical oncologists, surgical oncologists, radiation oncologists, pathologists, radiologists, and organ specific oncologists meet to find the best possible management for an individual patient considering the physical, social, psychological, emotional and financial status of the patient. It is very important for oncologists to be up to date with respect to the latest advancements in oncology. In response to this challenge, researchers at HPI and other research

institutes around the world are working towards developing an interdisciplinary tumor board. An example of such is shown in Figure 14.
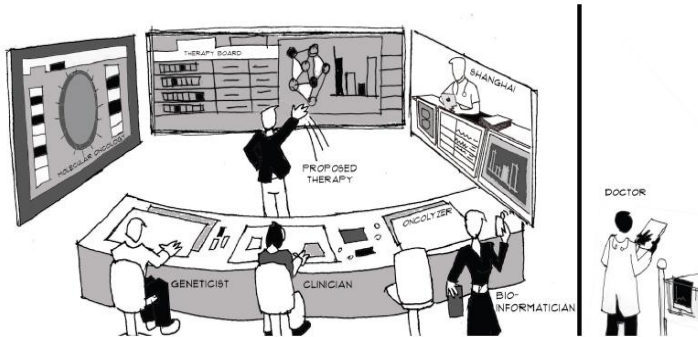
Figure 14. Interdisciplinary Interactive Real-Time Tumor Board (Schapranow, 2016)

This interdisciplinary tumor board is the novel idea and invention at the Hasso Plattner Institut, Potsdam which is currently under development for improved cancer care.

Use Case: Precision Oncology

Precision oncology involves identification of best treatment option for cancer patient and understanding of cell life cycle replication and management.
Lifecycle Management: Replication
The cell life cycle replication and management process involves the following stages:

Cell Cycle: Interphase

■ Interphase (I) consists of:
□ Gap 1 (G1), i.e. cell growth creating cell organelles

□ Gap 0 (G0) / Resting, i.e. cell stops division temporarily or forever
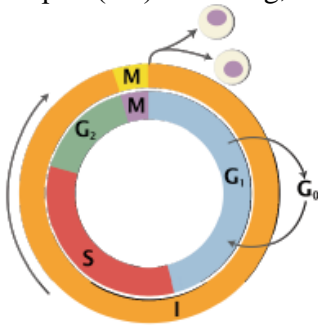
□ Synthesis (S) of DNA through replication of chromatids within the nucleolus
□ Gap 2 (G2), i.e. producing proteins for upcoming mitosis
■ Mitosis (M) is the process of cell division into two daughter cells

Mitosis: Prophase

Chromatin condenses into chromosomes
■ Nucleolus disappears
■ Spindle apparatus move to individual poles of the cell
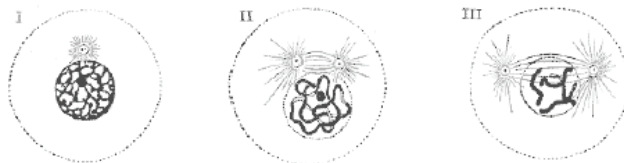
Henry Gray's Anatomy of the Human Body (Gray's Anatomy), 1918

Figure 15. Cell Replication Process (Mitosis)

Mitosis: Metaphase

Henry Gray's Anatomy of the Human Body (Gray's Anatomy), 1918

Figure 16. Mitosis: Metaphase

Mitosis: Telophase

Individual cell membranes form
■ Nucleoli reappear
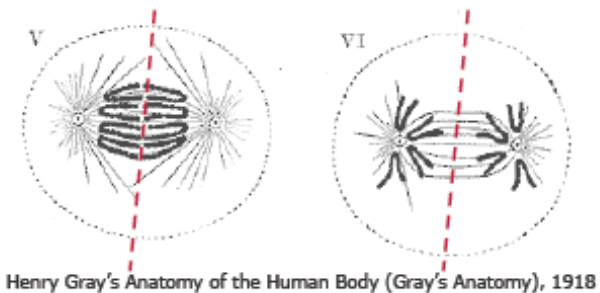■ Chromosomes unwind into more stable chromatin within nucleolus

Henry Gray's Anatomy of the Human Body (Gray's Anatomy), 1918

Figure 17. Mitosis:Telophase
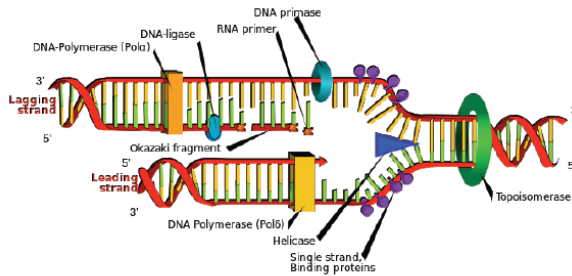
DNA Replication during Synthesis Phase

Figure 18. DNA Replication Process during Synthesis Phase

The three stages involved in the DNA replication process are:
1. **Initiation**

□ Topoisomerase unwinds/overwinds DNA
□ Helicase unzips DNA at specific origins
□ Primase is added to origin to bind polymerase

2. **Elongation**

□ DNA polymerase
– Extends DNA using a template strand in direction 5' ⟶ 3'
– Performs proofreading of replicated strand

3. **Termination:** Replication comes to an end

Mitosis results in two daughter cells carrying identical DNA
■ DNA polymerase performs proofreading of replicated strand

Compiling the Code: Transcription and Translation

The process of transforming DNA into proteins is divided in two stages: transcription, where RNA is produced using DNA templates and translation, where proteins are synthesized using RNA templates.

Transcription occurs inside the nucleus and itself can be divided in three stages: initiation, elongation and termination. And the translation process is also divided into three stages: Initiation, elongation and termination.

DNA SEQUENCING

Purpose: Transformation of analogous DNA into digital format (A/D converter)
■ **Input: Chunks of DNA**
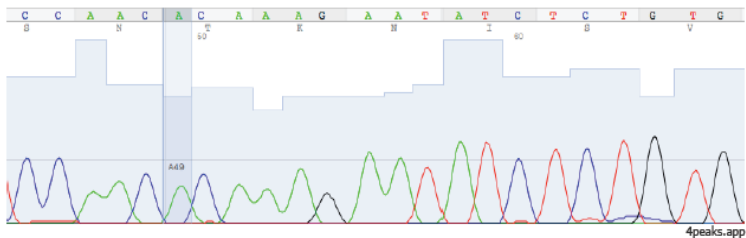■ **Output: DNA reads in digital form, e.g. in FASTQ format**

Figure 19. Analog/Digital DNA Converter

Output of Sequencing
File Formats: The genome sequenced digital output comes in one of the following formats.

FASTA: A FASTA format (FASTA, 2017) file contains text file information concerning nucleotides or peptide sequences. It consists of a description line followed by the correspondent sequence representation.

FASTQ: The FastQ format is quite similar to FASTA, it also contains text file information about nucleotides. However, it has an extra complementary sequence with the associated per base quality scores.

SAM and BAM: SAM stands for Sequence Alignment/Map. This format is tab-delimited and it is used to store sequence data aligned to a reference sequence (Li et al., 2009).

VCF: Variant Call Format (VCF) is a text file format used to store information about variants found at certain positions in a reference genome (Danecek, et al., 2011).

In this lecture, the illumine sequencing and the FASTQ file format is of interest. Figure 20 Shows FASTQ format as the output which is then used for further processing


Figure 20. FASTQ format

In the FASTQ output format one read is a quart-tuple comprising:
1. Sequence identifier /description
2. Raw sequence
3. Strand /direction
4. Quality values per sequenced base

Biological Pathways
A biological pathway is a sequence of interactions between molecules in a cell that result in a certain product of changes in a cell (Biological pathways, 2017). Those interactions aim to control the flow of information, energy and biochemical compounds in the cell and the ability of the cell to change its behavior in response to stimuli.

There are several types of biological pathways with the most commonly known ones' being metabolic, signaling and gene-regulation pathways. These are very important to understand the mechanisms that originate a disease as they provide clues on what genes, proteins and other molecules are involved in the pathway. Comparing two pathways, from a healthy person and from a person with a disease, researchers can find what triggered such disease. Figure 21. (Kyoto Encyclopedia of Genes and Genomes) is a biological pathway encyclopedia developed in Japan for interpretation of annotations.
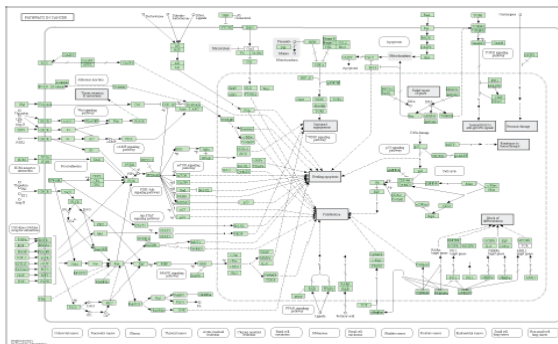
Interpretation of Annotations: BRAF Gene
Figure 21. Kegg (Kyoto Encyclopedia of Genes and Genomes)

DNA Sequencing machines. The human genome project (HGP) and research in next generation sequencing has resulted in the development of different sequencing machines and technologies. Figure 22(a) – (f) are examples of some of the sequencing machines.
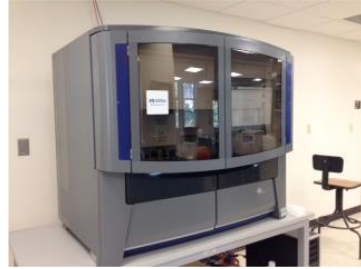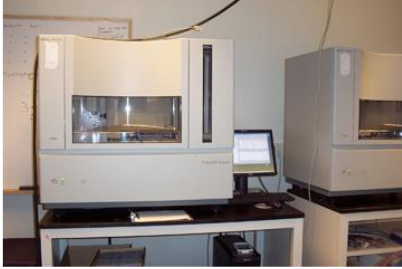
Figure 22 a. 2002: Sanger sequencing
b. 2006: Sequencing by Oligonucleotide Ligation and Detection (SOLiD)

c. 2005-2013 Roche-454 Sequencing
d. 2006: Solexa Illumina Sequencing

https://nanoporetech.com/products

e. Oxford Nanopore
f. 2013: PacBio

ABI Sequencing (1st gen)	**ABI Sequencing (2nd gen)**
2002: Sanger sequencing provides very high accuracy	2006: Sequencing by Oligonucleotide Ligation and Detection (SOLiD)
■ Accuracy: > 99.99%	■ Accuracy: > 99.99%
■ Throughput: 100 kbp / run (3hrs)	■ Throughput: 60 Gbp / run (5-10 days)
■ Read length: 0.6-1 kbp	■ Read length: 35-100 bp
■ Issues: time-intensive	■ Issues: time-intensive

Roche-454 Sequencing
2005-2013: Roche-454 Life Sciences launched first NGS device using Pyrosequencing / sequencing by synthesis approach
■ Accuracy: >99.9%
■ Throughput: 400-600 Mbp / run
■ Read length: 200-400 bp (2009) later up to 700 bp
■ Issues: Homopolymer repeat regions

Illumina Sequencing
2006: Solexa introduced Genome Analyzer
■ 2007: Illumina acquired Solexa
■ Accuracy: >99.9%
■ Throughput:
□ 2006: 1 Gbp / run (2006),
□ 2016: up to 1 Tbp / run (6 days)
■ Read length: 200-600 bp
■ Issues: cheap but less accurate

Oxford Nanopore
■ Vision: Very cheap and mobile long-read alternative
■ Accuracy: up to 99%
■ Throughput: approx. 10 Gbp / run (<48hrs)
■ Read length: 230-300 kbp
■ Issues: still early phase and behind expectations

Pacific Biosciences
2013: PacBio introduces long-read sequencer supporting innovative sequence assembling
■ Accuracy: >99% (at high coverage)
■ Throughput: 0.5-1 Gbp/run
■ Read length: up to 60 kbp (à DeNovo Alignment)
■ Issues: still comparable slow and lacks precision

Figure 23. Prof. Emuoyibofarhe observing a DNA sequencing Machine in the laboratory at the Department of Bioanalytics and Biosensorics at, Fraunhofer-Institut for Cell Therapy and Immunology Gohm, Potsdam, Germany.

Illumina Sequencing Process

1. Preparation

■ Double-stranded DNA is split into chunks of 200-600 bp length

■ Adaptors attached to DNA chunks

■ Separation of double-strand into two strands using sodium hydroxide

■ DNA chunks are washed across flowcell, i.e. DNA not binding to primers is removed

■ Polymerase Chain Reaction (PCR) is used for amplification of DNA chunks

■ Nucleotide bases and DNA polymerase are added to build bridges b/w primers

■ Double strand is split-up using heat à dense clusters of identical DNA sequences

■ Primers with fluorescently terminators are added, e.g. A, C, G, T + stop codon

■ Primers attach to DNA chunks and DNA polymerase attaches to terminator

■ Laser passes flowcell, i.e. each terminator type emits unique light

■ Terminators are removed and new terminators are added to next DNA position

Interpretation of Annotations: BRAF Gene dbSNP

Figure 24 Interpretation of Annotations: BRAF Gene dbSNP

DEEP NUERAL NETWORKS FOR GENOME INFORMATICS AND GENOME DATA ANALYSIS

Artificial neural networks are now widely used to solve various problems in genome informatics and molecular sequence analysis. With its many features and excellent capabilities for pattern recognition, generalization and classification, artificial neural network technology is well suited for genome informatics studies. Many important problems in genome informatics have been successfully addressed with artificial neural networks, and a vast literature has developed within the last two decades.

Deep learning are next generation artificial intelligence algorithms predicated on the idea of learning from hierarchical representations with a single algorithm or perhaps with a few hybrid algorithms. Examples of Deep Neural Networks include Convolutional neural networks (CNNs), Convolutional neural networks (CNNs) are one of the most successful deep learning models for image processing owing to their outstanding capacity to analyze spatial information (Krizhevsky et al., 2012), Zeng et al. (2016). Emuoyibofarhe and Ajisafe (2018) developed a Deep Convolutional Neural Networks for Early Skin Cancer Detection.

Recurrent Neural Networks (RNN) shows impressive results on challenging sequential prediction problems such as natural language processing, language translation, speech recognition. RNNs outperform CNNs and other deep neural networks on sequential data. Genomics data are typically sequential and often considered languages of biological nature. Recurrent models are thus excellent candidates for genomic data analysis, Cao et al.(2017). LSTM-based Neural Machine, Sønderby et al.. (2015) devised a convolutional LSTM networks to predict protein sub cellular localization from protein sequences, DanQ (Quang and Xie, 2016) is a hybrid convolutional and recurrent deep neural network for predicting the function of non-coding DNA.

Deep learning approaches for gene expression prediction have outperformed other existing algorithms. For example, Chen et al. (2016) presented a three-layer feed-forward neural network for gene expressions prediction of selected landmark genes achieved better performance than linear regression. Emuoyibofarhe and Raji (2018), Development of a Sequence to Sequence Model for Coronary Artery Disease using Genome Wide Association Study(GWAS).

The intersection of deep learning methods and genomic research may lead to a profound understanding of genomics that will benefit multiple fields including precision medicine (Leung et al., 2016), pharmacy (*i.e.* drug design) and even agriculture, *etc*. Take medicine for example, medical research and its applications such as gene therapies, molecular diagnostics and personalized medicine could be revolutionized by tailoring high-performance computing methods to analyzing available genomic datasets. Also, the process of developing new drugs takes a long period and is usually very costly.

All these benefits indicate the necessity of utilizing powerful and specially designed deep learning methods to foster the development of the genomics industry.
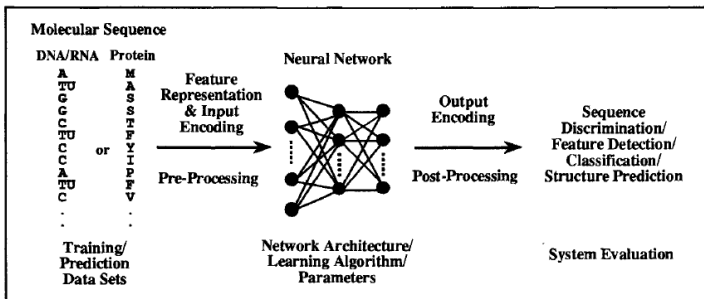
 Figure 25. Deep Neural Networks Applications for Genome Informatics

Deep Learning frameworks

Some commonly used deep learning frameworks are listed below.

Theano

Theano (http://deeplearning.net/software/theano/) is a Python library for deep learning. It was developed at the University of Montreal for research and development into state-of-the art deep learning algorithms. It handles operations on multidimensional arrays and has several optimizations including the use of GPU for computations.

TensorFlow

TensorFlow (https://www.tensorflow.org/) is an open source machine learning library developed by researchers and engineers at Google that uses data flow graphs for numerical computations. Mathematical operations are represented by nodes, while the graph edges represent the multidimensional data arrays, as tensors, that flow between them. It is cross-platform and has a C++ and Python interface. It also supports distributed computations in multiple CPUs and GPUs.

Caffe

Caffe (http://caffe.berkeleyvision.org/) is a Python deep learning library developed at Berkeley Vision and Learning Center. Its primary focus is convolutional neural networks and one of its benefits is the number of pre-trained networks that can be downloaded and used right away. It supports C++, Python and MATLAB interfaces.

DeepLearning4j

DeepLearning4j (https://deeplearning4j.org/) is a distributed deep learning framework developed in Java (and JVM languages) that can

integrate with Hadoop and Spark using multiple CPUs or GPUs. It supports multidimensional arrays by using ND4J(http://nd4j.org/).

In The Era of Artificial Intelligence, GPUs are the new CPUs

Why is the GPU getting so much attention now? The answer lies in the rise of deep learning, an advanced machine learning technique that is heavily used in AI and Cognitive Computing. Deep learning powers many scenarios including autonomous cars, cancer diagnosis, computer vision, speech recognition and many other intelligent use cases.

Like most of the ML algorithms, deep learning relies on sophisticated mathematical and statistical computations. Artificial Neural Networks (ANN), Convolutional Neural Networks (CNN) and Recurrent Neural Networks (RNN) are some of the modern implementations of deep learning. These neural nets emulate human brain with close resemblance to neuroscience. Each type of neural net is aligned with a complex use case like classification, clustering and prediction. For example, image recognition and face recognition use CNN while Natural Language Processing (NLP) relies on RNN. ANN, the simpler ones of all the neural networks is often used for predictions involving numerical data.

Modern GPUs provide superior processing power, memory bandwidth and efficiency over their CPU counterparts. They are 50–100 times faster in tasks that require multiple parallel processes such as machine learning and big data analysis.

The CPU (central processing unit) has often been called the brains of the PC. But increasingly, that brain is being enhanced by another part of the PC – the GPU (graphics processing unit), which is its soul.
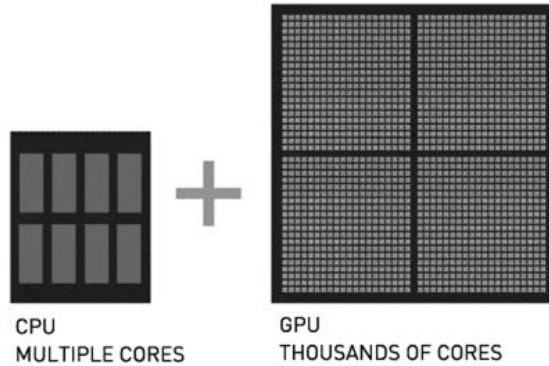
Figure 26. CPU (Central processing unit) vs the GPU (Graphics Processing Unit)

E-HEALTH AND TELEMEDICINE

My first encounter and subsequent research interest in e-health and telemedicine research started in 2006 with my involvement in the development of a framework for rural e-health readiness assessment of selected healthcare facilities in the Kwazulu Nathal region of South Africa (Ojo, Olugbara, Emuoyibofarhe, Adigun, Xulu and kabanda, 2006) during my post-doctoral fellowship at the Huawei/Telkom Center of Excellence for mobile e-services at the University of Zululand, Republic of South Africa. Subsequently, we developed an e-Health Management, Partnership and collaboration model for developing countries (Adigun, Emuoyibofarhe, Ojo and Dehinbo, 2006); which was presented at the 1st All Africa Technology Diffusion Conference, June 2006 Boksburg, Johannesburg, South Africa.

In 2007, when I returned back to Nigeria, I joined the society of telemedicine and e-health in Nigeria and continued to conduct research in e-health, mobile health (M-health), Telemedicine for sustainable quality rural e-health care service delivery.

In the section following, I will present my research activities in the e-health and telemedicine research niche over the past twelve years,

towards providing and delivering affordable and sustainable quality healthcare services in the developing country context.

What is E-Health?

E-health/Telemedicine is an emerging field in the intersection of medical informatics, public health and business, referring to health services and information delivered or enhanced through the Internet and related technologies.

E-Health and Telemedicine which literally means the use of information technology to exchange health information and provide healthcare services over a distance, has been shown by several studies in the last decade to have potential benefits and tremendous capabilities to bridge the gap of access to quality healthcare and reduce cost. E-health can also be described as facilitating healthcare service delivery through ICT or any electronic exchange of health related data through an electronic connectivity for improving efficiency and effectiveness of healthcare delivery or the use of ICTs in the health sector for clinical, educational, and administrative purposes, both at the local site and a distance (Mitchell 2000).

The role of ICT can no longer be ignored within the healthcare industry. In fact, for the healthcare industry to maintain and improve both clinical and business operations, it has to depend on Information Technology (IT) (Bernstein, Mccreless and Cote, 2007).

Prominent in the millennium development declaration or goals is the eradication of extreme poverty and, reduced mortality, improved health care systems and elimination of hunger (The Millennium Development Goals Report, United Nations, 2013).

Most developing countries are still far from achieving these goals because of neglect of the pivotal role of ICT in the pursuance of the MDG's. The cost effective provision of quality healthcare is a prominent social and governmental issue throughout the world. Reducing healthcare cost and physical movement, sharing of healthcare resources and improving communication while still maintaining universal high quality healthcare remains a serious challenge.

The advent of the internet, mobile wireless communication and other related enabling technologies serves as a platform for various information and communication technologies (ICT) service deliveries which have now become the major technological drivers for national development as is been witnessed in business and commerce (e-business, e-commerce), banking (e-banking, m-banking). However, one major area which has not enjoyed the significant application of ICT like the e-commerce and e-business in most developing nations is in the application of ICT to healthcare service delivery.

Telemedicine, means "medicine at a distance", encompasses all medical activities: diagnosis, treatment, prevention, education, and research (Craig, 1999). It is further defined as a way of distributing medical expertise and services to medically underserviced areas such as remote and rural areas using ICT as a communication platform (Malindi, 2011).

Different Areas of Telemedicine

• Telemedicine	Telemanagement
• Telesurgery	Teleophthamology
• Telementoring	Clinical Telemedic
• Telenursing	Teleneonatology
• Telelearning	Tele-Sonography
• Teleconsultation	Telediagnostics
• Telecare	e-Prescription
• Teleradiology	e-Pharmacy
• Tele or e-Cardiology	

Telemedicine can provide learning opportunities to the doctors and nurses in the rural areas and also provide a platform for second opinions among professionals. Additionally, it can save patients and physician's time and money as they will not have to travel far distances to provide or receive hospital services. Moreover, it can allow underprivileged rural hospitals to share equipment and human resources within well-equipped hospitals (Maheu, Whitten, and Allen, 2001)), (Malindi , 2011).

The Problem and Current state of Affairs

The healthcare sector in Nigeria and most developing countries are not only widely distributed and fragmented, but are paper based and exhibits a high degree of heterogeneity with strong local autonomy (Grimson *et al.,* 2011). Considering the changing demographics (particularly age structures, life styles and changing epidemiological profiles), demand for greater access to patient oriented quality care and the acute shortage of health care workforce in the country, the adoption of and investment in e-health/Telemedicine is a way forward.

Statistical Information Supporting Sub Saharan Africa's Need for Telemedicine (United Nations Population Division, 2004)

Population Data (Millions)

	1950	2000	2050
World		2,520	6,086	9,076
Africa		224	812	1.937
Asia		1,396	3,676	5,217
Europe	547	728	653	
Latin America / Caribbean		167	523	783
Northern America		172	315	438
Oceania		13	31	48

Source: United Nations Population Division, World Population Prospects 2004 Revision Group: a all types.

Physicians / 100,000 people

Italy	606	South Africa	35
USA	549	Nigeria	27
Canada	209	Zimbabwe	7
Egypt	211	Uganda	5
China	164	Malawi	1

The statistics shows that 31 African Countries have fewer than 10 Physicians per 100,000 people.

In order to address the above stated e-health challenges, I formed the Mobile and e-computing research group in 2007 and engaged various postgraduate research students to investigate various African contextual e-health challenges. To achieve our research objectives and goal, various research methodologies and tools were adopted including case study approach, Component Based Development, Web Service Technologies, Mobile and Wireless computing technologies, service oriented computing approach for developing software solutions, frameworks, models, prototypes and artifacts which address the African contextual needs in the Telemedicine, e-Health and m-Health domain.

Selected health care facilities and ICT infrastructures within Ogbomoso were identified for experimentation (see Figure 27). The goal of this work is to network selected hospitals in Ogbomoso in order to facilitate improved healthcare service delivery through resource aggregation and seamless exchange of electronic health records in cases of referrals and ambulatory services during emergencies. An Evolving Reference Architecture called LAUTECH e-Health Care Management System (LAUe-HCMS) was developed (Figure 28).

Given the enormous capital/funding requirement for the successful implementation of the e-health/Telemedicine project, collaboration and

funding partners were sought through a public-private-academia model (Figure 29). The mobile and e-computing research group entered into partnership with both local, national and foreign institutions such as Omatek Computers, Society for telemedicine and e-health in Nigeria (SFTeHIN), NEPAD, W.H.O, NARSDA, LAUTECH Teaching Hospital, UCH Telemedince Project, MTN, University of Zululand, Tshwane University of Technology, Pretoria, HPI Research School (ICT4D), University of Cape Town, Hasso Plattner Institute, University of Potsdam, Germany and Southern University, Baton Rouge USA.

Some of our research outputs over the years include but not limited to the under listed: Oladosu,., Emuoyibofarhe, Ojo and Adigun, (2009) developed a framework for Service-Oriented Mobile E-Health Service Discovery Infrastructure for Rural/Suburban Healthcare; Oladosu, Emuoyibofarhe,, Akomolafe, and Adewusi, (2010) further developed a Web-enabled Patient Case-note application. Emuoyibofarhe (2012) conducted a E-Healthcare/Telemedicine Readiness Assessment of Selected hospital in six (6) States in Western Nigeria. In this work Oyo, Osun, Ogun, Ondo, Lagos and Ekiti states in western Nigeria were chosen as the pilot study area, considering some critical factors of e-Health readiness such as need-change readiness, engagement readiness and structural readiness.

Leveraging on the abundant availability of mobile phone, and the need to bridge the language barrier between unlearned patients in rural communities and the doctors, Oladosu and Emuoyibofarhe (2012) developed a Yoruba—English Language Translator for Doctor—Patient Mobile Chat Application. In 2015, Lala, Emuoyibofarhe and Oladosu developed a Requirements Engineering Framework for Interoperable Distributed Rural E-Healthcare Services.
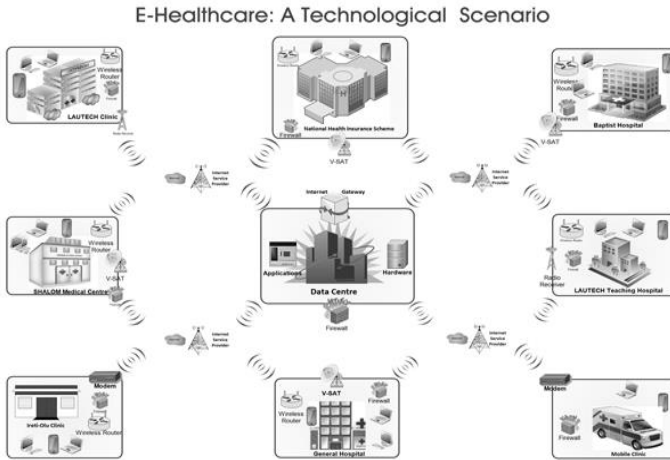
Figure. 27. A Proposed Network of Selected Hospitals and ICT Infrastructures in Ogbomoso for e-health Implementation

Wireless/Mobile tools in Developing Countries (Africa)

Nigeria is Africa's largest mobile market with more than 125 million subscribers and a market penetration of around 75% in early 2014. Given that Personal Computers (PC) are not affordable and available to most Nigerians, mobile solution/technology is the way out, given the abundance of mobile phones in Nigeria and its penetration even to rural communities. This work concentrates on the development of mobile health (m-health) solutions and applications. The chances of mobile wireless technology are bright in rural e-healthcare services provisioning where other technologies have failed.

The following technologies among others are employed in this project:
• Wireless technologies use: GSM/GPRS/3G, WiFi, WiMAX, WLL (Fixed or Mobile CDMA), Broadband wireless, Satellite, VSAT (Mobility vs Universal Access)
• Mobile devices: PDAs, Smartphone, Cellular phones, Tablet PCs, Laptops, smart cards, memory sticks, USB keys, sensors.

Figure 28 is the LAUTECH e-HealthCare Management system evolving reference architecture (LAUe-HCMS), the operational model of our research group.
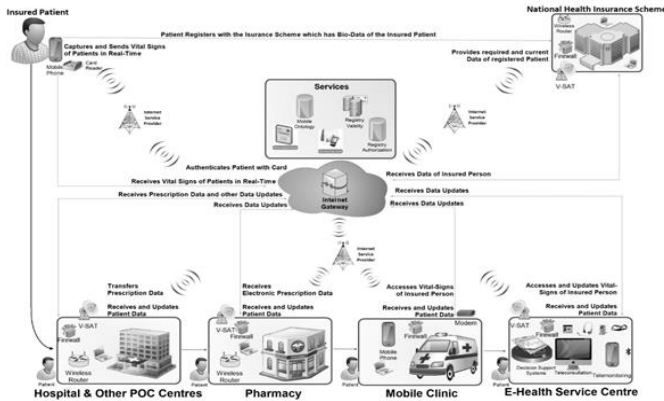
Figure 28. LAUe-HCMS Evolving Reference Architecture

Figure 29. E-Health partnership and Collaboration Model

National E-Healthcare Service Framework Design and Implementation

We hereby present our model of a national e-health framework which is workable for developing countries with little or no modification. A typical e-Healthcare service infrastructure includes the government, private and public organizations, equipment manufacturers, application developers, service providers and individuals. These providers together provide policies, connectivity, applications, systems, devices, insurance and skilled manpower required to have a functional e-Health infrastructure in the nation. These provisions serve direct and support infrastructure required by users in the e-Health community.

A typical m-health ecosystem comprises the following stakeholders:

i.   **Patients:** who require medical treatment

ii.   **Providers:** e.g. doctors, nurses, hospitals and nursing homes, which provide medical assistance and treatments.

iii. **Governmental agencies:** ensure the quality of the national health systems.

iv.   **Cost bearers:** e.g. insurance companies, which compensate the medical treatment costs.

v.   Other recognized stakeholders are independent regulatory bodies, application developers who develop e-Health applications and equipment manufacturers (EMs) who manufacture e-Health devices.
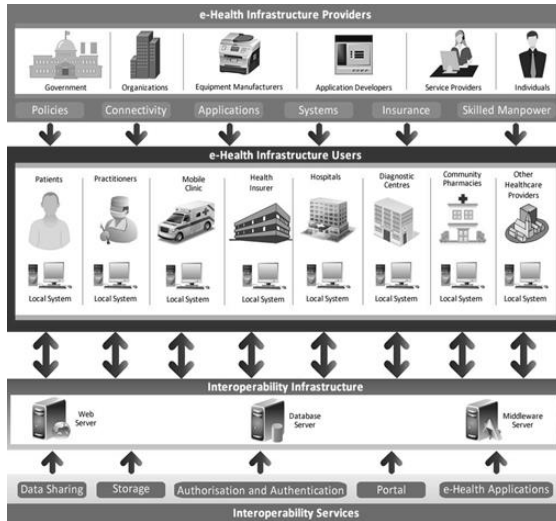
Figure 30. National Implementation and Operation of e-healthcare services

The e-Health infrastructure users include: Patients, Medical Practitioners, Mobile Clinics, Hospitals, Pharmacies, Diagnostic Centers and other Healthcare Providers. Each of these users has their local applications, systems and devices which are different from one another, though sometimes compatible with one another.

The core infrastructure is a server infrastructure which can be provided by a private organization or governmental organization such as NHIS (National Health Insurance Scheme). The e-Health users are connected to the server via an internet network. The server consists of the middleware services. The server serves as an enterprise bus to which users with different systems from different locations are connected to access the services.

Medical tele-management for chronic disease patient management

Medical tele-management is the combination of tele-monitoring and tele-consultation services for a more robust healthcare service package. The synergy of both services offers the possibility to continuously monitor out-patients with chronic conditions for proper post-treatment management to avoid relapse and a deteriorating health condition and at the same time provide a platform where health workers/professionals in rural settlements can consult or interact with their counterparts in urban areas.

Managing patients with chronic diseases in resource constrained developing countries is challenging, cost intensive and stressful for both the patient and caregiver. For out-patient with chronic disease, it will require repeated visits to the hospital over a long period of time. This can be very stressful and inconvenient for the patient. Tele-monitoring is a technology that allows the care giver or doctor to monitor vital reading of the patient from wearable biomedical sensors at a distance. Teleconsultation allows patient-Doctor audio/video consultation similar to face-to-face consultation. Amusan and Emuoyibofarhe (2018) developed a medical tele-management system for post-discharged patients with chronic diseases in resource constrained setting. Figure 31, is the Tele-management System Architecture. Emuoyibofarhe, Omotosho, Ajala and Adejumo (2018) implemented a health monitoring system for post-stroke management.
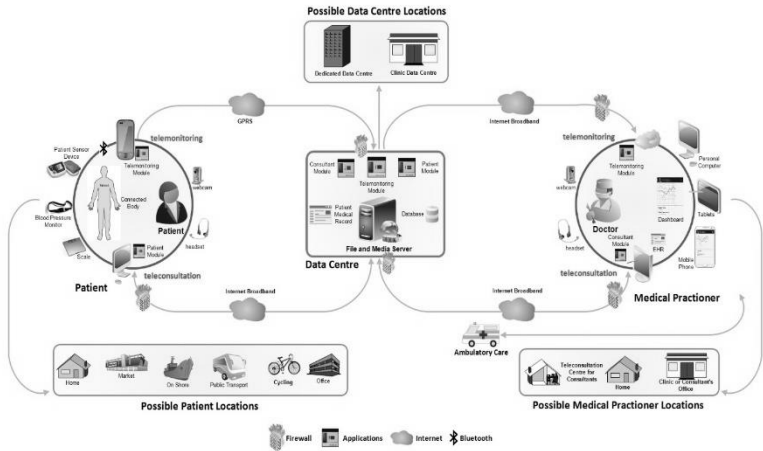
Figure 31. Tele-management System Architecture

BENEFITS OF E-HEALTH/TELEMEDICINE

- Opening up huge business opportunities by Translating the results of e-Health research to marketable and useful products
- Creating a reliable, timely, high quality and affordable health care services.
- Provisioning of cheap medical and pharmaceutical information.
- Easy Processing and analysis of patient images and data
- Alert, monitor and control the spread of communicable diseases.
- Encourage the adoption of ICT to improve and extend health care and health information systems.
- Medical and humanitarian assistance in disasters and emergencies.
- Making e-Health accessible to all citizens (equity).
- Reduce the cost of care and enhance e-prescription.
- Encourage the adoption of the health insurance scheme in developing Africa countries, thus opening up business chances for insurance firms in Africa.

Society for Telemedicine and eHealth in Nigeria (SFTeHIN)

The society for telemedicine and e-health in Nigeria is the first national eHealth Society in Nigeria and in Africa and the first to become a national member of the International Society for Telemedicine and eHealth with headquarters in Luxemburg.

I served as 2nd National Vice President, Society for Telemedicine and e-Health in Nigeria between 2011-2015 and later in 2016 when the Society was appointed as a member of the National Technical Committee on eHealth in August 2016 by the Honorable of Minister of Health. I was appointed to serve as a member of the strategic advisory board of the society for telemedicine and e-health in Nigeria. Listed below are some of the roles and Impact of the Society for Telemedicine and eHealth in Nigeria (SFTeHIN) on the Development of eHealth in Nigeria of which I have been and remain an active member and executive.
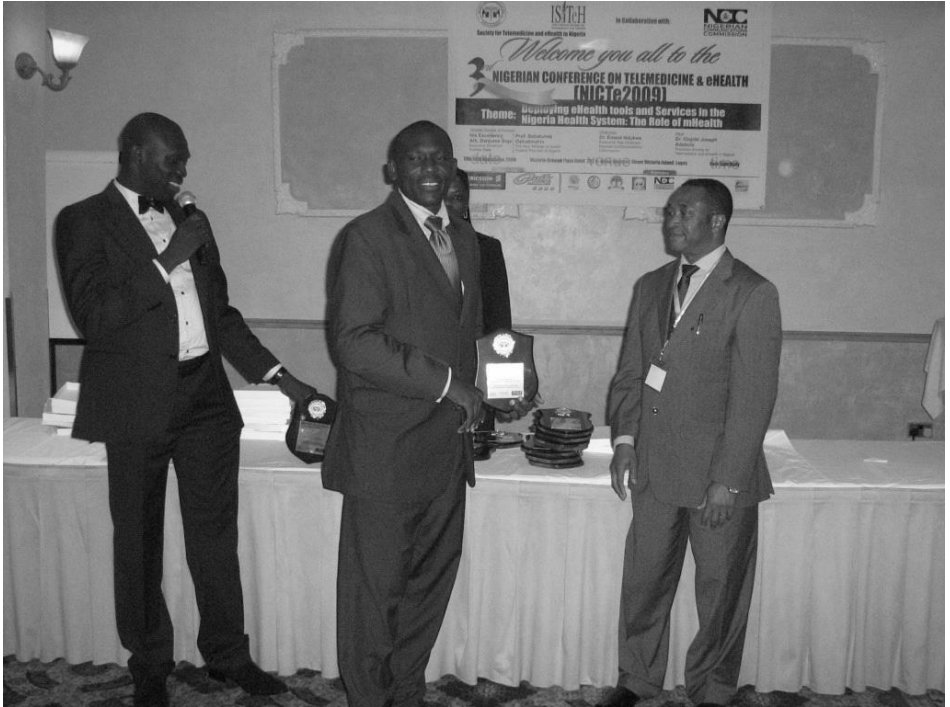
Figure 32. Receiving an Institutional Based E-Health Advocacy Award on Behalf of LAUTECH

Impact of the Society for Telemedicine and eHealth in Nigeria on the Development of eHealth in Nigeria

    i.   **General**
        a. First national eHealth Society in Africa to become national member of the International Society for Telemedicine and eHealth May 2005
        b. Organized in collaboration with World Health Organization a Pan African Conference on Telemedicine and eHealth September 2006

    c. Organizes an annual Scientific and educational conference on Telemedicine and eHealth since 2007 till date which serves as a capacity building event for the health and ICT workforce in Nigeria. It is known as Nigerian Conference on Telemedicine and eHealth (NICTe). This year is the 12th Edition.

    d. Conducted several workshops and seminars with several stakeholders as a capacity building event for the health and ICT workforce in Nigeria

1. Served in several national committees on Health and Telemedicine and eHealth

    a. Paid a courtesy visit to President Olusegun Obasanjo October 2006 which led to the creation of national telemedicine programme at the Federal Ministry of health.

    b. A national eHealth Committee was set up during the visit to President Olusegun Obasanjo but not inaugurated by the Federal Ministry of Health

    c. West Africa Health Ministers Ministerial Dialogue Planning December 2009

    d. Participated in the National Technical committee on Telemedicine set up by NARSDA to develop a national road map for Telemedicine in Nigeria May 2010

    e. Participated as Head of programme in the planning of the first national health ICT conference organized by Federal Ministry of Health December 2010

    f. Hosted the 17th annual Conference of the International Society for Telemedicine and eHealth in Abuja Nigeria November 2012

    g. National Technical Working Group on National Health Act, Federal Ministry of Health Nigeria, (2015)

    h. Member, National Technical Committee on eHealth, Federal Ministry of Health and Communications (2016)

    i.   Member, National Technical Working Group on Data System Technology. Federal Ministry of Health and Communications (2016)

    j.   Member National Human Resources for Health National Observatory (2017)

    k.   Proposed the establishment of National Technical Working Group on eHealth Policy, Legislation and Compliance. Currently a member. Federal Ministry of Health and Communications (2017)

ii.   Specific

1. Member, Technical Committee on the development of curriculum for Post-graduate Diploma and masters in Health Information Management (2018)
2. Contributed to the development of the national eHealth Strategy (2016)

CONCLUSION (UNTO WHOM MUCH IS GIVEN)

Mr. Vice Chancellor Sir, the three main functions of an academic in the university are: teaching, research and community service. It is commonly said that "unto whom much is given much is expected". Lautech has given me much and in return, I have endeavored over the last two decades to teach, conduct research locally and internationally and engage in community service to the benefits of mankind and the upliftment of the flag of LAUTECH. I have taught many generations of students both at the undergraduate and postgraduate levels. Four (4) of the students I taught are now full professors today in three different universities in Nigeria. While students I supervised at the Ph.D level some are currently Readers (Assoc. Profs), Senior Lecturers and so on. Permit me to mention the Ph.D students I have supervised in LAUTECH.

Table 2. PhD students successfully supervised by me

PhD students successfully supervised			
S/N	Name	Current Institution	Year of PhD
1.	Dr. Oladosu J.B.	LAUTECH	2011
2.	Dr. Araromi O.D.	LAUTECH	2011
3.	Dr. Mrs. Ajala A.F	LAUTECH	2012
4.	Dr. Akomolafe P.O.	University of Ibadan	2014
5.	Dr. Lala O.	BOWEN	2015
6.	Dr. Oyetunji Moses	Mountain Top Univ	2015
7.	Dr. Omotoso Adebayo	Landmark Univ	2016
8.	Dr. Awokola J. A.	Private Practice	2016
9.	Dr. Alamu F.O.	University of Lagos	2016
10.	Dr. Mrs. Amusan E.A.	LAUTECH	2017

I have been involved in both collaborative and individual research activities locally and internationally. My international research collaborations resulted into MoUs of academic and research cooperation with three different universities in three different countries of which staff and students of LAUTECH and others have benefitted and continue to benefit from. Namely the Hasso Plattner Institut, University of Potsdam, Potsdam Germany, Huawei-Telkom Center of Excellence of mobile e-services, University of Zululand, South Africa, and The International Center for Information Technology & Development, Southern University, Baton Rouge, Louisiana, USA. The following staff and Research students of mine have benefitted one form of grant or the other or fully paid trip and/or very attractive monthly stipend for various

kind of visit to either Germany, S.A or USA ranging from postdoc fellowships to short research visits.

Table 3. HPI Research Collaboration Beneficiaries'

Staff and My Research Students that I facilitated to visit Hasso Plattner Institut, Germany				
S/N	Name	Institution	Visit Type	Year
1.	Dr. O T. Arulogun	LAUTECH	Postdoc Fellowship	2012
2.	Dr. Mrs. Amusan E A	LAUTECH	Research Visit	2012
3.	Dr. Mrs. Emuoyibofarhe O. N	BOWEN	Postdoc Fellowship	2015
4.	Dr. Falohun Adeleye.	LAUTECH	Short Post Doc	2016
5.	Dr. Akomolafe P. O	Univ of Ibadan	Research Visit	2016
6.	Dr. Mrs. Adedeji O. T	LAUTECH	Research Visit	2014
7.	Dr. Oladosu J. B	LAUTECH	Research Visit	2017
8.	Dr. Awokola J. A	LAUTECH	Research Visit	2015
9.	Prof. Reju S. A	Univ. of Namibia	Research Visit	2017
10.	Prof. Adigun M. O	South Africa	Research Visit	2017
11.	Dr. Mrs. Baale A. A	LAUTECH	Research Visit	2018
12	Dr. Oluwaloseyi Jolababs	Topio	Research Visit	2016

13	Dr. Omotoso Adebayo	Landmark Univ.	Postdoc fellowship	2019

Table 4. UniZul Research Collaboration Beneficiaries'

Staff and My Research Students that I facilitated to visit Huawei Center of Excellence, University of Zululand, South Africa				
S/N	Name	Institution	Visit Type	Year
1.	Dr. Oladosu J. B	LAUTECH	Post-doctoral Fellowship	2012 to 2013
2.	Dr. Waziri O. V	FUT Mx	Post-doctoral Fellowship	2007
3.	Dr. Fagbola Tayo	LAUTECH/ FUOYE	Post-doctoral Fellowship	2018
4.	2 Undergrad Studs	LAUTECH	Full MSc scholarship	

Table 5. Southern University Research Collaboration Beneficiaries'

Staff and Researchers that I facilitated to visit Southern University, Baton Rouge , Loiusiana USA				
S/N	Name	Institution	Visit Type	Year
1.	Prof. Adewoye J. A	LAUTECH	Six Month Research Visit	2015
2.	Dr. O.T Arulogun	LAUTECH	Three Months Research Visit yet to visit	2018

Other research collaboration efforts which I am hoping will come to the lime light very soon to benefit others include HPI Research school (ICT4D) project at the University of Cape Town, South Africa and the Durban University Technology Durban, South Africa. These institutions I visited last year 2017 July.

I served on several committees of the Department, faculty and university. I served as the deputy dean of the faculty of engineering and technology between year 2009-2012 under the deanship of Prof. Adegbola and Prof. Olajide respectively. During this period, I invited the then Director General of NITDA, Prof. Cleopas Angaye to the faculty who donated twenty (20) computer systems, Computer Desks and chairs, a VSAT, inverter, UPS, Printer, photocopier and other items worth millions of Naira to the LAUTECH FET CAD Center.

During the short period that I served as acting director Lautech ICT, I gave direction and leadership for the development, implementation and deployment of the LAUTECH CBT facility still in use till date. Thanks to the vice chancellor and management for believing in my ability to deliver and for all the support rendered. Thanks also to the indefatigable LICT staff. I also implemented the e-payslip still in use today and the Lautech smart I.D card whose graphics was designed by Prof. ROM Kalilu, but coded and implemented by ICT under my leadership.

Mr. Vice Chancellor sir, I have contributed to both knowledge and human capacity development. I have served as external examiner to the departments of Computer Science in the following Universities for either undergraduate or postgraduate programmes or both in some cases;

    i.   University of Ibadan (Both Undergrad and post grad) 2013 - 2016, 2018

    ii.   University of Zululand South Africa, Postgrad   2012 - 2017

    iii.   University of Ilorin Postgrad 2018

    iv.   Kwara State University KWASU Malete Undergrad 2013 -2015

    v.   OAU Ile Ife Postgrad 2012-2018

    vi.   Federal Univ. of Tech Minna (Both Undergrad and post grad) 2011 – 2016

    vii.   Federal Univ. of Petroleum Resource Effurun Undergrad 2014 – 2016

    viii.   Ondo State Univ. of Tech Okitipupa   Undergrad   2018

I have also served as assessor for assessments for the professorial cadre for candidates in Covenant University, Ota, University of Ilorin and Bayero University Kano. I have also served as a team member on NUC panel for undergraduate accreditation and post graduate verification exercise to about a dozen universities across the nation.

I am a fellow of the Nigeria Computer Society and the 2nd Vice President of the Society for Telemedicine and e-Health in Nigeria between 2011-2013; I headed the Mobile and e-computing research group on mobile e-services and Telemedicine. I chaired and successfully hosted eight (8) series of the international conference on mobile e-services.

I mentored and took team highrise (Lautech student that represented Nigeria) to the Microsoft Imagine cup world finals in 2014 to Seattle USA and Team Highrise2 to second runner up in Nigeria 2018.

As a full professor in 2012, I was the first substantive Head ever of the Computer Science and Engineering Dept, I headed the committee that developed the proposal and road map of the LSEI and served as the pioneer coordinator of the Lautech Software Engineering Institute.

ACKNOWLEDGEMENTS/APPRECIATIONS

Mr. Vice Chancellor Sir, It's been a long journey of over forty (40) years, and obviously it couldn't have been my singular effort that has brought me to this point in life. A number of people have sacrificed and contributed in one way or the other to make this journey possible and hence I have debts of gratitude to pay. Firstly, to the King Immortal from whom life and all gifts come, I say "Thank you", "Thank you". "Thank you". ***Bless the LORD, O my soul: and all that is within me, . . . Bless the LORD, O my soul, and forget not his benefits***:

I will like to acknowledge the following people who played very significant roles in my life and during the journey:

1. My parents, Mr. Felix Asifor Emuoyibofarhe, a retired Airforce officer, thanks for your strict discipline and love. You actually wanted me to become a military General, but I chose not to pursue the military ambition in NDA but left NDA for the conventional university and today I am an academic General. I hope I didn't disappoint you so much. I am deeply grateful to my mother, Late (Mrs,) Alice Fokoro Emuoyibofarhe, a very strong pillar in my life. She died in 2016 of Cancer of the blood, she is the motivation for my interest in Cancer genomics. Alice Fokoro, though not much educated, sacrificed her last, sold her precious materials and properties and with dad's meager resources to get me educated, through Army Children School, Kawo, Kaduna, Govt. Day Secondary School, Kurmi Mashi, , Kaduna, and Federal University of Technology, Minna.

2. My late brother, Hamson Voke Emuoyibofarhe and sisters, Dolly Emuoyibofarhe, Nyta Emuoyibofarhe, Gladys Emuoyibofarhe, Rachael Emuoyibofarhe and Joy Emuoyibofarhe. You are all wonderfully appreciated.

3. My in-laws, Mr. Ordor A, Barr. Alujo J, Mr. and Mrs. Cookey Gam, Mr. Nweke Amoge: My uncles, Cousin and Nephews and Nieces.

4. My teachers that set the building blocks of my life from primary school through secondary school, Mrs. Kava, Mr. J. A Olopade, Mr. Edom, Mr. Esua, Mr. Ndokaife, Mr. Okotie, Mr. Korinthien, Mr. Omoh,

5. Permit me to specially recognize Mr. Arnold Douglass (aka Oyibo) my oldest friend who is here today. We both attended same primary school, and same secondary school. He played a very vital role in my academic life. He taught me and challenged me on how to read. He is a book worm himself. I also thank all class 88 GDSS SSI[A] book worms Ocholi S,, Sonuyi Yinka, Anche E, Monday Moses etc

6. Rtd. Warrant Officer Okoedoh John you played very significant role in my life spiritually and supported me financially to start up university education. Thank you.

7. My lecturers at FUT Minna. Prof. K.R Adeboye, Prof. Yomi Ayesimi, Prof. S. A Reju, Dr. P. B Sola, Dr. Ogwu (Oxford Don), Dr. Ezeako L, Dr. Bamkefa, Baba Bida, Prince Badmus

8. I want to specially thank Prof. S. A Reju my mentor and PhD supervisor for his contagious enthusiasm and interest in me and mentoring in I.T Consultancy. I also like to thank Prof. K. Onifade my PhD co-supervisor and Prof. N.I Akinwande for the roles they played during my Ph.D and beyond.

9. Prince Johnson Adeomowaye and Prof.(Mrs.) B.I.O Adeomowaye who were instrumental to my staying back in Ejigbo and my coming to Lautech. Thanks for your love, arm of true fellowship, encouragements, prayers and friendship over the years.

10. Dr. James Adesina of Baptist Hospital Ejigbo a friend indeed, thanks for the support all the way and particularly when my late brother was sick. Thanks also to Prof. and Mrs. Osundina for your encouragements and support when I lost my elder brother.

11. I appreciate Prof. R. O Ayeni of blessed memory, an academic father and my M.Tech supervisor, Prof. Edewor J. and Prof. T. Raji

12. My senior friends and sources of inspiration, Prof, J.K Oloke (Vice Chancellor Precious Cornerstone University, Ibadan), Prof. Odunola (Vice Chancellor Hallmark University, Ogun State), Prof. T. S. Ibiyemi (Vice Chancellor Achievers University, Owo), Prof. C. K Ayo (former Vice Chancellor Covenant University, Ota)

13. The various Vice Chancellors I have served under, Late Prof. A. M Salau who appointed me as a graduate assistant and under whom I became LI, Prof. T S Raji who approved a one year leave to enable me take up my post-doctoral fellowship award in South Africa in 2006. Prof. B.B Adeleke who promoted me to the senior lectureship position, under whom I partly served as

deputy dean of the faculty of Engineering and Technology and for his constant support and encouragement of our research group activities and e-health/Telemedicince conferences. Special thanks to Prof. A. S Gbadegesin, the Vice Chancellor under whom I was promoted to the professorial chair, I was appointed a substantive Head of department, served as acting director Lautech ICT and the pioneer coordinator of the Lautech Software Engineering Institute. Thank you sir, for believing in me and for all the support for our research collaborations and activities both locally and internationally. Finally the current Vice-Chancellor, Prof. M.O. Ologunde, a father figure and a role model over the years. Thank you for your interest in me, your support, smiles, words of advice and encouragement. While preparing this inaugural lecture, I came to you and you graciously made available several samples of past inaugural lectures which served as guidelines for me. You are appreciated.

14. All the past and present Deans and Heads of Departments in the faculty of Engineering and Technology, I appreciate the pioneer dean and grandfather of the faculty Rev. Canon Prof. E. B Lucas (Religio-Academia) for your support and constant presence at the Faculty postgraduate seminars during the period I was deputy dean. Thanks to Prof. J. O Ojediran (currently the VC of Bells University of Technology, Ota) for his always welcoming smiles and encouragements. Prof. A. A. Adegbola under whom I served as deputy dean for two years, it was nice working with you and moving the entire faculty forward with marked achievements in so many areas and particularly the postgraduate programme, CAD Center and FET International Conference. Prof. J. Olajide, under whom I also served as deputy dean for a period of one year. Before working with him as deputy dean, he has been very instrumental to bringing out some quality in me and assisting me in identifying my area of relevance in academics. Thanks for the roles played in coordinating, the assessment and evaluation process of my professorial promotion as the Dean. I really appreciate you. My Dean and Chairman

COPD, Engr. Prof. K A Adebiyi, thank you for the very friendly relationship we have enjoyed and maintained over the years and thank you for encouraging me and giving me the opportunity to give my inaugural lecture at this time. I appreciate your humble and approachable leadership disposition.

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