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## BIOGRAPHICAL SKETCH

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NAME: **MAKOLO**, Angela, U

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eRA COMMONS USER NAME (credential, e.g., agency login): **AUMAKOLO**

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POSITION TITLE: Lecturer, Computer Science Department, Group Leader, University of Ibadan Bioinformatics Group, University of Ibadan.

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EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)

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INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
University of Benin, Nigeria	B.Sc.	1990-1995	Computer Science
University of Ibadan, Nigeria	MSc.	2002-2004	Computer Science
University of Ibadan, Nigeria	Ph.D	2007-2012	Computer Science (Bioinformatics Option)
H3ABioNet (Human Health Hereditary in Africa Bioinformatics Network), ICIPE, Kenya.	Diploma	07-08, 2013	Train-the Trainer Bioinformatics Course and EBioKit Training
McMurrah Laboratory , Lawrence Berkeley National Laboratory, California, USA	Visiting Scholar	10-11, 2013	Bioinformatics
Massachusetts Institute of Technology(MIT), Boston, USA	Post-Doc	02-05, 2015	Bioinformatics

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### A. Personal Statement

I am a lecturer in the department of Computer Science, University of Ibadan, where I teach Computer Science and Bioinformatics Courses. I supervise PhD, MSc and undergraduate students specializing in Bioinformatics/Computational Biology.

Since 2012, I have been involved in advancing bioinformatics research and education in Africa. My PhD dissertation in Bioinformatics defended in October 2012 at the University of Ibadan, Nigeria included a Computational technique for mining Transcription Factors and DNA Binding Sites in *plasmodium falciparum*, a parasite that causes malaria. My research involves the development of efficient algorithms and Computational Methods for automated Genome Annotation which is critical to understanding and interpreting the bewildering mass of Genomic Sequence Data presently being generated by Molecular Biologists, with the view of improving the quality of life for Humanity. My Research aims to seize the unique opportunities offered by the advent of high throughput sequencing technologies to develop the computational tools necessary for a systematic understanding of genomic information. This is achieved by my ability to work closely with experimental scientists and health care providers with diverse expertise. We work across a wide range of organisms to validate computational predictions and think deeply about fundamental biological questions affecting life. The result of this interdisciplinary research group is that it allowed me to gain fundamental insight into the function, regulation and evolution of genomes.

For more than 14 years, I worked as an Information Technology professional in the industry before resigning in 2009 to follow my passion of teaching and research at the University of Ibadan. Specifically, I resigned from my position as the head of Management Information System (MIS) at the International institute of Tropical Agriculture, IITA, Ibadan after 12 years of meritorious service and bagging several awards such as best staff with outstanding performance appraisal for 3 consecutive years, best IT manager award etc.

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In 2013, I won the prestigious [Techwomen Emerging Leader](#) Award for excellence in Technology and leadership by the Institute of International Exchange (IIE) of the United States Department of States, USA. The Award entailed a professional mentorship in leading Technology organization in the United States. I was a Visiting Research fellow at McMurah Laboratory in the Bioinformatics Unit of the Life Sciences Division of Lawrence Berkeley National Laboratory, Berkeley, California. I worked with [Helen Budworth](#), in the development of Computational Models for Sequence analysis of antisense promoters and chromatin modifiers at triplet repeat regions providing an in-depth analysis of sequence motifs at triplet repeat regions to identify targets for triplet repeat disease treatments. While in the United States, I had a scientific tour of the [Joint Genome Institute](#) (JGI), [National Energy Research Scientific Computing Centre](#) (NERSC) and other leading IT companies in the Silicon Valley such as Yahoo, Google, Facebook, Microsoft, Oracle, Twitter, LinkedIn, Juniper Networks and Oracle. I had the opportunity of establishing research collaborations with Professor Carlos Bustamante, of the Stanford Department of Biomedical Data Science, Stanford University.

I also won the MIT-ETT Postdoctoral Training Fellowship (Massachusetts Institute of Technology-Empowering The Teacher) Award in 2015. It is an Empowering the Teachers training under the MIT Science and Technology Initiative Program (MISTI), for young African Faculties, to learn the best practice in Teaching and Research. While at MIT, I was exposed to rigorous pedagogical methods and research methodologies. I also had the opportunity of establishing research collaborations with leading researchers at MIT and Harvard, especially at the Broad Genomic Institute of MIT and Harvard where I worked with Professors Hazel Sive, Manolis Kellis and Ashlee Earl. In addition, I worked with Prof Raphael Isokpehi, of Bethune-Cookman University, Florida on a Cognitive Computational model for Interactive Visual Representations of Gene Transcriptional Direction Patterns in Microbial Genome; A project partly funded by National Science Foundation [HRD-1435186]; Prof Raphael Isokpehi is a collaborator with the University of Ibadan Bioinformatics Group..

I am the group leader of the University of Ibadan [Bioinformatics Research group](#). As the group leader, I oversee the different interdisciplinary projects that involve computational modeling, algorithm development, and analysis of genomic data. I also organize Bioinformatics workshops and seminars for researchers in the University of Ibadan and its environs using bioinformatics for their research. I provide bioinformatics support to different researchers in the Medical, Agricultural and Biological fields.

I am a collaborator with the NABDA Node of [H3ABioNet](#) (Human Health Hereditary in Africa Bioinformatics Network), An African Bioinformatics network for H3Africa Projects. I have attended several Bioinformatics Workshops organized by [H3ABioNet](#) and I am a volunteer with the [H3ABioNet](#) African Bioinformatics Education Committee. I was the class coordinator and one of the teaching assistants for the H3ABioNet Introduction to Bioinformatics Training 2016 (IBT-2016) Course in the University of Ibadan.

I have many publications in both local and international journals. I have attended many National and international conferences to present my research and won many awards.

<https://ng.linkedin.com/in/amakolo>

<http://bioinformatics.ui.edu.ng/sites/default/files/ANGELA%20MAKOLO.pdf>

<http://techmadel.org.ng>

## **B. Positions and Honors**

### **Positions and Employment**

06/1997-2009 Computer Programmer/Head of Management Information Systems, International Institute of Tropical Agriculture, IITA, Ibadan

09/2009- Present Lecturer, Computer Science Department, University of Ibadan.

05/2013-Present Group Leader, University of Ibadan Bioinformatics Research Group.

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## B.2. Academic and Professional Honors

- 2010 Best Ph.D Paper Award in the Research Consortium on Information Technology Innovations (RECITI 2010 Conference) of the Nigeria Computer Society, Delta State, Nigeria.
- 2010 The Vice Chancellor's Recommendation (Prof Olufemi Bamiro) for Development of a state of the arts web portal for the Post Graduate School, University of Ibadan.
- 2010 Best Ph.D paper Award in the Doctoral Consortium of ICT for Africa Conference, Uganda. March, 2012.
- 2013 H3ABioNet Fellowship, a Pan African Bioinformatics network for H3Africa Project. Kenya.
- 2013 TechWomen 2013 Emerging Leader Award by the Institute of International Exchange (IIE) of the United States Department of States, California, USA. October, November, 2013.
- 2013 Research Scholar Fellowship at McMurah Bioinformatics Laboratory in the Life Sciences Unit of Lawrence Berkeley National Laboratory, Berkeley, California.
- 2013 Invited speaker at LabTech Conference at Lawrence Berkeley National Laboratory, University California, USA- Paper delivered: Computing for Biology: The African perspective.
- 2013 Invited speaker at Computer Professionals of Nigeria Assembly. Paper delivered: Science and Technology Innovation in Tertiary Institutions in Nigeria.
- 2014 Organizer and Resource Person, Bioinformatics For Translational Research Workshop, University of Ibadan.
- 2014 Invited Speaker & Resource Person: H3ABioNet NABDA Metagenomics Data Analytics Workshop, IITA, Nigeria.
- 2014 Invited Speaker, NABDA Symposium on Genomic applications in Africa. Paper Delivered: Computational Thinking for Genomic Research in Africa.
- 2015 MIT Empowering the Teacher Fellowship at the Massachusetts Institute of Technology, MIT, USA.
- 2015 Invited Speaker on African Innovate Conference, MIT, SLOAN ; Paper Delivered: Visual Analytics for enhancing genomic Research in Africa.
- 2015 Invited Speaker, Pan Atlantic University (Former Lagos Business School), Lekki Lagos. Paper Delivered: The Science of Teaching, Learning and Research: MIT Best Practice.
- 2016 Organizer and Resource Person: A workshop on Application of Bioinformatics and Genomics for Translational Research in Health and Agriculture, University of Ibadan. July 12 &13 2016.

## C. Contribution to science

- [1] **Makolo, A. U.** (2005): A hybrid Software Development Methodology. *Proceedings of the 8<sup>th</sup> International Conference of the Nigerian Computer Society. (ICABUILD 2005)*, Vol. 16, pp 87-92, June 2005, Port-Harcourt, Nigeria.
  - [2] **Makolo, A. U**, Osofisan, A.O. (2012): STGEMS: A Computational Inference Algorithm For Motif Discovery. *In proceeding of ICT for Africa Conference, Uganda.* Pp 800- 815.
  - [3] **Makolo, A.U**, Osofisan, A.O. (2012) Computational Model for mining Transcription Factors and DNA Binding Sites in Plasmodium falciparum. *In Proceedings of Louisiana Academy of Sciences Conference, USA.* March 2012. Pp 34 -43.
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- [4] **Makolo, A.U** (2013): Computation for Biology- The African Perspective. In Proceeding of LabTech Conference, California, USA Pp 300-307.
- [5] **Makolo, A.U** and Osofisan ( 2013): A Survey of Computational Inference Algorithms, International conference on Science and Sustainable Development in Nigeria. Book of Abstracts, Pp 107, SSD 185.
- [6] **Makolo Angela** and Isokpehi Raphael (2015): Interactive Visual Representations of Gene Transcriptional Direction Patterns in Microbial Genomes In Conference of European Molecular Biology Organization on Visualization of Biological Data, VISBI 2015, USA.
- [7] **Makolo, Angela**, Ezekiel Adebisi and Osofisan Adenike (2011). Mining Structured Motifs with Gene Enrichment Motif Searching on Suffix tree. *Journal of Computer Science and its Applications* 18(1) : 79-91.
- [8] **Makolo, Angela**, Ezekiel Adebisi and Osofisan Adenike (2012). Comparative Analysis of Similarity Check Mechanism for Motif Extraction. *Journal of Computer Science and its Applications* . IEEE Afr J Comp & ICT January 2012 .Vol. 5(153) Pp 53-60.
- [9] **Makolo, Angela** (2013). Support Vector Machine for improving Performance of TCP on Hybrid Network . IEEE Afr J Comp & ICT 5(6) : 15-21
- [10] **Makolo, Angela**, Fatumo Segun (2014). Development of A Visualization tool for Plasmodium falciparum Metabolic Networks . *International Journal of Computer Science Issue* 11(5) : 152-158. USA
- [11] **Makolo, Angela** (2014). An Intelligent Pattern Searching Model with Suffix Structures. *Afr J. of Comp & ICTs*. IEEE Vol 7, No. 5. Pp9-23-28.
- [13] **Makolo, Angela** (2014). SSTRAP: A Computational Model for Genomic Motif Discovery *Journal of Computer Science and its Applications* 18(1) : 79-91
- [14] Taiwo Adigun, **Makolo Angela**, Segun Fatumo(2015): Input Dataset Survey of *In-Silico* Tools for Inference and Visualization of Gene Regulatory Networks (GRN), Science Publishing Group *Journal of Computational Biology and Bioinformatics*. Vol. 3, No. 6, 2015, pp. 81-87.
- [15] **Makolo Angela** and Olagunju TA.(2015) Computational identification of signaling pathways in protein interaction networks [ *F1000Research* 2015, **4**(ISCB Comm J):1522 UK,
- [16] **Makolo, Angela** and Nwobi Lucy (2015). Development of Food Calorie Converter for Nigeria. *Journal of Computer Science and its Applications* 21(1) : 79-91.
- [17] **Makolo Angela** and Sally Olatunde (2015), Gapped Motif Discovery With Multi-Objective Genetic Algorithm . Vol. 4, No. 6, 2016, pp. 81-87. Published by , Open Access Library Journal, USA.
- [18] **Angela Makolo (2016)** , A Comparative Analysis of Motif Discovery Algorithms. *International Journal of Computational Biology and Bioinformatics*. Vol. 4, No. 6, 2016, pp. 81-87. Published by Science Publishing Group, USA.
- [19] **Makolo Angela** and Taiwo Adigun (2016) Optimization of Clustering Algorithms for Gene Expression Data Analysis Using Distance Measures. *Journal of Intelligent Systems and Application* , USA.
- [20] **Makolo Angela** and Mope Oluwatosin (2016) Prediction And Classification Of Schistosoma Haematobium Infection Using Machine Learning. *International Journal of Computer Applications* Vol.136, No. 6, , pp. 81-87 USA.
- [21] **Makolo Angela** and Adesina Oluwatosin (2015). MEPVIEW: A Biological Metabolic Network Visualization Tool. EECScn2015 Research Conference, Massachusetts Institute of Technology, MIT, Boston, USA.

#### D. Research Support

List both selected ongoing and completed research projects (Federal or non-Federally-supported). Briefly indicate the overall goals of the projects and **responsibilities/role of the key person identified on the Biographical Sketch**.

#### Ongoing Research Support

Ref #: NSF [HRD-1435186]

PI: Prof. Raphael Isokpehi Date: May/2014- To Date

Funding Agency: National Science Foundation

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**Title:** A Cognitive Computational Model for Microbial Genes Adjacency Visualization and Tutoring.

**Goal:** The exponential increase in whole genome sequences of bacteria and archaea presents a source of large and complex data on functional and structural annotations of genes. The annotations for function and transcriptional direction of genes adjacent to a gene locus in genomes of bacteria and archaea can be informative on biological process that involve the gene. Therefore, we developed a computational pipeline to generate a 3-digit binary code for each protein-coding gene based on the transcriptional direction of adjacent genes. A binary code for 111 indicates that the adjacent genes are in same transcriptional direction. We then developed interactive visual representations of patterns of the binary code for a specific gene family in multiple microbial genomes. In particular, comparison of genomes from same genus has been useful for identifying member of the universal stress proteins (pfam00582) that are part of multi-gene transcription units. The findings are basis for experiments to evaluate stress response biomolecular networks. For ease of training users on this tool, we developed a cognitive intelligent tutor for using it. Our software tool Microbial Genes Adjacency Visualization Software (mGENAVIS) can be found on <http://bioinformatics.ui.edu.ng/geneadjacency>.

**Role:** Dr Angela Makolo is the Bioinformatics Researcher and Software Developer on this project.

**Ref #:** N/A

**PI:** Angela Makolo

**Date:** July/2015 – To Date

**Funding Agency:** Non

**Title:** Metabolic Pathway Viewer Software.

**Goal:** This project builds a computational model that provides a graphical visualization of Metabolic Pathways for organisms of Interest. This web based software enables translation of text format descriptions of biological networks into graphical visualization for ease of readability and making sense of the pathway data.

**Role:** Development of the algorithm and implementation of the software

**Ref #:** N/A

**PI:** Angela Makolo

**Date:** JULY/2015 – Date

**Funding Agency:** Non

**Title:** Dynamic and Multi-Scale Computational Tool of Latent Tuberculosis Networks Using Sigma-Pi Neural Network

**Goal:** Investigating issues related to latent tuberculosis data involves modeling higher order correlations of the data with nonlinear dependent parameters. Besides, it involves getting data from multi-scale platform accompany with several form of noises to reveal the biochemical components and their functions. Also, tools that solve issues related to latent tuberculosis have emerged more or less independently; a single computational model that would investigate all issues related to latent tuberculosis should be investigated so that the true picture of the interactions would be given. The aim of the research is to develop a computational model that would reveal both regulatory and metabolic networks in host-pathogen relationship of Mycobacterium Tuberculosis at latent stage from gene expression data. We propose to introduce sigma-pi units in a Recurrent Neural Network (RNN) to infer both the regulatory network and the metabolic networks that the regulated genes are involved in. The hybridized operation is to serve as the optimization technique by reducing the search space and by making the model to be implemented using parallel programming

**Role:** PI

**Ref #:** NIH-H3A-356

**PI:** Angela Makolo

**Date:** JULY/2017 – Date

**Funding Agency:** NIH-H3ABIONET

**Title:** Intelligent Systems for Building Cognitive and Visual Analytics tools for teaching Bioinformatics

**Goal:** Developing Intelligent tutors that will combine the techniques of artificial intelligence and human computer interaction in building the tutoring systems. This aims are bringing the skill of deploying intelligent tutoring systems for training delivery as well as to guide users of bioinformatics tools on the correct way of using such tools and drawing meaningful inferences without wasting time on learning how to use the tools and understanding the results.

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**Role: PI**

