BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
*Follow this format for each person. DO NOT EXCEED **FIVE (5)** PAGES.*

NAME: **MAKOLO**, Angela, U

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

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

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.)*

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
McMurah 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

A.   Personal Statement

I am a senior 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.

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 and 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, Manollis Kellis and Ashlee Earl. In addition, I worked with Prof Ralphael 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 the principal investigator for the University of Ibadan Node of H3ABioNet (Human Health Hereditary in Africa Bioinformatics Network), An African Bioinformatics network for H3Africa Projects.

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-	Senior Lecturer, Computer Science Department, University of Ibadan.
05/2013-	Group Leader, University of Ibadan Bioinformatics Research Group.

Other Experience and Professional Memberships

2013	Member, International Society for Computational Biology (ISCB)
2013	Member, H3ABioNet Committee on Education and Curriculum Review
2013	Fellow, TechWomen
2013	Emerging Leader by the Institute of International Exchange (IIE) of the United States Department of States.

2013	Invited speaker, LabTech Conference at Lawrence Berkeley National Laboratory, University California, USA- Paper delivered: Computing for Biology: The African perspective.
2013	Invited speaker, 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.
2013	Invited Speaker, NABDA Symposium on Genomic applications in Africa. Paper Delivered: Computational Thinking for Genomic Research in Africa.
2013	Fellow, MIT Empowering the Teacher at the Massachusetts Institute of Technology, MIT, USA.
2014	Invited Speaker, African Innovate Conference, MIT, SLOAN ; Paper Delivered: Visual Analytics for enhancing genomic Research in Africa.
2014	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.
2018	Organizer and Resource Person: A Symposium Bioinformatics and Genomics: Embracing the future University of Ibadan. September 3rd 2018.
2020	Designed and delivered the Bioinformatics Instructional Design Online Course as part of the H3ABioNet Bioinformatics Train-the-Trainer project
2020	Organized Adventure-Based Learning of Bioinformatics Data Investigation workshop at ISCB- Africa ASBCB 2021 Conference.

Honors

2008	International Institute of Tropical Agriculture, IITA Staff of the Year with three years consecutive outstanding performance Appraisal.
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.
2012	Best Ph.D paper Award in the Doctoral Consortium of ICT for Africa Conference, Uganda. March, 2012.
2013	TechWomen Emerging Leader Award for Excellence in Technology and Innovation.
2015	Total E&A Scholarship for Outstanding African Faculty for MIT-ETT Award

C. Contribution to science

1. My early focus was on the development of algorithms and software for solving specific computing problems.This was manifested in my earlier works on the analysis and improvement of software

development methodologies and optimization of algorithms. These efforts were documented in the following publications

   a.   Makolo, A. U. (2005): A hybrid Software Development Methodology. Proceedings of the 8th International Conference of the Nigerian Computer Society. (ICABUILD   2005), Vol. 16, pp 87-92, June 2005, Port-Harcourt, Nigeria.
   b.   Makolo, Angela   (2013). Support Vector Machine for improving Performance of TCP on Hybrid Network . IEEE Afr J Comp & ICT 5(6) : 15-21

2.   My research focus soon shifted to the application of my computational skills in algorithm design and development to solving specific biological problems which was motivated by the vast amount of data made available to biologists through high throughput sequencing technologies. The immediate challenge was the development of efficient algorithms to aid biologists to understand these vast data and draw meaningful and useful biological inferences. Also needed were models to aid understanding of organisms and the biological processes involving the organisms. My research contributions in this regard are as follows

   a.   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.
   b.   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.
   c.   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.
   d.   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.
   e.   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.
   f.   Makolo Angela and Olagunju TA.(2015) Computational identification of signaling pathways in protein interaction networks [F1000Research 2015, 4(ISCB Comm J):1522 UK]

3.   My activities in designing computational tools for understanding Plasmodium falciparum, the malaria parasite, led to the development of the Suffix Tree Algorithm to mine structured motifs in Plasmodium genome.

   a.   Makolo, Angela, Ezekiel Adebiyi 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.
   b.   Makolo, Angela, Ezekiel Adebiyi 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.
   c.   Makolo, Angela   (2014). An Intelligent Pattern Searching Model with Suffix Structures. Afr J. of Comp & ICTs. IEEE Vol 7, No. 5. Pp9-23-28.
   d.   Makolo, Angela   (2014). SSTRAP: A Computational Model for Genomic Motif Discovery Journal of Computer Science and its Applications 18(1) : 79-91
   e.   Makolo Angela and Salihu Okatahi (2015), Gapped Motif Discovery With Multi-Objective Genetic Algorithm . Vol. 4, No. 6, 2016, pp. 81-87. Published by , Open Access Library Journal, USA.
   f.   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.

4.   The need to further make easier the process of understanding the large datasets available from high throughput sequencing technologies necessitated my foray into visual analytics of genomic data. In

collaboration with a seasoned expert in visual analytics, I developed tools to visualize large genomic data of pathogens in order to better understand the genetic bases of the pathogens.

a. 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

b. 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.

c. Makolo Angela and Adesina Oluwatosin (2015). MEPVIEW: A Biological Metabolic Network Visualization Tool. EECScon2015 Research Conference, Massachusetts Institute of Technology, MIT, Boston, USA

d. 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.

e. Makolo Angela and Lamidi, U.A. (2018). Motif Discovery in DNA Sequences Using an Improved Gibbs (iGibbs) Sampling Algorithm. *Journal of Computer Science and System Biology,* Vol. 11. No. 5 : 296-305.

f. Makolo Angela and Ibijola, A.S. (2018). Protein Secondary Structure Prediction using Deep Neural Network and Particle Swarm Optimization Algorithm. *International Journal of Computer Applications.* Vol. 181. No. 28 : 1-8.

g. Makolo Angela (2019). Transcription Direction Patterns of Adjacent Genes in Mycobacterium Tuberculosis Using GENAVIS. *Computational Biology and Bioinformatics.* Vol. 7. No. 1 : 1-4.

h. Adigun, T. and Makolo, A.U. (2019). Discovering Gene Co-Expression Modules Using Fuzzified Adjusted Rand Index. *Computational Biology and Bioinformatics.* Vol. 7. No. 2 : 11-21.

i. Makolo, A.U. and Maminor, G.U. (2020). A Computational Model for Clustering of Protein Sequences using a Self-Organizing Map and an Alignment-free Algorithm. *University of Ibadan Journal of Science and Logics in ICT Research (UIJSLICTR)*, Vol. 5. No. 1 : 1-10.

j. Makolo A. U and Olarenwaju S. (2021). Prediction of Benign and Malignant Tumor Cells in Human   Brest Using Machine Learning Techniques. Egyptian Computer Science Journal Vol .45. No 2: 14-23

k. Angela U. Makolo , Olubukola Smile , Kehinde B. Ezekiel , Antoinette M. Destefano, Junell L. McCall and Raphael D. Isokpehi (2022) Leveraging H3Africa Scholarly Publications For Technology-Enhanced Personalized Bioinformatics Education. MDPI Education. Science Journal . Vol 12, No 859: 1-17.

l. Makolo A. and Nkemelu D.(2022) Cognitive Tutoring in the use of Bioinformatics Tools *University of Ibadan Journal of Science and Logics in ICT Res earch (UIJSLICTR)*, Vol. 7. No. 2

m. S Cadmus, T Olagunju, A Makolo, V Akinseye, T Falodun, O Lawal, O Babalola, S Akingbesote, A Akinwumi, O Sokoya, A Moronfolu, C Kunle-Ope, E Osman (2022)
NTBP: A Geo-Genomic Repository of TB Data in Nigeria International Journal of Infectious Diseases, Elsevier .Vol 116, Supplement,, Page S102(USA)

n. Makolo A.U and Opoola Sunday (2022) Computational Dynamic Feature Extraction from Anonymized Medical Images Journal of Computer Science and Information Technology
 Vol 11,No 1 1-9 . (USA)

o. Modupe O. Coker, Olayinka A. Kotila, Taiwo O. Adigun,Temitayo V. Lawal, Adeniyi F. Fagbamigbe,   Angela U. Makolo, Mobolaji M. Salawu , David T. Ajayi Paul E. Oluniyi, Judith U. Oguzie, Anise N.Happi, Anne G. Hoen, Chinedum P.
(2023) Data science training needs in sub-Saharan Africa: Implications for biomedical research and therapeutics capacity. Open Research Africa 6:21

p. *Temitayo Adebanji Olagunju, Angela Uche Makolo, Andreas Gisel (2023).* Ds-Seq: an integrated pipeline for in silico small RNA sequence analysis for host-pathogen interaction studies EMBnet.journal, [S.l.], v. 29, p. e1037, ISSN 2226-6089. Available at: <https://journal.embnet.org/index.php/embnetjournal/article/view/1037>.

q. Raphael D Isokpehi, Amos O Abioye, Rickeisha S Hamilton, Jasmin C Fryer, Antoinesha L Hollman, Antoinette M Destefano, Kehinde B Ezekiel, Tyrese L Taylor, Shawna F Brooks, Matilda O Johnson, Olubukola Smile, Shirma Ramroop-Butts, Angela U Makolo, Albert G Hayward. (2024) Visual Analytics for Robust Investigations of Placental Aquaporin Gene Expression in Response to Maternal SARS-CoV-2 Infection. *Analytics* 2024, *3*, 116-139. https://doi.org/10.3390/analytics3010007

r. Angela Makolo, Pelumi Stephen Gboyega (2024) Computational prediction of small molecules targeting Lassa fever drug target using quantitative structure activity relationship (QSAR) and random forest algorithm. Journal of Computational Biology and Bioinformatics Research. Vol 3(1)

D. Research Support

Completed Research Support (completed during the last 5 years) :
H3ABioNet University of Ibadan Bioinformatics Group Node
Ref # : NIH 5U24HG006941-09   PI: PROF. MULDER, NICOLA   15-AUG-2017 - 30-JUN-2022
Title: H3ABIONET: INFORMATICS SOLUTIONS FOR H3AFRICA Awardee Organization: UNIVERSITY OF CAPE TOWN
Goal: H3ABioNet aims to develop a robust and innovative informatics network that addresses the complex needs of genomics researchers from clinical and biological data collection to genomic data generation and analysis and ultimately to impactful translation health research. The network will be the H3Africa data coordinating centre, hosting the data prior to submission to public repositories and providing access to data in line with the needs and consent of PIs and participants. It will ensure that data is quality controlled, standardized and interoperable. In order to facilitate adequate exploitation of genomic data, H3ABioNet will improve the user experience with genomics tools, adapting them, where necessary, for African data. The network will also go beyond this by seeking innovative data integration and translational solutions to enable comprehensive systems level analysis of diseases to ensure African scientists not only remain internationally competitive, but lead the way in translational research with tangible benefits for patients.
Role: University of Ibadan H3ABioNet Node PI

Ref # Grant No TETFund/DR&D/CE/NRF/STI/VOL.1) : Nigerian Goverment (TETFUND)   PI: Prof S.I.B Cadmus   Date: Dec/2019 – Dec/2021
Title: Bioinformatics Resources for Geo-Genomic Information Surveillance on Drug Resistant Mycobacterium Isolates from Nigeria
Goal: This project proposes to: i) analyse specimens (i.e. culture isolates) of drug resistant (DR)- Tuberculosis (TB) patients with whole genome sequencing (WGS) and compare results obtained with those of conventional genotypic and phenotypic DST with a view to investigating resistance mutations and genes associated with DR among TB patients ii) carry out WGS and molecular analysis to investigate the genetic diversity, evolutionary trend, phylogeny, and possible strain-dependent virulence features of Mtb among DR-TB clinical patients in Southwestern Nigeria, iii) additionally, we propose to create a bioinformatics resource platform comprising of a

data repository and computational tools for the analysis of the geo-genomic data generated in order to support knowledge discovery in the control of DR-TB in Nigeria.
Role: CO-PI

Ref #: NSF [HRD-1435186]   PI: Prof. Raphael Isokpehi   Date: 08/2017 - 07/2020
Title: Developing Quantitative Expertise in the Undergraduate Biology Curriculum (QEUBiC)
Goal: To provide learning experiences for undergraduate biology majors to develop quantitative and computational skills for biological discovery and analysis. The project has two specific objectives: 1) to infuse data science competencies in research-oriented courses and 2) to develop three new courses. The project will infuse concepts of data flow, data analytics and data curation in a series of five research-oriented biology core courses. In addition, a Cognitive Computational Model for Microbial Genes Adjacency Visualization was developed and an intelligent Tutoring software to teach the use of this software. Our software tool Microbial Genes Adjacency Visualization Software (mGENAVIS) can be found on http://www.geneadjacency.org
Role: Collaborator (Bioinformatics Researcher and Software Developer)