

CURRICULUM VITAE

- I. (a) Name: Angela Uche Makolo
(b) Date of Birth: 22 September, 1972
(c) Department: Computer Science
(d) Faculty: Science
- II. (a) First Academic Appointment: Lecturer II, 1 September, 2009
(b) Present Post with date: Senior Lecturer, 1 October, 2016
(c) Date of Last Promotion: 1 October, 2016
(d) Date Last Considered (in cases where promotion was not through): Not Applicable

***NB: Associate Professor In View, applied since 2020**

III. University Education (With Dates):

- (a) University of Benin, Edo State, Nigeria 1990 - 1995
(b) University of Ibadan, Ibadan, Nigeria 2002 - 2004
(c) University of Ibadan, Ibadan, Nigeria 2007 - 2012

IV. Academic Qualifications (With dates and granting bodies):

- (a) BSc. Computer Science, University of Benin. 1995
(b) MSc. Computer Science, University of Ibadan. 2004
(c) PhD. Computer Science, University of Ibadan. 2012

V. Professional Qualifications and Diplomas (With dates)

- (a) Oracle Certified Professional (OCP). 2000
(b) H3ABioNet Bioinformatics Certificate. 2013
(c) Massachusetts Institute of Technology,
Postgraduate Certificate in Teaching. 2015

VI. Scholarships, Fellowships and Prizes (with dates) in
Respect of Undergraduate and Postgraduate work only:

- (a) H3ABioNet Fellowship, a Pan African
Bioinformatics Network, Kenya. August, 2013
(d) TechWomen 2013 Emerging Leader Award
California, USA. November, 2013

- (e) Research Scholar Fellowship at McMurah Laboratory
at Lawrence Berkeley National Laboratory,
Berkeley, California. October, 2013.
- (f) MIT-ETT Fellowship at Massachusetts Institute
of Technology, for Teaching and Research. May, 2015.

VII. Honours, Distinctions and Membership of Learned Societies:

- (a) ISCB (International Society for Computational Biology)
- (b) CPN (Computer Professionals Registration Council of Nigeria)
- (c) NBGN (Nigerian Bioinformatics & Genomic Network)

VIII. Details of Teaching/Work Experience:

(a) Work Experience:

- (i) Software Engineer, International Institute of Tropical Agriculture 1997 - 2009
- (ii) Lecturer II, University of Ibadan. 2009 - 2013
- (iii) Lecturer I, University of Ibadan. 2013 - 2016
- (iv) Senior Lecturer, University of Ibadan 2016 to date

(b) Teaching Experience:

(i) <u>Undergraduate Courses:</u>	<u>Course Unit</u>
CSC 101 Introduction to Computer Science	4
CSC 231 Introduction to Fortran	3
CSC 333 Software Engineering I	4
CSC 301 Computer Centre Management	2
CSC 391 File System Management	3
CSC 433 Software Engineering II	4
(ii) <u>Postgraduate Courses:</u>	
CSC 724 Computing for Bioinformatics	3
CSC 725 Programming Lab for Bioinformatics	3
CSC 763 Advanced Software Engineering	3
MCS 736 Software Engineering	3
MCS 725 Project and Change Management	3
MCS 731 Integrating IS Functions	3

(iii) Project Supervision

Completed:

BSc. - 124

MSc. - 91

PhD - 4

Ongoing:

BSc. - 4

MSc. - 7

PhD - 4

Successful PhD Supervised

1. Dr Taiwo Adigun A Multi-layer Perceptron Model of Gene Regulatory Network with Fuzzified Adjusted Rand Index. June 2021.
2. Dr Temitayo Olagunju : A Computational model of multi-layer gene regulatory network for host/pathogen studies : Cassava and Cassava Mosaic Disease as a Case Study December 2021.
3. Dr Olaitan Awe : An Improved Model for the Identification of Protein-coding and Non-coding Region in Transcriptomes using Machine Learning. August 2023.
4. Dr Kemi Osuntokun : Biclustering Analysis of Micro Array Data Using a Combinatorial Firefly Differential Evolution Algorithm . July 2023

(c) Administrative Responsibilities and Community Service:

Administrative Responsibilities

- | | | |
|-------|--|--------------|
| (i) | Departmental Time Table Coordinator | 2013 - 2017 |
| (ii) | Course Adviser | 2013 - 2018 |
| (iii) | MBC & MSC Project Coordinator | 2015 to date |
| (iv) | Member, Departmental Finance Committee | 2013 - 2014 |
| (v) | Member, Examination Committee | 2015 - date |
| (vi) | Postgraduate Coordinator | 2018 - date |
| (vii) | Postgraduate Seminar Coordinator | 2017 - date |

Community Development

- | | | |
|--------|---|--------------|
| (viii) | Convener, Bioinformatics Workshop, University of Ibadan | 2016 - 2019 |
| (ix) | Convener, TechMadel, A Tech club for girls in Ibadan. | 2013 to date |
| (x) | Principal Investigator, UI node of H3 Africa | |

- | | | |
|---------|---|-----------------------------|
| | Bioinformatics Network (H3ABioNet) | 2017 to date |
| (xi) | Speaker and Local Organising Committee Techwomen For Nigerian Women and Youths , Nigeria | 2018 |
| (xii) | Local Organising Committee member (LOC), 1st Nigerian Bioinformatics Conference, Lagos. | 2019 |
| (xiii) | Local Organising Committee (LOC) member, Nigerian Women in Information Technology Association. | 2018-2019 |
| (xiv) | Resource Person, Introduction to Bioinformatics Training. | 2017-2024 |
| (xv) | Resource Person, Learning Adventure in Bioinformatics Data Investigation Workshop in ISCB Africa Conference | June 7th 2021. |
| (xvi) | Programme Committe, Abstract Review Cordinator 2 nd Nigerian Bioinformatics Conference Kwara state | 11– 3th October 2021 |
| (xvii) | Convener & Resource Person, Bioinformatics Symposium Celebrating 10 years of University of Ibadan Bioinformatics Group | 20 th April 2023 |
| (xviii) | Convener & Resource Person, Adventure-Based Learning of Bioinformatics A workshop for female students of University of Ibadan | 27th April 2023 |
| (xix) | Convener & Resource Person, Project Management Workshop Celebrating TechMadel @ 10 | 27th April 2023 |
| (xx) | Local Organising Committee member (LOC) Conference of the Society for the Advancement of ICT & Comparative Knowledge (SOCTHADICKconf'23), Ibadan, Nigeria, 29th October – 1st November 2023 | |

IX. Research:

(a) Completed:

1. Computational Inference Technique for Mining Structured Motifs.
2. Modelling Metabolic Pathways of various model organisms using Visual Analytics and Machine Learning Techniques.
3. ESTEMKIT: An Educational Computer game for teaching STEM (Science Technology, Engineering and Mathematics) subjects to students in Secondary Schools in Nigeria.
4. GENAVIS : A tool for modelling Transcription Direction Patterns of Adjacent Genes in Mycobacterium Tuberculosis .
5. A Dynamic and Multi-Scale Computational Tool for Latent Tuberculosis Networks Using Sigma-Pi Neural Network.

(b) In Progress :

1. A Multi-layer Perceptron Model of Gene Regulatory Network with Fuzzified Adjusted Rand Index. This project started in 2016, the aim is to develop a Multi-layer Perceptron model to reconstruct biological networks of higher order correlation genetic data. Adjusted Rand Index was modified using Fuzzy set to develop Fuzzified Adjusted Rand Index (FARI), which was incorporated into Multi-Layer Perceptron (MLP) neural network method to model a Gene Regulatory Network (GRN). The FARI part was used to investigate and establish the expression trends of genes in an expression profile data, while MLP part was used for the inference modeling. The FARI produced co-expression modules, which were used to generate the co-expression network. Detected hub genes from the co-expression network were functionally active and biologically relevant when their pathway profiling in Kyoto Encyclopedia of Genes and Genomes (KEGG) database were checked. The expected outcome is a computational model for reconstruction of Gene Regulatory Network. The project is estimated to be completed in April 2021.

5. A Computational model of multi-layer gene regulatory network for host/pathogen studies : Cassava and Cassava Mosaic Disease as a Case Study. This project commenced in 2017, the aim is to develop a Multi-Layer Network(MLN) model of gene regulatory network in a host/pathogen interaction. This model was tested using a 2-layered MLN consisting of gene co-expression and small RNA-gene target interaction information of five genotypes of Cassava with clearly different phenotypes in response to Cassava Mosaic disease infection. The small RNA profile of the Cassava genotypes was first obtained from unstructured raw sequence data through classification and annotation of the sequences. The sequence reads were classified as host, virus, conserved and novel small RNAs. Gene expression analysis revealed the pattern of expression of the small RNAs in the different pairwise combination of the genotypes as experimental conditions. The gene targets of the classified and profiled small RNAs across all the genotypes were predicted and this served as the input data for the second layer of the GRNs. The current stage of the project is the validation of the preliminary results obtained. Expected outcome is a computational model for host/pathogen interaction studies involving small RNAs. The project is expected to be completed in January 2022.

6. Bioinformatics Resources for Geo-Genomic Information Surveillance on Drug Resistant Mycobacterium tuberculosis (*Mtb*) Isolates from Nigeria. This project started in 2019 in collaboration with Prof. S.I.B Cadmus, Veterinary Medicine, University of Ibadan. The aim of the project is to explore the use of whole genome sequencing (WGS) and molecular analysis to

investigate the genetic diversity, evolutionary trends, phylogenetic relatedness of clinical *Mtb*, and to develop a secured cloud-based bioinformatics pipeline, consisting of a geo-genomic data repository and a visual analytic framework, for *Mtb* analysis in Nigeria. Over 590 patients have been recruited with sputum sample collection and these have been cultured in the lab for *Mtb* isolates extraction. The isolates will soon be sent for sequencing prior to bioinformatics analysis. The portal to host the data is already under development and will be completed within the next 2 months. The Expected outcome of the project is a geo-genomic portal for TB surveillance in Nigeria. The project is estimated to be completed in December 2021.

(c) Project, Dissertation and Thesis:

- (i) Makolo, A. U. (2004): An Hybrid Software Development Methodology: MSc Project University of Ibadan. 125p.
- (ii) Makolo, A. U. (2012): Computational Inference Technique for Mining Structured Motifs. PhD Thesis. University of Ibadan. 250p.

X. Publications:

(a) Books Already Published: Nil

(b) Chapters in Books Already Published: Nil

(c) Articles that have Already Appeared in Refereed Conference Proceedings:

1. **Makolo, A. U.** (2005). TRADRAD: A hybrid Software Development Methodology. In Ajibike O. Itegboje, (Ed.). *Information Technology Capacity Building. Proceedings of the 8th International Conference of the Nigerian Computer Society. (ICABUILD 2005)*, Port-Harcourt, Nigeria. 14-17 June, 2005, 87 – 91pp. (Nigeria) (Contribution: 100%).
2. **Makolo, A. U.** and Osofisan, A. O. (2012). Computational Model for mining Transcription Factors and DNA Binding Sites in Plasmodium falciparum. In *Proceedings of 86th Annual Conference of Louisiana Academy of Science*, Louisiana, United States of America. 3-5 March, 2012. 21 – 27pp. (United States of America) (Contribution: 80%).
3. **Makolo, A. U.** (2013). Computation for Biology - The African Perspective. In *Proceeding of LabTech Conference, California, United States of America*. 8-11 October, 2013. 87-94pp. (United States of America) (Contribution : 100%).

- *4. Awe, O. I., **Makolo, A. U.** and Fatumo, S. (2017). Computational Prediction of Protein-Coding regions in human Transcriptomes : An application to the elderly. *In Proceedings of International Rural and Elderly Health Informatics Conference*. Togo. 7-10 December, 2017. 1-4pp. (Togo) (Contribution : 45%).
5. Makolo A.U (2023) Developing Bioinformatics Capacity Amongst Educators for Career Mentorship in the Bioinformatics Field. *In Proceedings of the 2023 Conference of the Society for the Advancement of ICT & Comparative Knowledge (SOCTHADICKconf'23)*, Nigeria, 29th October – 1st November, 2023 (Nigeria) (100%).
6. Bamidele Oluwade, Morufu Amusa, Tinuke Oladele, Clement Bewaji and Angela Makolo(2023) On the Codebook of a genetic encoder model of the e-Coli bacterium in DNA computing. *In Proceedings of the 2023 Conference of the Society for the Advancement of ICT & Comparative Knowledge (SOCTHADICKconf'23)*, Nigeria, 29th October – 1st November, 2023 (Nigeria) (20%)

(d) Patents and Copyrights:

Nil

(e) Articles that have Already Appeared in Learned Journals:

7. **Makolo, A. U.**, Adebisi, E. F. and Osofisan, A. O. (2011). Mining Structured Motifs with Gene Enrichment Motif Searching on Suffix tree. *Journal of Computer Science and its Applications*. Vol. 18. No. 1: 1-9. (Nigeria) (Contribution: 70%).
8. **Makolo, A. U.**, Adebisi, E. F. and Osofisan, A. O. (2012). Comparative Analysis of Similarity Check Mechanism for Motif Extraction. *IEEE African Journal of Computer Science & ICT*. Vol. 5. No. 1: 1-9. (Nigeria) (Contribution: 70%).
9. **Makolo, A. U.** (2012). Support Vector Machine for improving Performance of TCP on Hybrid Network. *IEEE African Journal of Computer Science & ICT*. Vol. 5. No. 6: 107-112. (Nigeria) (Contribution: 100%).
10. **Makolo, A. U.** and Fatumo, S. (2014). Development of a Visualization Tool for *Plasmodium falciparum* Metabolic Networks. *International Journal of Computer Science Issues*. Vol. 11. No. 5: 152-158. (United States of America) (Contribution: 70%).

11. **Makolo, A. U.** (2014). An Intelligent Pattern Searching Model with Suffix Structures. *IEEE African Journal of Computer Science & ICT*. Vol. 7. No. 5: 23-28. (Nigeria) (Contribution: 100%).
12. **Makolo, A. U.** (2014). SSTRAP: A Computational Model for Genomic Motif Discovery. *Journal of Computer Science and its Applications*. Vol. 20. No. 1: 79-84. (Nigeria) (Contribution: 100%).
13. Adigun, T., **Makolo, A. U.** and Fatumo, S. (2015). Input Dataset Survey of In-Silico Tools for Inference and Visualization of Gene Regulatory Networks (GRN). *Computational Biology and Bioinformatics*. Vol. 3. No. 6: 81-87. (United States of America) (Contribution: 45%). (Current Volume of Journal is 18).
14. **Makolo, A. U.** and Nwobi, L. (2015). Development of a Food to Calorie Converter Mobile Application; A Case Study of Nigerian Foods. *Journal of Computer Science and its Applications*. Vol. 21. No. 1: 1-8. (Nigeria) (Contribution: 70%).
15. **Makolo, A. U.** (2015). A Comparative Analysis of Motif Discovery Algorithms. *Computational Biology and Bioinformatics*. Vol. 4. No. 1: 1-9. (United States of America) (Contribution: 100%).
16. **Makolo, A. U.** and Olagunju, T. A. (2015) Computational Identification of Signaling Pathways in Protein Interaction Networks. *F1000Research ISCB Comm J* Vol 4. No. 1 : 1-10 (United Kingdom) (Contribution : 70%).
17. **Makolo, A. U.** and Suberu, S. (2016). Gapped Motif Discovery With Multi-Objective Genetic Algorithm. *Open Access Library Journal*. Vol. 3. No. 1: 1-6. (United States of America) (Contribution: 70%) . (Current volume of journal is 8).
18. **Makolo, A. U.** and Adigun, T. (2016). Optimization of Clustering Algorithms for Gene Expression Data Analysis Using Distance Measures. *International Journal of Computer Applications*. Vol. 139. No.13: 4-8. (United States of America) (Contribution: 70%).
19. **Makolo, A. U.** and Akinyemi, M. (2016). Prediction and Classification of Schistosoma Haematobium Infection Using Machine Learning. *International Journal of Computer Applications*. Vol. 136. No. 8: 32-39. (United States of America) (Contribution: 70%).
- *20. **Makolo, A. U.** and Lamidi, U. A. (2018). Motif Discovery in DNA Sequences Using an Improved Gibbs (iGibbs) Sampling Algorithm. *Journal of Computer Science and Systems Biology*, Vol. 11. No. 5 : 296-305. (Belgium) (Contribution : 70%).

- *21. **Makolo, A. U.** 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. (United States of America) (Contribution :70%).
- *22. **Makolo, A. U.** (2019). Transcription Direction Patterns of Adjacent Genes in Mycobacterium Tuberculosis Using GENAVIS. *Computational Biology and Bioinformatics*. Vol. 7. No. 1 : 1-4 (United States of America) (Contribution : 100%).
- *23. 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 (United States of America) (Contribution : 50%).
- *24. Adigun, T. and **Makolo, A. U.** (2019). Multilayer Perceptron based Model of Large-Scale Gene Regulatory Network. *International Journal of Computer Applications*. Vol. 178. No. 42: 6-15. (United States of America) (Contribution : 50%).
- *25. **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. (Nigeria) (Contribution : 70%) (Published : June 2020).
- *26. Osuntokun, O. D., Adeyemo, A. B. and **Makolo, A. U.** (2020). A Review of Biclustering Algorithms for Data Mining Analysis of Gene Expression Data. *University of Ibadan Journal of Science and Logics in ICT Research (UIJSLICTR)*, Vol. 5. No. 1 : 64-76. (Nigeria) (Contribution : 35%) (Published : June 2020).
27. **Makolo, A.U** and Obotu Ojobo (2020) Motion Planning In Metabolic Pathways Using Probabilistic Roadmap and A* Algorithms. *International Journal of Computer Science Issues*. Vol. 17. No. 6: 48 -57. (United States of America) (Contribution: 70%).
28. **Makolo A. U** and Olarenwaju S. 2021. Prediction of Benign and Malignant Tumor Cells in Human Breast Using Machine Learning Techniques. *Egyptian Computer Science Journal* Vol .45. No 2: 14-23. (Egypt) (75%)
29. **Makolo A. U** and Rukayat Olapojoye (2021). Bayesian –ANFIS Student Model for an Intelligent Tutoring System. *International Journal of Applied Information Systems*. Vol 12. No 37: 16-22. (United States of America) (Contribution: 70%).
30. **Makolo A. U** and Tayo Adeboye (2021) Credit Card Fraud Detection System Using Machine Learning. *International Journal of Information Technology and Computer Science(IJITCS)*, Vol.13, No.4: 24-37 (United States of America) (Contribution: 70%).

31. **Angela U. Makolo** 1, 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. .(Switzerland) (Contribution 25%)
32. **Angela Makolo** and Goodness Ayinmode (2022) Design and Development of an Online Purchase System for Residents of a University Community. International Journal of Applied Information Systems. Vol 12. No 39: 43-51. (United States of America) (Contribution: 70%).
33. **Makolo A.** and Nkemelu D.(2022) Cognitive Tutoring in the use of Bioinformatics Tools ` *University of Ibadan Journal of Science and Logics in ICT Research (UIJSLICTR)*, Vol. 7. No. 2 :1-7. (Nigeria) (Contribution : 70%).
34. 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) (Contribution :30%).
35. **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) (Contribution 70%)
36. **Makolo A.U** and Festus Ajiboye (2023) Prediction of Sequences and Comparative Drug- likeness Ggenomic Signature of NGS. Journal of Computer Science and Information Technology Vol 11,No 3 34-45 . USA (Contribution 70%)
37. **Makolo A.U** and Oluwasegun V. Dada (2023) Ethnicity Classification: A Machine Learning Approach . Egyptian Computer Science Journal Vol. 47 No.1 1-10 (Egypt) (Contribution 70%)
38. 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 (USA) (20%)
39. *Temitayo Adebajji 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.I.], v. 29, p. e1037, ISSN 2226-6089. (Swizerland), (40 %)*
40. Raphael D Isokpehi, Amos O Abioye, Rickeisha S Hamilton, Jasmin C Fryer, Antoinessa 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. (USA) (20%).
41. **Angela Makolo** and 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). (USA) (70%)

(f) Books, Chapters in Book and Articles Already Accepted for Publication:

42. **Makolo A. U** (2022) Introduction to Bioinformatics . ISBN: 978-021-977-3, Lecture Note for University of Ibadan Distance Learning. (Nigeria) (Contribution: 100%).
43. **Makolo A. U** (2024) Personalized and Facilitated Learning of Bioinformatics ISBN: 978-978-8550-08-02. A Textbook Endorsed by African Bioinformatics Network for H3Africa (100%)

(g) Technical Reports and Monographs:

Nil

* Publications which have appeared/been accepted since last promotion.

XI. Major Conferences Attended with Papers Read (in the last 5 years):

1. H3Africa Consortium Conference and African Society for Human Genetics and Computational Biology Conference, Kigali, Rwanda. September 17th -21st 2018.

Paper Read: **Makolo, A. U.** (2018). Computational Model for Bioinformatics Train-the-Trainer Resource using Design Thinking Framework for H3Africa (H3-Human Health Hereditary).

2. 1st Nigerian Bioinformatics Conference with the theme: Bioinformatics in the era of Genomics in Africa taking place at the Nigeria Institute of Medical Research (NIMR), Lagos, Nigeria. June 25-26th 2019.

Paper Read: **Makolo, A. U.** and Ezekhanaya, C. (2019). GeAnnotate: A Computational Pipeline for Genome Annotation and Metabolic Pathway Reconstruction in Plants.

3. International Society for Computational Biology Africa, (ISCB Africa) Conference 2021 Virtual Conference from June 7th to 10th 2021.

Paper Read: Temitayo Olagunju, **Makolo, A. U.** and Andreas Gisel. (2021). Development of a multi-layer gene regulatory network perturbation simulation model for host-pathogen interaction studies GeAnnotate: A Computational Pipeline for Genome Annotation and Metabolic Pathway Reconstruction in Plants.

4. 2nd Conference of the Nigerian Bioinformatics and Genomics Network, Landmark University, Kwara State, Nigeria.. October 11th -13th 2021.

Paper Read: Temitayo Olagunju, **Makolo, A. U.** and Andreas Gisel. (2021). Ds-Seq: An Automated Pipeline for Genome-wide Small RNA Profiling in Host-Pathogen Studies

5. Eighth International Conference on Emerging Diseases and Surveillance, 2021

Virtual Conference from November 4th -6th , 2021.

Paper Read: 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. NTBP: A Geo-Genomic Repository of TB Data in Nigeria .

6. International Society for Computational Biology Conference, Las Vegas, United States of America November 7th -11th 2022.

Paper Read: Onyewuchi Njoku and Makolo, A. U. (2022). Investigation of Universal Stress Proteins from Mycobacterium Tuberculosis.

7. Conference of the Society for the Advancement of ICT & Comparative Knowledge Nigeria, 29th October – 1st November, 2023.

Paper Read: **Makolo, A. U.** (2023) Developing Bioinformatics Capacity Amongst Educators for Career Mentorship in the Bioinformatics Field.



Dr. Angela U. Makolo

Date:

XII. Ten Best Publications that Reflect the Totality of my Contributions to Scholarship:

1. **Makolo, A. U.**, Adebisi, E. F. and Osofisan, A.O. (2011). Mining Structured Motifs with Gene Enrichment Motif Searching on Suffix tree. *Journal of Computer Science and its Applications*. Vol. 18. No. 1: 1-9. (Nigeria) (Contribution: 70%).
2. **Makolo, A. U.** (2013). Computation for Biology - The African Perspective. *In Proceeding of LabTech Conference, California*. 8-11 October, 2013. 87-94pp. (United States of America) (Contribution : 100%).
3. **Makolo, A. U.** (2014). An Intelligent Pattern Searching Model with Suffix Structures. *IEEE African Journal of Computer Science & ICT*. Vol. 7, No. 5: 23 - 28. (Nigeria) (Contribution: 100%).
4. **Makolo, A. U.** (2014). SSTRAP: A Computational Model for Genomic Motif Discovery. *Journal of Computer Science and its Applications*. Vol.18, No. 1: 79-91. (Nigeria) (Contribution: 100%).
5. **Makolo, A. U.** (2015). A Comparative Analysis of Motif Discovery Algorithms. *Journal of Computational Biology and Bioinformatics*. Vol. 4, No. 1: 1-9. (United States of America)

(Contribution: 100%).

6. **Makolo, A. U.** and Olagunju, T. A. (2015) Computational identification of signaling pathways in protein interaction networks. *F1000Research ISCB Comm J*. Vol 4. No. 1 : 1-10 (United Kingdom) (Contribution : 70%).
7. **Makolo, A. U.** and Lamidi, U. A. (2018). Motif Discovery in DNA Sequences Using an Improved Gibbs (iGibbs) Sampling Algorithm. *Journal of Computer Science and Systems Biology*, Vol. 11. No. 5 : 296-305. (Belgium) (Contribution : 70%).
8. **Makolo, A. U.** 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. (United States of America) (Contribution :70%).
9. **Makolo, A. U.** (2019). Transcription Direction Patterns of Adjacent Genes in Mycobacterium Tuberculosis Using GENAVIS. *Journal Of Computational Biology and Bioinformatics* Vol. 7. No 1 : pp 1-4 (United States of America) (Contribution : 100%).
10. **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. (Nigeria) (Contribution : 70%) (Published : June 2020).

Research Focus

My main research area is Computational Biology/Bioinformatics. I have also worked in Machine Learning and Software Engineering. The understanding of complete genomes, their biological networks, and their evolutionary mechanisms using novel algorithms and machine learning techniques for knowledge discovery is the core of my research. It 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.

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 with diverse expertise, working across a wide range of model organisms to validate computational predictions, obtain new datasets and think deeply about foundational biological questions affecting life. The result of this interdisciplinary research is that it allowed acquisition of fundamental new knowledge into the function, regulation and evolution of genomes by taking advantage of emerging technologies and data types, inventing new computational models that exploit the unique nature of biological

problems, and ensuring that computational results benefit from expert experimental validation to confirm new insights. This knowledge is aimed at designing interventions such as drug targets, vaccines and other practices that are aimed at controlling traits of organisms of interest.

Specifically, computational approaches that exploit the genome-wide nature of biological datasets to derive common rules and genomic signatures used to annotate functional DNA elements, reconstruct their regulatory circuits, and understand their evolutionary principles are developed.

In the area of Machine Learning, extensive work has been done in developing and implementing machine learning models. Supervised and unsupervised machine learning techniques have been used in prediction of genomic data set with the aim of identifying unique patterns and interactions between the various gene components.

The focus in Software Engineering research has been principally in the area of development of software process methodologies and using them in the design and implementation of applications. A hybrid software process model was conceptualized and its efficiency in application software development was demonstrated in various research outputs.

Signature

Date