

CONTACT

Address: Biostatistics and Computational Biology Branch, NIH/NIEHS
111 T W Alexander Dr, Rall Building, Research Triangle Park, NC 27709

Email: atiteykomlan@gmail.com ; atiteydavidkomlan@yahoo.fr

Mobile: +1 4028179597

Languages: English, French, Chinese

Website: <https://komlanatitey.github.io/komlanatitey/eglikokotako.html>

ABOUT ME

I am a Computational Biologist more than five years of experience leading research that spans Bayesian statistics, and the analysis of high-dimensional single-cell data, with a strong track record of developing innovative methodologies to address complex biological questions.

EDUCATION

PhD in Electrical Engineering (Specialization: Computational Biology)

Swansea University, United Kingdom | Oct 2016 – Oct 2019

Thesis: Computational Models and Bayesian Analysis of Genetic Networks

- Focused on probabilistic modeling, Bayesian inference, and the statistical analysis of gene regulatory networks.

Thesis Advisors: Dr. Pavel Loskot, and Prof. Paul Rees

M.Eng. in Information and Communication Engineering

Harbin Engineering University, China | Sep 2013 – Dec 2015

Thesis: A Novel Prediction algorithm for Multi-Target Tracking

- Focused on the application of statistical signal processing and predictive modeling approaches for tracking multiple targets

Master's Thesis Advisor: Dr. Yan Cang

Chinese Language Studies

Harbin Engineering University, China | Sep 2012 – Aug 2013

- Completed language and cultural immersion in preparation for advanced studies

M.Sc. in Solid State Physics

University of Lome, Togo | Oct 2006 – Nov 2007

Thesis: A Dynamical Theory of Electromagnetism Based on Maxwell's Equations

- Focused on Physical modeling and mathematical derivation within the framework of electromagnetic

Master's Thesis Advisor: Prof. Toyi Assih

B.Sc. in Physics

University of Lome, Togo | Oct 2003 – Nov 2006

- Emphasized core principles of physical sciences and quantitative analytical methods.

CERTIFICATION

Data Science: Machine Learning

Havard University (Online), MA, USA | Jul 2023

- Covered supervised and unsupervised learning, regression, classification, clustering, feature engineering, and model validation using statistical methods.

Advisor: Prof. Rafael Irizarry

High-Dimensional Data Analysis

Havard University (Online), MA, USA | Jul 2023

- Focused on statistical techniques for high-dimensional biological datasets, including PCA, t-SNE, UMAP, autoencoders, and clustering algorithms.

Advisor: Prof. Rafael Irizarry

RESEARCH FOCUS AND INTEREST

- Development of statistical methodologies and computational tools to support applications in drug development and immunotherapy for immune-related diseases.
- Modeling and integration of high-dimensional multi-omics and spatial-temporal data for robust biological inference.
- Statistical modeling of single-cell and spatial omics data to uncover molecular interactions between immune cells and disease-affected cells.
- Application of machine learning and mechanistic modeling to develop hybrid statistical models for studying disease-immune dynamics.
- Detection and validation of disease-associated driver genes using statistical frameworks to support early diagnosis, treatment strategies, and prevention effort.

COMPUTATIONAL RESEARCH

Core Competencies and Technical Expertise:

- Statistical Inference • Probabilistic & Deterministic Modeling
- High-dimensional Data Analysis • Immune Response Modeling
- Machine Learning • Deep Learning • AI • Bioinformatics
- Single-cell and Spatial Transcriptomics • Functional Genomics
- Data Visualization • Data Warehousing • Hierarchical Clustering
- Programming: R, Python, MATLAB, Unix/Linux

Developed Software Tools:

- **MIBCOVIS** - Benchmarking Methods for High-Dimensional Data Reduction: github.com/NIEHS/MIBCOVIS
- **DEGBOE** - Variational Bayesian-Based Conditional Prediction: github.com/KomlanAtitey62/DEGBOE
- **MMQE** - Agent-Based Modeling of Dynamic Systems: [github.com/komlanAtitey/Multiscale Multicellular Quantitative Evaluator-MMQE](https://github.com/komlanAtitey/Multiscale_Multicellular_Quantitative_Evaluator-MMQE)
- **GIBOOST** - Optimizing Functions Through Data Integration: github.com/NIEHS/GIBOOST
- **magicSubclonal** - AI tool for subclonal gene identification: <https://github.com/komlanAtitey/magicSubclonal>
- **CancerTrace** - Tool for Identifying Driver and Modulator Genes: <https://github.com/komlanAtitey/CancerTrace>

RESEARCH EXPERIENCE

Research Fellow

Biostatistics and Computational Biology Branch (BCBB), National Institute of Environmental Health Sciences (NIEHS), NIH

Nov 2020 – Present | 40 hours/week

- Developed and applied hybrid statistical models combining agent-based approaches with ordinary differential equation (ODE) modeling to simulate immune cell proliferation and the dynamics of cytokine and chemokine signaling.
- Developed Bayesian statistical models coupled with spatial dynamics of cell-type distributions and gene expression to capture gene-gene interactions and mutation processes, explicitly accounting for tumor microenvironment heterogeneity.
- Applied Bayesian statistical methods to model discrete Bayesian networks, integrating dynamic and spatial principles of gene-gene interactions and cellular microenvironment heterogeneity to analyze genetic and cellular variability for identifying cancer driver genes.
- Developed computational tools leveraging Bayesian multimodal inference for biological clustering and ontology, combined with Markov transition modeling and advanced visualization techniques, to enhance interpretation of high-dimensional spatial single-cell datasets.
- Directed statistical integration strategies incorporating Bayesian model integration, statistical optimization, and spatial-temporal structure preservation using discrete Markov models to advance insights from complex, large-scale single-cell biomedical data.

Postdoctoral Research Associate*Department of Biochemistry, University of Nebraska – Lincoln*

Oct 2019 – Oct 2020 | 40 hours/week

- Developed a mechanism-based, multiscale, multicellular model of the immune system incorporating ordinary differential equation (ODE) modeling to capture dynamic biological processes.
- Integrated experimental data with computational models, combining ODE modeling and agent-based modeling to simulate immune responses and disease progression.

Doctoral Researcher*College of Engineering, Swansea University, United Kingdom*

Oct 2016 – Oct 2019

- Conducted statistical analysis of gene expression dynamics in biological systems using Bayesian inference methods.
- Modeled mRNA and protein distributions using stochastic processes combined with Bayesian modeling and posterior sampling techniques.
- Quantified uncertainty in biochemical reaction rates and gene regulation using histogram fitting, Bayesian inference, stochastic modeling, and goodness-of-fit tests to infer gamma-distributed molecule counts.

TEACHING AND MENTORING**Graduate Mentor***Biostatistics and Computational Biology Branch (BCBB), NIH/NIEHS, Research Triangle Park, NC*

Jan 2021 – Present | 10 hours/week

- Mentoring graduate students in statistical programming and analysis of high-dimensional single-cell data.
- Guiding students on best practices in data preprocessing, visualization, and interpretation of complex biomedical datasets.

Lecturer in Statistical Inference (Summer School Program)*Biostatistics and Computational Biology Branch (BCBB), NIH/NIEHS, Research Triangle Park, NC*

Jan 2021 – Present | 2 hours/week

- Designed and delivered lectures on key statistical inference topics, including hypothesis testing, regression, and confidence intervals.
- Developed course materials and assignments, facilitating student understanding through real-world examples and hands-on learning.
- Fostered interactive learning environments through discussions and group activities.
- Provided individual support to students, addressing content-related queries and offering personalized feedback.
- Coordinated with faculty and staff to ensure smooth delivery and logistics of the course.

Mathematics Demonstrator (Math Café)*College of Engineering, Swansea University, United Kingdom*

Feb 2017 – Jun 2019 | 6 hours/week

- Assisted graduate and undergraduate students with R and MATLAB programming, as well as core mathematical concepts.
- Simplified advanced mathematical techniques for students of diverse academic backgrounds.
- Offered one-on-one and small group support to strengthen students' problem-solving skills.

Physics Teacher*High School of Adidogome, Lomé, Togo*

Sep 2007 – Aug 2012 | 30 hours/week

- Planned and delivered physics curricula aligned with national education standards.
- Developed and administered assessments to evaluate conceptual understanding and practical application.
- Provided tailored instructional support to students with varying learning needs and academic levels.

PUBLISHED MANUSCRIPT

- Atitey, K., Hughes, C.E. and Fusco, J.C., 2025. CancerTrace: Multi-Stage Single-Cell Analysis of Networked Cancer Evolution for Driver and Modulator Gene Identification. *Computational and Structural Biotechnology Journal*.
 - *CancerTrace – Software tool*
- Atitey, K., Hughes, C.E. and Fusco, J.C., 2025. Physics-informed AI with Chemical Master Equation Dynamics for Driver-Gene Subclone Detection and Risk Labeling. *Computational and Structural Biotechnology Journal*.
 - *magicSubclonal – Software tool*
- Atitey, K., Jian-Liang Li, and Anchang, B., 2025. Boosting data interpretation with GIBOOST to enhance visualization of complex high-dimensional data. *Briefings in Bioinformatics* 26.4 (2025): bbaf415.
GIBOOST – Software tool
- Atitey, K., Motsinger-Reif, A.A. and Anchang, B., 2024. Model-based evaluation of spatiotemporal data reduction methods with unknown ground truth through optimal visualization and interpretability metrics. *Briefings in Bioinformatics*, 25(1), p.bbad455.
 - *MIBCOVIS – Software tool, 1,700 + downloads.*
- Atitey, K., 2022. DEGBOE: Discrete time Evolution modeling of Gene mutation through Bayesian inference using qualitative Observation of mutation Events. *Journal of biomedical informatics*, 134, p.104197.
 - *DEGBOE – Software tool, 5,300 + downloads.*
- Atitey, K. and Anchang, B., 2022. Mathematical modeling of proliferative immune response initiated by interactions between classical antigen-presenting cells under joint antagonistic IL-2 and IL-4 signaling. *Frontiers in molecular biosciences*, 9, p.777390.
 - *MMQE – Software tool, 6,500 + downloads.*
- Atitey, K., Loskot, P. and Rees, P., 2019. Elucidating effects of reaction rates on dynamics of the lac circuit in Escherichia coli. *Biosystems*, 175, pp.1-10.
- Atitey, K., Loskot, P. and Rees, P., 2018. Inferring distributions from observed mRNA and protein copy counts in genetic circuits. *Biomedical Physics & Engineering Express*, 5(1), p.015022.
- Atitey, K., Loskot, P. and Rees, P., 2018. Determining the transcription rates yielding steady-state production of mRNA in the lac genetic switch of Escherichia coli. *Journal of Computational Biology*, 25(9), pp.1023-1039.
- Atitey, K., Loskot, P. and Mihaylova, L., 2019. Variational Bayesian inference of hidden stochastic processes with unknown parameters. *arXiv preprint arXiv:1911.00757*.
- Loskot, P., Atitey, K. and Mihaylova, L., 2019. Comprehensive review of models and methods for inferences in bio-chemical reaction networks. *Frontiers in genetics*, 10, p.549.
- Atitey K., Cang Y. A novel prediction algorithm in Gaussian-mixture probability hypothesis density filter for target tracking. In Image and Graphics: 8th International Conference, ICIG 2015, Tianjin, China, August 13-16 2015, Proceedings, Part I 8 2015 (pp. 373-393). Springer International Publishing.

MANUSCRIPT UNDER REVIEW

- Atitey, K., Anchang, B. MarkovCellNet: Statistical Inference of Time-Evolving Cell Populations via Compositional Markov Models. *American Statistical Association*
- Atitey, K., Anchang, B. PICDGI: Predicting Immunosuppressive Cancer Driver Genes via Gene-Gene Interaction Features. *Journal of Biomedical Informatics*.
- Atitey, K. DiMEXP: Diffusion-Based Markov Modeling of Local-to-Global Gene Expression Dynamics for the Identification of Non-Driver Gene Modulators. *Computer Methods and Programs in Biomedicine*

CONFERENCE PRESENTATION

- **Atitey, K.**, Anchang, B. Beyond Mutation Frequency: A Bayesian Framework for Identifying Functional Cancer Drivers from Single-Cell Data. International Conference on Intelligent Systems for Molecular Biology (ISMB), Liverpool, England, July 20-24
- **Atitey, K.**, Anchang, B. Boosting Data Interpretability with GIBOOST to Enhance Visualization of High - Dimensional Data. International Conference on Intelligent Systems for Molecular Biology (ISMB), Montreal, Quebec, Canada, July 12-16, 2024.
- **Atitey, K.**, Anchang, B. Benchmarking framework for optimal visualization and interpretability of high-dimensional separable data. ISMB 2021 (https://www.youtube.com/watch?v=S0iIWgQ_QHg&t=2s).

POSTER PRESENTATION

- **Atitey, K.**, Anchang, B. Optimizing single-cell spatiotemporal delay variations to identify key features driving progression, *ISMB 2023*, July 2023.
- **Atitey, K.**, Anchang, B. Multicellular and Multiscale Modeling of Proliferative Immune Response Under Joint Synergistic and Antagonistic Cytokine Signaling, *ISMB 2022*, July 2022.
- **Atitey, K.**, Loskot, P. A Bayesian inference framework for statistical evaluation of protein production data from in-silico cell experiments. *The 41st Research Students' Conference in Probability and Statistics*. July 2018. University of Sheffield (UK).

INVITED TALKS

- **External**
 - Group discussion with graduate students in Systems Biology and Computational Biology, Purdue University, West Lafayette, IN | Nov 2021
 - Presented forensic science methods to student audience, Wake Young Men's Leadership Academy, Raleigh, NC | Apr 2025
- **Internal: Speaker at the Friday Seminar Series, Biostatistics and Computational Biology Branch**
 - Delivered a presentation on MIBCOVIS: A software Tool for Benchmarking High-Dimensional Data Reduction Methods | Oct 2022
 - Presented DEGBOE: A Software Tool for Variational Bayesian-Based Conditional Prediction | Jul 2021
 - Unveiled MMQE: A Software Tool for Agent-Based Modeling of Dynamic Systems. | Dec 2021
 - Presented GIBOOST: A Software Tool for Function Optimization via Data Integration. | Jun 2024

AWARDS AND SCHOLARSHIPS

Quantitative Approaches in Spatial Multi-Omics for Guiding Personalized Medicine | June 2025

- Event hosted by Biomedical Data Science Innovation Lab (BDSIL), Nashville, Tennessee

Codeathon: Clinical and Single-Cell Transcriptomics for Pneumonia | Sep 2023

- Event hosted by NIAID, CZI, BV-BRC, and Northwestern University in Chicago

Award for PAIR-UP UNC Imaging Workshop | Jan 2023

- Workshop hosted by the University of North Carolina at Chapel Hill in North Carolina.
The workshop provides training in advanced microscopy considerations for imaging live cells using transmitted light, fluorescent probes, and fluorescent biosensors

Award for PAIR-UP Imaging Workshop | Oct 2022

- Workshop hosted by the Rockefeller University Bio-Imaging Resource Center in New York.
The workshop provides training in advanced fluorescence microscopy and super-resolution techniques for live cell imaging

Award for Research Excellence (FARE 2022), in USA | Jul 2022

- NIH Awarded Study Section: Informatics/Computational Biology/Systems Biology
<https://www.niehs.nih.gov/careers/research/fellows/involvement/awards/excellence/index.cfm>

United Kingdom Highly Prestigious Zienkiewcz PhD fully funded Scholarship | Feb 2016

- Scholarship for the PhD research in Engineering, Swansea University, United Kingdom
Reserved for top calibre students (outstanding academic performance with a minimum of a First Class Honors Degree). This scholarship is opened to UK, EU and International students

China Scholarship Council (CSC) - Highly Competitive Full Master's Scholarship | Mar 2012

- Awarded a fully funded CSC for a Master's degree in Engineering at Harbin Engineering University, Harbin, Heilongjiang, China.