

## CURRICULUM VITAE

**ESKEZIEA YIHUNIE DESSIE, PhD**

**Postdoctoral Research Fellow**

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### CONTACT INFORMATION

#### Professional Address:

Indiana University School of Medicine

Department of Medicine, Division of Pulmonary, Critical Care, Sleep & Occupational Medicine

R3C400, 1101 W 10th Street

Indianapolis, IN 46202

**Email:** [edessie@iu.edu](mailto:edessie@iu.edu) | [estu2003@gmail.com](mailto:estu2003@gmail.com)

**ORCID** | [Google Scholar](#) | [GitHub](#) | [Linkedin](#)

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### RESEARCH INTERESTS

AI-driven bioinformatics, biostatistics, data science, Transcriptomics analysis, Epigenomics and genomics multi-omics integration, microbiome, precision medicine, Cancer, asthma, and allergic diseases

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### EDUCATION

#### **Ph.D. in Bioinformatics and Medical Engineering** | June 2021

Asia University, Taichung, Taiwan

*Dissertation:* Statistical and Machine Learning Methods for Developing Prognostic Models Using RNA-seq Data

*Advisor:* Ka-Lok NG, PhD

#### **M.Sc. in Biostatistics** | February 2013

Addis Ababa University, Addis Ababa, Ethiopia

*Thesis:* Determinants of Contraceptive Use Among Married Women in Ethiopia:

Ordinary Logistic and Multilevel Logistic Regression Analyses

#### **B.Sc. in Statistics** | August 2008

University of Gondar, Gondar, Ethiopia

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### APPOINTMENTS

#### **Postdoctoral Research Fellow** | August 2025 – Present

Indiana University School of Medicine, Indianapolis, IN

Division of Pulmonary, Critical Care, Sleep & Occupational Medicine

*Supervisor:* Tesfaye B. Mersha, PhD

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- Develop novel causal inference frameworks for trans-mQTL analysis in asthma using explainable AI
- Lead multi-omics integration projects combining genomics, epigenomics, and metabolomics
- Collaborate with clinical and computational investigators; contribute to NIH and institutional grant proposals.

**Postdoctoral Research Fellow** | October 2021 – August 2025

Cincinnati Children's Hospital Medical Center, Cincinnati, OH

Asthma Research Division, Department of Pediatrics

*Supervisor:* Tesfaye B. Mersha, PhD

- Led multi-omics integration studies for asthma, atopic dermatitis, and allergic diseases
- Developed computational pipelines for causal methylation–gene–phenotype analysis
- Published 4 first-author papers in high-impact journals
- Designed statistical analysis plans for NIH-funded projects.
- Mentored graduate students

**Postdoctoral Researcher** | July 2021 – August 2021

China Medical University Hospital, Taichung, Taiwan

Epigenome Research Center and Center for Precision Medicine

*Supervisor:* **Jan-Gowth Chang**, MD, PhD

- Developed nine-gene machine learning signature for lung adenocarcinoma survival prediction (AUC = 0.86)
- Conducted large-scale multi-omics analyses using TCGA, GEO, and in house datasets

**Doctoral Researcher** | February 2018 – June 2021

Asia University, Taichung, Taiwan

Department of Bioinformatics and Medical Engineering

*Advisor:* Ka-Lok Ng, PhD

- Developed novel statistical methods for cancer prognostic model development
- Published 3 first-author papers on cancer biomarker discovery
- Presented research at international conferences (IEEE BIBE)
- Contributed to grant proposals for Taiwan Ministry of Science and Technology

**Lecturer of Statistics** | September 2014 – July 2017

Debre Markos University, Debre Markos, Ethiopia

Department of Statistics

- Taught undergraduate courses: Multivariate Analysis, Biostatistics, Categorical Data Analysis, Regression Analysis, Design of Experiments, Statistical Theory

- Supervised 6 undergraduate thesis projects
- Served on departmental curriculum development committee
- Provided statistical consulting to government agencies and NGOs

**Lecturer of Statistics** | February 2013 – January 2014

Aksum University, Aksum, Ethiopia

Department of Statistics

- Taught undergraduate statistics courses: Statistical Methods I & II, Sampling Theory
- Developed new course materials for applied statistics
- Mentored undergraduate research projects

**Graduate Assistant** | April 2009 – August 2011

Aksum University, Aksum, Ethiopia

Department of Statistics

- Assisted faculty with teaching undergraduate statistics courses
- Conducted tutorials and study sessions for 60+ students per semester
- Graded assignments and examinations

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**PUBLICATIONS**

**Peer-Reviewed Journal Articles (*First Author*)**

1. **Dessie, E.Y.**; Ding, L.; Satish, L.; Mersha, T.B. Co-Expression Network and Machine Learning Analysis of Transcriptomics Data Identifies Distinct Gene Signatures and Pathways in Lesional and Non-Lesional Atopic Dermatitis. *Journal of Personalized Medicine* **14**(9):960, 2024. [SCI-indexed, Q1]
  2. **Dessie, E.Y.**; Ding, L.; Mersha, T.B. Integrative analysis identifies gene signatures mediating the effect of DNA methylation on asthma severity and lung function." *Clinical Epigenetics* **16**(15), 2024.
  3. **Dessie, E.Y.**; Gautam, Y.; Ding, L.; Altaye, M.; Beyene, J.; Mersha, T.B. "Development and validation of asthma risk prediction models using co-expression gene modules and machine learning." *Scientific Reports* **13**(1):11279, 2023.
  4. **Dessie, E.Y.**; Chang, J.-G.; Chang, Y.-S. A nine-gene signature identification and prognostic risk prediction for patients with lung adenocarcinoma using novel machine learning approach. *Computers in Biology and Medicine* **145**:105493, 2022.
  5. **Dessie, E.Y.**; Tu, S.-J.; Chiang, H.-S.; Tsai, J.J.P.; Chang, Y.-S.; Chang, J.-G.; Ng, K.-L. Construction and Validation of a Prognostic Gene-Based Model for Overall Survival Prediction in Hepatocellular Carcinoma Using an Integrated Statistical and Bioinformatic Approach. *International Journal of Molecular Sciences* **22**(4), 2021.
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6. **Dessie, E.Y.**; Tsai, J.J.P.; Chang, J.-G.; Ng, K.-L. A novel miRNA-based classification model of risks and stages for clear cell renal cell carcinoma patients. *BMC Bioinformatics* **22**(10), 2021.

#### **Peer-Reviewed Journal Articles (Co-Author)**

7. Huang, C.-H.; Zaenudin, E.; Tsai, J.J.P.; Kuru, N.; **Dessie, E.Y.**; Ng, K.-L. Dissecting molecular network structures using a network subgraph approach. *PeerJ* **8**: e9556, 2020.

#### **Manuscripts in Preparation**

8. **Dessie, E.Y.**; Stein, M.M.; Mersha, T.B. Integrative analysis of microbiome, DNA methylation, and metabolites reveals environmental influences on asthma in immigrant populations. s
9. **Dessie, E.Y.**; Mersha, T.B. Integrative multi-omics analysis reveals sex-specific cis and trans-mQTLs in asthma.
10. **Dessie, E.Y.**; Amal, I. Mersha, T.B. Genetic ancestry differences in IgE-mediated peanut allergy in African Americans.

#### **Conference Presentations and Abstracts**

11. **Dessie, E.Y.**; Gautam, Y.; Mersha, T.B. Comprehensive analysis of epigenome and transcriptome-based correlation network analysis in severe asthma risk prediction." *Journal of Allergy and Clinical Immunology* **151**(2):AB105, 2023.  
[Invited oral presentation, AAAAI Annual Meeting, San Antonio, TX]
12. Zaenudin, E.; Wijaya, E.B.; **Dessie, E.Y.**; Reddy, M.V.; Tsai, J.J.P.; Huang, C.-H.; Ng, K.-L. "A Parallel Algorithm to Generate Connected Network Motifs." *IAENG International Journal of Computer Science* **46**(4), 2019. [EI-indexed]
13. **Dessie, E.Y.**; Wijaya, E.B.; Huang, C.-H.; Agustriawan, D.; Tsai, J.J.P.; Ng, K.-L. "Identification of Several Core Overexpressed MicroRNAs that Could Predict Survival in Patients with Ovarian Cancer." *Proceedings of 2018 IEEE 18th International Conference on Bioinformatics and Bioengineering (BIBE)*, Taichung, Taiwan, October 29-31, 2018.

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## **GRANTS AND FUNDING**

### **Grant Proposal | In Development**

*Project Title:* TRACE: Trans-mQTL Atlas of Causal Epigenetic Regulation in Asthma Using Machine Learning and Explainable AI

*Role:* Principal Investigator

*Status:* Preliminary data complete, full proposal in final review

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## **TEACHING EXPERIENCE**

### **Graduate-Level Instruction**

## **Introduction to Bioinformatics Programming | Spring 2020, 2021**

Asia University, Taichung, Taiwan

*Department of Bioinformatics and Medical Engineering*

- Taught graduate students R, Python, and command-line tools for bioinformatics
- Covered RNA-seq analysis, genomic data visualization, and pipeline development
- Course enrollment: 25 students per semester
- Student evaluations: 4.6/5.0 average

## **Undergraduate-Level Instruction**

**Debre Markos University, Ethiopia | 2014–2017**

- Multivariate Analysis, Biostatistics, Categorical Data Analysis, Regression Analysis, Design of Experiments, Statistical Theory of Distribution

**Aksum University, Ethiopia | 2009–2014**

- Statistical Methods I & II, Applied Probability, Sampling Theory and Distribution, Research Methods

**Teaching Philosophy:** Student-centered, and active learning approach.

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## **MENTORING AND ADVISING**

### **Graduate Students (Informal Mentoring)**

**University of Cincinnati | 2023–2025**

- PhD student, statistical genetics and data processing from GEO, TCGA data
- Technical training in R, Python, and bioinformatics tools

### **Undergraduate Thesis Supervision**

**Debre Markos University, Ethiopia | 2014–2017**

- Supervised undergraduate thesis projects in statistics and biostatistics
- All students successfully defended and graduated

### **Statistical Consulting**

**Government and NGO Consulting | 2010–2017**

- Conducted training workshops on SPSS, Stata, and R (15 trainees)
  - Delivered 3-day workshop on data analysis in R for Debre Markos University academic staff professionals
  - Provided statistical methodology consulting services
  - Field Data Collection Supervisor | Central Statistical Agency, Addis Ababa, Ethiopia.
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## **PROFESSIONAL SERVICE**

### **Peer Review Activities**

**Manuscript Reviewer for:**

- *Frontiers in Genetics* (1 reviews)
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- *Scientific Reports* (1 reviews)
- *Genes* (1 reviews)

### Professional Memberships

- **American Academy of Allergy, Asthma & Immunology (AAAAI)** | December 2022 – Present
- **Ethiopian Statistical Association** | September 2010 – Present
- **Asia University Quantum AI Research Center (QAIRC)** | September 2025 – Present

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## INVITED PRESENTATIONS

### Oral Presentations

1. **Comprehensive analysis of epigenome and transcriptome-based correlation network analysis in severe asthma risk prediction.**  
American Academy of Allergy, Asthma & Immunology (AAAAI) Annual Meeting  
San Antonio, TX | February 26, 2023  
*Session:* Genetics and Epigenetics of Asthma [**Invited speaker**]
2. **Identification of Several Core Overexpressed MicroRNAs that Could Predict Survival in Patients with Ovarian Cancer.**  
IEEE 18th International Conference on Bioinformatics and Bioengineering (BIBE)  
Taichung, Taiwan | October 29-31, 2018

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## HONORS AND AWARDS

- **AAAAI PhD Travel Scholarship** | February 2023 | \$1,400  
American Academy of Allergy, Asthma & Immunology
- **Asia University PhD Full Scholarship** | 2018–2021  
Covered full tuition, fees, and living stipend for 4 years

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## TECHNICAL SKILLS

### Statistical and Computational Methods

- **Advanced statistical, and biostatistics methods** such as: Multivariate analysis, survival analysis, regression modeling (linear, logistic, Cox), mixed-effects models, Bayesian methods, causal inference, mediation analysis, high-dimensional data analysis
- **Machine Learning** such as: Random forests, gradient boosting, support vector machines, neural networks, ensemble methods, feature selection, model validation, cross-validation, hyperparameter optimization
- **Genomics** such as: RNA-seq analysis, differential expression, DNA methylation analysis (450K/EPIC arrays), eQTL/mQTL, GWAS, metabolomics, microbiome

pathway enrichment, gene ontology, co-expression network analysis (WGCNA), graph neural network

### **Programming Languages and Software**

- **Expert:** R (tidyverse, Bioconductor, caret, WGCNA, ggplot2, data.table), Python (pandas, scikit-learn, matplotlib, seaborn, NumPy, TensorFlow, PyTorch)
- **Proficient:** SAS, STATA, SPSS, Bash scripting, Linux/Unix command line
- **Bioinformatics Tools:** PLINK, MatrixEQTL, STAR, Bowtie2, HISAT2, GATK, Samtools, Bedtools, and Cystoscope
- **Version Control:** Git, GitHub, GitLab
- **High-Performance Computing:** Experience with HPC clusters
- **Reproducible Research:** R Markdown, and Jupyter Notebooks

### **Data Visualization**

- ggplot2, ComplexHeatmap, Plotly, matplotlib, seaborn, GraphPad Prism
- Publication-quality figure preparation

### **Other Technical Skills**

- Electronic Health Records (EHR) data analysis
- Clinical trial design and analysis
- Power and sample size calculations
- Database management (SQL basics)
- Microsoft Office Suite (Word, Excel, PowerPoint, advanced Excel functions)

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## **PROFESSIONAL DEVELOPMENT**

### **Workshops and Training ( CCHMC October -2021-August 2025)**

- Causal Inference in Biostatistics, Advanced Machine Learning for Genomics. Grant Writing Workshop, HPC cluster training, Advanced gene Mapping).

### **Certifications**

- **Human Subjects Research (HSR) CORE** | CITI Training | Valid: 06/07/2024 – 06/08/2027
- **Good Clinical Practice** | CITI Training | Valid: 10/20/2021 – 06/28/2027
- **Children Research Ethics** | CITI Training | Valid: 10/2019 – Present
- **Export Controls Course** | CITI Training | Valid: 10/20/2021 – Present
- **Biomedical Researcher** | CITI Training | Valid: 09/2030

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## **LANGUAGES**

- **English:** Fluent (speaking, reading, writing)
- **Amharic:** Native

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## **RESEARCH STATEMENT**

My research develops computational methods and bioinformatics tools for causal inference in multi-omics data to uncover the molecular architecture of complex diseases, including cancer, asthma, lung diseases, and allergic conditions. By integrating statistical genetics, epigenetics, gene regulatory networks, machine learning, and explainable AI, I map causal pathways from genomic variation through DNA methylation to phenotype—advancing from association to mechanistic understanding of how genetic and epigenetic factors interact with environmental exposure in disease etiology.

My research addresses a fundamental question: **How do trans-mQTLs act through context-specific gene regulatory networks to causally influence phenotype beyond cis-mQTL effects?** I am leading development of TRACE (Trans-mQTL Atlas of Causal Epigenetic Regulation), the first framework applying causal inference to trans-mQTL regulatory networks. TRACE integrates genome-wide trans-mQTL discovery, CIMLA-SHAP causal attribution across SNP→CpG→TF→gene regulatory cascades in disease versus control populations, sex-stratified network analysis, and multi-omic validation to address missing heritability in complex diseases.

My work spans computational and applied data analysis in statistical genetics, epigenetics, genome informatics, gene regulatory network reconstruction, and omics integration. I have developed causal mediation frameworks linking CpG methylation to asthma severity (*Clinical Epigenetics*, 2024), ensemble disease prediction models incorporating multiethnic admixture (*Scientific Reports*, 2023; *Computers in Biology and Medicine*, 2022), and network biomarkers for atopic dermatitis (*Journal of Personalized Medicine*, 2024).

My goal is to translate CpG-based causal discoveries into clinically actionable biomarkers through collaborative partnerships with clinical investigators, advancing precision medicine across cancer, respiratory, and allergic diseases.

### **Collaborative Philosophy:**

I believe the most impactful science emerges from interdisciplinary collaboration. I actively seek partnerships with clinical investigators (to ensure biological relevance), experimental biologists (for validation), and computational scientists (for methodological innovation). My publications reflect this collaborative approach, with co-authors spanning pediatrics, genetics and computational biology.

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## **REFERENCES**

**Available upon request**

**Potential referees include:**

1. **Tesfaye B. Mersha, PhD**  
Professor of genetics



Indiana University  
school of Medicine  
Email: [tmersha@iu.edu](mailto:tmersha@iu.edu)

*Relationship:* Postdoctoral mentor (2021-2025)

2. **Ka-Lok Ng, PhD**

Professor, Department of Bioinformatics and Medical Engineering  
Asia University, Taiwan  
Email: [ppiddi@gmail.com](mailto:ppiddi@gmail.com)

*Relationship:* PhD advisor (2018-2021)

3. **Tesfaye B. Mersha, PhD**

Professor of Biostatistics  
Director, Data Management and Analysis Center, Cincinnati children's medical  
center  
Email: [mekibib.altaye@cchmc.org](mailto:mekibib.altaye@cchmc.org)

*Relationship:* Research Collaborator