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| Faculty |
| A person wearing glasses and a pink shirt  AI-generated content may be incorrect.  Feseha Abebe-Akele, PhD  [fabebeakele@ecsu.edu](mailto:fabebeakele@ecsu.edu) |

# Biographical Sketch

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| Name | Position Title |
| Feseha Abebe-Akele | Assistant Professor |
| Institution | Department/Division |
| Elizabeth City State University | Natural Sciences |

**Education and Training**

A list of all professional education and/or training.

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| Institution, Location | Degree (if applicable) | Year(s) | Field of Study |
| University of New Hampshire, Durham, NH, USA | PhD | 2006-2013 | Genetics |
| University of New Hampshire, Durham, NH, USA | MSC | 2006-2013 | College Teaching In Science |
| Seneca College of Arts and Sciences. North York, Ontario, Canada | MSC equivalent Postgraduate Diploma | 2004 | Bioinformatics |
| Addis Ababa University Graduate School, Addis Ababa, Ethiopia | MSc Biology | 1991-1993 | Molecular Biology |
| Addis Ababa University Graduate School, Addis Ababa, Ethiopia | BSc Biology | 1991-1993 | Biology |

**Positions and Honors**

Positions in chronological order (as space allows), including present position.

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| * 08/2019 – current, Elizabeth City State University (ECSU), Assistant Professor of Biology * 09/2016 – 05/2019, Texas A&M International University, Assistant Professor of Biology * 12/2013-08-2016, Hubbard Center for Genome Studies, (Postdoctoral fellow). Lead Bioinformatician and Bioinformatics Supervisor * 12/2009-12/2013, Hubbard Center for Genome Studies. Bioinformatics Support. * 08/2006-11/2009, University of New Hampshire Genetics Program, Durham, NH Graduate Teaching and Research Assistant * 08/2004-08/2006, Division of Experimental Therapeutics, University Health Network, Toronto, ON. Research Assistant, Junior Bioinformatician * 200-2004, Royal Trust of Canada, Toronto Canada. Money Market desk coordinator. * 1984-1991, Ministry of Education, Ethiopia. Biology Teacher and Department Head |

**Relevant Publications**

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| * Rai R, Swanson E, Sarkar I, Lama D, Abebe-Aleke F, et. al. 2017. Permanent draft genome sequence of the French bean symbiont Rhizobium sp. strain RSm-3 isolated from the Eastern Himalayan region of India. Genome Announce 5:e00175-17. * Mahoney LL, Sargent DJ, Abebe-Akele F, et. al. (2016) A High-Density Linkage Map of the Ancestral Diploid Strawberry, Fragaria iinumae, Constructed with Single Nucleotide Polymorphism Markers from the IStraw90 Array and Genotyping by Sequencing. The plant genome. 2016 vol. 9(2) \_\_1-\_\_14 - doi:10.3835/plantgenome2015.08.0071 * Oshone R, Hurst IV SG, Abebe-Akele F, et. al., (2016) Permanent Draft Genome Sequences for Two Variants of Frankia sp. Strain CpI1, the First Frankia Strain Isolated from Root Nodules of Comptonia peregrina. Genome Announc. Jan/Feb 2016 vol. 4 no. 1 e01588-15 * Abebe E, Abebe-Akele F, Morrison J, Cooper V, Thomas WK. An insect pathogenic symbiosis between a Caenorhabditis and Serratia. Virulence. 2011 Mar-Apr;2(2):158-61. doi: 10.4161/viru.2.2.15337. Epub 2011 Mar 1. PMID: 21389770; PMCID: PMC3100764. * Feseha Abebe-Akele, et. al., (2015) Genome sequence and comparative analysis of a putative entomopathogenic Serratia isolated from Caenorhabditis briggsae. BMC Genomics 16:531 doi:10.1186/s12864-015-1697-8 |

**Other Products**

List up to 5 products (in chronological order) with the most relevance to the proposed project. Products may include but are not limited to policy briefs, software tools, online dashboards and community meeting presentations.

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| * Bioinformatics programming: Python, JAVA, Perl, C# and task automation using BASH shell scripting. * Database Programming: MySQL, MSSQL Server (Certified by Microsoft) * Unix/Linux Server/System administration User Account management, Automation, Maintenance * Curriculum Development in College Teaching * Reviewer of Journals: Elsevier, Gene; NRC Genome * Grant Reviewer: GRFP at NSF. * Grant Reviewer: Swiss National Science Foundation (SNSF). * Co-Pi: Texas A&M International University (TAMIU) STEM High-End Computational Resource, June 2019. ($325,795). |

**SGX3 Bioinformatics Resources.**

The Science Gateway Exchange (SGX3) offers a various web-based platforms that provide access to tools, data, and computational resources. These gateway resources are particularly valuable for bioinformatics applications, including Next Generation Sequencing (NGS) data analysis, as they facilitate access to high-performance computing (HPC) resources and specialized bioinformatics tools.

In the enhanced course, we will incorporate the following SGX3 and related resources:

1. **EDGE Bioinformatics Science Gateway**  
   • **Purpose:** Assists biologists, educators, and public health professionals in processing NGS data.  
   • **Features:**
   * Supports various NGS workflows, including quality control, alignment, and variant calling.
   * Provides a user-friendly interface for non-experts.
   * Facilitates data sharing and collaboration among users.  
     • **Access:** Available through the ACCESS Science Gateways portal (ACCESS Support).
2. **NAIRR (National AI Research Resource)**  
   • **Purpose:** Expands access to high-performance computing, datasets, and AI tools for research and education.  
   • **Features:**
   * Provides compute allocations that can support large-scale NGS and microbiome analyses.
   * Enables integration of machine learning approaches in bioinformatics pipelines.  
     • **Access:** Requests can be made via the NAIRR pilot platform, often integrated with ACCESS resources.
3. **Jupyter Notebooks and JupyterHub**  
   • **Purpose:** Offers an interactive computational environment for teaching and hands-on data analysis.  
   • **Features:**
   * Students can run code, visualize results, and annotate analyses in one environment.
   * Can be hosted on institutional HPC clusters, cloud platforms, or integrated into SGX3-supported gateways.
   * Encourages reproducibility and transparency in NGS data analysis.  
     • **Access:** Available through multiple ACCESS-affiliated hubs and via local deployment.
4. **projectEUREKA!**  
   • **Purpose:** Connects researchers and educators with computational and data science training and resources.  
   • **Features:**
   * Curated training materials on using HPC, gateways, and workflows in life sciences.
   * Facilitates networking and collaboration across institutions.  
     • **Access:** Supported within the ACCESS ecosystem and promoted through SGX3 workshops.
5. **GitHub Workflows (CI/CD for Bioinformatics)**  
   • **Purpose:** Introduces version control and automation of NGS pipelines.  
   • **Features:**
   * Students learn how to manage code repositories for reproducible bioinformatics.
   * Automates quality checks, testing, and deployment of pipelines.
   * Enables collaborative contributions to shared course repositories.  
     • **Access:** Freely available on GitHub, with integrations to HPC and SGX3 gateway environments.