


Boahemaa Adu-Oppong, Ph.D.

St. Louis, MO 
Available to Relocate

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https://abenaa07.github.io/ 

Experienced Computation and Bioinformatics Scientist with 10 years of experience in large-scaled sequencing data analysis in the microbial genomics field and pipeline development in the Amazon Cloud environment. Strong research professional with over 10 publications. Extensive experience with mentoring, leading code reviews and influencing best practices within an agile dev/ops environment. Hopes to leverage computational skills to help others make sense of complex data.

Skills

Expert: Bioinformatics, Programming skills (Python, R, SQL, Shell scripting), Linux/Unix, Writing, Verbal communication, Data Processing, Interpersonal skills, Visual Studio Code, Version Control (GitHub), Docker

Advanced: Statistics, Design (Adobe Illustrator, Photoshop), Coaching, Computer Science

Intermediate: Machine Learning

Education

JULY 2017

Ph.D. in Biology and Biomedical Sciences / Washington University in St. Louis

Awards:

- Distinguished Individual Leader – Arts and Sciences Graduate School
- Edward A. Bouchet Fellow
- Gerry & Bob Virgil Ethic of Service
- NSF Graduate Fellowship – Scholarship for 3 years of Graduate School

B.S. in Ecology and Evolutionary Biology / Rice University

Awards:

- Julian Huxley Award – top award for undergraduate research
- Mellon Mays Fellow

Experience

APRIL 2020 – PRESENT

Field Bioinformatic Scientist/ Field Application Support, Thermo Fisher Scientific, St. Louis, MO

- Provided computational support for Ion Torrent Sequencing Products.
- Awarded the West Sequencing Field Application Scientist 4i Award where colleagues vote on an individual who contributed to team and customers with respect to Thermo Fisher's 4i values.
- Technologies and data sources used: Unix, MySQL, Bash, Python, Javascript, AWS

JANUARY 2020 – PRESENT

Adjunct Instructor & Senior Tutor/ Washington University in St. Louis, St. Louis, MO

- Instructor of 24 students with over 240 hours of in class instruction and act as substitute instructor
- Tutored over 300 hours for over 35 students with an average rating of 4.9/5
- Technologies and data sources used: Advanced Excel/VBA, Python, R, Advanced Statistics, Machine Learning (Scikit-Learn, Keras, Tensorflow), Tableau, JavaScript (D3.js, Leaflet.js), HTML5/CSS (Bootstrap), API Interactions, Databases (SQL/NoSQL, MongoDB, MySQL, PostgreSQL), IaaS/PaaS Offerings (Shiny, Flask, Heroku, AWS), Big Data (AWS, Hadoop, Spark), IDEs (VS Code, Jupyter, R Studio), and Git/Github.

OCTOBER 2017 – APRIL 2020

Data Scientist / Genomics & Data Science, Bayer Crop Science, St. Louis, MO

- Engineered a metagenomics pipeline to be enabled in the Amazon Cloud Environment (AWS).

- Decreased costs for assembling and annotating metagenomes by 50%.
- Collaborated with scientists to develop a strategy to mine novel toxins from metagenomes.
- Coached an intern in developing a R ShinyApp that merged information from various databases to enable stakeholders in gene discovery and nomination.
- Awarded the Bronze Presidential Service Award for over 100 volunteer hours in a calendar year.
- Technologies and data sources used: Python, NCBI, ENSEMBL, R, MySQL, BLAST, Visual Studio Code, GitHub, Docker

JANUARY 2015 – DECEMBER 2016

Director of Young Scientist Program (YSP) / Division of Biology and Biomedical Sciences, Washington University in St. Louis

- Managed a team of over 100 volunteers in promoting STEM education
- Outperformed previous Directors by increasing volunteer retention, participants, external and internal requests and received the Outstanding YSP Director Award.
- Fundraised over \$100,000 at the inaugural YSP Gala
- Partnered with various news agencies to promote STEM education such as the national podcast Science Friday.

Projects

JUNE 2011 – JULY 2017

Urine Microbiome & Root-Endophytic Microbiome/ Division of Biology and Biomedical Sciences, Washington University in St. Louis

- Spearheaded, designed and executed novel experiments to characterize the microbial community of human bladders as it relates to human health (urinary tract infections) and the root-endophytic microbial community to understand the interplay between plant microbiome and plant yield
- Performed multi-variate statistical (ADONIS, PERMANOVA, CAP, PCOA, PCA) and phylogenetic analysis (SNP, Core Genome Tree, Average Nucleotide Identity) on datasets using R.
- Sequenced and assembled over 100 bacterial/fungal/viral genomes to determine pathogenicity computationally using bioinformatic predictive tools.
- Technologies used: Python, R, Centrifuge, Kraken, Trimmomatic, Spades, MetaPhlan, shotgun sequencing, Illumina Library Prep, FastTree, Muscle, Statistics, HMMER, BLAST, QIIME, amplicon sequencing

Public Outreach

JANUARY 2019 – DECEMBER 2019

Biotech Data Fluency Mentoring Program / Bayer Crop Science

- Led the Biotech wide Data Fluency Mentoring Program where mentees executed their business goal by attaining a new data fluency skill taught by the mentor.
- Managed 7 committee members and over 30 mentors and mentees.

JANUARY 2019 – DECEMBER 2019

Best Practices Data Science Analytics Team / Bayer Crop Science

- Organized 8 code reviews in Python and R for the entire Data Science and Analytics organization.

JULY 2018 & OCTOBER 2018 & AUGUST 2019

Software Carpentry Instructor / Bayer Crop Science

- Led courses in Python and certified to teach Python.

Selected Publications

1. The gut microbiome defines social group membership in honey bee colonies. Cassondra L. Vernier, Iris M. Chin, **Boahemaa Adu-Oppong**, Joshua J. Krupp, Joel Levine, Gautam Dantas, Yehuda Ben-Shahar. Science Advances. 2020 Oct 14.
2. Prairie plants harbor distinct and beneficial endophytic bacterial communities. **Boahemaa Adu-Oppong**, Scott Mangan, Chris Catano, Jonathan Myers, Claudia Stein, Gautam Dantas. PlosOne. 2020 June 25.

For more please visit: <https://abenaa07.github.io/publications/>