Boahemaa Adu-Oppong, Ph.D.

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Experienced Computation and Bioinformatics Scientist with 9 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 5 publications. Extensive experience with mentoring, leading code reviews and influencing best practices within an agile dev/ops environment. Hopes to leverage computational skills to build bioinformatic pipelines and tools to answer complex biological questions.

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 Products.
- Technologies and data sources used: Unix, MySQL, Bash

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
- Tutored over 250 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 enabled 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. 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.
2. Local confinement of disease-related microbiome facilitates recovery of gorgonian sea fans from necrotic-patch disease. Elena Quintanilla, Catalina Ramírez-Portilla, **Boahemaa Adu-Oppong**, Gretchen Walljasper, Stefanie P Glaeser, Thomas Wilke, Alejandro Reyes Muñoz, Juan A Sánchez. Scientific Reports. 2018 Oct 2.

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