

Mohamed Abuelanin

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Summary

Computer Scientist & Bioinformatician With a track record of developing innovative bioinformatics tools and frameworks, I harness computational power to drive biological discovery and accelerate genomics research. Leveraging my strong foundation in computer science and expertise in bioinformatics, I bridge the gap between data analysis and scientific insight, empowering researchers to uncover new biological breakthroughs.

Education

University of California, Davis <i>Ph.D. in Computer Science</i> <ul style="list-style-type: none">Thesis: Petabyte-scale sequence characterization	Davis, CA Sep. 2020 – Jun. 2024
Nile University <i>M.Sc. in Communication and Information Technology: kmer-based sequence partitioning;</i>	Giza, Egypt Mar. 2017 – Aug. 2020
Higher Technological Institute <i>B.Sc. in Electrical Engineering (Biomedical Engineering emphasis)</i> <ul style="list-style-type: none">Thesis: ML-Based Taxonomic Classification by DNA Chaos Game Representation	10th of Ramadan City, Egypt Sep. 2011 – Jan. 2017

Teaching Experience

Marine Biological Laboratory <i>Teaching Assistant, Gene Regulatory Networks Workshop</i>	Woods Hole, MA Oct. 2023
University of California, Davis <i>Data Analysis Collaboratory 2023 workshop at UC Davis.</i>	Davis, CA Jun 2023
University of California, Davis <i>Lead Teaching Assistant, ECS 161: Enhanced course content and engagement</i>	Davis, CA Jan. 2021 – Apr. 2021
Nile University <i>Teaching Assistant: Graduate courses: ML, Big Data, and advanced NGS Data Analysis</i>	Giza, Egypt Mar. 2019 – Aug. 2020

Appointments

University of California, Davis <i>Graduate Student Researcher, DIB-LAB</i>	Davis, CA Sep. 2020 – Present
Artronix <i>R&D Contract Engineer: Led embedded systems and software projects</i>	Egypt Jan. 2013 – Nov. 2017

Projects

kProcessor	Efficient Sequence K-mer indexing and Analysis
DBRetina	Gene Overlap Super Network.
kSpider	K-mer based ultrafast pairwise DNA clustering tool.
Sourmash	Quickly analyze genomic and metagenomic data sets.
denovo-rnaseq	De novo assembly, Differential gene expression, and annotation workflow.
guidedPartitioner	RNA-Seq guided-partitioning for purified transcriptome assembly.
kDecontaminer	RNA-Seq Decontamination tool for a cleaner denovo transcriptome assembly.
genoFreq	Tool for summarizing and visualizing genetic variation across samples.
Codon Optimization Tool	A tool for optimizing cDNA sequences using codon usage bias for DNA vaccines.

Skills

Python, C++, Bash, Rust, Git, Docker, HPC & Cloud Computing, Full-stack Development, CI, Snakemake

References

C. Titus Brown (PI), ctbrown@ucdavis.edu; **Tamer Mansour (CO-PI)**, tahmed@ucdavis.edu