

MODUPEORE O. ADETUNJI

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modupeore@gmail.com | 302-415-4154
LinkedIn: <http://www.linkedin.com/in/modupeore>
Website: <http://modupeore.github.io>

EDUCATION

UNIVERSITY OF DELAWARE

Newark, DE

PhD, Bioinformatics and Systems Biology

May 2019

GPA: 3.98/4.0

Skills: Bioinformatics, Databases, Big Data Analytics, Next Generation Sequencing, Computational Biology, and Statistics

UNIVERSITY OF DELAWARE

Newark, DE

Masters of Science, Bioinformatics and Computational Biology

December 2014

GPA: 4.0/4.0

Thesis: *Improving Eukaryotic Genome Assembly through Application of Single Molecule Real-Time Sequencing Data.*

REDEEMER'S UNIVERSITY

Ogun State, Nigeria

Bachelor of Science in Biochemistry

August 2009

CGPA: 4.2/5.0 - Dean's Honors List (all semesters)

Senior Thesis: *The Effect of Artemisinin-based Antimalarial Drug, Anate® on Specific Enzyme Activities in the Erythrocytes and Hepatocytes of Rats.*

SKILLS

LANGUAGE: PHP; HTML; Perl, Python programming language; Shell scripting.

OPERATING SYSTEMS: Unix /Linux; Windows Operating Systems.

PIPELINE DEVELOPMENT: Nextflow, Docker.

VERSION CONTROL: git

Big Data Analysis: Genomics, Transcriptomics, Variant Analysis using NGS, TGS platforms

DATABASE: Design; Implementation and Administration of MySQL; NoSQL [FastBit, MongoDB].

STATISTICS: R, Matlab.

VISUALIZATION: Cytospace, Seqmonk, IGV, UCSC Browser

RESEARCH EXPERIENCE

UNIVERSITY OF DELAWARE

Newark, DE

Bioinformatics Graduate Research Assistant, Schmidt Lab

January 2015 - Present

- Conducting research on Selection Signatures in commercial birds using transcriptome sequencing data.
- Developing several automated workflows for NGS data processing and analysis.
- Created a local hybrid database application and toolkit for storing and connecting transcriptome NGS metadata, gene expression profiling and variant analysis results from different various bioinformatics tools (**TransAtlasDB** - <https://modupeore.github.io/TransAtlasDB/>)
- Developed a Perl and/or Nextflow Variant Analysis Pipeline for DNaseq and RNAseq data from either the Fastq files or alignment files (SAM/BAM format) with TopHat2, HISAT2, STAR, BWA, BowTie2, Picard tools and GATK.
- Developed web-user interface for transcriptome gene-expression MySQL and NoSQL database using HTML and PHP.
- Designed the database solution for storage of large amount of transcriptome analysis (RNAseq) metadata and variant information using open source RDBMS and NoSQL platform and created the webpages to interact with both databases seamlessly.
- Developed pipeline workflows for transcriptome variant detection and annotation analysis.

UNIVERSITY OF DELAWARE

Newark, DE

Bioinformatics Graduate Research Assistant, CBCB Bioinformatics Core

January 2012- December 2014

- Provided solutions and informative insights in designing workflows for the assembly of large genomes
- Developed novel pipeline workflows for genome assembly of large eukaryotic genomes using SMRT sequencing and next-generation sequencing data.
- Performed comparative genomics and variant detection analysis on High Throughput Sequencing data using various reference genome alignment tools.
- Evaluated genome assembly alignment and variants using different reference assemblers and variant detection tools.
- Involved in core bioinformatics research and support/services to end users at CBCB (Center for Bioinformatics and Computational Biology).

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PROFESSIONAL EXPERIENCE

ROCHE DIAGNOSTICS CORP.

Pleasanton, CA

Bioinformatics Research, Sequencing Summer Intern

June 2016 - August 2016

- Improved and automated our target enrichment analysis workflow using Nextflow and SGE (Sun Grid Engine).
- Reduced server clutter by implementing custom bash/perl scripts for metrics and cleanup of temporary directories.
- Created shareable and successful deployable packages of our pipeline for our external clients using Docker and integrated the Nextflow pipeline with Docker.
- Contributed in meetings and gave presentations on projects progress for the group.

PUBLICATIONS

- Modupeore O Adetunji, Susan J Lamont, Carl J Schmidt; TransAtlasDB: an integrated database connecting expression data, metadata and variants, *Database*, Volume 2018, 1 January 2018, bay014, <https://doi.org/10.1093/database/bay014>.
- Barthold JS, Pugarelli J, MacDonald ML, Ren J, Adetunji MO, Polson SW, Mateson A, Wang Y, Sol-Church K, McCahan SM, Akins RE, Devoto M, Robbins AK. Polygenic inheritance of cryptorchidism susceptibility in the LE/orl rat. *Molecular Human Reproduction*. 2015. doi: 10.1093/molehr/gav060.

PRESENTATIONS

- Modupeore Adetunji, Sara Jastrebski and Carl Schmidt. Comparative Analysis of Signatures of Gene Selection between Two Distinct Bird Lines using Transcriptomic Data. Plants and Animal Genome XXVI (PAG 2018), San Diego, California, USA, January 13-17, 2018.
- Modupeore Adetunji and Carl Schmidt. TransAtlasDB: An informatics system for Transcriptome Analysis Data. Plants and Animal Genome XXV (PAG 2017), San Diego, California, USA, January 14-18, 2017.
- Modupeore Adetunji and Carl Schmidt. An Integrated Database connecting Expression data, Meta-Data and Variants. Plants and Animal Genome XXIV (PAG 2016), San Diego, California, USA, January 9-13, 2016.
- Modupeore Adetunji, Chris Ashwell, Max Rothschild, Susan Lamont, Mike Persia, Carl Schmidt. Characterization of Transcriptome Associated SNPs in the Chicken. Plants and Animal Genome XXIII (PAG 2015), San Diego, California, USA, January 10-14, 2015.
- Modupeore Adetunji (May 2014). Improving Eukaryotic Genome Assembly through Application of Single Molecule Real-Time Sequencing Data. Center for Bioinformatics and Computational Biology Seminar Series. University of Delaware.
- Adetunji MO, Hollman A, Nasko D, Triska Martin (October 2012). Development of a Cluster-Based Sequence Compression Pipeline. Center for Bioinformatics and Computational Biology Seminar Series. University of Delaware.
- Modupeore Adetunji (May 2012). Evaluating Reference Alignment Algorithms for Genomic Variant Detection. Center for Bioinformatics and Computational Biology Seminar Series. University of Delaware.
- Polson SW, Adetunji MO, Chen C, Huang H and Wu CH. 2012 CBCB Research Symposium on Bioinformatics and Systems Biology. May 24, 2012.

HONORS & AWARDS

University Doctoral Fellowship Award	2018 - 2019
GHC Scholar.	2017
CRA-W, Grad Cohort Workshop Travel Award.	2014 - 2017
Travel Grant for NSF: High Performance Computing in Life/Medical Science Workshop.	2012

WORKSHOPS

Grace Hopper Women in Computing Workshop. Orlando, FL.	September 2017
JMP Statistical Software Workshop	November 2017
CRA-W Graduate Cohort Workshop	2014 - 2017
Data Carpentry Bootcamp, Newark, DE.	March 2017
Center for Cell Circuits Computational Genomics Workshop, Cambridge, MA.	January 2017
CyVerse Tools and Services Workshop, Newark, DE.	February 2016
Software Carpentry Bootcamp, Newark, DE.	September 2014

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PacBio Bioinformatics Workshop, Baltimore, MD.
High Performance Computing in Life/Medical Science Workshop.

June 2013
July 2012

MEMBERSHIP

International WeLoveU Foundation.
Association of Computing Machinery (ACM), UD Chapter.
American Red Cross Association.
Bioinformatics Student Association, UD.
Black Graduates Student Association, UD.
Computing Research Association (CRA).
Grace Hopper Computing Scholar.
CISsters, UD.

ACTIVITIES

Helper for Data Carpentry Workshop at University of Delaware.	March 2017
Vice President of the Bioinformatics Student Association (BiSA), UD.	2016 - 2017
Helper for Software Carpentry Workshop at University of Delaware	September 2014
Treasurer of the Bioinformatics Student Association (BiSA), UD.	2012 - 2013
Teaching Assistant for RNA-SEQ Data Analysis Workshop. CBCB, UD	May 2012
Participant in the NSF: High Performance Computing in Life/Medical Science Workshop at the Virginia Bioinformatics Institute (VBI) at Virginia Tech.	July 2012