

# MODUPEORE O. ADETUNJI

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LinkedIn: <http://www.linkedin.com/in/modupeore>

Website: <http://modupeore.github.io>

## EDUCATION

### UNIVERSITY OF DELAWARE

Newark, DE

PhD, Bioinformatics and Systems Biology

May 2018

GPA: 3.98/4.0

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

September 2005 - 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; Python, Perl programming language; Shell scripting.

**OPERATING SYSTEMS:** Unix /Linux; Windows Operating Systems.

**PIPELINE DEVELOPMENT:** Nextflow, Docker.

**VERSION CONTROL:** git

**NGS Analysis:** RNAseq (Illumina miseq), DNAseq (Illumina hiseq, PacBio RS)

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

**TOOLS:** Statistics (R, Matlab); Genomic Assembly, Transcriptomic Assembly Variant Analysis, Variant Annotation tools (Tuxedo suite, BWA, CLC Genomics Workbench, Samtools, GATK, VEP, SNPEff, Annovar, Blast, David); De novo assemblers and error detection tools (SOAPdenovo, Velvet, Trinity, PBJelly, PBcR pipeline, Celera assembler); Visualization software (Cytospace, Seqmonk, IGV, UCSC Browser); Microsoft Office (Word, Powerpoint, Excel).

## RESEARCH EXPERIENCE

### UNIVERSITY OF DELAWARE

Newark, DE

Bioinformatics Graduate Research Assistant, Schmidt Lab

January 2015 - Present

- Developing 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.
- 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 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.
- Designed a lossless relational database (MySQL) for storage and manipulation of gene expression data, variant detection and annotation analysis from RNAseq assemblies.
- Developed pipeline workflows for transcriptome variant detection and annotation analysis.

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.

## HONORS, MEMBERSHIP, ACTIVITIES

|  |                |
|--|----------------|
| Participant in the CRA-Women 2017 Workshop at Washington, DC.  | April 2017     |
| Helper for Data Carpentry Workshop at University of Delaware.  | March 2017     |
| Vice President of the Bioinformatics Student Association (BiSA), UD.   | 2016 - 2017    |
| Participant in the CRA-Women 2016 Workshop at San Diego, CA.   | April 2016     |
| Participant in the CRA-Women 2015 Workshop at San Francisco, CA.   | April 2015     |
| Helper for Software Carpentry Workshop at University of Delaware   | September 2014 |
| Participant in the CRA-Women 2014 Workshop at Santa Clara, CA.   | April 2014     |
| Treasure 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      |

## PUBLICATION

- Modupe 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.
- Modupe 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.
- 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.
- Modupe 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.