

THINH B. VO

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Education

Bachelors for Biological Data Science: Bioinformatics | Graduation: Fall 2020
Virginia Commonwealth University, Richmond Virginia

Associate Degree in Biology | Graduated: Spring 2015
Northern Virginia Community College, Woodbridge Virginia

Relevant Coursework:

- **BNFO 201** | Introduction to Computation in Bioinformatics, including basics of handling sequence data, data representation, computer organization, and programming in Python.
- **BNFO 251-252** | Bacteriophage Discovery, including scientific journaling, genome annotation, basic bioinformatics research.
- **BNFO 301** | Introduction to Bioinformatics, practical and theoretical introduction to the tools and techniques needed to obtain and interpret a variety of genome-related data types.
- **BNFO 300** | Molecular Biology Through Discovery, study of molecular biology using the raw material and experiment design.
- **BNFO 420** | Application in Bioinformatics, applying integrative biological, computational, and quantitative skills to complete bioinformatics projects.
- **BNFO 492** | Independent Study at Boyd lab.
- **CMSC 302** | Introduction to Discrete Structures.
- **CMSC 255/256** | Introduction to Java and Data Structures using Object Oriented Programming.
- **BIOL 300** | Cellular and Molecular Biology.
- **BIOL 540** | Molecular Genetics.
- **STAT 321** | Statistical Computing, research data quantitative analysis, statistical test and visualization using SAS and R programming.

Experience

Institute for System Biology – Cancer Genomic Cloud - Internship | GDIT
Bioinformatics Engineering Intern, 06/2020-present

- Develop Bioinformatics workflows on Google Cloud Platform (GCP):
 - Snakemake, CWL, WDL, Nextflow pipelines
- Create front-end web pages to display the workflows, documentations:
 - Git Version Control for back end data
 - Documentation in ISB-CGC read the docs

https://isb-cgc.appspot.com/programmatic_access/

<https://isb-cgc.appspot.com/workflow/>

<https://github.com/isb-cgc/RunningWorkflows-on-the-GoogleCloud>

BOYD LAB - Internship | Virginia Commonwealth University
Programmer, 01/2020-present

- Assemble *Haematomyzus elephantis*'s endosymbiont sequences from Sequence Read Archive data
- Metabolic pathways annotation
- Phylogenetic study

<https://rampages.us/bboydlab/people/>

Ramhacks - Carmax Transfer Price Selector | Virginia Commonwealth University Hackathon
Back-end Programmer

- Set up back-end codes in Flask, worked on the authentication and database accesses to connect to Front-end design using Firebase frameworks in Python

<https://devpost.com/software/carmax-transfer-price-selector>

Professional Membership

Society of Bioinformatics | VCU
President, 08/2020-present

Projects

***Haematomyzus elephantis* Endosymbiont Genome Analysis** | sequence assembly, phylogenetic.

Sequence Alignment Tool | rewrote a global alignment tool applying object-oriented programming approach.

SARS-CoV-2 S-protein Disulfide Bridge Stabilization in Silico | *Team Leader, Programmer* | Using Python to work with pdb data format to do protein structure analysis to predict potential site for cysteine substitution (a technique used in vaccine research).

Novel Phage Holin Protein Classification | The study of novel bacteriophage Holin protein, including phylogenetic analysis and protein classification. <https://wiki.vcu.edu/display/phagelab/Kyle+Vo>

Angiopoietin-Tie, and Integrin Cancer Pathway Experiment Design | Molecular Cancer Experiment Design

<http://www.people.vcu.edu/~elhajj/bnfo300/19/Units/Proposal/draft/Vo-draft.docx>

I-TASSER study | basic research into threading protein modelling technique though I-TASSER

Skills

Computing | Java, Python, HTML, Blast, Linux, Git Version Control, I-TASSER, Pymol, Chimera, Dynamut, Pandas, NumPy, HHPRED, Matplotlib, BioPython, BowTIE2, ABYSS, SamTools, BAM, SRATools, SAS, SAS-SQL, R programming, TMHMM, Clustal, MUSCLE, Putty, Filezilla, Trimmomatic, FASTQC, Nextflow, WDL, CWL, Snakemake, Docker, Bootstrap3, RST, Hisat2, Stringtie, Conda, Google Cloud Platform, Kotlin, Android Studio, flask, firebase, postman.

Wet Lab Techniques | Genome Annotation, Journal Annotation, Cell Passage, Centrifuge, Pipette, Autoclave

Digital | Adobe Photoshop, Paint

Languages | ACTFL Certified Vietnamese and English