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VAISHNAVI VENKAT

Georgia Institute of Technology

EDUCATION

Master of Science, Bioinformatics (2014-present)
Georgia Institute of Technology, USA

Bachelor of Engineering, Biotechnology (2010-2014)
C.M.R Institute of Technology, India

SKILLS

Programming Languages:
Python, Perl, C++, C#, R

Tools:
Chimera, VMD, AMBER, Geneious, CLC workbench, Samtools, Sailfish, Tuxedo, Autodock Vina

Technology and Concepts Worked With:
Whole genome sequence analysis, Genome assembly, Gene prediction, Comparative genomics, Molecular Dynamic Simulation, RNA-seq, Cancer genomics

INTERNSHIP

ABiL, IHRC Inc.
Bioinformatics Intern
06.2015-08.2015
• Develop a computational genomics pipeline
• Assess, evaluate and document different tools used for Genome Assembly

Bigtec Labs
Research Intern
02.2014 − 05.2014
• Building and testing microfluidic cartridges according to given protocol
• Analysis of PCR data and Spectrophotometry data

Geomarine Biotechnologies
Lab Intern
01.2014
• Studying quorum sensing in V. *harveyi*
• Antimicrobial Screening of cowpea plant

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ACADEMICS

Graduate Research Assistant
Guide: Dr. Patrick McGrath, Georgia Tech
01.2015-current
• Developed homology model for different receptors in C. *elegans*
• Used molecular dynamics (AMBER) to predict ligands in silico

Human Computational Genomics Class Fall 2015
Guide: Dr. Fredrik Vannberg, Georgia Tech
• Developed DNA analysis pipeline for analyzing risk for ovarian cancer
• Developed RNA analysis pipeline for evaluating tissue of origin and monitoring effectiveness of cancer treatment using biomarkers

Computational Genomics Class Spring 2015
Guide: Dr. King Jordan, Georgia Tech
• Developed scalable, automated pipeline for Gene Prediction for unassembled NGS sequence provided by CDC
• Developed semi-automated typing tool for species delineation, serotype/serogroup identification and molecular characterization

HealthPlot
Health Informatics Class Spring 2015
• Developed an application to assists primary care physicians during patient visits
• Coded a patient similarity search for finding similar patients based on condition and treatment history

Studying and Modelling of Conserved Sites in Human GPCR
Guide: Dr. Patrick McGrath, Georgia Tech
08.2014-12.2014
• Using Geneious to do multiple sequence alignment
• Develop a python script that Chimera can use to visualize conserved sites.

Tuxedo vs. Sailfish: A Comparative Study
Genomics and Bioinformatics Class Fall 2014
• Comparing the Tuxedo and Sailfish pipelines used for analysis of different gene expression from RNA-seq data sets

Checking Tuberculosis Drug Adherence in Patients
Guide: Dr. Phani Kumar Pullela, CMR Institute of Technology
02.2014-06.2014
• Selection, screening and spectrophotometric analysis of food coloring
• Development of android app to implement drug adherence testing in patients

Teacher Assistant
• February 2014 – June 2014: Management and IPR
• August 2013 – December 2013: Food Biotechnology

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