JOHN VIVIAN

EDUCATION

2015–Present   University of California, Santa Cruz

Doctor of Philosophy in Bioinformatics

Department of Biomolecular Engineering
Computational Genomics Lab, Genomics Institute.
Distributed computing, RNA-seq, large-scale cancer genomics, statistical analysis, machine learning, and visualization.
Advisors: Dr. David Haussler, Dr. Benedict Paten

2013–2014   University of California, Santa Cruz

Masters of Science in Biomolecular Engineering & Bioinformatics

Department of Biomolecular Engineering
Capstone Paper: *Methods for Analysis of Nanopore Reread Data*
Used hidden markov models as a primary means of modeling "rereads" of a single molecule being translocated through a protein nanopore via a helicase motor.
Advisors: Dr. Mark Akeson, Dr. Kevin Karplus

2010–2012   University of California, Santa Cruz

Bachelors of Science in Bioengineering

Department of Biomolecular Engineering
Final Project: *DNA Adapters for Nanopore Sequencing*
Created a protocol for attaching adapter oligos to both synthesized and genomic inserts that allow the adapted construct to interface with a biological nanopore with the help of $\Phi 29$ DNA polymerase.
Advisor: Dr. Mark Akeson

RESEARCH EXPERIENCE

1/2015–Present   Graduate Researcher

UC Santa Cruz Genomics Institute

Working for the Computational Genomics Lab with a focus on distributed computing for large-scale genomics projects and applications. Developed a series of analysis pipelines with emphases on portability, reproducibility, efficiency, and scalability.
Reference: Dr. Benedict Paten · +1 (831) 459-5232 · benedict@soe.ucsc.edu

09/2013–12/2014   Graduate Researcher

UC Santa Cruz Nanopore Lab

Ran and analyzed single-molecule biological nanopore experiments for determining the effectiveness of improving accuracy by "rereading." Created a hidden markov model to detect differences in methylation state and quantified improved accuracy by rereading.
Reference: Dr. Mark Akeson · +1 (831) 459-1038 · makeson@soe.ucsc.edu
Reference: Dr. Kevin Karplus · +1(831) 459-4250 · karplus@soe.ucsc.edu

06/2012–01/2013   Junior Specialist

UC Santa Cruz Nanopore Lab

Ran and analyzed single-molecule biological nanopore experiments for distinguishing epigenetic modifications on cytosine. Created scientific figures and videos for publications. Designed and modeled prototype nanopore device.
Reference: Dr. Robin Abu-Shumays +1 (831) 459-5537 · roabu@soe.ucsc.edu

April 2017   Toil enables reproducible, open source, big
biomedical data analyses

Nature Biotechnology

Toil is portable, open-source workflow software that supports contemporary workflow definition languages and can be used to securely and reproducibly run scientific workflows efficiently at large scale. We used Toil to process over 20,000 RNA-seq samples to create a consistent meta-analysis of five datasets free of computational batch effects. Nearly all the samples were analysed in under four days using a commercial cloud cluster of 32,000 preemptable cores.

Authors: **Vivian J**, *et al.*

November 2016   UCSC Genome Browser

Nucleic Acids Research

I contributed over 7,500 wiggle tracks derived from samples from the Genotype Tissue Expression Consortium that were used to build signal graphs for the GTEx Signal Hub, which is an extension of the GTEx Gene Expression Track.

Authors: Tyner C, *et al.*

October 2013   Error rates for Nanopore Discrimination
Among Cytosine, Methylcytosine, and
Hydroxymethylcytosine Along Individual
DNA Strands

Proceedings of the National Academy of Science

Epigenetic modifications to nucleotides influence gene regulation and can be used to predict genetic disease. Current next-generation sequencing devices can only read canonical base identity. The M2MspA nanopore can distinguish between unmodified cytosine, methylcytosine, and hydroxymethylcytosine using machine learning methods. The accuracy of this discrimination is sequence dependent, and characterized for each sequence context.

Authors: Schreiber J, Wescoe ZL, Abu-Shumays R, **Vivian J**, Baatar B, Karplus K, Akeson M.

TEACHING EXPERIENCE

Summer 2016   BD2K Summer Workshop Teacher

UC Santa Cruz

Created and taught a week-long bioinformatics bootcamp to undergraduates from around the country. Taught the basics of Git, cloud computing, shell, Python, notebooks, visualization, and gave lectures on evolution, mutation, and next generation sequencing. Materials: Github repository.
Reference: Dr. Judith Canner · jcanner@csumb.edu

Spring 2014   Teacher's Assistant

UC Santa Cruz Baskin Engineering

Python Programming for Biologists (BME-160). I taught six hours of section a week, held office hours, and graded homework.
Reference: Dr. David Bernick · +1 (831) 459-2061 · dbernick@soe.ucsc.edu

Winter 2014   Teacher's Assistant

Lab manager and assistant for the senior design class of 2014 (BME-123B). Graded students' final projects and presentations.
Reference: Dr. Mark Akeson · +1 (831) 459-1038 · makeson@soe.ucsc.edu

TECHNICAL SKILLS

Languages	PYTHON, RUST, GIT, DOCKER, R — acquainted with SCALA, MATLAB, RUBY, JAVASCRIPT
Markup/Web	LaTeX, MARKDOWN, HTML, CSS
Data Analysis	PANDAS, MACHINE LEARNING, BAYESIAN INFERENCE, HIDDEN MARKOV MODELS
Cloud	AMAZON WEB SERVICES, MICROSOFT AZURE
Visualization	ADOBE ILLUSTRATOR, MATPLOTLIB, SEABORN, HOLOVIEWS, AUTOCAD
Laboratory	NANOPORE EXPERIMENTATION, GEL ELECTROPHORESIS, PCR, OLIGO DESIGN, PROTEIN CULTURE & EXPRESSION, DNA PURIFICATION

POSTERS AND PRESENTATIONS

11-6-18	Treehouse Childhood Cancer Initiative, *Santa Cruz, CA*
1-30-17	National Institute of Health BD2K Scientific Advisory Board, *Santa Cruz, CA*
7-11-16	GTEx Consortium Project Community Meeting, *Stanford, CA*
11-28-15	National Institute of Health BD2K All Hands Meeting, *Bethesda, MD*
11-4-15	Festival of Genomics, *San Mateo, CA*
10-5-15	Center for Research in Storage Systems, *Santa Cruz, CA*
9-7-15	Presented to BD2K consortium, *Santa Cruz, CA*
6-17-15	PanCancer Analysis of Whole Genomes, *Aptos, CA*

ACADEMIC ACCOMPLISHMENTS AND HONORS

UC Santa Cruz	Winter 2014 · Received an 'Outstanding' Rank (21) from a National Institute of Health panel for a National Human Genome Research Institute grant (1 R01 HG007827-01) which funded the nanopore reread project.
	Fall 2012 · Recognition for Achievement in Undergraduate Research
	Fall 2011 · Dean's Honor List
CSU Bakersfield	Fall 2007 · Hawk Honors Scholarship and Honors Program