

# JOHN VIVIAN

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## PROFILE

My interests are related to statistical inference and machine learning which I hope to integrate into my eventual PhD thesis. I spend most of my time doing software development for the Genomics Institute at UC Santa Cruz. In my spare time I play drums with two different groups, dabble in piano, study data analysis and read.

## SKILLS

<i>Languages</i>	PYTHON, R – Familiar with: SCALA, MATLAB, RUBY
<i>Markup and Web Design</i>	LaTeX, MARKDOWN, HTML, CSS, JAVASCRIPT
<i>Visualization</i>	ADOBE ILLUSTRATOR, MATPLOTLIB, SONY VEGAS, AUTOCAD, ADOBE PHOTOSHOP
<i>Computational Techniques</i>	HIDDEN MARKOV MODELS, DATAFRAME OPERATIONS, DATA ANALYSIS
<i>Laboratory Techniques</i>	GEL ELECTROPHORESIS, PCR, OLIGO DESIGN, PROTEIN CULTURE & EXPRESSION, NANODROP, DNA PURIFICATION, FINE MOTOR SKILL MANIPULATION

## EXPERIENCE

	<i>1/2015–Present</i>	<b>Graduate Researcher</b>
<i>UC Santa Cruz Big Data Genomics</i>		Working for the Computational Genomics Lab whose focus is distributed computing for large scale genomics projects and applications. Developed a series of analysis pipelines that use in-house pipeline architecture. Reference: DR. BENEDICT PATEN · +1 (831) 459-5232 · <a href="mailto:benedict@soe.ucsc.edu">benedict@soe.ucsc.edu</a>
	<i>09/2013–12/2014</i>	<b>Graduate Researcher</b>
<i>UC Santa Cruz Nanopore Lab</i>		Ran and analyzed single-molecule biological nanopore experiments for determining the effectiveness of improving accuracy by ‘rereading.’ Created and programmed theoretical hidden markov models to model real-world phenomena seen by the system our group designed. Reference: DR. MARK AKESON · +1 (831) 459-1038 · <a href="mailto:makeson@soe.ucsc.edu">makeson@soe.ucsc.edu</a> Reference: DR. KEVIN KARPLUS · +1(831) 459-4250 · <a href="mailto:karplus@soe.ucsc.edu">karplus@soe.ucsc.edu</a>
	<i>Spring 2014</i>	<b>Teacher’s Assistant</b>
<i>UC Santa Cruz</i>		Helped teach a research programming class in python (BME-160). I taught six hours of section a week, held office hours, and graded homework. Reference: DR. DAVID BERNICK · +1 (831) 459-2061 · <a href="mailto:dbernick@soe.ucsc.edu">dbernick@soe.ucsc.edu</a>
	<i>Winter 2014</i>	<b>Teacher’s Assistant</b>
		Acted as lab manager and assistant for the senior design class of 2014 (BME-123B). I also assisted in grading students’ final projects and presentations. Reference: DR. MARK AKESON · +1 (831) 459-1038 · <a href="mailto:makeson@soe.ucsc.edu">makeson@soe.ucsc.edu</a>
	<i>06/2012–01/2013</i>	<b>Junior Specialist</b>
<i>UC Santa Cruz Nanopore Lab</i>		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](mailto:roabu@soe.ucsc.edu)

## EDUCATION

<p><i>Doctor of Philosophy in Bioinformatics</i></p> <p><i>Masters of Science in Biomolecular Engineering &amp; Bioinformatics</i></p> <p><i>Bachelors of Science in Bioengineering</i></p>	<p>2015–Present</p> <p>University of California, Santa Cruz</p> <p>Department of Biomolecular Engineering Computational Genomics Lab, Genomics Institute. Large scale cancer genome analysis. Advisors: DR. DAVID HAUSSLER, DR. BENEDICT PATEN</p>
	<p>2013–2014</p> <p>University of California, Santa Cruz</p> <p>Department of Biomolecular Engineering Capstone Paper: <i>Methods for Analysis of Nanopore Reread Data</i> 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</p>
	<p>2010–2012</p> <p>University of California, Santa Cruz</p> <p>GPA: 3.2 · Department of Biomolecular Engineering Final Project: <i>DNA Adapters for Nanopore Sequencing</i> 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 <math>\Phi</math>29 DNA polymerase. Advisor: DR. MARK AKESON</p>

## PUBLICATION

<p><i>Proceedings of the National Academy of Science</i></p>	<p>October 2013</p> <p>Error rates for Nanopore Discrimination Among Cytosine, Methylcytosine, and Hydroxymethylcytosine Along Individual DNA Strands</p> <p>Epigenetic modifications to nucleotides influence gene regulation and can be used to predict genetic disease. Current so-called 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: Jacob Schreiber, Zachary Wescoe, Robin Abu-Shumays, John Vivian, Baldandorj Baatar, Kevin Karplus, Mark Akeson</p>
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## ACADEMIC ACCOMPLISHMENTS AND HONORS

<p><i>CSU Bakersfield</i></p>	<p>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 our project.</p>
	<p>Fall 2012 · Recognition for Achievement in Undergraduate Research</p>
	<p>Fall 2011 · Dean’s Honor List</p>
	<p>2007 · Hawk Honors Scholarship and Honors Program</p>

December 23, 2015