

# Daniel Hui

Generic version, updated 2/25/17 – address and contact info removed

## EDUCATION

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University of Pittsburgh, B.S. Computer Science with Honors, Expected Spring '17, GPA: 3.5/4.0

## PROGRAMMING LANGUAGES AND SOFTWARE USAGE

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**Scripting:** Perl, Bash/Linux shell, Python

**Compiled:** Java, C

**Statistical:** R, Matlab

**Web:** HTML, CSS, JavaScript

**IDEs/Editors:** Vim, Eclipse

**Version Control:** GitHub

### Select Bioinformatics Software:

SAMtools, Bowtie2, BEDtools, UCSC Genome Browser, FastQC, Cutadapt, STAR, Picard, mothur, MetaPhlan2

## RESEARCH EXPERIENCE

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Rangos Research Center, Children's Hospital of University of Pittsburgh Medical Center

Research Assistant

*Summer 2014 – Present*

Summer Research Internship

*Summer 2014, 2015*

### Sequencing Analysis

- Developed entire analysis pipelines for data from high-throughput next-generation sequencing techniques, including whole genome metagenomics for the eye's microbiome, and ATAC-seq for differential expression
- Created efficient and well-documented scripts for custom analyses such as summarizing and reporting results, data processing or formatting, and automating analyses in parallel in a cluster environment
- Benchmarked different protocols and software at all analysis steps including initial quality trimming, additional pre-processing, alignment, all downstream analyses, and visualization
- Analyzed over 600 metagenomics samples across more than 4 terabytes of raw data
- Implemented and assured quality for analysis pipelines for RNA-seq for differential expression, 16S rRNA sequencing for study of the gut microbiome, and Hi-C data to improve haplotype phasing
- Collaborated with wet-lab scientists and senior members of the group – presented summary and visualization of findings every few weeks

### Web Applications

- Developed web application that displays t-SNE plots and k-means clusters for single cell RNA-seq datasets
- Utilized R package Shiny, experience with Amazon Web Services
- Created and maintain lab website using HTML and CSS – [www.pitt.edu/~wec47](http://www.pitt.edu/~wec47)

### Tool Development

- Created toolkit that automatically does all input formatting and pre-processing, and statistical output summary for four popular software that infer local ancestry
- Most code written in Perl, some R – all documentation and source code available at [www.pitt.edu/~wec47/lait.html](http://www.pitt.edu/~wec47/lait.html)

Research Assistant – Department of Biomedical Informatics, University of Pittsburgh

*Spring 2014*

- With a small team, created visualization software that displays the ontologies of user-input genes in a treemap
- Most code in Java, also used JSON and D3 JavaScript library

## AWARDS

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Honors College Health Sciences Fellowship

*Summer 2016*

Chancellor's Undergraduate Research Fellowship

*Fall 2015*

## OTHER

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Select Coursework: Graduate Algorithm Design, Machine Learning, Honors Applied Statistics, Simulation, Artificial Intelligence, Algorithm Implementation, Programming Web Applications, Genetics, Biology I/II, Organic Chemistry I

Vice President – Future Business Leaders of America, Radnor High School, Radnor PA

*2012-2013*

- Placed 3rd in state-wide exam for "Introductory Technology Concepts", competed in nationals

Clerk – West Chester Hospital, Cardiology Consultants of Philadelphia, West Chester PA

*Summer 2012*