

Taylor D. Lee

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OBJECTIVE	To acquire a position as a Frontend Engineer Apprentice with Fetch.	
EDUCATION	<i>Bachelor of Arts, Mathematics</i> <i>Bachelor of Arts, Studies in Applied Mathematics (Individualized Major)</i> Edgewood College, Madison, WI, 2013	
HONORS	<i>Dean's List</i> Edgewood College <i>Mid-Career Physicist Award</i> Edgewood College	
COMPUTER SKILLS	<i>Languages & Software:</i> Python, MATLAB, R, LaTeX, Java, C, Sage, Javascript, HTML, CSS, Angular, BASH, HTCondor. <i>Operating Systems:</i> Unix, Mac OSX, Windows. <i>Databases:</i> MySQL, CouchDB, MongoDB	
UW-Madison CS COURSES	CS 240, CS 252, CS 302, CS 352, CS 354, CS 367, CS 412, CS 435	
EXPERIENCE	<i>Underwriting Intern</i>	Summer 2012
	Group Health Cooperative of South Central Wisconsin, Madison, WI	
	<ul style="list-style-type: none">Calculated Increase in premiums for large groups based on in house formulas.	
	<i>Actuarial Assistant Internship</i>	Late Summer 2012
	Huttleston and Associates, Madison, WI	
	<ul style="list-style-type: none">Developed HTML parsers with Python which collected premium data for individual health plans from Dane County's four largest HMOs, including all ages, genders, and smoking preferences.	
	<i>Student Hourly Programmer</i>	August 2014 - August 2015
	University of Wisconsin-Madison, Dept. of Bacteriology	
	<ul style="list-style-type: none">Worked as a Programmer for the Bacteriology Lab of Federico Rey. The Lab's research focused on the human gut microbiome. Gained valuable experience in Bioinformatics. Learned to use HTCondor and SLURM with HTC and HPC respectively. Participated in an RNA-Seq discussion group that met at WID and a Metagenomics seminar group that met at MSB.Sharpened experience with Python and Shell scripting. Installed and used a vast array of Bioinformatics software, including Prokka, a prokaryote Annotation pipeline, and installed QIIME (Quantitative Insights Into Microbial Ecology), a 16S software pipeline with a broad range of dependencies.Managed a collection of 93 bacteria genomes, and developed an RNA-seq pipeline that read in SAM files and GFF files, and output an excel table with the number of hits each gene from each bug in each sample received.	
	<i>Student Hourly Programmer</i>	August 2015 - March 2016
	University of Wisconsin-Madison, Dept. of Mechanical Engineering, Advanced Composite Materials Group	

- Currently working as a programmer for a Mechanical Engineering group, developing a web application that will allow information from testing 3D printed-objects to be saved to a MongoDB database. Working with a Python Web Framework called Tornado and an HTML template language called Jinja2.
- Database will allow advanced data aggregation and provide crucial information for future designs. Currently working to make the application richer with AngularJS.
- Also used Javascript library THREE.js to help grad student in group visualize the results of algorithms that fill in surfaces with lines that represent the toolpath of the 3D printer.

Angular 2+ Developer
HealthConnect.Link

May 2017 - Sept 2017

- Worked as a Angular 2+ Developer for a non-Profit startup called HealthConnect.Link. Used Angular 2 and NGRX to build a advanced search menu that would allow users to specify with precision what non-for profit services they are interested in.

React Developer
DataChat

Feb 2018 - May 2018

- Worked as a React Developer for a startup called DataChat.

Associate Research Specialist

Jan 2019 - Nov 2019

Laboratory of David O'Connor, University of Wisconsin-Madison Department of Pathology

- Worked as a Associate Research Specialist in the Laboratory of David O'Connor. Performed a number of Bioinformatics related tasks, including running an Allele assembly pipeline on servers at UW-Madison's Center for High Throughput Computing with HTCondor, as well as the development of an Allele annotation pipeline. I oversaw the submission of over 500 alleles to IPD, the Immuno Polymorphism Database, which is hosted by the European Molecular Biology Laboratory.

PROJECTS

Computational Number Theory: Cohen-Lenstra Heuristics for Cubic Number Fields Spring 2013

University of Wisconsin-Madison

- Used the Mathematical Computing Software Sage to compute the Fractional Ideal Class Groups of Non-Cyclic Cubic Number Fields within the University of Wisconsin-Madison Mathematics Department's Collaborative Undergraduate Research Laboratory. Our computation extends far beyond other online databases by a factor of 1000, in terms of discriminant bound. This project involved remotely connecting to a Math Department server and managing a large file system while constantly writing Python and Shell Scripts.