

Portland. OR

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Summary_

Currently an **Associate Data Scientist** at Vacasa in Portland, OR. I have 3+ years working in data analytics and research in various aspects for both business and science. I am comfortable jumping into unfamiliar projects and trying new things and have experience using a variety of tools and techniques. I have experience working with a fledgling data science team and communicating to both non-technical stakeholders and engineers alike.

Skills_

Programming Python, PostgreSQL, Git, Bash

Data Science Pandas, Numpy, Jupyter, Data Visualization, Feature Engineering, Linear Algebra, Statistics, Predictive Modeling, Machine Learning

Other Documentation, AWS (redshift, s3)

Experience_

Vacasa Portland, OR

Associate Data Scientist

Jul 2018 - PRESENT

- · Worked closely with both software engineers and stakeholders to create machine learning models to help with business needs.
- A big item was significantly improving an old model used to predict cleaning times. Worked with various people in the business to start the initial pass as well as further working on reporting the progress of the model and features chosen. For the project, it was important to be able to present the technical aspects in a way that was understandable for non-technical people. End product was a model widely used by the business.

JUNIOR ANALYST Sep 2017 - Jul 2018

- Building training set for machine learning model to predict owner churn, identifying gaps in owner data, and identifying indicators to help determine at risk owners.
- Presented work to COO and other upper management to show current status of project and working hands on with the direction of the model.
- Gained experience on showing why a project might not be worth continuing despite the want and what can be done to make the project work in the future.

ANALYST INTERN Jun 2017 - Sep 2017

University of Oregon - Institute of Molecular Biology

Eugene, OR

BIOINFORMATICIST - SELKER LAB

Oct 2016 - May 2017

- Updated and managed scripts for analysis of ChIP-seq and RNA-seq data.
- Compared ChIP-seq datasets looking at differences in RNA pol II binding between different strains of n. crassa. Done using various data analysis programs and automated using R and bash scripting.

SCIENTIFIC PROGRAMMER - HARMS LAB

Sep 2015 - May 2017

- Developed a GUI using PyQt5 for python API that analyses isothermal calorimetry (ITC) data. Along with this, wrote documentation for GUI using sphinx on Read the Docs as well as a C extension to calculate the binding polynomial in the API.

 Repo: https://github.com/harmslab/pytc-gui and https://github.com/harmslab/pytc
- Developed an extension of a phage display analysis pipeline. Researched and implemented different methods of data clustering.
 Repo: https://github.com/harmslab/phagedisplay

Publications

Hiranmayi Duvvuri, Lucas C. Wheeler, and Michael J. Harms

Biochemistry

PYTC: OPEN-SOURCE PYTHON SOFTWARE FOR GLOBAL ANALYSES OF ISOTHERMAL TITRATION CALORIMETRY DATA

2018

Education

B.S. IN BIOCHEMISTRY

University of Oregon

Eugene, OR

Sep 2011 - Sep 2016

• focus on biology, chemistry, and computer science