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ERIN GILL, PhD

Website: https://eringill.github.io
GitHub: https://github.com/eringill
LinkedIn: https://www.linkedin.com/in/erin-e-gill-phd
Blog: https://vancouvercodeprojects.hashnode.dev/

SKILLS

Programming Languages: Python | R | SQL | HTML | CSS | Bootstrap
Python Libraries: Pandas | Matplotlib | Seaborn | Plotly | Bokeh | scikit-learn Keras | Tensorflow | SciPy | Numpy
Technical Skills: statistics | machine learning | pipeline development | dashboard development | AWS | data visualization | data cleaning | cloud deployment | Linux server deployment | git | database design

EXPERIENCE

Simon Fraser University, Burnaby, BC — *Research Associate*

FEB 2020 - PRESENT

- Designed and deployed a PostgreSQL database on AWS RDS to store Canadian SARS-CoV-2 case and sequencing information.
- Developed and iteratively improved an interactive dashboard that is hosted on Heroku. The dashboard automatically downloads data from multiple sources to display live Canadian SARS-CoV-2 case, vaccination and hospitalization data [1].
- Created a ML software package in Python that automatically detects outliers in time series data using multiple statistical strategies and forecasts future timepoints.
- Analyzed BC socioeconomic and COVID-19 vaccination data from multiple sources. Built and evaluated linear regression models to determine factors influencing vaccine uptake.

IMV Inc., Dartmouth, NS — *Research Scientist*

FEB 2019 - SEP 2019

- Analyzed and visualized gene expression data from clinical trial participants in R via GLM regression to produce actionable insights for drug mechanism of action.

R.E.W. Hancock Lab, University of British Columbia, Vancouver, BC — *Research Associate and RNA-Seq Program Manager*

JAN 2014 - APR 2018

- Built and improved pipelines on a Linux server with Bash scripts for breaking down and analyzing large amounts of complex data.
- Utilized random forest machine learning approaches in R to identify sets of genes driving disease etiology.
- Developed a novel statistical algorithm in R to identify gene expression signatures associated with diseases that have overlapping symptomologies, thus enabling greater diagnostic accuracy [2].

- Analyzed dozens of gene expression datasets in R using CRAN and Bioconductor software packages to generate insight into the biological processes underlying sepsis, cystic fibrosis, asthma and bacterial virulence.

Indel Therapeutics Inc., Vancouver, BC — *Postdoctoral Intern - Virtual Screening (Drug Development)*
AUG 2012 - NOV 2013

- Performed *in silico* ligand docking with protein structures to select small molecules with antimicrobial activity for *in vitro* testing.
- Identified potential antimicrobial drug targets computationally, reducing the time spent on downstream activities by orders of magnitude.

F. Brinkman Lab, Simon Fraser University, Burnaby, BC — *Postdoctoral Researcher / Project Manager*
FEB 2009 - JUL 2012

- Performed *in silico* ligand docking with protein structures to select small molecules with antimicrobial activity for *in vitro* testing.

EDUCATION

University of British Columbia — *PhD (Genetics)*
Dalhousie University — *BSc (Biochemistry and Biology)*

TECH COMMUNITY OUTREACH

Co-leader of Codecademy Vancouver Code Projects Chapter
MAY 2021 - PRESENT

- Hosting monthly meetups to teach less-experienced individuals how to code [3].
- Developing and disseminating online learning resources that enable novices to work at their own pace.

PUBLICATIONS

- I have co-authored 27 peer-reviewed publications. They can be viewed here [4].

REFERENCES AND LINKS

[1] https://canadacoviddashboard.herokuapp.com/

[2] https://pubmed.ncbi.nlm.nih.gov/33692808/

[3] https://community.codecademy.com/vancouver-code-projects/

[4] https://tinyurl.com/38yft8hx