Gurkamal Deol

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EDUCATION

UNIVERSITY OF GUELPH
Master of Bioinformatics
Aug 2019 | Guelph, ON

WESTERN UNIVERSITY
Bsc. in Genetics and Pharmacology
June 2017 | London, ON

SKILLS

LANGUAGES
Python
R
SQL
HTML and CSS
Shell - Bash

MACHINE LEARNING
Scikit-Learn
Glmnet
CARET
Tensorflow
RDKit

TOOLS
UNIX
PostgreSQL
Github
Virtual Box
Jupyter
Google Compute Engine

DATA ENGINEERING
Hadoop
Tableau

EXPERIENCE

CYCLICA | Bioinformatics Developer (co-op)
April 2019 - August 2019 | Toronto, ON

- Created and maintained a database of 300 million rows using PostgreSQL.
- Built and monitored indexes to bring down processing times from minutes to seconds.
- Wrote complex SQL queries using complex joins, grouping, aggregation, nested subqueries.
- Added the ability to perform complex cheminformatics querying by integrating functions from RDKit - such as molecular similarity searching.

WESTERN UNIVERSITY | Research assistant
April 2016 – June 2017 | London, ON

- Thesis Project: Detecting Prostate Cancer Using Tumor-Activatable Minicircles Encoding the Biomarker SEAP
- Data collection using: Bioluminescence imaging of cells; Western blotting; BCA assays; Immunocytochemisty; PSA testing - ELISA kit.
- Producing Minicircles - Steps include transgene cloning, DNA extraction/isolation; cloning, plasmid purification.

PROJECTS

PREDICTING ENVIRONMENTAL CARCINOGENS | github/gdeol4

- Conducted a novel case study using molecular fingerprints as features to classify compounds as carcinogens.
- Demonstrated the following concepts from Scikit-learn: fixing class imbalance using the ADASYN algorithm, parameter tuning, logistic regression, k-nearest neighbor, and gradient boost algorithms.
- Evaluated model accuracy with metrics such as AUC scores, f1-scores, and confusion matrices.

EXAMINING BANK CHURN USING A GEOSEGMENTATION MODEL | github/gdeol4

- Built a logistic regression model with Gretl by using variance inflation factors (VIF) and odds ratios for feature engineering.

DRUG DECODER | github/gdeol4

- Created a web app which converts common drug names to their SMILES (molecular structure) format using Pandas and Numpy libraries and Flask

FAQ2VAR | (FASTQ to variant calling pipeline) | github/gdeol4

- Created a variant pipeline to be used which takes FASTQ input files returns variant calling format (VCF) files.
- Pipeline written in bash and using the following tools: sickle, sabre, SamTools, HTSlib, BCFtools, bwa.