

Gurkamal Deol

gurkamal.com | github.com/gdeol4
gdeol4@uwo.ca | 226.688.7704 |

EDUCATION

UNIVERSITY OF GUELPH
MASTER OF BIOINFORMATICS
Sept 2017 | Guelph, ON

WESTERN UNIVERSITY
BSC. IN GENETICS AND
PHARMACOLOGY
June 2017 | London, ON

SKILLS

LANGUAGES

Python
R
SQL
HTML and CSS
Shell
Hadoop

MACHINE LEARNING

Scikit-Learn
Glmnet
CARET
Tensorflow
RDKit

TOOLS

UNIX
PostgreSQL
Github
Virtual Box
Jupyter
Google Compute Engine

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 - an open source molecular modeling toolkit.

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; Immunocytochemistry; 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.

DRUG DECODER | GITHUB/GDEOL4

- Created a web app which converts common drug names to their SMILES (molecular structure) format to help scientists reduce manual searching time.
- Wrote the drug conversion processes in python, utilizing the Pandas and Numpy libraries.
- Used Flask to create the web app with secure form submissions and ability to delete all uploaded data for privacy.

FAQ2VAR | (FASTQ TO VARIANT CALLING PIPELINE) | GITHUB/GDEOL4

- Created a variant pipeline to be used with fastq type files containing genomic information and returns a variant calling format (VCF) file. Intermediary .BAM and .SAM files can also be used.
- Written in bash and using the following tools: sickle, sabre, SamTools, HTSLib, BCFtools, bwa.