## T: 604.822.9677 | F: 604.822.9676 | science.coop@ubc.ca | www.sciencecoop.ubc.ca







https://nafabrar.github.io https://github.com/nafabrar +1 778-929-4772

nafis.abrar@alumni.ubc.ca

# **EDUCATION**

B.Sc. in Computer Science 4th year at University of British Columbia

Vancouver

Focus on Machine Learning

Notable courses: Intelligent Systems/AI, Machine Learning, Advanced Database, Computer Vision, Software Engineering, Statistical Learning.

**WORK** 

Jan 2019-Present

#### DATA SCIENTIST

■ Toronto

at ScotiaBank (Artificial Intelligence and Machine Learning Team)

- Currently working on Scotiabank's global fraud detection Al software by applying ensemble methods for prediction and inference.
- Performed sensitivity analysis and hyperparameter tuning to improve model performance.
- Set up multiple pipelines using Microsoft Azure and Docker to parallelize the training phase. This resulted in a speed up of 50%.
- Presented results to business stakeholders and potential custom-

Jan 2018 - • Aug

## SCIENTIFIC SOFTWARE DEVELOPER

Vancouver

at BC Cancer Research Centre (Sohrab Shah Lab)

- Worked on a machine learning research project for integrating genomic data with imaging data of cancer cells to classify dead/ alive cells. The classifier resulted in an prediction accuracy of 84%.
- Performed data analysis and implemented machine learning algorithms for cancer cell clustering problems and Microsoft hololens cell visualization app using Python libraries.
- Implemented, extended and documented python APIs and REST interfaces.

May 2017 - 🐞 Sept 2017

# **FULL STACK WEB-DEVELOPER**

Vancouver

at UBC EOSC (Earth and Ocean Sciences)

- Contributed to the backend of the UBC EOSC website by creating models, views and forms using Django.
- Exported CSV files from older Drupal7 UBC website and wrote Python scripts that automatically created objects in the new Django website using the CSV data. This resulted in loading 1000+ records in the new website.



### **RELEVANT PROJECTS**

June 2018

## PIMS BC DATA SCIENCE NLP CAPSTONE PROJECT (COMM100)

Language: Python Frameworks: Pandas, Scikit Learn, TextBlob, spaCy

- Worked in a team of 10 to determine intent and create knowledge base from live chat transcripts. The data set was provided by Comm100 which includes online chat sessions.
- The goal of the project was to cluster or correlate chat sessions and build a knowledge base in an automated way using mathematical models.

http://workshop.bcdata.ca/2018/finalpres/comm100-slides.

October-Present Personal Projects

#### MACHINE LEARNING/DATA SCIENCE

Language: Python Frameworks: Pandas, Scikit Learn

- Implemented supervised and unsupervised machine learning algorithms with Python (pandas, numpy). The following algorithms are implemented: Linear Regression, Kmeans, KNN, RBF-Kernels and Stochastic Gradient Descent.
- Built a sentiment analyser that extracts data from Twitter given a topic. The data from the Twitter API is then processed to give a result of how people feel about the user provided topic.
- Worked on computer vision projects such as scene recognition with bag of words, face detection in a scaled representation, local invariant features and RANSAC.

## Programming Languages

Competent (1 year) Projects: Restaurant App, Advanced Calculator, DNS Server, FTP Client, Gym Database using JDBC

Basic (8 months) Projects: FTP Server, x86 implementation

Python Competent (2 years) Projects: Machine learning algorithms, Django-UBC EOSC website, Rhoads, NLP

SOL Competent (1 year) Projects: GYM Database, UBC EOSC website

Unix/bash Competent(1 year)



#### Web development and Design

HTML and CSS -Competent(4 months) Projects: UBC Eosc website, Rhoads website

TypeScript\* -Basic (3 months) Projects: Insight UBC

Django -Proficient (8 months) Projects: UBC EOSC website, Rhoads website



### Machine Learning/Data Science

- Python scikit-learn, Pandas, matplotlib
- PySpark\*
- Xaboost\*
- TensorFlow\*
- Microsoft Azure

<sup>\*</sup>Current learning for work project



- Github
- Docker
- Jira



### Publication

Scalable whole genome sequencing of 40,000 single cells identifies stochastic aneuploidies, genome replication states and clonal repertoires.

https://www.biorxiv.org/content/early/2018/09/13/411058