# Jean Charle Yaacoub

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#### **INTERESTS**

I have experience across a wide range of DL topics from conventional CNNs to NLP and recently I am working on a project utilizing Graph NNs and foundation models like ESM for precision oncology.

#### **EDUCATION**

## **MSc in Applied Computing**

September 2022 - December 2023

University of Toronto, Department of Computer Science Artificial Intelligence Concentration

Courses:

CSC2559 Trustworthy ML

CSC2552 Topics in Computational Social Science

CSC2231 Visual and Mobile Computing Systems (Winter)

CSC2545 Advanced Topics in ML – Causal Learning (Winter)

**Bachelor of Computing (Honors)** 

Queen's University of Kingston, Department of Computer Science

Artificial Intelligence Specialization

4.16 GPA

#### **WORK EXPERIENCE**

# **Princess Margaret Cancer Centre – UHN**

Jan 2024 - Present

(Full-time)

Research Analyst

## **Princess Margaret Cancer Centre – UHN**

May 2023 – December 2023

September 2018 – June 2022

(Intern)

Co-op Master's Student

- Worked on project to improve precision oncology using GNNs (see MutDTA below).
- Collaborated with others in the lab to help brainstorm ideas and provide feedback during group meetings and 1-1s.

#### Vancouver Prostate Centre - UBC Lab

August 2020 - December 2021

(On and off between part-time and full-time)

Undergraduate Academic Assistant

- Helped to improve the performance of the Deep Docking model designed to accelerate the drug discovery process. This included optimizing code to run up to 3x faster and improving the model's architecture to be more accurate.
- Co-led the design and development of a GUI web application that made Deep Docking more accessible.
- Helped review and write papers for submission.

## **NOTABLE PROJECTS**

## **UofT MScAC Thesis Project - MutDTA**

May – Dec 2023

GNNs with Protein Dynamics for Enhanced Drug Targeting - github.com/jyaacoub/MutDTA

Project looking at using GNNs for binding affinity prediction to improve precision oncology for cancer patients. Researched, designed, and iterated on models under limited resources which required creative solutions to overcome with distributed multi-node computing. Additionally, leveraged existing ESM-2 foundation protein language model to improve prediction results.

## CSC2231 - Visual and Mobile Computing Systems Project

Winter 2023

Federated Learning Vision Transformers - github.com/jyaacoub/FL-ViT

A project Looking at optimizing the performance of Vision Transformers under a federated learning environment. Implemented in python using <u>flower</u> library to perform distributed training under simulated and real-world conditions with clients containing varying levels of processing power.

# CSC2559 - Trustworthy ML Project

Fall 2022

Cross-Domain Attacks in NLP - github.com/jyaacoub/Cross-Domain-Attacks-NLP

As a team of two we explored the transferability of adversarial examples across problem domains in NLP to get a better understanding of the intuition behind their existence in NLP. I helped review papers and

implement solutions for testing. We found that transferability across domains was weak, signaling that adversarial examples come from high level features of language similar to CV which arise from "non-robust features".

# OpenAl Hackathon for Climate Change

Net Zero AI – github.com/jyaacoub/CSR\_summarizer

2022 Nov 11-14

Fall

Led a team in developing a tool to create meaningful summaries from lengthy Corporate Social Responsibility reports. I helped bring people together, organize and divide up tasks. I was also in charge of the backend programming; utilizing the OpenAl APIs to perform semantic search and summarization via GPT-3 text completion.

Winter 2022

# CISC 499 - Undergraduate Project

Powerful Puzzling - github.com/QuMuLab/PowerfulPuzzling

Designed and implemented a novel jigsaw puzzle solver that works with island pieces (group of 2 or more connected pieces). I came up with a matching algorithm that utilized color and shape characteristics to connect the segmented pieces together. I also acted as the team leader, organizing, and tracking tasks that needed to be done via GitHub projects.

# CISC 474 – Reinforcement Learning Project

Fall 2021

"Playing Atari with Deep Reinforcement Learning" - github.com/jamesgleave/DeepRL-ATARI
Replicated the results from the 2013 DeepMind paper on Atari games. Oversaw programming the Deep
Q-Learning model architectures to be tested using TensorFlow. Also helped design the test environment
and utilize transfer learning to speed up training.

#### Mayors Innovation Challenge/QHacks

Cycle AI - devpost.com/software/cycle-ai

Winter 2020 Feb 1-31

As a team of 4 we developed Cycle AI, an app that uses ML to classify certain articles of trash/recyclables to incentivize awareness of what a user throws away. Here I oversaw programing the frontend and connecting it to the Computer Vision model in the backend. With this we were the winning team overall at QHacks (hackathon hosted by Queen's University) and got the opportunity to compete in a pitch competition against Kingston's brightest students in the Mayor's Innovation Challenge.

#### **TECHNICAL SKILLS**

Programming Languages: Python, JavaScript, Java, C, MATLAB, and Prolog.

Machine Learning: PyTorch, pytorch-lightning, torch\_geometric, Scikit-learn, and Matplotlib.

HPC and Distributed Learning: SLURM, Ray[Tune,Train], Flower

Web development: Flask, SQL

#### **PUBLICATIONS**

Yaacoub J.C., Gleave J., Gentile F., et al. "DD-GUI: a graphical user interface for deep learning-accelerated virtual screening of large chemical libraries (Deep Docking)", *Bioinformatics*, Volume **38**, Issue 4, 15 February 2022, 1146–1148. <a href="https://doi.org/10.1093/bioinformatics/btab771">https://doi.org/10.1093/bioinformatics/btab771</a>

Gentile F., Yaacoub J.C., Gleave J., et al. "Artificial Intelligence-Enabled Virtual Screening of Ultra-Large Chemical Libraries with Deep Docking", *Nature Protocols*, **17**, 4 February 2022, 672-697. https://doi.org/10.1038/s41596-021-00659-2

Gentile F., Fernandez M., Ban F., et al. "Automated discovery of noncovalent inhibitors of SARS-CoV-2 main protease by consensus Deep Docking of 40 billion small molecules" *Chem. Sci.*, **12**, 17 November 2021, 15960-15974. <a href="https://doi.org/10.1039/D1SC05579H">https://doi.org/10.1039/D1SC05579H</a>