

BANG CHI DUONG

<https://bangchi.tk>

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SKILLS

- **Languages:** Python, R, C++, Java, Javascript, SQL, HTML5, CSS3, Perl
- **Frameworks:** React, Bootstrap, Typescript, NodeJS, Express, TensorFlow
- **Machine Learning:** Generalised Linear Model, Classification, Dimension Reduction Analysis

EDUCATION

- **University of British Columbia** Vancouver, Canada
Bachelor of Computer Science (BCS); GPA: 82.70/100.00 Sep 2017 – Apr 2020
- **University of Guelph** Guelph, Canada
Master of Bioinformatics; GPA: 91.00/100.00 Sep 2016 – Aug 2017
- **University of Toronto** Toronto, Canada
Bachelor of Science (Hons) in Physics, Statistics and Chemistry; GPA: 3.73/4.00 Sep 2012 – Aug 2016

EXPERIENCE

- **Ubisoft - La Forge** Montreal, Canada
AI Programmer Sep 2018 – Dec 2018
 - **Maya nCloth Data Simulation:** Generate a pool of nCloth data in Maya to capture a wide range of dynamics, including internal/external collisions such as human body and wind
 - **Deep Learning for Cloth Simulation:** Train neural networks for both linear and non-linear dynamics of a cloth that run entirely in the subspace, leading to computation that scales proportionally to the number of subspace modes rather than the number of simulation elements; also, complex environmental interactions including collisions with external objects are tested
 - **Potential Impact:** Compared to a highly optimised simulation engine currently shipped in AAA game products, the method achieves a five times speed-up on average versus the low-quality baseline, while approaching the quality of the high-quality simulation data
- **Structural Genomics Consortium (SGC)** Toronto, Canada
Bioinformatics Analyst May 2017 – Aug 2017
 - **Visualisation:** Analysed sequencing data using R, with graphical visualisations such as multidimensional scaling, principal component plot, heatmaps, and volcano plots, supported by different R packages such as ggplot2, limma, and edgeR
 - **Differential Analysis:** Constructed Generalised Linear Models and a Peptide-based Model, resulting in about 1000 differentially expressed genes (RNA-Sequencing data) out of a pool of approximately 13,600 genes, and about 200 differentially expressed proteins (proteomic data) out of a pool of approximately 4,500 proteins

PROJECTS

- **Movie Review Web App - JavaScript/React/Bootstrap/NodeJS:** Find movies using API of The Movie Database (TMDb); write own reviews, find and follow others' reviews; <https://cs490-project-movie.herokuapp.com/>
- **Car Detection - Python:** Detect cars in images using Linear-SVM model on features extracted from HOG method
- **Lossy Image Compression - C++:** Compress images using space partitioning trees, specifically 2-D trees
- **Convex Hull - C++:** Find a convex hull, and an intersection region (if exists) of a convex polygon with an arbitrary polygon in images, using Graham Scan and Sutherland-Hodgman algorithms
- **Classification Methods - R:** Predict cancer severity as malignant or benign, on a mammographic dataset, using k-fold cross-validation to compare multiple classifiers: logistic regression, linear and quadratic discriminant analyses, support vector machine, random forest, adaptive boosting, and k-nearest neighbours

OTHERS

- **Tutor:** Provided Maths/Stats/Physics tutoring services to university and high school students
- **Teaching Assistant:** Prepared high school students for the Physics CAP exam
- **Choir Member:** Performed in a choir at senior/retirement homes biweekly