

# BANG CHI DUONG

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## SKILLS

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

## EDUCATION

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- **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

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- **Ubisoft - La Forge** Montreal, Canada  
*AI Programmer* Sep 2018 – Dec 2018
  - **Maya nCloth Data Acquisition:** Generated and extracted a pool of cloth and soft body data using Maya nCloth engine, and capture a wide range of dynamics, including self-collision, external collisions with rigid bodies, and external forces such as wind strength, noise, and directions
  - **Fast and Stable Cloth/Soft-body Real-time Simulation:** Trained neural networks to learn non-linear dynamics of six cloth-related systems including soft bodies and predict future motion trajectory that run entirely in a compressed linear subspace of 256 bases from a 7,500-9,000 degrees of freedom full-space
  - **Vertex Normals Approximation:** Trained a linear regression model to approximate cloth's vertex normals from the cloth subspace compressed representation
  - **Result:** Combined data driven techniques and subspace methods with GPU decompression optimisation, to achieve a realistic and high performance runtime, upto 7,000 times speedup from offline physics simulation, in a real-time interactive application including cloth and soft body self-collision and external collisions, in exchange for expensive precomputations and some extra memory usage
- **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 1,000 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

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- **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

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- **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