# Dong-Jo (Dongjo) Ban

# **EDUCATION**

**ADDRESS:** 251 10<sup>th</sup> Street NW, THD307A • Atlanta, GA • 30318 **CELL:** (419) 705-8402 • **E-MAIL:** dongjoban17@gmail.com

WEBSITE: dongjoban17.github.io

Georgia Institute of Technology | Atlanta, GA

Master of Science in Bioinformatics, 4.0/4.0 GPA, Dec 2018 (Expected)

The Ohio State University | Columbus, OH

Bachelor of Science in Computer & Information Science (Minor in Statistics), May 2017

**SKILLS** (Basic Proficiency Marked with \*)

Languages: Python, R, Bash, Perl, PHP\*, Javascript\*, Java\*, SQL\* Technologies: Unix/Linux, Rstudio, Photoshop, Illustrator, Laravel\*

## WORK EXPERIENCE

Graduate Research Assistant, Aug 2017 - Current

Jordan Lab, School of Biological Sciences | Atlanta, GA

Computatational Method For Predicting Metabolites With Anticancer Properties

- Extracted and reformatted data from various sources (GEO, KEGG, HMDB, etc.) for analysis.
- Performed gene expression analysis on microarray and RNA-Seq data.
- Predicted clinically relevant metabolites that are down-regulated in cancer cells.

McDonald Lab, Integrated Cancer Research Center | Atlanta, GA

Assessing the Impact of Aberrant Epigenetic Changes on Allele-specific Expression (ASE) in Ovarian Cancer

• Examining the effect of perturbing epigenetic controls by using a histone deacetylase inhibitor (Trichostatin A) and a DNA methyltransferase inhibitor (decitabine) in an ovarian cancer cell line (HEY-A8).

#### Research Technician I (Tech Temp), May 2018 - Aug 2018

McDonald Lab, Integrated Cancer Research Center | Atlanta, GA

Examining Allele-specific Expression in Cancer Cell Lines and Ovarian Cancer Patients

- Developed pipeline for data pre-processing (quality control) and allele-specific downstream (alignment, variant calling, etc) analysis using whole-exome and RNA sequencing data.
- Created figures and visualizations to present data and findings.

#### Student Intern, Jun 2016 - Apr 2017

Payne Lab, Department of Biomedical Informatics | Columbus, OH

Retrospective Analysis of Drug Repurposing Hypotheses in Melanoma Using EHR Data

- Integrated EHR and administrative data to determine drug exposure of the patients.
- Developed algorithms for covariate detection within patients' records, including melanoma stage and surgical therapy.
- Evaluated survival outcomes using Cox-Regression models and hazard ratios. The results showed that around 50% of patients that have taken NSAIDs were less likely to die from melanoma.

Manuscript in Preparation

Regan K, Ban D, Kil J, Gascon G, Latchana N, Suarez-Kelly L, Pinette A, Li F, Carson WE, Payne PRO, Retrospective Analysis of Electronic Health Record and Administrative Data for Drug Repurposing Hypothesis Evaluation in Melanoma

## **LEADERSHIP & AWARDS**

Global Leadership Initiative (Aug 2016 - May 2017), Cohort Member Korean International Student Organization (Aug 2015 - Aug 2016), VP Office of International Affairs (Jul 2015 - Jan 2017), Peer Advisor Republic of Korea Army (July 2012 – April 2014)

Computational Biology Faculty Research Awards (2017, 2018), Georgia Institute of Technology Certificate of Commendation (2014), Presidential Security Service