

Dong-Jo (Dongjo) Ban

ADDRESS: 251 10th Street NW, THD307A • Atlanta, GA • 30318

CELL: (419) 705-8402 • **E-MAIL:** dongjoban17@gmail.com

WEBSITE: dongjoban17.github.io

EDUCATION

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 *)

Programming: Python, R, Bash, Perl, PHP*, Javascript*, Java*, SQL*

Bioinformatics: BLAST, SAMtools, GATK, BWA, STAR2, FastQC, RNA-SeQC, SRA Toolkit

Technologies: Rstudio, macOS, Unix/Linux, Photoshop, Illustrator, Laravel*

RELEVANT EXPERIENCE

Graduate Research Assistant, Aug 2018 – Current

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 HEY-A8 Cell Line and Ovarian Cancer Patients

- Developed pipeline for data pre-processing and downstream allele-specific analysis using whole-exome and RNA sequencing data.
- Compared allele-specific expressions of primary and metastatic samples of ovarian cancer patients.
- Identified genes displaying allele-specific expression that are shared across primary and metastatic samples.

Graduate Research Assistant, Aug 2017 – May 2017

Jordan Lab, School of Biological Sciences | Atlanta, GA

Computational 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.

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.

LEADERSHIP & AWARDS

Computational Biology Faculty Research Awards (2017, 2018), Georgia Institute of Technology

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

Certificate of Commendation (Feb 2014), Presidential Security Service

Republic of Korea Army (Jul 2012 – Apr 2014)

REFERENCES

I. King Jordan

Associate Professor, Director of Bioinformatics Program
School of Biological Sciences, Georgia Institute of Technology
950 Atlantic Drive
Atlanta, GA 30332
404-385-2224
king.jordan@biology.gatech.edu

John F. McDonald

Professor, Director of Integrated Cancer Research Center, CSO of Ovarian Cancer Institute
School of Biological Sciences, Georgia Institute of Technology
315 Ferst Drive NW
Atlanta, GA 30332
404-385-6630
john.mcdonald@biology.gatech.edu

Evan Clayton

PhD Student, Bioinformatics
School of Biological Sciences, Georgia Institute of Technology
315 Ferst Drive NW
Atlanta, GA 30332
732-570-5903
eclayton3@gatech.edu