

Dong-Jo (Dongjo) Ban

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EDUCATION

Georgia Institute of Technology | Atlanta, GA

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

Relevant Coursework: Applied Genomics and Bioinformatics, Computational Genomics, Data & Visual Analytics, Programming for Bioinformatics, Biostatistics

The Ohio State University | Columbus, OH

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

Relevant Coursework: Data Mining & Analysis, Mathematical Statistics, Data Structures & Algorithms, Database Systems, Capstone Design: Information Systems

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, IGV

Operating Systems: macOS, Unix/Linux, Windows

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 HEY-A8 using next-generation sequencing (NGS) data.

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 (TCGA).
- 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.

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
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