Djina Pajkic

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Cover Letter

My computer programming experience consists of nearly two years of research lab data-analysis using Python software. My research was focused on illuminating genetic differences and variation among different strains of model organisms (Behavioral genetics in Drosophila melanogaster; Drug Response Variation in Caenorhabditis elegans) at the University of Toronto.

I began to be interested in Computer Science during my employment in the Fraser Lab. To supplement my efficiency to conduct research, I completed a Python programming course at the University of Toronto. The course facilitated my ability to generate and optimize software for high-throughput image data analysis through python programming and provided me with working knowledge of Python software. My work, which illustrated that cyanide response varies over different developmental stages, was analyzed using high-throughput image data analysis that I helped develop and has contributed to two papers. One was accepted and the other is under review for publication; one of which has me listed as second author.

I have since been studying online and in a full time immersive Bootcamp course at Lighthouse Labs. I am confident that I have the necessary skills to begin working as a Junior Developer where I will be able to continue my learning.

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PROFESSIONAL SUMMARY

I am an Honours B.Sc. University of Toronto graduate and have discovered a new passion for coding. After two years of research experience that included data analysis using Python software I have decided to transition into Web Development, Full Stack. I have completed an immersive Full-Time Web Development Program at Lighthouse Labs in Toronto and am ready to begin working as a Junior Developer.

EXPERIENCE

RESEARCH SCIENTIST AND LAB TECHNICIAN

Dr. Andrew Fraser Laboratory - Donnelly Centre For Cellular And Biomolecular Research, University of Toronto - Toronto ON, CAN, April 2013 - December 2015

My full-time employment in Dr. Fraser's lab advanced my research experience involving the model organism C. elegans in regards to natural genetic variation research. I have aided and gained experience in developing assays, analyzing data using Python software, presenting data in a stimulating way and preparing data for publication.

RESEARCH SCIENTIST/STUDENT

Dr. Andrew Fraser Laboratory - Donnelly Centre For Cellular And Biomolecular Research, Toronto ON, CAN, September 2013 - March 2014

Project: Study of Natural Genetic Variation in C. elegans via a Neurotransmitter Drug Screen Uncovers Two Drugs with Putative Variant Loci. Natural variation is very important; every single individual is different in numerous ways, many of which are genetically determined. Despite being profoundly alike in our biology, different individuals will respond to the same substrates differently; regarding this project, the focus is on drug response variation. A panel of eighteen drugs, pertaining to the nervous system, were screened by using genotypically diverse C. elegans isolates, and exposing them to different drug concentrations. By examining the drug's effect at two developmental stages (early - L1 and late - adult), a clearer picture of variation was uncovered. Seven drugs showed an effect on worms and one (chlorpromazine) exhibited a clear difference in drug response between isolates. Therefore, unearthing the disparity between isolates will shed light on the genetic basis for variability in drug susceptibility between individuals.

PRESENTER

Undergraduate 3MT - University of Toronto, Toront ON, CAN, April 2014

Participated in the first Undergraduate Three Minute Thesis competition at the University of Toronto. 3MT challenges students to give a compelling presentation of their independent research in only three minutes to a panel of non-specialist judges.

VOLUNTEER

Sunnybrook Hospital, University of Toronto, Toronto ON, CAN, August 2010 - August 2012

Through the volunteer program, I've witnessed the quality of care health professionals provide on a daily basis as well as the type of environment hospital life conveys. In addition to Sunnybrook, I've also volunteered at a number of academic events such as symposiums/conferences and talks held by researchers at the University of Toronto. Total number of hours: 250+.

VICE PRESIDENT OF COMMUNICATIONS

Biotechnology Society, University of Toronto - Toronto ON, CAN, September 2010 - April 2011

I was elected as VP of communications for the Biotechnology Society at the University of Toronto. My duties included bringing awareness and educating students about the innovative and expanding field known as biotechnology through seminars presented by researchers within the industry and academia.

RESEARCH ASSISTANT
Dr. Marla Sokolowski Laboratory - Department of Cell and Systems Biology, University of Toronto - Toronto ON, CAN, September 2012 - February 2014
Hands-on experience with fundamental molecular techniques, as well as familiarization with Drosophila rearing, has provided me with valuable research experience that I will require for further prospects.

PROJECTS

A HIGH-THROUGHPUT IMAGE-BASED ASSAY TO MEASURE THE ACUTE EFFECTS OF DRUGS ON C. ELEGANS
Generated and optimized software for high-throughput image data analysis through python programming. Illustrated that cyanide response varies over different developmental stages.

NATURAL VARIATION IN GENE EXPRESSION MODULATES THE SEVERITY OF MUTANT PHENOTYPES.
Validated RNAi data showing natural variation in the electron transport chain via potassium cyanide dose-response curve variation.

EDUCATION

HONOURS B.SC.
University of Toronto • Toronto ON, CAN • 2014

SKILLS

TWO YEARS EXPERIENCE - DATA ANALYSIS PYTHON NUMPY ARRAYS, MATPLOTLIB, D3 **JAVASCRIPT** AJAX **JQUERY** RUBY **RUBY ON RAILS** PHOTOSHOP **SINATRA** NODE.JS **REACT** MYSQL **HTML5** CSS3 **GENETICS** BIOTECHNOLOGY **MICROSOFT OFFICE** MOLECULAR BIOLOGY **WINDOWS AND MAC OS** DNA, RNA, PROTEIN PREPARATION AND HANDLING **MAGIC TOOL ANALYSIS** QUANTITATIVE IMAGE ANALYSIS SOFTWARE **MICROARRAY CHIP TECHNOLOGY** SERBIAN **CROATIAN** BOSNIAN **MEGA4** NEXT GEN SEQUENCING **MSA** NCBI/BLAST

CONTACT

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