BRIANNA K. RICHARDSON

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EDUCATION

University of Florida — **Gainesville, FL**
Ph.D., Human-Centered Computing — May 2020

University of Maryland Baltimore County (UMBC) — **Baltimore, MD**
B.S., Bioinformatics & Computer Science, **GPA: 3.6** — May 2018

HONORS/AWARDS

Marc U*Star Scholar — **Fall 2016 – May 2018**
Meyerhoff Scholar — **Fall 2014 – May 2018**

SKILLS

Programming: MATLAB, Python, C/C++, R, Java, SQL, Perl, NASM assembly language
Applications: GitHub, Bitbucket, Android Studio
Operating Systems: Linux, OS, Windows, MacOS
Scripting: JavaScript, PHP, HTML, Bootstrap Frameworks

WORK EXPERIENCE

B&D Consulting — **Hagerstown, MD**
Block Chain Intern — June 2018– August 2018

- Contributed to a Hyperledger software for optimizing energy use in households
- Led a mini-project to create a hybrid web application for visitors to login to the office

UMBC Computer Science Department — **Baltimore, MD**
Introduction to Computer Science Teacher Assistant — August 2017– May 2018

- Led a discussion class, guiding computer science majors through the theoretical computer science, programming through Python, and using a cluster for the first time
- Worked with a team of TAs to create assignments, grade assignments, & lead office hours to assist students through lab, homework, and project assignments

Varsity Tutors — **Baltimore, MD**
Tutor — March 2017 – May 2018

- Mentored undergraduate and graduate students through Computer Science courses, providing supplemental instructions, exam preparation, & project assistance
- Prepared students to gain the best score possible on projects, exams, & additional assignments
- Worked with students both in-person and online to get tasks done quickly and efficiently

The Graduate School — **Baltimore, MD**
Front Desk Position — September 2015 – May 2018

- Professionally answered phone calls directed to the graduate school about UMBC graduate programs and the application process
- Utilized organization and multitasking skills to process incoming mail and file applications in the PeopleSoft system

VOLUNTEER EXPERIENCE

REACH (Assistant Director, volunteer) **May 2015 – May 2018**

- Partnered with a female from an inner-Baltimore high school as a mentor and an advisor, giving advice about being both a minority and a female in the STEM and professional workplace
- Worked together with mentee on a scientific project about the effects of external stresses on pregnant fish, teaching the scientific method along the way

RESEARCH EXPERIENCE

University of Maryland, Baltimore County **August 2016 – April 2018**
Department of Biomedical Engineering (intern)
Advisor: Dr. Gregory Szeto

- Uses analytical techniques to normalize and interpret proteomic data from diseased mice with different treatments
- Project the techniques with the best results onto multiscale data to identify networks or biological processes influential in diseases and treatments
- Utilize a plethora of programs, including Treeview, Matlab, several packages in RStudio, and several statistical algorithms featured as add-ins on major applications.

Princeton University **June 2015 – August 2017**
Lewis-Sigler Institute for Integrative Genomics (intern/employee)
Advisor: Dr. Anastasia Baryshnikova

- Contributed to the first compilation project involving the Saccharomyces Cerevisiae deletion collection and its use in phenotypic screening.
- Utilized different programming languages, including Python and Matlab, to import, interpret, and export data in a user-friendly format

Boston University **June 2017- August 2017**
Department of Bioinformatics (intern)
Advisor: Gabriel Girzu, Rajita Menon, Dr. Kirill Korolev

- Created a pipeline to analyze RNASeq data from the microbiota of biopsy samples from patients with several different forms to Irritable Bowel Disease (IBS)
- Utilize machine learning to differentiate between diseases and identify outlying microbiota for successful pre-symptomatic disease prediction

College of Charleston **June 2016 - August 2016**
Department of Computer Science (intern)
Advisor: Dr. Paul Anderson

- Analyzed RNA-seq data from 21 patients with NSCLC utilizing traditional, univariate expression analysis, such as DiffSplice and CuffDiff, and multivariate, statistical approaches such as, Elastic Net and Random Forest
- Utilized several different bioinformatics packages within R, including glmnet, randomforest, and CummeRbund; and also worked with packages in Python, including MISO