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Objective:

I have a passion for working with large, complex data sets, and the biological, statistical, and programming skills necessary to remain on the cutting edge of the field of bioinformatics. My lifelong fascination with science and technology, and my desire to contribute to the improvement of human health have both been major driving forces in my career. In addition to providing me with access to rich sources of data, I am seeking a position that challenges me to develop the best methods for exploring and interpreting such datasets to identify, characterize, and share the most robust and impactful discoveries.

Education:

Bachelor of Science in Neuroscience with Honors (Received May 2008)
Brown University, Providence, Rhode Island, GPA 3.8
Undergraduate Thesis Title:
Cloning, expression, and purification of the $5HT_{3A}R$ M3-M4 linker using TM1526 as a protein scaffold

PhD in Neuroscience (Received May 2018)
Icahn School of Medicine at Mount Sinai, New York, New York, GPA 3.9
PhD Thesis Title:
Using induced pluripotent stem cells derived from patient blood samples for transcriptional modeling and the evaluation of IGF-1 treatment in Phelan-McDermid Syndrome

Additional coursework:

• **CSCI E-52: Intro to CS with C, PHP, & JavaScript** (Fall 2009; Harvard Extension) • **Machine Learning** (Fall 2018; Coursera)

Standardized Tests:

MCAT (Taken June 2009): Verbal-10, Physics-12, Biology-12, Writing-O

GRE (Taken October 2009): Verbal-590, Math-800, Writing-5.0

Research Experience:

• **Undergraduate Researcher, Department of Molecular Pharmacology, Physiology, and Biotechnology, Brown University – Hawrot Lab (July 2006-May 2008)**

In this lab I worked under Professor Edward Hawrot with the graduate student Joao Paulo providing guidance to establish a platform in prokaryotes for the expression of human neurotransmitter receptors. For this project, I sub-cloned serotonin and cholinergic receptors into plasmids, expressed and purified them from *E. coli*, and confirmed their sequence via mass spectrometry.

- **Research Technician, Massachusetts General Hospital – Genetics and Aging Unit – Tanzi Lab (August 2008-July 2010)**

For this position, I worked with Dr. Martin Zhang under the direction of Dr. Rudolph Tanzi to identify novel Alzheimer's Disease (AD) candidate genes and therapeutics. To do this, I screened and prioritized genes and compounds associated with AD via prior evidence and used a human *in vitro* model to assess disease-associated cleavage activity via RNA- and protein-based assays.

- **Senior Research Technician, Columbia University Medical Center – Taub Institute – Clark Lab (August 2010-July 2011)**

For this work I studied the genetics of Parkinson's Disease (PD) and Dementia with Lewy Bodies (DLB) under the guidance of Dr. Lorraine Clark with training from Dr. Miguel Verbitsky and Sergey Kisselev. For one component of this work, I utilized Sequenom technology to genotype allelic variants for SNPs associated with PD and DLB through GWAS data. I also performed breakpoint mapping of CNVs identified in patients with PD and DLB using qPCR.

- **Graduate Researcher, Icahn School of Medicine at Mount Sinai – Department of Neuroscience – Buxbaum Lab (August 2011-September 2018)**

For this position I worked in the lab of Dr. Joseph Buxbaum to study PhelanMcDermid Syndrome (PMS) using patient samples from the Seaver Autism Center.

Using blood from these patients, I generated induced pluripotent stem cells and differentiated them into human neurons. As a primary endpoint, I performed RNA sequencing on these neurons to identify transcriptional differences associated with PMS, as well as novel drug candidates. I performed all stages of the sequencing analysis using a combination of Unix and Python for the trimming and alignment of reads, and R for the downstream bioinformatic analyses. The downstream pipeline incorporated data cleaning via outlier removal, covariate modeling and correction, and comparative and network analyses using a combination of PCA, correlation, linear regression, differential expression, gene set enrichment, and network modeling.

During my graduate training, I also worked as part of a large, multidisciplinary team, the CommonMind Consortium, to develop a neurobiological model of schizophrenia using RNAseq from human postmortem brain samples from more than 500 individuals. For this role, I used R to estimate cell type fractions in brain tissue using publicly available gene expression signatures, as well as Perl to quantify RNA editing levels at more than 2.5 million sites.

- **Senior Scientist, Bristol-Myers Squibb (May 2019-Present; Celgene from May 2019-November 2019)**

My work at Bristol-Myers Squibb was focused on the stratification of solid tumor samples from oncotherapeutic trial patients into highly robust and clinically and biologically relevant groups via integrative clustering of multi-omic data. To accomplish this, I performed evaluation of clinical and quality control data, normalization and correction for batch effects, clustering with prior and novel methods, survival analysis,

functional characterization, and integration with paired immunolabeling, CNV, and proteomic data. To socialize my results, I deployed interactive bioinformatic applications with R shiny.

In this role, I also helped develop clinical diagnostic assays for the screening and identification of patient groups with differential outcome or treatment response. Additionally, I have continued to develop my bioinformatic skillset by learning how to utilize and interpret single-cell and spatial transcriptomic datasets to identify biomarkers of cancer progression and better elucidate cancer biology and interactions with the tumor microenvironment.

While this position started as a hybrid office/remote role, I moved to working fully remotely during the Covid pandemic, and in doing so, I displayed my exceptional self-motivation and organizational skills, as well as my ability to remain highly collaborative even in a virtual office environment.

Publications

- Loss-of-function of ATXN1 increases Abeta levels by potentiating beta-secretase processing of APP. Zhang C, **Browne A**, Child D, Divito JR, Stevenson JA, Tanzi RE. J Biol Chem. 2010 Jan 22.
- Familial Alzheimer's Disease Mutations in Presenilin 1 Do Not Alter Levels of the Secreted Amyloid-beta Protein Precursor Generated by beta-Secretase Cleavage. Zhang C, **Browne A**, Kim DY, Tanzi RE. Curr Alzheimer Res. 2009 Dec 1.
- Curcumin decreases amyloid-beta peptide levels by attenuating the maturation of amyloid-beta precursor protein. Zhang C, **Browne A**, Child D, Tanzi RE. J Biol Chem. 2010 Sep 10.
- Amyloid-β Production Via Cleavage of Amyloid-β Protein Precursor is Modulated by Cell Density. Zhang C, **Browne A**, Divito JR, Stevenson JA, Romano D, Dong Y, Xie Z, Tanzi RE. J Alzheimers Dis. 2010 Aug 30.
- Genome-wide association study identifies candidate genes for Parkinson's disease in an Ashkenazi Jewish population. Liu X, Cheng R, Verbitsky M, Kisselev S, **Browne A**, Mejia-Sanatana H, Louis ED, Cote LJ, Andrews H, Waters C, Ford B, Frucht S, Fahn S, Marder K, Clark LN, Lee JH. BMC Med Gen. 2011 Aug 11.
- Gene expression elucidates functional impact of polygenic risk for schizophrenia. Fromer M, Roussos P, Sieberts SK, Johnson JS, Kavanagh DH, Perumal TM, Ruderfer DM, Oh EC, Topol A, Shah HR, Klei LL, Kramer R, Pinto D, Gümüş AH, Cicek AE, Dang KK, **Browne A**, … Sklar P. Nature Neuroscience 2016 Sep 26.
- Disruption of the KH1 domain of Fmr1 leads to transcriptional alterations and attentional deficits in rats. Golden CEM, Breen MS, Koro L, Sonar S, Niblo K, **Browne A**, DiMarino D, DeRubeis S, Baxter MG, Buxbaum JD, Harony-Nicolas H. bioRxiv 2018 Jun 9.
- Transcriptional signatures of participant-derived neural progenitor cells and neurons implicate altered Wnt signaling in Phelan-McDermid syndrome and autism. Breen MS*, **Browne A*,** Stathopoulos S, Brennand K, Buxbaum JD, Drapeau E *Molecular Autism* **11**, 53 (2020). *Equal contribution

- Direct comparison of circulating tumor DNA sequencing assays with targeted large gene panels. Yu L, Lopez G, Rassa J, Wang Y, Basavanhally T, **Browne A**, Huang CP, Dorsey L, Jen J, Hersey S. PloS one. 2022 Apr 28;17(4):e0266889.

Awards and Honors

- Granted an UTRA fellowship for undergraduate research (Summer 2007)
- Awarded Honors at graduation for undergraduate thesis (May 2008)
- Awarded Neuroscience T32 grant for my PhD research (Fall 2011-Summer 2013)
- Awarded a Systems and Developmental Biology and Birth Defects T32 grant for my graduate thesis project (September 2013-August 2015)
- Awarded a Research Fellowship from the Seaver Center for Autism Research and Treatment for my graduate thesis project (September 2015-August 2017)

Computer Skills and Software:

R UNIX Python shiny Docker AWS Git TensorFlow/keras