Andrew Browne, Ph.D.

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PROFESSIONAL SUMMARY

Experienced bioinformatician with a Ph.D. in Neuroscience and 12 years of experience, specializing in multi-omic integration, biomarker/classifier development, single cell biology, and AI/ML modeling. Proven track record in developing robust disease models and integrating large-scale datasets to drive impactful discoveries in human health and drug development.

WORK EXPERIENCE

Independent Data Science Consultant (Boston, MA) **07/2023 – Present**

- Created predictive financial models using option chain data applied to PyTorch neural networks.
- Established a streamlined workflow for identifying outcome-associated multi-omic biomarkers.
- Developed an agentic system for converting text into structured Obsidian knowledge bases with retrieval-augmented generation (RAG) query capability.
- Built a dashboard for identifying cell-type specific vulnerabilities in Alzheimer's Disease using multi-omic single cell data from the Seattle Alzheimer's Disease Brain Cell Atlas (SEA-AD).

Senior Scientist at Bristol-Myers Squibb (Cambridge, MA) **05/2019 – 06/2023**

- Integrated multi-omic data (e.g. RNAseq, WES, and proteomics) to develop comprehensive disease models and identify robust and meaningful patient subtypes in solid tumor settings.
- Developed AI/ML classifiers to differentiate patient samples using multi-modal clinical data.
- Cross-translated classifiers and insights between bulk, single-cell, and spatial transcriptomic datasets to better resolve disease biology and tumor microenvironment.
- Applied solid tumor disease modeling and classification strategy to patient-derived cell line and organoid models with CRISPR-mediated modulation of genes implicated in disease progression.
- Created interactive tools and dashboards for data visualization, interpretation, and evaluation.
- Spearheaded the utilization and harmonization of real-world data to augment existing analyses.
- Supported the development of clinical diagnostic assays for patient identification and screening.
- Mentored a PhD-level summer intern in immuno-oncology biomarker research to guide project development and foster technical and professional growth.
- Collaborated regularly with a diverse team of bioinformaticians, clinicians, and wet-lab scientists across groups within and outside the organization.

Graduate Researcher at Icahn Sch. of Medicine at Mt. Sinai (New York, NY) **09/2011 – 08/2018**

- Developed transcriptional models of neurodevelopmental and neuropsychiatric disease using postmortem and cell-derived RNA sequencing from human neural samples.
- Created transcriptomic workflows from raw sequencing through downstream analysis such as differential expression, cell-type deconvolution, eQTL enrichment, and network modeling.
- Worked in highly collaborative and cross-disciplinary teams of clinicians and researchers.
- Provided neuroscience research mentorship to undergraduate and high school students.

EDUCATION

Icahn School of Medicine at Mount Sinai (New York, NY) **09/2011 – 05/2018**
Doctorate of Philosophy in Neuroscience GPA: 3.9

Brown University (Providence, RI) **09/2004 – 05/2008**
Bachelor of Science in Neuroscience, *with Honors* GPA: 3.8

TECHNICAL SKILLS

Bioinformatics: Multi-omic analysis, single-cell and spatial transcriptomics, real-world and clinical data integration, cell type deconvolution, gene-set enrichment, dashboard and workflow development

Statistical Methods: AI/ML predictive modeling and classifier development, dimensionality reduction, correlation, clustering, survival analysis, linear/log/mixed modeling, time series analysis

Programming Tools: R (Bioconductor, shiny, tidyverse, Seurat, ggplot2), Python (PyTorch, pandas, scanpy), Unix, Git, RAG, agentic workflows, AWS, Docker, Cursor, Jira/Confluence

PUBLICATIONS

- Zhang W, Ghaffari S, **Browne A**, Macintosh C, Lu X, Dang H, Lopez G, Wang K. Unveiling Candidate Drivers in Cancer Progression Using Somatic-IV Analysis. *bioRxiv* 2025 Feb 26. https://doi.org/10.1101/2025.02.20.638369
- Jeyaraju DV, Hayati S, Polonskaia A, Alapa M, Ugidos M, **Browne A**, Risueño A, Hagner P, Gupta V, Talpaz M, Hernandez C. Fedratinib Induces Cytokine Changes Correlating with Clinical Response in Ruxolitinib Exposed Myelofibrosis Patients: Biomarker Analysis from the Freedom Trial. *Blood*. 2022 Nov 15; 140 (Supplement 1): 3865–3867. https://doi.org/10.1182/blood-2022-166407
- Reiss DJ, **Browne A**, Fox B, Ratushny AV, Wang M, Biankin AV, Lila T. Abstract C085: Spatial arrangements of immune cells of the pancreatic ductal adenocarcinoma tumor microenvironment correlated with outcomes in the phase 3 APACT trial. *Cancer Res.* 2022 Nov 15; 82 (22_Supplement): C085. https://doi.org/10.1158/1538-7445.PANCA22-C085
- Egger R, Fisher A, Drage M, Trillo-Tinoco J, Abel J, **Browne A**, … Baxi V. Identification of clinically relevant spatial tissue phenotypes in large-scale multiplex immunofluorescence data via unsupervised graph learning in non-small cell lung cancer. *Journal for ImmunoTherapy of Cancer*. 2022 Nov 7; **10.** https://doi.org/10.1136/jitc-2022-SITC2022.1277
- Gjini E, Trillo-Tinoco J, **Browne A**, … Bowden M. Integrative molecular profiling of high-grade primary prostate cancer identifies patients with a biomarker profile that favors the combination of standard of care (SOC) therapy with immunotherapy. *Journal for ImmunoTherapy of Cancer*. 2020 Dec 10; **8.** https://doi.org/10.1136/jitc-2020-SITC2020.0733
- Lila T, Biankin A, **Browne A**, Reiss DJ, Lu B, Pierce D, Ratushny A, Tsai KT, Lata S, Kamalakaran S, Babak T. Abstract PO-008: Multi-omic Profiling of primary pancreatic adenocarcinomas obtained from the APACT adjuvant trial of nab-paclitaxel+ gemcitabine vs gemcitabine. *Cancer Res*. 2020 Nov 15; 80 (22_Supplement): PO–008. https://doi.org/10.1158/1538-7445.PANCA20-PO-008
- Breen MS*, **Browne A***, Hoffman GE, Stathopoulos S, Brennand K, Buxbaum JD. Transcriptional signatures of participant-derived neural progenitor cells and neurons implicate altered Wnt signaling in Phelan-McDermid syndrome and autism. *Molecular Autism*. 2020 Jun 19; **11**, 53. *equal contribution https://doi.org/10.1186/s13229-020-00355-0
- Golden CEM, Breen MS, Koro L, Sonar S, Niblo K, **Browne A**, DiMarino D, DeRubeis S, Baxter MG, Buxbaum JD, Harony-Nicolas H. Disruption of the KH1 domain of Fmr1 leads to transcriptional alterations and attentional deficits in rats. *Cerebral Cortex*. 2019 Mar 16; Volume 29, Issue 5, Pages 2228–2244. https://doi.org/10.1093/cercor/bhz029
- 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. Gene expression elucidates functional impact of polygenic risk for schizophrenia. *Nat Neurosci*. 2016 Sep 26; **19**, 1442–1453. https://doi.org/10.1038/nn.4399
- 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. Genome-wide association study identifies candidate genes for Parkinson's disease in an Ashkenazi Jewish population. *BMC Med Genet*. 2011 Aug 3; **12**, 104. https://doi.org/10.1186/1471-2350-12-104
- Zhang C, **Browne A**, Divito JR, Stevenson JA, Romano D, Dong Y, Xie Z, Tanzi RE. Amyloid-β Production Via Cleavage of Amyloid-β Protein Precursor is Modulated by Cell Density. *J Alzheimers Dis.* 2010 Oct 1; 22(2):683-984. https://doi.org/10.3233%2FJAD-2010-100816
- Zhang C, **Browne A**, Child D, Tanzi RE. Curcumin decreases amyloid-beta peptide levels by attenuating the maturation of amyloid-beta precursor protein. *J Biol Chem.* 2010 Sep 10; 285(37):28472-80. https://doi.org/10.1074/jbc.m110.133520
- Zhang C, **Browne A**, Child D, Divito JR, Stevenson JA, Tanzi RE. Loss-of-function of ATXN1 increases Abeta levels by potentiating beta-secretase processing of APP. *J Biol Chem*. 2010 Jan 22; 285(12): 8515–8526. https://doi.org/10.1074%2Fjbc.M109.079079