

Muhammad Elsadany

New York City, NY • [E-mail](#) • [LinkedIn](#) • [GitHub](#) • [Portfolio](#) • [ORCID](#)

EXPERIENCE

REGENERON, INC., REGENERON GENETICS CENTER (RGC)

Tarrytown, NY

Associate Manager, Clinical Informatics

JUN 2026 – PRESENT

- Developing and maintaining scalable software tools to automate the processing, QC, and harmonization of EHRs, surveys, and digital device data for millions of individuals.
- Partnering with cross-functional scientists (genetics, epidemiology, drug design) to interpret complex health data and guide therapeutic programs.

OPENAI

Remote

Consultant

MAY 2026

- **Model Evaluation:** Contributed to the evaluation and assessment of reasoning for GeneBench-Pro.

UNIVERSITY OF IOWA, DEPARTMENT OF PSYCHIATRY, MICHAELSON LAB

Iowa City, IA

Temporary Professional Employee

MAY 2026

- **App development:** Developed a desktop app to host one of the language tasks developed during my Ph.D. and allow interactive feature extraction and analysis.

Graduate Research Assistant

JUN 2022 – MAY 2026

- **Drug Discovery & Pharmacogenomics:** Engineered a computational framework to predict psychiatric drug response and neurological side effects by integrating genetic data (GWAS, eQTL), gene expression, and drug perturbation profiles.
- **Multi-Modal Data Fusion:** Architected and implemented scalable data processing pipelines for diverse datasets, including genetic variants (SNP-array), multi-modal neuroimaging (sMRI, fMRI, DWI), behavioral surveys, audio recordings, and clinical interviews.
- **Single-Cell Multi-Omics Analysis:** Developed a novel analytical pipeline for single-nuclei multi-omics (RNA+ATAC) data, implementing a bootstrapped pseudo-bulk strategy and mixed-effects models (lmmSeq) to identify cell-type-specific transcriptional responses to human brain stimulation, validated via cross-species comparison.
- **Leadership & Mentorship:** Supervised and trained 9 undergraduate interns and 5 graduate students in computational biology methods, statistical analysis, and research best practices.

REGENERON, INC., REGENERON GENETICS CENTER (RGC)

Tarrytown, NY

Ph.D. Intern

JUN 2025 – AUG 2025

- **Genetic Target Discovery:** Applied structural equation modeling (SEM) to decompose the shared genetic architecture between depression, anxiety, and body composition, defining novel latent factors.
- **Multivariate Genomics:** Conducted multivariate GWAS and GWAS-by-subtraction to identify genetic loci specific to shared and unique latent factors, to identify and prioritize potential therapeutic targets.
- *Supervisor: Frank Wendt, Ph.D.*

UNIVERSITY OF IOWA, GRADUATE COLLEGE

Iowa City, IA

Graduate Teaching Assistant

2024

- **BIOL:3212 (Bioinformatics):** Instructed senior undergraduate and graduate students (n=30) on core bioinformatics concepts and led hands-on computational workshops.
- **GENE:6200 (Seminar):** Facilitated discussion groups and managed course logistics for a PhD-level seminar course (n=37).

EDUCATION

UNIVERSITY OF IOWA

Iowa City, IA

Ph.D. – Interdisciplinary Graduate Program in Genetics (Computational Genetics)

AUG 2021 – MAY 2026

- Advisor: Jacob Michaelson, Ph.D.
- Dissertation: "[Mechanistic Triangulation Across Molecular, Circuit, and Behavioral Scales](#)"

ZEWAIL CITY FOR SCIENCE AND TECHNOLOGY (ZC-UST) ABET-accredited.

Giza, Egypt

B.S., Biomedical Sciences (Computational Biology and Genomics), Cum Laude

SEP 2017 - JUN 2021

- A premier institution dedicated to educating Egypt's top-performing STEM students.
- Dissertation: "Comparative Transcriptome Analysis of Alzheimer's, Huntington's, and Parkinson's Diseases"

- **Programming & Statistical Languages:** R, Python, SQL, UNIX Shell, MATLAB
- **Data Platforms & Clinical Data:** Databricks, Amazon Redshift, Electronic Health Record (EHR) data, data querying relational data modeling, and large-scale healthcare data analysis
- **Statistical & Machine Learning Modeling:** Linear/mixed effects models, logistic/Poisson regression, structural equation modeling (SEM), mediation analysis, hypothesis testing; dimensionality reduction (PCA, sPLS, CCA), cluster analysis, TensorFlow
- **Genomics & Multi-Omics Analysis:** GWAS, polygenic scores (PGS), genomic SEM, eQTL analysis, TWAS; bulk, single-cell, and spatial RNA-seq; ATAC-seq, differential expression, and cell-cell communication
- **Neuroimaging & Multimodal Data:** Structural, functional, and diffusion MRI (sMRI/fMRI/DWI); audio analysis, facial landmarking, and NLP
- **Software & Platforms:** R shiny, Git, high-performance computing (HPC), AWS cloud, REDCap, Qualtrics, Seurat, RRHO2, lmmSeq, plotly, ggplot2

RESEARCH PROJECTS

COMPUTATIONAL DRUG DISCOVERY & PHARMACOGENOMICS

Polygenic Drug Response Signatures for Psychiatric Disorders | University of Iowa, Michaelson Lab

- Developed a computational tool integrating genetic data (GWAS, eQTL, RNA-Seq) to generate personalized treatment recommendations for psychiatric disorders, with a focus on ADHD.
- Scaled the application to cohorts with 88,000+ participants (SPARK, ABCD) and validated predictions against behavioral scales (CBCL, BPM) and neuroimaging (fMRI) data.
- **Poster:** *Biological Psychiatry* (DOI: 10.1016/j.biopsych.2023.02.769)

Mapping Brain-Wide Drug Effects using Deep Learning | University of Iowa, Michaelson Lab

- Built a deep learning model that integrates brain-wide gene expression (Allen Institute) and fMRI trait maps with drug perturbation signatures (CMAP, LINCS) to predict functional brain activity changes for 838 compounds.
- Delivered insights through an interactive R Shiny application featuring 3D brain visualizations, linking compounds to phenotypic effects via Neurosynth and Neuromaps.

SINGLE-CELL MULTI-OMICS & CROSS-SPECIES VALIDATION

Gene Expression Signature of Human Brain Stimulation | University of Iowa, Michaelson Lab

- Engineered an end-to-end computational pipeline for single-nuclei multi-omics (RNA+ATAC) data, implementing a bootstrapped pseudo-bulk strategy and mixed-effects models (lmmSeq) to identify cell-type-specific responses to electrical stimulation.
- Validated translational relevance through cross-species comparison (RRHO) with mouse models, identifying conserved gene sets.
- Manuscript in review (DOI: 10.1101/2023.09.21.558812)

NEUROeSTIMator: A Deep Learning Model for Neuronal Activation | University of Iowa, Michaelson Lab

- Contributed to the development of a deep learning model (NEUROeSTIMator) that estimates neuronal activation from transcriptomic data (scRNA-seq, spatial).
- Demonstrated model robustness by associating outputs with patch-seq electrophysiology and across species and cell types.
- **Publication:** *Nature Communications* (DOI: 10.1038/s41467-023-44503-5)

MULTIMODAL PHENOTYPING & DIGITAL BIOMARKERS

Exceptional Ability: A Multimodal Cognitive Study | University of Iowa, Michaelson Lab

- Designed and implemented a multimodal analysis pipeline integrating NIH-Toolbox/IQ scores, a custom language task, acoustic feature extraction (audio), interview transcription (Whisper AI), facial landmarking (computer vision), and structural/functional/diffusion MRI.
- Developed a 10-minute language task that effectively captures cognitive performance, demonstrating potential as an efficient digital biomarker.

Linguistic Signatures of Bipolar Disorder from Social Media | University of Iowa, Michaelson Lab

- Applied NLP (topic modeling, sentiment analysis) and GPT-4 embeddings to Reddit comments to identify language patterns and temporal mood cycles in users with bipolar disorder.
- Extracted behavioral features such as sleep patterns and comment frequency to track disease-relevant trends.

Transcriptional Analysis in Neurodegeneration | Zewail City, Center for Genomics

- Conducted a meta-analysis of nuclear-encoded mitochondrial genes across 8 neurodegenerative diseases (Alzheimer's, Parkinson's, Huntington's, etc.) using RNA-seq data (DESeq2, Limma).
- Identified common transcriptional pathways and potential therapeutic targets, with a focus on Friedreich's ataxia.
- **Publication:** *Frontiers in Genetics* (DOI: 10.3389/fgene.2021.749792)

ADDITIONAL INFORMATION

• Selected Presentations

- **International Society for Autism Research (INSAR) Annual Meeting** (2025) | *Oral Presentation*
- **Society of Biological Psychiatry Annual Conference** (2023) | *Poster Presentation*
- **HawkIDDRC Program Retreat** (2024) | *Data Blitz Presentation* (100+ attendees)
- **Computational Psychiatry Symposium** (2022, 2023, 2024) | *Poster Presentations (3)*
- **Intel International Science and Engineering Fair (ISEF)** (2015) | *Poster Presentation* | *National Finalist*

• Works

- **Elsadany, M.** (2026). Mechanistic triangulation across molecular, circuit, and behavioral scales. Doctoral dissertation, University of Iowa.
 - ProQuest: <https://www.proquest.com/openview/0f4e3c7be02e52cb3b403462a78ca0e0/1?pq-origsite=gscholar&cbl=18750&diss=y>
- Abdelsalam, N. A., **Elsadany, M.**, & Badr, E. (2026). Common Dysregulated Pathways and Genes in Alzheimer's, Parkinson's, and Huntington's Diseases: A Computational Analysis to Nominate Candidate Gene Targets for Drug Repurposing. *bioRxiv*, 2026.2007.2022.739294.
 - DOI: 10.64898/2026.07.22.739294
- Han, Y., Yaghi, M.H., Polo, J., **Elsadany M.** et al. Diagnostic accuracy of intravesical prostatic protrusion (IPP) for bladder outlet obstruction using urodynamics as reference standard: a systematic review and meta-analysis. *World J Urol* 44, 539 (2026).
 - DOI: 10.1007/s00345-026-06664-y
- Casten, L. G., Tener, A., **Elsadany, M.**, Yang, J. S., Strang, J. F., & Michaelson, J. J. (2026). Migration genetics link excitatory neurons to ancient selection and economic growth. *bioRxiv*.
 - DOI: 10.64898/2026.02.05.703995
- Chatterjee, S., **Elsadany, M.**, et al. (2025). The gene expression signature of electrical stimulation in the human brain. *bioRxiv*.
 - DOI: 10.1101/2023.09.21.558812
- Bliese, S.R., Basu, B., Beyer, S.E., **Elsadany, M.**, et al. (2025). Single-cell resolution spatial transcriptomic signature of the retrosplenial cortex during memory consolidation. *Molecular Psychiatry*.
 - DOI: 10.1038/s41380-025-03331-3
- Bahl, E., Chatterjee, S., Mukherjee, U., **Elsadany, M.**, et al. (2024). Using deep learning to quantify neuronal activation from single-cell and spatial transcriptomic data. *Nature Communications*, 15, 779.
 - DOI: 10.1038/s41467-023-44503-5
- Casten, L. G., Koomar, T., **Elsadany, M.**, et al. (2024). Lingo: an automated, web-based deep phenotyping platform for language ability. *medRxiv*.
 - DOI: 10.1101/2024.03.29.24305034
- **Elsadany, M.**, Thomas, T. T., Michaelson, J. J. (2023). 529. Polygenic Drug Response Signatures and Their Associated Behavioral Patterns. *Biological Psychiatry*, 93(9), S308.
 - DOI: 10.1016/j.biopsych.2023.02.769
- **Elsadany, M.**, Elghaish, R. A., Khalil, A. S., et al. (2021). Transcriptional Analysis of Nuclear-Encoded Mitochondrial Genes in Eight Neurodegenerative Disorders. *Frontiers in Genetics*, 12, 749792.
 - DOI: 10.3389/fgene.2021.749792

- **Honors, Awards & Grants**
 - **Zewail City Scholarship** for Undergraduate Studies (2017-2021) | *Awarded based on academic excellence*
 - **Misr El-khair Scholarship** for Undergraduate Studies (2017-2021) | *Awarded based on high school excellence*
 - **ITAC & ITIDIA Grant** for Undergraduate Thesis Project (2020-2021) | *10k EGP*
 - **National Finalist**, Intel International Science and Engineering Fair (ISEF) (2015)
- **Languages:** English (Professional Proficiency), Arabic (Native)