HPI·MS

Mount Sinai

Hasso Plattner Institute for Digital Health at Mount Sinai

2027

GET TO KNOW OUR MENTORS

A GUIDE TO
HPIMS
MENTORS

OUR MENTORS & RESEARCH AREAS

01	ANKIT SAKHUJA	AI for Critical Care
02	BEN GLICKSBERG	Multimodal AI for Health
03	BILAL NAVED	Safe AI for Clinical Care
04	JACK HUMPHREY	Genomics of Neurodegenerative Disease
05	LI SHEN	AI for Genomics
06	MATTEO DANIELETTO	Digital Biomarkers and Health
07	TOWFIQUE RAJ	AI and Neurodegenerative Disease
08	SCOTT RUSSO	Stress, Immunity, and Mental Health
09	SIKANDER HAYAT	AI for Scientific Discovery
10	VIKAS PEJAVER	AI for Genetic Disease
11	VINCENZO FIORE	Computational Psychiatry
12	EUGENIA ALLEVA	AI for Women's Health
13	JASON LIU	AI-Driven Precision Medicine

ABOUT

Ankit Sakhuja, MBBS, MS is an Associate Professor of AI and Human Health and Medicine, Data Driven & Digital Medicine, and NIH-funded physician scientist at the Icahn School of Medicine at Mount Sinai.

He serves as Associate CMIO for AI and Critical Care for Mount Sinai Health System, System Chief of AI Operations and Assurance in the Windreich Department of AI and Human Health, and System Director of Research, Technology and Innovation for the Institute for Critical Care Medicine.

An intensivist and nephrologist, his research focuses on reinforcement learning for clinical decision-making, generative AI for clinical care, and predictive modeling for critical illness.

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ANKIT SAKHUJA

AT A GLANCE +

The Mount Sinai AI Assurance Lab studies **how artificial intelligence can improve the care of critically ill patients**. Its research spans three core areas: **reinforcement learning for clinical decision-making**, including methods to learn optimal treatment strategies from complex physiologic and clinical data; **generative AI in medicine**, including agentic systems for clinical reasoning and rigorous evaluation of large language models for accuracy, reliability, and safety; and **predictive modeling of critical illness**, using multimodal data to understand disease onset, trajectory, and recovery. Across these areas, the lab emphasizes methodological rigor, clinical relevance, and translation into practice.

Click here to visit lab website

AI ASSURANCE LAB

AVAILABLE PROJECTS +

1. Real-Time AI for Sepsis Detection

Develop and validate an agentic framework for real-time sepsis identification and compare its performance with existing clinical tools, including SepsisNow and EPIC V2.

2. Multimodal Foundation Model for Sepsis

Develop and validate a multimodal foundation model that integrates diverse clinical data to improve the detection and characterization of sepsis.

AI ASSURANCE LAB



BEN GLICKSBERG

ABOUT +

Benjamin Glicksberg, PhD is an Associate Professor of AI and Human Health at the Icahn School of Medicine at Mount Sinai.

He serves as Chief of Entrepreneurship and Innovation in the Windreich Department of AI and Human Health. Founding Director of the Center for AI in Children's Health within the Mindich Child Health and Development Institute, and Director of the Digital Discovery Program within the Hasso Plattner Institute for Digital Health.

His research focuses on applying machine learning to multi-modal and multi-omic patient data to advance personalized medicine. He also co-founded ArtemisAI Labs, which delivers real-time, objective health assessments at the bedside using audiovisual monitoring, with a primary focus on neonatal care.

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AT A GLANCE +

The Glicksberg Lab develops **multimodal AI representations of patient state**. The lab integrates routinely collected clinical data — including electronic health records, laboratory results, and medical imaging — with audiovisual signals such as facial movement, voice, and body movement to offer a **higher-fidelity, continuous, and objective window into how patients are actually doing**. Through prospective studies, the lab aims to **capture patient state more faithfully than any single data source allows**. These methods are developed, applied, and validated across a range of clinical domains including cardiology, psychiatry, neurodegenerative diseases, and pediatrics.

Click here to visit lab website

GLICKSBERG LAB

AVAILABLE PROJECTS +

1. Computer Vision for Wound Care

Develop deep learning methods for automated pressure injury staging from bedside images, including a prospective comparison of smart glasses versus smartphone capture at the point of care.

2. Pose Estimation in the Neonatal and Pediatric ICU

Develop smartphone-based video AI methods for continuous, contactless monitoring of sedation depth and neurologic status in critically ill children.

3. Audiovisual Biomarkers of Mental Health

Develop models using pose, speech, and acoustic modeling to track depression and anxiety severity across the care continuum, moving beyond episodic self-report.

4. Audiovisual Signals of Cardiac Health

Integrate cardiac sounds, three-lead ECG, and audiovisual data captured during cardiology evaluations to identify digital biomarkers of cardiac health.

GLICKSBERG LAB

AVAILABLE PROJECTS (CONT.)

5. Multimodal N-of-1 Monitoring in Rare Disease

Develop a patient-specific framework that integrates audiovisual and physiologic signals to quantify disease state in individuals with rare genetic disorders.

6. Video-Based Motor Assessment in Movement Disorders

Develop automated methods to quantify movement from routine video in Parkinson's disease and pediatric movement disorders.

7. Generative AI for Clinical Diagnostic Reasoning

Evaluate how large language models support or distort diagnostic reasoning through a multi-institutional study of AI-assisted clinical decision-making.

ABOUT

Bilal Naved, PhD is an Instructor of AI and Human Health and an Eric and Wendy Schmidt AI in Human Health Fellow at the Icahn School of Medicine at Mount Sinai.

He also serves as Co-Founder and Chief Product Officer of Clearstep, a venture-backed health technology company focused on clinically intelligent patient navigation and access.

As a biomedical researcher and health technology entrepreneur at Mount Sinai, his work focuses on evaluating patient-facing AI agents through prospective, multi-center clinical studies and developing evidence-based approaches to improve access, safety, and healthcare delivery.

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BILAL NAVED

AT A GLANCE +

Dr. Bilal Naved's research aims to develop and validate **AI systems designed to improve clinical care across the patient journey**, from initial symptoms through diagnosis, treatment, and post-discharge follow-up. The research focuses on three core aims: **making medical AI provably safe**, **scaling how clinical AI is evaluated**, and **building evidence for AI-enabled care delivery**.

Current work includes studying and validating the first clinical formal language by evaluating for safety-critical errors, testing whether LLMs can translate clinical guidelines into clinician-approved logic, and assessing its extension beyond triage to diagnosis and treatment. A second research focus is building generative patients that simulate diverse real-world patient interactions, allowing clinical AI systems to be tested for safety and performance at scale. Another area of research involves prospective, randomized, multi-site studies of conversational and agentic AI across the full care episode. Together, these efforts establish the safety framework, the evaluation science, and the clinical evidence needed to move patient-facing AI from ad hoc adoption to rigorous, equitable, clinician-governed deployment at national scale.

RESEARCH FOCUS

AVAILABLE PROJECTS +

1. Validating the Clinical Domain-Specific Language (DSL) for Provably Safe Medical AI

Study and validate our clinical formal language, a precise, citation-linked DSL that clinicians can read and write directly, which a compiler translates into fixed, machine-checkable rules an AI must obey. Contribute to evaluating LLM-assisted extraction of triage logic from society guidelines and primary literature into the DSL, blinded A/B comparisons of LLM-extracted versus human-edited DSL logic, and independent-clinician validation panels that break the self-referential loop in which the authors of clinical rules also write their own test cases.

2. Evaluating LLMs for Clinical Triage

Systematically evaluate frontier models (ChatGPT, Gemini, Claude, and domain-specific clinical tools) on triage accuracy, under-triage rates, and safety-critical errors, benchmarked against our 11,609-vignette clinician-curated gold standard.

3. Testing the Resilience of Hybrid Deterministic-Probabilistic Architectures

Evaluate whether hybrid AI architectures that combine LLMs with deterministic clinical safety rules can maintain safe recommendations when patients challenge or resist guidance. Analyze multi-turn conversations and assess safety, resilience, and model behavior under different forms of patient pushback.

RESEARCH FOCUS

AVAILABLE PROJECTS (CONT.)

4. Voice Automated AI Triage

Evaluate voice-based AI for clinical triage through vignette-based testing and prospective deployment studies. Projects may examine clinical accuracy, conversational quality, patient trust, escalation, and differences in performance across age, acuity, and language-preference groups.

5. Developing Specialist Referral Appropriateness Rubrics

Develop evidence-based, specialist-informed criteria for determining when patients should receive an in-person specialist visit, an e-consult, or continued primary-care management. Students may conduct structured specialist interviews, analyze areas of agreement and disagreement, and contribute to methodology and implementation research.

6. Quantifying Ambulatory Care Capacity

Analyze Mount Sinai ambulatory care data to identify visits that may be appropriate for asynchronous or virtual care. Projects may examine operational definitions of potentially avoidable in-person visits, identify service lines with the greatest opportunities for capacity recovery, and evaluate the implications for health-system operations.

RESEARCH FOCUS



JACK HUMPHREY

ABOUT

Jack Humphrey, PhD, is an Assistant Professor of Neuroscience at the Icahn School of Medicine at Mount Sinai.

He is a geneticist and computational RNA biologist whose research focuses on understanding the genetic and molecular mechanisms underlying neurodegenerative disease.

His work spans amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), and Alzheimer's disease, with a focus on developing and applying computational approaches to study gene expression, mRNA splicing, and genetic variation. He integrates multiple types of genomic data to identify genetic factors and molecular mechanisms that contribute to neurodegeneration.

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AT A GLANCE

The Humphrey Lab investigates the **genetic and molecular mechanisms underlying neurodegenerative disease**, using **RNA biology as a link between genetic variation and disease**. The lab develops and applies computational genomics methods to large, patient-derived datasets to study diseases, including **amyotrophic lateral sclerosis** (ALS), **frontotemporal dementia** (FTD), **progressive supranuclear palsy** (PSP), and **Alzheimer's disease**.

The lab integrates statistical genetics and functional genomics to disentangle causal genetic drivers of disease from mere consequences. A particular focus is understanding how genetic variation affects **mRNA splicing**, a fundamental cellular process that drives regulatory diversity in the brain, and is affected in disease through changes in RNA-protein interactions. The lab has an interest in developing new computational methods to quantify mRNA splicing from sequencing reads, including **long-read, single-cell, and spatial approaches**.

Click here to visit lab website

HUMPHREY LAB

AVAILABLE PROJECTS +

1. Assessing Genetic Convergence Across Neurodegenerative Diseases

We recently demonstrated that ALS and PSP, two neurodegenerative diseases with distinct pathologies and clinical features, share a genetic risk factor in the MOBP gene, suggesting that oligodendrocyte dysfunction is a convergent feature of disease (Fodder et al, 2026, medRxiv). This project would take the analysis genome-wide to identify further shared genetic links across multiple diseases, using a combination of statistical genetics (genetic correlation, fine-mapping), and functional genomics (colocalization, Mendelian randomization) to prioritize new gene targets.

2. Identifying Signatures of Splicing Dysfunction in Single Cells

ALS, FTD, and Alzheimer's disease share the hallmark pathology of TDP-43 mislocalization, a critical RNA-binding protein that when dysfunctional causes a range of mRNA splicing changes. We previously demonstrated that TDP-43 pathology can be quantified from RNA sequencing in bulk brain tissues (Prudencio et al, 2020, JCI). We have now generated single-cell RNA-seq across multiple ALS and FTD donors and have developed methods to quantify TDP-43-associated splicing in individual cells. This project would integrate multiple single-cell datasets to measure TDP-43 splicing signatures across a range of neurodegenerative diseases and identify clinical and genetic associations.

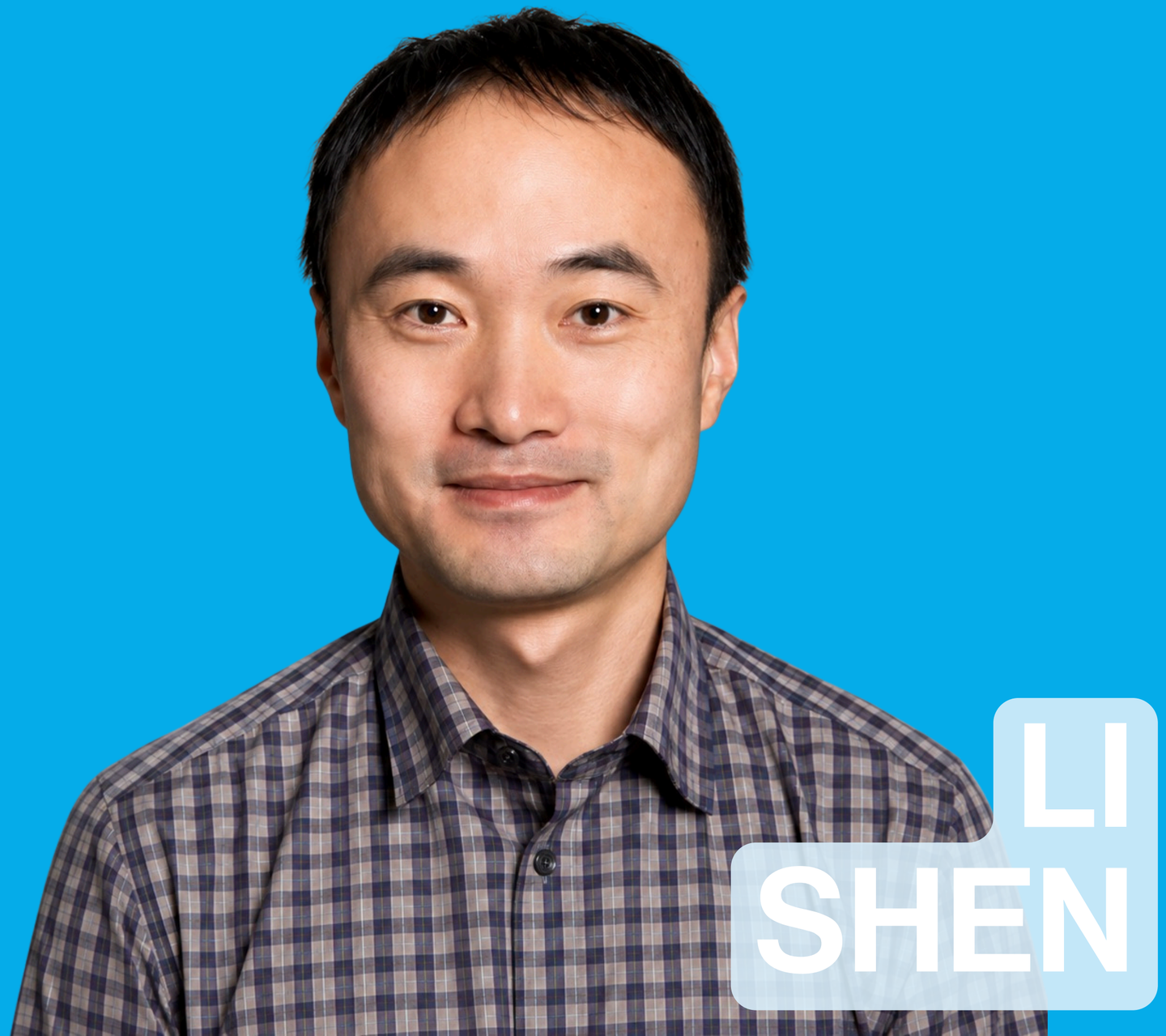
ABOUT

Li Shen, PhD, is a Professor of Neuroscience and AI and Human Health at the Icahn School of Medicine at Mount Sinai.

He is a computational genomics and machine learning researcher whose work focuses on building next-generation AI systems to understand the human genome.

His research spans open genome AI foundation models, genomic language models, personalized gene-expression prediction, and genome reasoning models that combine biological evidence with interpretable reasoning. A central goal of his program is to develop powerful, transparent, and openly available genome AI models that enable researchers to investigate how genetic variation shapes molecular function, cellular phenotypes, and human disease.

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AT A GLANCE +

The Shen Lab develops **open genome AI systems that can read, model, and reason about the human genome**. The lab aims to move beyond models that merely recognize patterns in DNA toward foundation models that can predict molecular phenotypes, analyze individual genomes, and provide biologically grounded explanations of genetic variation.

Research spans four interconnected areas: **open genome AI foundation models** for predicting molecular phenotypes from long genomic sequences; **personal gene-expression prediction** to connect individual genetic variation with tissue-specific molecular phenotypes and disease susceptibility; **genomic language models** that learn representations of genome organization and regulatory function; and **genome reasoning models** that integrate sequence, functional predictions, biological annotations, and scientific knowledge to explain the effects of genetic variants.

Together, these projects pursue a broader vision: an open and scientifically transparent genome AI ecosystem capable of predicting what a genome does, explaining why it does it, and revealing how its effects differ from one person to another.

Click here to visit lab website

SHEN LAB

AVAILABLE PROJECTS +

1. Scaling and Extending OmniGenome

Develop new capabilities for OmniGenome, an open genome AI foundation model for predicting molecular phenotypes from long genomic sequences. Projects may explore model architecture, sparse attention, computational efficiency, training stability, and evaluation across genomic prediction tasks.

2. Grounding Genome Reasoning Models

Investigate methods such as retrieval-augmented generation to connect predictive and explanatory genome reasoning models with trusted genomic databases, scientific literature, and sequence-to-function predictions, making model outputs more evidence-based, transparent, and resistant to hallucination.

3. Learning From Personal Genomes With Genomic Language Models

Leverage Mount Sinai patient data to investigate how genomic language models can learn from individual genome sequences and better understand how genetic variation influences gene regulation, molecular phenotypes, and disease risk.

4. Improving Personal Gene-Expression Prediction Accuracy

Develop accurate, robust, and generalizable machine-learning algorithms to predict tissue-specific gene expression from individual genomes, exploring new architectures, novel loss functions, regularization methods, training strategies, and evaluation frameworks.

SHEN LAB



MATTEO DANIELETTO

ABOUT

Matteo Danieletto, PhD is an Assistant Professor of AI and Human Health at the Icahn School of Medicine at Mount Sinai.

He serves as Associate Director of AI and Human Health in the Windreich Department of AI and Human Health and leads the engineering efforts of the Digital Discovery Program.

His team developed eHive, a platform for research studies that integrates diverse data streams, including wearable data, in a HIPAA-compliant environment. His team also leads the AIHH-Vision initiative, focused on data integrity and pipeline development for video data collected via smart glasses. His expertise in software development and machine learning has advanced research in inflammatory bowel disease, skin disorders, and Lyme disease. He contributes to data engineering efforts for The Mount Sinai Million Health Discoveries Program and leads the engineering effort for the ECGCopilot initiative, which aims to advance AI-driven cardiac diagnostics.

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AT A GLANCE +

Dr. Matteo Danieletto's research centers on **developing and applying multimodal sensing and machine-learning methods to extract clinically meaningful digital biomarkers from real-world, free-living data**. The research spans hardware, software, and secure data infrastructure for collecting and analyzing physiological, behavioral, and environmental data from wearable devices, smartphones, cameras, and emerging mixed-reality platforms such as Apple Vision Pro and Meta AI Glasses.

This work integrates wearable biosignals, mobile sensor data, and audio-visual data to develop scalable, secure, and interoperable digital health technologies that translate everyday device data into actionable insights for disease prediction, monitoring, and clinical decision-making. The ultimate goal is to transform continuous real-world data into clinically useful information that can **support earlier diagnosis**, **better informed treatment decisions**, and **improved patient outcomes**.

RESEARCH FOCUS

AVAILABLE PROJECTS +

1. Digital Biomarkers With Apple Vision Pro

Develop an application that uses the Apple Vision Pro's cameras and spatial-computing capabilities to extract digital biomarkers relevant to a specific clinical condition.

2. Digital Biomarkers From Apple Watch PPG

Analyze photoplethysmography (PPG) signal data collected from Apple Watch to identify digital biomarkers associated with patient health and physiologic status.

3. Privacy-Preserving On-Device AI for Digital Health

Design an architecture and application that integrates outputs from multiple algorithms running on smartphones or remotely, exploring the use of foundation models that can operate directly on-device to enable privacy-preserving analysis.

RESEARCH FOCUS

ABOUT

Towfique Raj, PhD, is a Professor of Neuroscience, Neurology, Genetics and Genomic Sciences, AI and Human Health, and Immunology and Immunotherapy at the Icahn School of Medicine at Mount Sinai.

He is a member of the Ronald M. Loeb Center for Alzheimer's Disease, the Friedman Brain Institute, and the Icahn Institute for Data Science and Genomic Technology, and serves as Co-Director of the Genomics Core of the Alzheimer's Disease Research Center.

His foundational work established myeloid cells, including monocytes and microglia, as the primary cell types through which genetic risk for Alzheimer's and Parkinson's disease acts. His lab has developed widely used public genomic resources, including MiGA, isoMiGA, SingleBrain, and BigBrain, and increasingly develops AI and machine learning approaches to decode the regulatory genome of neurodegenerative disease.

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TOWFIQUE RAJ

AT A GLANCE +

The Raj Lab investigates the **molecular mechanisms underlying neurodegenerative diseases**, including Alzheimer's disease (AD), Parkinson's disease (PD), and amyotrophic lateral sclerosis (ALS). We are a hybrid computational and experimental lab that integrates **human genetics**, **single-cell and spatial genomics**, **immunology**, and **machine learning** to obtain a **systems-level understanding of disease**.

A central focus is defining how disease risk variants act in myeloid cells (microglia and monocytes) to drive neurodegeneration. The Raj Lab maps quantitative trait loci (xQTLs) across brain and immune cell types, builds large single-cell atlases of the aging and diseased brain, and models disease variants in iPSC-derived microglia carrying AD/PD-relevant alleles. Increasingly, the lab develops and applies AI/ML methods, including genomic sequence-to-function deep learning models, single-cell foundation models, and LLM-based agentic tools, to predict the regulatory effects of disease variants, model perturbation responses in microglia, and accelerate target discovery and drug repurposing for neurodegeneration.

Click here to visit lab website

RAJ LAB

AVAILABLE PROJECTS +

1. Learning the Regulatory Code of Alzheimer's Disease Genomes With Deep Learning

Fine-tune genomic deep learning models (e.g., AlphaGenome/Enformer-class sequence-to-function models) on microglia and brain multiomic datasets (SingleBrain, BigBrain, MiGA) to predict the effects of non-coding Alzheimer's and Parkinson's disease risk variants, with experimental validation in iPSC-derived microglia.

2. Developing a Microglia Foundation Model for Perturbation Prediction

Train single-cell foundation models on large-scale microglial datasets and genetic or pharmacologic perturbation screens to predict how perturbations alter microglial states and identify potential therapeutic targets in Alzheimer's and Parkinson's disease.

3. Single-Cell Dissection of Glial Regulatory Landscapes in α-Synucleinopathies

Using our single-nucleus multiomic atlases of the substantia nigra and myeloid atlas in α-synucleinopathies (AION-Myeloid), map cell-type-specific regulatory programs and integrate Parkinson's disease GWAS to identify causal cell states and variants (e.g., protective P2RY12 variant rs3732765, functionally characterized in iPSC-microglia and miBrain models).

RAJ LAB



SCOTT RUSSO

ABOUT

Scott Russo, PhD, is an endowed Professor of Psychiatry, Neuroscience, and Immunology and Immunotherapy in the Nash Family Department of Neuroscience at the Icahn School of Medicine at Mount Sinai.

He serves as Director of the Center for Affective Neuroscience and the Brain Body Research Center at the Icahn School of Medicine at Mount Sinai

A renowned neurobiologist, he is internationally recognized for his contributions to understanding the neural and immunological basis of neuropsychiatric disorders. His translational studies of the immune system in depression have changed the way we think about mental illness providing detailed mechanisms by which disturbances in peripheral immunity lead to changes in complex behavior. He has also dissected the circuitry in the brain that controls abnormal social behaviors—including aggression and violence—leading to new perspectives on social dysfunction in people with neuropsychiatric illness.

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AT A GLANCE +

The Russo Lab investigates **how stress affects the brain and body** and how these changes contribute to **mental health disorders** such as depression and anxiety. The research combines studies in animal models with research involving people with depression and anxiety, using both laboratory and computational approaches to uncover how the brain and immune system respond to stress.

A major focus is the identification of liquid biomarkers — measurable biological signals in body fluids — that may help characterize stress-related disorders. The program studies **inflammatory monocyte-derived factors**, **microRNAs**, and **extracellular vesicles**, also known as exosomes, and uses predictive modeling to investigate their relationships with symptoms and behavioral measures of anhedonia. Ultimately, the Russo Lab aims to **identify biological mechanisms** to explain why some individuals are more vulnerable to stress-related disorders and guide the development of better treatments.

Click here to visit lab website

RUSSO LAB

AVAILABLE PROJECTS +

1. Immune Biomarkers of Depression and Stress-Related Disorders

Analyze biological and clinical data to identify liquid biomarkers associated with depression, PTSD, and post-acute sequelae of SARS-CoV-2 infection (PASC), with an emphasis on predictive modeling and integrated biomarker signatures.

RUSSO LAB

ABOUT

Sikander Hayat, PhD is an Associate Professor in the Cardiovascular Research Institute and an Associate Professor of AI and Human Health at the Icahn School of Medicine at Mount Sinai.

He is a computational biologist whose research combines single-cell and spatial transcriptomics, multi-omics, and artificial intelligence to uncover insights into disease biology and identify potential therapeutic targets.

He has led multi-omics studies of cancer, kidney disease, heart failure, and athersclerosis, with a focus on immune-stromal interactions and fibrosis.

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SIKANDER HAYAT

AT A GLANCE +

Dr. Sikander Hayat's research focuses on **developing multi-agent AI systems for scientific discovery**, integrating single-cell and spatial transcriptomics with large language models and multimodal foundation models. The research focuses on using AI to generate and evaluate biomedical hypotheses, identify potential therapeutic targets, and support scientific study design.

A central goal is to move beyond black-box prediction toward **explainable, mechanism-aware AI** that can **integrate biological knowledge, generate testable hypotheses, and support experimental reasoning.**

RESEARCH FOCUS

AVAILABLE PROJECTS +

1. Multi-Agent AI for Biomedical Hypothesis Generation
Develop multi-agent AI systems that can generate biomedical hypotheses, propose study designs, and support scientific discovery.

2. Improving AI-Generated Hypothesis Scoring and Explainability
Develop algorithms to improve the evaluation, ranking, and interpretability of AI-generated hypotheses.

3. Multimodal AI for Mechanistic Discovery
Integrate multimodal biological data with mechanistic knowledge and foundation models.

4. Evaluation Frameworks for AI-Assisted Scientific Discovery
Develop rigorous evaluation frameworks and open benchmarks for assessing AI systems used in biomedical research and scientific reasoning.

RESEARCH FOCUS



VIKAS PEJAVER

ABOUT

Vikas Pejaver, PhD, is an Assistant Professor of Genetics and Genomic Sciences and AI and Human Health at the Icahn School of Medicine at Mount Sinai.

He is a member of multiple working groups within the Clinical Genome (ClinGen) Reserouce and Impact of Genomic Variation on Function (IGVF) consortia and co-chairs the Analysis, Modeling, and Prediction Workstream within the Atlas of Variant Effects (AVE) Alliance.

His research focuses on developing and applying machine learning and artificial intelligence methods to understand how genetic variation relates to molecular function and disease phenotypes, using genomic, protein, and electronic health record data. His work particularly focuses on rare genetic variants and diseases, using approches including semi-supervised learning, model calibration, and language modeling across basic, translational, and clinical applications.

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AT A GLANCE +

The Pejaver Lab develops and applies **machine learning and AI methods to connect genetic variation with molecular function and clinical disease**, with a particular emphasis on **rare genetic diseases**. The lab integrates genomic data, protein structure and function, and electronic health record data to accelerate the discovery, diagnosis, and treatment of rare diseases.

Click here to visit lab website

PEJAVER LAB

AVAILABLE PROJECTS +

1. Calibrating AI Models for Genetic Variant Effect Prediction

Develop and evaluate methods to improve the calibration and reliability of AI models that predict the functional effects of genetic variants.

2. Predicting Variant Effects on Protein Structure and Function

Develop machine-learning approaches to predict how genetic variants alter protein structure and function.

3. Identifying Rare Genetic Diseases From EHRs and Clinical Notes

Develop AI methods to identify patients with rare genetic diseases using electronic health records and clinical notes.

PEJAVER LAB

ABOUT

Vincenzo G. Fiore, PhD is an Assistant Professor of Psychiatry at the Icahn School of Medicine at Mount Sinai.

His research focuses on computational psychiatry and the use of computational models to understand decision-making, goal-directed behavior, and habit formation in healthy and clinical populations.

His work particularly examines neural, reinforcement learning and Bayesian computational models of health and aberrant behavior in human and non-human animals, with a specific focus on disorders of compulsivity, including substance use disorders, behavioral addictions, eating disorders, and obsessive-compulsive disorder. These methods are also used in model-based analyses of fMRI and neurophysiological data, with the aim of developing comprehensive models of the neural dynamics of cortico-thalamo-striatal circuits, under aminergic modulation.

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VINCENZO FIORE

AT A GLANCE +

The Fiore Lab investigates the **neurocomputational mechanisms underlying decision-making, goal-directed behavior, and habit formation in healthy and clinical populations**, with a particular focus on how these processes are altered in **psychiatric disorders**.

The research relies on **computational models of behaviour and neural dynamics**, bridging **computational theory**, **mechanistic implementation**, and **clinical interpretation** to inform our understanding of clinical phenomena.

Click here to visit lab website

FIORE LAB

AVAILABLE PROJECTS +

1. Predictive Connectome Fingerprints of Decision-Making in Obsessive-Compulsive Disorder

Investigate whether task-based whole-brain functional connectivity can provide individualized neural fingerprints of OCD. Using existing fMRI data from decision-making tasks, the project will combine computational modeling of behavior with connectome-based predictive modeling to characterize individual differences in decision-making and their relationship to clinical symptom severity.

FIORE LAB



EUGENIA ALLEVA

ABOUT +

Eugenia Alleva, PhD is an Assistant Professor of AI and Human Health and Obstetrics, Gynecology and Reproductive Sciences at the Icahn School of Medicine at Mount Sinai. Trained as both a physician and digital health scientist, she bridges gynecology and computational sciences to advance women's health.

Her research applies machine learning and natural language processing to gynecological and obstetrical conditions, including endometriosis, dysmenorrhea, and heavy menstrual bleeding (HMB). In 2025, she received a Wellcome Leap Missed Vital Sign grant to develop AI/ML tools for early detection and treatment of HMB, a condition affecting over 30% of reproductive-age women worldwide.

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AT A GLANCE +

The Alleva Lab develops **computational methods for women's health research using real-world clinical data**. Our work integrates electronic health records, survey instruments, medical imaging, and retrospectively collected physiological signals into models that support **risk prediction** and **phenotyping** for **menstruation-related disorders**.

ALLEVA LAB

AVAILABLE PROJECTS +

1. Develop AI Methods to Identify Patients With Rare Genetic Diseases Using EHRs and Clinical Notes

Physiological signal processing for real-world wearable data. Continuous physiological data collected outside the clinic is dominated by artifact, non-wear, and irregular sampling. This project concerns the design of physiologically motivated filtering for a single measure, and how much the resulting summary statistics depend on those preprocessing choices.

2. Physiological Markers of Heavy Menstrual Bleeding

Heavy menstrual bleeding is thought to produce measurable physiological consequences, including cardiovascular compensation for blood loss, but the evidence in wearable data is thin. This project examines whether such a consequence is detectable in continuous monitoring data when observations are anchored to the menstrual cycle rather than to calendar time.

3. Aligning Representations Across Clinical Modalities

Clinical records, images, tissue, and physiological signals describe the same patient in different languages, and a model built on one of them sees only part of the picture. This project concerns the alignment of learned representations from two modalities into a shared space, and what alignment buys when patients are missing one of them, as most patients are.

ALLEVA LAB

AVAILABLE PROJECTS +

4. Agent-Based Harmonization of Multi-Site Clinical Data

Research groups collecting the same clinical concepts describe them in different variable names, units, and coding conventions, and reconciling them is currently slow manual work. This project investigates whether a language-model agent can propose mappings between site-level data dictionaries and a common schema, and how those proposals should be evaluated against expert judgment.

5. Learning Pelvic Ultrasound Structure From Sparse Labels

Transvaginal ultrasound studies arrive as large collections of frames varying in anatomy and imaging plane, of which only a small fraction is ever expertly annotated. This project applies adversarial and generative approaches to train classifiers that recognize imaging plane and anatomical structure from sparsely labeled data.

6. Autonomic Markers and Menstrual Pain (CRAMP Study)

Menstrual pain varies widely between people and within the same person across cycles, and the physiological correlates of that variation are poorly characterized. This project explores the relationship between wearable-derived autonomic measures, such as heart rate variability, and reported pain severity, including how two differently sampled data streams can be compared at all.

ABOUT

Jason Liu, PhD, is an Assistant Professor in Artificial Intelligence and Human Health and Psychiatry at the Icahn School of Medicine at Mount Sinai.

He received his PhD from Yale University, where he also completed his postdoctoral training. His research focuses on developing interpretable AI approaches that integrate wearable devices, digital health data, and human genetics to better understand neurological and psychiatric disorders and advance precision medicine.

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AT A GLANCE +

The Liu Lab works at the intersection of artificial intelligence, digital health, and genomics to advance precision medicine, **developing interpretable AI approaches that integrate data from wearable devices, clinical records, and human genetics to better understand health and disease**.

The research focuses on how continuous, real-world measurements of physiology and behavior, including activity, sleep, and heart rate, can provide new insights into neurological and psychiatric disorders. By combining these measurements with genetic and clinical data, the Liu Lab aims to 1) **identify biomarkers of disease**, 2) **understand individual differences in disease progression and treatment response**, and 3) **uncover genes and biological mechanisms that could inform the development of new therapeutics**. The work spans AI, deep learning, time-series analysis, statistical genetics, and computational biology, with opportunities to develop novel computational methods and apply them to large-scale biomedical datasets.

Click here to visit lab website

LIU LAB

AVAILABLE PROJECTS +

1. Using AI and Wearables to Understand and Predict Medication Response

Explore how wearable devices and AI can provide objective, real-world measurements of medication response. Analyze patterns in activity, sleep, heart rate, and other physiological signals, aiming to identify signatures of treatment benefits and side effects, understand individual differences in medication response, and predict long-term treatment outcomes. Develop machine learning models, analyze longitudinal wearable data, and identify digital biomarkers of treatment response, with applications to psychiatric and neurological conditions.

2. Using AI and Genome-Wide Association Studies to Uncover the Genetics of Human Disease

Integrate AI-derived wearable phenotypes with large-scale genetic data to discover genes and biological mechanisms underlying neurological and psychiatric disorders. By developing more precise, continuous measures of health and disease from wearable data, we aim to improve genome-wide association studies (GWAS) and identify genetic variants and pathways associated with disease susceptibility, symptoms, and progression. Develop interpretable AI methods, conduct large-scale GWAS, and perform statistical and functional genomic analyses to investigate the genetic basis of diseases such as Parkinson's disease and psychiatric disorders.

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