MitoOmics–GPU

A Cross-Modal “Mito Health Index” (MHI) from EV/MDV Proteomics + Single-Cell

Nvidia Accelerate Omics Hackathon

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NVIDIA

UCI University of California, Irvine

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Northeastern University

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Why Mitochondria ?

1. **Powerhouse** of the cell
2. **Biomarker** for disease and cellular health

3. **It reflects**
    a. metabolic capacity and
    b. cellular adaptation to stress
    c. disease severity and progression.
    d. mitochondrial QC pathways
    e. easily detected in blood

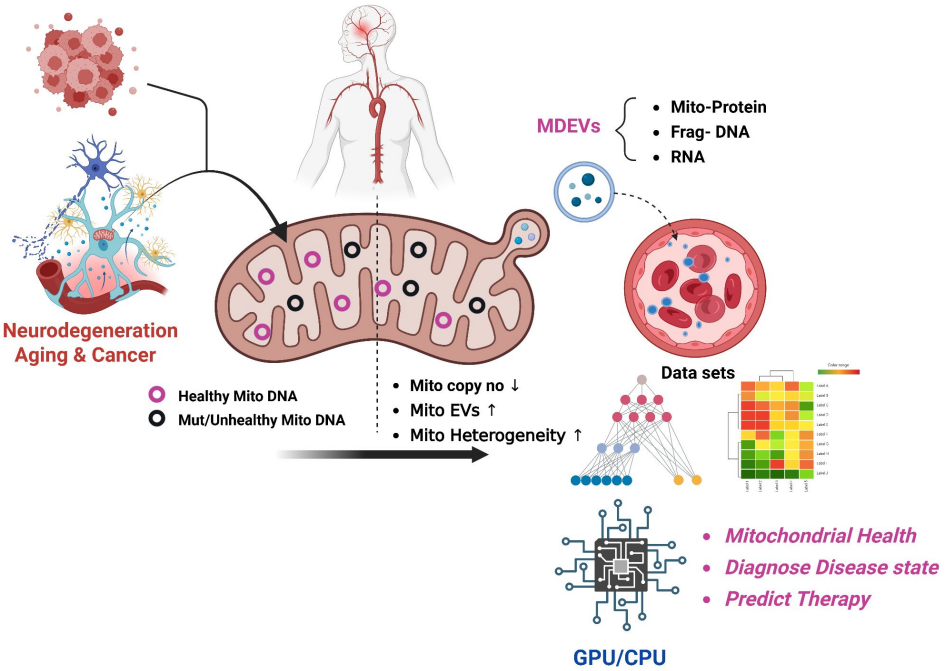
4. **mtDNA copy and MDEVs determines:**
    i. disease risk progression
    ii. therapeutic monitoring
    iii. Determine mitochondrial resilience and mitochondrial fitness

5. Integration Multi Omics data sets, Multimodal imaging and Clinical outcomes
   Determine mitochondrial metrics for potential therapeutic intervention

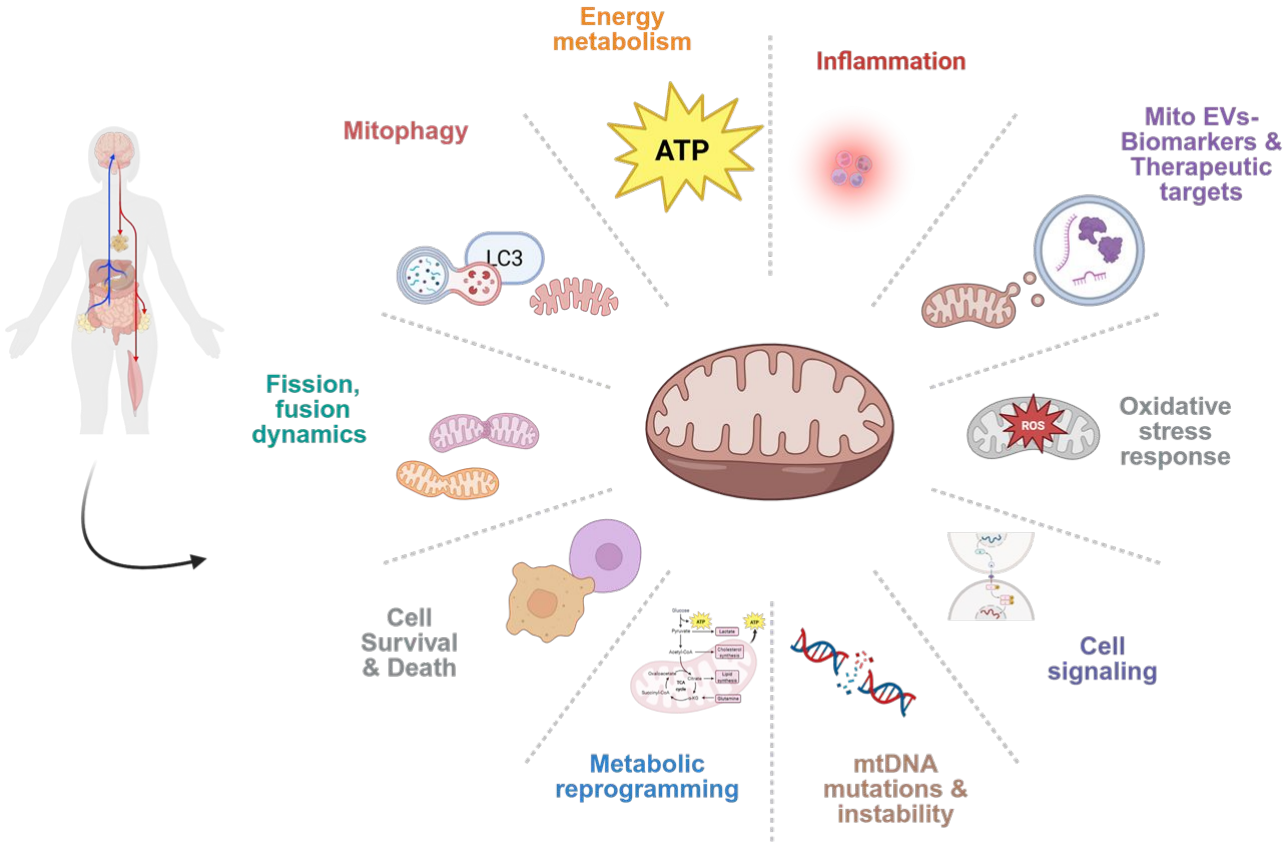
Objective

To develop GPU-accelerated pipeline to quantify and visualize mitochondrial health index (MHI) via circulating extracellular mitochondrial derived vesicle (EV/MDV) proteomics to mitochondrial DNA copy-number, from scRNA-seq with clear CPU-GPU speedups and a tidy PR to scverse/rapids-single cell.

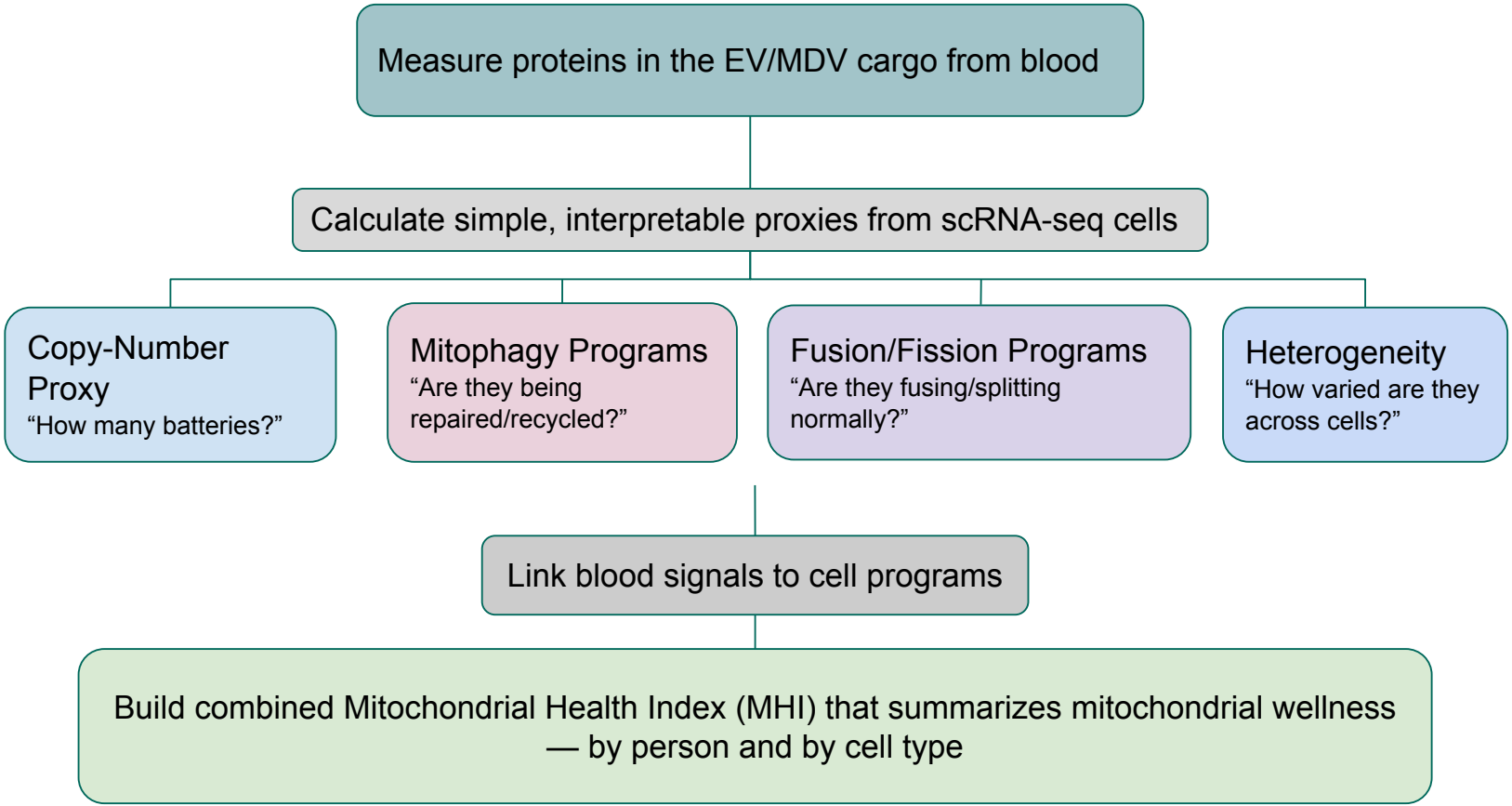
To accelerate and predict mitochondrial health, biogenesis, heterogeneity and disease condition for potential therapeutic targets



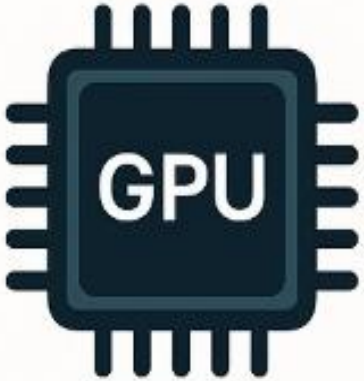
Mitochondria Fate In Health and Disease: at crossroads?

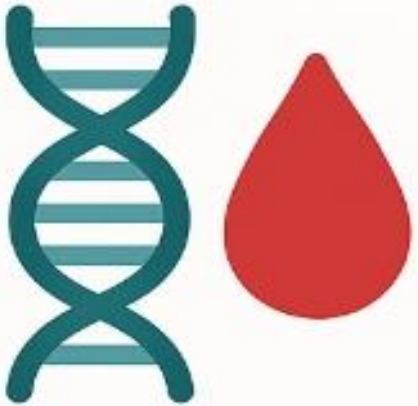


Computational Workflow



GPU acceleration





Why GPUs matter:

Huge datasets ⟶ GPUs crunch them **much faster**

What's new vs. today:

Combines blood and single-cell signals

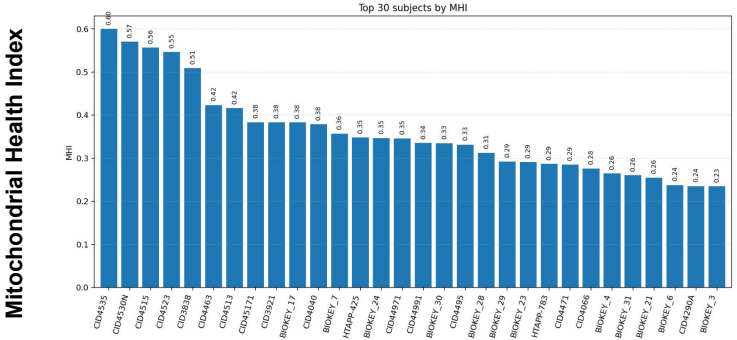
Generates MHI

Who benefits and how:

Researchers/clinicians

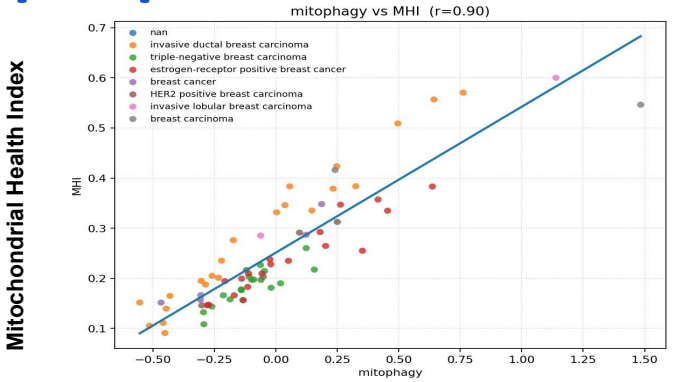
Trials/biotech

Key Insights - output plots



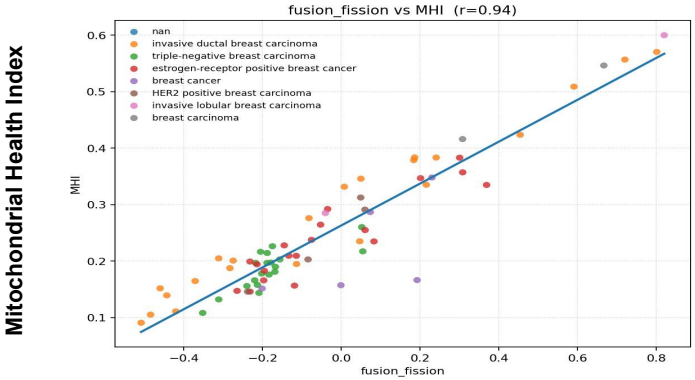
Mitochondrial Health Index

Patient Datasets/Biological Identifier



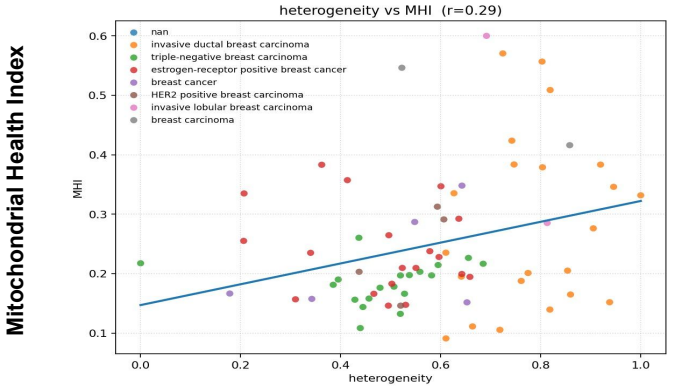
Mitochondrial Health Index

Mitophagy (mito-recycling)



Mitochondrial Health Index

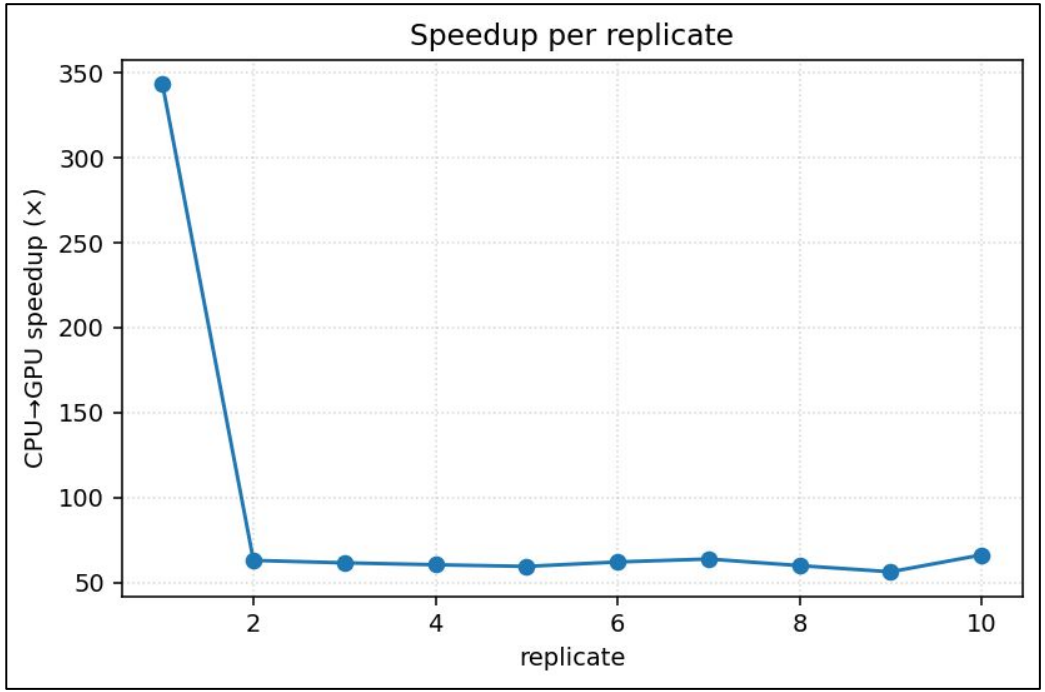
Mitochondrial Biogenesis Fusion and Fission



Mitochondrial Health Index

Mitochondrial Heterogeneity

Key Insights - GPU/CPU comparison speedups



rep	CPU(s)	GPU(s)	speedup
1	2.016	0.006	343.50×
2	0.366	0.006	62.95×
3	0.343	0.006	61.53×
4	0.331	0.005	60.40×
5	0.330	0.006	59.42×
6	0.348	0.006	62.04×
7	0.345	0.005	63.77×
8	0.332	0.006	59.88×
9	0.374	0.007	56.24×
10	0.384	0.006	66.21×

Key takeaways

01	Biological Implications	• Biomarker discovery • Disease prediction, prognosis, progression etc • Patient stratification for effective drug response • Improve quality of life & reduce economic burden
02	What we learnt?	• Predictive Models • Data Integration Pipelines • Visualization Dashboards • Tools for Biomarker Discovery
03	Future Directions	• Cross-disease biomarker • Precision medicine • Bridging bench-to-bedside • Develop therapeutic interventions targeting mitochondrial health

Conclusion and Future directions

Summary

Unified MHI (EV/MDV proteomics + scRNA-seq)

GPU-accelerated single-cell analysis

Open-source pipeline (ready for integration)

Future Directions

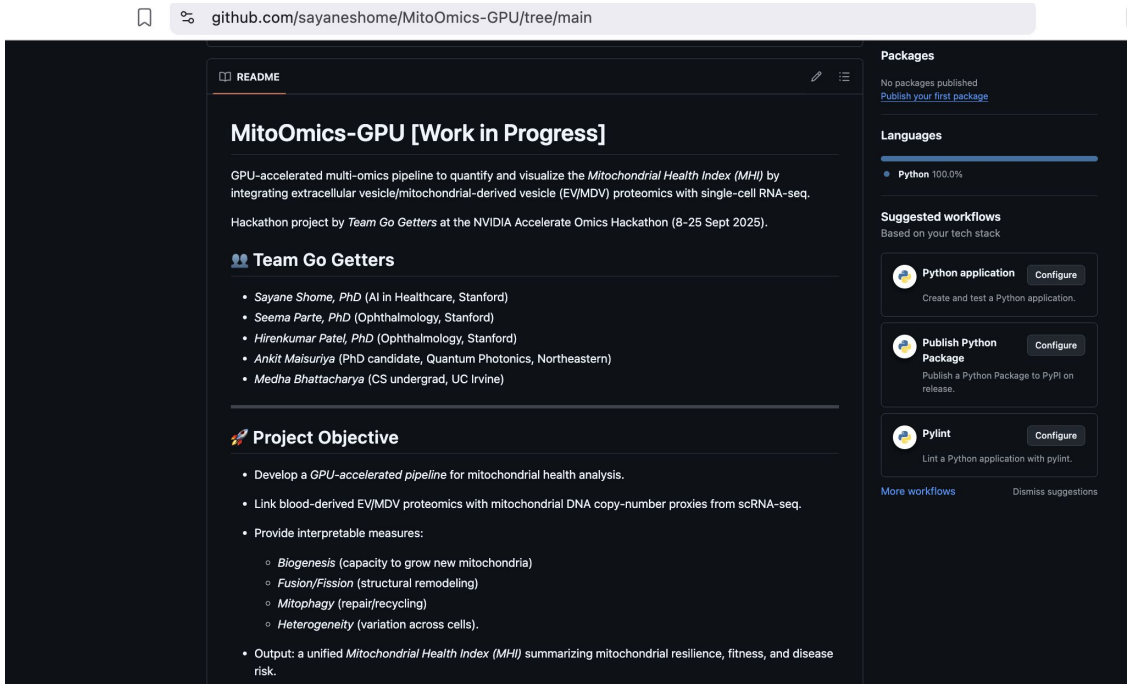
Add more modalities (scATAC, etc.)

Web-server/pip access for biologists/end-users

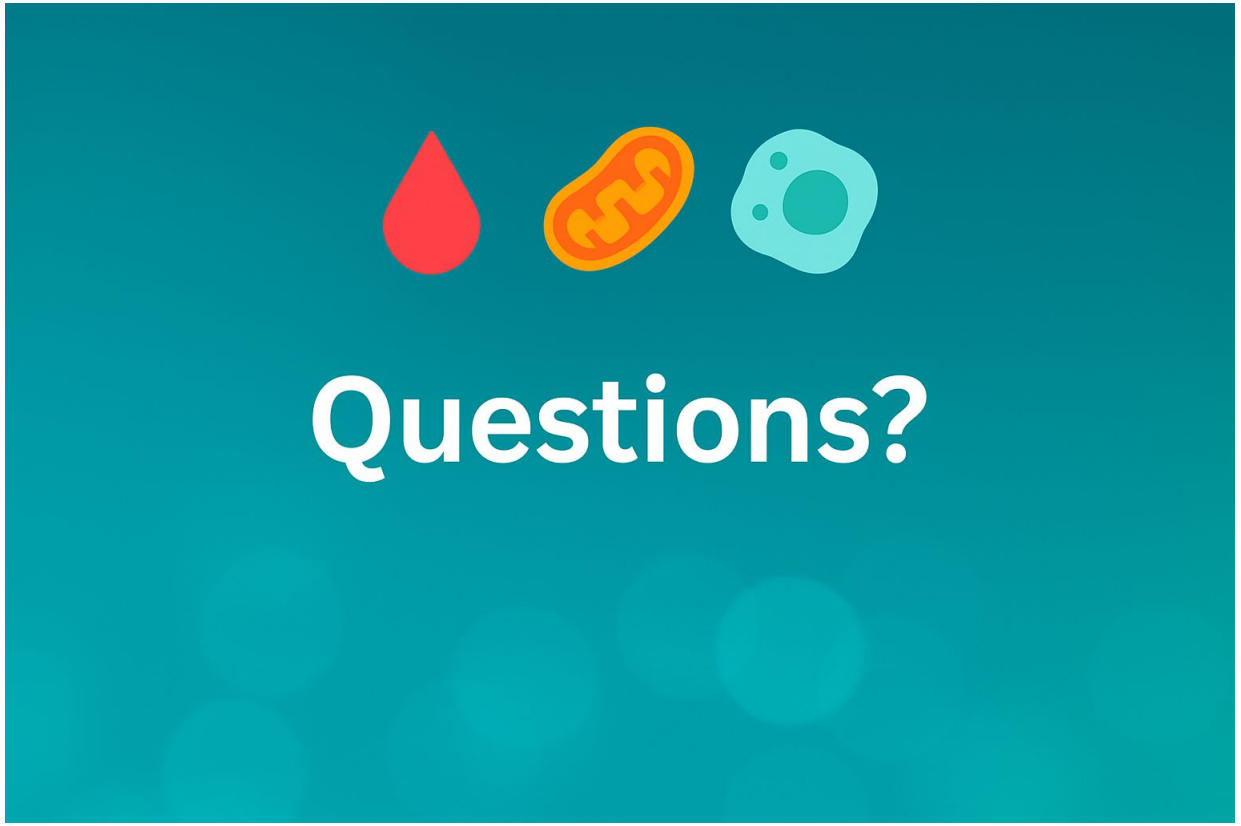
Clinical validation with partners & cohorts

ML upgrades: pattern discovery & prediction on MHI

Github and Contact details



Contact : sshome@stanford.edu


Questions?