

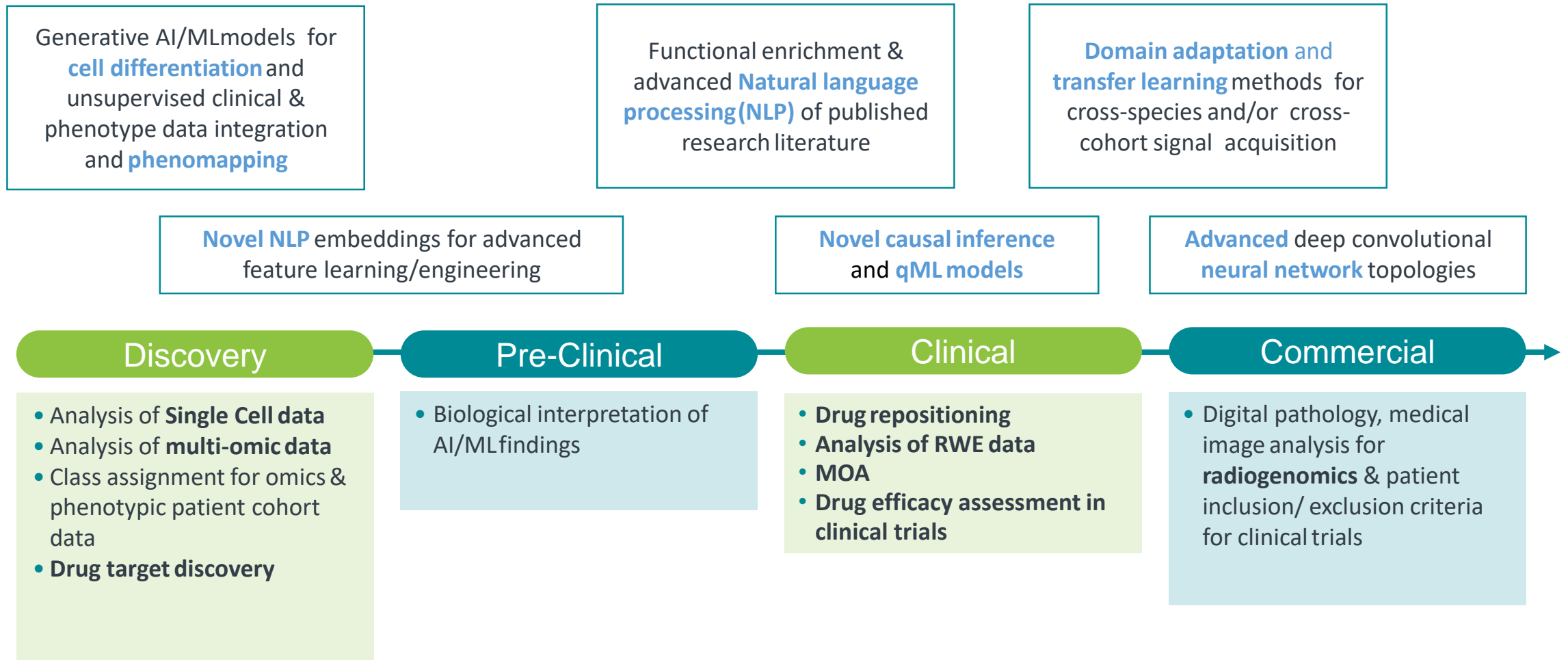


## *Reimagining AI in Biopharma*

*Tom Chittenden, PhD, DPhil, PStat  
Chief Scientific Officer, President of R&D, SAB Chairman  
Lecturer on Pediatrics, BCH & Harvard Medical School*

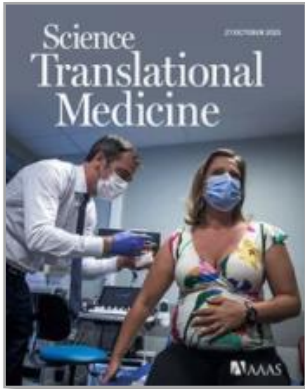
The Lab of the Future Congress USA  
10 March 2023

# AI/SciML Platform for Drug Discovery and Drug Development



# Scientific Impact in the Biomedical Sciences

Featured on Cover  
Accompanying Editorial

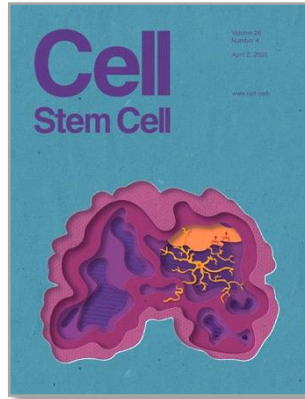


Identification of driver genes for critical forms of COVID-19 in a deeply phenotyped young patient cohort [link](#)



Quantum processor-inspired machine learning in the biomedical sciences [link](#)

Featured at NHLBI



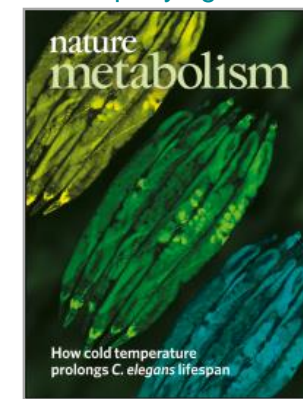
Smooth muscle cell reprogramming in aortic aneurysms [link](#)

Accompanying Editorial



Chronic mTOR activation induces a degradative smooth muscle cell phenotype [link](#)

Accompanying Editorial



Endothelial TGF- $\beta$  signaling drives vascular inflammation and atherosclerosis [link](#)

Accompanying Editorial

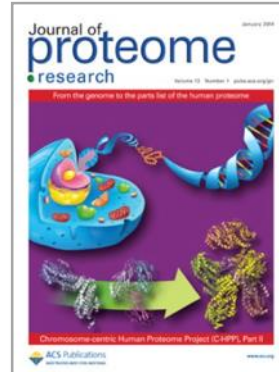


Endothelial ERK1/2 signaling maintains integrity of the quiescent endothelium [link](#)

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Enhancing retrosynthetic reaction prediction with Deep Learning Using multiscale reaction classification [link](#)

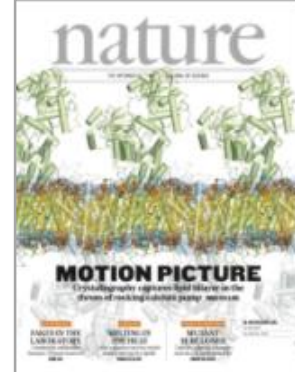


Proteomic analysis and identification of cellular interactors of the giant ubiquitin ligase HERC2 [link](#)

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Somatic mutation in single human neurons tracks developmental and transcriptional history [link](#)



FGF-dependent metabolic control of vascular development [link](#)

Accompanying Editorial



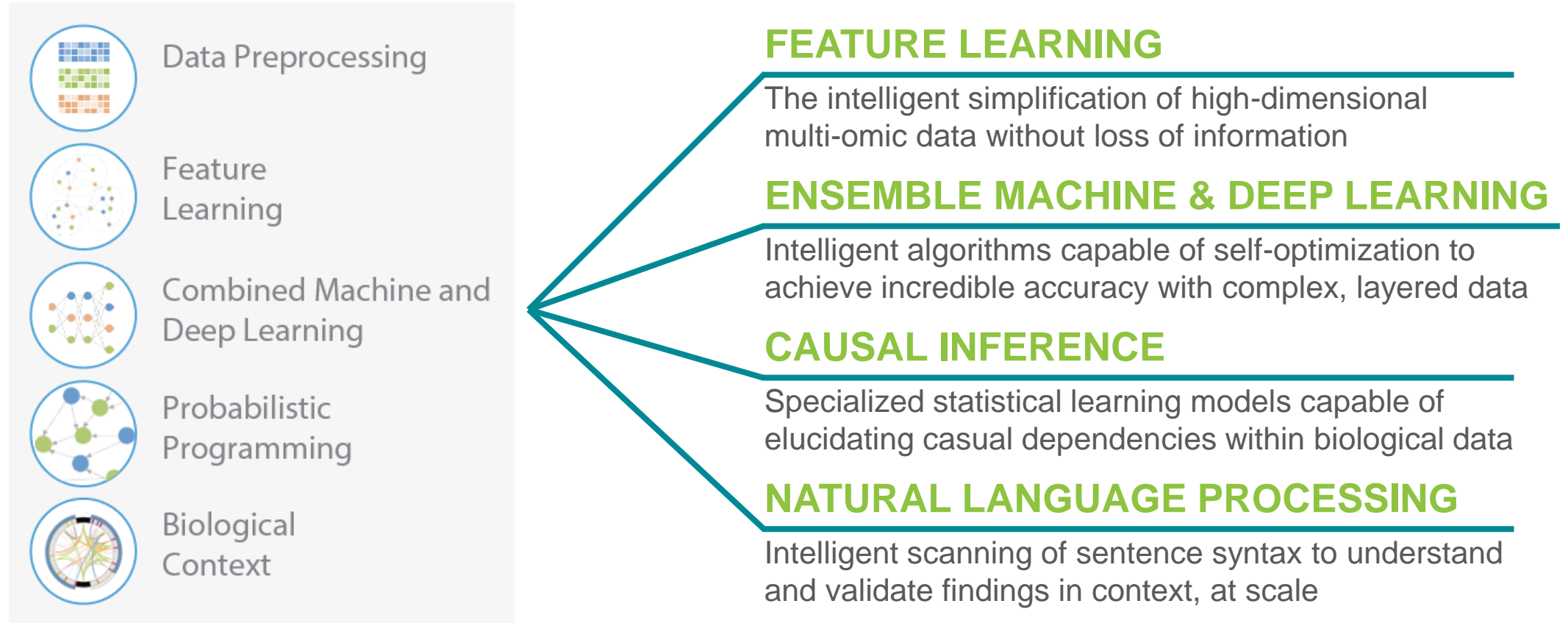
Aging & neurodegeneration are associated with increased mutations in single human neurons [link](#)



Shear-induced Notch-Cx37-p27 axis arrests endothelial cell cycle to enable arterial specification [link](#)

# Ensemble AI/SciML and Precision Medicine

The computational power of modern AI/ML technology is well-positioned to uncover new and actionable insights from the exponentially growing pool of biological data.



The combination of several AI/SciML methods create a proprietary ensemble AI/SciML strategy capable of revealing novel patterns and causal dependencies in disparate and varied biological data.

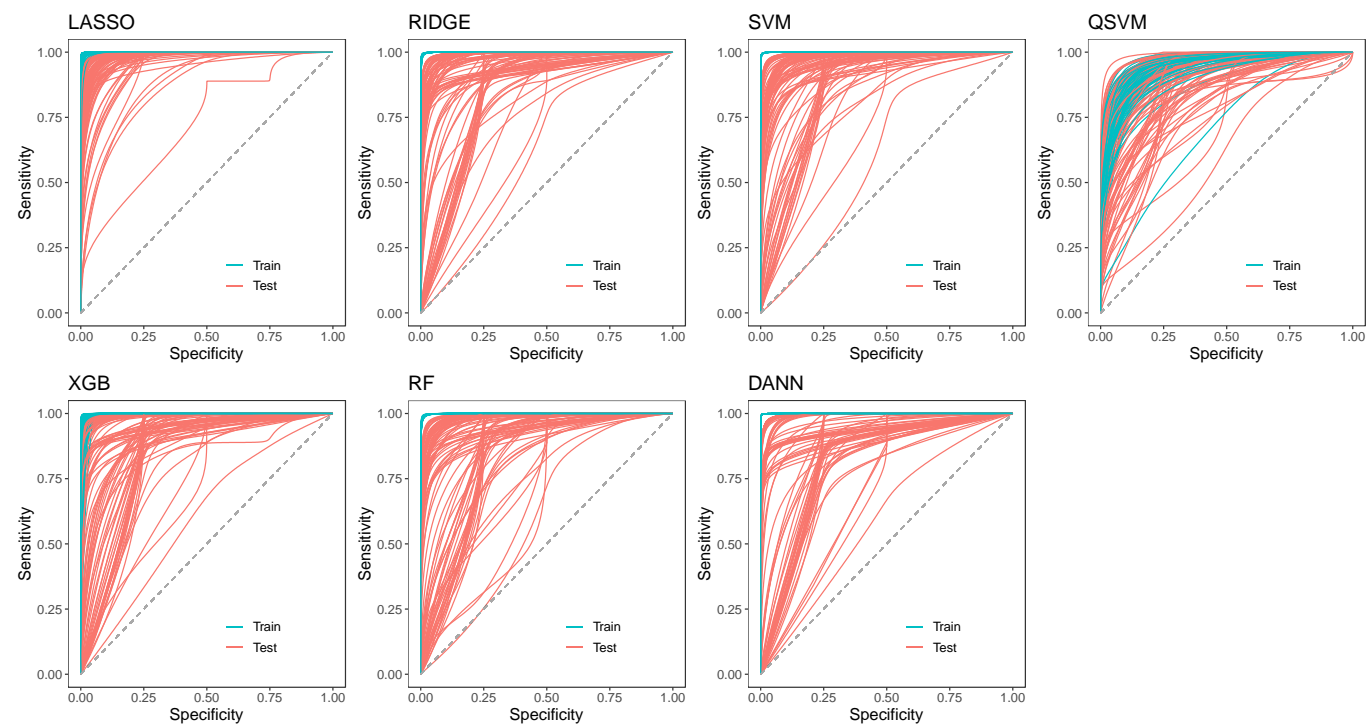
# COVID-19 Severity Study: Ensemble AI/SciML/qML approach to compare critical vs non-critical patients

- Unique study design focused on adults younger than **50 without co-morbidities or age-related decline**
- During height of first wave (before corticosteroid use), our collaborators at Strasbourg recruited COVID-19 patients with **ARDS requiring mechanical ventilation** and matched patients who were sick enough to be hospitalized but **required oxygen without assisted ventilation**

Group	Description	Whole blood RNA-Seq	Plasma Proteomics	PBMC Proteomics	WGS
Critical	Severe COVID patients with ARDS requiring ventilators	<b>46</b>	45	34	47
Non-critical	Control COVID patients hospitalized and given oxygen but not ICU care	<b>23</b>	23	21	25
COVID negative controls	Healthy controls from blood donors at same hospital	22	22	22	22



Cohort 1 RNA-seq: Critical(ARDS) vs non-critical groups with ensemble strategy comprising 7 different AI/ML algorithms including Quantum SVM (69 patients total) – Leads to stable gene feature sets to allow for subsequent causal inference (other methods produce variable gene lists)



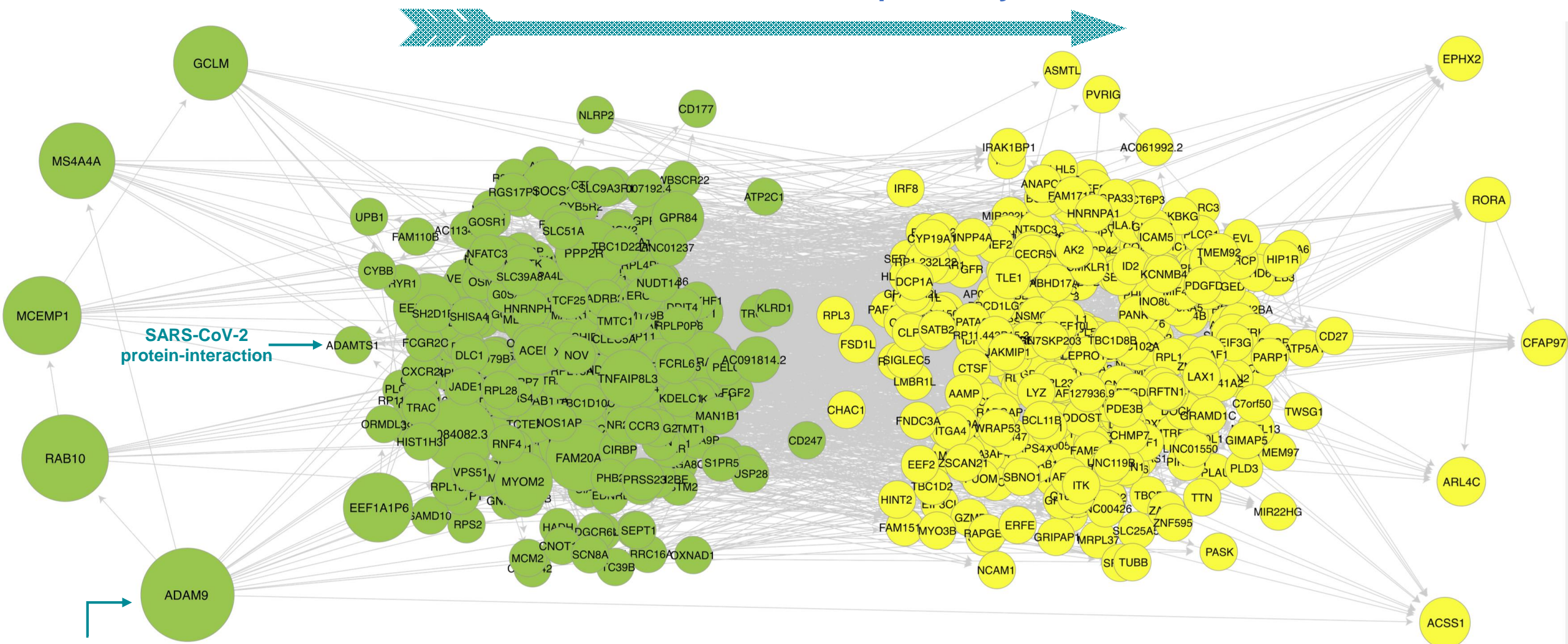
	LASSO	Ridge	SVM	qSVM
Accuracy (Train/Test)	0.9991 ± 0.0004 / 0.9677 ± 0.0050	1.0000 ± 0.0000 / 0.9169 ± 0.0072	1.0000 ± 0.0000 / 0.9223 ± 0.0075	0.9245 ± 0.0028 / 0.8677 ± 0.0121
Balanced Acc. (Train/Test)	0.9987 ± 0.0006 / 0.9503 ± 0.0078	1.0000 ± 0.0000 / 0.8990 ± 0.0094	1.0000 ± 0.0000 / 0.9068 ± 0.0092	0.9189 ± 0.0039 / 0.8607 ± 0.0118
AUROC (Train/Test)	<b>1.0000 ± 0.0000 / 0.9908 ± 0.0036</b>	<b>1.0000 ± 0.0000 / 0.9547 ± 0.0075</b>	<b>1.0000 ± 0.0000 / 0.9633 ± 0.0070</b>	<b>0.9667 ± 0.0029 / 0.9386 ± 0.0081</b>
F1 (Train/Test)	0.9993 ± 0.0003 / 0.9780 ± 0.0034	1.0000 ± 0.0000 / 0.9404 ± 0.0052	1.0000 ± 0.0000 / 0.9487 ± 0.0049	0.9426 ± 0.0020 / 0.9095 ± 0.0071
MCC (Train/Test)	0.9980 ± 0.0009 / 0.9251 ± 0.0118	1.0000 ± 0.0000 / 0.8128 ± 0.0169	1.0000 ± 0.0000 / 0.8364 ± 0.0161	0.8339 ± 0.0065 / 0.7398 ± 0.0198

	XGB	RF	DANN
Accuracy (Train/Test)	0.9952 ± 0.0008 / 0.9146 ± 0.0076	1.0000 ± 0.0000 / 0.9254 ± 0.0072	1.0000 ± 0.0000 / 0.9131 ± 0.0083
Balanced Acc. (Train/Test)	0.9930 ± 0.0012 / 0.8932 ± 0.0100	1.0000 ± 0.0000 / 0.9072 ± 0.0094	1.0000 ± 0.0000 / 0.9032 ± 0.0097
AUROC (Train/Test)	<b>0.9999 ± 0.0000 / 0.9443 ± 0.0079</b>	<b>1.0000 ± 0.0000 / 0.9360 ± 0.0091</b>	<b>1.0000 ± 0.0000 / 0.9435 ± 0.0081</b>
F1 (Train/Test)	0.9964 ± 0.0006 / 0.9391 ± 0.0054	1.0000 ± 0.0000 / 0.9467 ± 0.0052	1.0000 ± 0.0000 / 0.9359 ± 0.0062
MCC (Train/Test)	0.9893 ± 0.0018 / 0.8061 ± 0.0181	1.0000 ± 0.0000 / 0.8308 ± 0.0168	1.0000 ± 0.0000 / 0.8091 ± 0.0185

High accuracies with AUROC of test sets from 0.94 to 0.99

# Integrated AI/SciML and Structural Causal Modeling on top of 600 RNA-seq genes from critical (ARDS) vs non-critical groups

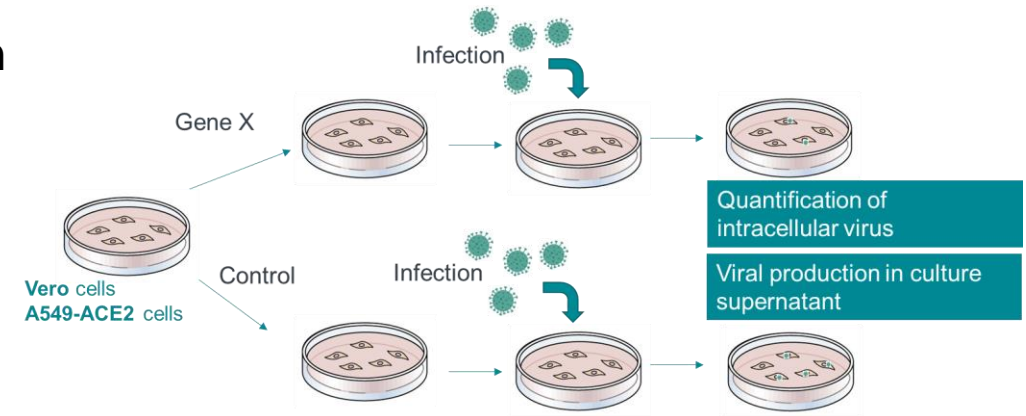
Putative flow of Causal Dependency



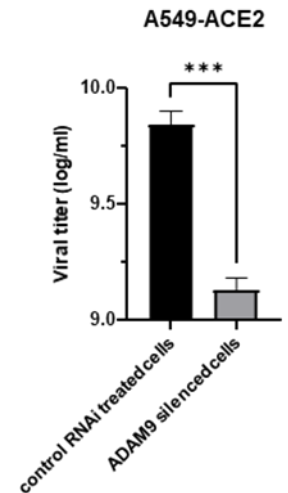
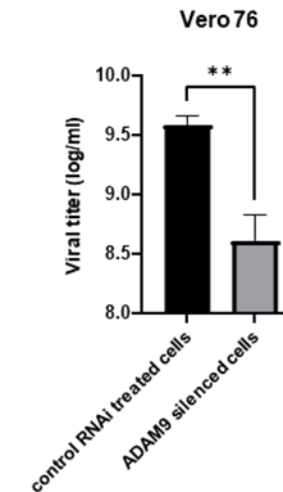
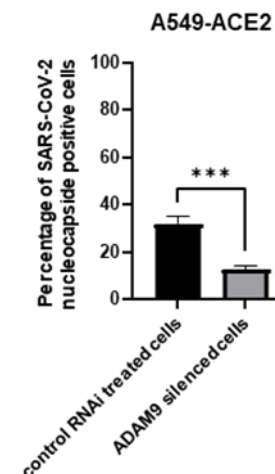
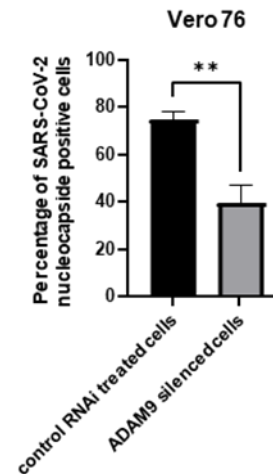
Carapito et al., *Science Translational Medicine* 2021

# COVID-19 project – Experimental Validation of AI/SciML Findings (effects of ADAM9 silencing on viral uptake and replication)

- Silencing Gene X inhibits SARS-CoV-2 uptake and replication in human lung epithelial cells: ***strong empirical evidence of molecular mechanism of action*** driving complex disease etiology
- Actively pursuing a possible **first AI/ML-based repositioning** of a drug currently in Phase III trials ADAM9+ tumors



Carapito, R *et al.*, *Science Translational Medicine* 2021

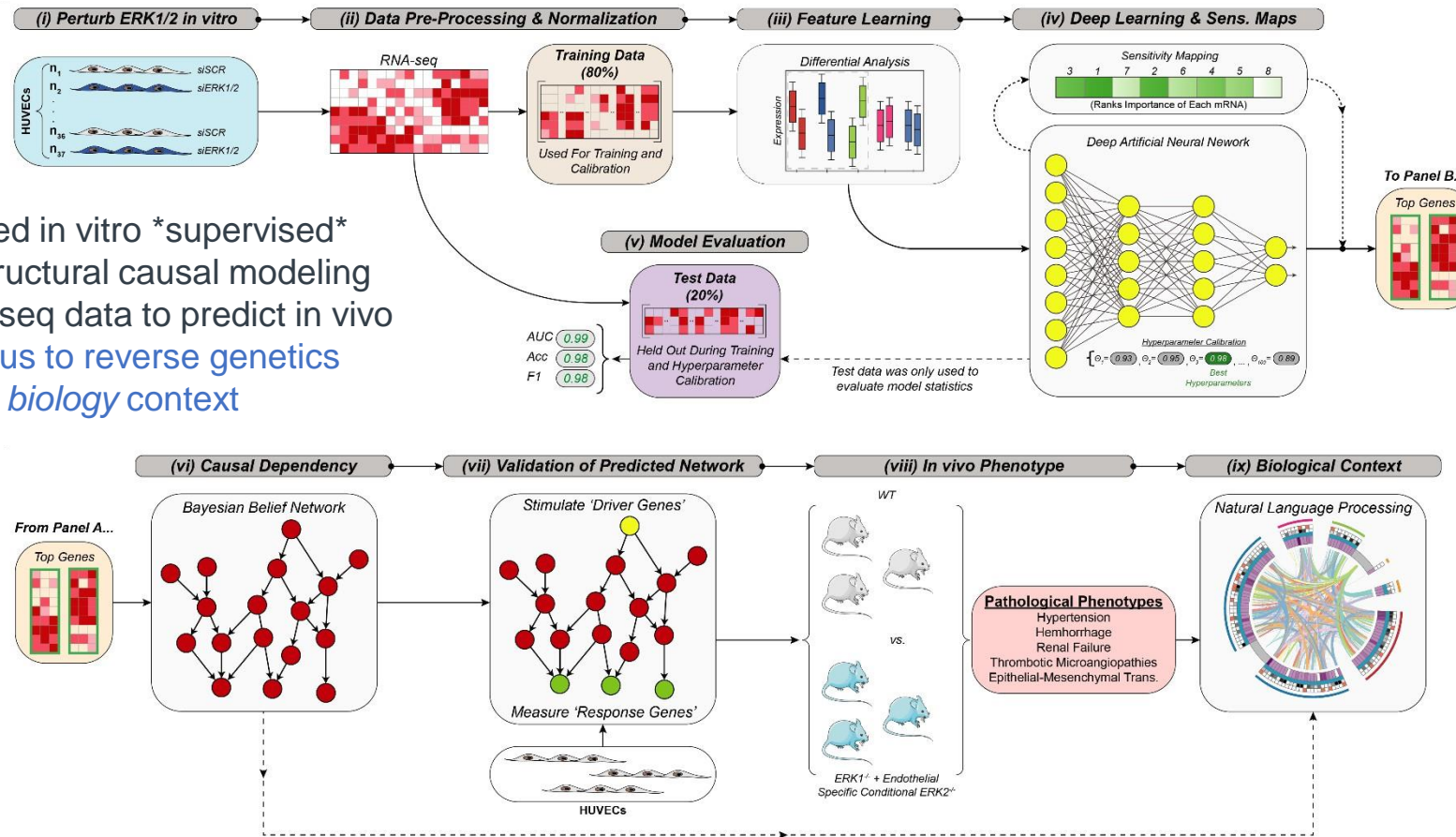




# *In Silico* Phenotype Projection: Identifying Causal Drivers of CVD (Hypertension, Vascular Hemorrhage, and Renal Failure)

(Ricard et al., *JEM* 2019)

Example of integrated in vitro \*supervised\* classification and structural causal modeling (SCM) of bulk RNA-seq data to predict in vivo phenotype. Analogous to reverse genetics with added *systems biology* context

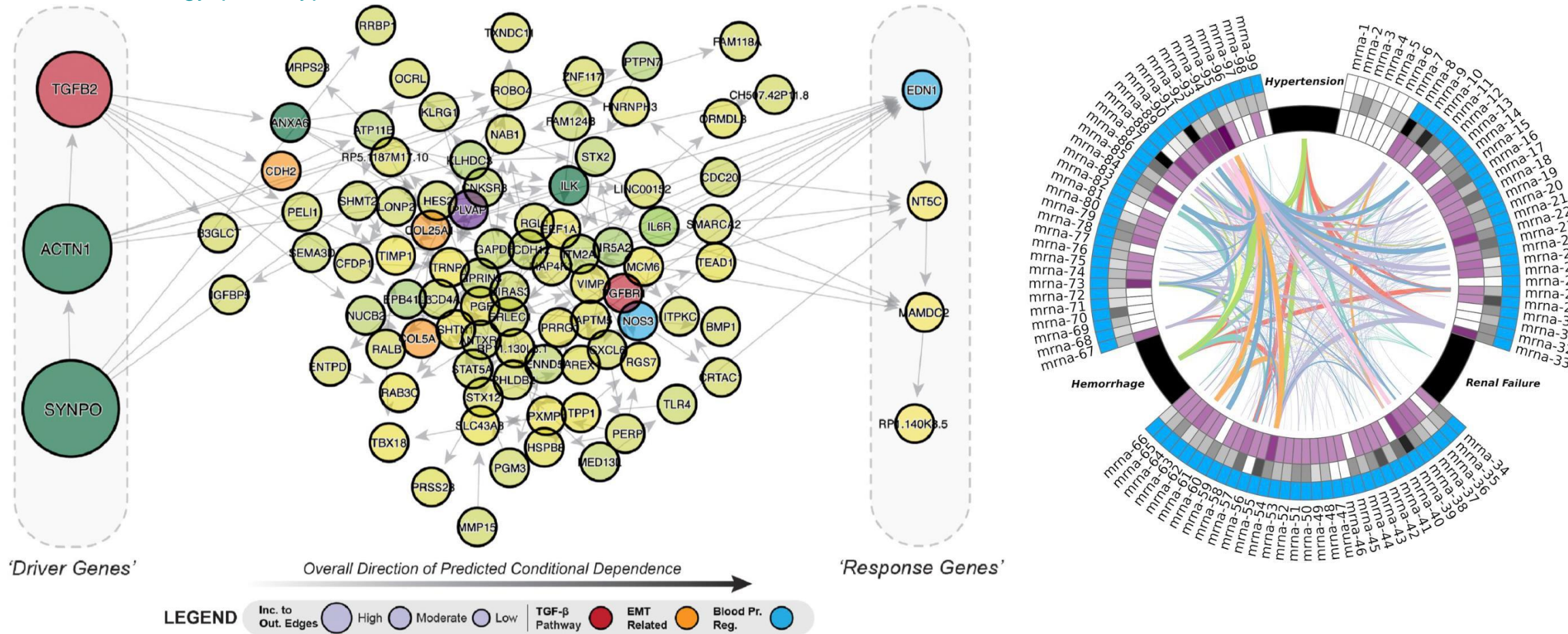


Research Collaboration with Yale Cardiovascular Research Center  
Deep Learning, Structural Causal Modeling, and NLP of Bulk and Single Cell RNA-seq Data

# In Silico Phenotype Projection: Identifying Causal Drivers of CVD (Hypertension, Vascular Hemorrhage, and Renal Failure)

Example of causal structural modeling (SCM) of bulk RNA-seq analysis, which is downstream  
\*supervised\* bulk RNA-seq analysis on previous slide to derive putative causal drivers of disease  
etiology, phenotype, etc.

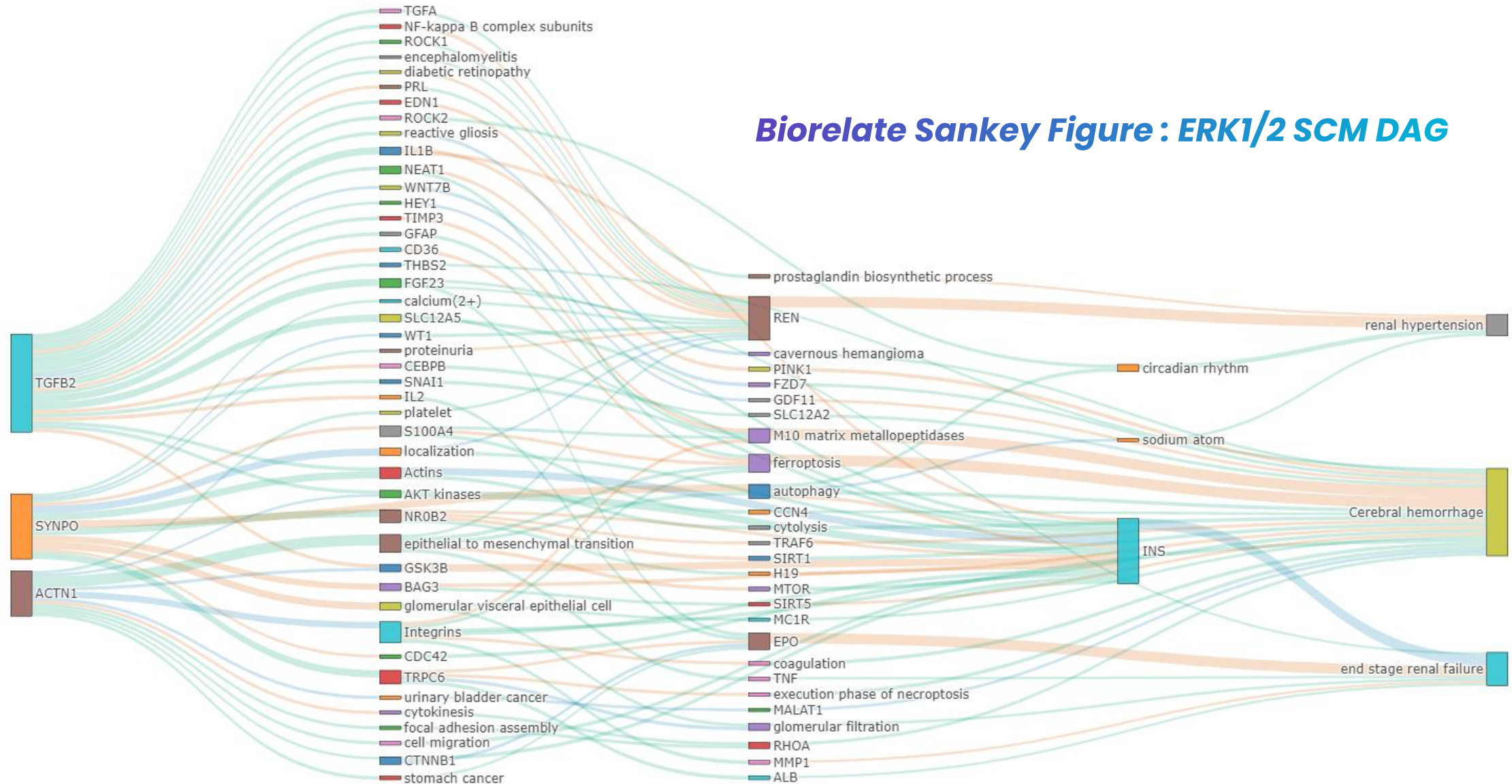
(Ricard et al., *JEM*2019)



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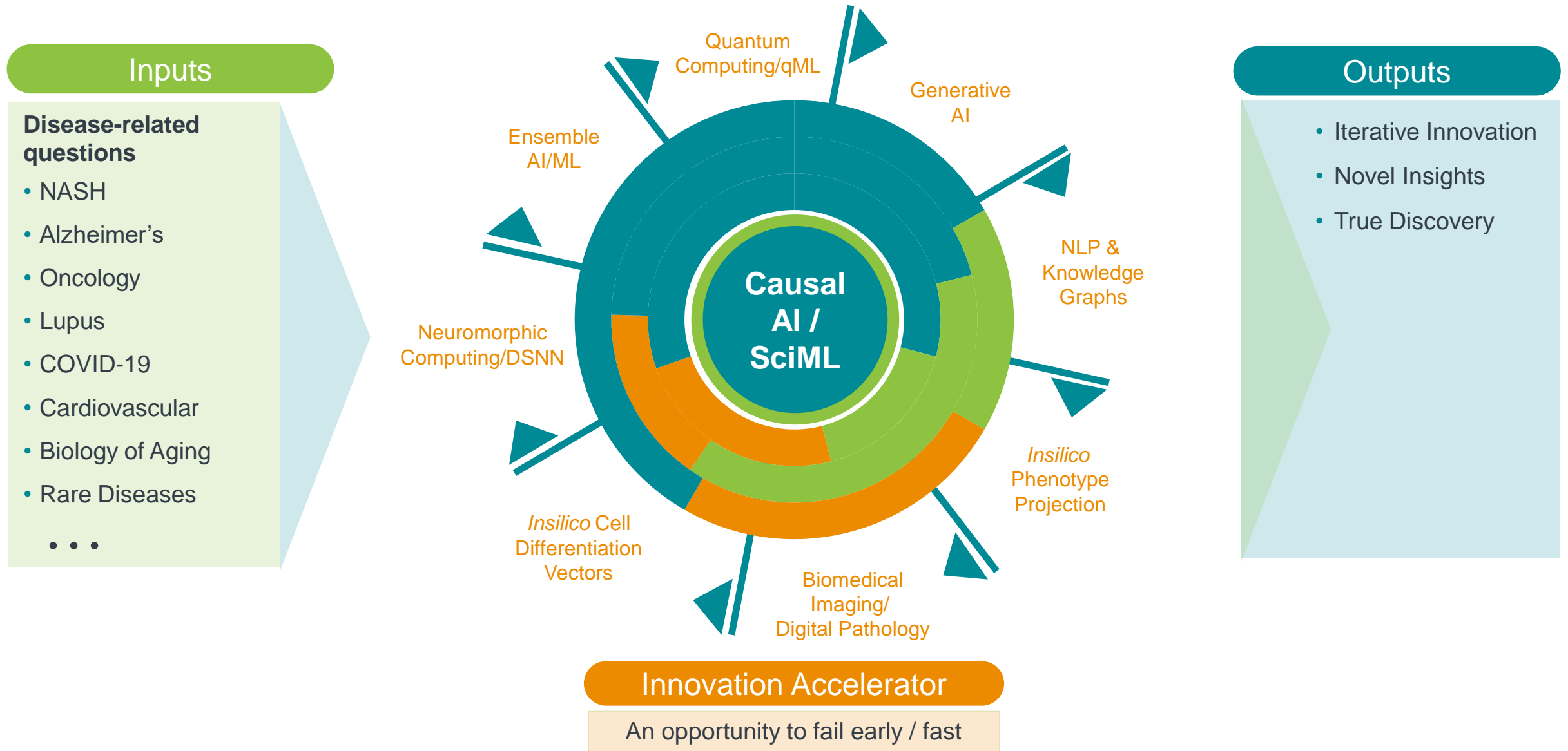


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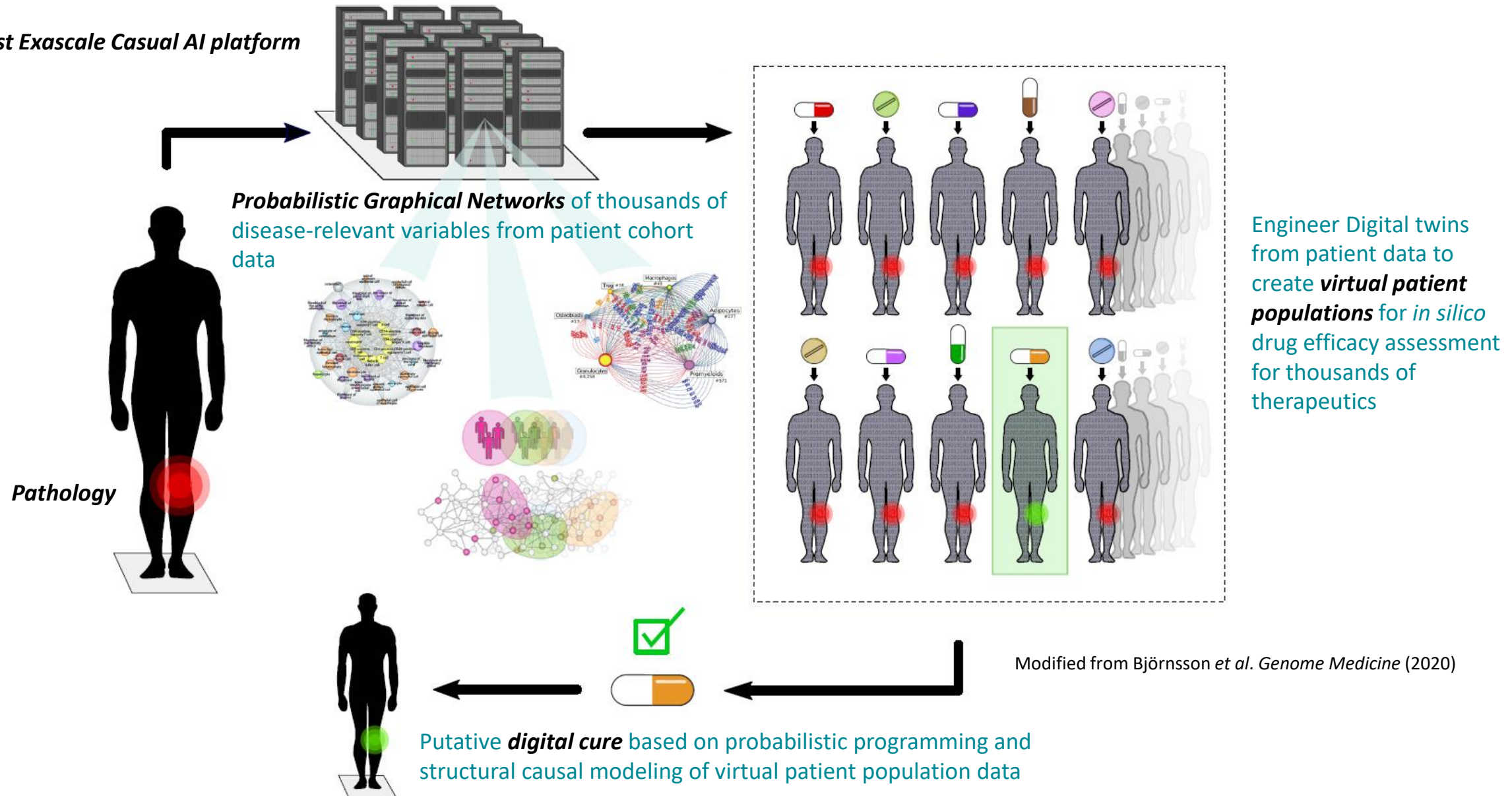
# A Novel AI/SciML R&D Innovation Engine





# The future of drug target discovery and drug development

**World's first Exascale Casual AI platform**  
(Oracle)



Modified from Björnsson *et al. Genome Medicine* (2020)

# Acknowledgements

## BioAI Health

- Alan Jerusalmi
- Michael James
- Krishna Bairavi
- Ayushi Shah
- Mike Bonham
- John Cogswell

## Queen Mary University of London

- Sir Mark Caulfield
- Andrew Livingston
- Greg Slabaugh

## Elucidata

- Abhishek Jha
- Devika Benoy

## Biorelate

- Mark Hughes

## Oracle

- Alison Derbenwick Miller
- Ryan Payton

## Genuity Science

- Jeff Gulcher
- Hannes Smarason
- Judith Conroy
- Amy Swearingen

## Genuity AI Research Institute

- Sweta Bajaj
- Jose Malagon Lopez
- Richard Li
- Allison McLean
- Raony Guimaraes
- Tiago Magalhaes
- Chris Hoefler

## Boston Children's Hospital Harvard Medical School

- Chris Walsh

## Cardiovascular Research Center Yale University Medical School

- Mike Simons

## University of Southern California

- Daniel Lidar
- Razieh Mohseninia

## University of Tennessee Health Science Center

- Hao Chen

## University of Strasbourg Medical Center

- Seiamak Bahram
- Raphael Carapito