AI methods development in multi-omics

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THE OHIO STATE UNIVERSITY
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IMMUNO-ONCOLOGY INFORMATICS GROUP
IOG
PELOTONIA INSTITUTE FOR IMMUNO-ONCOLOGY

BMBL
Bioinformatics and Mathematical Biosciences Lab

Overview: from big multi-omics data to biological knowledge

Big multi-omics Data
generated by
High-throughput Sequencing

AI and Bioinformatics
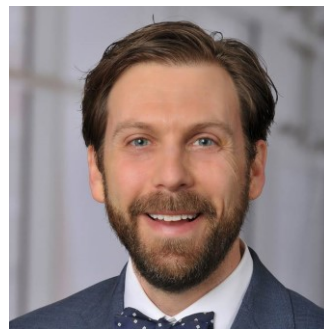
Knowledge
in
Human health and disease

Dr. Lang Li
Genome editing

Dr. Lijun Cheng
Multi-omics integration

Dr. Xia Ning
Proteomics

Dr. Dan Stover
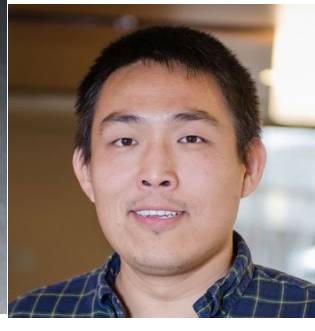*Clinical genomics, Circulating DNA and CNV*

Dr. Brian Searle
Proteomics

Dr. Dongjun Chung
Genomics

Dr. Kin Fai Au
Epigenomics and Long-read sequencing

Dr. Qin Ma
Genomics and Transcriptomics Single cell multi-omics

Strengths and active grants

- Dan Stover, PIN ALLIANCE (MPI), Power in Numbers using Harmonized GWAS and Toxicity Data

- Dan Stover, R21CA259985 (PI), Video Intervention to Address Pre-Test Patient Education for Tumor Genomic Testing

- Xia Ning, R01GM118470 (MPI), Computational tools for proteoform identification by top-down data independent acquisition mass spectrometry

- Brain Searle, R01GM133981-01 (co-I), A universal multiplexing approach to unlock the hidden proteome

- Kin Fai Au, R01GM136886 (PI), Experimental and bioinformatics platform for epigenome analysis using nanopore sequencing

- Dongjun Chuang, R21HG012482 (MPI): Statistical Power Calculation Framework for Spatially Resolved Transcriptomics Experiments

- Qin Ma, R01GM131399 (PI), Construction of cell-specific gene co-regulation signatures based on single-cell transcriptomics analysis

- Qin Ma, NSF1546869 (PI): A reinforced imputation framework for accurate gene expression recovery from single-cell RNA-seq data

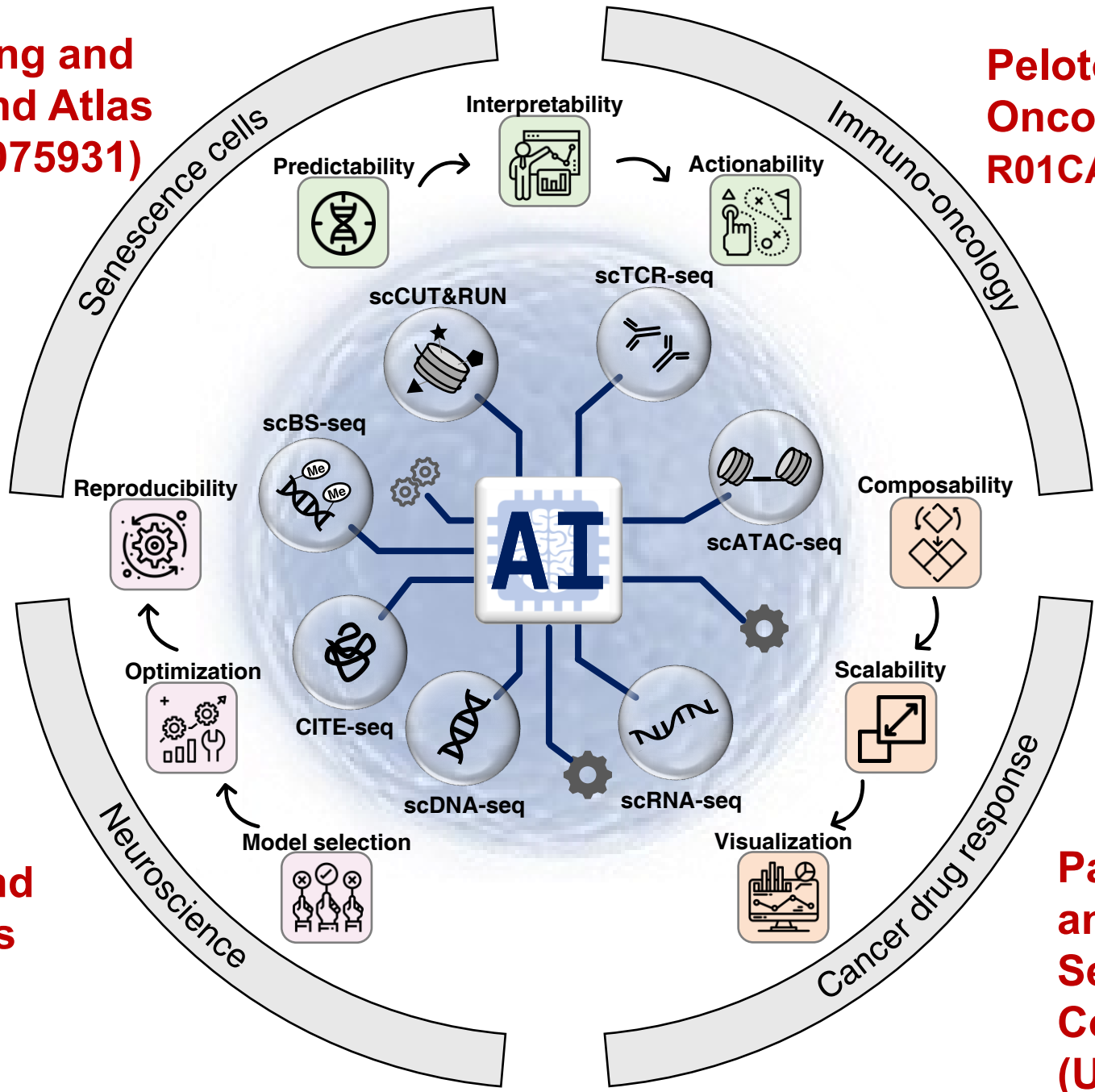**TriState SenNET (Lung and Heart) Tissue Map and Atlas consortium (U54AG075931)**

Mauricio Rojas   Ana L. Mora

Spinal cord injury and Alzheimer's diseases (R01DK126008 and R56AG066782)

Dana McTigue   Hongjun Fu

Pelotonia Institute for Immuno-Oncology (R01AI162779 and R01CA262069)

Zihai Li   Haitao Wen
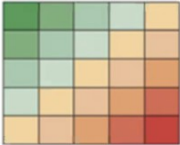
Participant Engagement and Cancer Genome Sequencing: Coordinating Center (U24CA252977)

John Bridges   Electra Paskett

Senescence cells

Immuno-oncology

Cancer drug response

Neuroscience

Predictability
Interpretability
Actionability
scTCR-seq
scCUT&RUN
scBS-seq
Reproducibility
scATAC-seq
Composability
AI
Optimization
Scalability
CITE-seq
scDNA-seq
scRNA-seq
Visualization
Model selection

What do we need

RFA-HG-22-010: Multi-Omics for Health and Disease - Data Analysis and Coordination Center

- Faculty recruitment for metabolomics and microbiome data with AI experiences

- Dedicated local and cloud computing resources for AI methods

- Tool development technician for package development implementation and maintenance

- Graduate student recruitment avenue with AI and multi-omics training