

# Bioinformatics Research Development and Updates

**Qin Ma, PhD**

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Section Chief of Computational Biology and Bioinformatics

Department of Biomedical Informatics

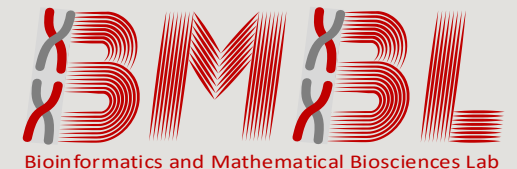
Leader of the Immuno-Oncology Informatics Group

Pelotonia Institute for Immuno-Oncology



**THE OHIO STATE UNIVERSITY**

WEXNER MEDICAL CENTER

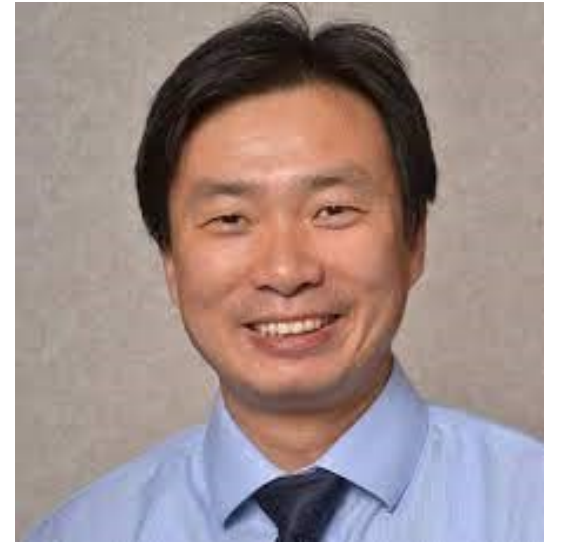


# Bioinformatics and Computational Biology Section

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## Goals and vision

- Assemble and organize a team full of expertise in bioinformatics, computational biology, biostatistics, and deep learning to systematically solve biomedical problems. (currently >10 faculty members)
- Enhance and promote independent research programs and collaborations and communications among Section members; Bridge different research communities and facilitate program/grant development.
- Advance the opening of new and creative ways in which biomedical research and education activities can couple with broader impacts.
- The success of these activities can promote computational and data sciences in translational research, drive interdisciplinary collaborations, and reflect BMI values.



Dr. Lang Li, BMI Chair

# Immuno-Oncology Informatics Group (IOIG) - PIIIO

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## Mission of IOIG

- Assemble and organize a team full of expertise in biostatistics, bioinformatics, and deep learning to systematically solve immuno-oncological problems.
- Enhance and promote collaborations and communications among PIIIO members, aiming to bridge different research communities and facilitate program/grant development.
- Other priorities will include but not limited to training sections that engage and invigorate PIIIO faculty and students and inviting reputed researchers within and outside OSU for seminar series.

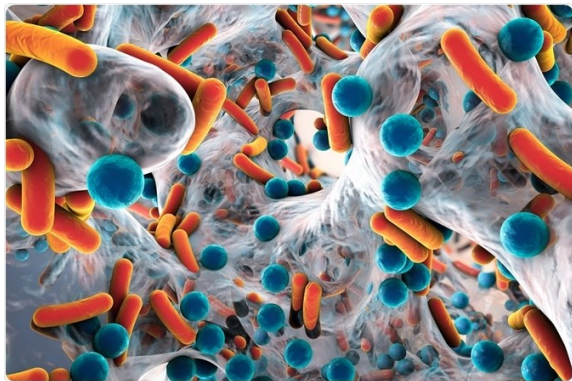


Dr. Zihai Li, PIIIO director

# Bioinformatics and Mathematical Biosciences Lab (BMBL, 2015-now)



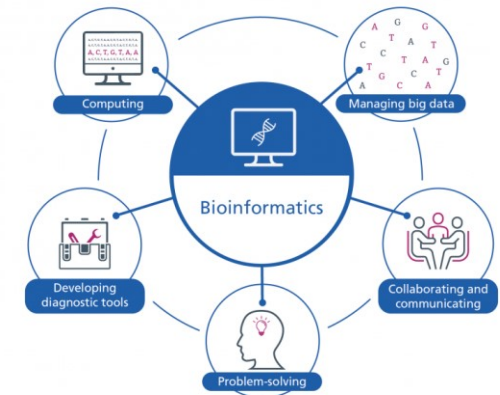
New bio-technology  
New single-cell sequencing



New computational models and  
algorithms (e.g., deep learning)



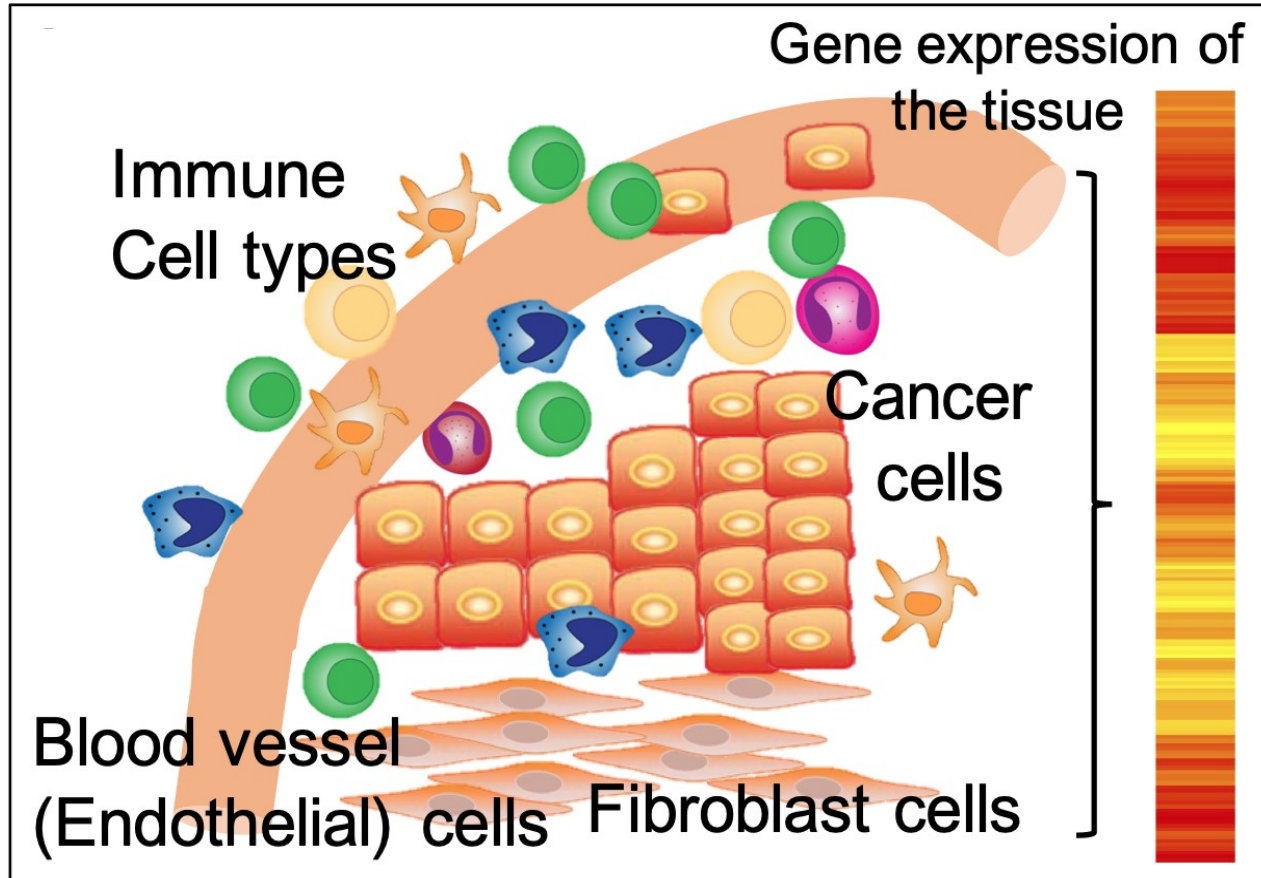
Bioinformatics infrastructure  
development



NIH (R01, R35, and R21, with BDMA and GCATS);  
NSF (SCH, EDGE, IIBR, with special panels)

NIH (U01-ITCR, U24-PECGS, and  
U54-SenNet, with special panels)

## BMBL research interests



- Who are they (cellular heterogeneity)?
- What are their activities (molecular profiles, e.g., genes and proteins)?
- How do they communicate with each other (cell-cell interactions)?
- What is the impact on disease initiation and development?

## **A note before introducing specific projects**

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**I submitted quite a lot of intake forms...**

**But only few projects were funded...**

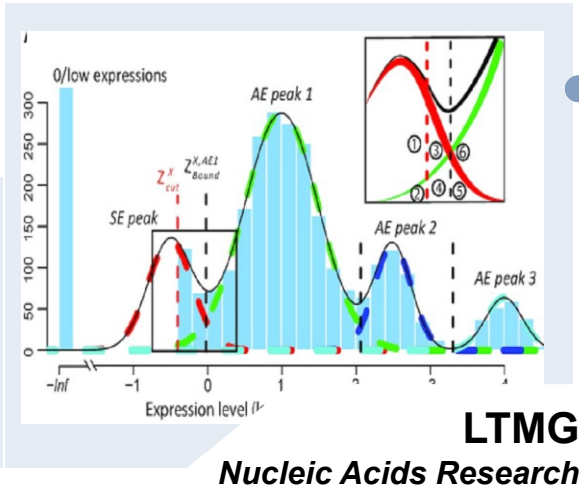
**So, I feel sorry about wasting your time...**

**Guess what? I will keep submitting intake forms in the future...**

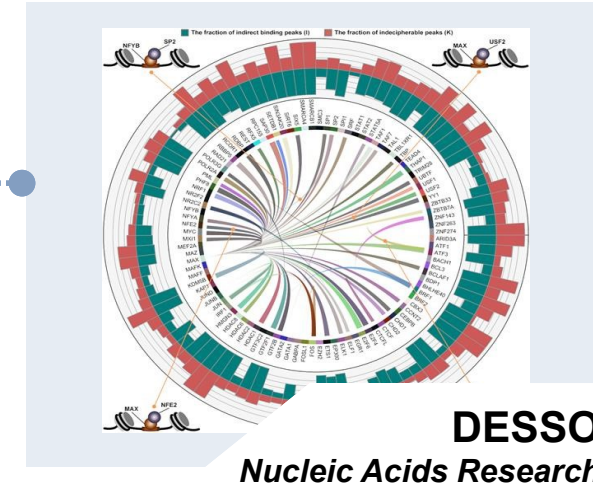


# #1 R01GM131399 (PI): Construction of cell-specific gene co-regulation signatures based on single-cell transcriptomics analysis

- Statistical modeling
- Qualitative representation of regulatory signal
- Improve cell clustering, DEG, module detection



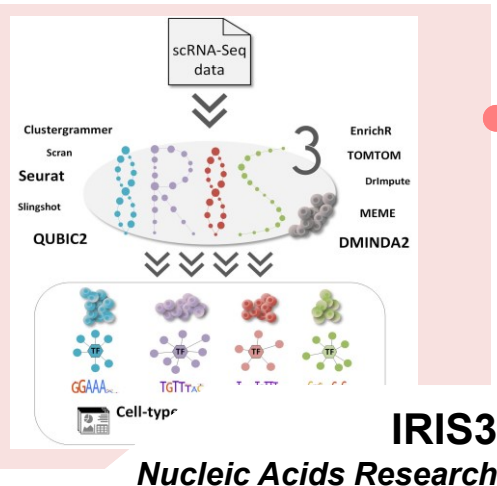
2019



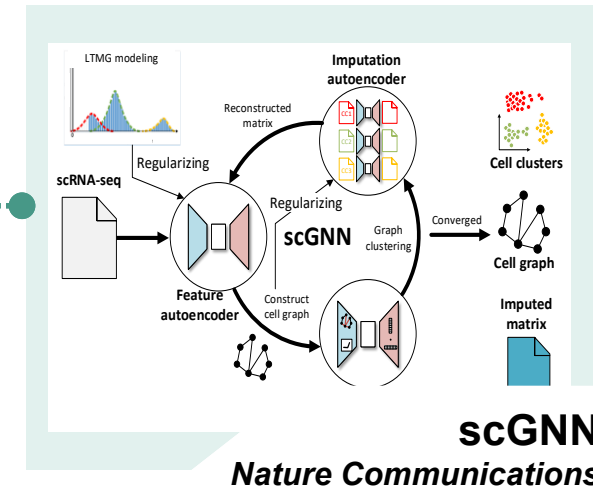
- Deep learning (Convolutional neural network)
- ChIP-seq analysis
- Motif prediction
- Shape motif
- Tethering binding

2020

- First cell-type-specific regulon pipeline
- Composable framework
- scRNA-seq analyses
- Heterogeneous regulatory mechanism
- Web interface



2021

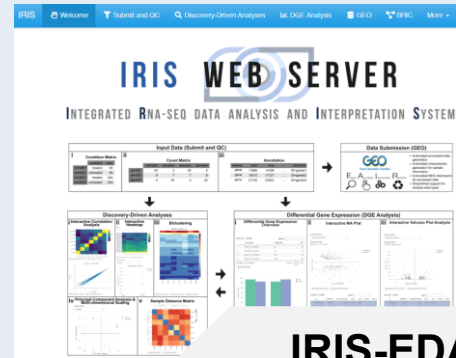


- First graph neural network (GNN) model for scRNA-seq
- Gene imputation
- Cell clustering
- Cell-cell communications
- Iterative autoencoder

# #2 NSF1546869 (OSU PI): Adapting Perennial Crops for Climate Change: Graft Transmissible Effects of Rootstocks on Grapevine Shoots

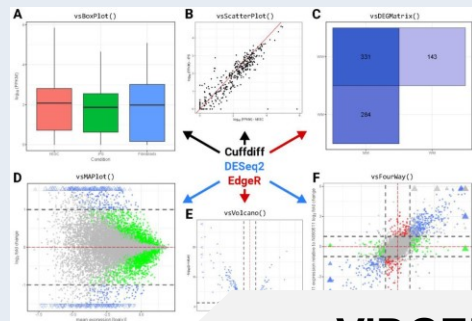


- RShiny webserver
- RNA and scRNA-seq
- Hypothesis-driven and discovery-driven analyses
- Integrative data analysis



**IRIS-EDA**  
*Bioinformatics*

- R package
- RNA-seq
- DEG analysis
- Visualization
- Interpretation



**ViDGER**  
*Brief. Bioinform.*



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

2018

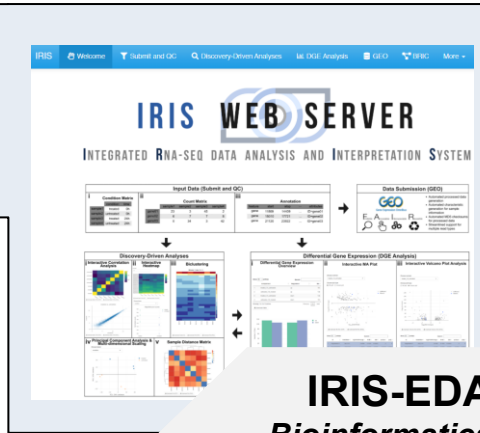
2019

2020

2021

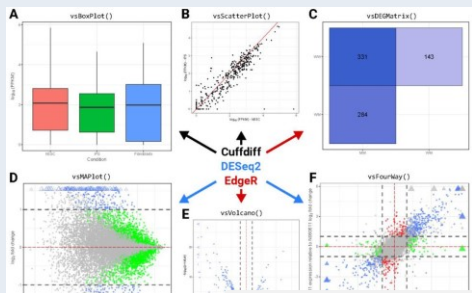
2022

- RShiny webserver
- RNA and scRNA-seq
- Hypothesis-driven and discovery-driven analyses
- Integrative data analysis

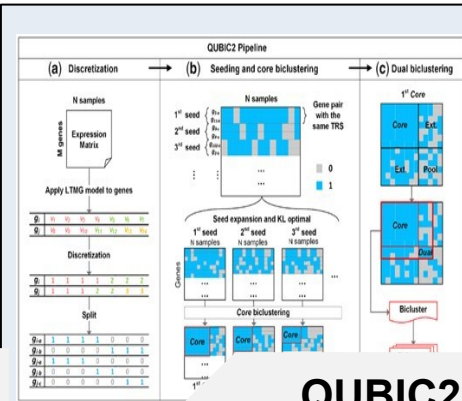


**IRIS-EDA**  
*Bioinformatics*

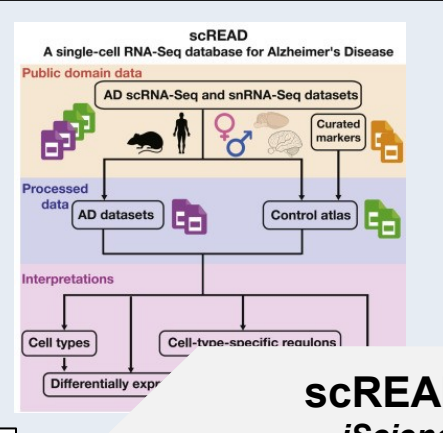
- R package
- RNA-seq
- DEG analysis
- Visualization
- Interpretation



**ViDGER**  
*Brief. Bioinform.*



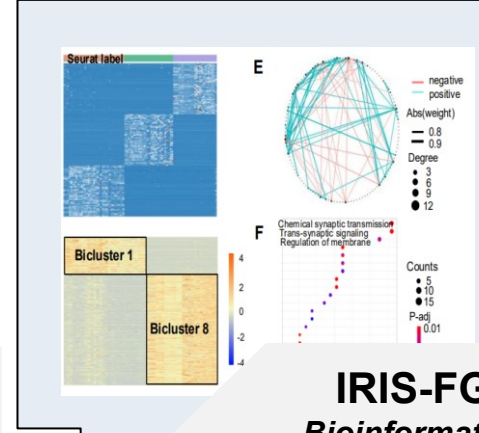
**QUBIC2.0**  
*Bioinformatics*



**scREAD**  
*iScience*

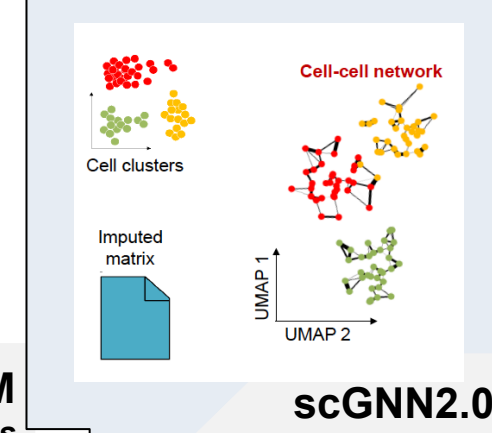
- Web database
- Alzheimer's disease
- scRNA-seq & snRNA-seq
- Data analyzing
- Results interpretation

- C++ package
- Biclustering of scRNA-seq
- Co-expression gene module
- Cell clustering



**IRIS-FGM**  
*Bioinformatics*

- Bioconductor package
- scRNA-seq
- Functional gene module
- Systemic visualization and interpretation



**scGNN2.0**  
*Bioinformatics*

- R package
- Bulk and scRNA-seq
- Gene imputation
- Cell clustering and cell-cell network

## #4 U24CA252977 (MPI): The Participant Engagement and Cancer Genome Sequencing (PE-CGS): Coordinating Center

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- Provides administrative support and scientific guidance to the Network's researchers and community partners.
- Facilitates the development and coordination of outreach and communications channels.
- Leads the development and implementation of standardized approaches to data collection and processing, including the guidance of best practices in participant engagement.
- Facilitates well-organized communication plans and research standards within the Network and contributes to the broader dissemination and implementation of findings and experience of the Network.



John Bridges, PhD



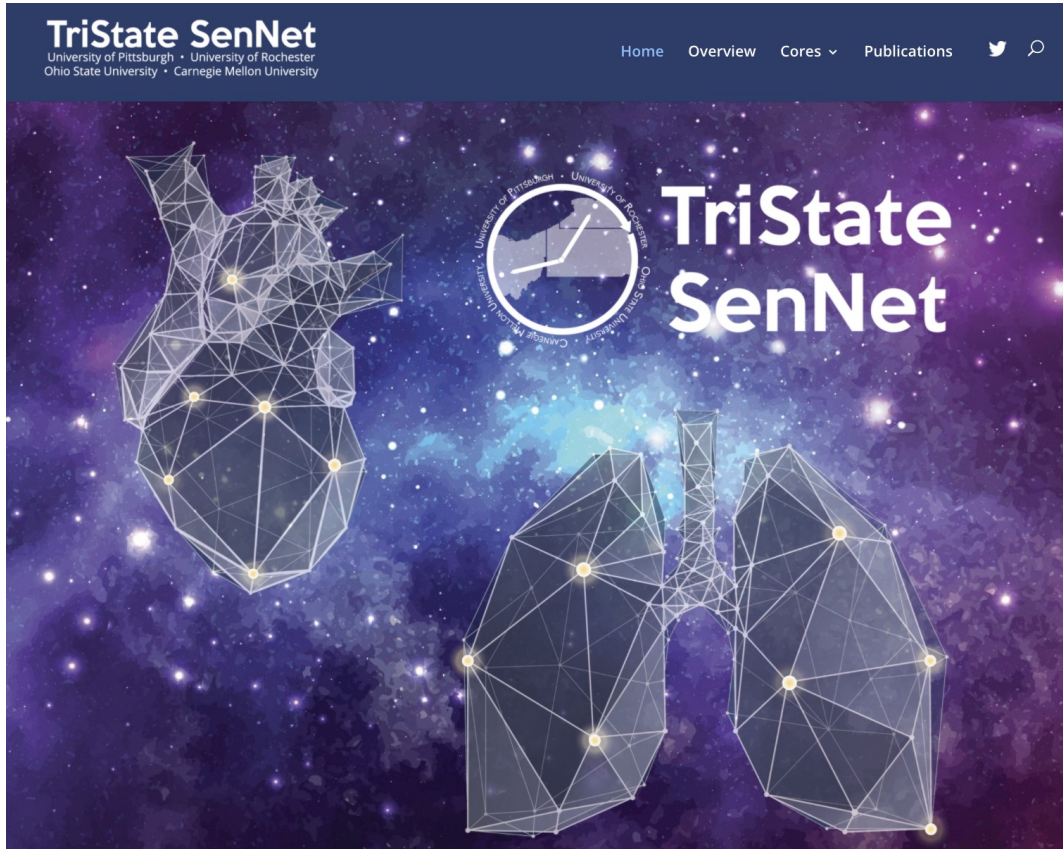
Qin Ma, PhD



Electra Paskett, PhD



## #5 U54AG075931 (Data Core PI): TriState SenNet Tissue Mapping Center (TMC)



Program was established to comprehensively identify and characterize the differences in senescent cells across the body, across various states of human health, and across the lifespan.

- The TriState SenNet Consortium seeks to comprehensively map **senescent cells** in the human heart and lung.
- To better characterize the senescent cell population and underlying molecular program, and to identify the physiologically relevant triggers for senescent cell formation.



Mauricio Rojas



Ana L. Mora



## #6 R21HG012482 (MPI): Statistical Power Calculation Framework for Spatially Resolved Transcriptomics Experiments

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- We will develop a rigorous power analysis framework for spatial transcriptome experiments.
- We will develop an interactive web interface and an R package for power analysis of spatial transcriptome
- The proposed power analysis framework will be developed and evaluated using simulation data, HST data in the public domain, and in-house spatial transcriptome datasets from collaborators.
- The statistical framework that will be developed in this project, along with the open-source software implementing this framework, will provide essential tools for the optimal design of future spatial transcriptome experiments.



Dr. Dongjun Chung

## Co-I grants for bioinformatics support

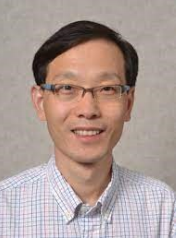
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**NIH (R01), co-I (PI: Haitao Wen):** Targeting immune inhibitory molecule SUSD2 to reverse immunosuppression.



**NIH (R01), co-I (PI: Zihai Li):** Targeting GRP94-TGF-beta pathway for cancer immunotherapy



**NIH (R01), co-I (PI: Hongjun Fu):** Ectodermal-neural cortex 1 and neuronal vulnerability to tau pathology in Alzheimer's disease



**NIH (R01), co-I (PI: Dana McTigue):** Spinal cord injury causes liver pathology and metabolic dysfunction

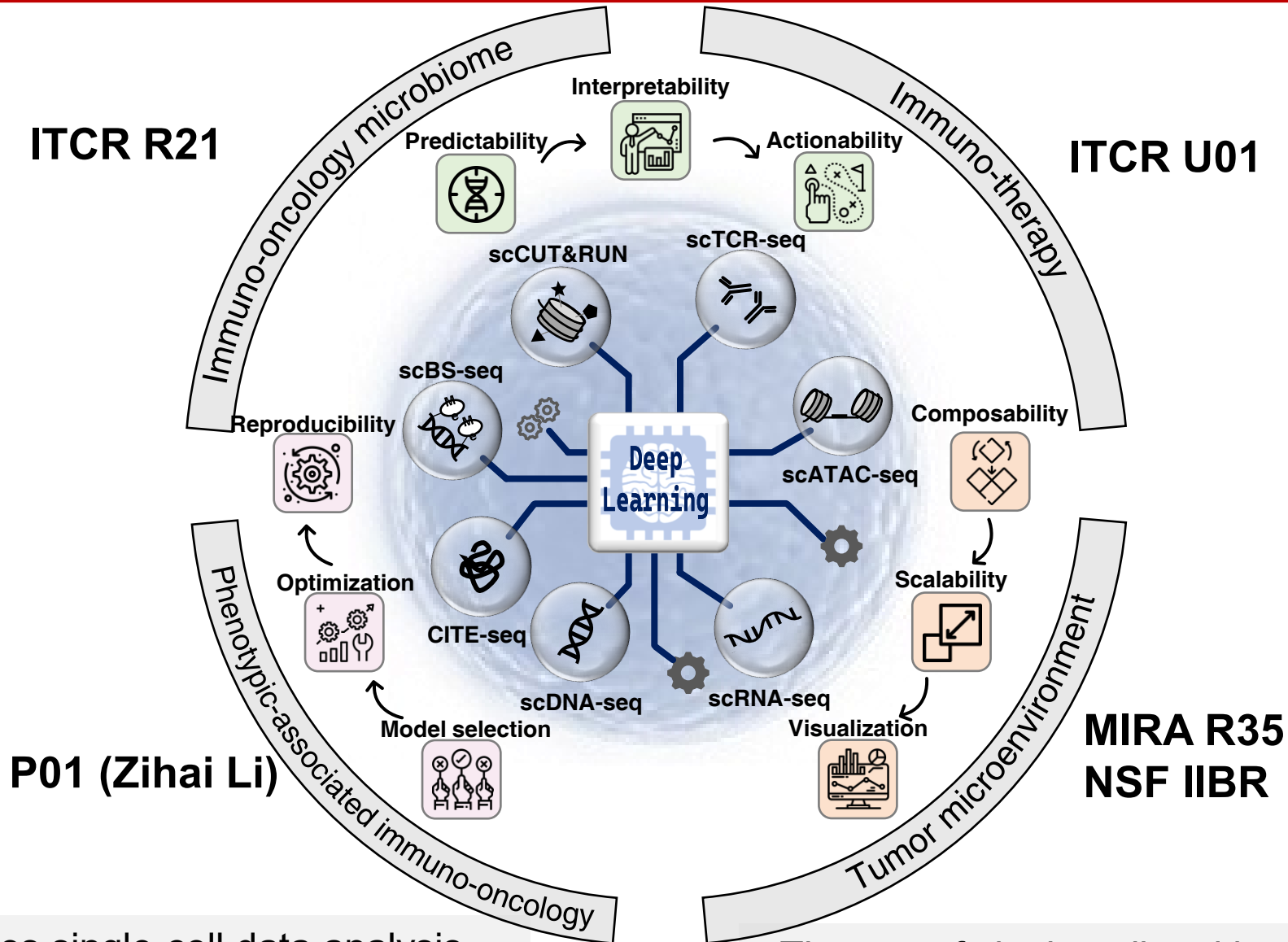


**NIH (R01), co-I (PI: Tamar Gur):** Prenatal neuroinflammation: maternal microbiome contributions and behavioral consequences



**NIH (R01), co-I (PI: Xuefeng Liu):** Conditionally reprogrammed cell model for castration-resistant prostate cancer

# Develop DL methods for new hypothesis generation



Deep learning shapes single-cell data analysis  
*Nature Reviews Molecular Cell Biology*, 2022

The use of single-cell multi-omics in immuno-oncology  
*Nature Communications*, 2022



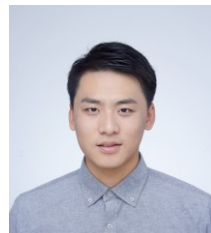
# Acknowledgement



Anjun Ma, PhD  
Research Sci  
*IRIS3, scGNN,  
scDEAL, DeepMAPS*



Yang Li, PhD  
Postdoc  
*DESSO*



Yuzhou Chang  
PhD candidate  
*IRIS-FGM, RESEPT*



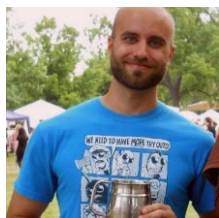
Cankun Wang, MS  
Research Sci  
*IRIS3, scREAD*



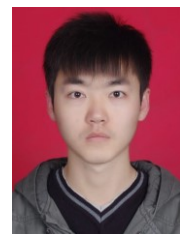
Xiaoying Wang  
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*DeepMAPS*



Adam McDermaid,  
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*VIDGER*



Brandon Monier,  
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*IRIS-EDA*



Jinyu Yang, MS  
Graduate student  
*DESSO, DMINDA2*

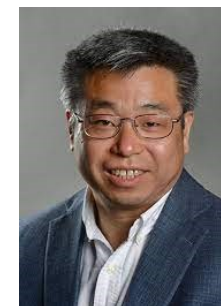


Jun Xie, MS  
Graduate student  
*QUBIC2*



Junyi Chen, PhD  
Visiting scholar  
*scDEAL*

## Collaborators



Prof. Dong Xu  
University of Missouri  
Deep learning methods



Prof. Auru Zhang  
Duke University  
Statistical modeling



Prof. Chi Zhang  
Indiana University  
Gene regulation

## Grants Management Office (GMO)!!



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<https://u.osu.edu/bmb/>