



# Spatial Multi-Omics Meets AI: Turning Tissue into Actionable Insight

*Designing Insightful Spatial Multi-Omics Studies: From Sample to Signal*

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data for **life** >

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## LEGACY BRANDS



## The experience you need

Aliri, global CRO, is committed to solving industry challenges by bringing innovative bioanalytical and spatial solutions to biotech and pharma, as the complexity of the drug development landscape continues to rise.

# Aliri France: Integrated Spatial Solutions for Translational Impact

- **Early Biomarker Discovery**

Single-cell, spatially resolved biomarkers improve patient stratification and guide precision medicine approaches.

- **Target Validation**

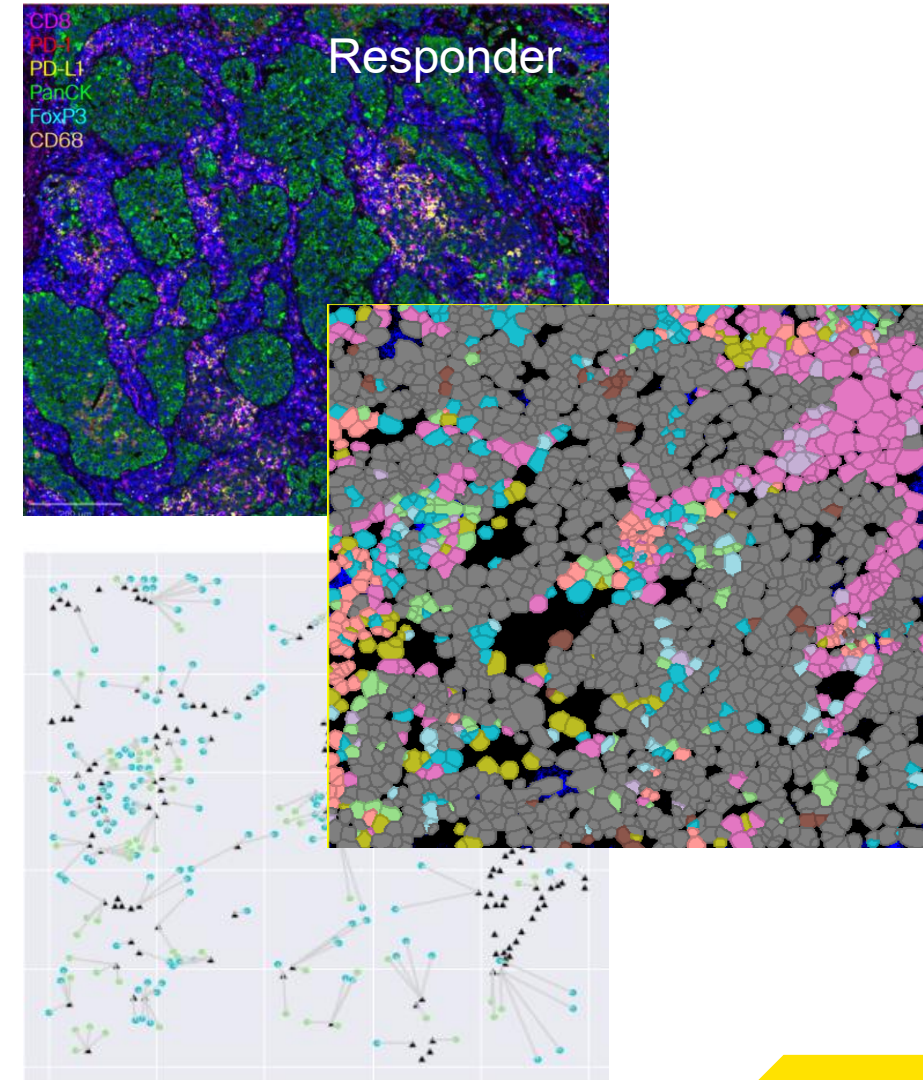
Confirms target expression in the native microenvironment to ensure biological relevance and therapeutic validity.

- **Mechanism of Action (MoA) Studies**

Reveals spatial dynamics of drug response across cell types and compartments, uncovering key interaction networks.

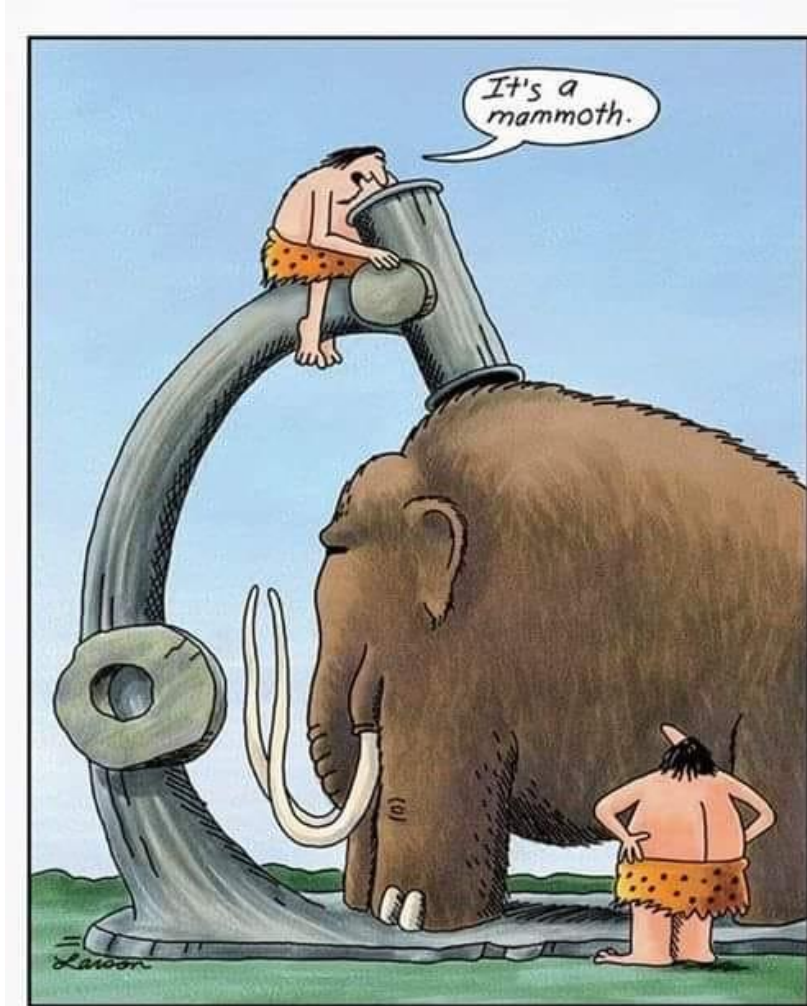
- **Spatial-Driven Data Integration**

Custom bioinformatics unify spatial, single-cell, and bulk omics data to extract integrated insights for clinical translation.



## From Classification to Context: Why Spatial Multi-Omics Matters

- In drug development, classification systems aim to predict outcomes and match therapies to disease subtypes.
- But traditional bulk or single-omic approaches often miss the spatial organization of biological signals.
- Spatial multi-omics bridges this gap—capturing the architecture, cell-cell relationships, and local signaling networks that drive treatment response.
- With AI-enhanced data integration, we can go beyond labels to derive truly actionable insights from tissue context.

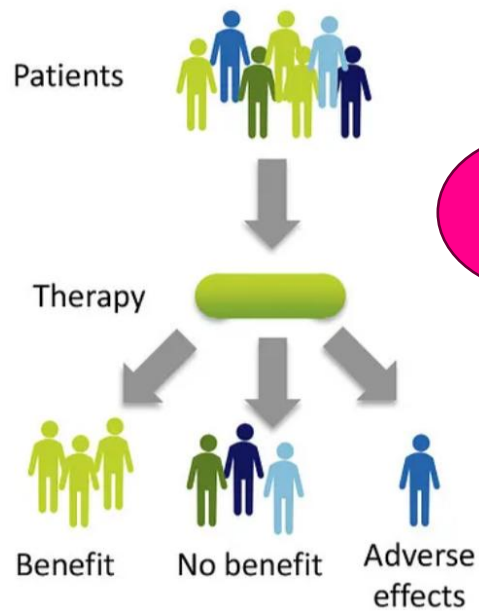


Early microscope

# Precision Medicine Needs More Than Biomarker

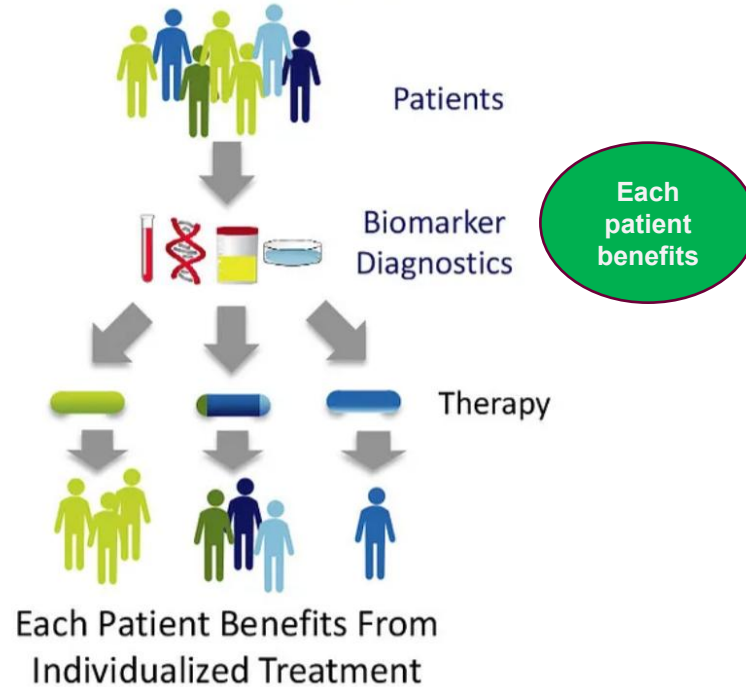
## Without Personalized Medicine:

Some Benefit, Some Do Not

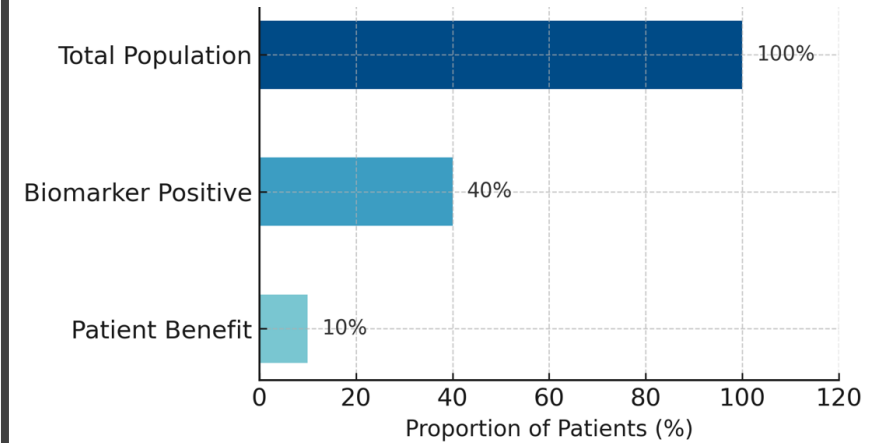


## With Personalized Medicine:

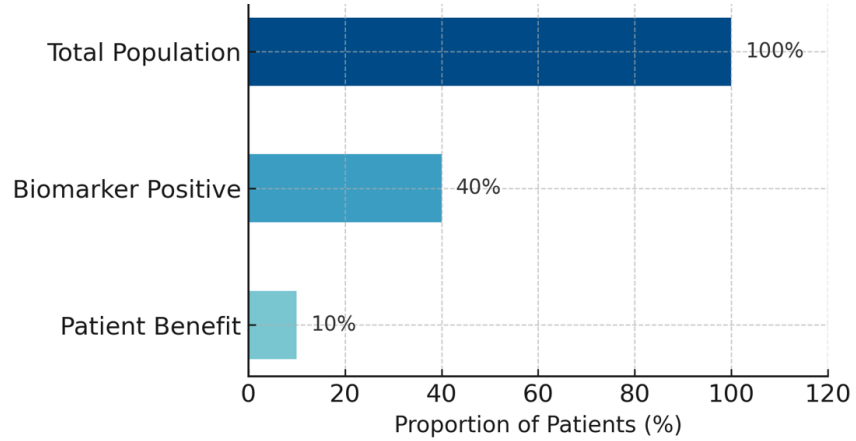
Each Patient Receives the Right Medicine For Them



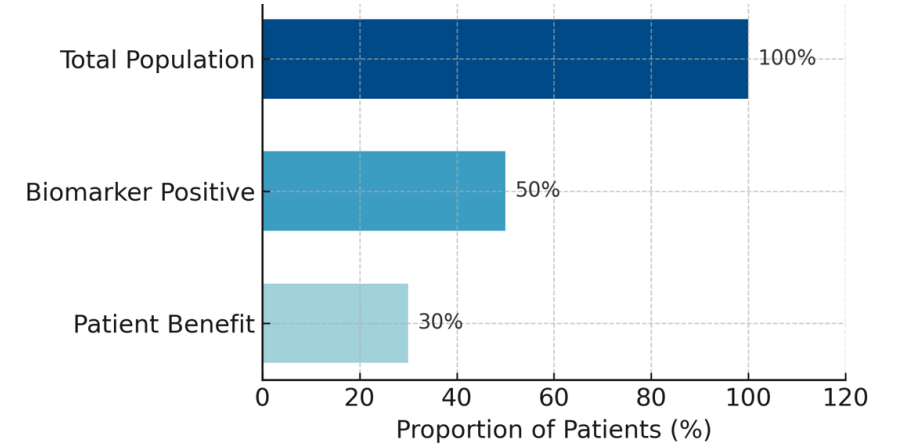
## Biomarkers have limitations



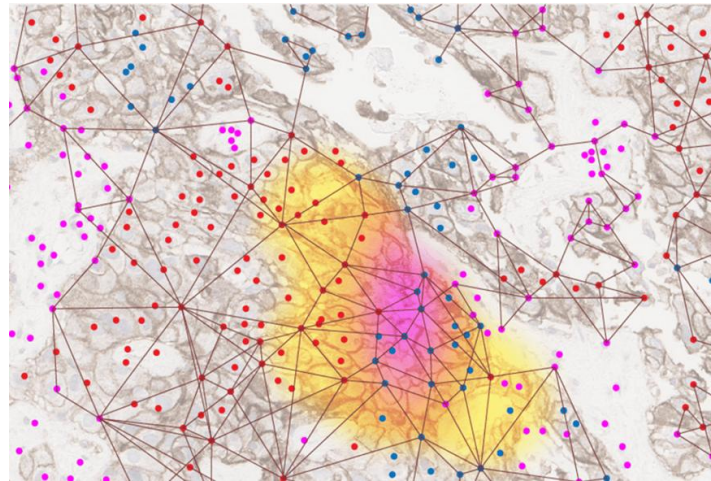
# Overcoming Biomarker limitation with AI



Improving Biomarker  
with AI



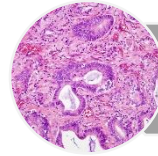
Signature Biomarker



Nucleai Team, February ,2024

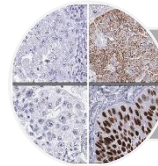
## Biomarkers exists in multiple types

**Histology:** Examines tissue structure under a microscope to detect abnormalities.



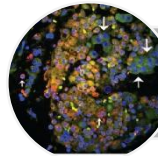
Histology

**Immunohistochemistry:** Identifies proteins in tissues, often used for cancer biomarkers.



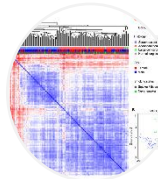
IHC

**Immunofluorescence :** Detects multiple proteins simultaneously to analyze immune responses in tumors.



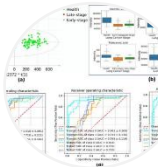
mIF

**Transcriptomics:** Studies RNA to identify active genes in diseases like cancer.



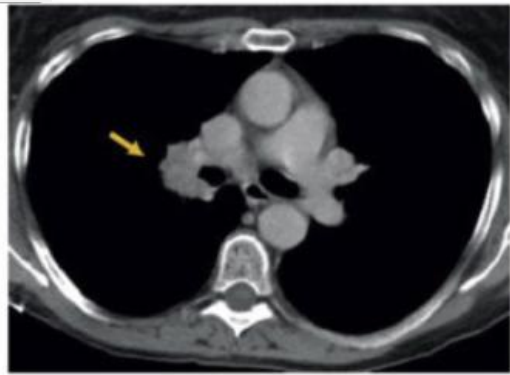
Transcriptomics

**Metabolomics:** Analyzes metabolites to understand disease-related metabolic changes.



Metabolomics

# Checkpoint inhibitor immunotherapy improve survival

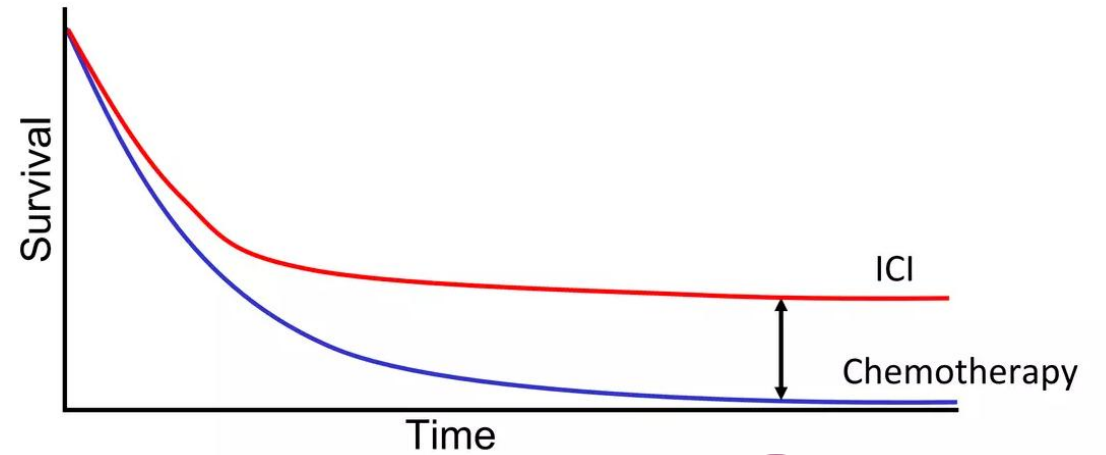


Baseline (April 2013)

Atezolizumab started  
→



Week 15 (August 2013)

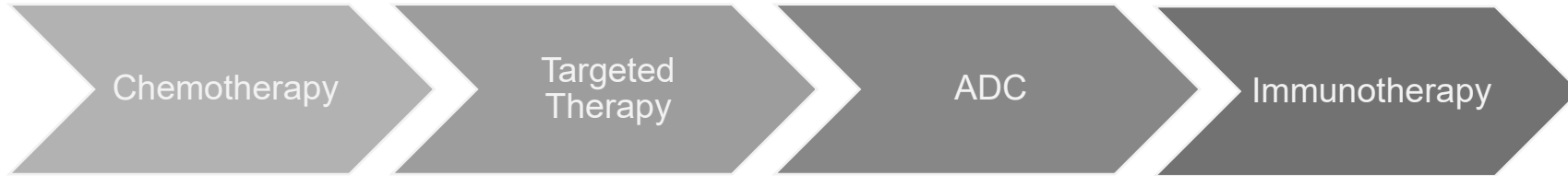


The biomarker are focused on tumor cells and Tumor microenvironment.

Only in a subset of patients

Modified from Ribas A et al., Clin. Cancer Res. 2012. Clinical Lung Cancer, September 2020.

# Expanded therapy options requires expanded biomarkers

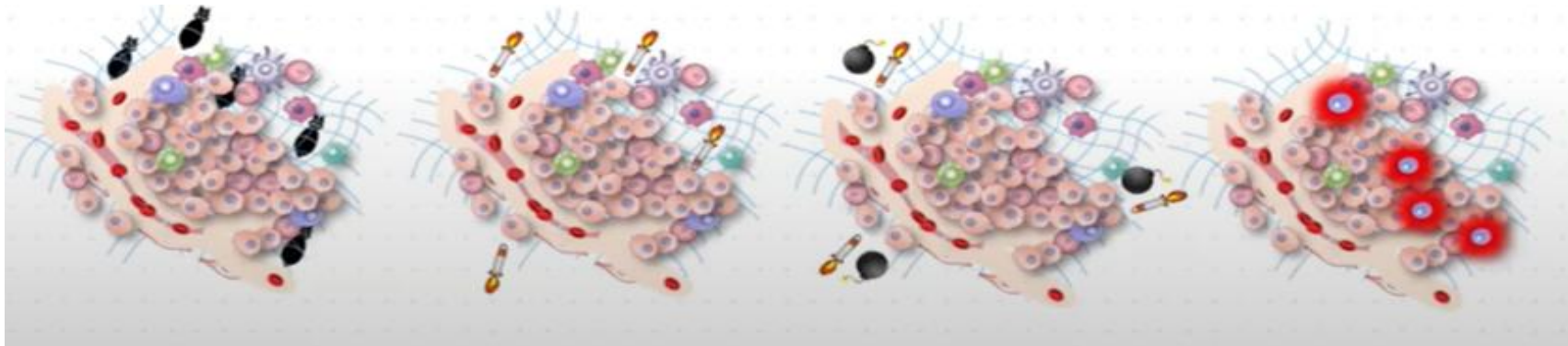


- Cell Type
- Proliferation

- Cell Type
- Target
- Resistance

- Cell Type
- Target
- Payload
- Bystanders

- Cell Type
- TME
- Germline
- Resistance



## Immunotherapy

- Pan tumor potential
- Patients negative for a biomarker still get benefit
- Tumor Cells + TME

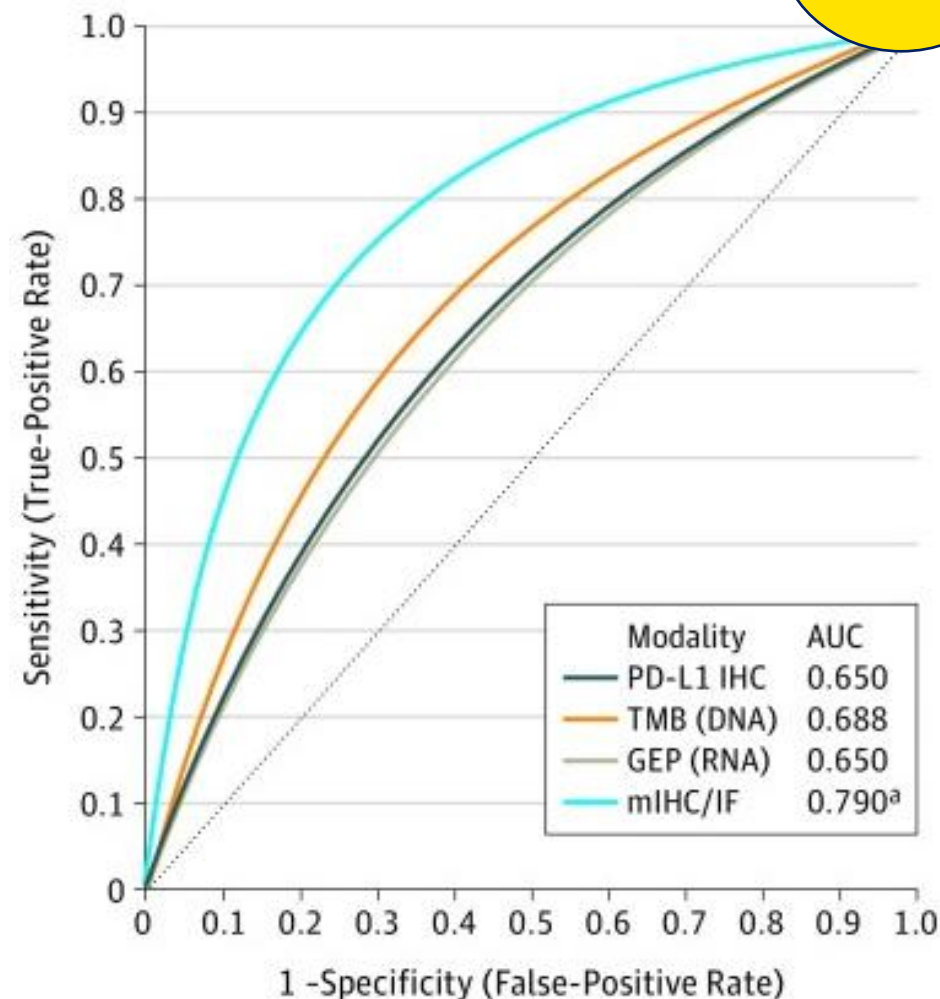
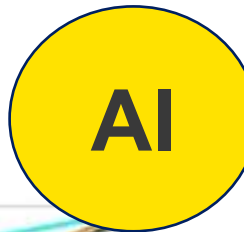
# The Power of Spatial Omics in Precision Medicine

**Immunotherapy Prediction Challenge:** Predicting success has been hard because traditional bulk analysis cannot capture specific interactions between tumor and immune cells.

**Spatial Omics Maps Cell Interactions:** It uncovers the precise location of immune and tumor cells within tissues, providing critical context for predicting treatment responses.

**AI Enhances Predictions:** AI processes complex spatial omics data to make more accurate, individualized predictions, facilitating faster and more effective drug development.

Increase Predictability  
Improved Accuracy  
Integration Multi-Omics



Comparison of Biomarker Modalities for Predicting Response to PD-1/PD-L1 Checkpoint Blockade. *JAMA Oncol.* 2019;5(8):1195-1204

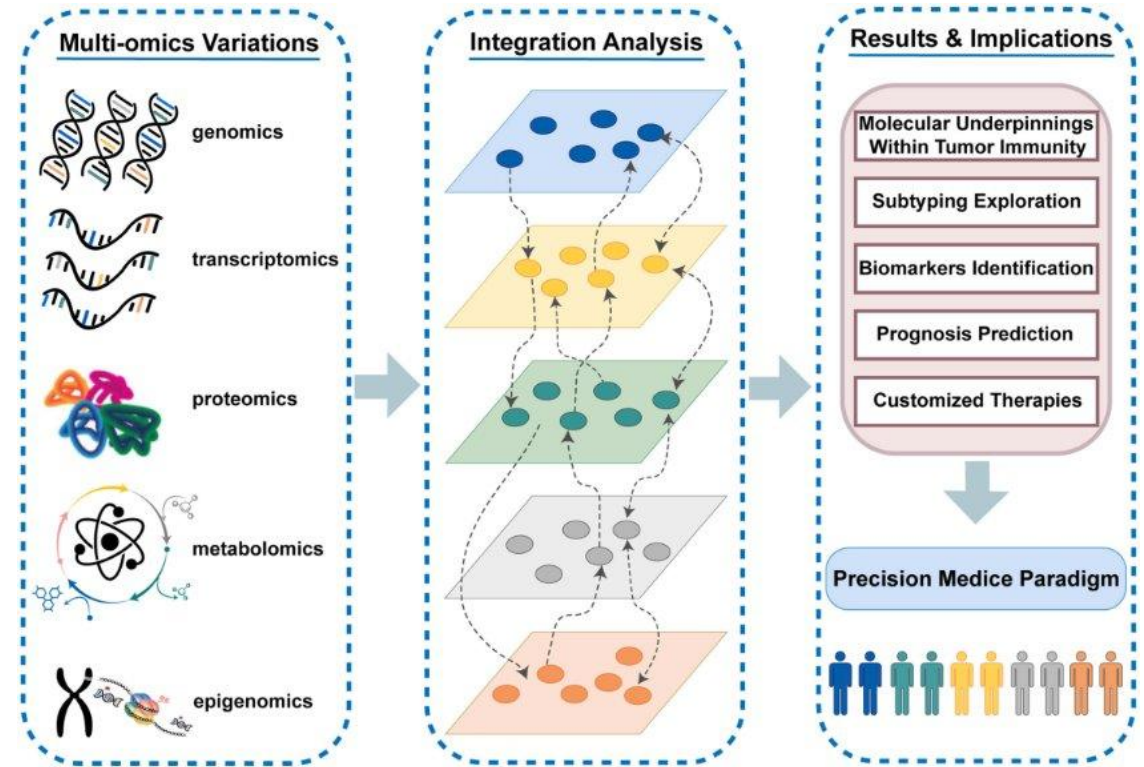


# Combining AI and Spatial Omics for Precision Medicine

Integration of multiple omics genomic, transcriptomics proteomic, and metabolomic data

Provides comprehensive insights into biological processes: multiple biological factors across these omics layers.

➡ Critical for understanding complex diseases like cancer

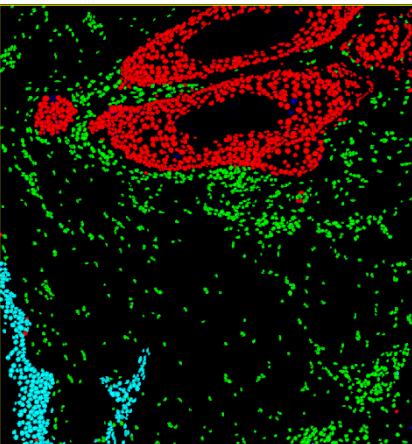
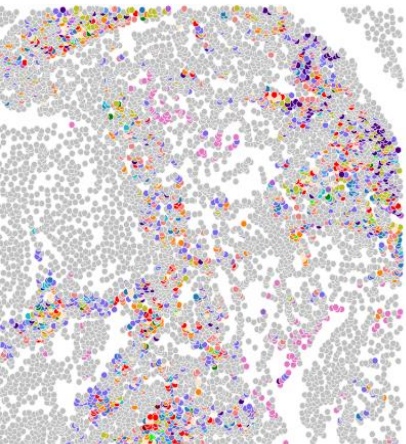
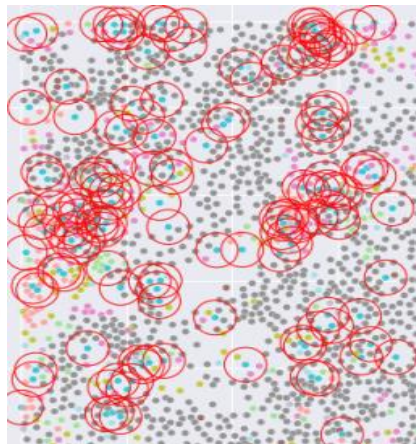
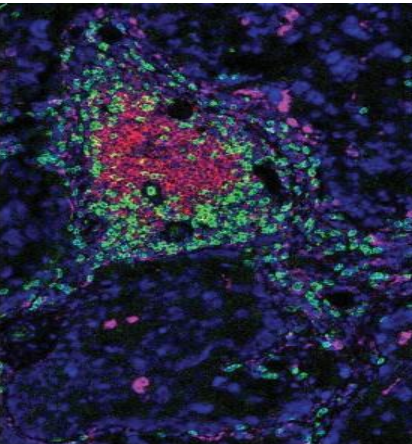


# Deep Learning and Machine Learning Pipeline



Model Results	Area Classification (tumor, stroma..)	Cell classification (Tumor, Lymphocyte, Plasma cell...)	Secondary Structures (TLS)

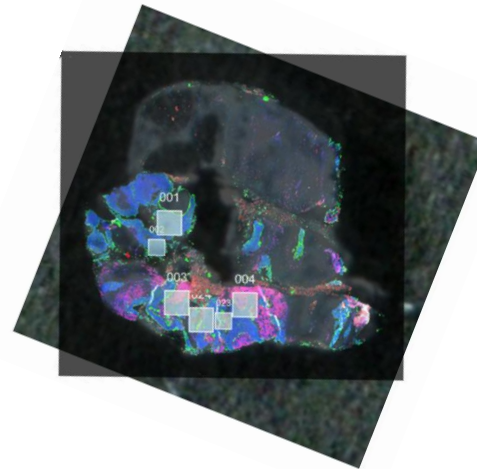
Spatial Features Category

Area region features	Cellular distribution features	Cellular Interactions Features	TLS features
			

# Multi-omics data analysis – Methodology

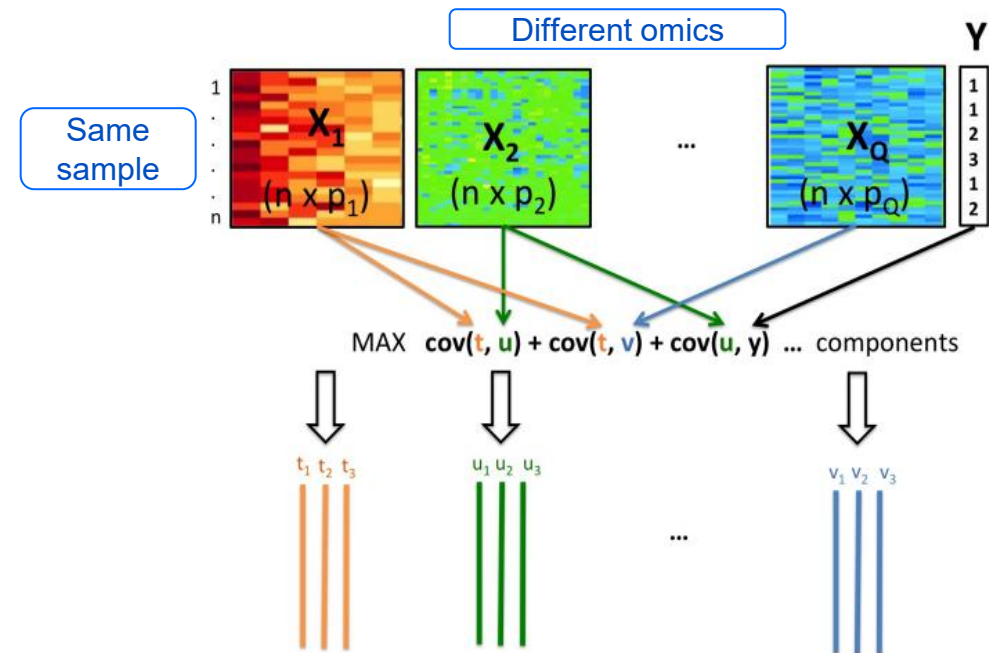
- Clinical data
  - Classes:** Responder and Non-Responder

- Spatial Proteomics
- Spatial Transcriptomics
- Spatial Metabolomics

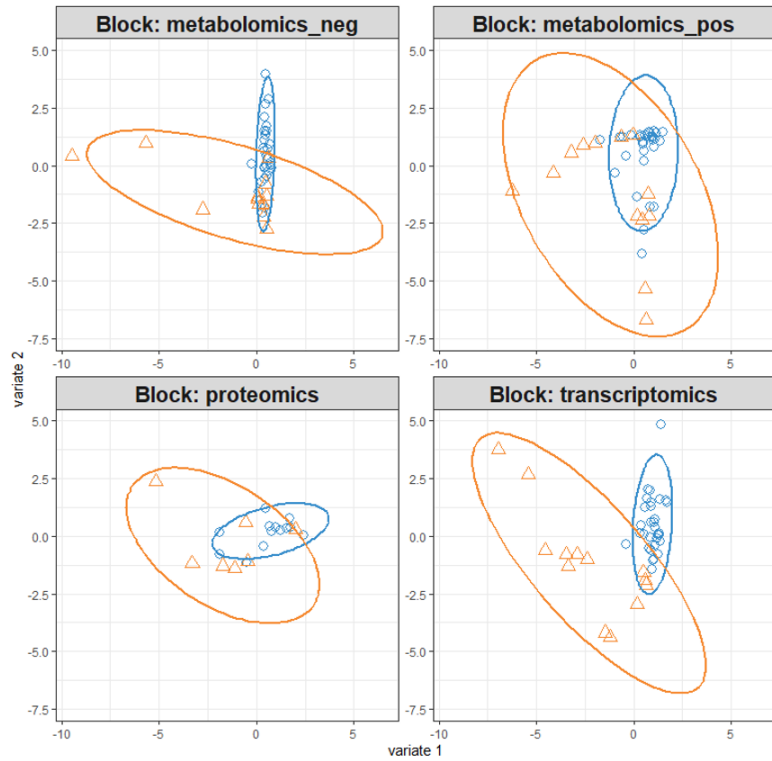


Region of Interest (ROI)

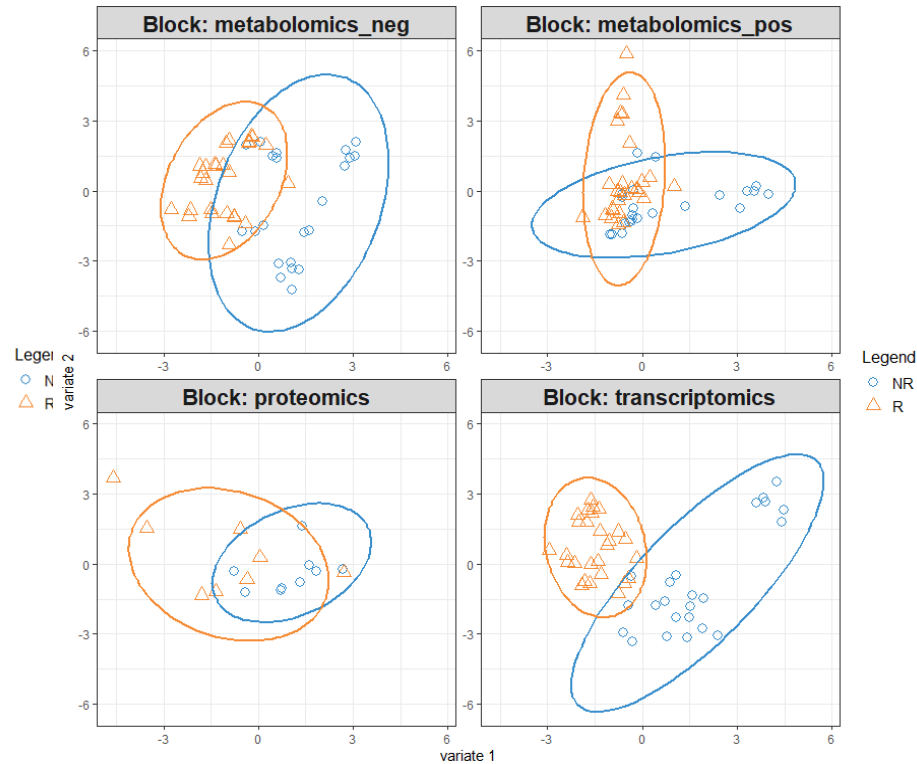
Data Integration Analysis for Biomarker discovery using Latent variable approaches for Omics studies (**DIABLO**)



# Class Separation



Tumor

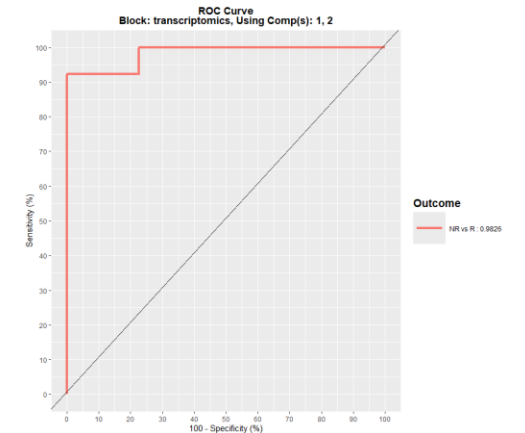


Interface

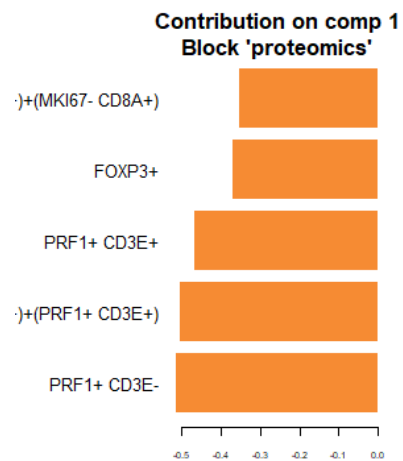
(Balanced) Error rate is the proportion of incorrect predictions out of the total number of predictions, weighted by the number of samples in each class.

\$centroids.dist

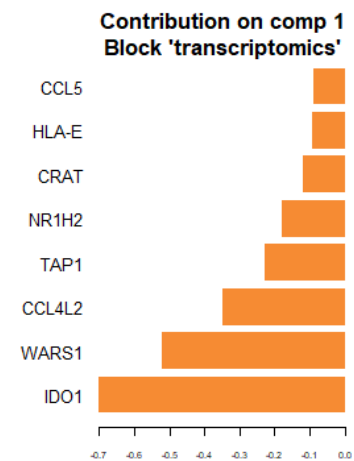
	comp1	comp2
NR	0.03548387	0.06451613
R	0.50000000	0.36153846
Overall.ER	0.17272727	0.15227273
Overall.BER	0.26774194	0.21302730



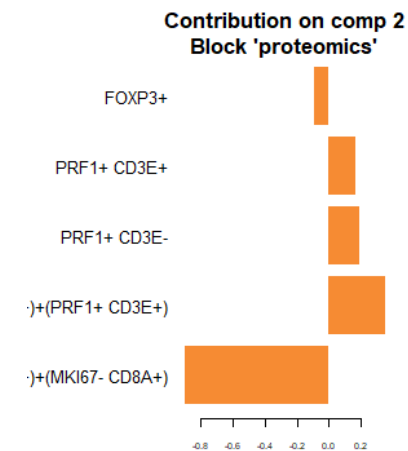
# Identification of Key Variables - Tumor



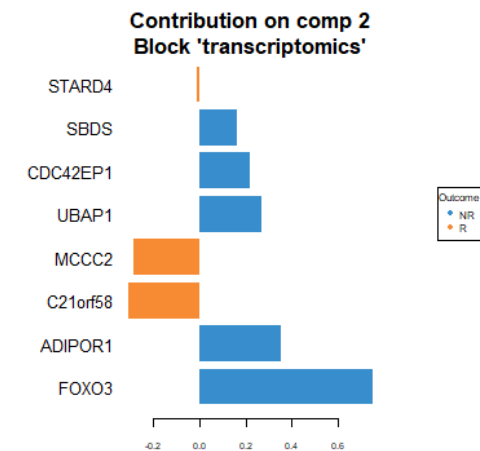
Outcome  
• NR  
• R



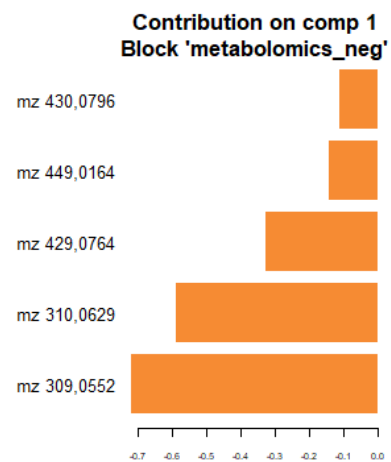
Outcome  
• NR  
• R



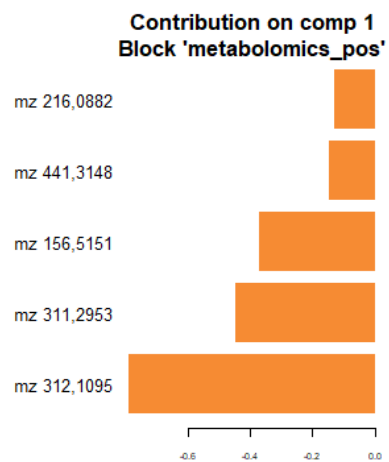
Outcome  
• NR  
• R



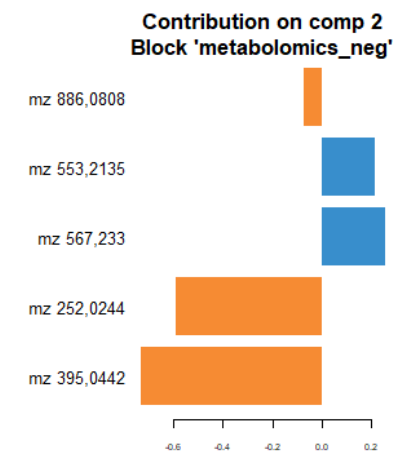
Outcome  
• NR  
• R



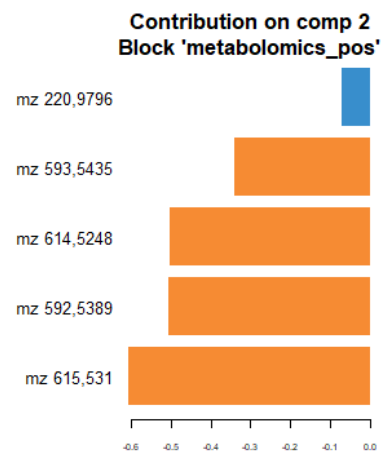
Outcome  
• NR  
• R



Outcome  
• NR  
• R

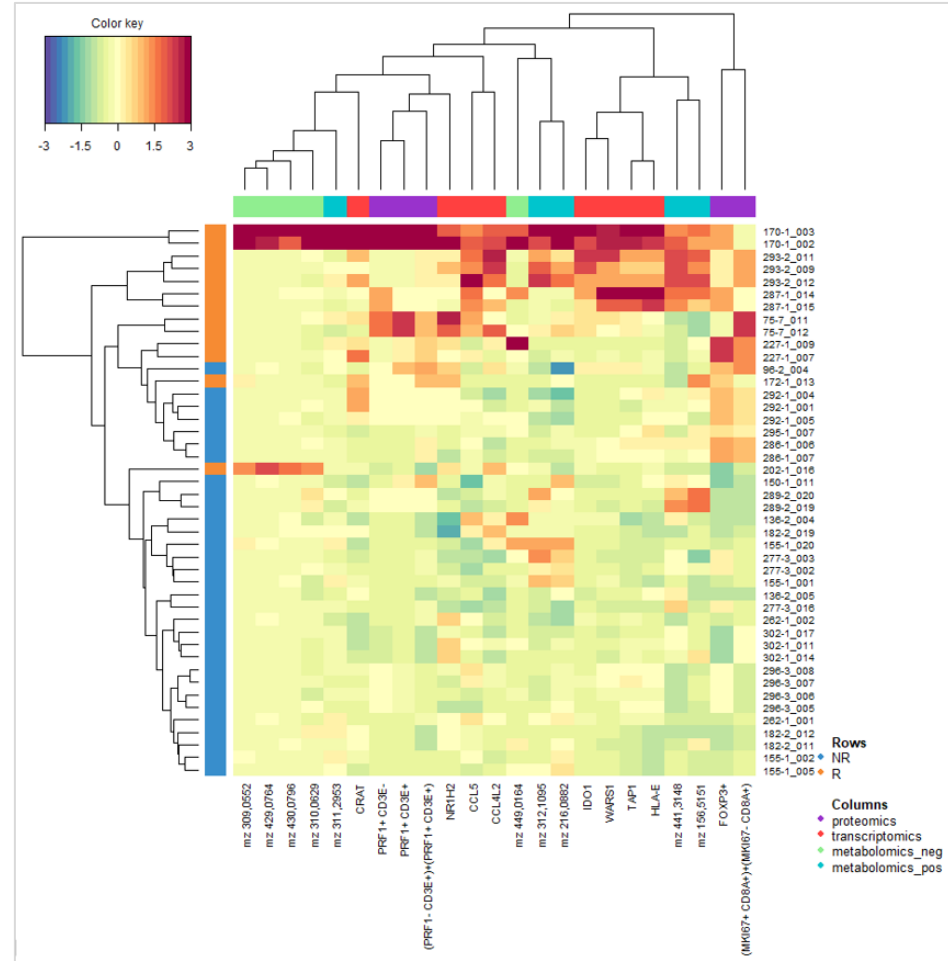
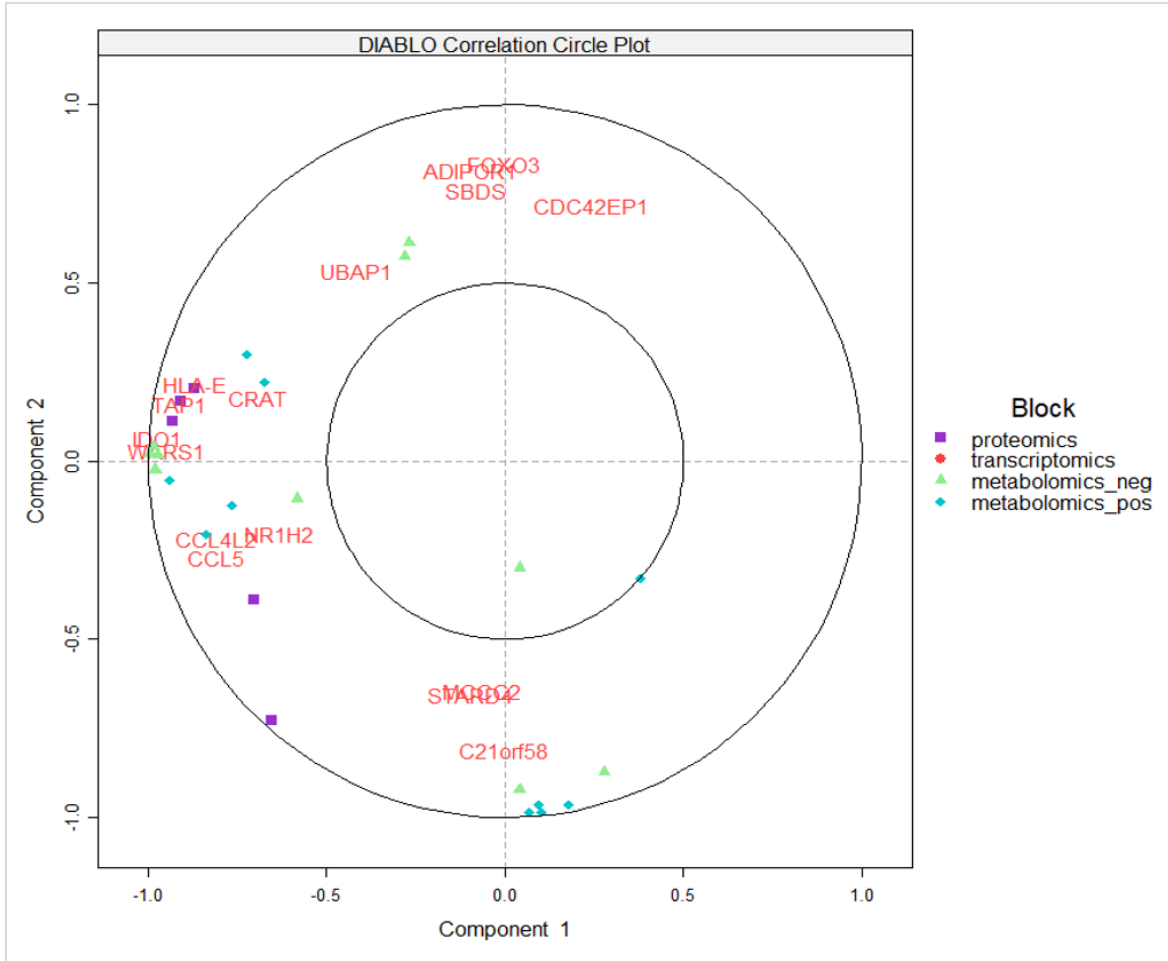


Outcome  
• NR  
• R



Outcome  
• NR  
• R

# Relationships Between Omics Modalities – Tumor




# AI and multimodal patient data for better, faster clinical trials

## Improved Predictive Power for Treatment Response

- AI models, when trained on spatial omics data, can more accurately predict treatment responses by analyzing the spatial arrangement and molecular states of cells.
  - This allows for precise identification of patient subgroups most likely to benefit from specific treatments.
- By integrating AI and spatial omics early in drug development, companies can better predict treatment efficacy, reducing late-stage trial failures and improving clinical success rates.

## Unlocking the power of spatial omics with AI

Kyle Coleman, Amelia Schroeder & Mingyao Li

 Check for updates

Spatial omics technologies have transformed biomedical research by offering detailed, spatially resolved molecular profiles that elucidate tissue structure and function at unprecedented levels. AI can potentially unlock the full power of spatial omics, facilitating the integration of complex datasets and discovery of novel biomedical insights.

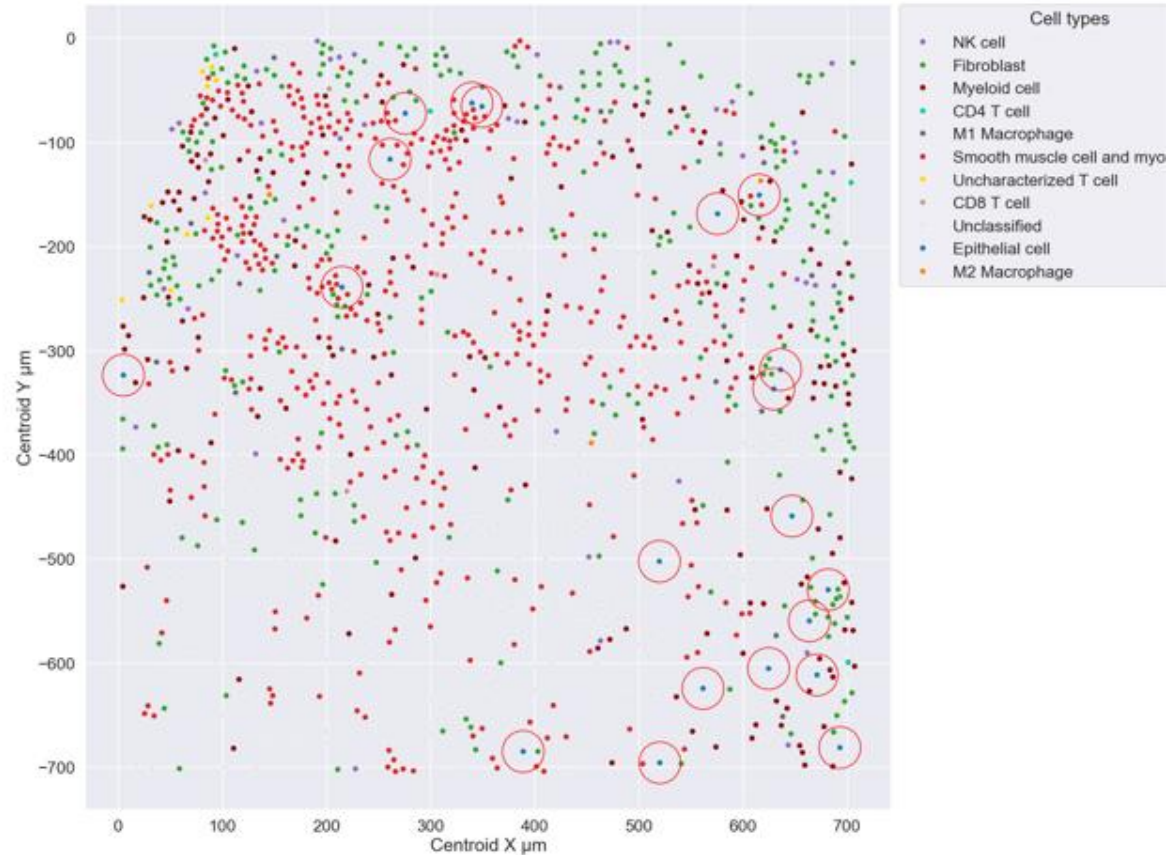
Spatial omics technologies have ushered in a new era of biomedical research, offering unprecedented insights into the organization of tissues through spatial molecular profiling. These technologies

to tumors, influencing both the effectiveness of treatments and the behavior of the tumor. As a result, accurate identification and localization of these rare cell types is crucial for studying the tumor microenvironment and for developing effective treatments. Therefore, there remains a crucial need to achieve spatially resolved, full transcriptome measurements at the real single-cell level.

We suggest that the gaps in spatial transcriptomics might be bridged with single-cell RNA sequencing (scRNA-seq) data, which provide full transcriptome measurements at the cellular level but lack spatial context. This integration can be achieved by training a deep learning model on spatial transcriptomics data to infer the spatial coordinates of cells within a paired scRNA-seq dataset<sup>4</sup>. Another method involves learning the relationship between the expression levels of genes using an scRNA-seq dataset and imputing the unmeasured genes in an imaging-based spatial transcriptomics

# Acknowledgments

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Sandra Delebecq  
Richard Ruez





**Thank You for your Attention**

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