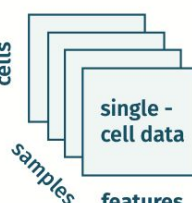


# ScaiVision AI platform: project workflow to facilitate drug development

## INPUT

**1**


**Endpoint A**



cells  
samples  
single - cell data  
features

vs

**Endpoint B**




single - cell data

Multiparametric sc datasets:

<b>Endpoint A</b>	vs	<b>Endpoint B</b>
scRNA-seq	vs	responder vs non-responder
CITE-seq	vs	healthy vs disease
CytoF	vs	mild vs severe
Flow cytometry	vs	active vs non-active
+ other data types	vs	high quality vs low quality
+ clinical data	vs	regression vs classification


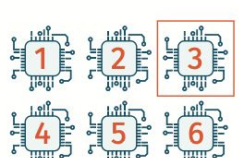
## DATA ANALYSIS

**2**



Train a network to find endpoint-specific patterns in the data

Validate predictive performance of the models and select one

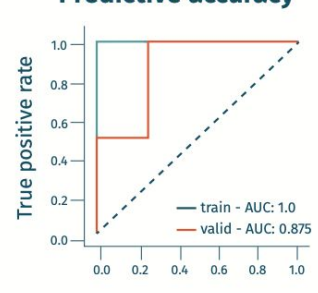



- Cell-type **agnostic** → works across different indications and tissues
- Data augmentation → discoveries from **few samples**
- Cluster-free → retains **single-cell resolution** → sensitive to rare events
- Shallow AI network → **explainable predictive performance**

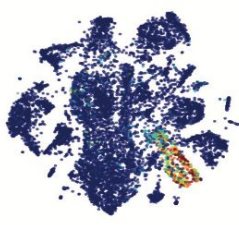
## OUTPUT

**3**

**Predictive accuracy**



**Predictive cell identity**



**Consolidated signature**

feature 014

feature 021

feature 055

feature 167

**Predict endpoints for new samples**  
**Extract cellular and molecular biomarker profiles**

## 4

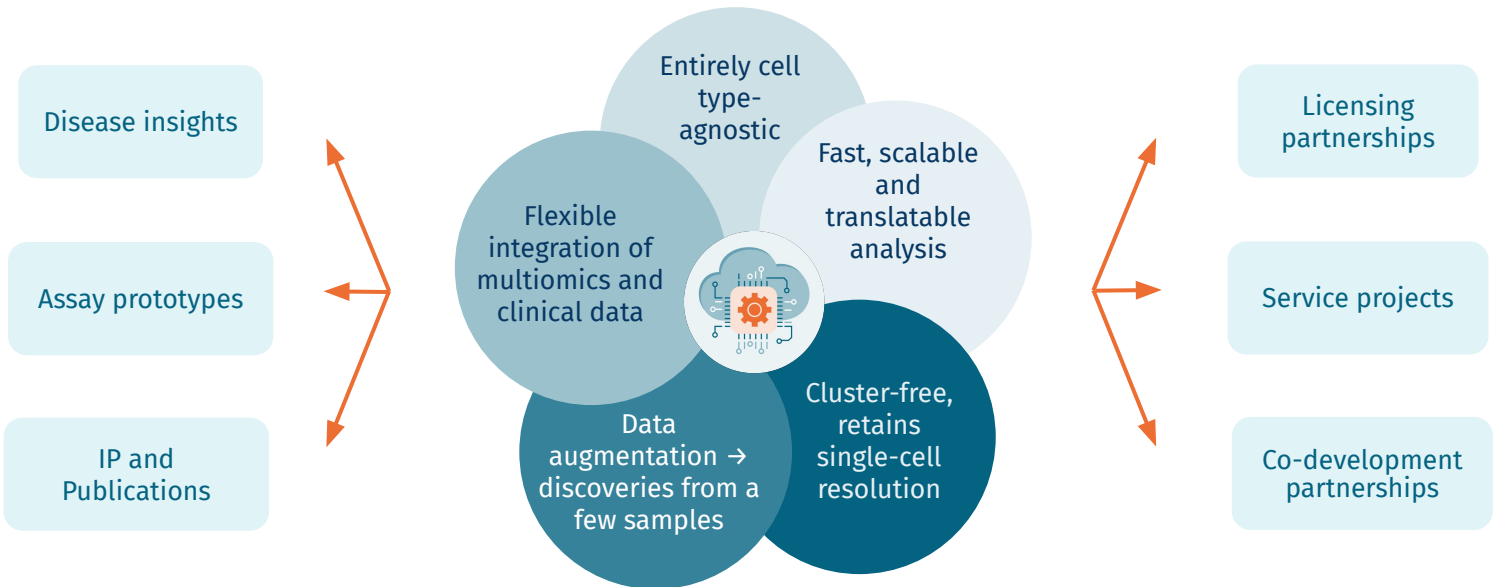
**Prototype of routine assay**  
PCR, Flow Cytometry



# True precision medicine through single-cell science

Generating clinically relevant insights from single-cell data

ScaiVision™ unravels hidden secrets of complex single-cell multiomics data to extract composite biomarkers associated with different cell populations. Using a convolutional neural network and representation learning, ScaiVision automatically learns molecular patterns associated with relevant clinical outcomes. These signatures can then be applied to classify new samples and develop diagnostic assay prototypes.



## ScaiVision predicts clinical response and toxicity in CAR T cell therapy of lymphoma patients

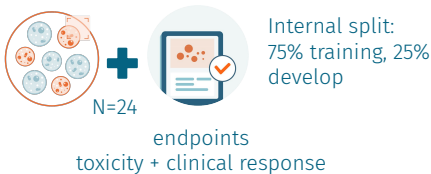
ScaiVision predicts clinical response with 85% accuracy and detects specific CD4<sup>+</sup> and CD8<sup>+</sup> T cell populations enriched for markers of memory and depleted for markers of exhaustion and inflammation associated with complete response.

ScaiVision identifies a complex cellular signature that predicts high-grade toxicities with 100% accuracy.

### 1) ScaiVision Model Training

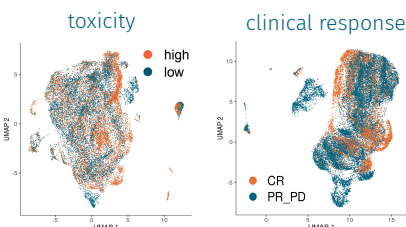
#### Experimental setup:

Deng et al., 2020, Nat Med



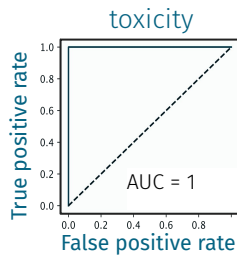
#### Technology: scRNA-seq

CAR T infusion product

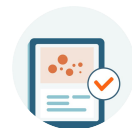


### 2) Endpoint prediction

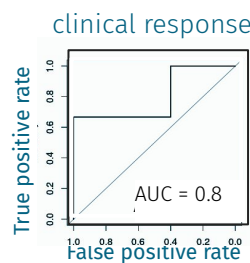
#### Performance:



ScaiVision predicts high-grade toxicities with **100%**

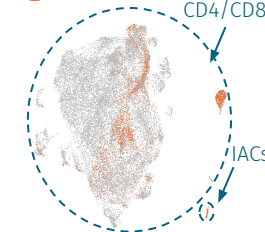


and clinical response with **85% accuracy**

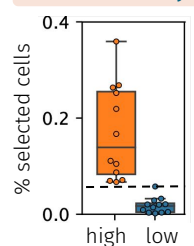


### 3) Highlights

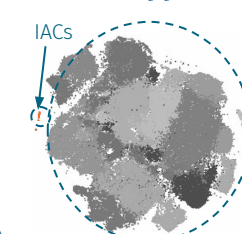
#### scaiVision®



#### 100% sensitivity



#### Standard approach:



#### 58% sensitivity

