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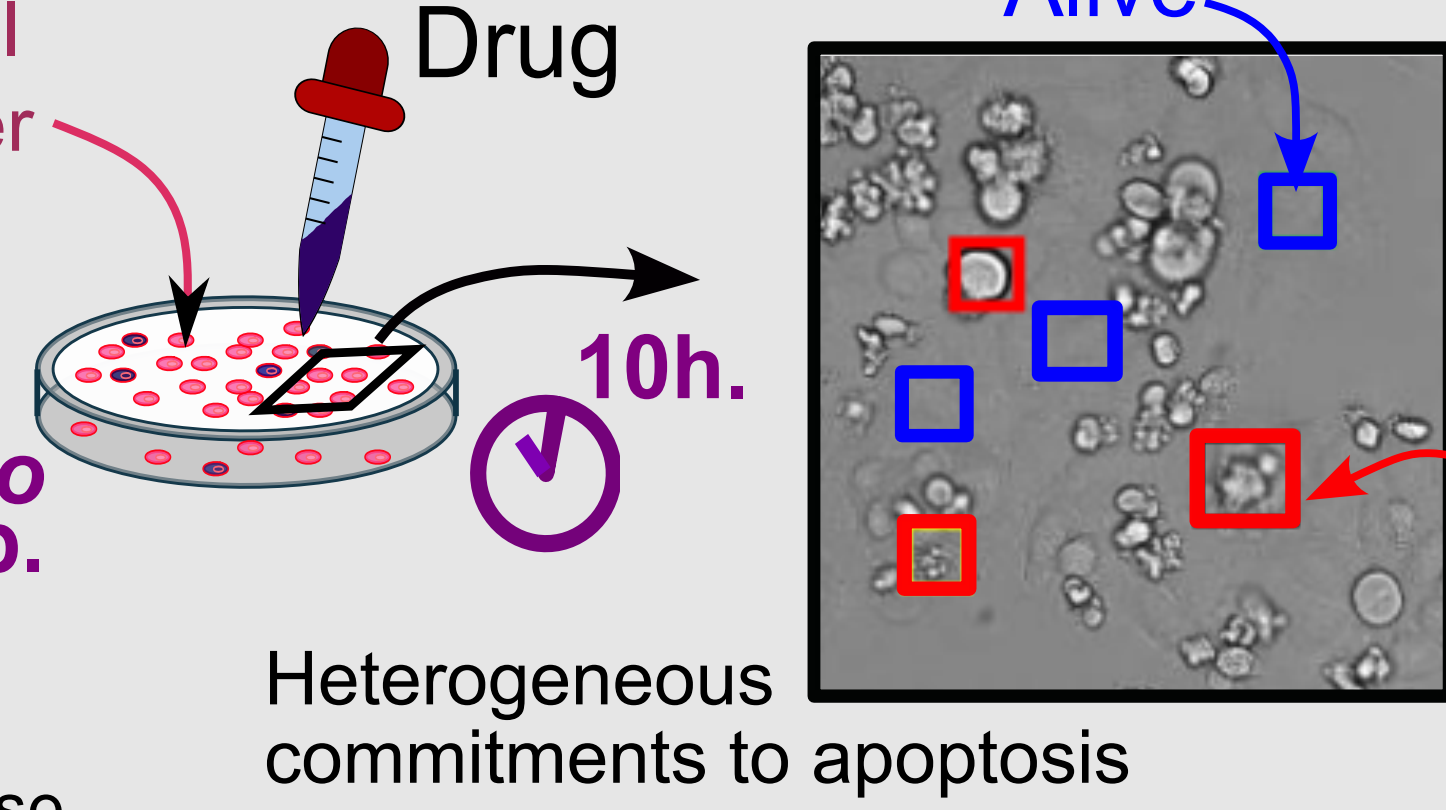
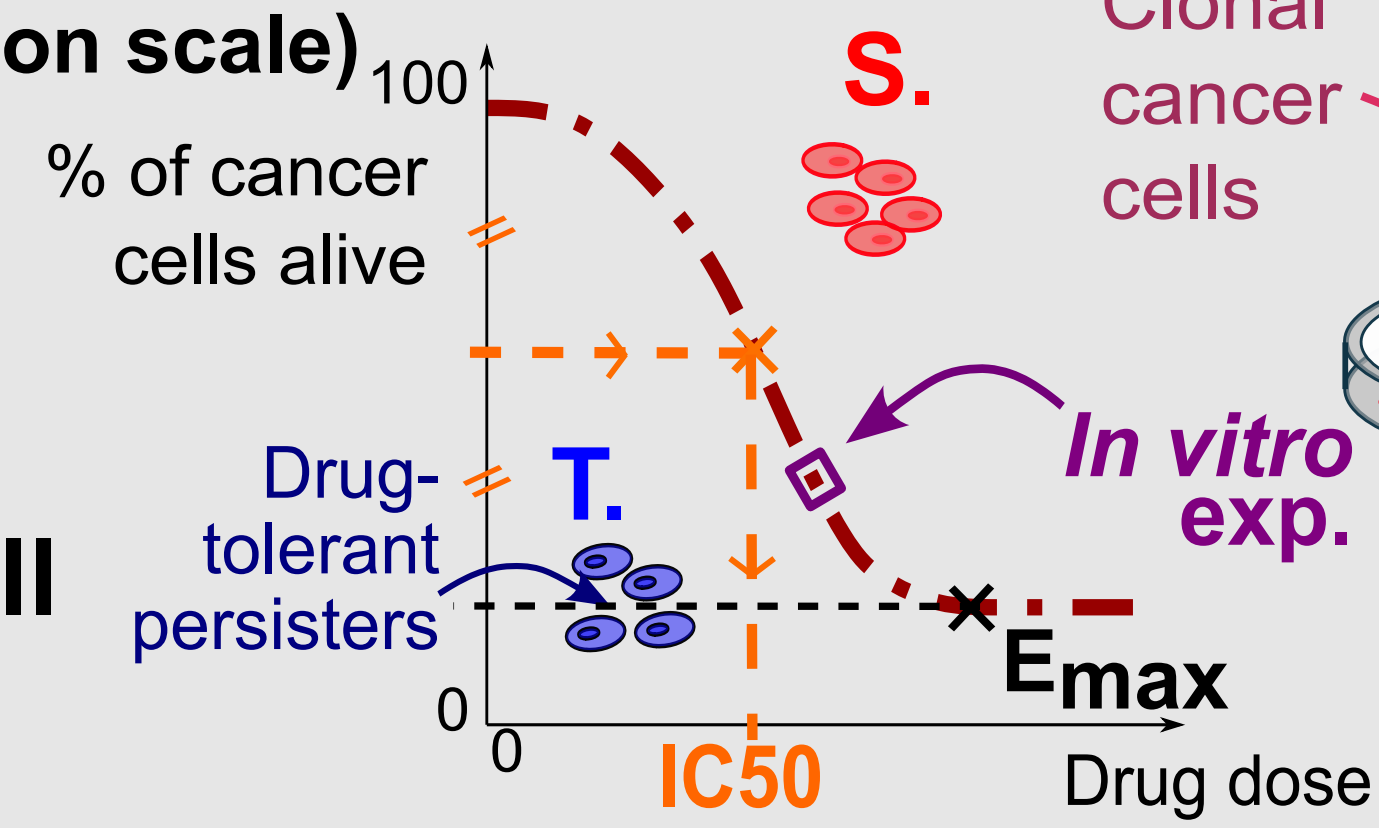
# Integrating Machine Learning (ML) methods in single-cell experimental workflow increases throughput and accuracy for target identification in immuno-oncology

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## Problems

Methods to evaluate drug-efficacy are static and don't consider single-cell heterogeneity

Pharmacological profile (population scale)



No rational way to find biomarkers of drug-tolerance and therapeutic targets for drug-combination

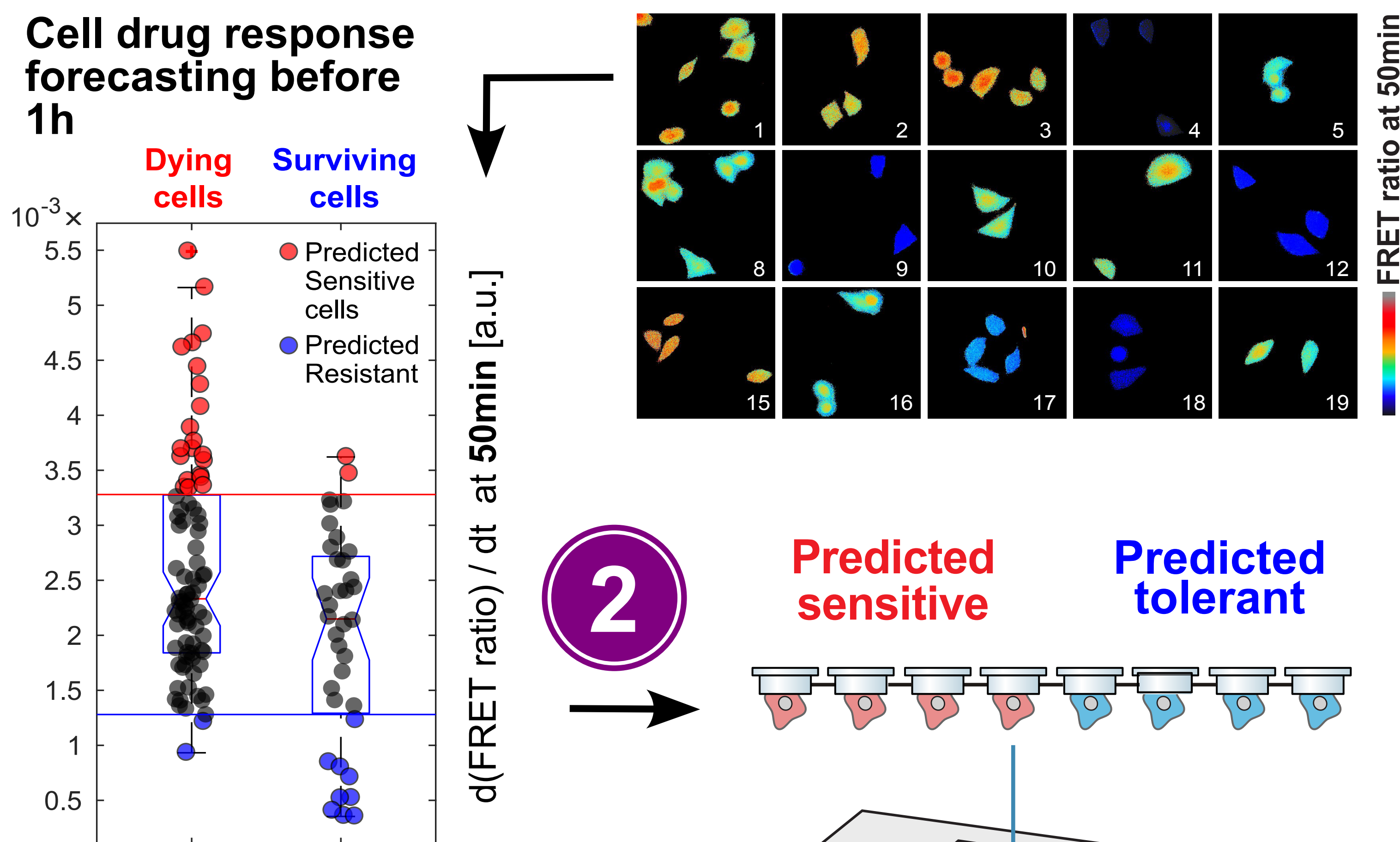
**Therapeutic failure**

## Our technical solution

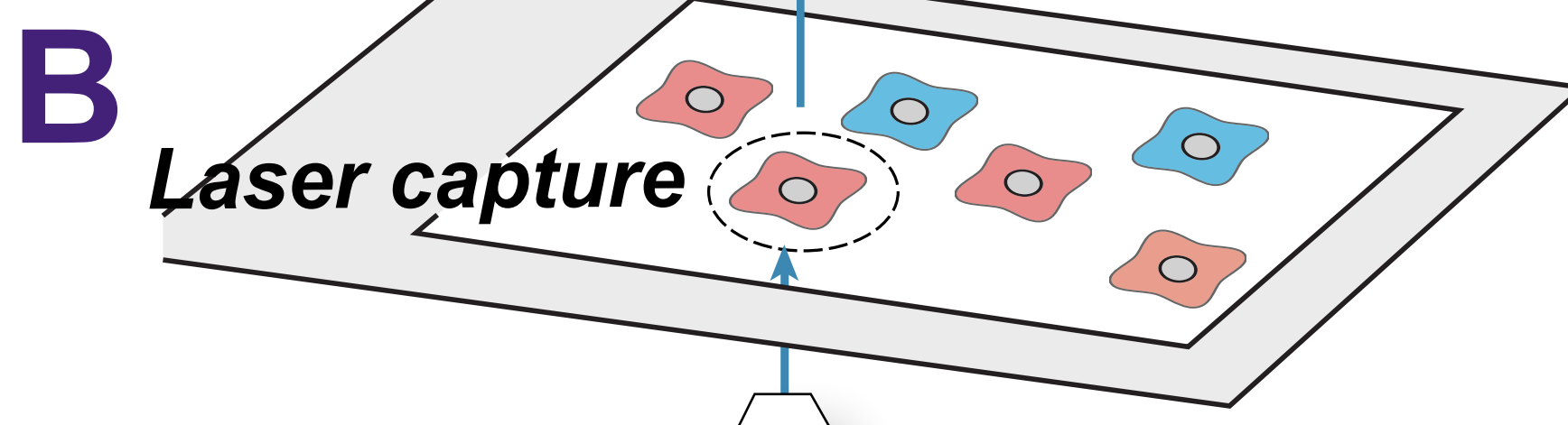
### FATE-SEQ

**Drawback:** Only 4% of the cells were isolated for profiling during proof of concept with the death-ligand TRAIL<sup>1,3</sup>

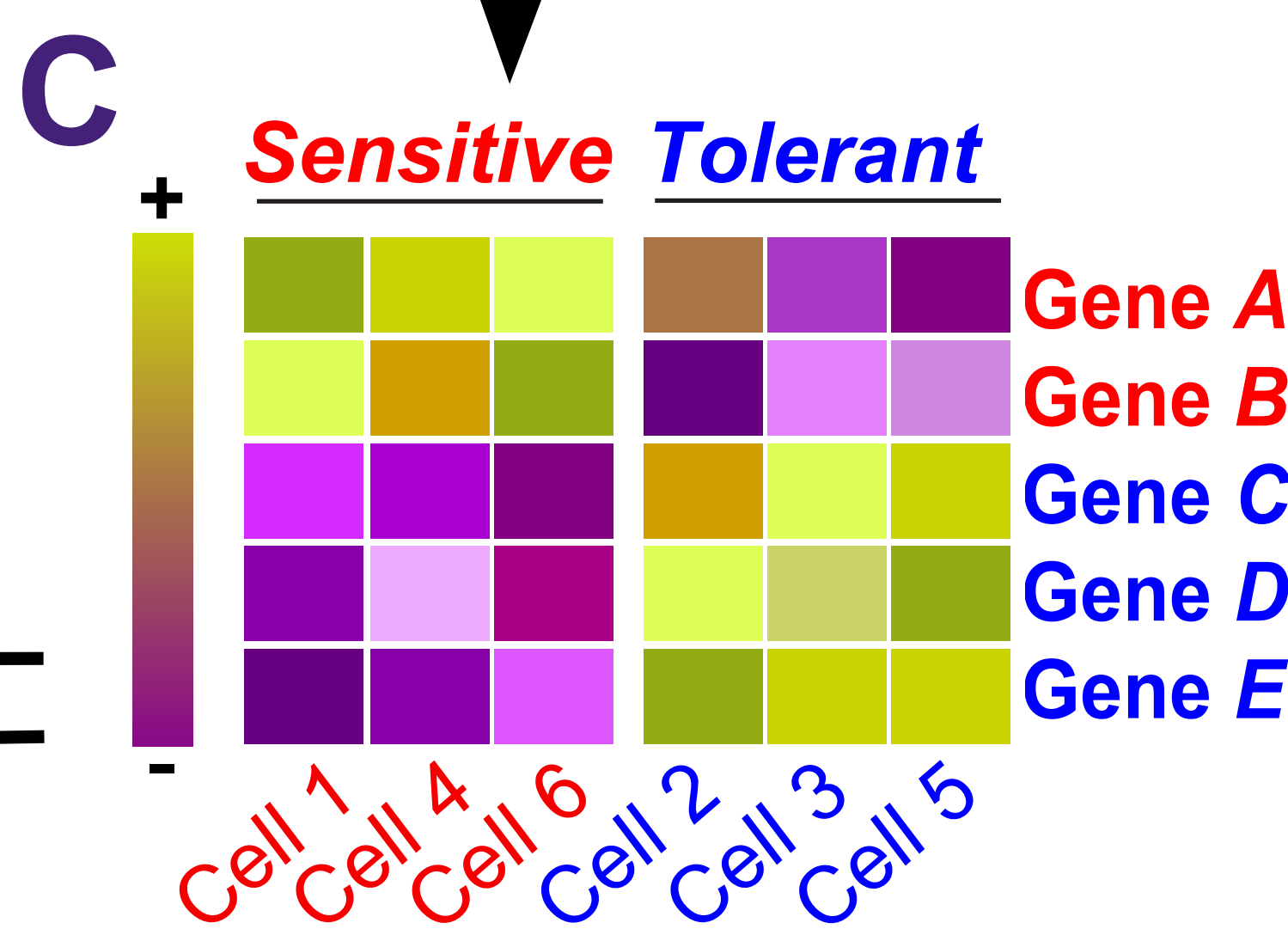
### A Single-cell drug response dynamics by live-cell microscopy



Same-cell isolation by laser-capture microdissection



Single-cell transcriptomic profile by single-cell RNA sequencing



### 3 GENetRank Gene prioritization<sup>4</sup>

Therapeutic targets + Molecular profile of drug efficacy + Cell-based assay validation

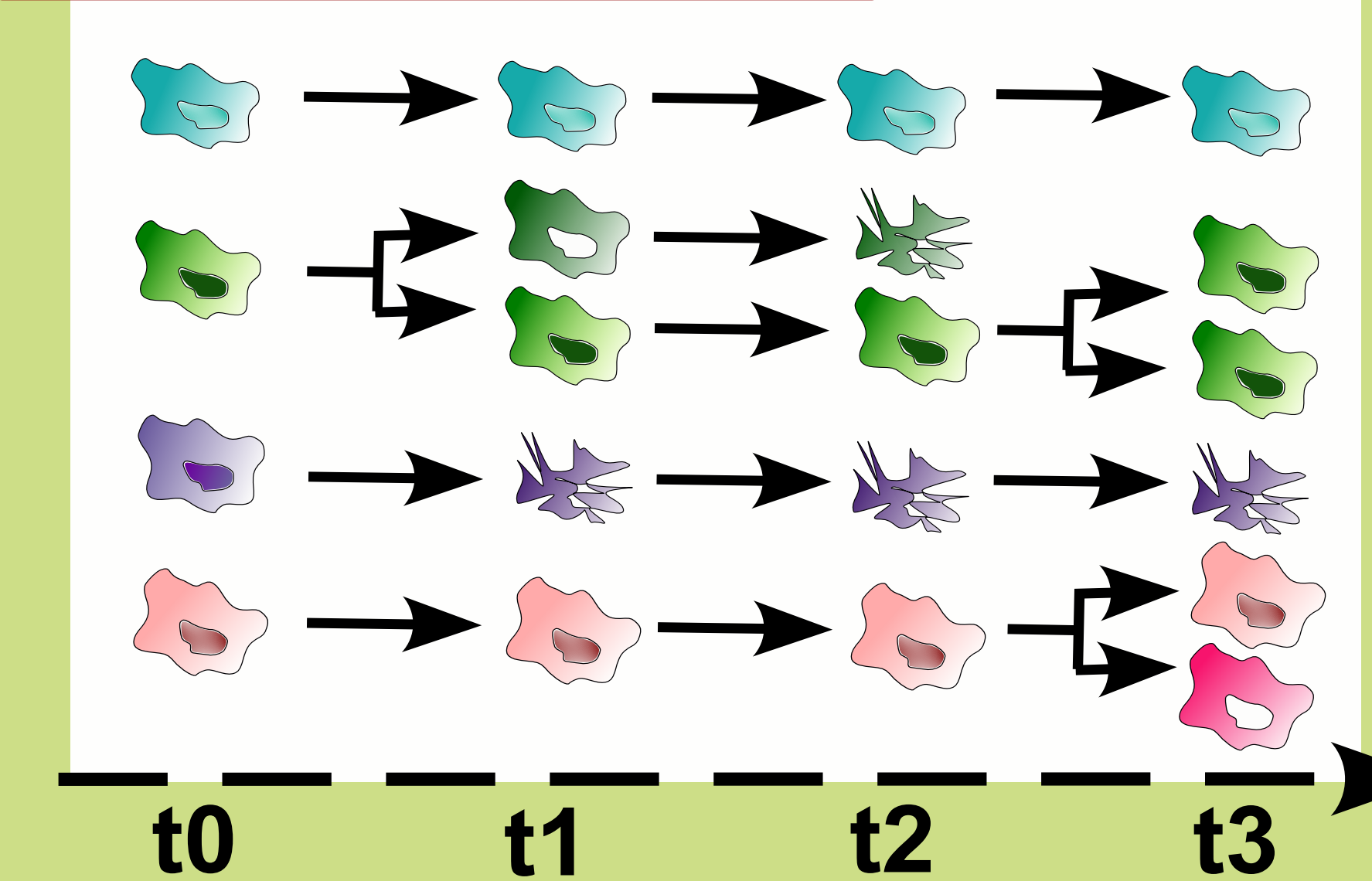
#### References:

1. Meyer et al. Cell systems 11.4 (2020): 367-374.
2. Péré, et al. Foundations Of Systems Biology in Engineering, IFAC conference (2022).
3. Bian et al. STAR protocols 3.3 (2022): 101600.
4. Sales-de-Queiroz et al. PLoS One (2022): 17(11):e0268956.
5. Shrikumar et al. International conference on machine learning. PMLR (2017).

## Our improvements with ML

### Cell tracking

Accuracy = 97%  
All cells predicted



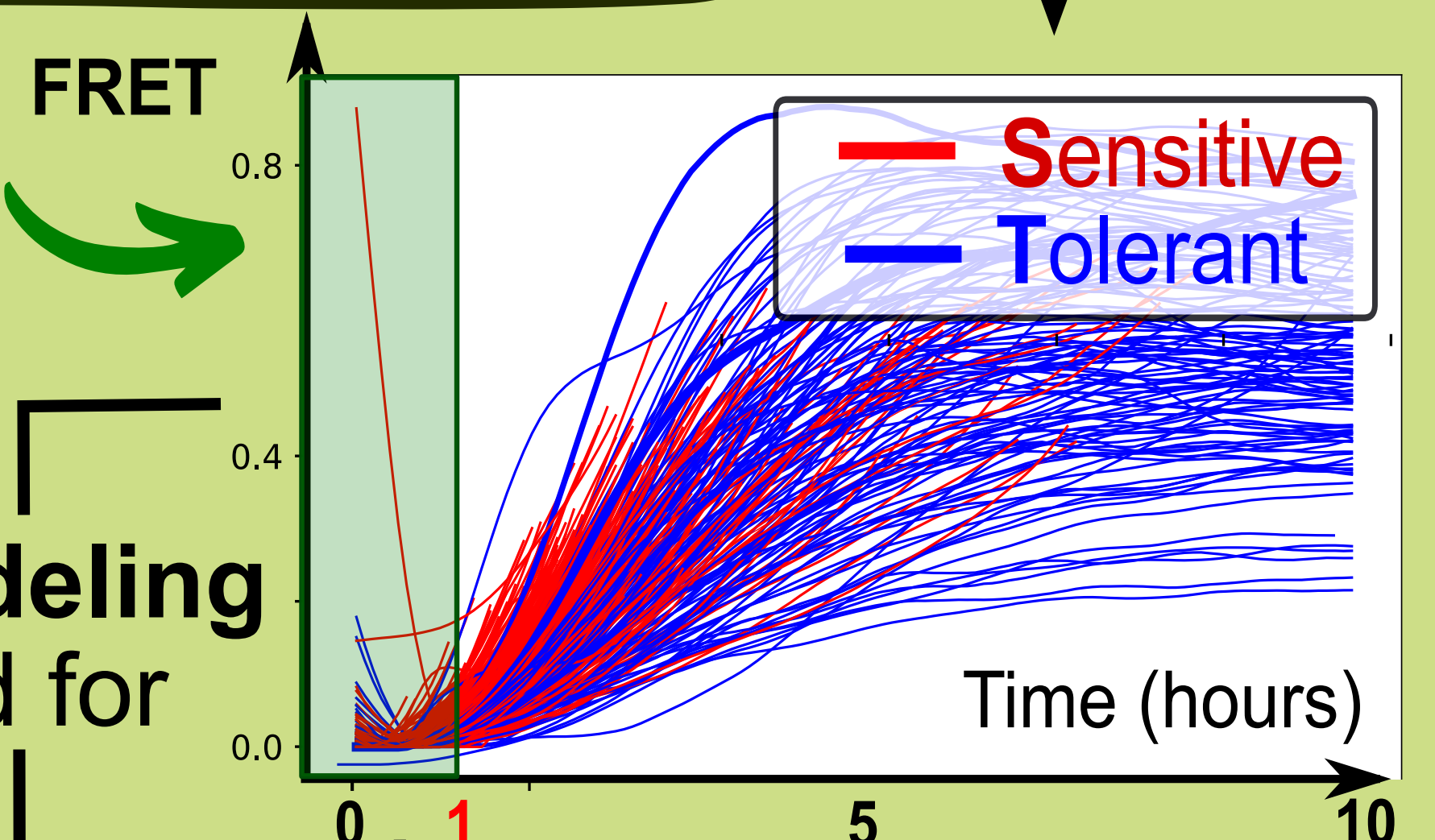
Cell Segmentation + Tracking with U-Net

+ Automatic Detection of cell lineage with correlation filters  
+ Fluorescent time-trajectories extraction

### Cell-fate forecasting

Sparse & short time-trajectories

Mathematical modeling of apoptosis<sup>2</sup> fitted for each cell



eDRUG early Drug Response UpGraded ML classifier

2 x more cells isolated with the same precision

Augmented feature input space

### Gene prioritization

Attribution scores = gene rank

- Gene A 80%
- Gene C 74%
- Gene D 99%
- Gene E 45%

