

A large, colorful molecular structure composed of various colored spheres (blue, green, red, yellow, orange, pink, white) connected by thin white rods, set against a light blue background. The structure is positioned on the left side of the image, with a faint silhouette of a human head in profile behind it.

FROM  
MOLECULE TO  
PATIENT

ASCPT 2019  
ANNUAL MEETING



Identifying biological signals differentiating  
responders and non-responders  
to MPDL3280A (Anti-PDL1) in NSCLC  
using QSP modeling of immune checkpoints

Vincent Lemaire, Genentech

March 16, 2019



## Modeling platform goals

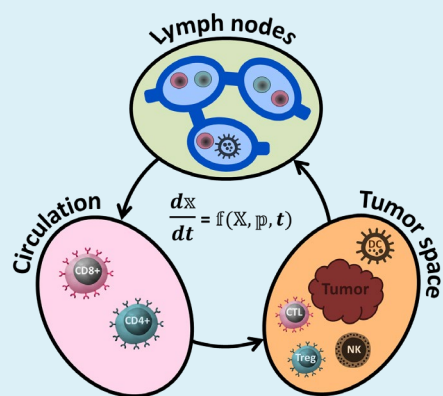
1. Help prioritizing combinations of immune checkpoint inhibitors
2. Address project-specific questions related to the clinical development of ongoing CIT programs

E.g.

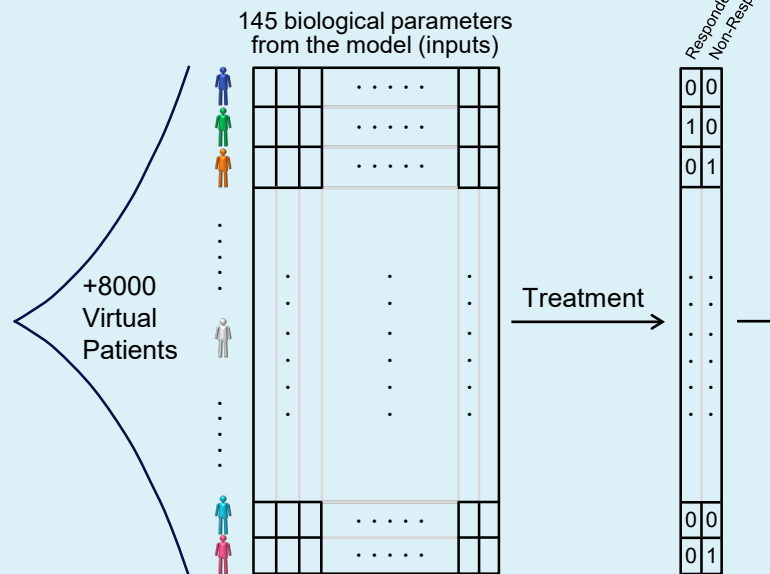
- Clarify complex dose-response relationships
- Identify signals of response (biomarkers)
- Assess synergy in combination treatments
- Optimization of dose scheduling
- Assessment of treatment duration
- Evaluation of combination sequencing effects
- Patient stratification (responder vs. non-responder)

# Overview of the approach

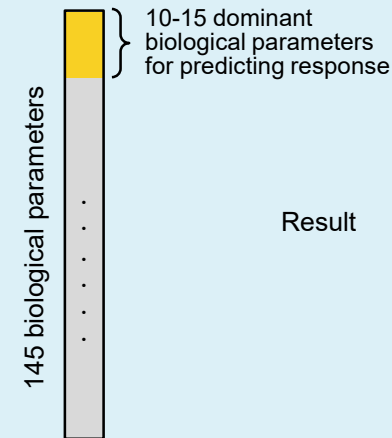
## QSP Model



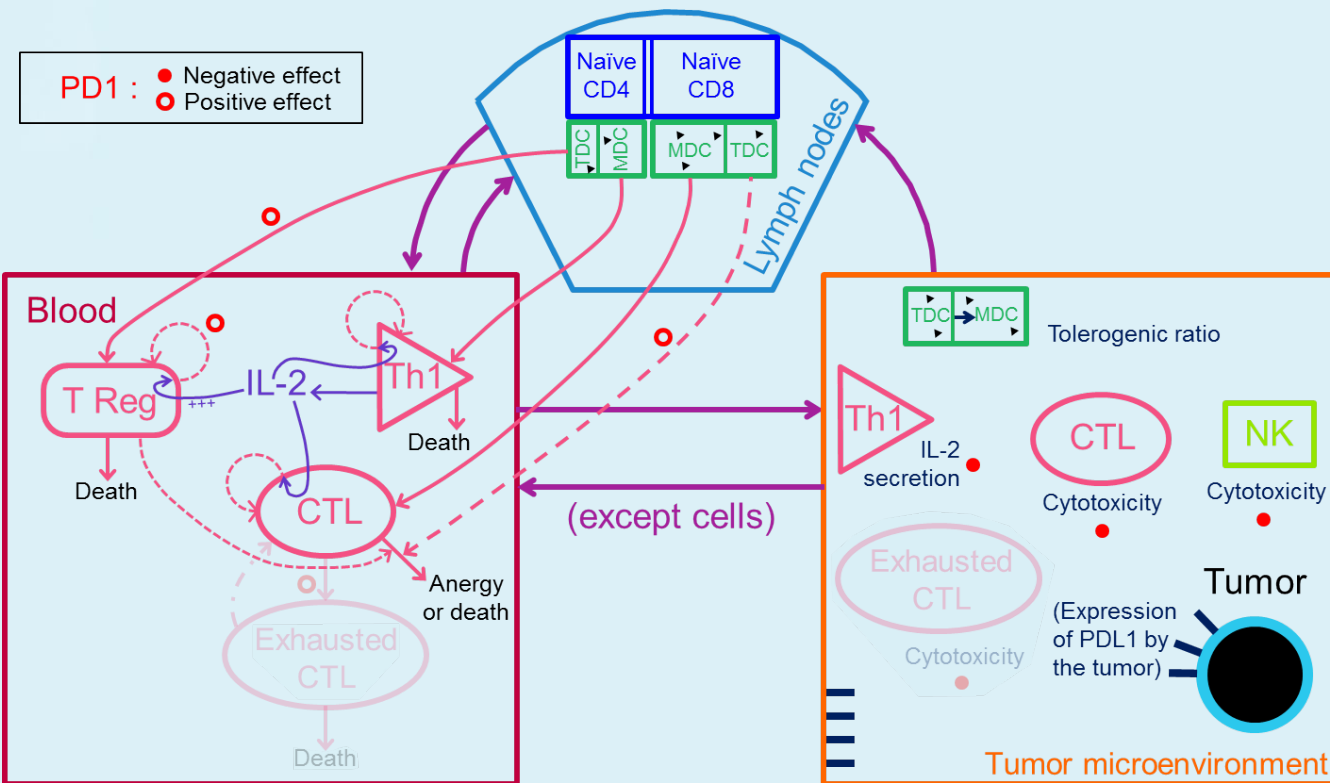
## Virtual Population

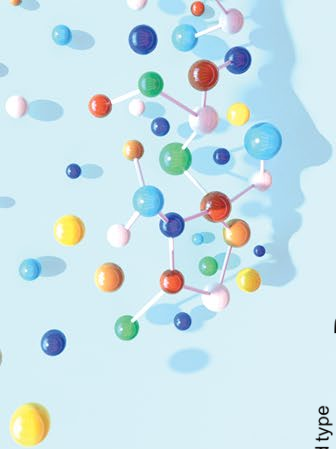


## Machine Learning Analysis



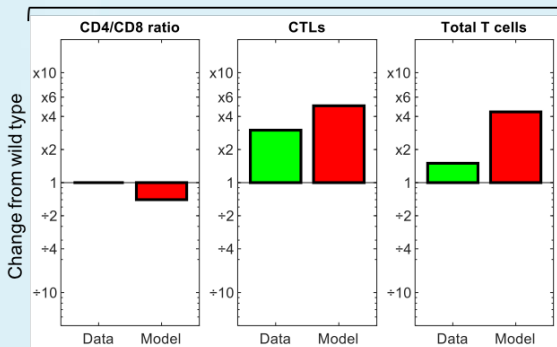
# Overview of the biology in the model



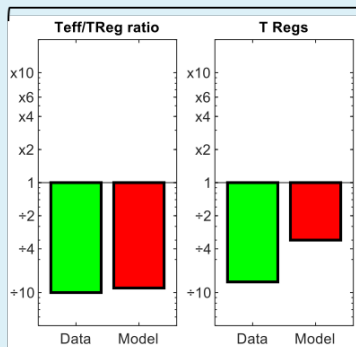


# Virtual patients must satisfy basic biology

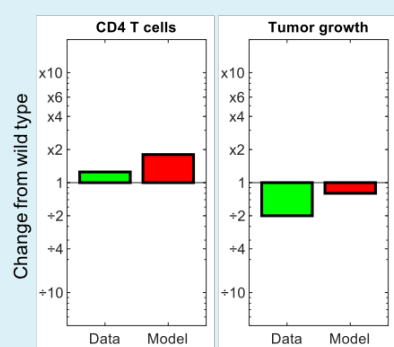
### PD1 knockout



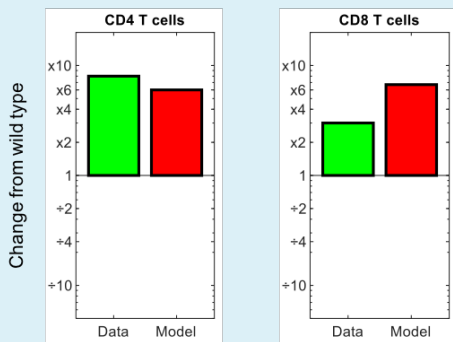
### PDL1 knockout



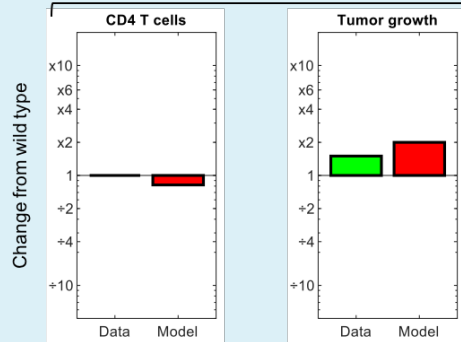
### Imm Ckpt 2 knockout



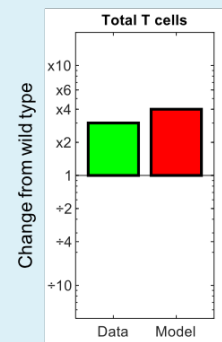
### Imm Ckpt 3 knockout



### CTL depletion



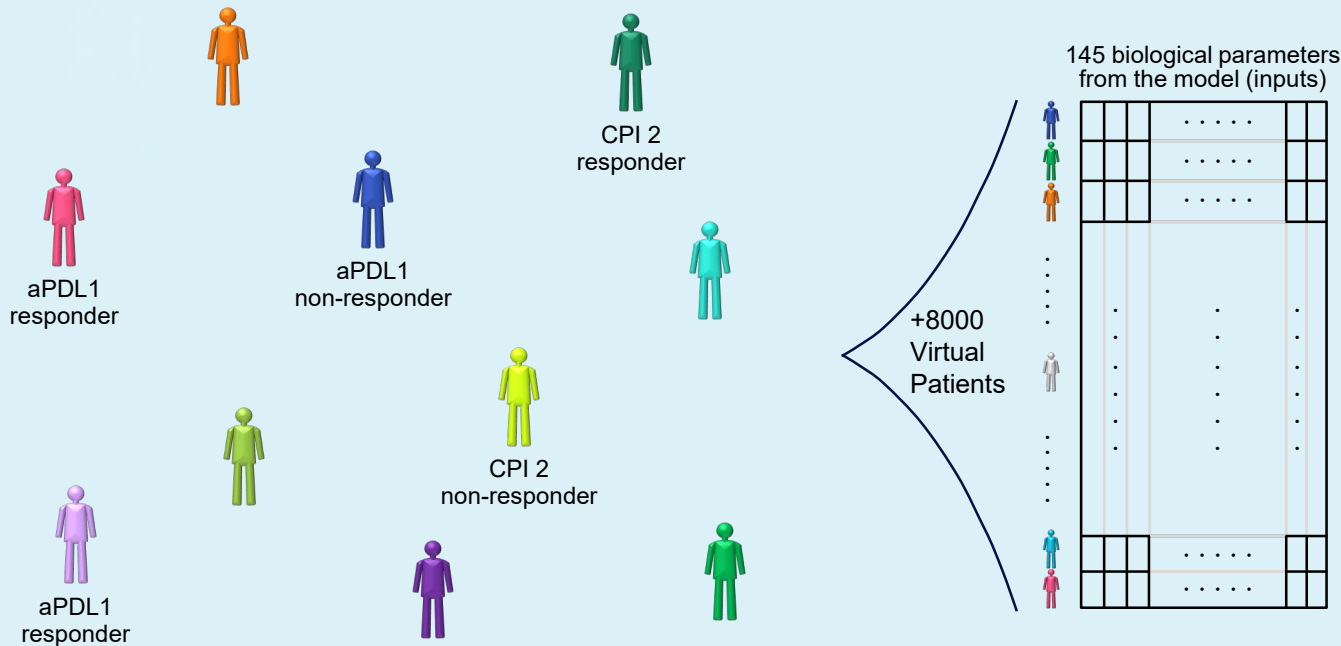
### T Regs depletion



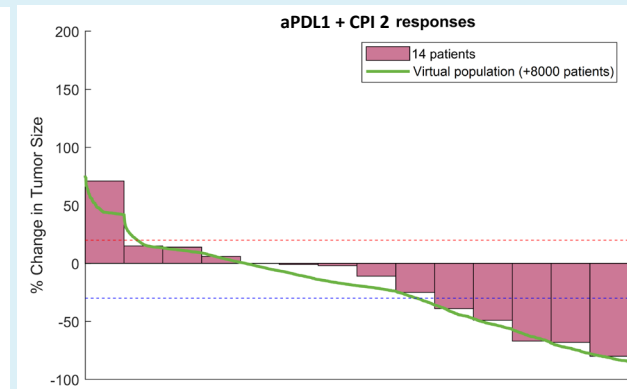
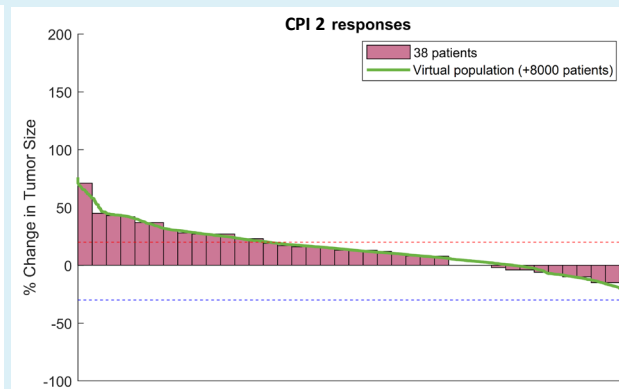
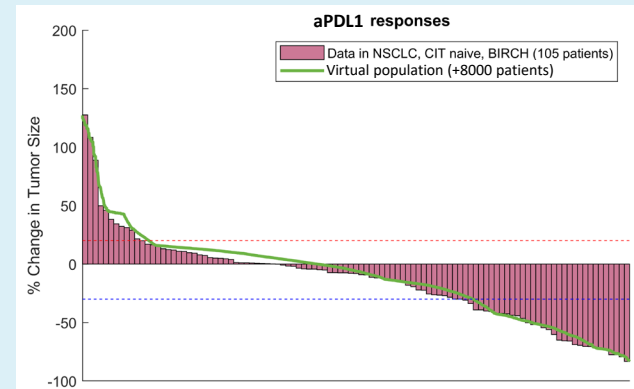
\* Imm Ckpt = Immune Checkpoint



# Virtual population with high diversity in biology



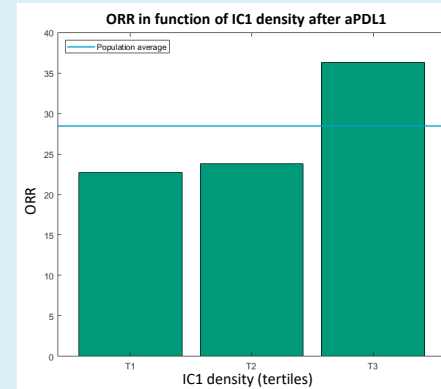
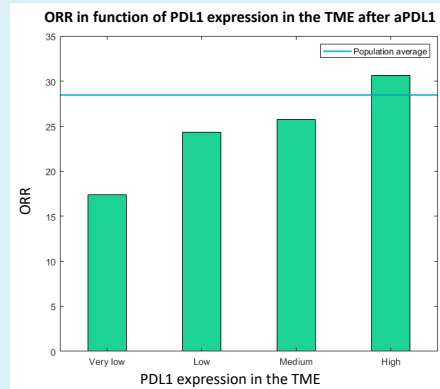
# Calibration of the virtual population to match clinical response data





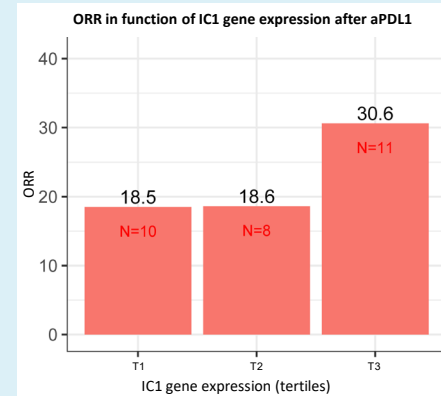
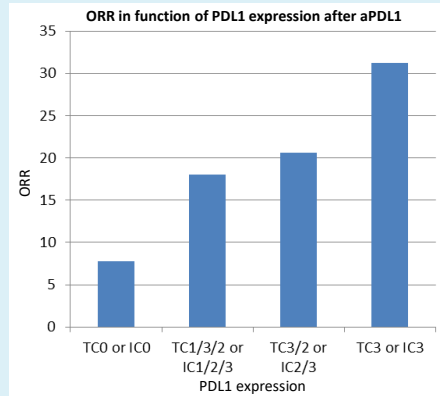
# Pieces of model and virtual population validation

Model



Model

Data



Data

# Machine learning approach & results

Identify differences in biology which separate aPDL1 responders and non-responders

Using the Machine Learning algorithms:

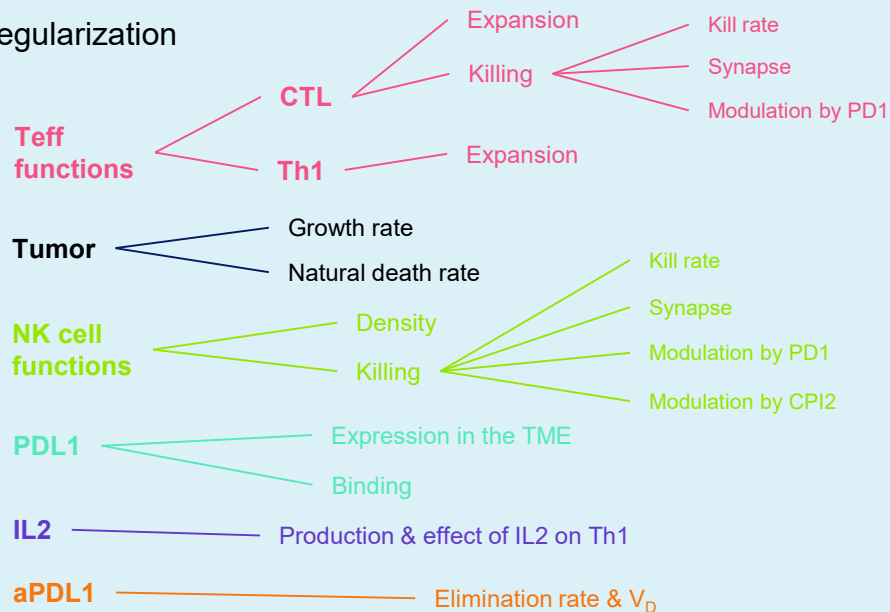
- Multivariate linear regression with LASSO regularization
- Support Vector Machine (SVM)

## LASSO:

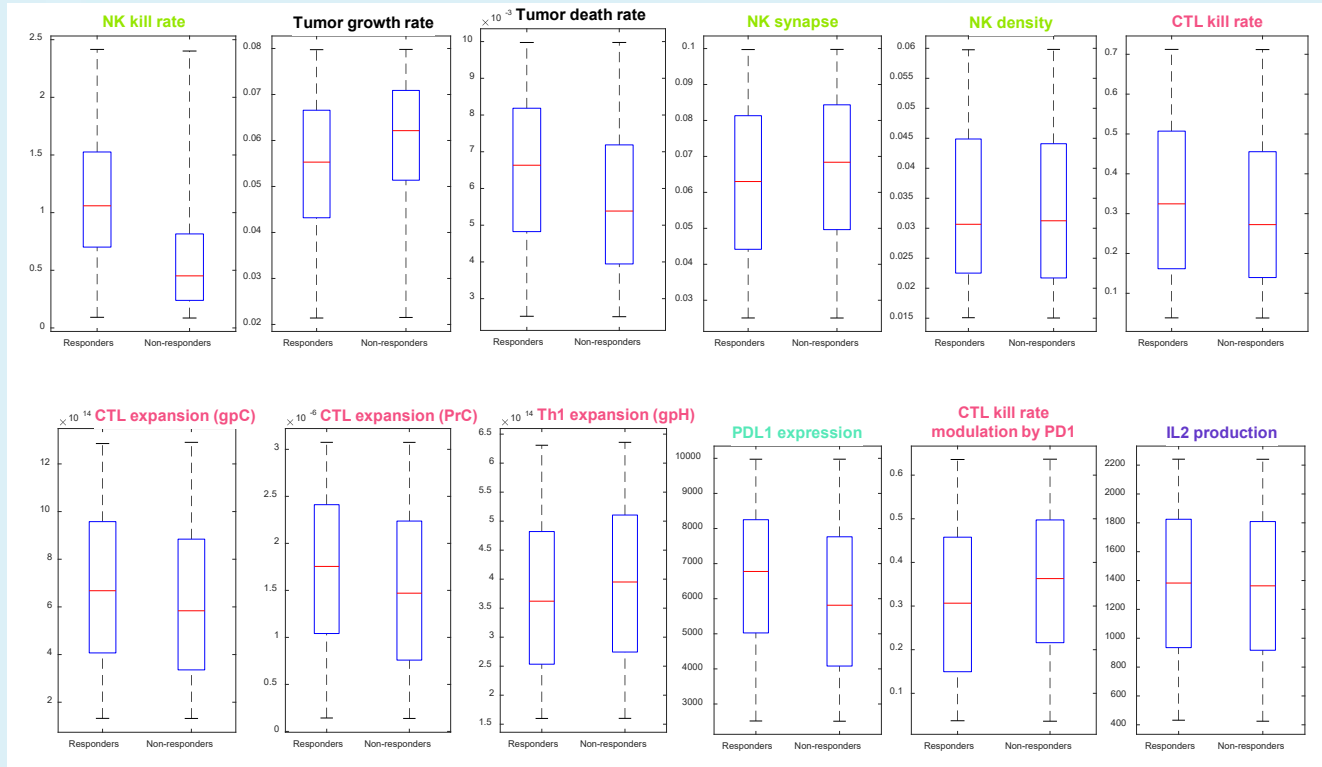
Parameters	Coefficients
kk	-0.566
beta	0.387
kapop	-0.299
KDK	0.183
Pi50pkPD1	0.181
K	-0.178
kc	-0.149
gpC	-0.122
PrC	-0.105
gpH	0.0677
KDPD1	0.0622
Pi50pcPD1	0.0458
PrH	0.0437
KDC	0.0383
PDL1tO	-0.0338
gpI	-0.0334
keaPDL1	-0.0227

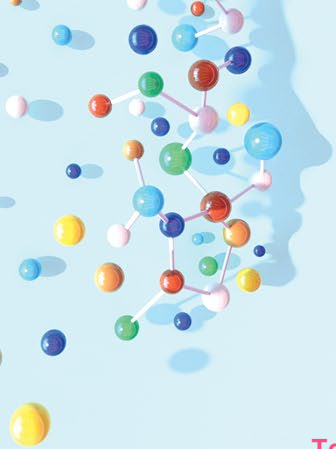
## SVM:

Parameters	Coefficients
kk	-1.92
beta	1.73
kapop	-1.35
Pi50pkPD1	1.28
gpC	-0.73
KDK	0.646
PrC	-0.611
KDPD1	0.501
gpH	0.485
PDL1tO	-0.476
kc	-0.415
Pi50pkCPI2	-0.361
kkCPI2	-0.341
kcCPI2	-0.326
Pi50pcPD1	0.297
K	-0.231
ErI	-0.189

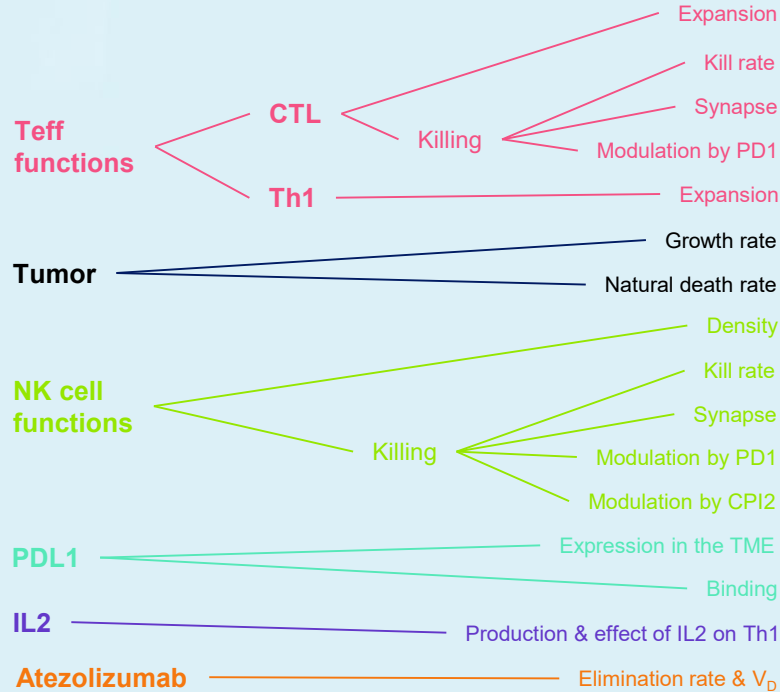


# Biological signals need to be considered together for prediction



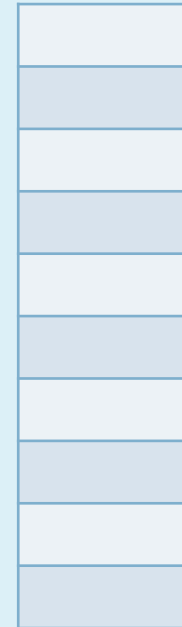


# Collaboration & partnership with biomarker scientists



A clinically measurable panel of biomarkers

Translate into



# Acknowledgements

**Clinical Pharmacology (M&S):** Anand Rotte, Jin jin, Matts Kågedal, Xiaofei Zhou, René Bruno, Mathilde Marchand

**Clinical Pharmacology (CIT):** Kari Morrissey, Helen Winter, Yachi Chen

**PKPD:** Saroja Ramanujan, Kapil Gadkar, Justin Feigelman, Iraj Hosseini

**Oncology Biomarkers:** Sami Mahrus, Priti Hegde, Sanjeev Mariathasan, Romain Banchereau, Namrata Patil

**Roche:** Benjamin Ribba, Jonathan Wagg, Jean-Eric Charoin

**Research:** Andrey Shaw

**Early Clinical Development:** Raymond Meng, Mike Flanagan

**Others:** Dan Blaney (gRED), Craig Amundsen (IT cluster), Sam Marshalik (Mathworks)

