

Notch
THERAPEUTICS

Making drugs from T cells: Quantitative Analysis of CAR-T Pharmacology

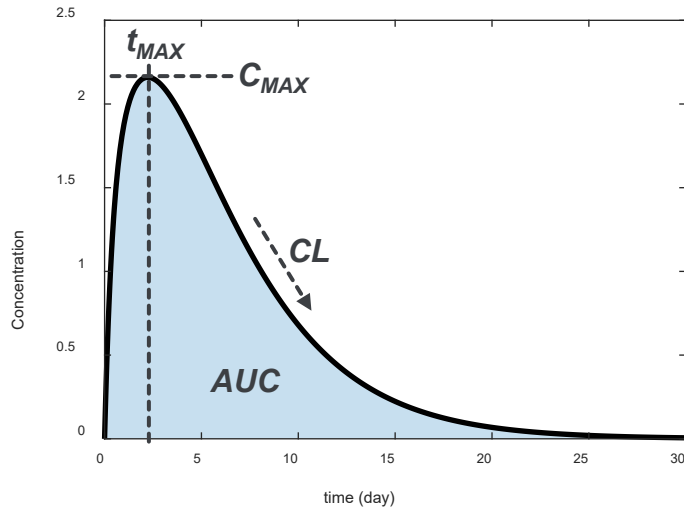
FOCIS Cancer Immunity & Immunotherapy Course

June 20, 2023

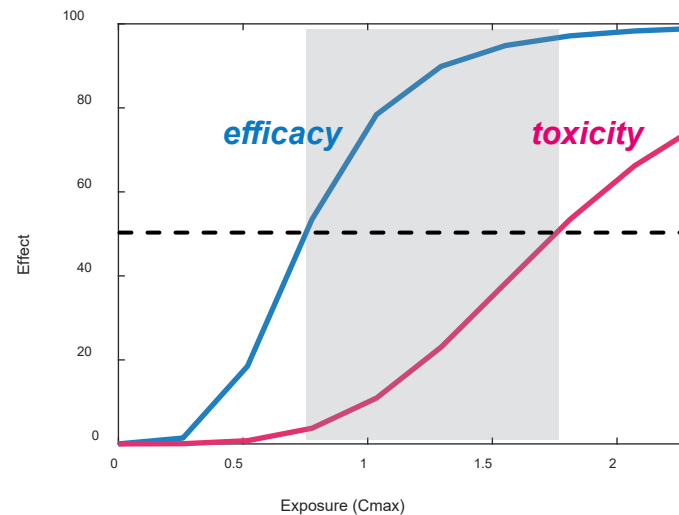
Daniel Kirouac

Pharmacometrics: Quantitative Pharmacokinetics & Pharmacodynamics (PKPD)

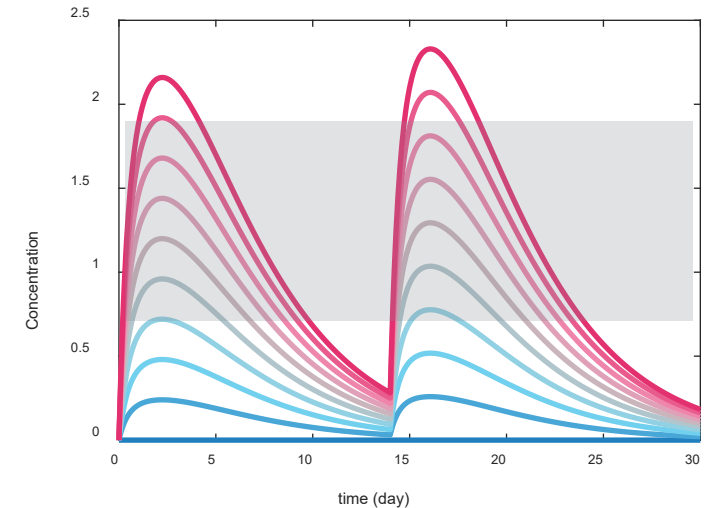
Pharmacokinetics (PK):
Dose-Exposure



Pharmacodynamics (PD):
Exposure-Response



PKPD:
Dose regimen optimization



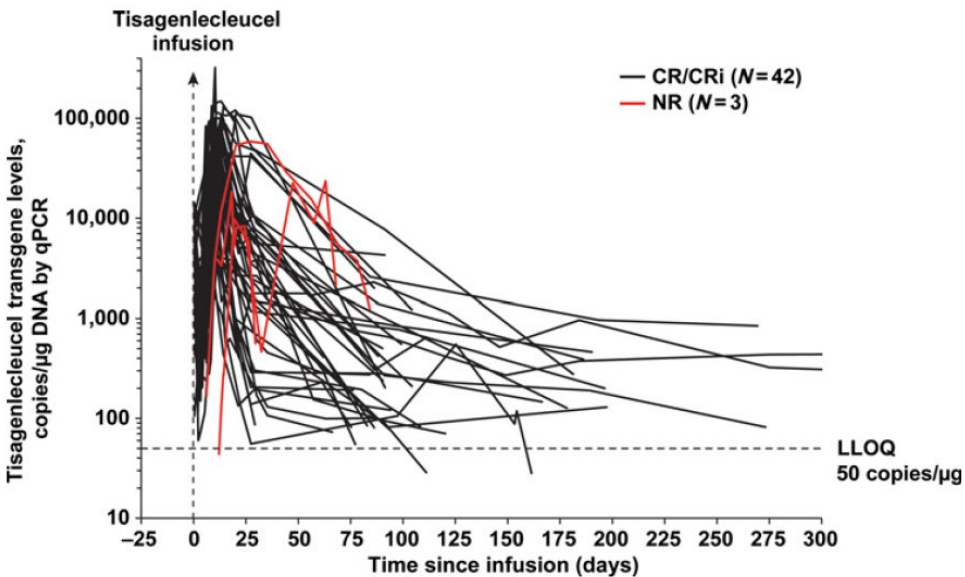
C_{max} : maximal concentration
 T_{max} : time at C_{max}
 AUC: Area under the Curve
 CL: Clearance rate (\sim half-life⁻¹)

$$\text{Effect} = E_{max} \cdot \left(\frac{C^k}{C^k + EC50^k} \right)$$

Therapeutic index: $EC50(\text{efficacy}) - EC50(\text{tox})$

How do we apply these quantitative metrics to adoptive T cell therapy?

Adoptive T cell therapy: what drives exposure/response?



Mueller KT, Waldron ER, Grupp SA, et al (2018) Clinical Pharmacology of Tisagenlecleucel in B-Cell Acute Lymphoblastic Leukemia. Clin Cancer Res 24(24):6175-6184

Distribution

- Where do T cells go?
- Does proliferation/expansion occur in tissues or blood?

Cell Expansion

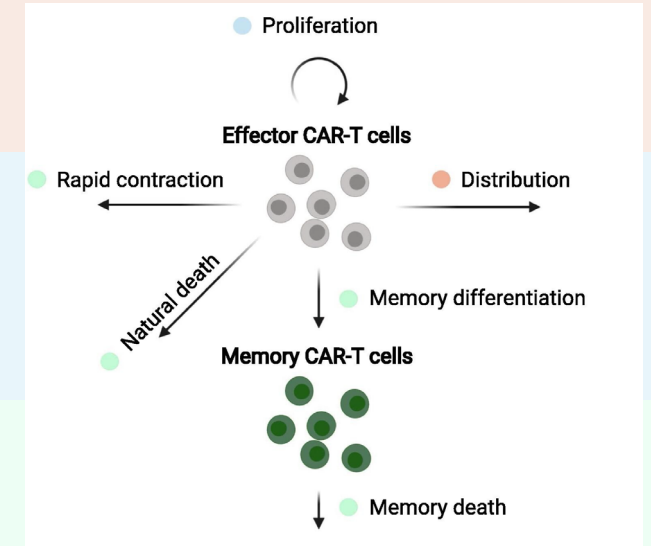
- Memory vs. exhaustion phenotype...sometimes
- Intrinsic proliferative capacity of the cells
- CAR design & expression
- Patient cytokine levels
- Tumor burden

Contraction & Clearance/Persistence

- Memory cell generation following antigen clearance
- Competition from host T cells for 'space'
- Allogeneic elimination (host vs. graft)

Anti-tumor efficacy & toxicity (CRS)

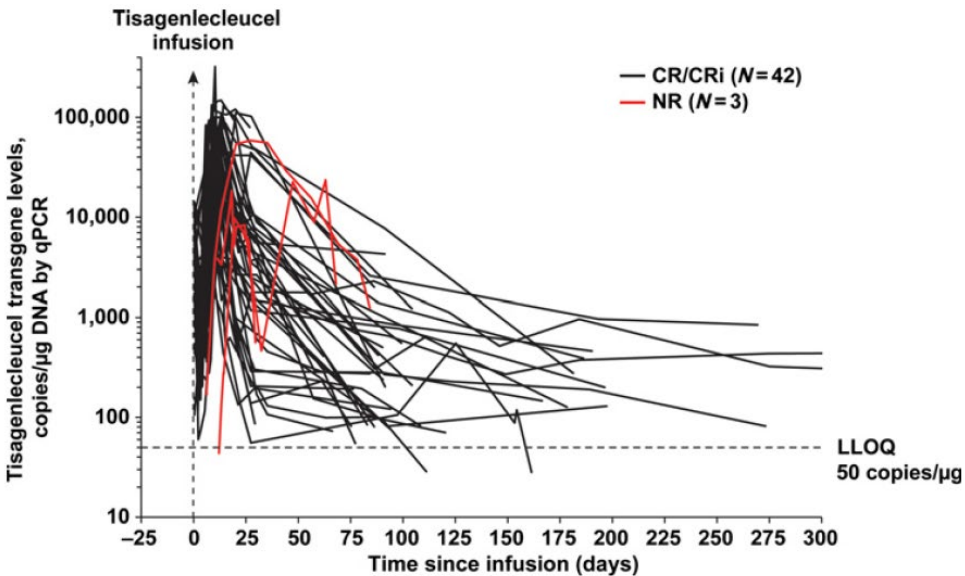
- Exposure (Cmax / AUC)
- Intrinsic cytotoxic potency
- CAR design & expression
- Tumor Microenvironment inflammatory/anti-inflammatory signals
- Tumor homing/penetration**



Qi T, McGrath K, Ranganathan R, et al (2022) Cellular kinetics: A clinical and computational review of CAR-T cell pharmacology. Adv Drug Deliver Rev 188:114421.

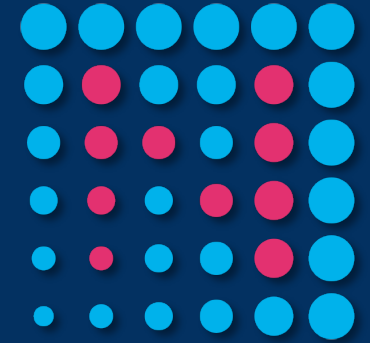
Adoptive T cell therapy: what drives exposure/response?

Outline

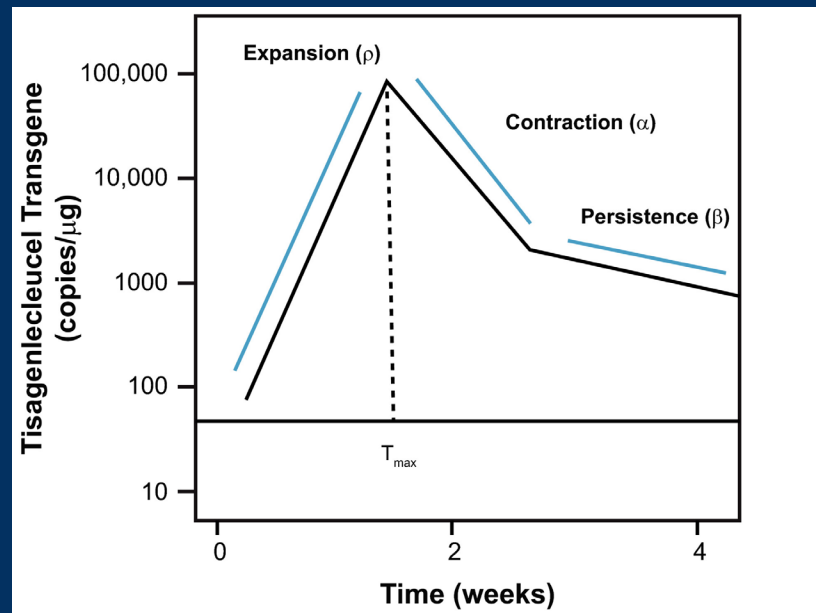


Mueller KT, Waldron ER, Grupp SA, et al (2018) Clinical Pharmacology of Tisagenlecleucel in B-Cell Acute Lymphoblastic Leukemia. Clin Cancer Res 24(24):6175-6184

1. What pharmacometrics predict patient response?
 - *Empirical* pharmacokinetic (PK) modelling
2. What cell-intrinsic properties of the CART product underly the wide clinical variability?
 - *Mechanistic* PKPD modelling of Tcell:tumor interactions
 - *Machine learning* model for predicting response
3. What patient-intrinsic factors mediate response?
 - A. T cell bio-distribution*
 - B. Tumor inflammation
 - C. Lympho-depletion regimen & patient response
 - D. Host vs. Graft (allogeneic clearance)



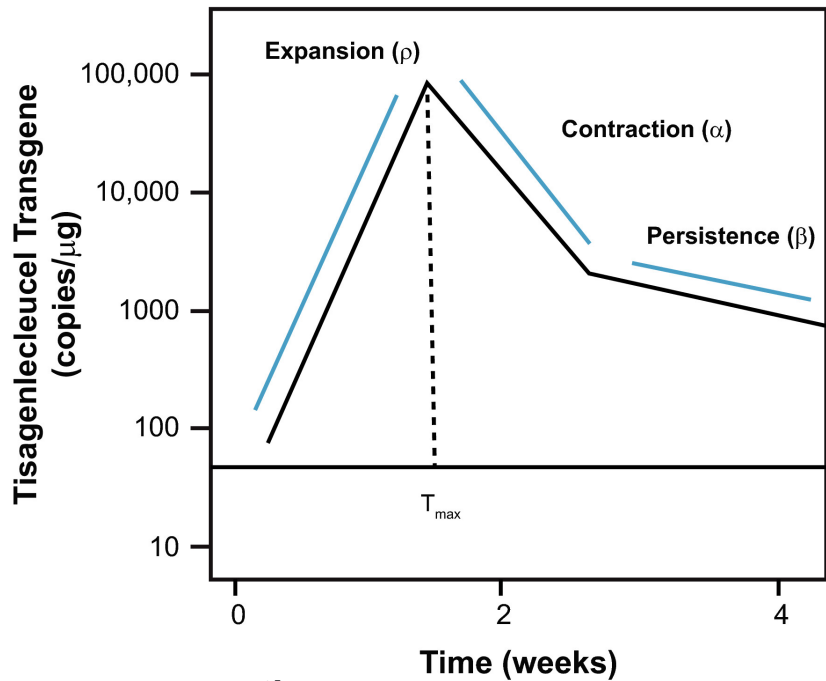
1. What CAR-T pharmacometrics predict response?



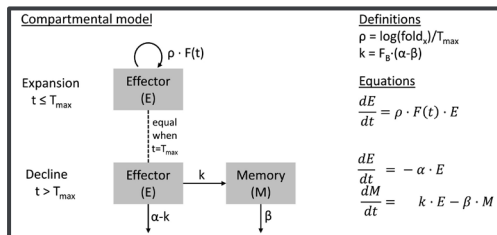
CAR-T pharmacokinetic (“cellular kinetics”) model

Developed for Kymriah (TISAGENLEUCEL-T) BLA

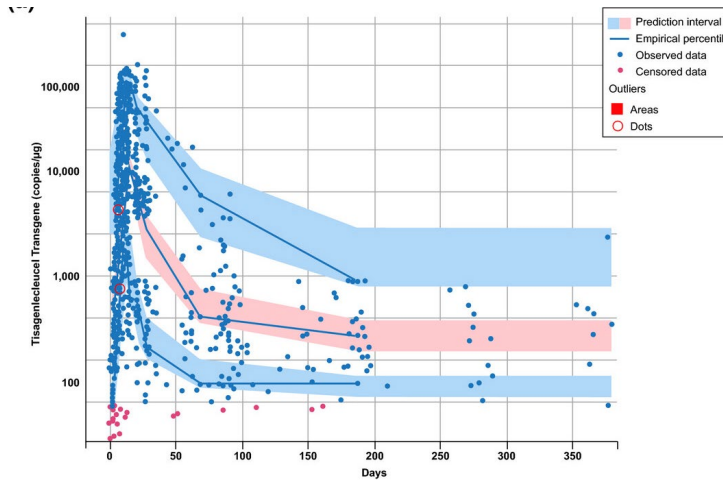
Empirical model quantifies PK curves



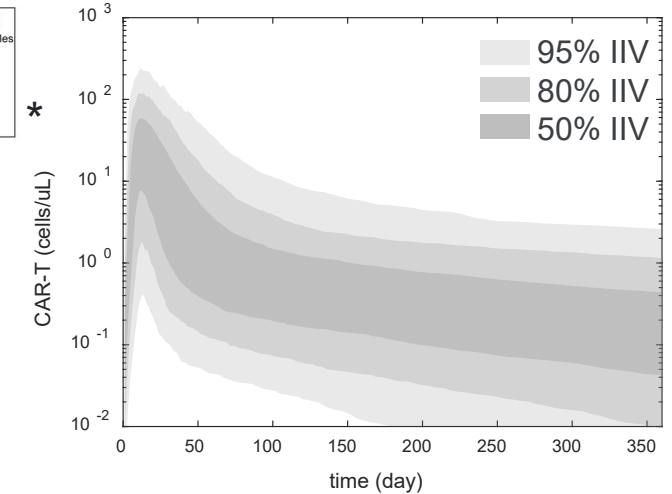
math



PK simulations vs. clinical data



Internal model simulations



*Kalos et al (2011) Sci Transl Med 3:73-95.

Model parameters

PARAMETER	THETA (mean)	ETA (variance)
Cmax	24000 (counts/ug)	0.65
Tmax	9.3 (day)	0.38
foldX (Cmax/C ₀)	3900	2.4
Fb (fraction Tm at tmax)	0.0079	0.8
Alpha (contraction)	0.16 day ⁻¹	0.91
Beta (persistence)	0.0032 day ⁻¹	0.86

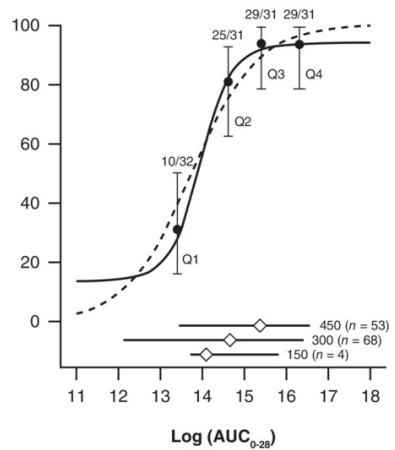
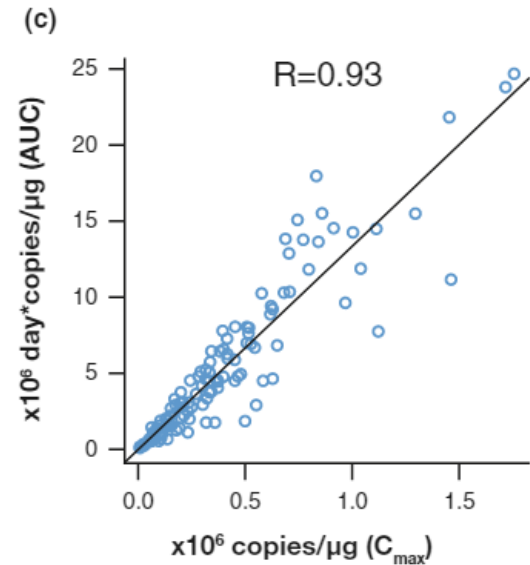
CAR-T exposure-response analyses

Abecma in Multiple Myeloma

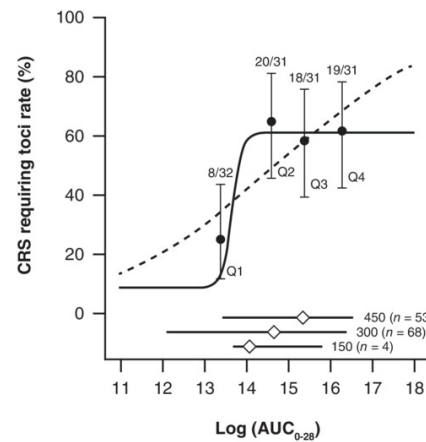
AUC ~ Cmax

AUC (or Cmax) drives response & toxicity (CRS)

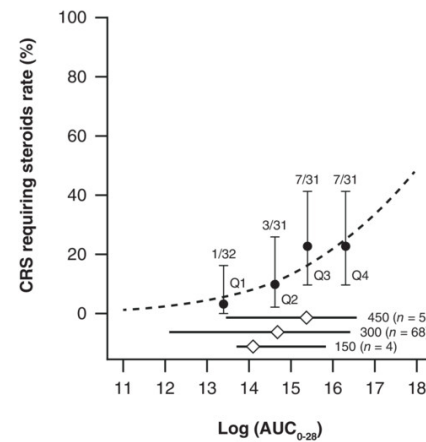
Response vs. dose and CRS



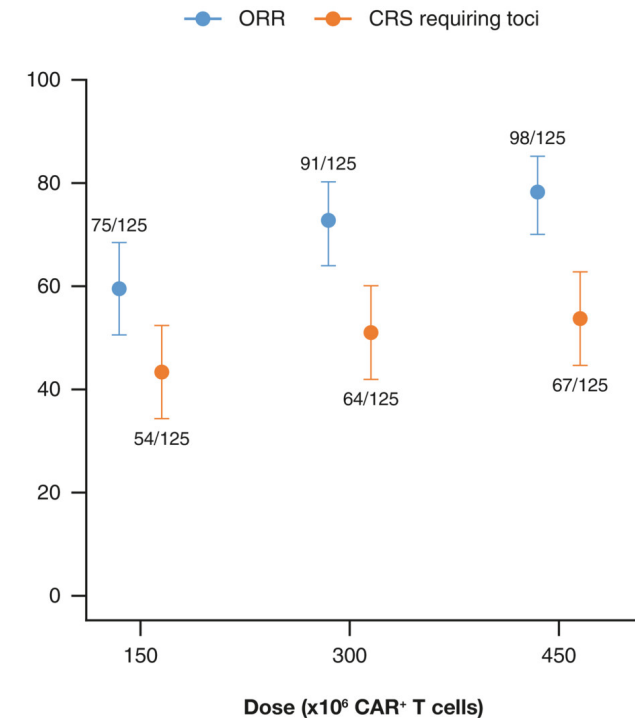
Parameter	Estimate (%RSE) on the logit scale
E ₀	-2.83 (43.0)
E _{max}	2.29 (37.0)
Log (EC ₅₀)	2.64 (0.96)
H	3.25 (19.7)
Sex (female vs male)	1.78 (38.3)



Parameter	Estimate (%RSE) on the logit scale
E ₀	-2.37 (43.5)
E _{max}	0.44 (47.3)
Log (EC ₅₀)	2.61 (0.71)
H	4.67 (27.9)



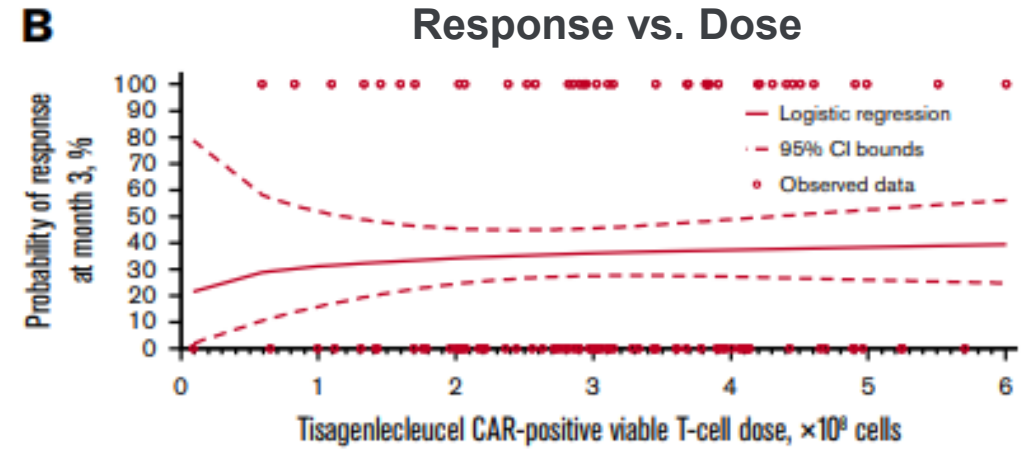
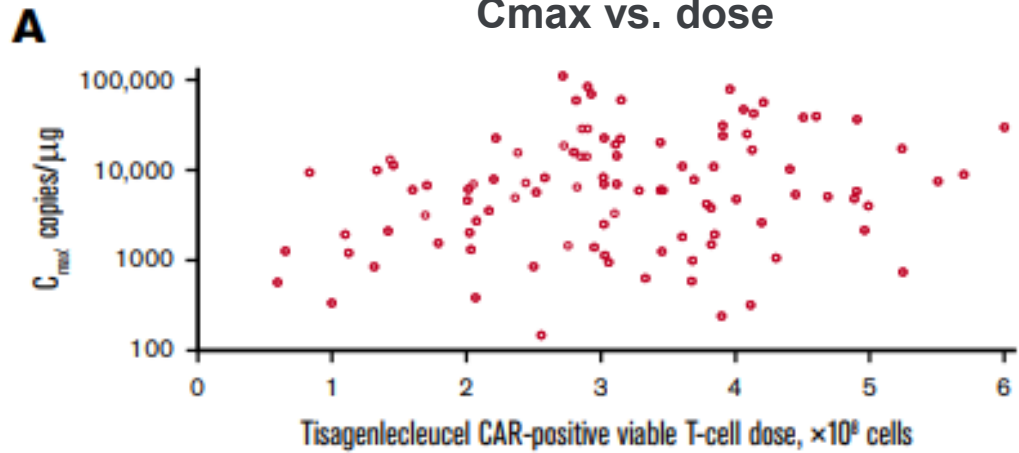
Parameter	Estimate (%RSE) on the logit scale
Intercept	-11.1 (37.2)
Slope	0.61 (43.5)



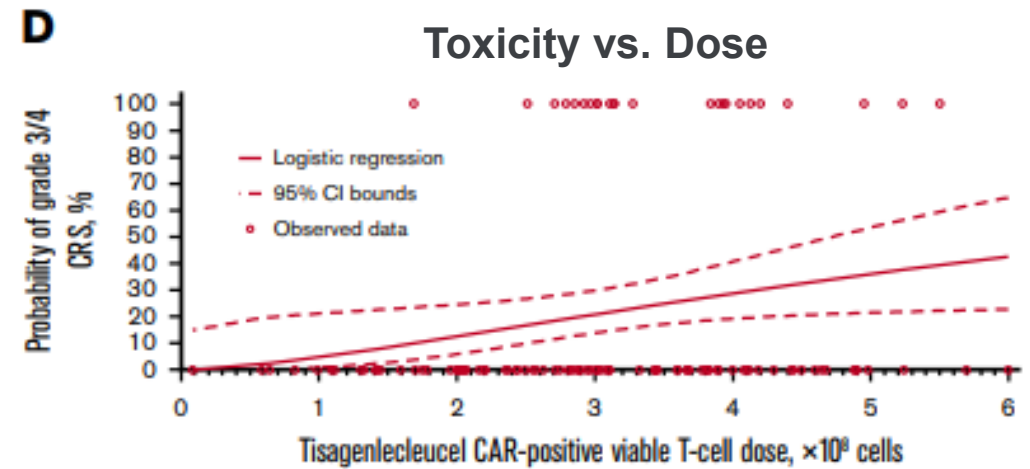
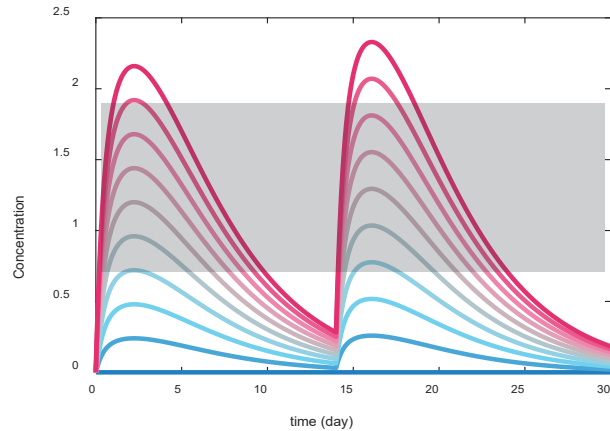
Connarn JN, Witjes H, Geffen M van Z, et al (2023) Characterizing the exposure–response relationship of idecabtagene vicleucel in patients with relapsed/refractory multiple myeloma. *Cpt Pharmacometrics Syst Pharmacol*. <https://doi.org/10.1002/psp4.12922>

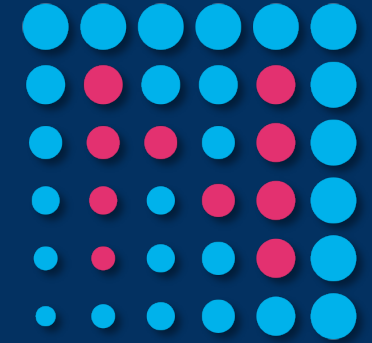
Inter-individual variability (IIV) washes out dose-responses

Kymriah in DLBCL

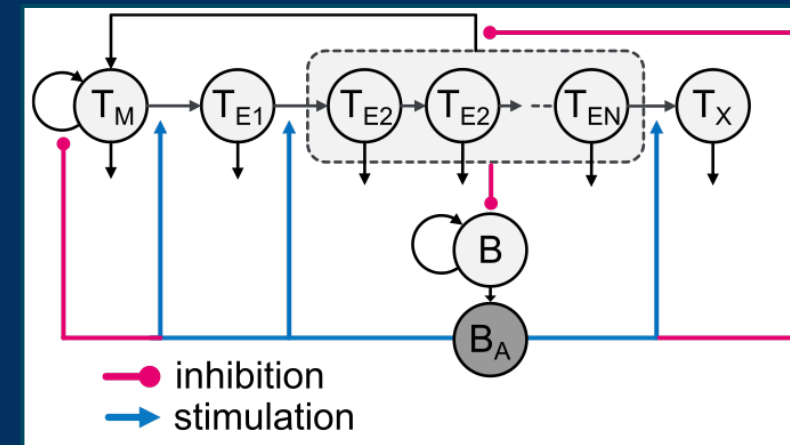
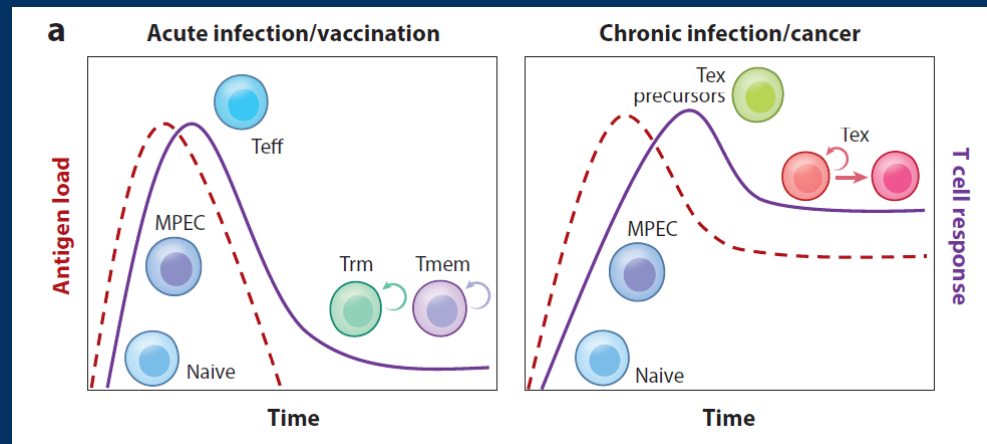


Impossible to dose-optimize (current)-CARTs





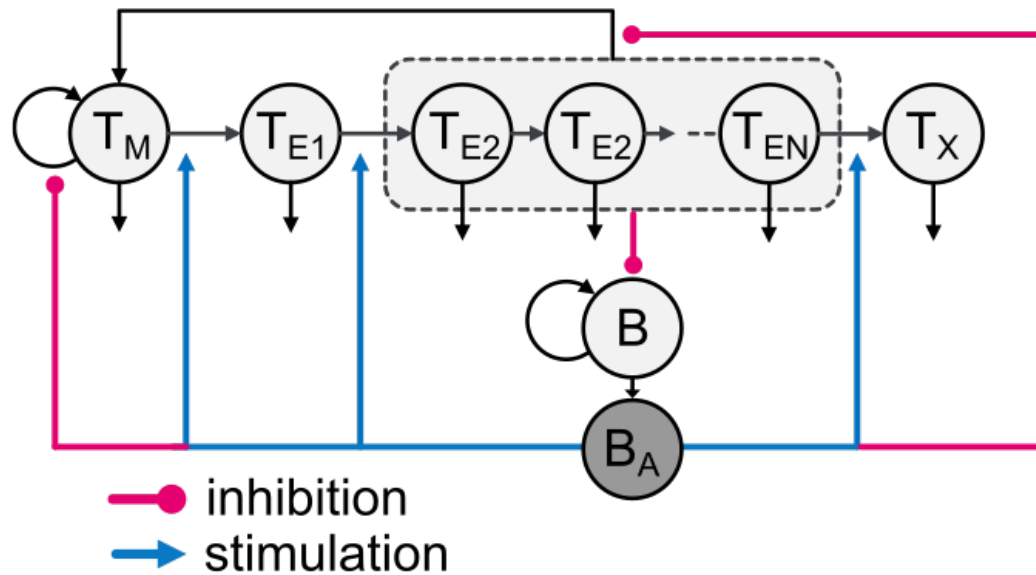
2. What cell-intrinsic properties underly clinical variability and response?



McLane LM, Abdel-Hakeem MS, Wherry EJ (2015) CD8 T Cell Exhaustion During Chronic Viral Infection and Cancer. *Annu Rev Immunol* 37:1–39.

DC Kirouac, C Zmurchok, A Deyati, J Sicherman, C Bond, PW Zandstra. *Deconvolution of clinical variance in CAR-T pharmacology and response.* *Nat Biotech* 2023

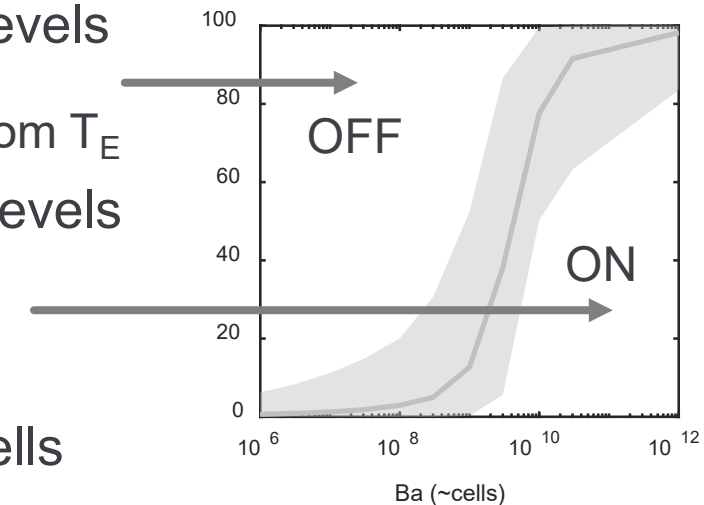
“Toggle switch” model structure and assumptions



- T_M : memory T cells
- T_E : effector T cells
- T_X : exhausted T cells
- B: B cells (tumor)
- B_A : B cell antigen

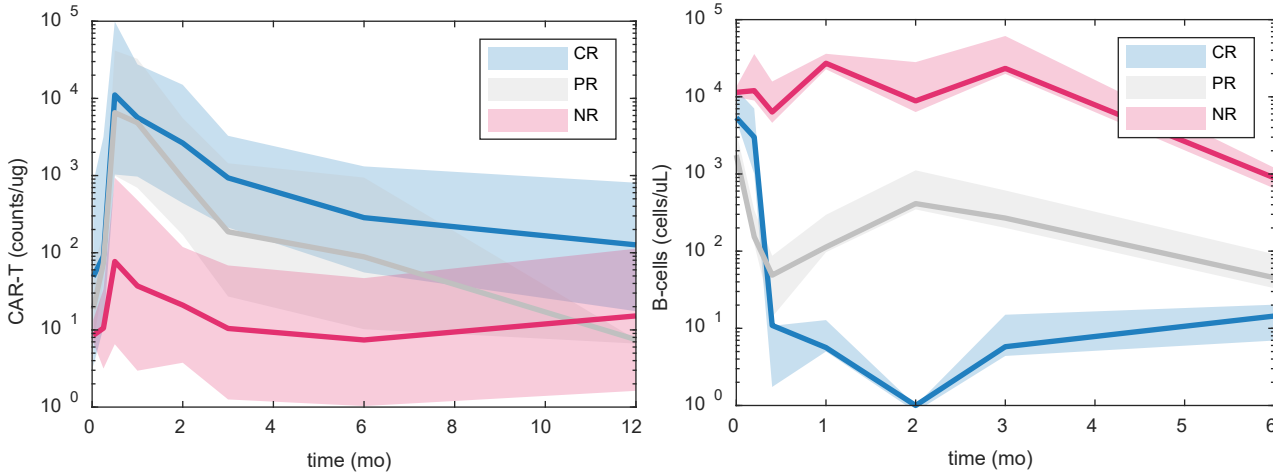
T cell differentiation *toggle switch*

- Low antigen (B_A) levels
 - T_M self-renewal
 - T_M regeneration from T_E
- High antigen (B_A) levels
 - T_M differentiation
 - T_E proliferation
 - T_E exhaustion (T_X)
- T effectors kill B-cells
- N cell divisions within T_E compartment



Model training data: *Kymriah* in Chronic Lymphoblastic Leukemia PKPD profiles, CAR-T product transcriptomes and immuno-phenotypes vs. response

Population mean PKPD: *Kymriah* in Chronic Lymphoblastic Leukemia (CLL)

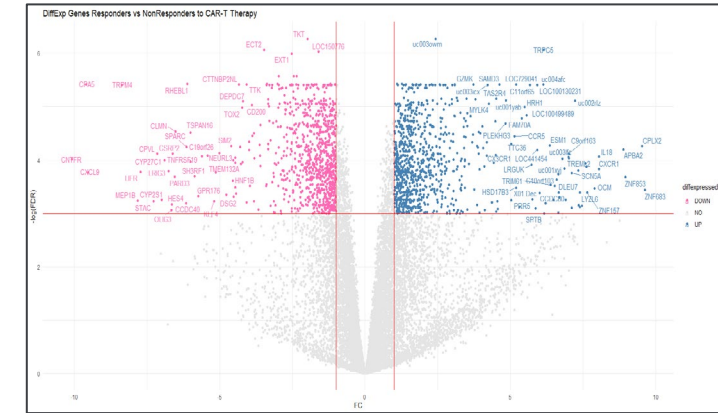


*mean ± std, digitized from publication
CR=8, PR =5, NR=25

CR = Complete Response
PR = Partial Response
NR = Non-Response

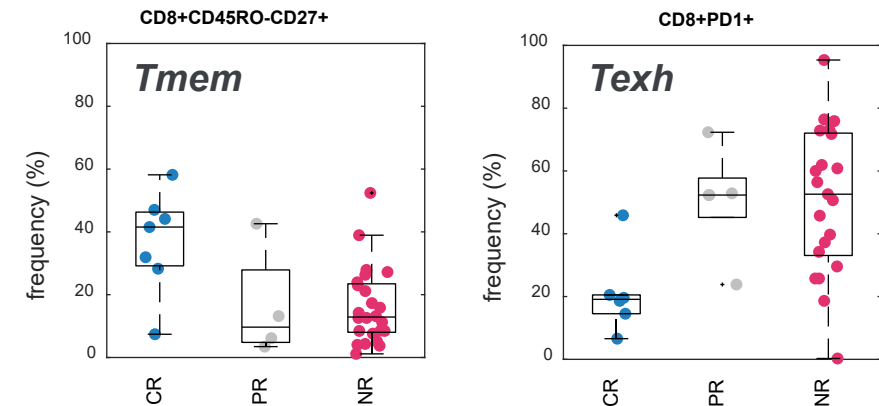
- Can we recapitulate the pharmacokinetics & tumor dynamics (PKPD) based on T cell biology?
- What kinetic parameters / molecular features distinguish robust vs. poor responding patients?

Pre-infusion CAR-T transcriptomes



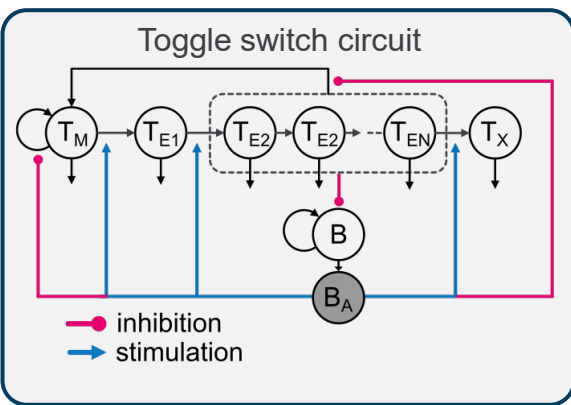
CR=5, PR =5, NR=21

Pre-infusion CAR-T immunophenotype



Model development and validation workflow

Conceptual model of T cell biology



Mechanism-based dynamical model

Math

$$\dot{x} = f(x, y, z, w, v, u, t)$$

$$\dot{y} = g(x, y, z, w, v, u, t)$$

$$\dot{z} = h(x, y, z, w, v, u, t)$$

$$\dot{w} = i(x, y, z, w, v, u, t)$$

$$\dot{v} = j(x, y, z, w, v, u, t)$$

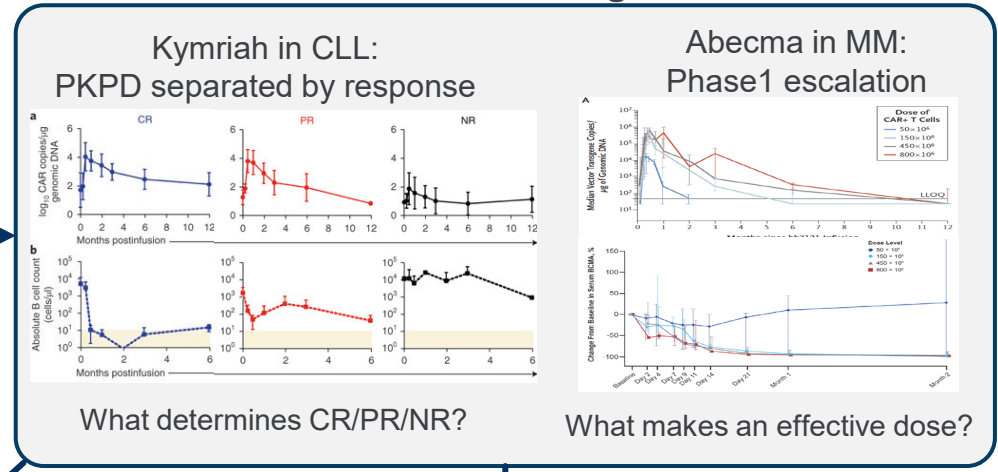
$$\dot{u} = k(x, y, z, w, v, u, t)$$

Executable code

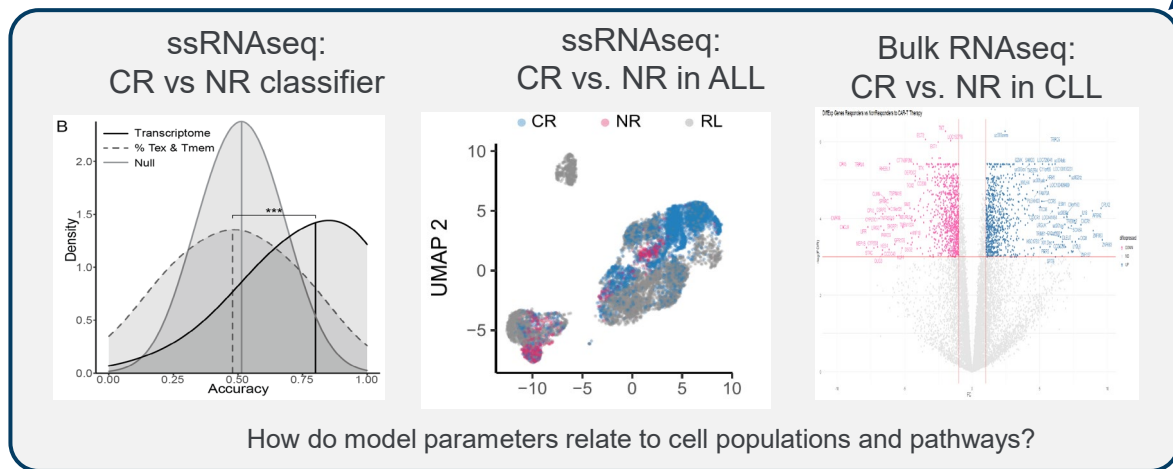
```

%% LOAD MODEL
mk = absolute_path('MPEPD_v3'); % loads MAPP project as 'mk'
model = mk.m;
Param_table = readtable('MPEPD_v3_ParameterTable.csv');
Param_table.Properties.VariableNames(1) = 'NAME';
Param_table.CLASS = categorical(Param_table.CLASS); %converts cell
Param = Param_table.NAME; %pulls out names as cell array
Fobservariables = Param_table.NAME(Param_table.CLASS=='SPECIES');
Param_table.NAME = categorical(Param_table.NAME);
Fobser = {'dose'}; %define which species may be dosed
test_maximum_sim_time = 500;
configureObj = optionsObj(model);
set(configObj, 'MaximumWallClock', 1); %test maximum time to run
set(configObj.SolverOptions, 'RelativeTolerance', 1e-6); %set
set(configObj.SolverOptions, 'AbsoluteTolerance', 1e-7); %set
convert into function handle
F = createSimFunction(model, Param, Fobservariables, Fobser);
% PACK into structure
OD_fit_pops = fit_pops;
OD_data = data;
OD_MODEL = F;
OD_Param_table = Param_table;
OD_cell_dose = cell_dose;
OD_BO = BO;
OD_scaling_factor = scaling_factor;
% RUN
[MSR_sim_output] = MPEPD_v3_P00_Faetta_OD(F, OD, OD);
MSR_output = MSR_output.MSR_output;
Four = sim_output.Four
                    
```

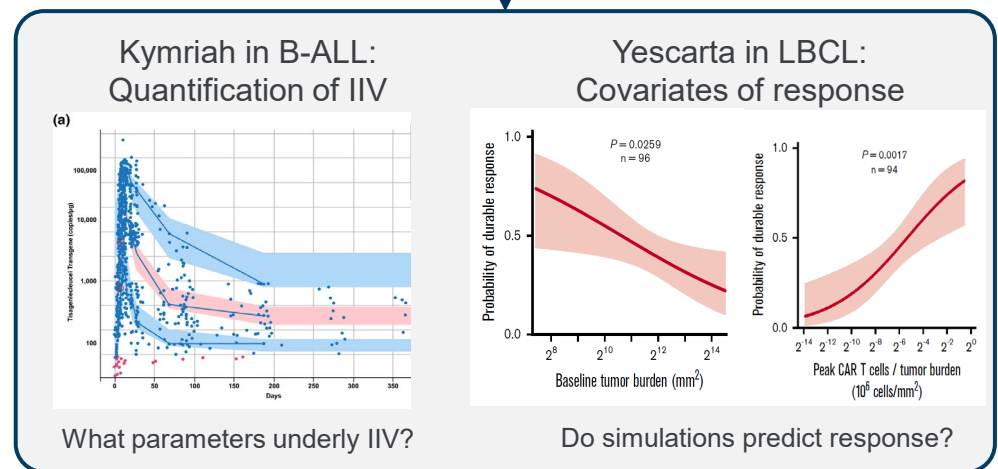
Clinical Training Data



Genomic "Validation" Data



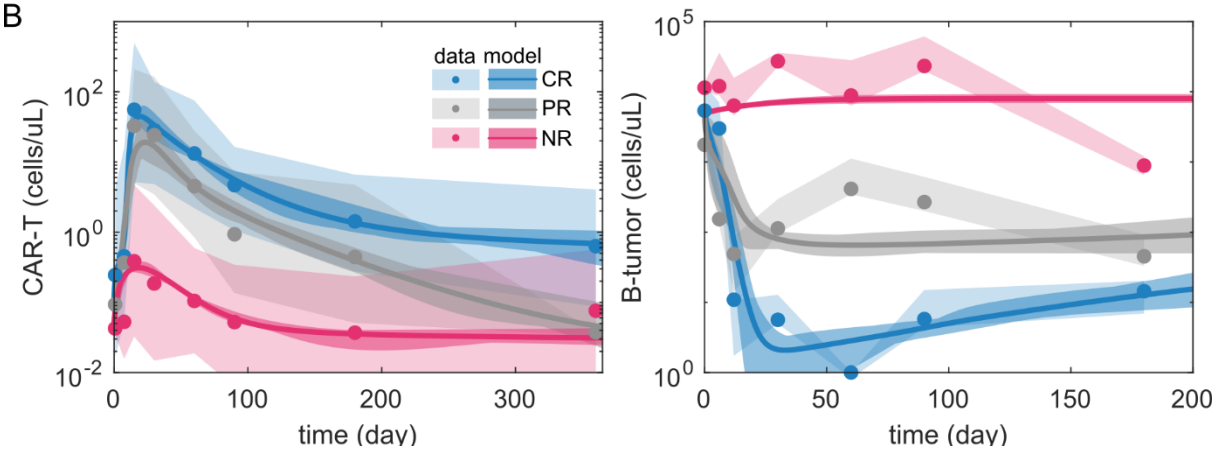
Clinical Validation Data



Model calibration & analysis

What features (model parameters) separate clinical outcomes?

Model calibration

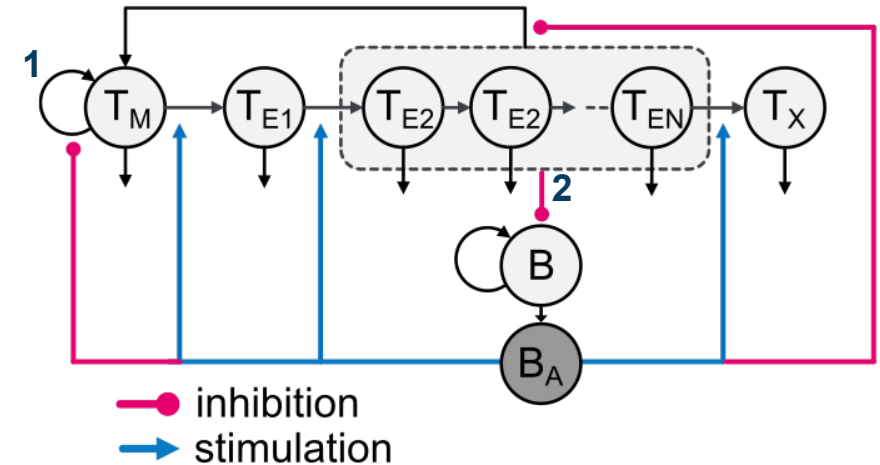
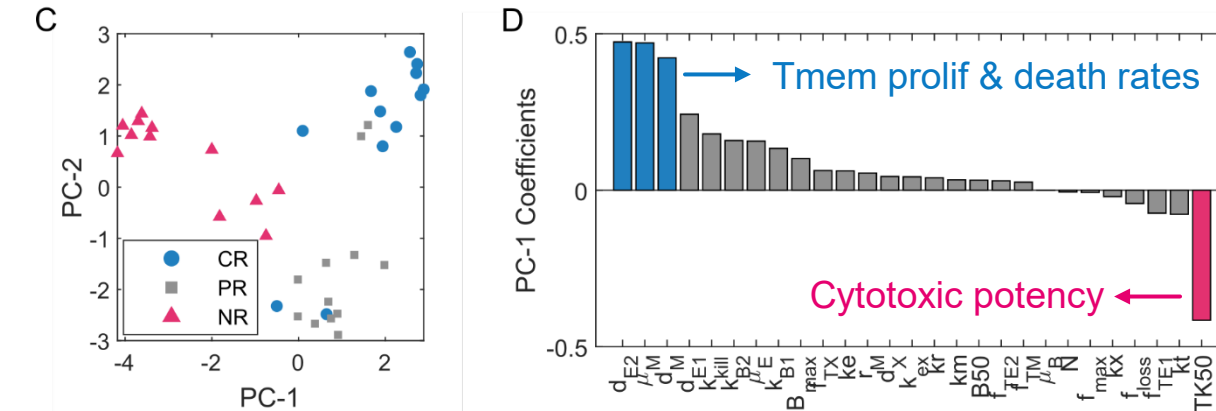


What differentiates CR vs. NR ?

CAR-T products in CR vs. NR show:

1. Heightened memory cell turnover (μ_M, d_M)
2. Heightened cytotoxic potency ($TK50$)
3. Little difference in Tmem/Texth frequency

Parameter Analysis



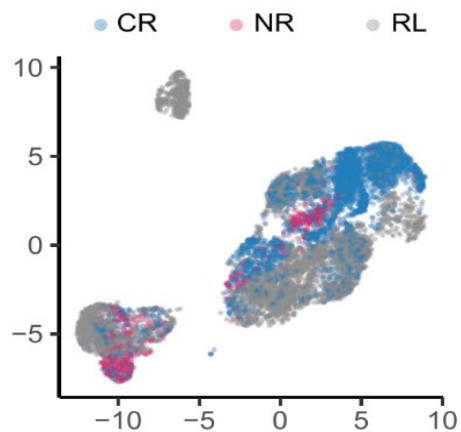
*Assume Dose = 10^8 cells, Tumor burden = 10^{10} cells (median reported); Estimate parameters using PSO: simulations represent 90% confidence intervals

'Validation' of model inferences via single-cell transcriptomes

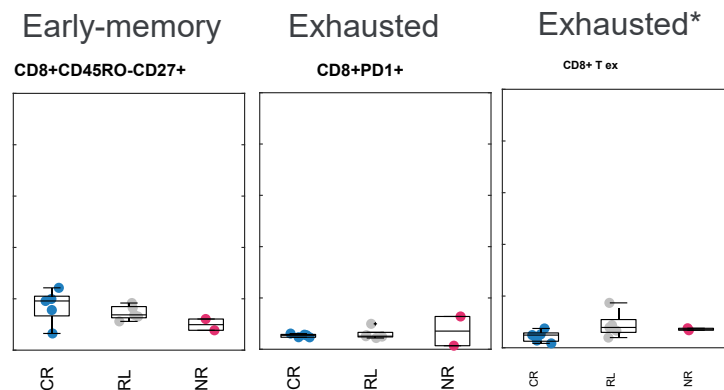
Mathematical inferences assessed in an additional blood cancer: Acute Lymphoblastic Lymphoma

T cell composition (memory vs. exhausted cells) does not substantially vary by response category

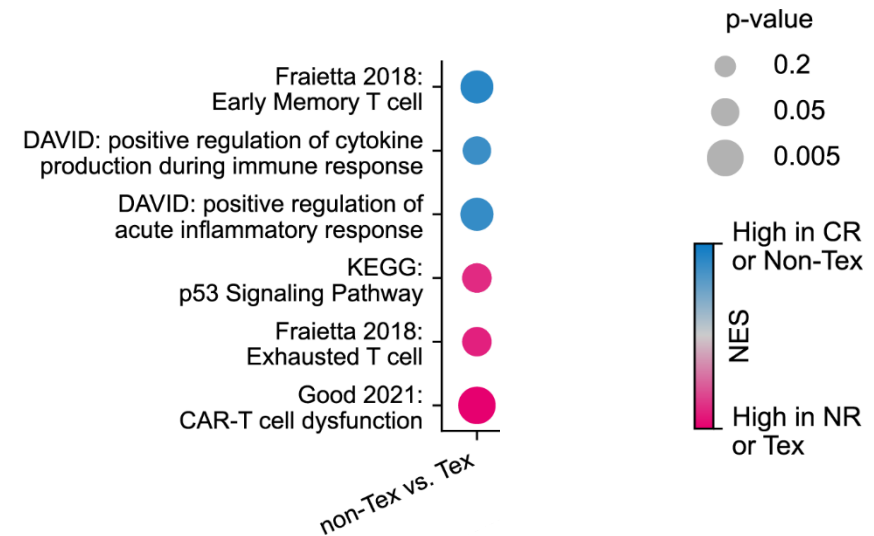
scRNAseq: Kyrmiah in ALL annotated by Response



T cell population frequencies by response category



Cell-intrinsic differences



***ProjecTILS annotation:** Andreatta M, Corria-Osorio J, Müller S, et al (2021) Interpretation of T cell states from single-cell transcriptomics data using reference atlases. Nat Commun 12:2965.

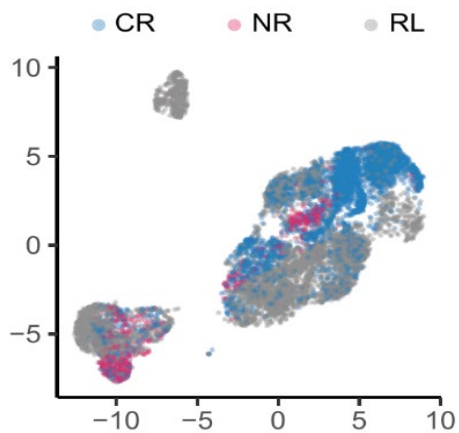
CART Dysfunction: Good CR, Aznar MA, Kuramitsu S, et al (2021) An NK-like CAR T cell transition in CAR T cell dysfunction. Cell.

'Validation' of model inferences via single-cell transcriptomes

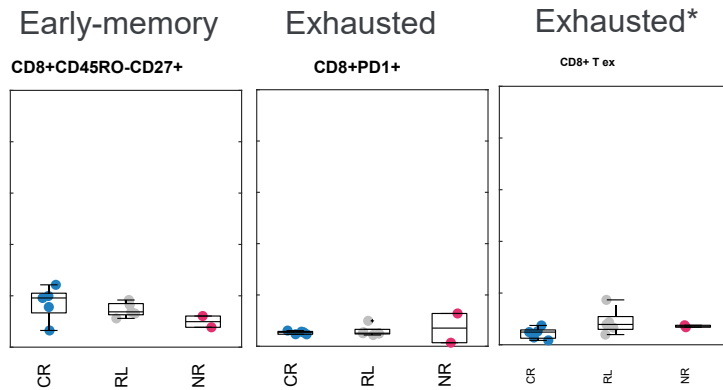
Mathematical inferences assessed in an additional blood cancer: Acute Lymphoblastic Lymphoma

T memory cells from NR patients display intrinsic functional deficits analogous to T cell exhaustion

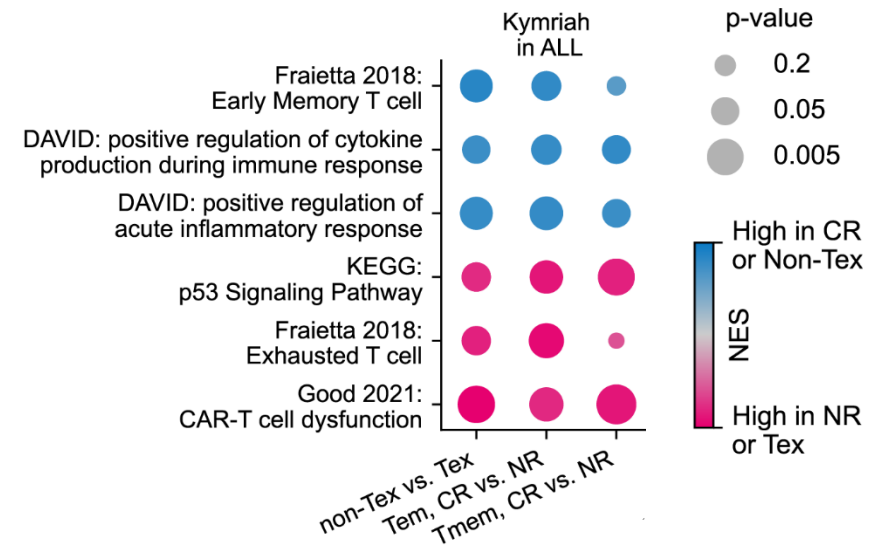
scRNAseq: Kymriah in ALL annotated by Response



T cell population frequencies by response category



Cell-intrinsic differences



***ProjectTILS annotation:** Andreatta M, Corria-Osorio J, Müller S, et al (2021) Interpretation of T cell states from single-cell transcriptomics data using reference atlases. Nat Commun 12:2965.

CART Dysfunction: Good CR, Aznar MA, Kuramitsu S, et al (2021) An NK-like CAR T cell transition in CAR T cell dysfunction. Cell.

Tem, Tmem cells from NR samples appear functionally exhausted

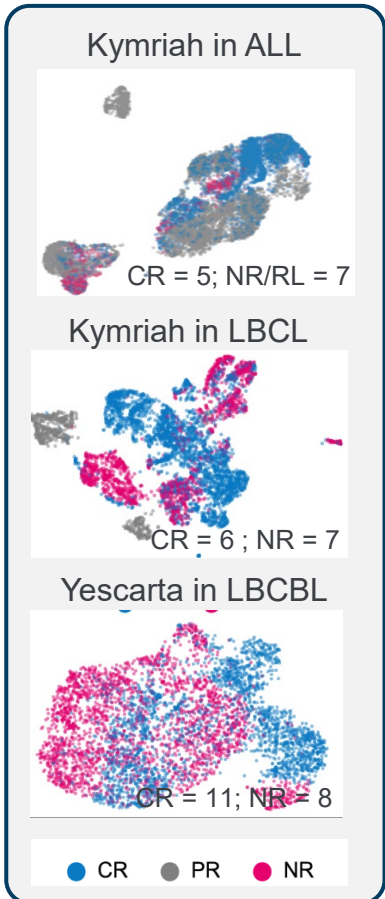
***Tem:** defined via ProjectTILS algorithm

***Tmem:** defined via CD8+CD45RO-CD27+ CITEseq tags

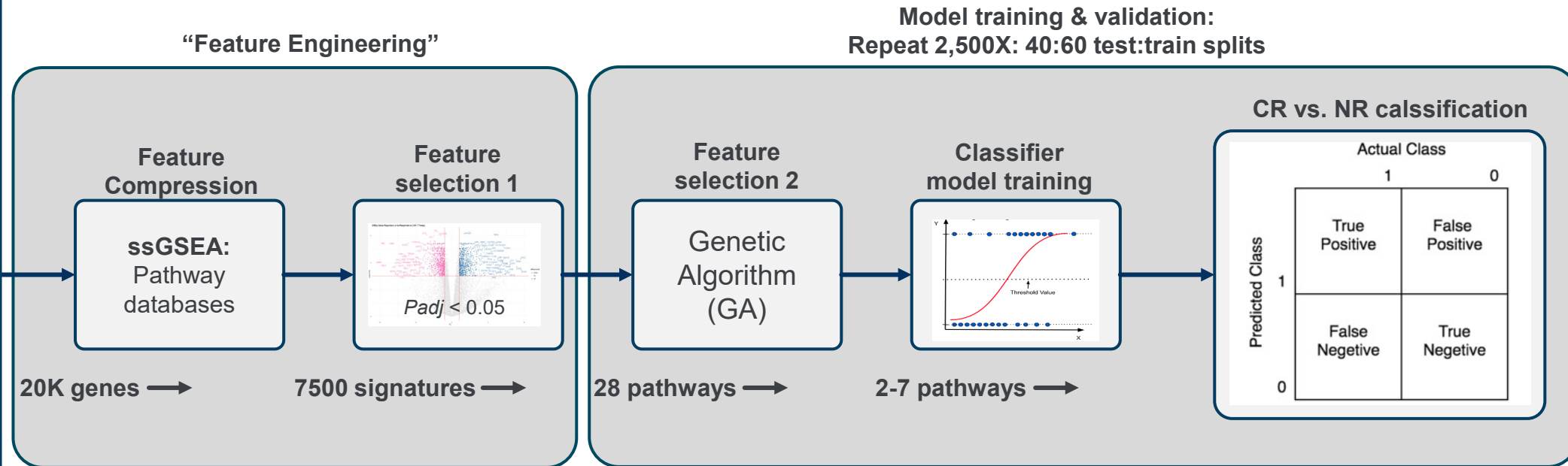
CAR-T clinical response prediction

Are pre-infusion CAR-T transcriptomes predictive of clinical response (CR vs. NR)?

scRNAseq pre-infusion CAR-Ts
CR/NR/PR classes



Machine learning workflow



$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

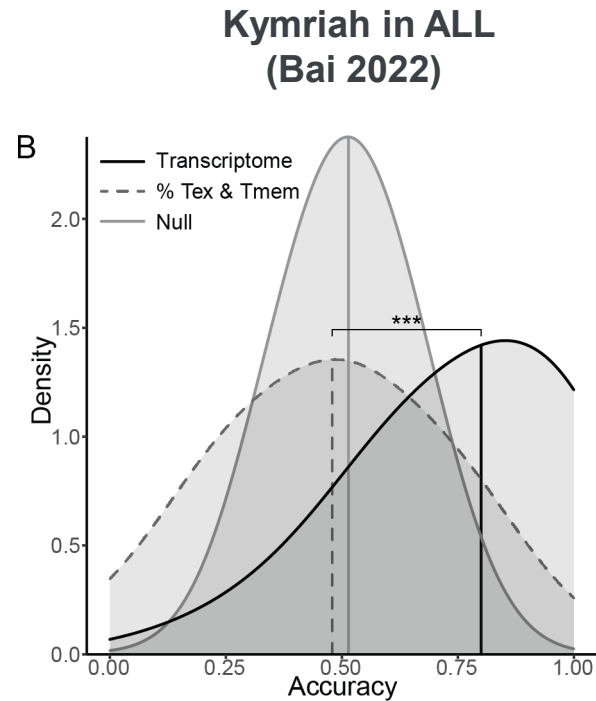
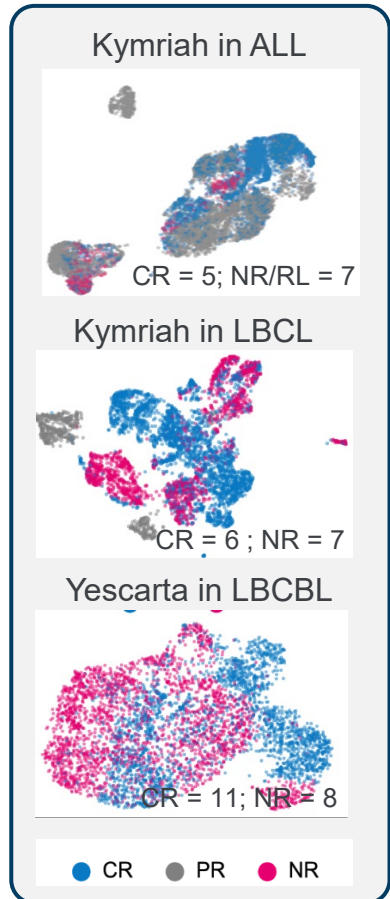
Lage P, small N problem: the central challenge in biomedical genomics

CAR-T clinical response prediction

Are pre-infusion CAR-T transcriptomes predictive of clinical response (CR vs. NR)?

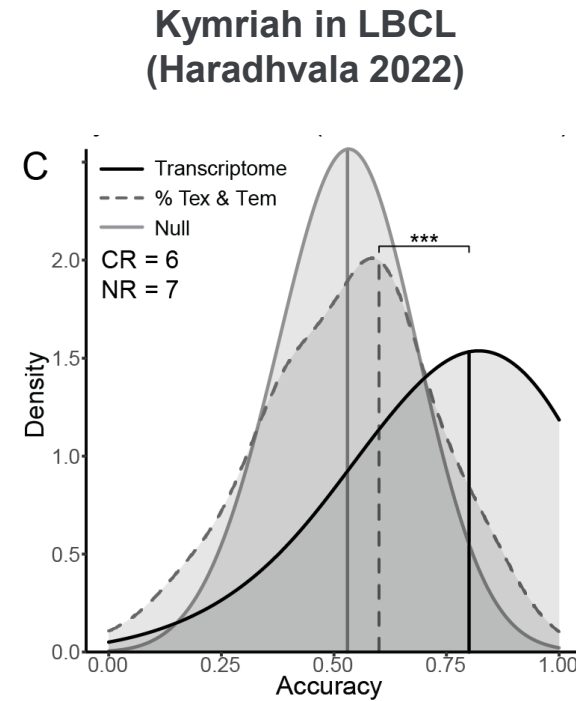
Predictive accuracy of response classification using 60:40 train:test splits

scRNAseq pre-infusion CAR-Ts
CR/NR/PR classes

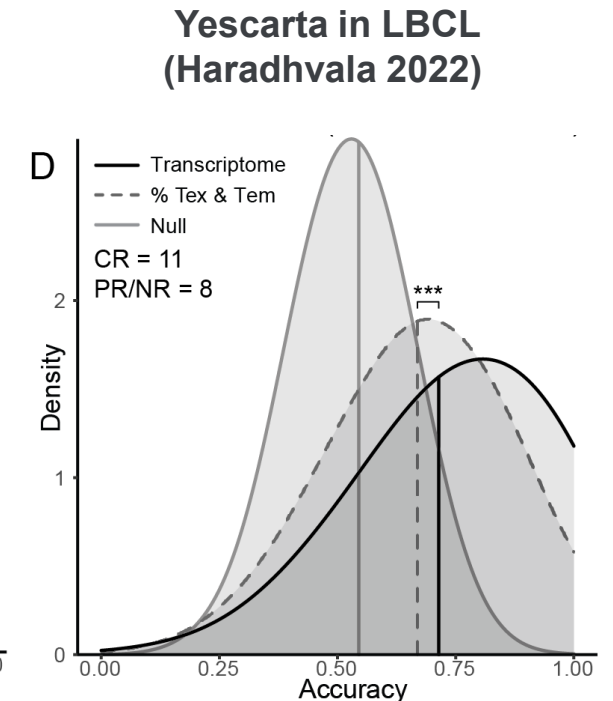


Accuracy = 80%
Tmem, Tex: CITESeq data
CR = 5; NR/RL = 7

*** $P < 10^{-8}$ (rank-sum test)



Accuracy = 80%
Tmem, Tex: ProjectTILS*
CR = 6; NR = 7



Accuracy = 71%
Tmem, Tex: ProjectTILS
CR = 11; NR/PR = 8

Functional attributes predictive of clinical outcomes are CART-cell-intrinsic & indication-agnostic
Transcriptome > 'gold standard' immunophenotyping

CAR-T clinical response prediction

What transcriptional signatures are predictive of CAR-T response?

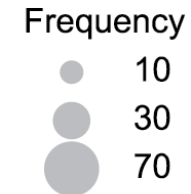
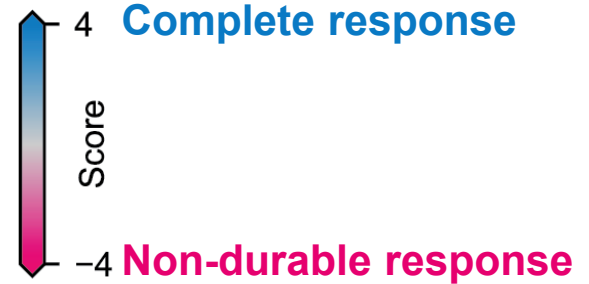
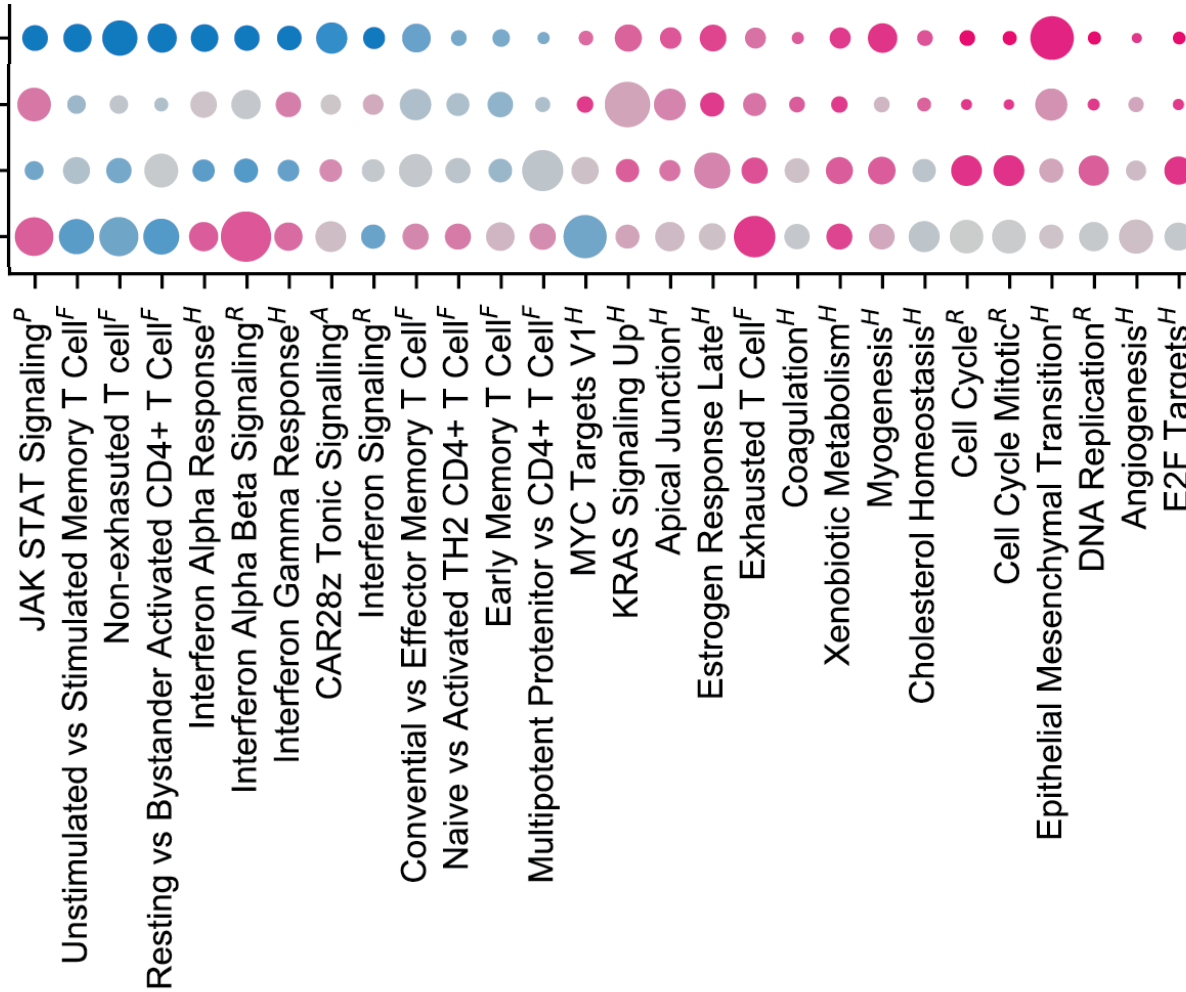
CAR-T Response Score-card

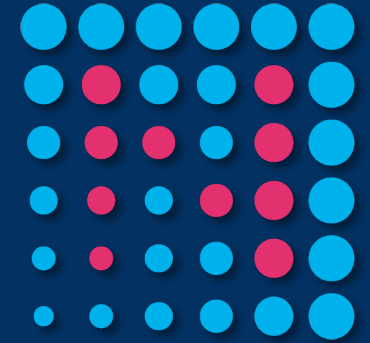
Accuracy

90%
80%
80%
71%

Kymriah in CLL
Kymriah in ALL
Kymriah in LBCL
Yescarta in LBCL

P: PROGENy
F: Fraietta 2018
H: Hallmark
R: Reactome
A: Albert 2018





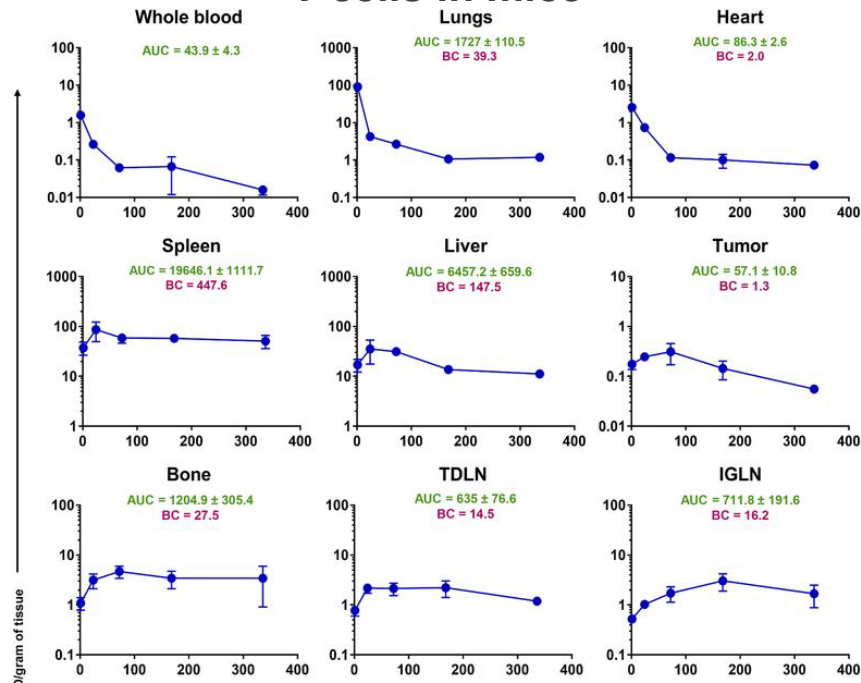
3. Patient-intrinsic factors mediating response

- A. T cell biodistribution
- B. Tumor Inflammation
- C. Response to Lympho-depletion & host-T cell competition
- D. Host vs. Graft response (allogeneic elimination)

3A. Adoptive T cell Biodistribution

Where do CAR-Ts go once administered? What happens in tissues vs. Blood?

Pharmacokinetics & biodistribution of radio-labelled T cells in mice

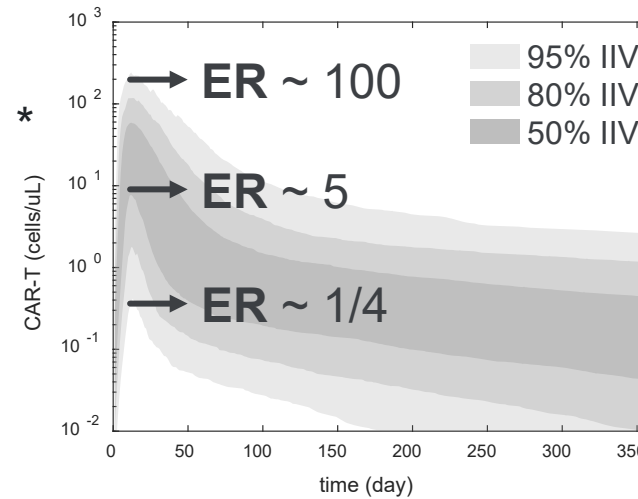


***BC** = Biodistribution Coefficient.
= AUC of T cells in tissue vs. blood

Majority of administered T cells distribute to lungs, spleen, liver, kidney & lymph nodes.

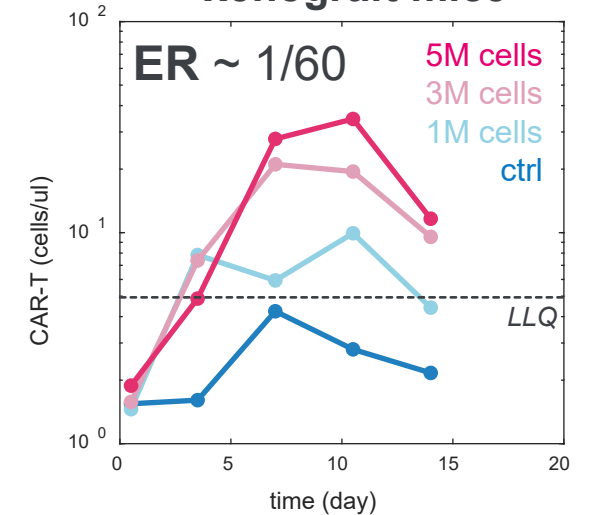
Pharmacology 'accounting' in man vs. mouse

Kymriah in B-ALL



***ER** = Expansion Ratio. How many cells do you detect at Cmax per infused?
= $C_{max} \cdot V_{blood} / \text{Dose}$

Kymriah in NALM6 xenograft mice

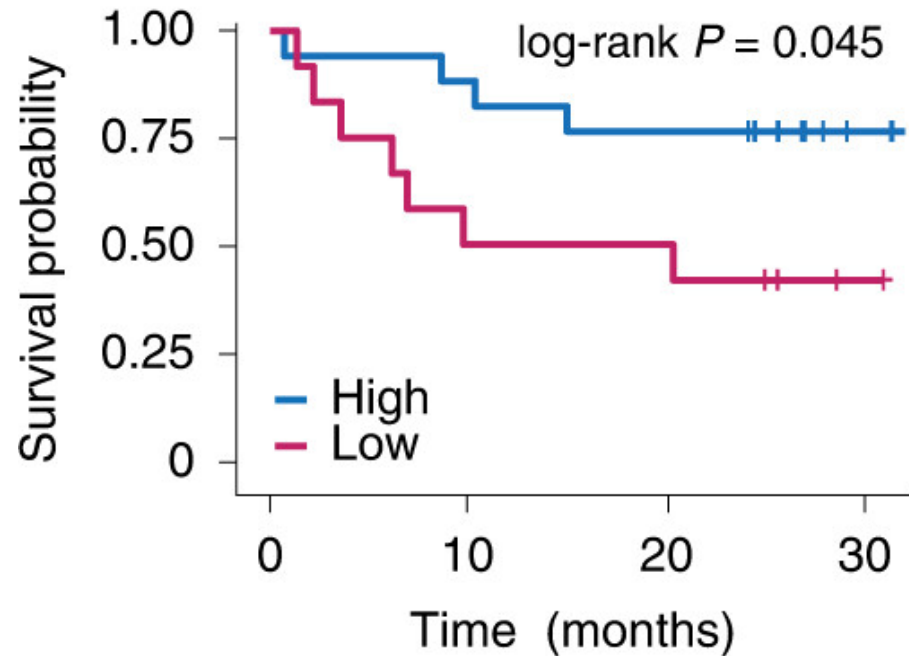


Q: Where do the majority of CARTs distribute
Q: Where does the 'action' happen (tissue vs. blood)?

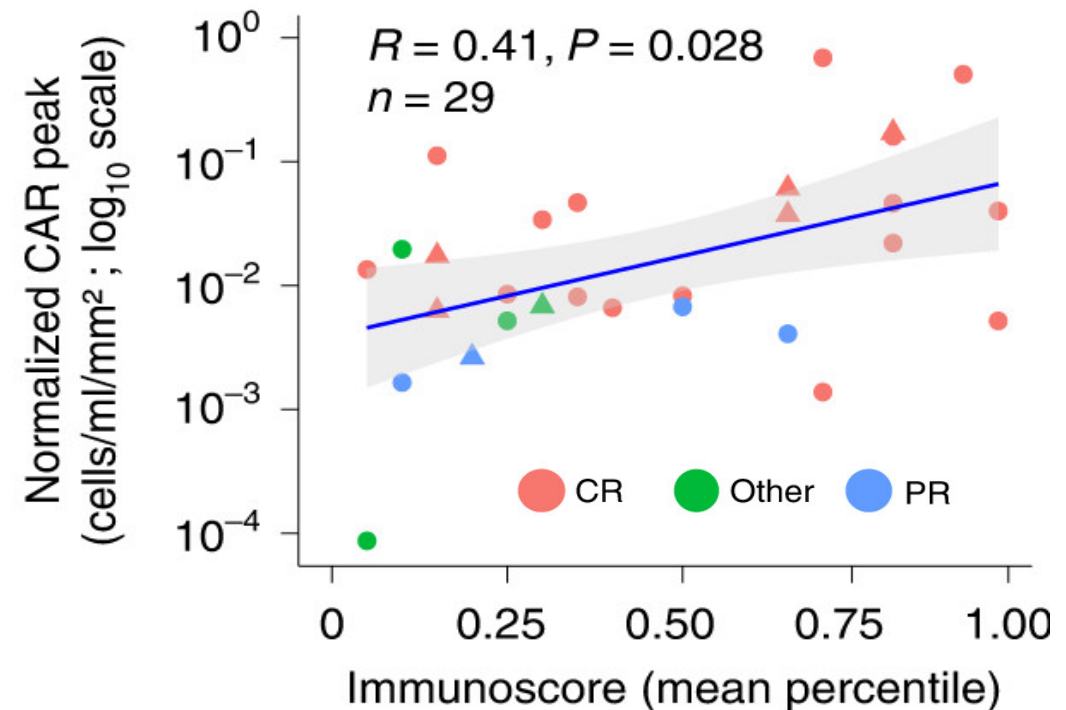
3B. Tumor inflammation and CAR-T response

Yescarta (CD19-CAR-T) in DLBCL: ZUMA-1 trial

'Immunoscore' (Tumor inflammation) is the most significant patient-intrinsic predictor of CAR-T response



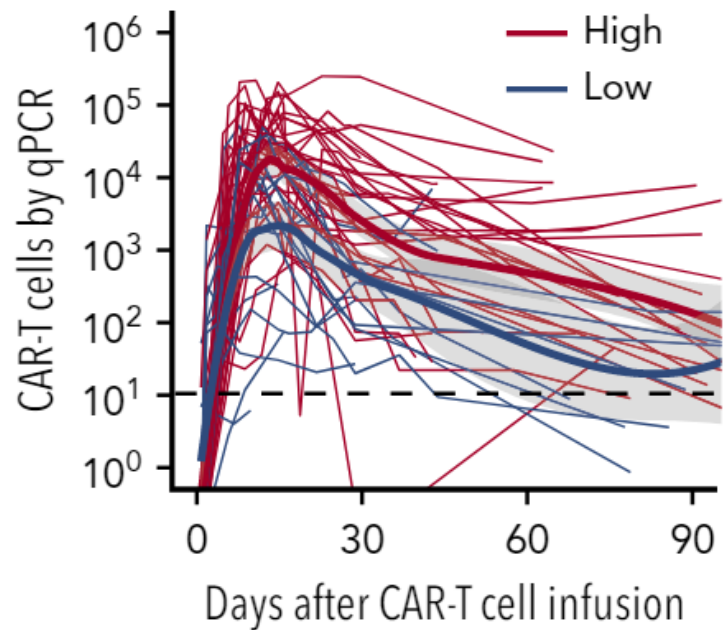
Immunoscore (Tumor inflammation) also drives Cmax



Q: How would pre-existing TILs influence CAR-T expansion?

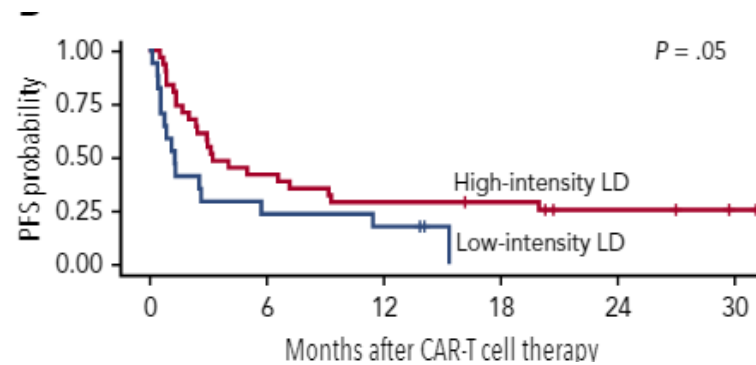
3C. Lympho-depletion intensity & response via IL7 availability?

Lymphodepletion intensity drives CART expansion

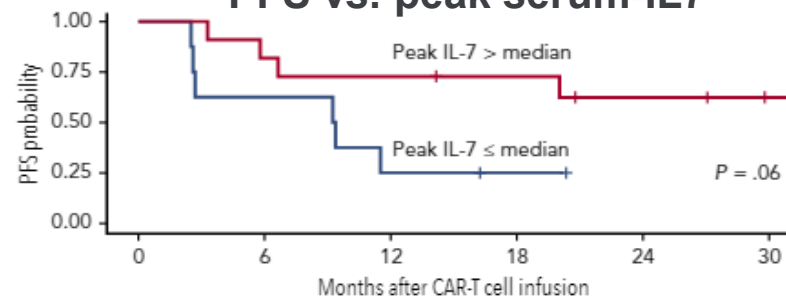


*60 vs. 30 mg/kg cyclophosphamide, CD19 CART therapy in NHL

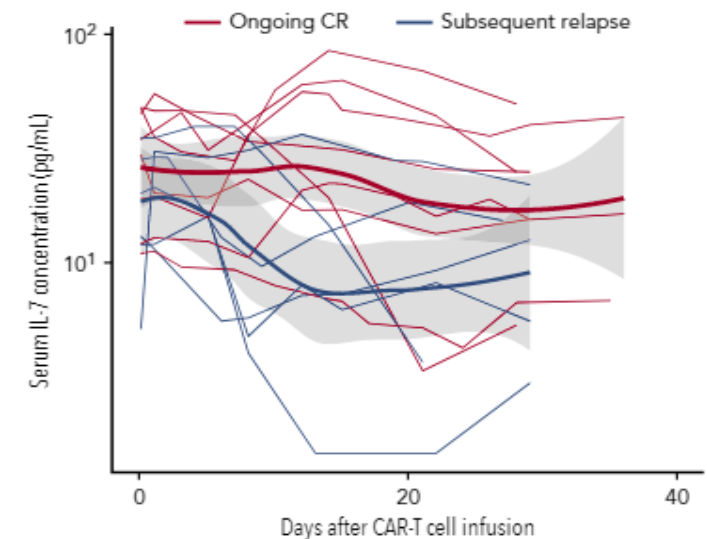
PFS vs. lymphodepletion



PFS vs. peak serum-IL7



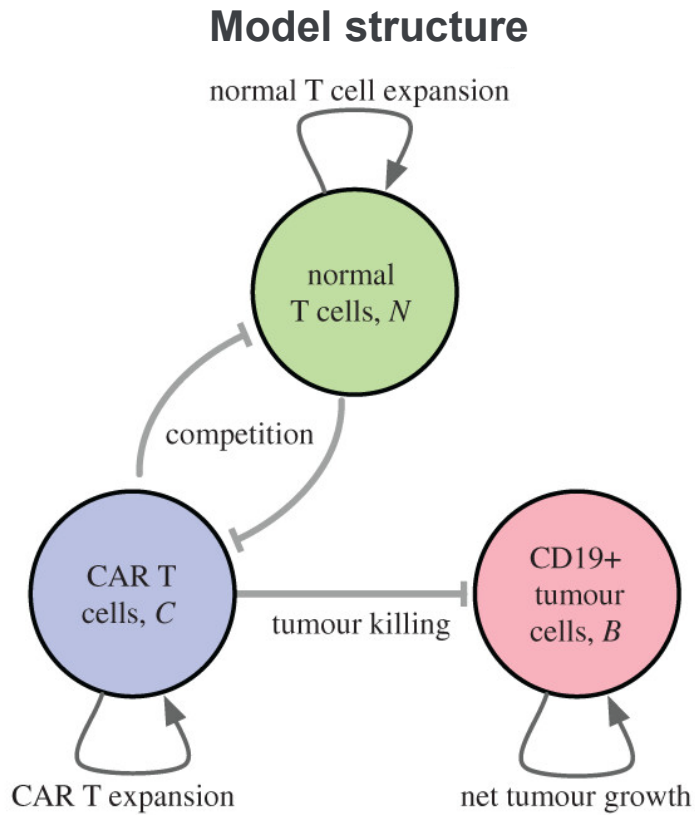
Lymphodepletion intensity drives IL7 expression



Q: How does Lympho-depletion intensity affect CART-T expansion and peak IL7 concentration?

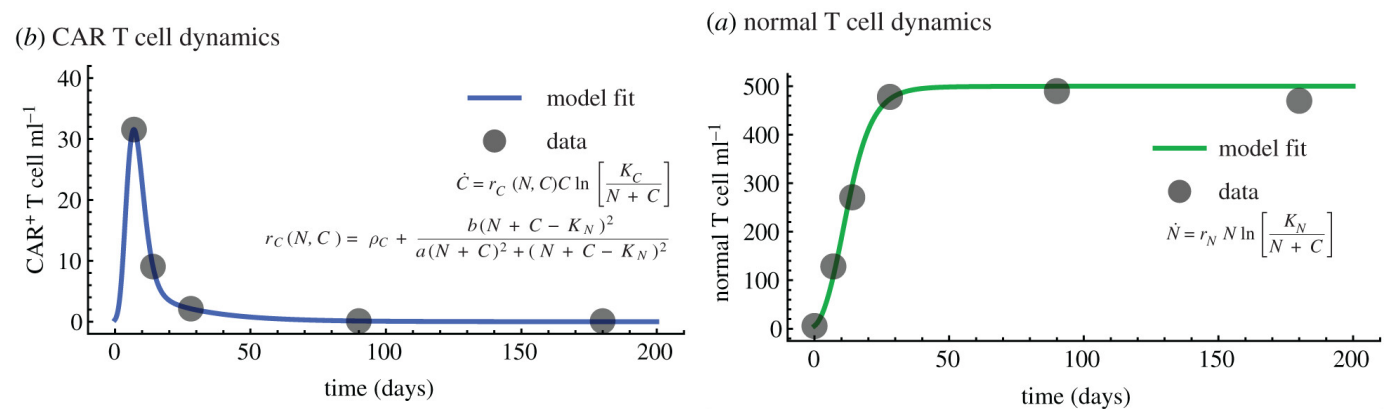
Q: Can we *mimic* intense-LDT via cytokine support?

Competition between Adoptive vs. Patient T cells

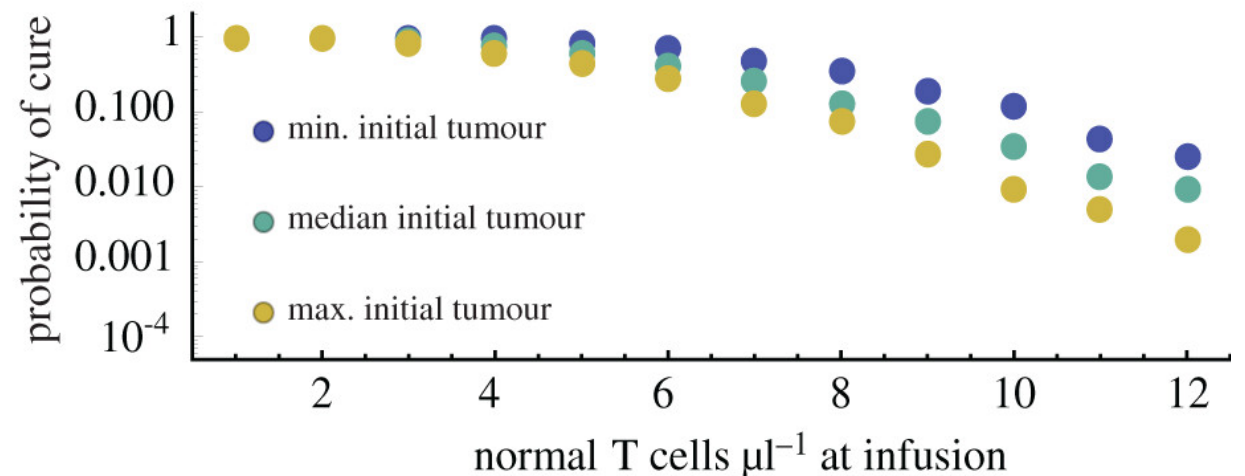


Q: What is the mechanism underlying T cell competition for limited 'space'?

Model fitting: Yescarta in LBCL (ZUMA-1) CAR-T and Host-T cell kinetics



Model simulations: Response vs. Tumor burden & LDT depth

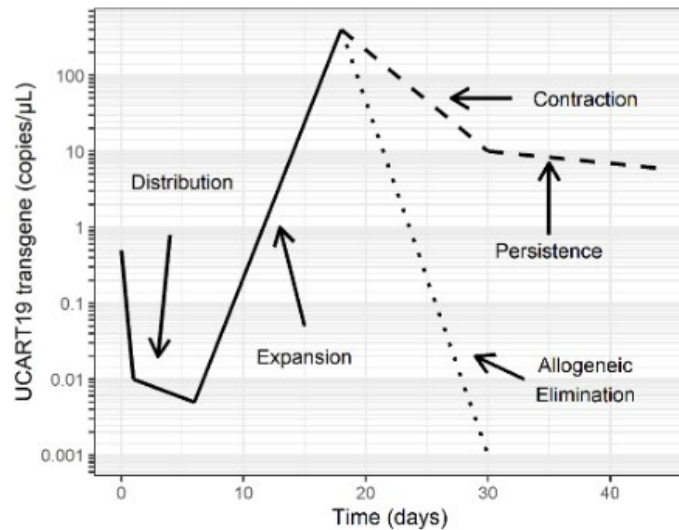


3D. Host vs. Graft response (allogeneic elimination)

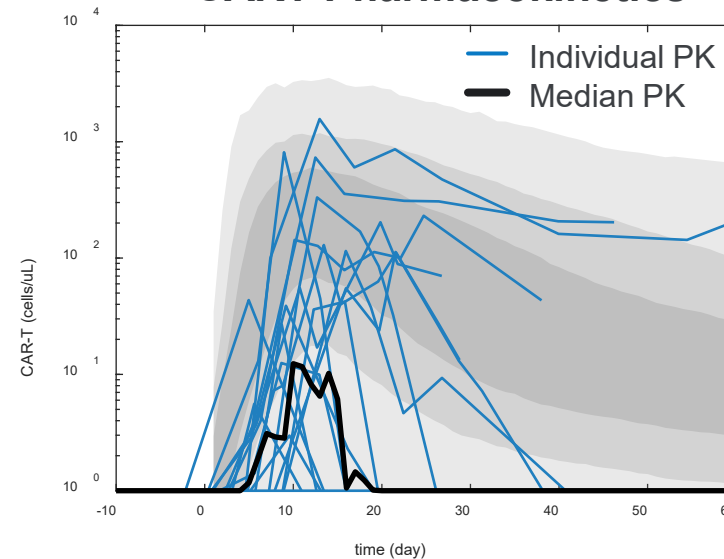
Host T cells actively clear (allogenic) T cell grafts

UCART19 in B-ALL: The first reported allogeneic CAR-T clinical data
CD19-CART, allogeneic (healthy donor-derived) T cells, *TRAC^{-/-}*

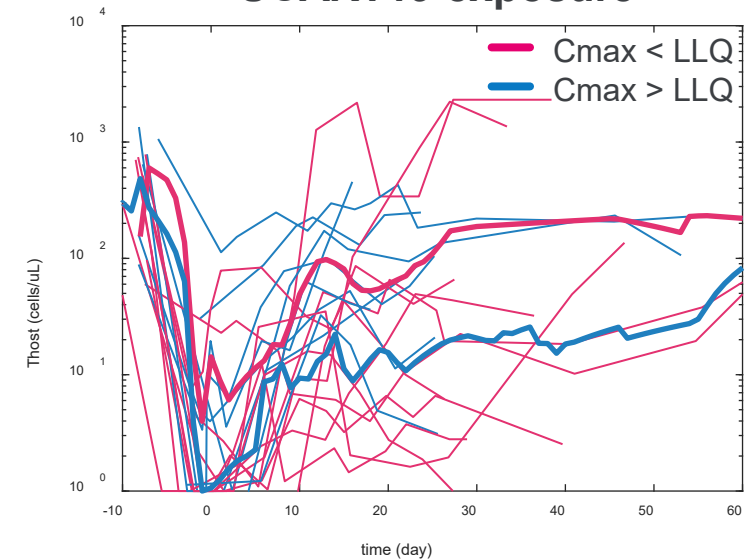
Allogeneic Elimination



UCART19 vs. Kymriah CART Pharmacokinetics



Host T cell reconstitution ~ UCART19 exposure



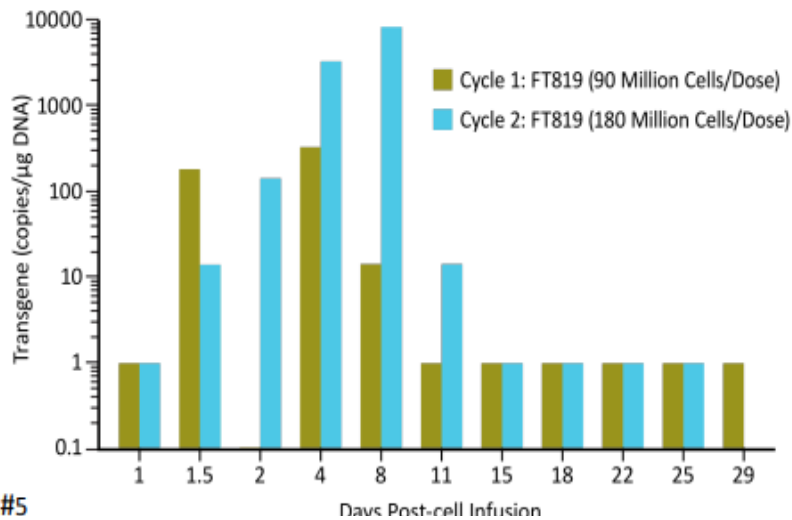
- Deeper LDT & slower T cell reconstitution ~ greater allogeneic CART exposure
- Q: How would additional gene edits (i.e. MHC-knock out) affect allo-clearance rates

Data digitized from: Derippe T, Fouliard S, Marchiq I, et al (2022) Mechanistic modeling of the interplay between host immune system, interleukin 7 and UCART19 allogeneic CAR-T cells in adult B-cell acute lymphoblastic leukemia. *Cancer Res Commun* 2:1532–1544.

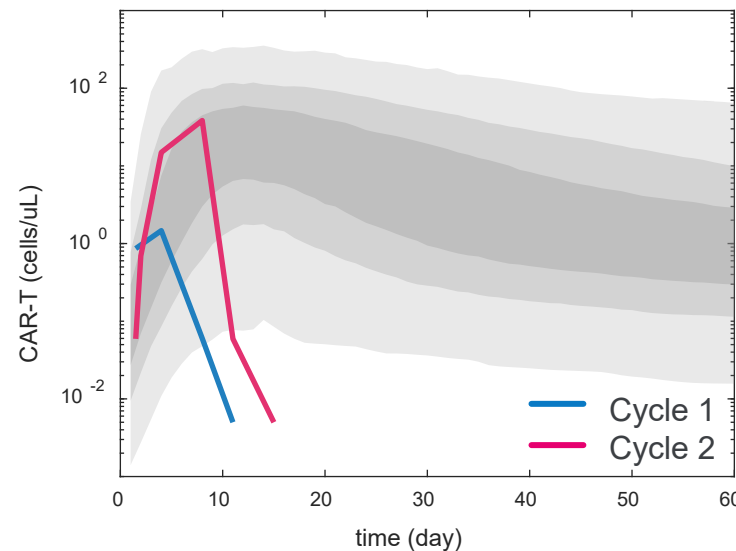
The next frontier: iPSC-derived CAR-Ts

FT819: The first reported clinically tested iPSC-derived CART CD19-CART, allogeneic (iPSC-differentiated) T cells, *TRAC*^{-/-}

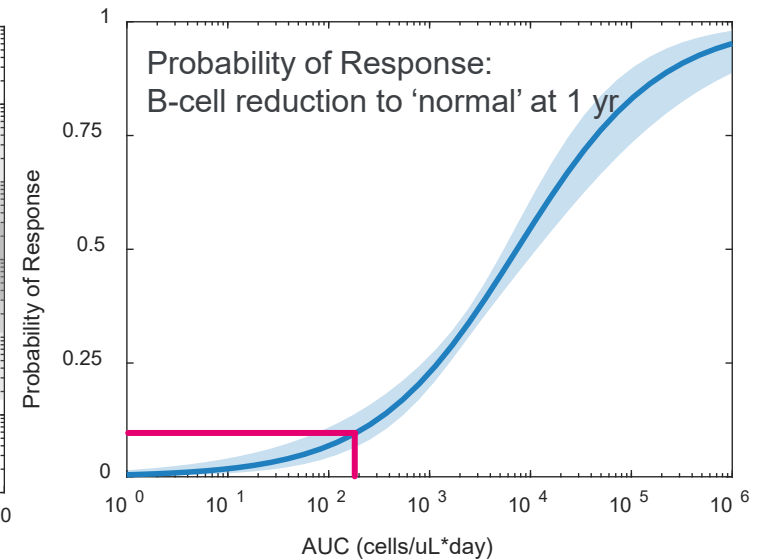
PK data digitized from ASH poster
*n=1 patient



FT819 vs. Kymriah
CART Pharmacokinetics



AUC vs. Durable Response



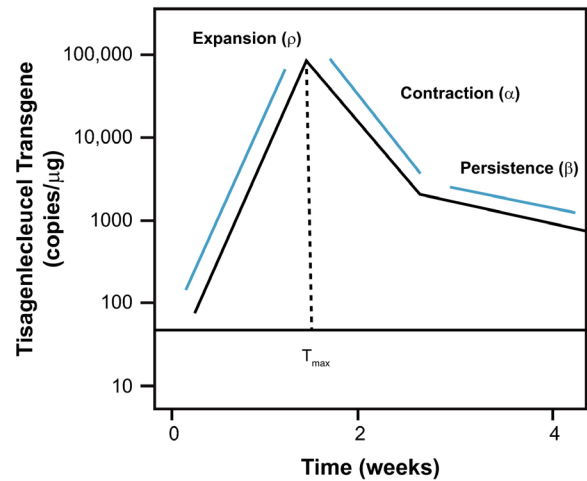
- Both robust cell expansion + persistence (AUC) is required for clinical activity

Q: Why are (FT819) iPSC-CARTs incapable of persistence - *Cell intrinsic* deficit vs. *allogeneic*-clearance?

Summary

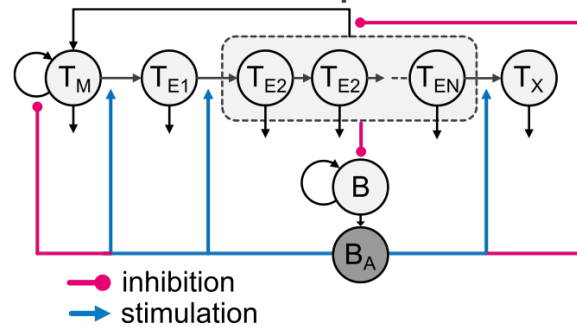
1. Empirical PKPD models

- Cmax predicts response
- High variability makes dose-optimization infeasible



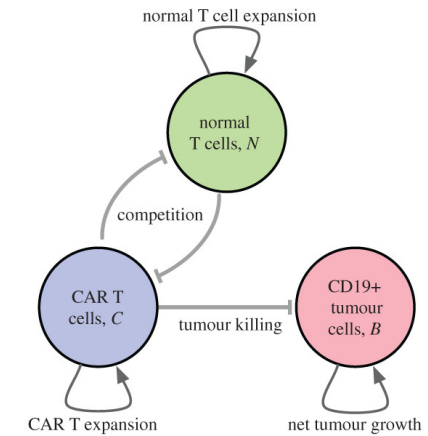
2. Mechanistic modelling & machine learning

- Product intrinsic-proliferation of memory cells is important for clinical response
- Predictive features are buried in CART transcriptomes



3. Patient-intrinsic effects

- Biodistribution, inflammatory state, lympho-depletion response, and Host vs Graft affect PK and response



Mathematical models can enable CAR-T design, optimization and data interpretation
Quantitative data is required to translate measurements to kinetic parameters

Thank You!



Vancouver, BC

- ✓ Developmental immunology
- ✓ Systems Biology and T cell pharmacology



Seattle, WA

- ✓ Protein and genome engineering
- ✓ Translational sciences
- ✓ Cancer biology

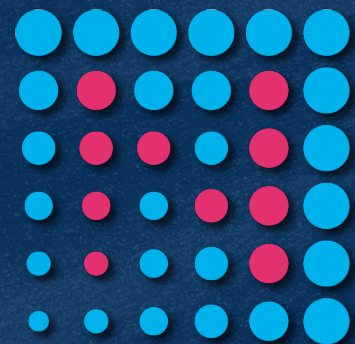


Toronto, ON

- ✓ GMP iPSCs and gene editing
- ✓ T cell manufacturing
- ✓ QA/QC

Avisek Deyati,
Jordan Sicherman
Cole Zmurchok
Peter Zandstra,
Chris Bond,
Gregory Block
Irja Elliott Donaghue

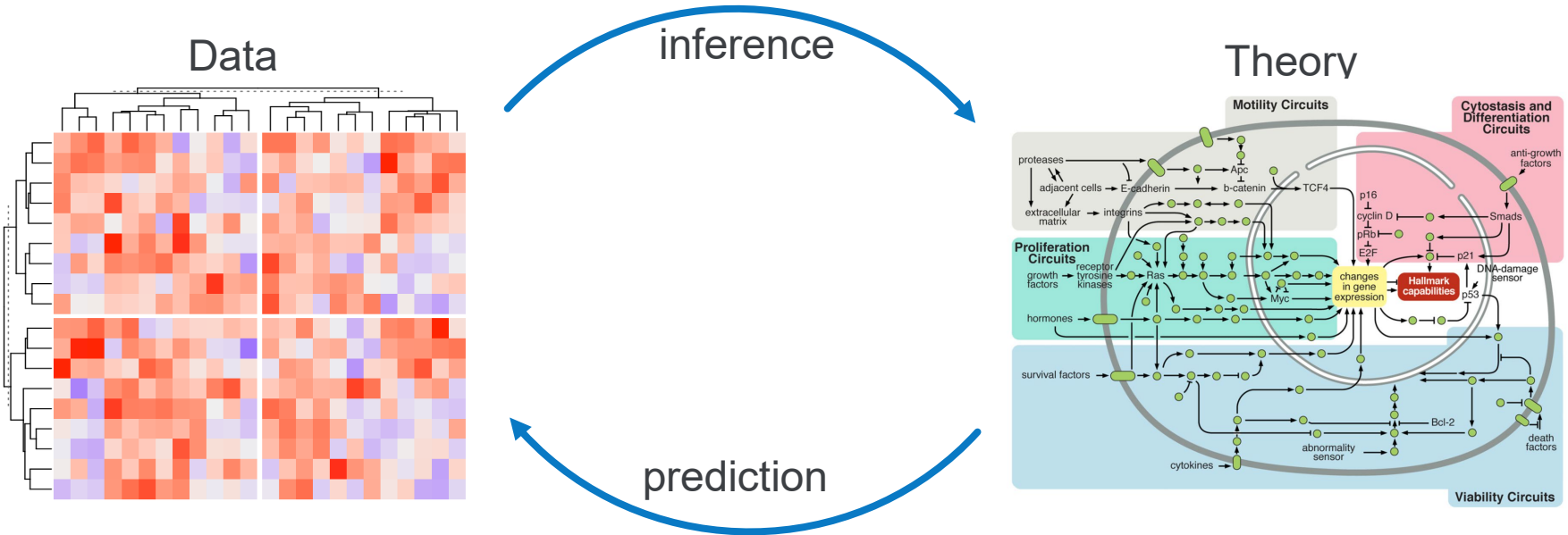




Notch
THERAPEUTICS

What value does modelling bring to drug development?

The biological mechanisms underlying experimental data are often complex and non-intuitive



The number of possible experiments to conduct is infinite

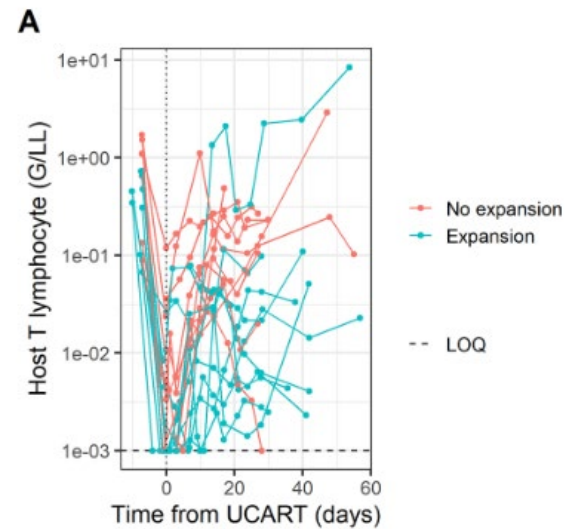
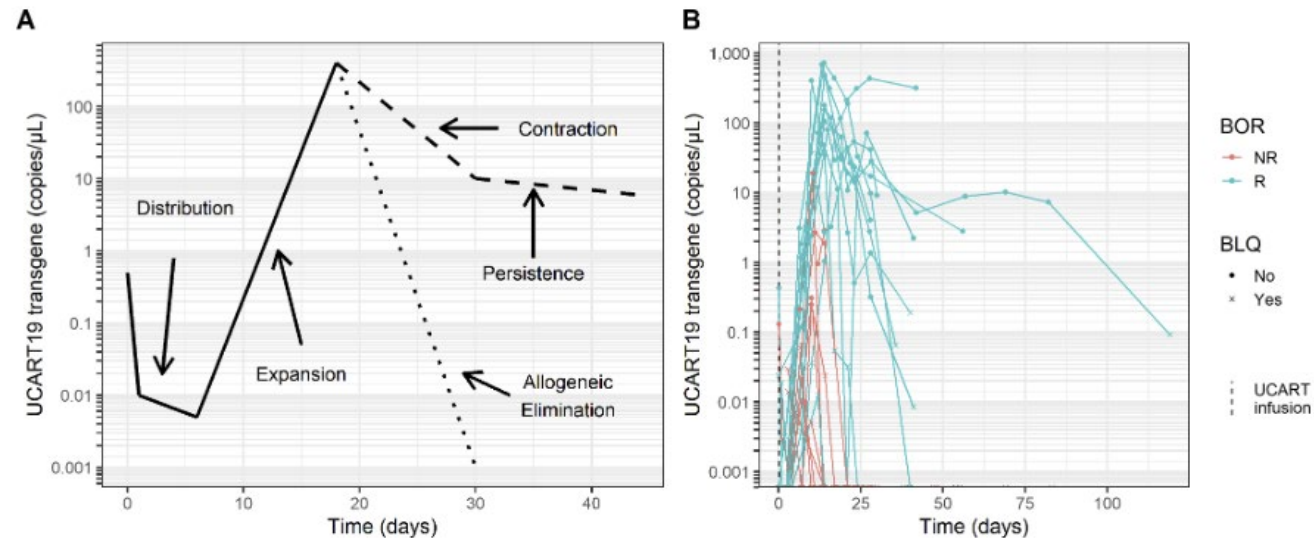
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 CD19-CART, allogeneic (healthy donor-derived) T cells, *TRAC^{-/-}*

C_{max} predicts response

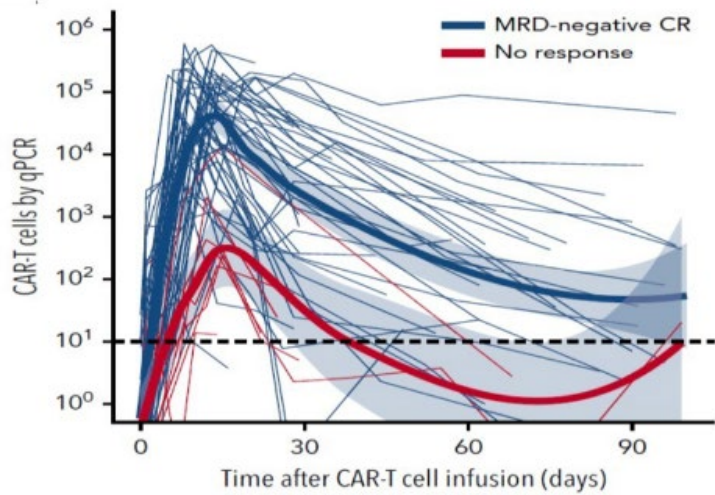
Host T cell reconstitution limits CAR-T expansion



Dupouy S, Marchiq I, Derippe T, et al (2022) Clinical Pharmacology and Determinants of Response to UCART19, an Allogeneic Anti-CD19 CAR-T Cell Product, in Adult B-cell Acute Lymphoblastic Leukemia. *Cancer Res Commun* 2:1520–1531.

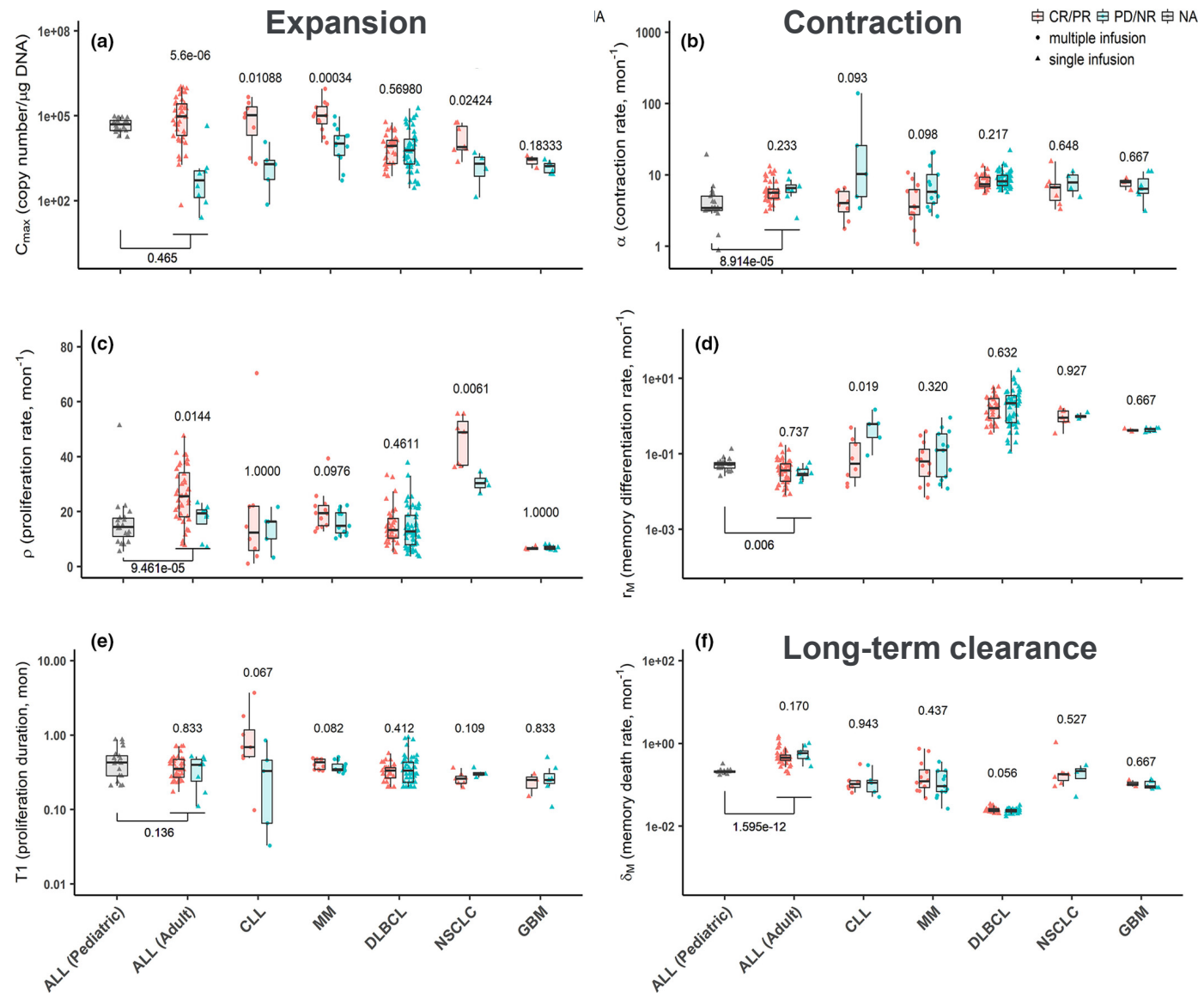
Initial expansion (C_{max}) predicts response for multiple CAR-Ts

Clearance does not (for autologous products)



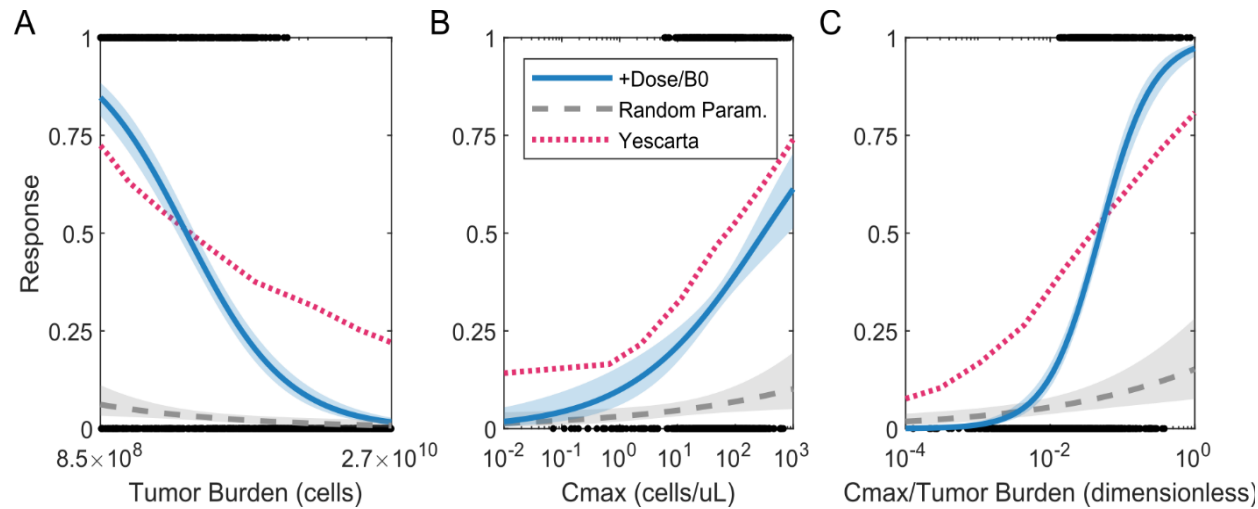
Liu C, Ayyar VS, Zheng X, et al (2020) Model-based Cellular Kinetic Analysis of Chimeric Antigen Receptor-T Cells in Humans. Clin Pharmacol Ther.

Cell Kinetic model to data from 7 CART trials (Jansen)



Model-based insights into clinical response: cell dose & tumor burden

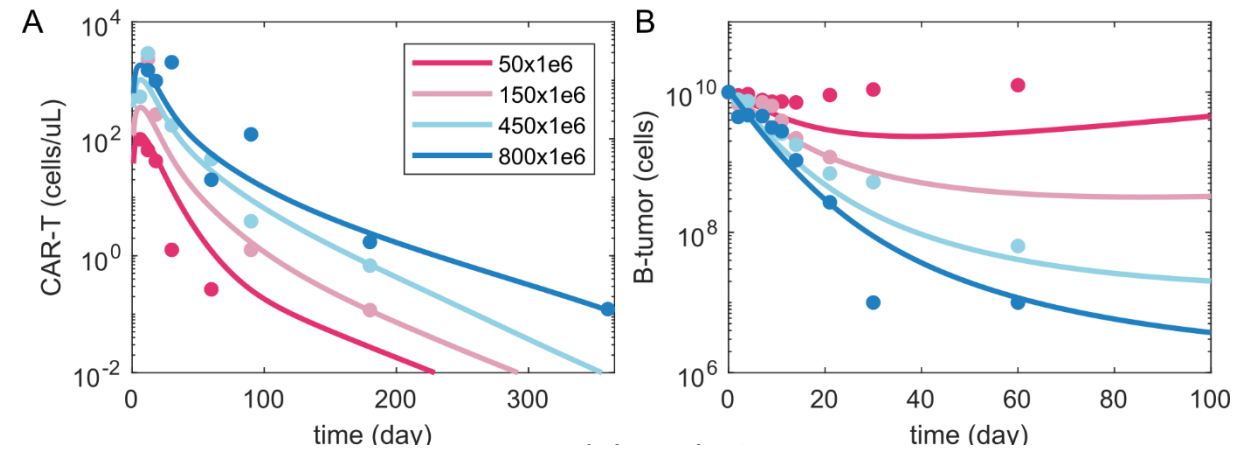
Predicted covariates of response: Cmax vs. Tumor Burden
Virtual Populations vs. Yescarta in LCBCL (ZUMA-1)



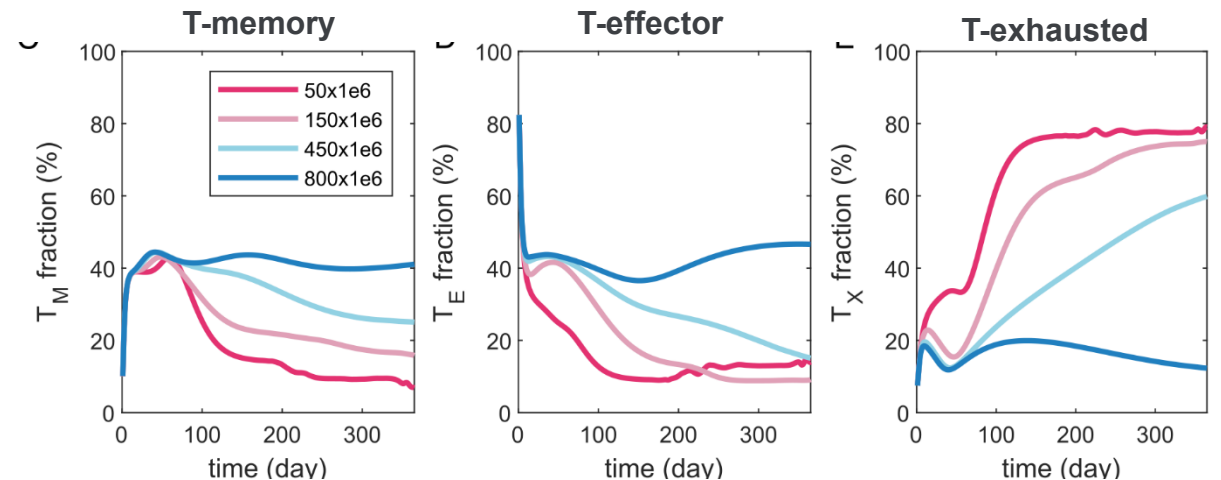
Data source: Locke FL, Rossi JM, Neelapu SS, et al (2020) Tumor burden, inflammation, and product attributes determine outcomes of axicabtagene ciloleucel in large B-cell lymphoma. Blood Adv 4:4898–4911.

Mechanism-based models can *predict* biological processes underlying clinical observations

Model training: Ph1 Abecma dose escalation (BCMA, Multiple Myeloma)

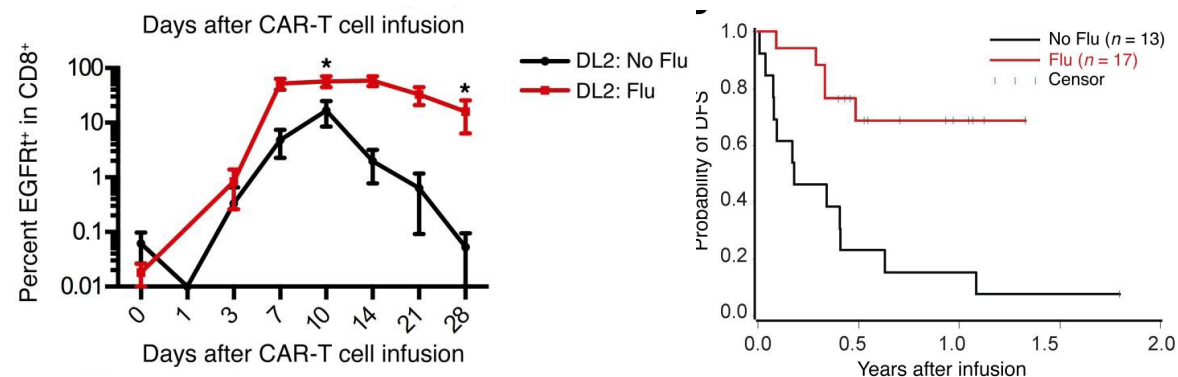


Predicted sub-population dynamics: Ph1 dose escalation



Lympho-depletion intensity & response via IL7 availability?

Cyclophosphamide (Cy) vs. Cy + Fludarabine (Flu): CD19-CART therapy in B-ALL

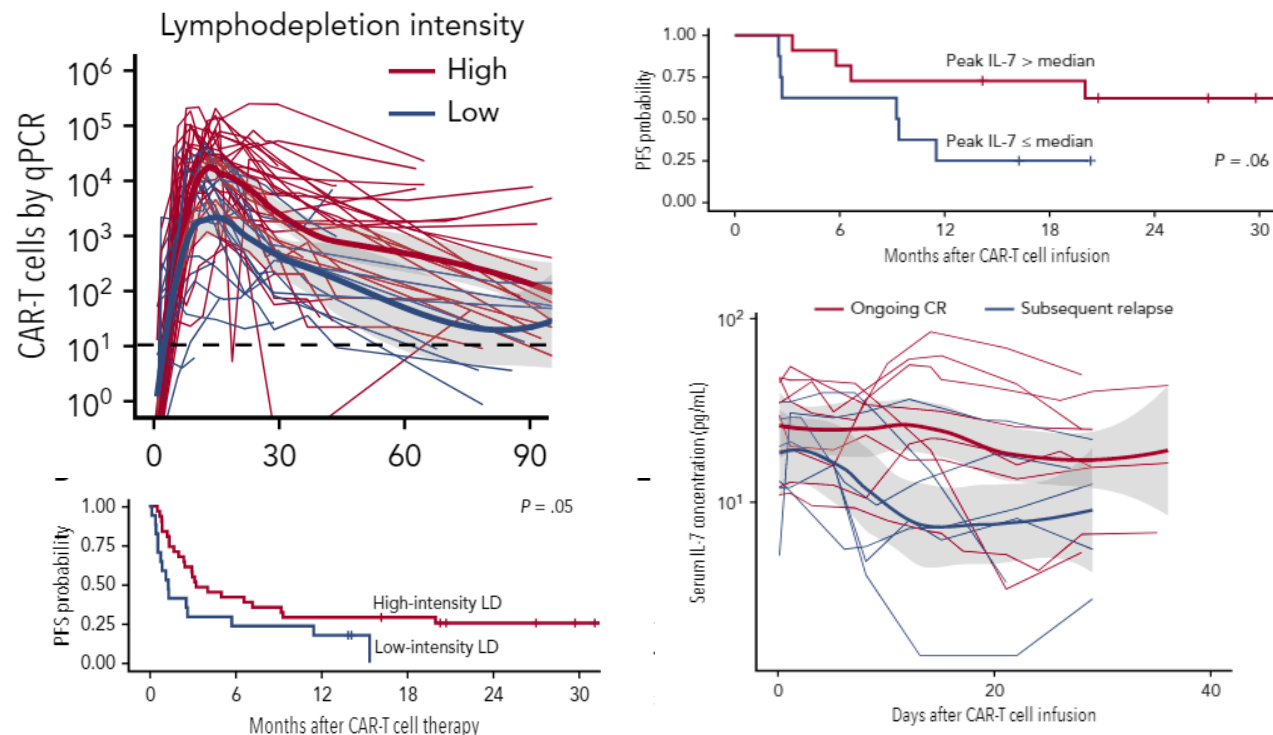


Turtle CJ, Hanafi L-A, Berger C, et al (2016) CD19 CAR-T cells of defined CD4+:CD8+ composition in adult B cell ALL patients. J Clin Invest 126:2123–2138.

Q: How does Lympho-depletion intensity affect CAR-T expansion and peak IL7 concentration?

Q: Can we *mimic* intense-LDT via cytokine support?

High vs. Low-intensity Cy+Flu: CD19-CART therapy in NHL



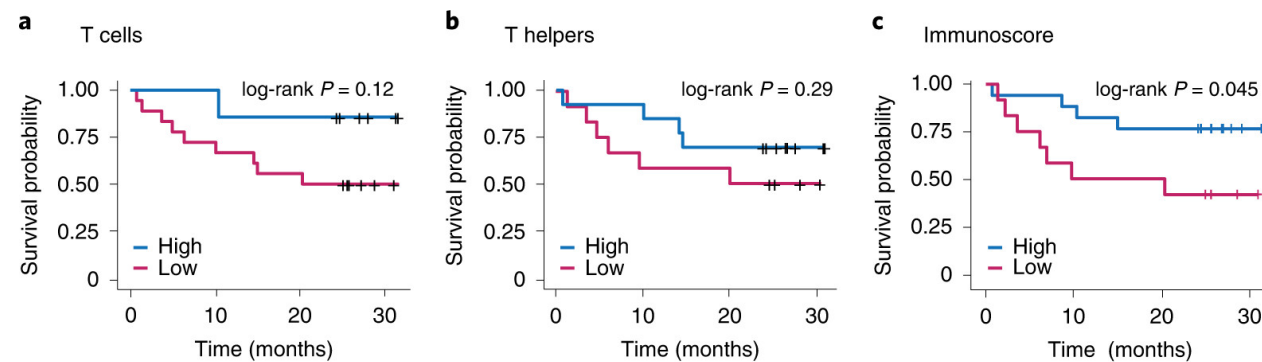
*60 vs. 30 mg/kg cyclophosphamide

Hirayama AV, Gauthier J, Hay KA, et al (2019) The response to lymphodepletion impacts PFS in patients with aggressive non-Hodgkin lymphoma treated with CD19 CAR T cells. Blood 133:1876–1887.

3B. Tumor inflammation and CAR-T response

Yescarta in DLBCL: ZUMA-1

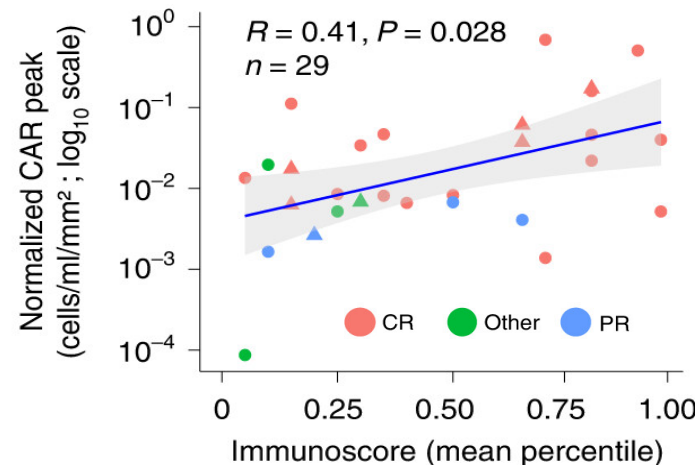
T cell inflamed tumors ~ improved survival



Immunoscore is the most significant “co-variate” Cox-regression (statistical) model

Variable	N	HR (95% CI)	P value
Immunoscore			
High	17	Reference	
Low	12	412.45 (2.63, 64,685.90)	0.020
Gender			
Female	13	Reference	
Male	16	0.51 (0.05, 5.27)	0.569
Subtype			
GCB	18	Reference	
ABC	4	0.00 (0.00, Inf)	0.999
N/A	1	0.00 (0.00, Inf)	1.000
Unknown	6	2.00 (0.12, 34.57)	0.634
IPI			
Low	6	Reference	
Intermediate	10	0.64 (0.02, 16.94)	0.787
High	13	0.06 (0.00, 16.40)	0.327
Baseline tumor burden (SPD)	29	1.00 (1.00, 1.00)	0.018
BCL2 overexpression			
Yes	16	Reference	
No	8	0.07 (0.00, 2.16)	0.127
Unknown	5	0.00 (0.00, Inf)	1.000
c-MYC overexpression			
Yes	10	Reference	
No	14	202.19 (3.98, 10,283.23)	0.008
Unknown	5	0.00 (0.00, Inf)	1.000
BCL6 overexpression			
Yes	15	Reference	
No	10	6.52 (0.65, 65.49)	0.111
Unknown	4	Inf (0.00, Inf)	0.999

Tumor inflammation ~ Cmax (CART expansion)



Q: How would pre-existing TILs influence CAR-T expansion?