

Application of Quantitative Systems Pharmacology in Early Clinical Development for Immuno-Oncology Drug Combinations

2019 Multi-Scale Modeling Consortium Meeting

Brian J. Schmidt, PhD

March 6th, 2019

Agenda

- Introduction to mechanistic modeling vis a vis QSP
 - QSP at BMS
 - General considerations for developing and applying models
- QSP application workflows (very high level)
- I-O QSP model application examples
 - Drug x

QSP at BMS

- 8 Dedicated QSP modelers in the Quantitative Clinical Pharmacology group
- Substantial & continual investment in platform development and approaches

Oncology & Immuno-Oncology

- ◆ 3 I-O Platforms
- ◆ Antibody-Drug Conjugate Platform
- ◆ Physiologically-Based Tumor Receptor Occupancy

Cardiovascular Disease

- ◆ Heart Failure
- ◆ Thrombosis

Additional Platform Resources

- ◆ Diabetes/Metabolic Diseases

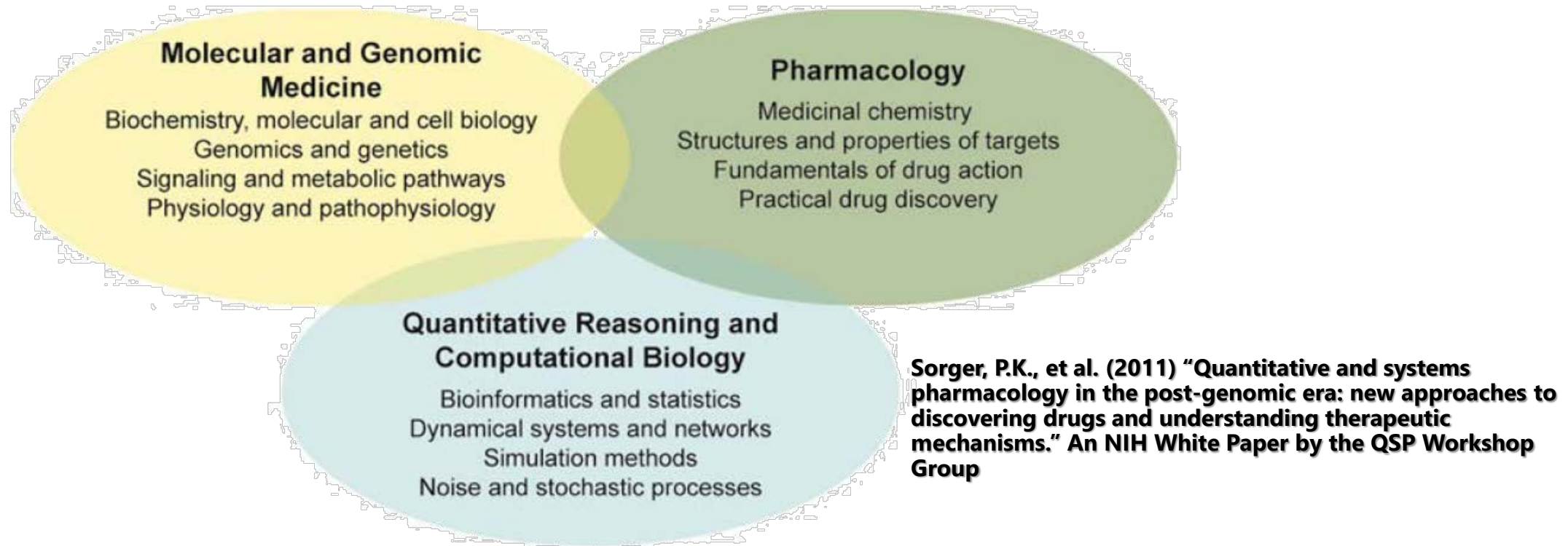
Immunoscience

- ◆ Rheumatoid Arthritis
- ◆ Immunogenicity
- ◆ Crohn's Disease
- ◆ Ulcerative Colitis
- ◆ Psoriatic Arthritis
- ◆ Systemic Lupus Erythematosus

Fibrosis

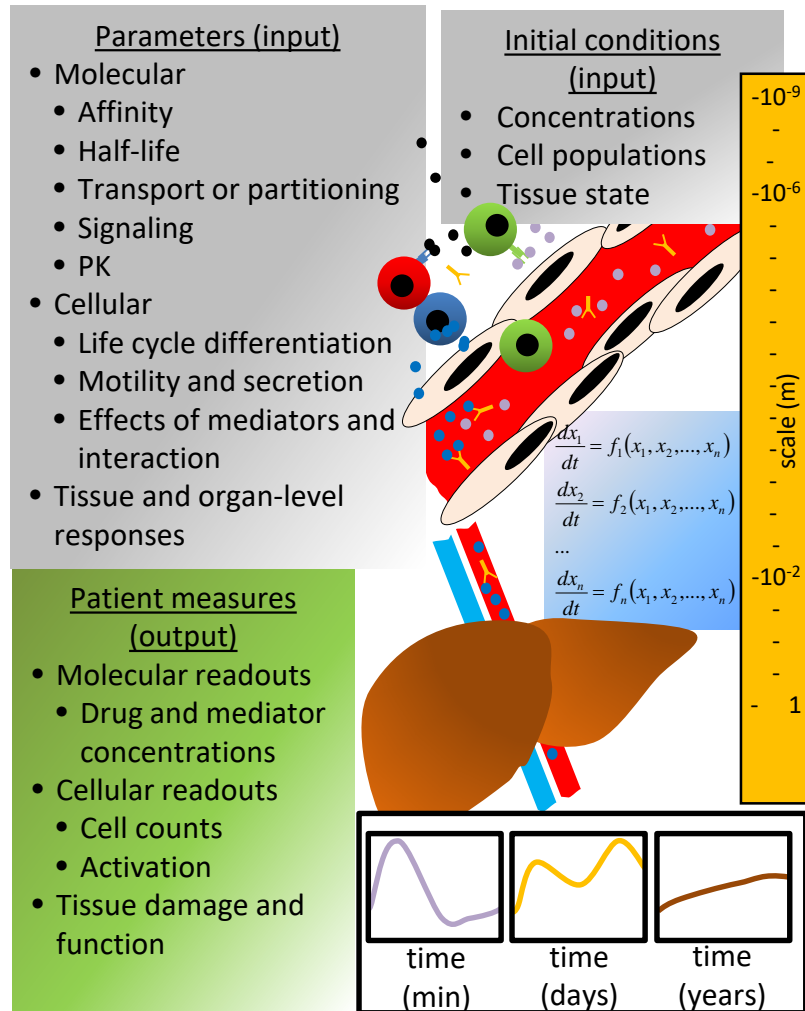
- ◆ Nonalcoholic Steatohepatitis
- ◆ Pulmonary Fibrosis

Quantitative Systems Pharmacology (QSP)



“Quantitative analysis of the dynamic interactions between drug(s) and a biological system that aims to understand the behavior of the system as a whole, as opposed to the behavior of its individual constituents”
(van der Graaf & Benson 2011, *J Pharm Sci*)

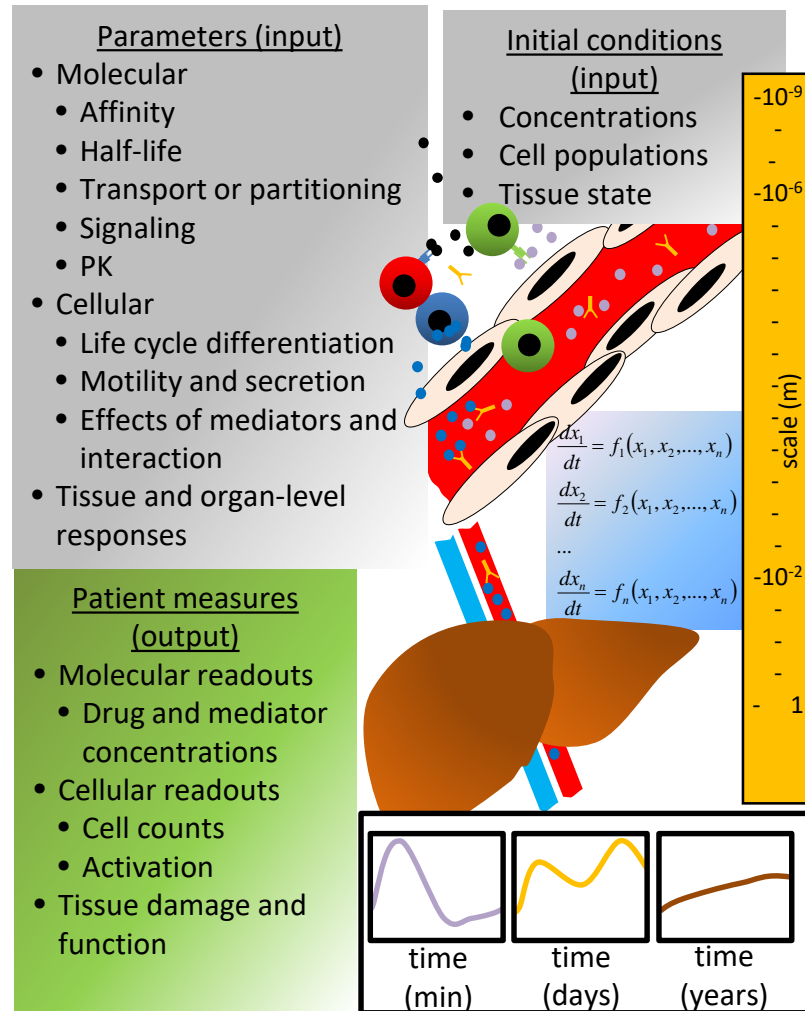
QSP model introduction (1)



Drug Discov Today (2013) 18(3-4): 116-127

- Mechanistically link target modulation to disease outcome
- Pathway modeling informed by quantitative measurements:
 - In vitro measures (in-house, literature)
 - Mini-models to extract pathway parameters
- Multiple clinical datasets for modeled assets:
 - Lesion response
 - Gene expression
 - IHC
- Model scales vary
 - Narrowly focused (single asset with well-defined, narrow biology)
 - In-between: asset-level combinations
 - **Focus on prioritized biomarkers**
 - **Stage development**
 - **Can work towards bigger platforms**
- Disease-scale platform
 - **Larger biomarker panels**

QSP model introduction (2)



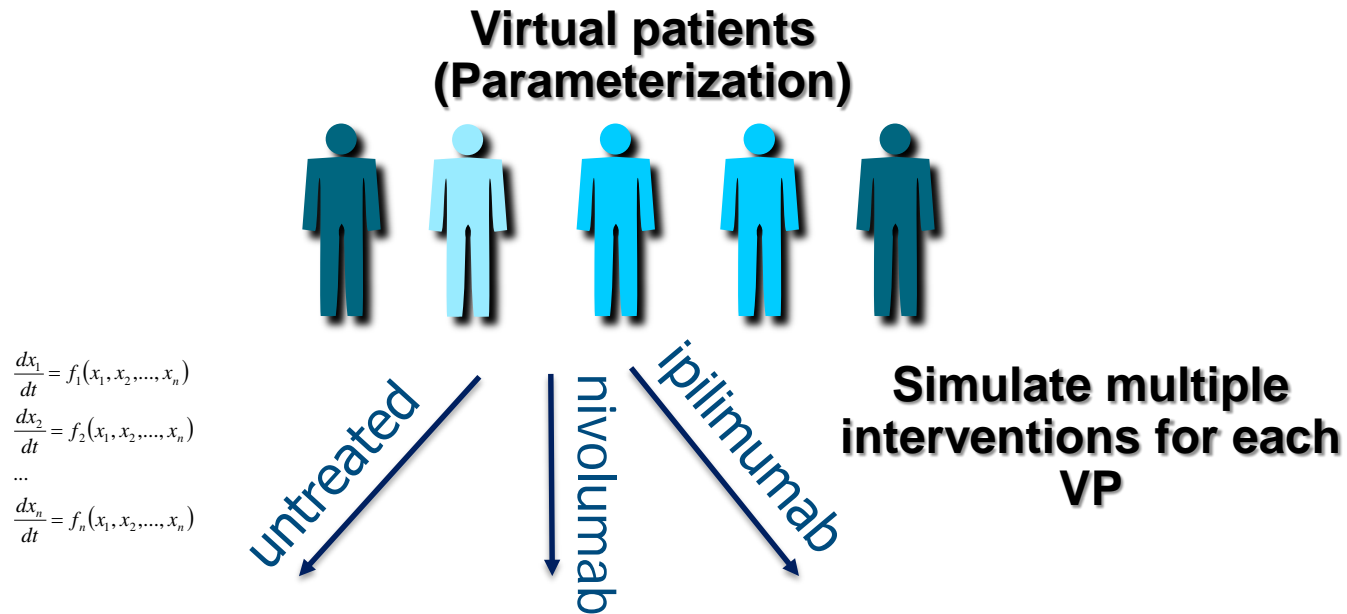
Drug Discov Today (2013) 18(3-4): 116-127

- System focus: provide predictions and analyses before trial data are available for a new intervention/therapy
- Calibrate model for related therapies
 - Lesion responses, for example on nivolumab
- Evaluate model performance from withheld data
- **Stronger extrapolation principal if data available for therapies that perturb related pathways**
- Challenges and risk mitigation
 - Many parameters
 - Mini-models for parameter extraction from experiments
 - Train on outcomes
 - Only accept solutions that agree with observed clinical outcomes
 - Availability of data
 - Initially focus on tumor types where the best data are available and accessible
 - Clearly communicate where additional pathway or outcome training & validation data will be beneficial

Agenda

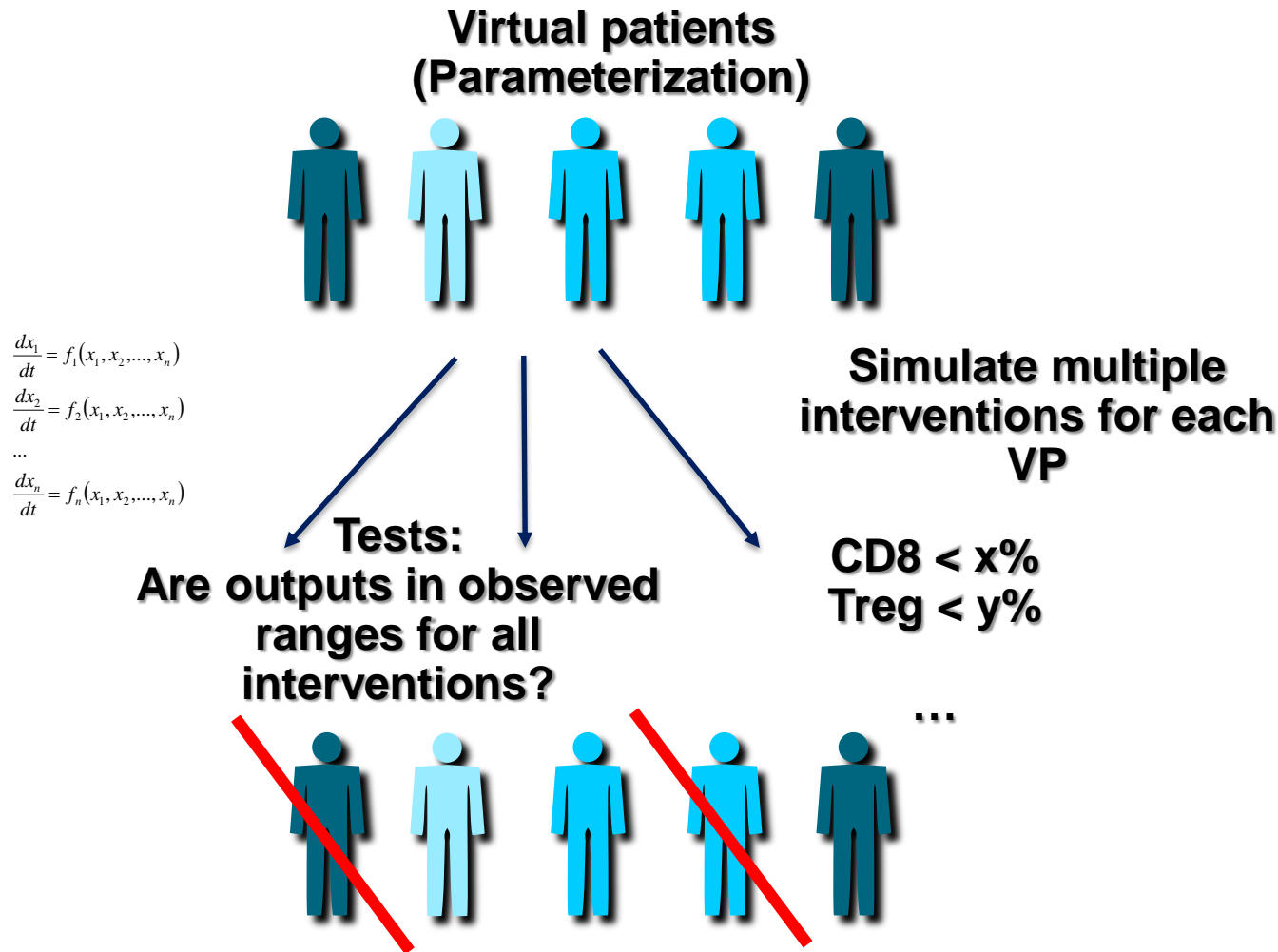
- Introduction to mechanistic modeling vis a vis QSP
 - QSP at BMS
 - General considerations for developing and applying models
- QSP application workflows (very high level)
- I-O QSP model application examples
 - Drug x

Methods: virtual patient cohort (1)



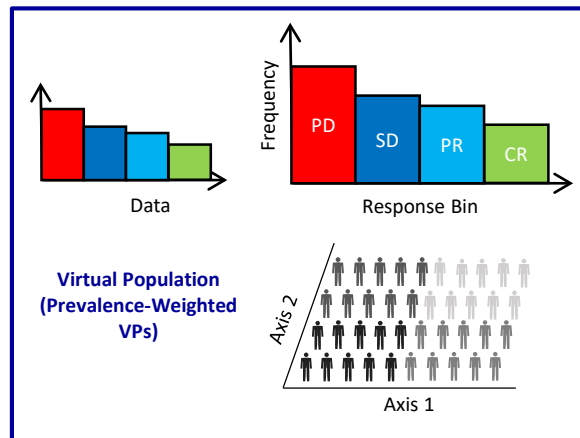
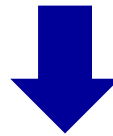
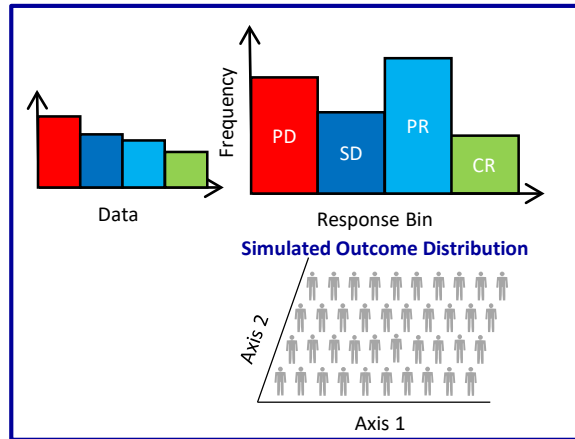
- Alternate model parameterizations are sampled (biomarker diversity)
- Multiple interventions (therapies) are simulated for each virtual patient

Methods: virtual patient cohort (2)



- Alternate model parameterizations are sampled (biomarker diversity)
- Multiple interventions (therapies) are simulated for each virtual patient
- Biomarker and response data are used to:
 - Guide reasonable parameter bounds
 - Set acceptance criteria on simulated outcomes
 - Plausible VPs must pass numerous acceptance criteria from data

Methods: virtual population



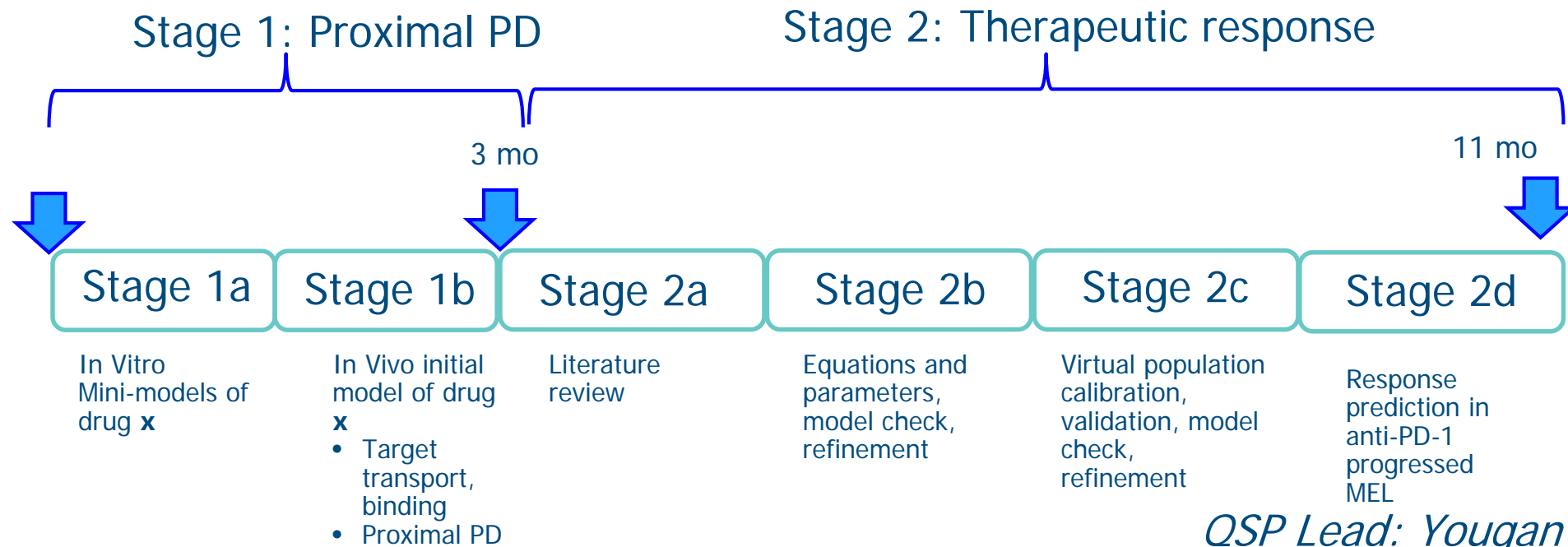
- Simulations also need to match observed statistics
- Often accomplished with “prevalence weight” to create a virtual population
 - Simultaneous fit
 - Multiple biomarkers and response for each therapy
 - Multiple therapies
- Uses multiple statistical tests and dependent on data to match
 - Summary statistics
 - Distributions
 - Bins
 - Multivariable

Agenda

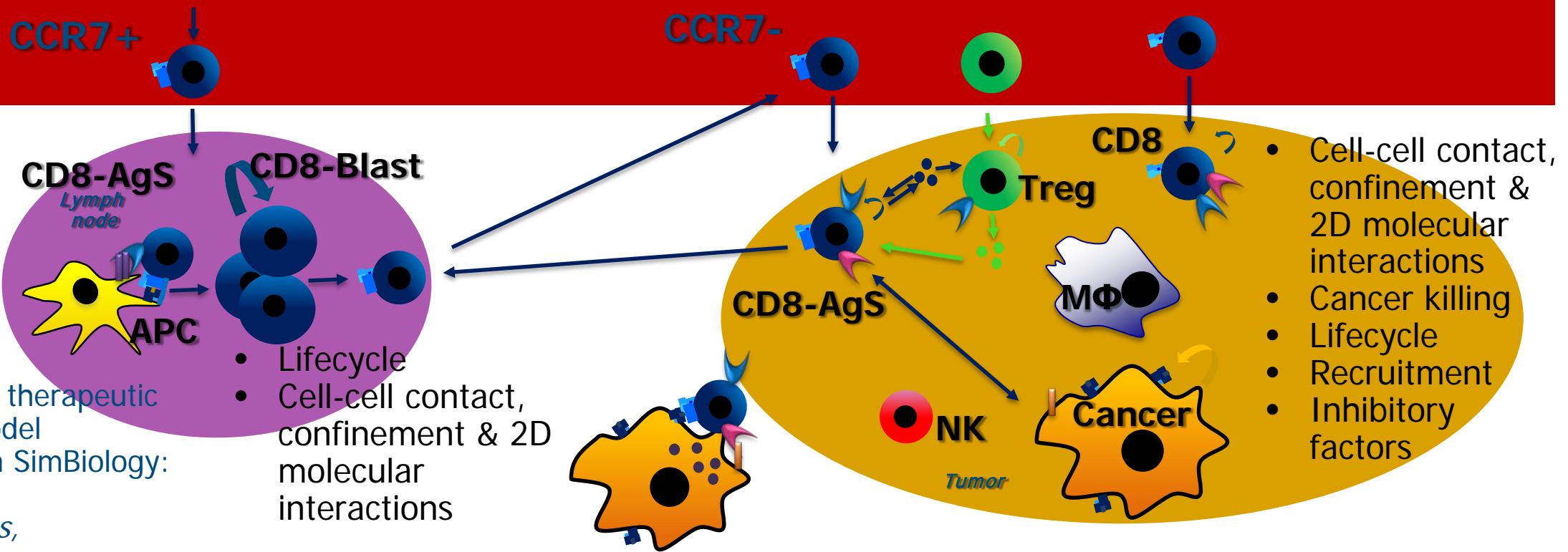
- Introduction to mechanistic modeling vis a vis QSP
 - QSP at BMS
 - General considerations for developing and applying models
- QSP application workflows (very high level)
- I-O QSP model application examples
 - Drug x

I-O platform 1: initial development to support dose expansions & ongoing trials for drug x

- Questions
 - What is the anticipated dose response of drug **x** in anti-PD-1 progressed MEL?
 - What is the role of biomarkers in the response?
- Multi-step approach



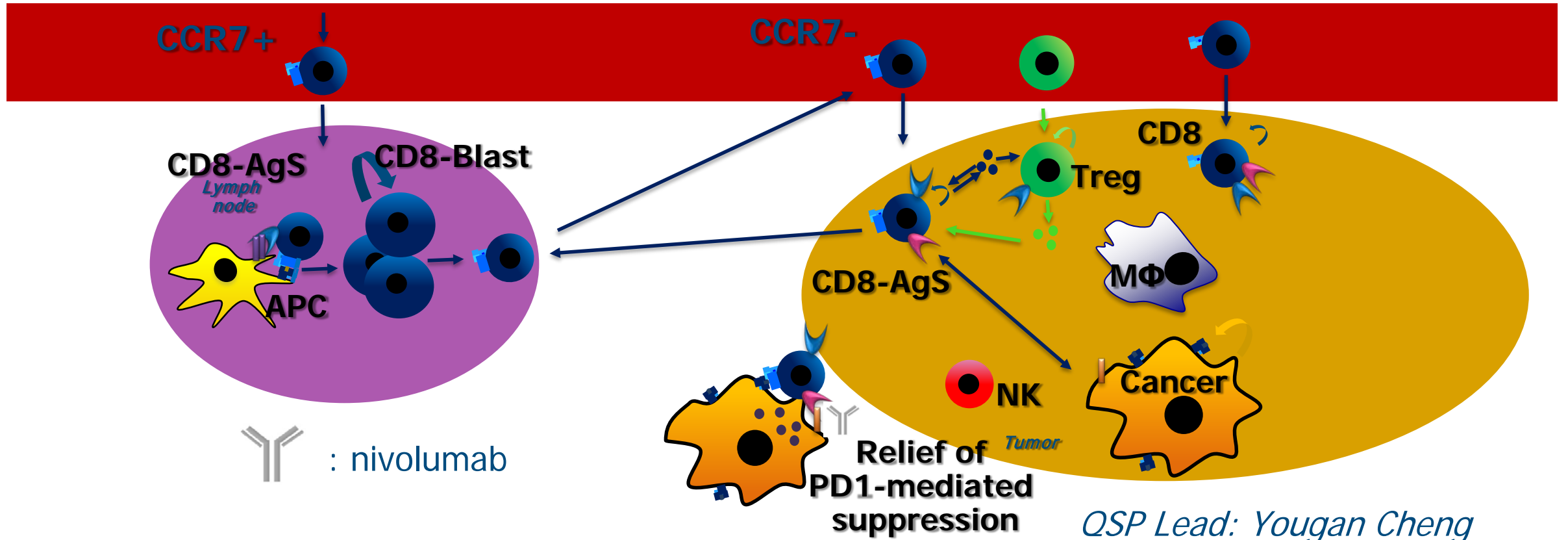
Overview of I-O platform 1



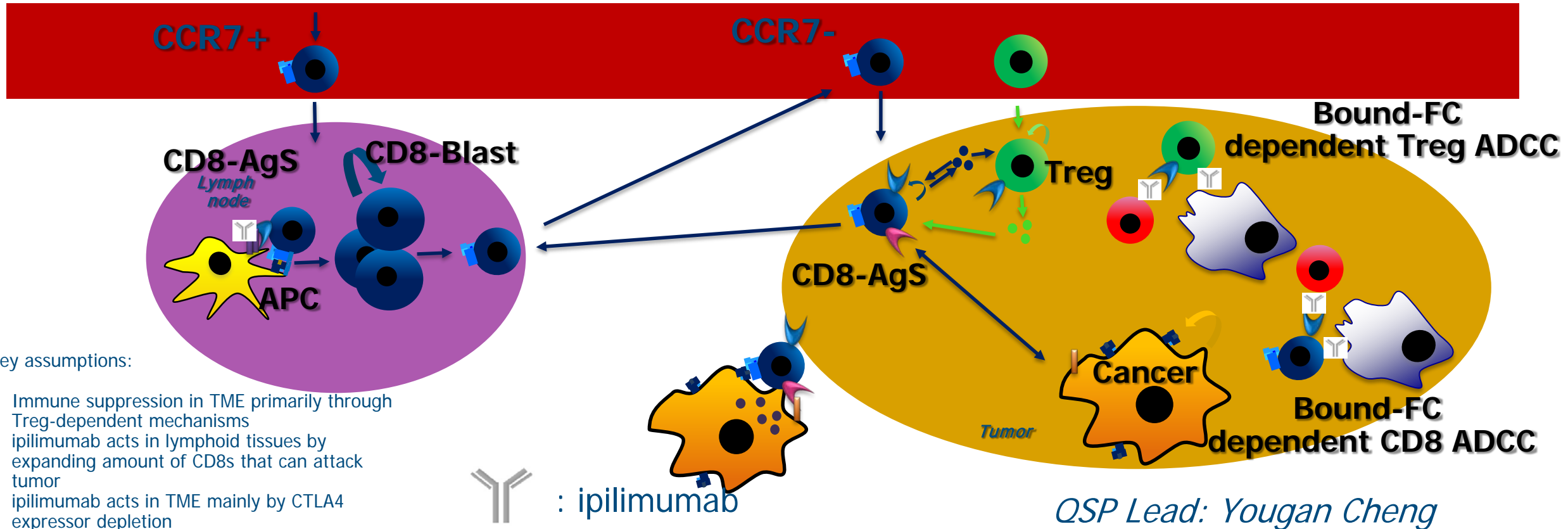
Combination therapeutic response model
 Developed in SimBiology:
 66 ODEs,
 236 reactions,
 212 rules

QSP Lead: Yougan Cheng

Implemented nivolumab mechanism



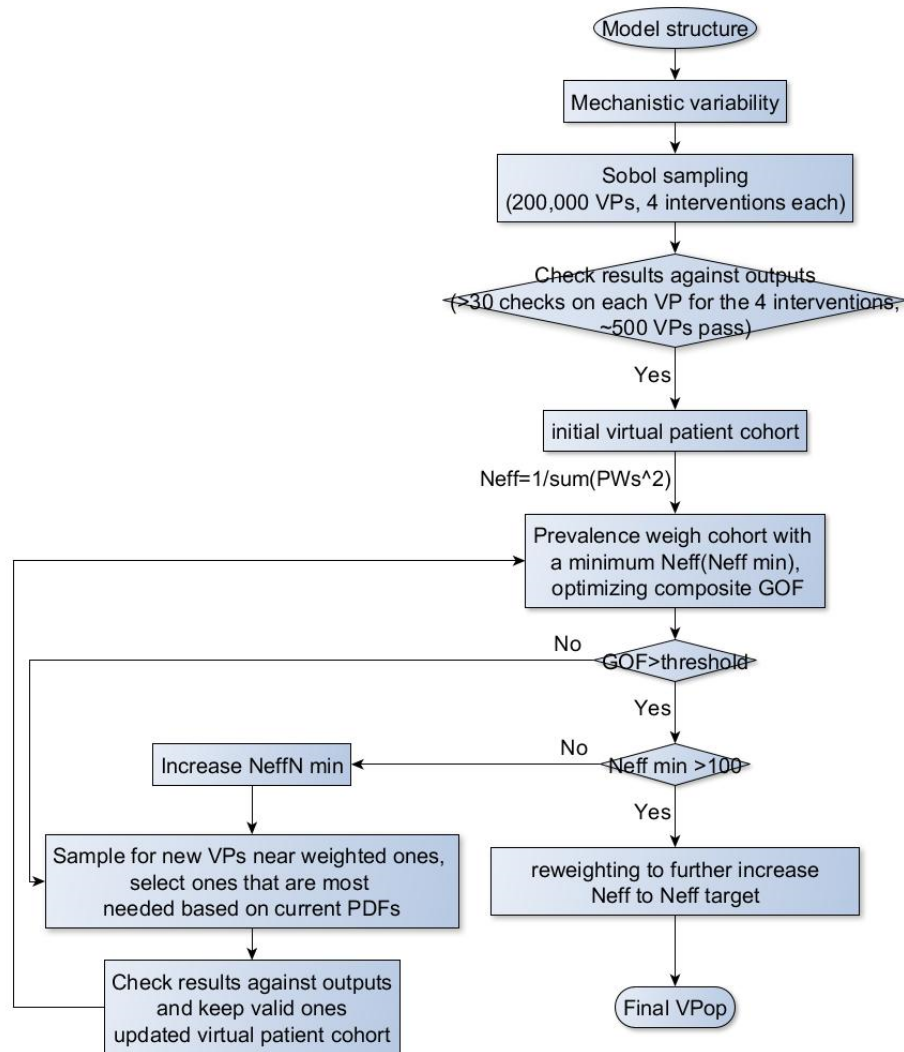
Implemented ipilimumab mechanism



Key assumptions:

- Immune suppression in TME primarily through Treg-dependent mechanisms
- ipilimumab acts in lymphoid tissues by expanding amount of CD8s that can attack tumor
- ipilimumab acts in TME mainly by CTLA4 expressor depletion

Algorithmic VPop development



Is the incorporated physiologically feasible mechanistic variability able to explain the observed biomarker/response diversity?

Run on 64 core server using QSPToolbox:

<https://github.com/BMSQSP/QSPToolbox>

“expandVPopEffN.m”

Cheng Y, et al. (2017) QSP Toolbox: Computational Implementation of Integrated Workflow Components for Deploying Multi-Scale Mechanistic Models. AAPS J 19(4), 1002-1016.

QSP Lead: Yougan Cheng

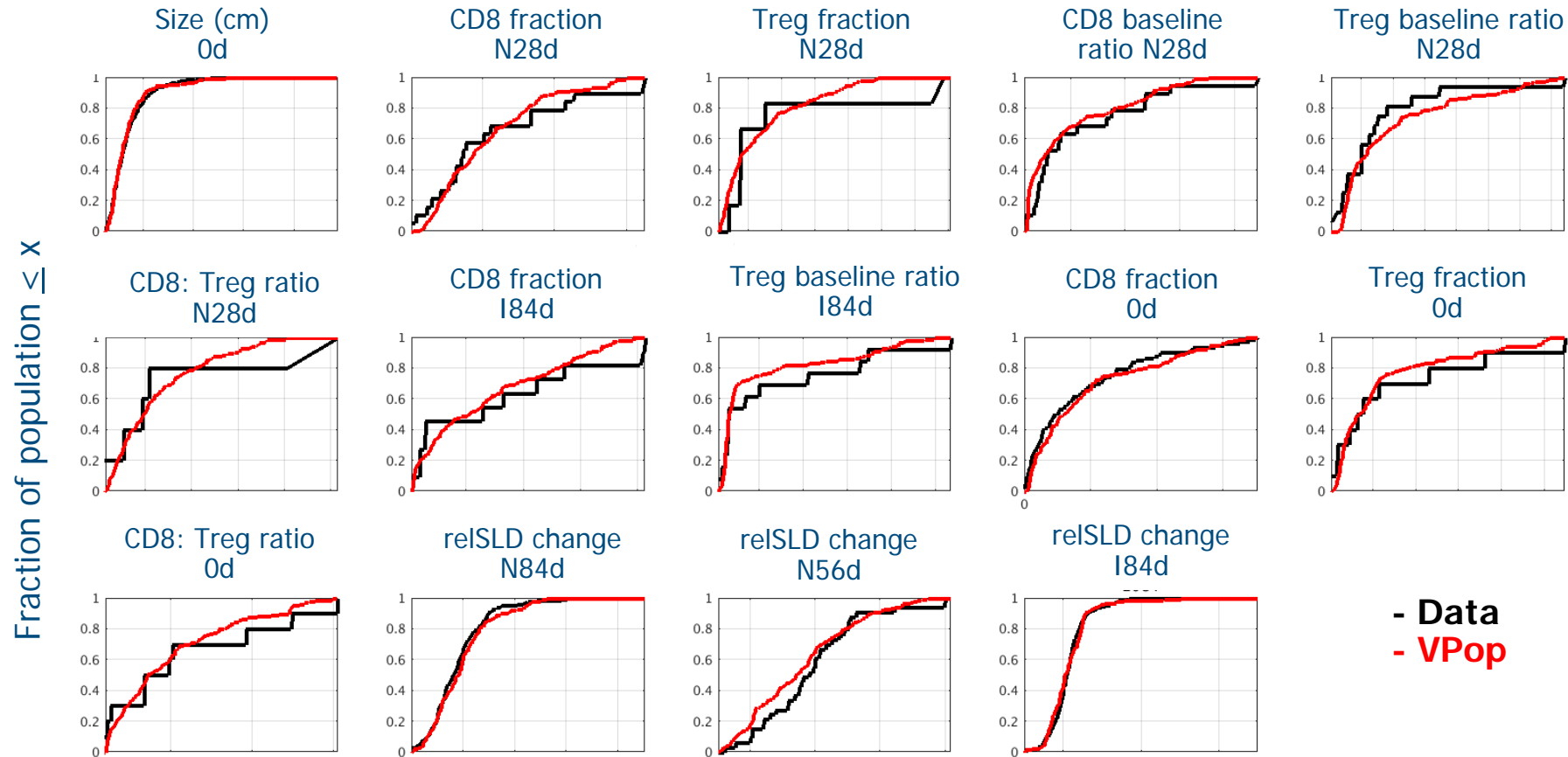
Response calibration

- Focus on 3 month time point (first lesion scans; minimize dropouts)
- Calibrate to all patients where we have data at 3 months
- Calibrate to on-treatment VPs

The VPop is fitted against various biomarker *bins, mn/sd and distributions* (a total of *51 simultaneous fits*). The *composite goodness of fit (range: 0-1)* of these 51 simultaneous fits is *0.71*. Typically, a VPop is considered accepted if the composite goodness of fit is *greater than 0.05*.

QSP Lead: Yougan Cheng

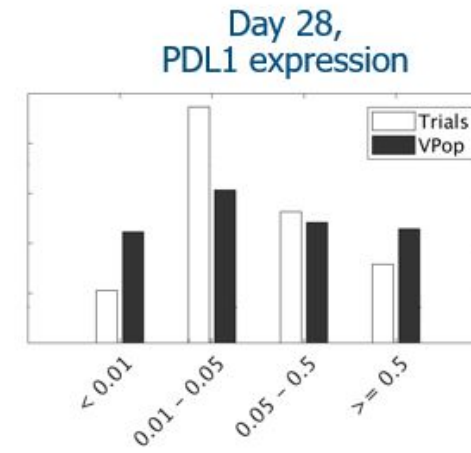
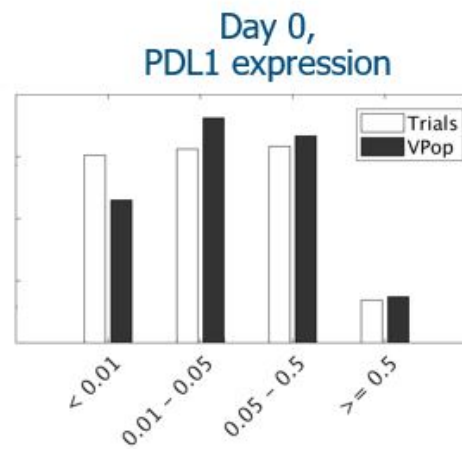
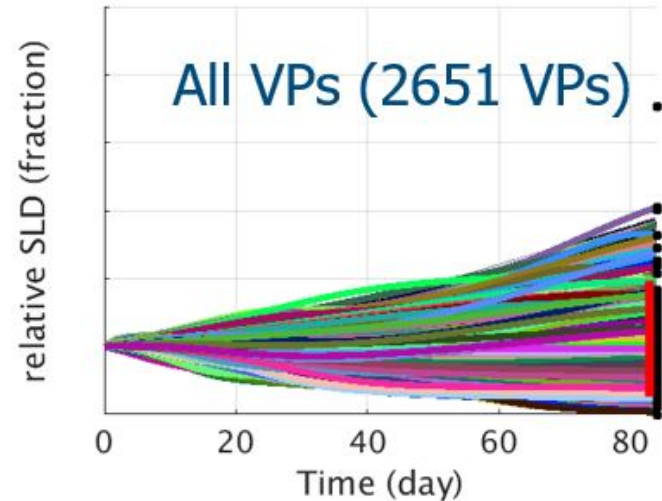
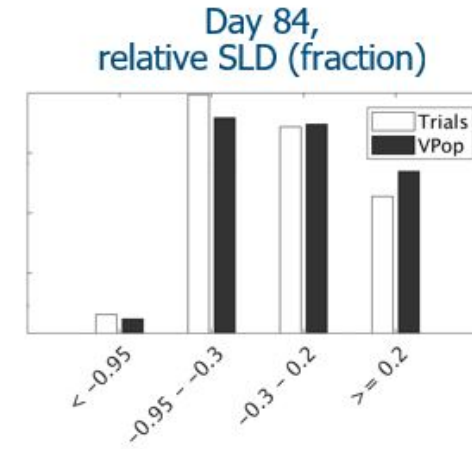
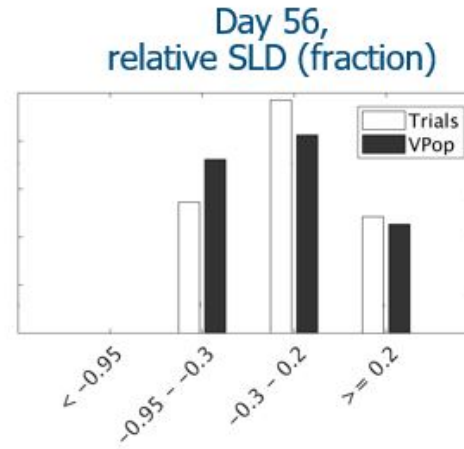
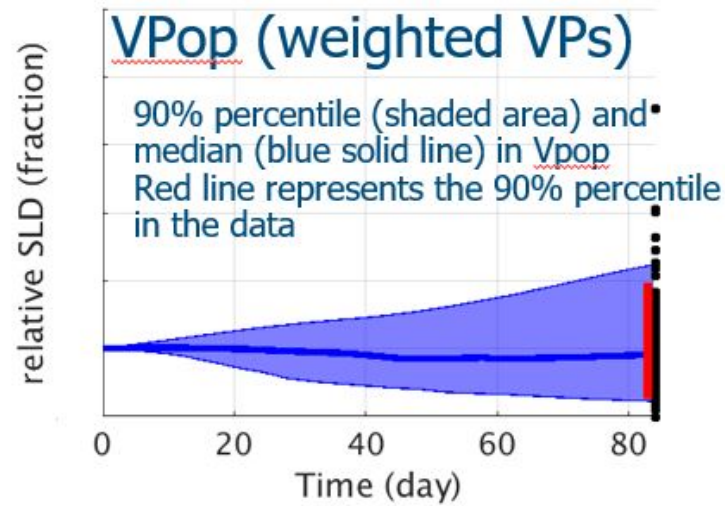
VPop captures clinical distributions



Cumulative distribution functions (CDFs) shown

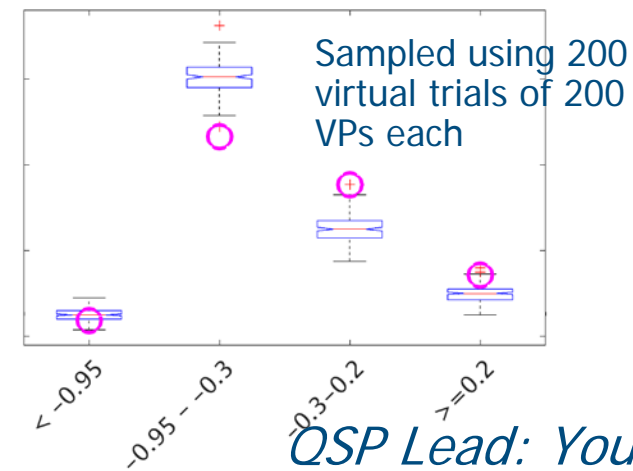
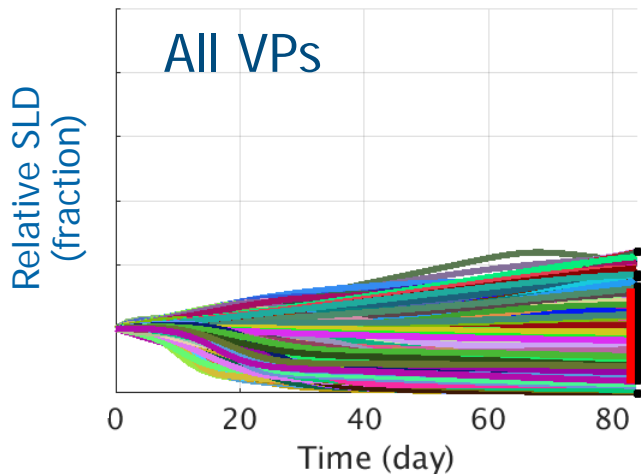
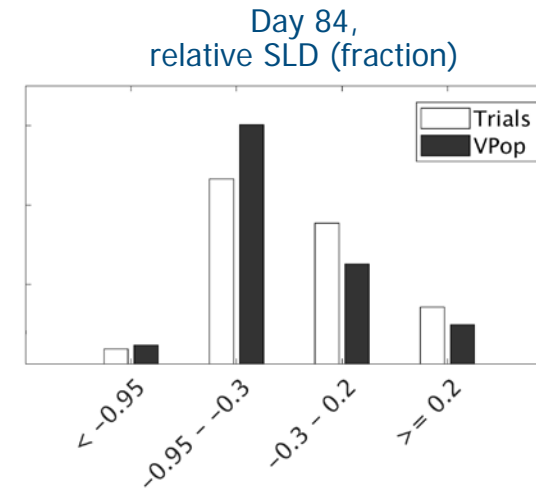
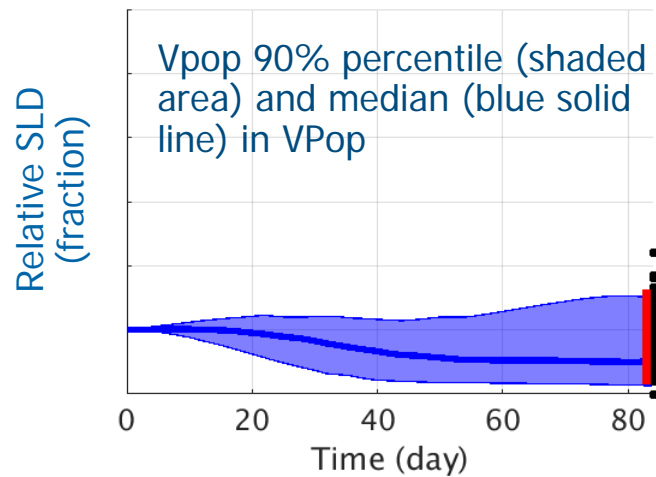
QSP Lead: Yougan Cheng

Nivolumab: simulated lesion response and PDL1



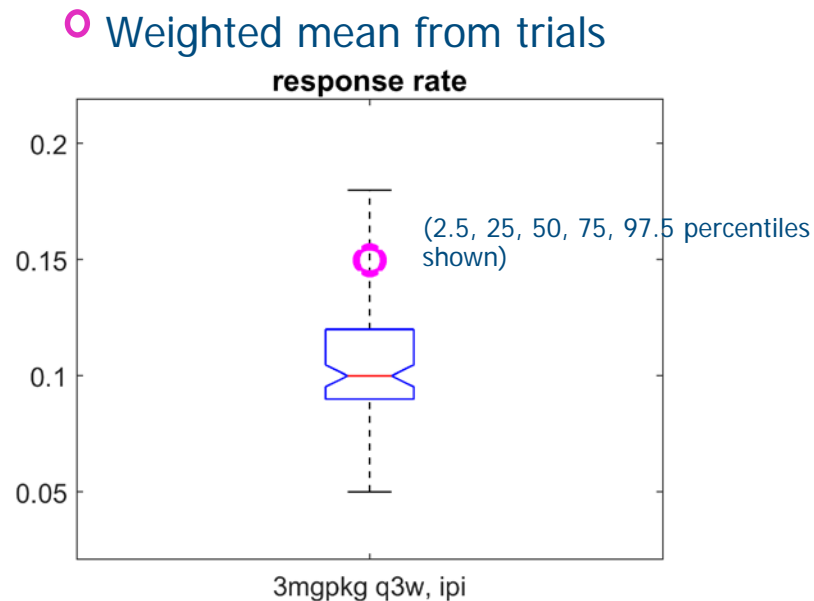
QSP Lead: Yougan Cheng

Model validation: BLIND PREDICTION of nivolumab & ipilimumab combo therapy



QSP Lead: Yougan Cheng

Model validation: BLIND PREDICTION of ipilimumab after progression on nivolumab



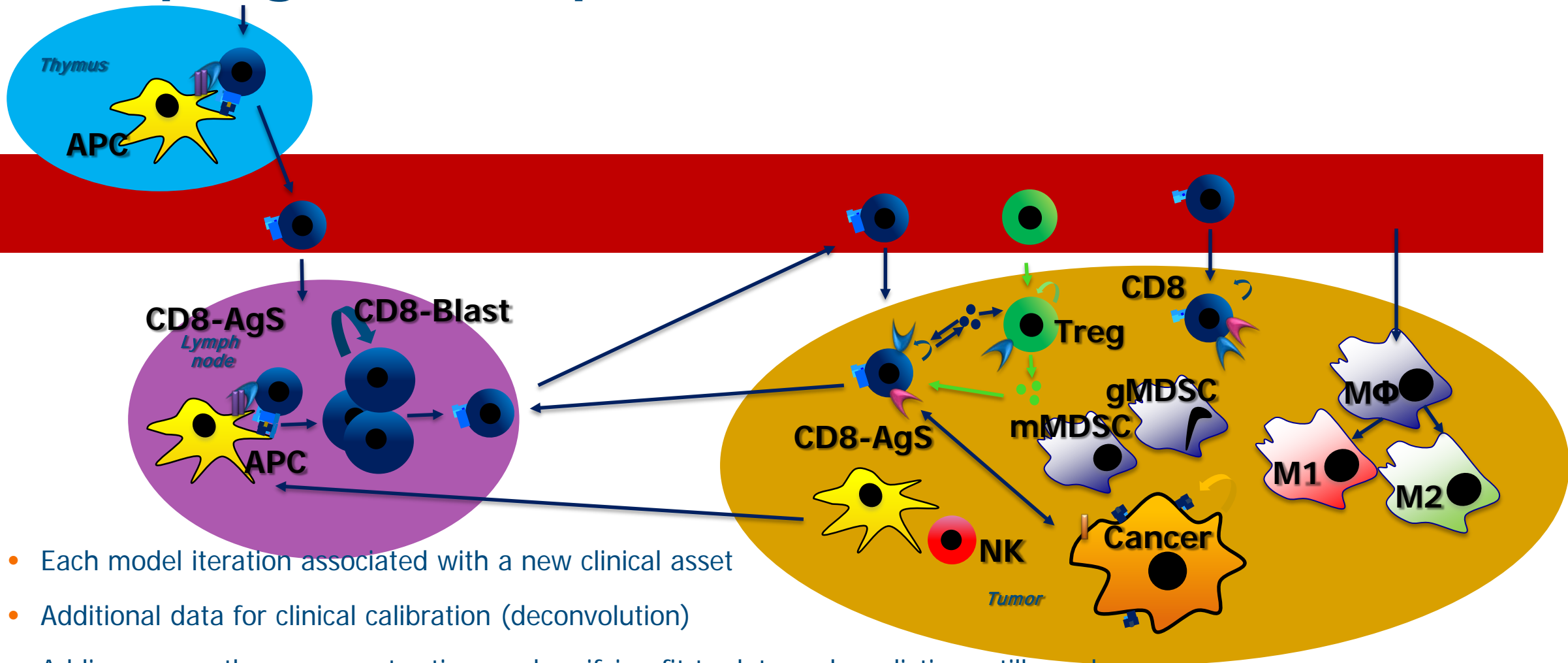
- Ipilimumab efficacy after progression on anti-PD1 therapy in melanoma:
 - 0.5 (N=8) Jacobsoone-Ulrich A, et al. Melanoma Res. 2016
 - 0.1 (N=40) Bowyer S, et al. Br J Cancer. 2016
 - 0.22 (N=9) Aya F, et al. Future Oncol. 2016
 - 0.16 (N=47) Zimmer L, et al. Eur. J. Cancer 2017
 - 0.13 (N=97) Long V, et al. Pigment Cell melanoma Res 2017
- “In summary, although there are no prospective trials to assess the efficacy of ipilimumab in patients with metastatic melanoma whose disease progressed during frontline treatment with an anti-PD-1 agent, we can surmise that approximately 10% to 20% of patients will achieve a response to second-line ipilimumab.” -Svetomir Markovic and Richard W. Joseph

QSP Lead: Yougan Cheng

Model impact for drug x (so far)

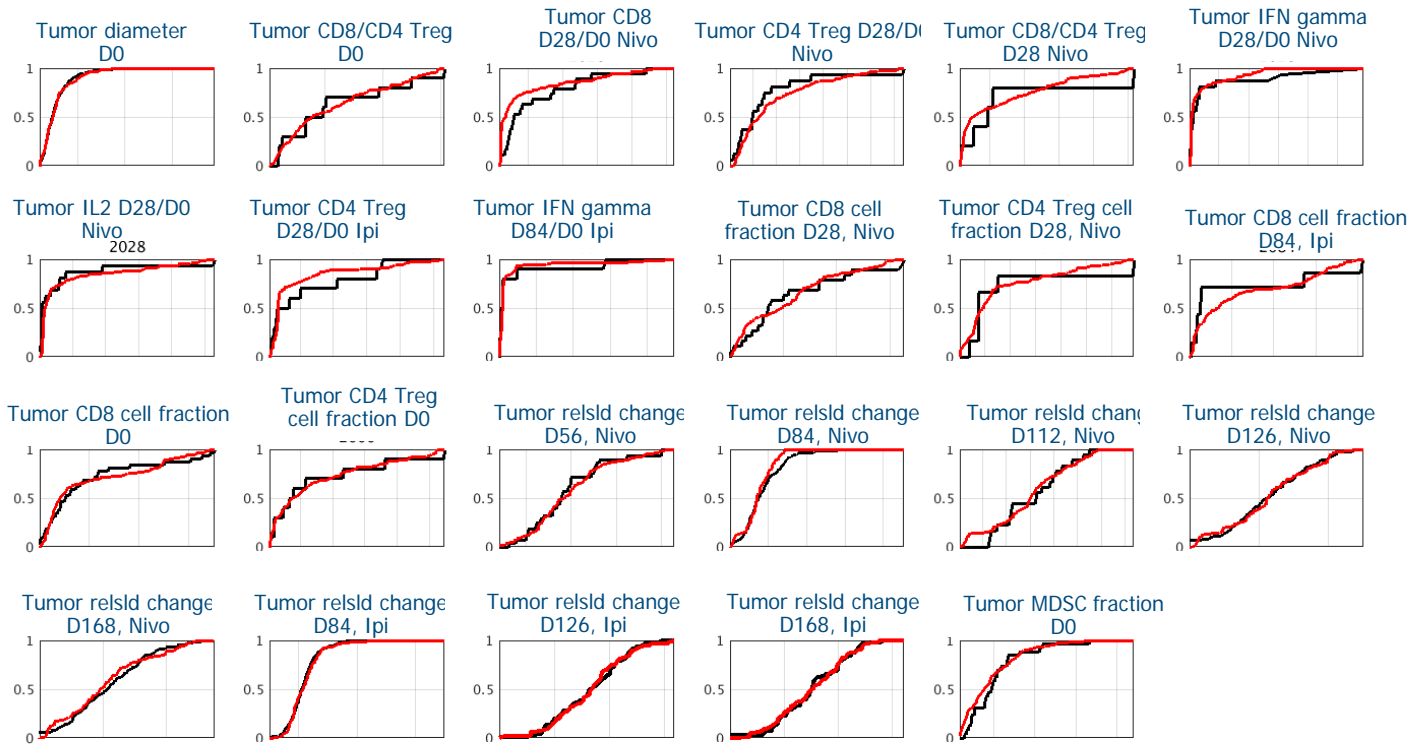
- Proximal PD model predicted some clinical immunological activity at a very low starting dose for drug x early in development, subsequently confirmed
- Current model impacts with development team
 - Model predicts drug x has a biphasic dose response in anti-PD-1 progressed MEL, so far qualitatively observed in a broader dose escalation cohort but small N
 - Model has been used to provide guidance on unexpected relationship observed between cell type y and lesion response
 - Model has been used to provide guidance on the impact of dose fractionation on cell type y and lesion response
- CURRENT CHALLENGES
 - Note calibrating tumor-type specific responses
 - Have small N and multiple tumor types in early clinical development

New programs: stepwise addition of new MOAs

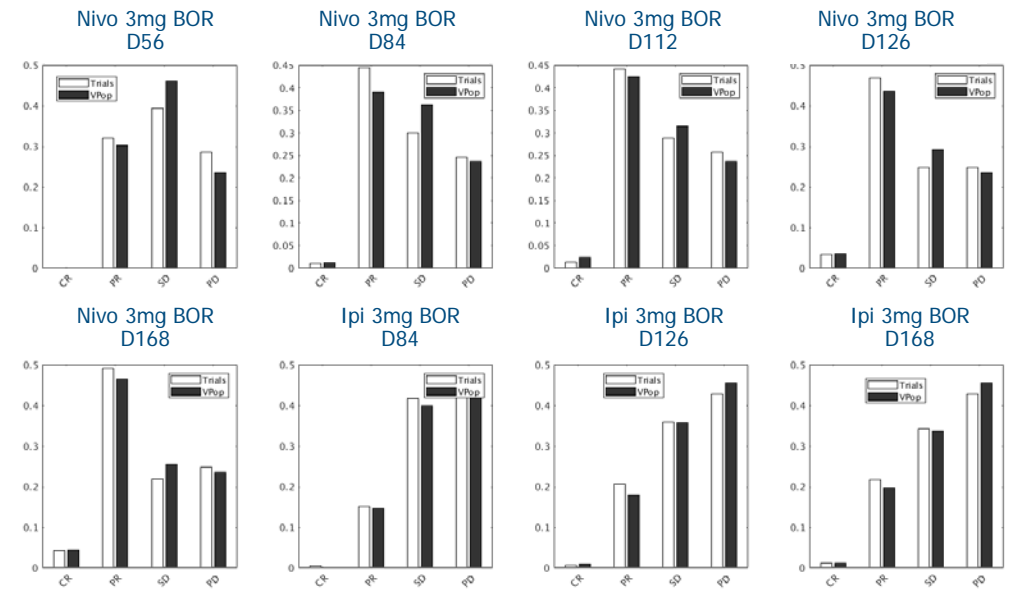


- Each model iteration associated with a new clinical asset
- Additional data for clinical calibration (deconvolution)
- Adding new pathways one-at-a-time and verifying fit to data and predictions still good
- gMDSC/mMDSC, M1/M2 macrophage polarization, NK life cycle, DC maturation, soluble mediators; Th subsets

Calibration of even more tumor endpoint distributions



BOR for ipilimumab and nivolumab Up to 6 months so far



- Truer CR classification and CR/PD censoring, here out to 6 months
- Using RNA-seq to calibrate cell markers or net protein production where it makes sense

Acknowledgements

- Session organizers
 - Jeff Saucerman, Feilim Mac Gabhann, Colleen Kuemmel, Sarah Dunsmore
- BMS QSP & QCP
 - Yougan Cheng, Craig J. Thalhauser, Tarek A. Leil
- BMS CP
 - Akintunde Bello, Amit Roy, Ming Zheng
- Virtual Systems Pharmacology (computational infrastructure)
 - Jyotnsa Pagidala, Shep Smithline, Marko Miladinov, Brian Wong, Dan Bachalis, Radha Konduri, Russel Towell, Karun Pothacamury
- Translational Bioinformatics
 - Nathan Siemers, Don Jackson, Petra Ross-MacDonald
- Biologics Discovery California
 - Minhua Han, Christine Bee, John Engelhardt, Natalie Bezman, Paula So