

A novel positive feedback loop sets a dose-dependent threshold for T cell differentiation

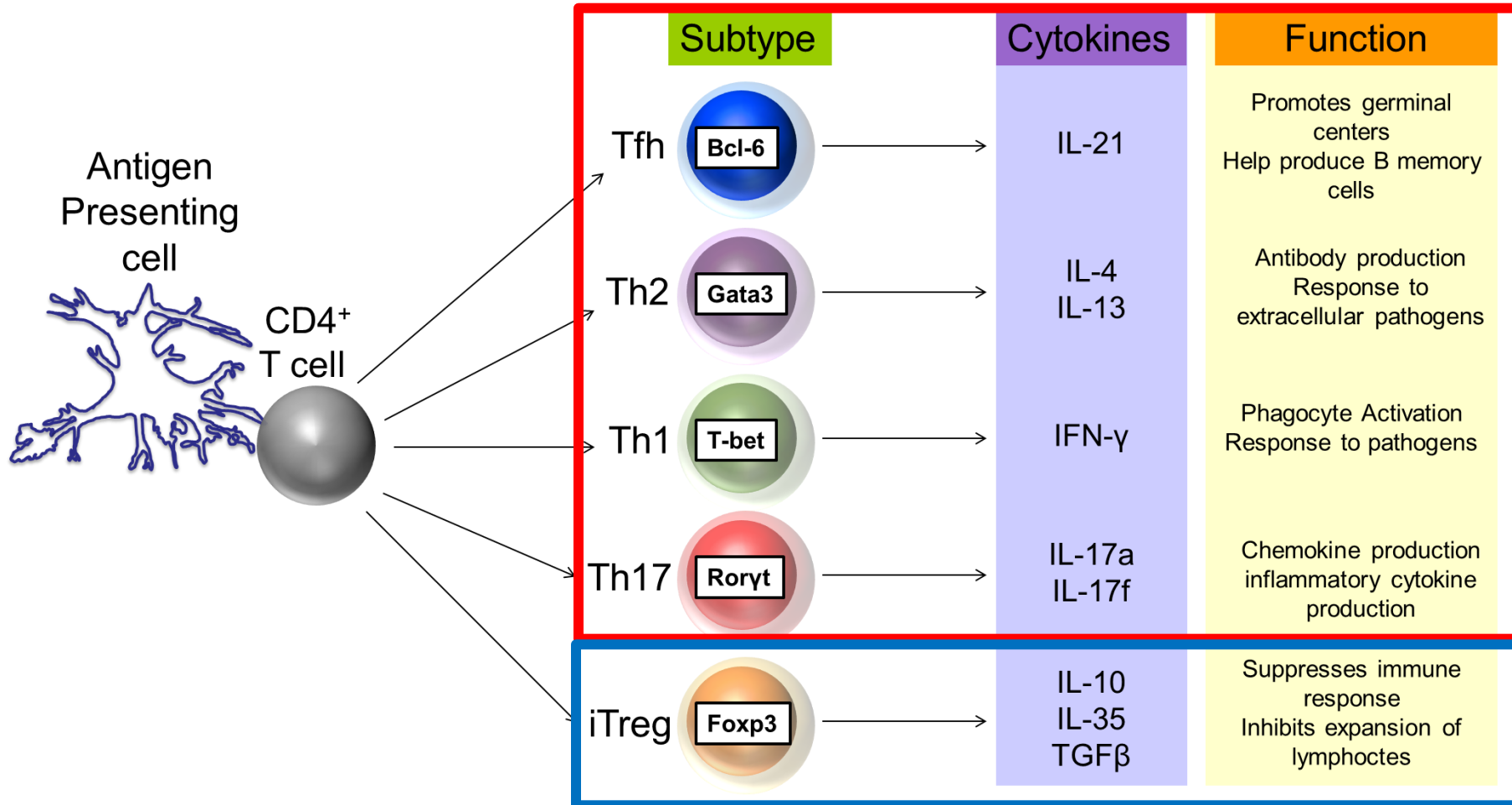
Robert P. Sheehan

Department of Computational and Systems Biology

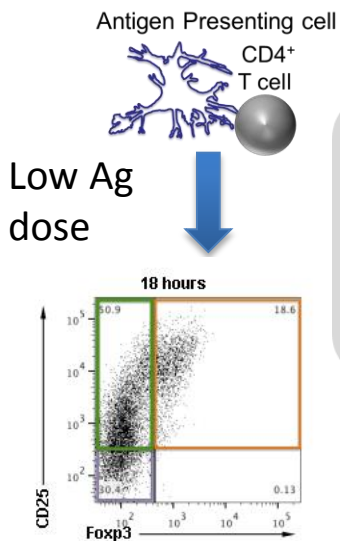
University of Pittsburgh



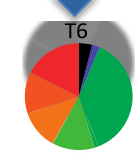
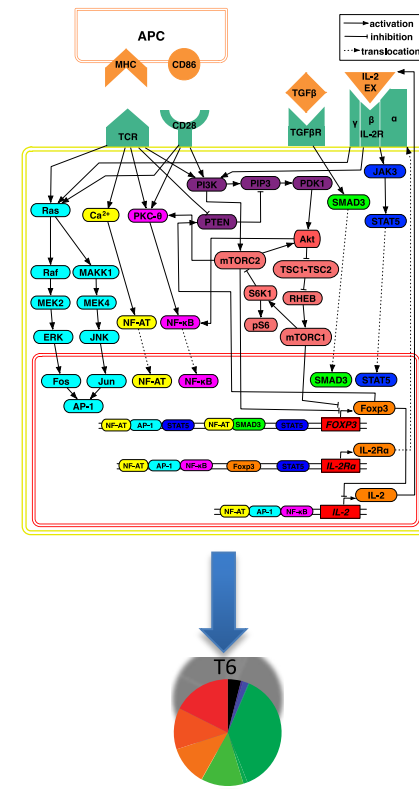
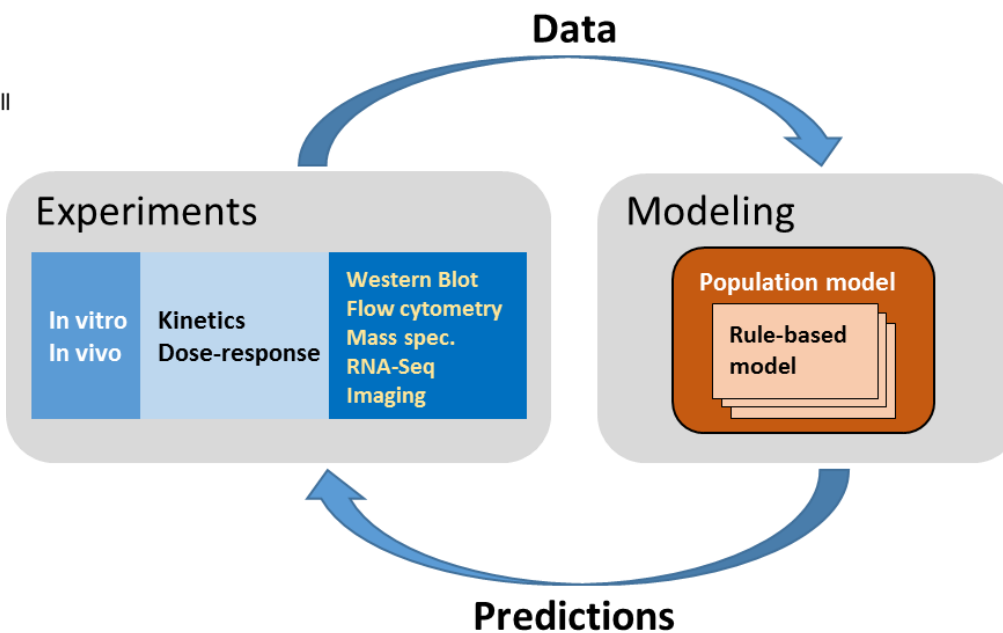
Helper T cell fate determination



Systems Biology Approach to T Cell Differentiation

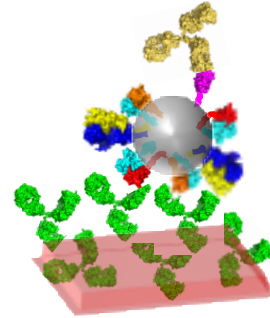
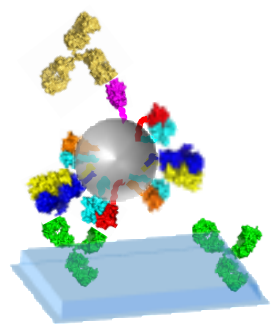


Morel Lab



Faeder Lab

Antigen dose controls level of Treg induction

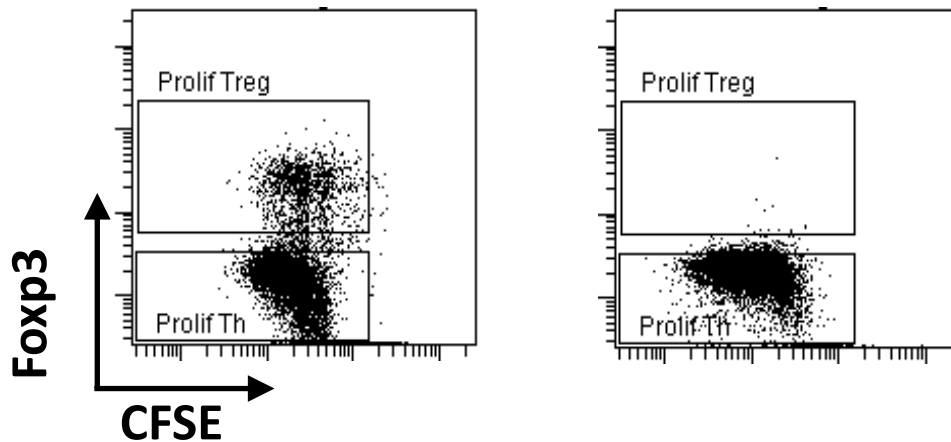


soluble aCD28

plate-bound aCD3

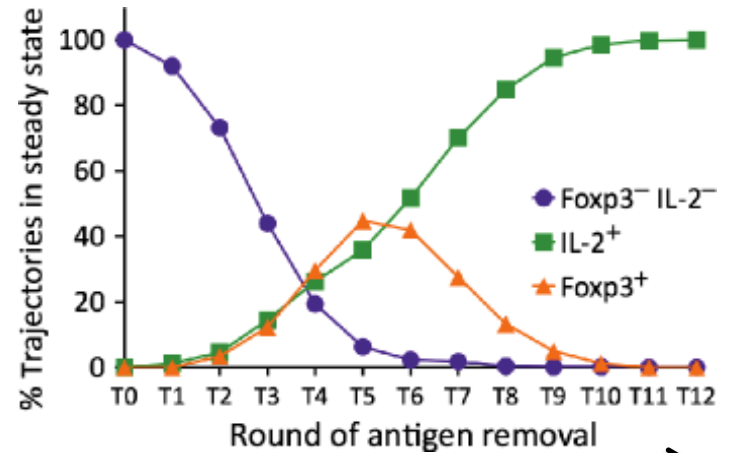
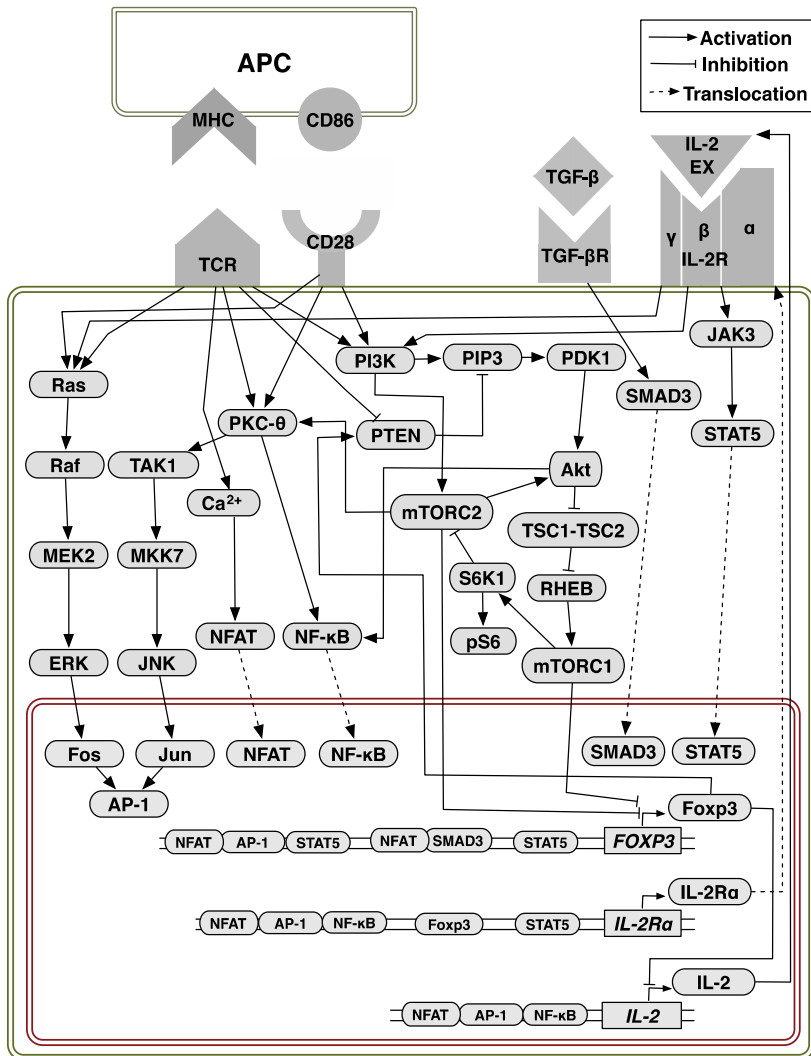
(0.25 $\mu\text{g/ml}$ aCD3) Low Ag dose

High Ag dose (1 $\mu\text{g/ml}$ aCD3)

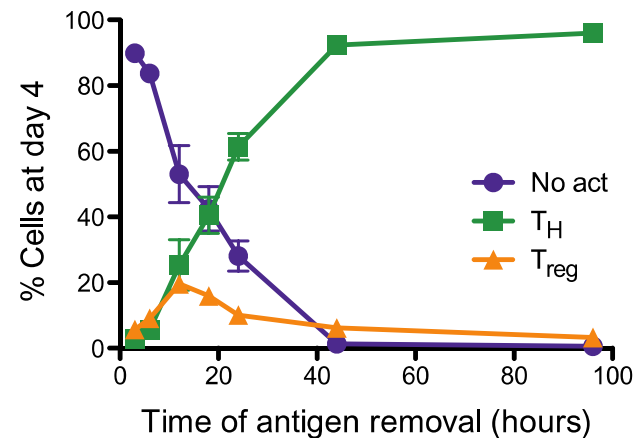


No cytokines are added

Logical model of T cell differentiation

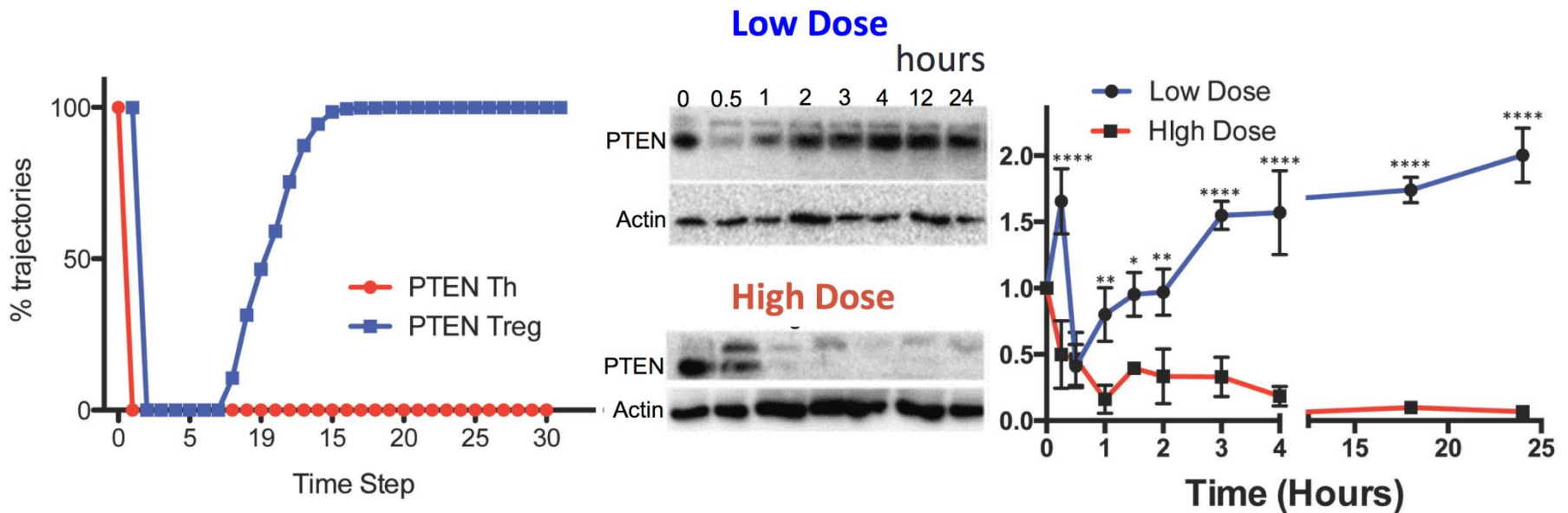


TCR signal duration



Model prediction: differential kinetics of PTEN

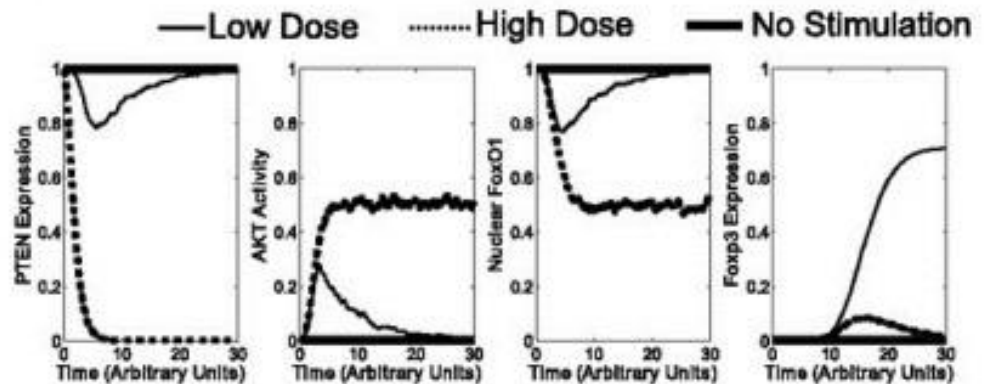
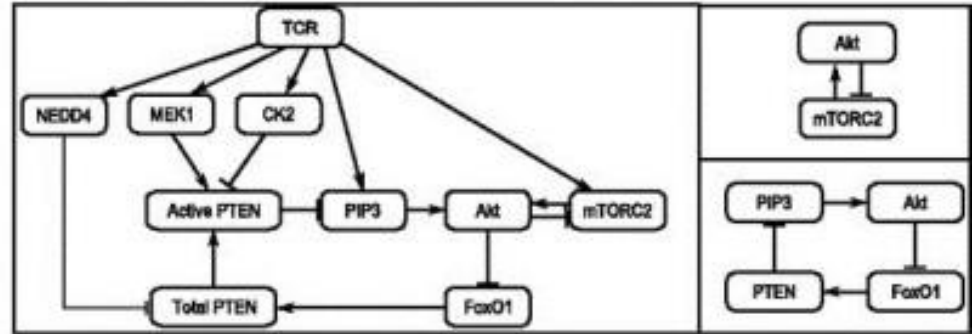
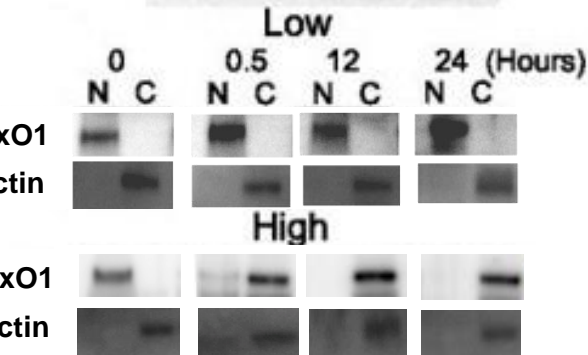
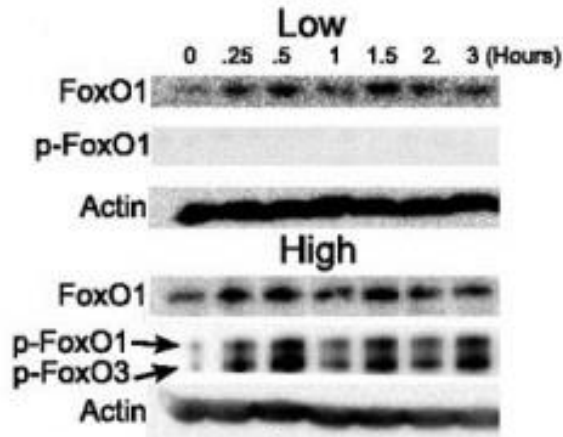
Experiments: Dr. Bill Hawse



Miskov-Zivanov et al. *Science Signaling* (2013)

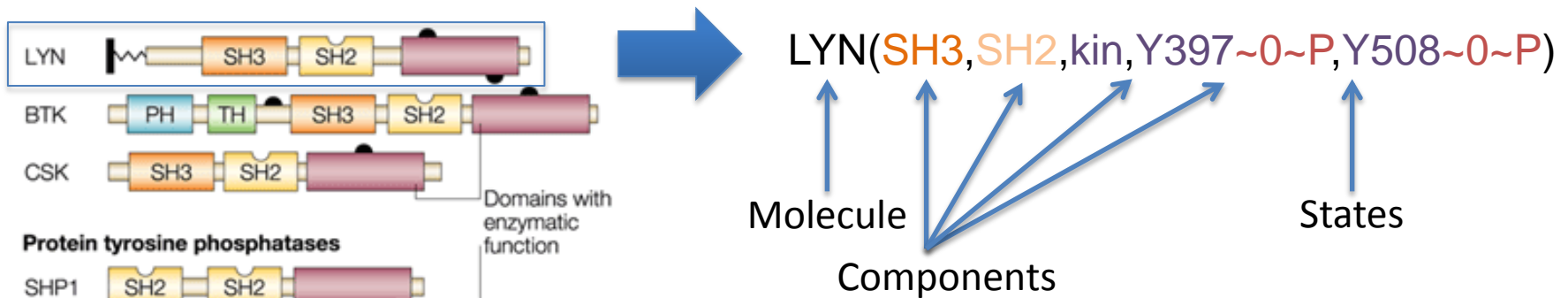
Hawse et al., *J. Immunol. Cutting Edge* (2015)

FoxO1 plays a critical role in PTEN regulation

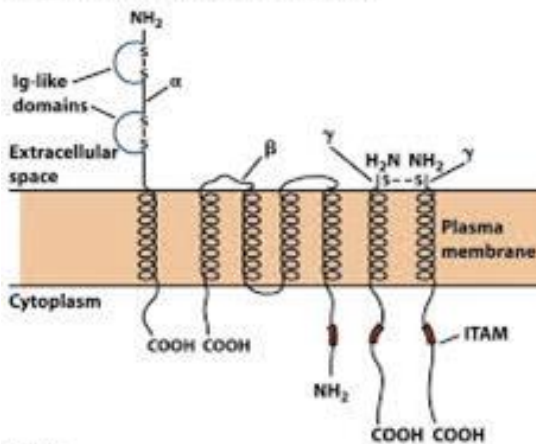


Rule-based Modeling (RBM)

Molecules are modeled as *structured objects*



FcεRI: High-affinity IgE receptor

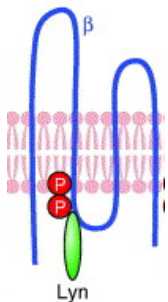


FcεRI(a_Ig, b_Y218~0~P, g_ITAM~0~P)

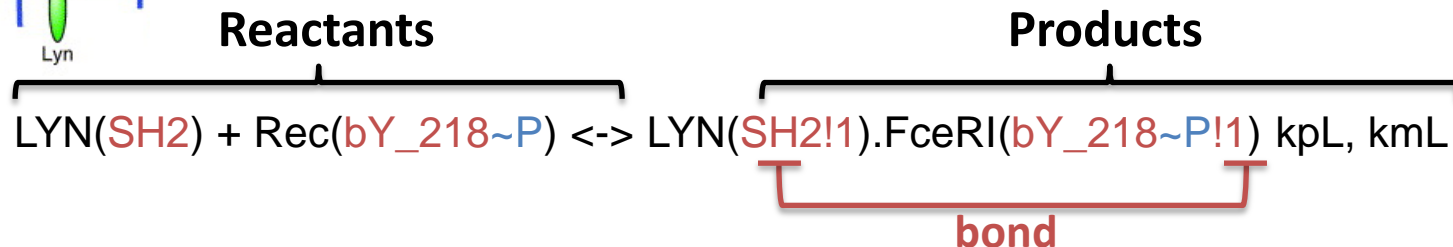
Figure 13-42
 Kelly, Alberts/MOLECULAR CELL BIOLOGY
 © 2007 W. H. Freeman and Company

Rule-based Modeling (RBM)

Rules define the interactions of molecules



“Lyn SH2 domain binds to phosphorylated Tyr 218 on the β subunit of Fc ϵ RI ”



Center – elements modified by the action of the rule

Context – elements required for reaction to occur but not modified

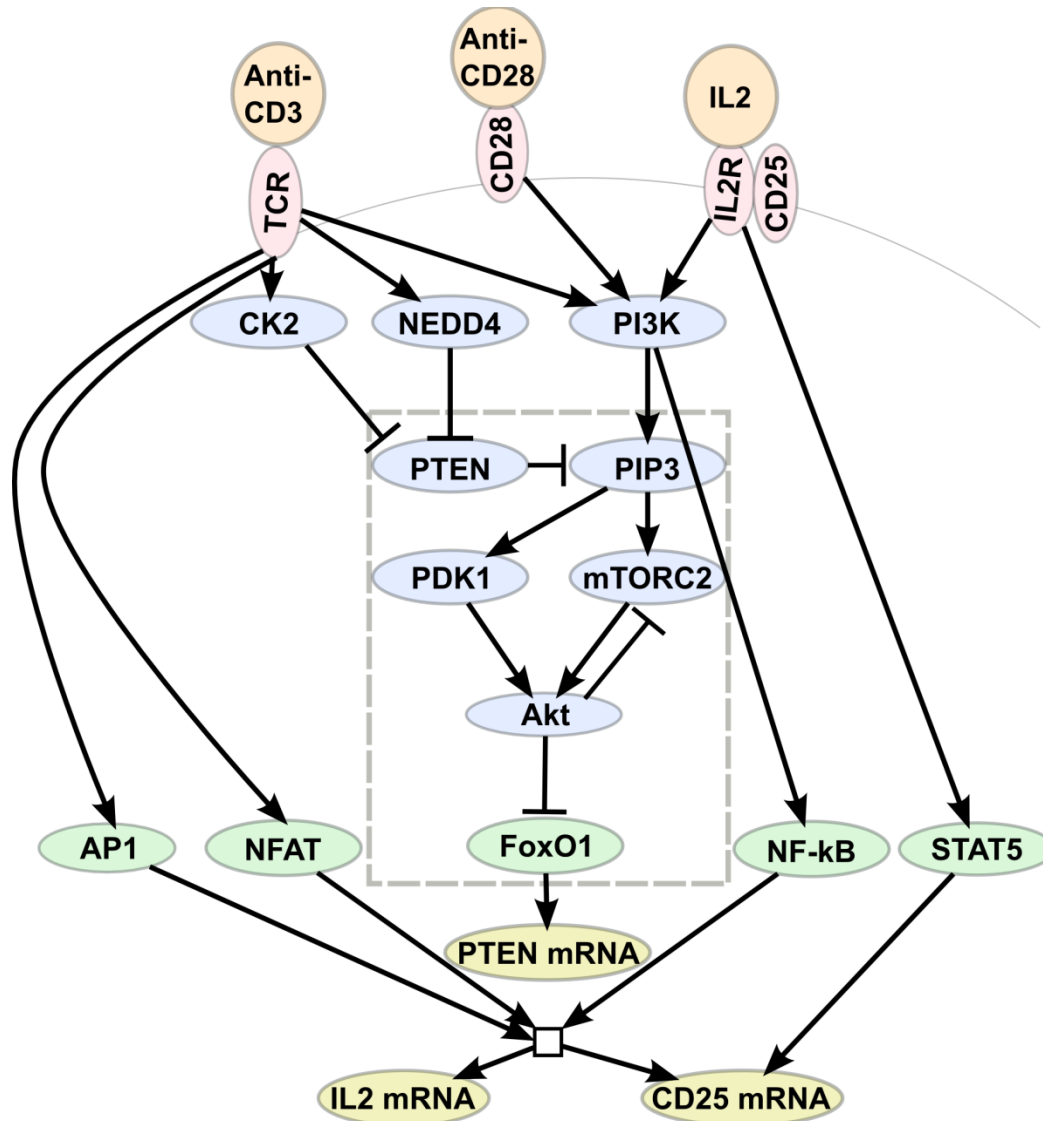
“Don’t write don’t care” – elements not mentioned may be in any state

➔ *One rule can generate reactions involving many different species*

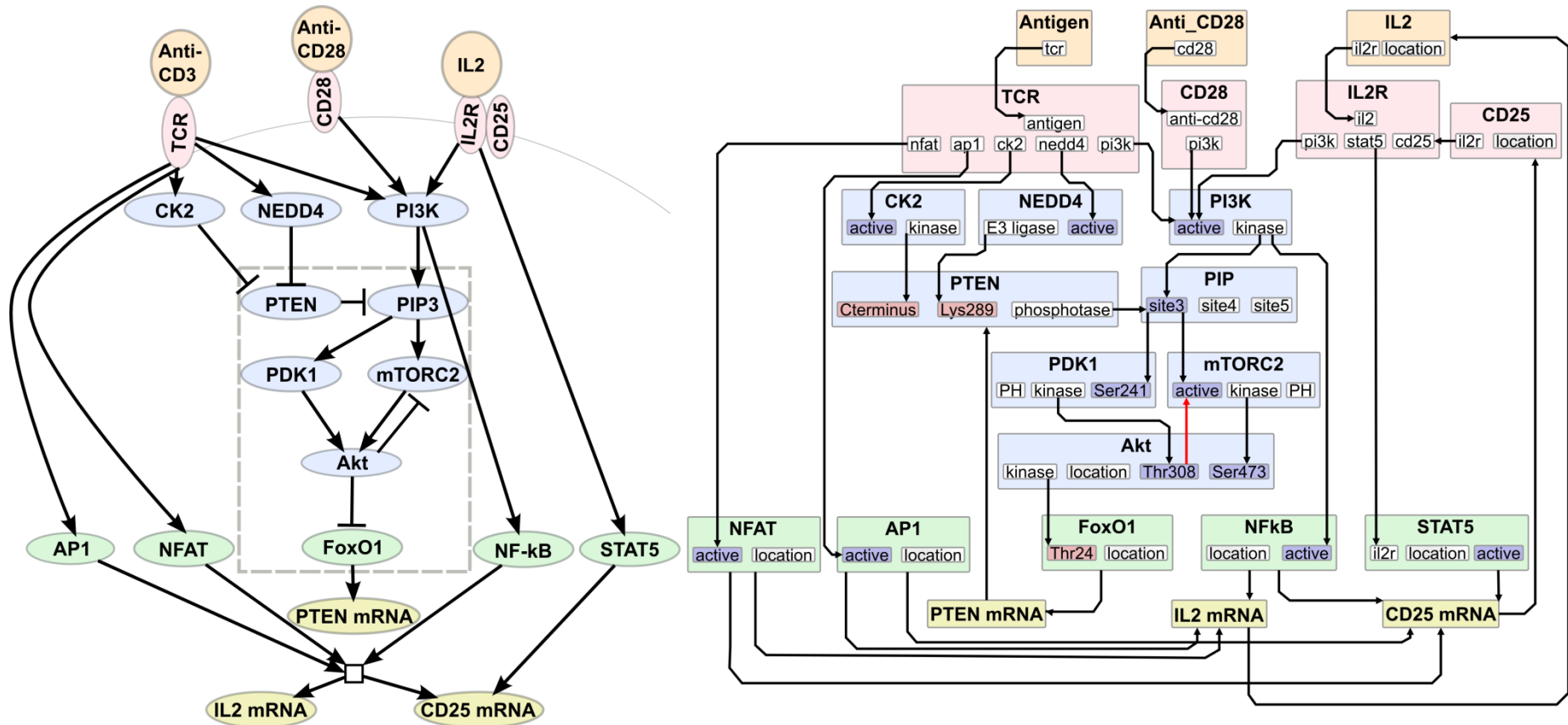
Reaction rate determined by **Mass Action kinetics**

$$\text{rate forward} = \text{kpL} * [\text{LYN}(\text{SH2})] * [\text{Rec}(\text{bY_218}\sim\text{P})]$$

Rule based modeling of TCR signaling

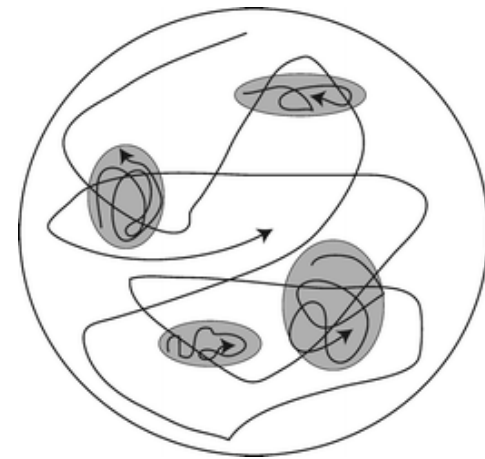
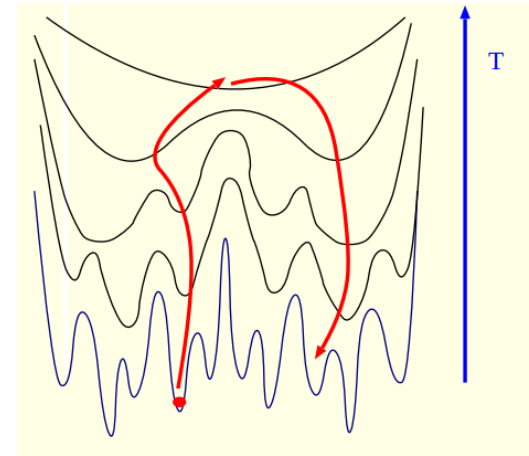


Rule based modeling of TCR signaling

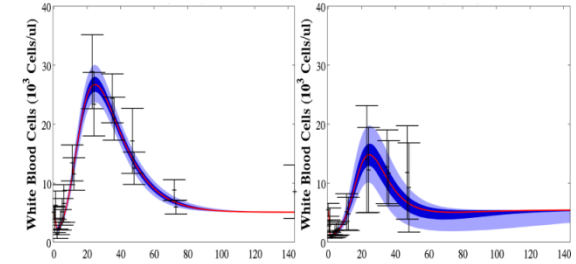
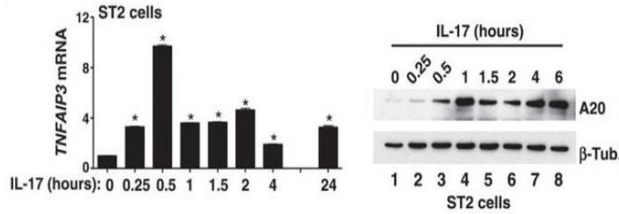


Parameter Estimation: Parallel Tempering

- Replica exchange Bayesian MCMC
- Allows for efficient sampling of multi-dimensional parameter space
- Run parallel MCMC chains at different temperatures
- Higher temperatures smooth the energy landscape, allowing for global sampling
- Chains switch temperatures when new local minima are found
- Prior distributions constrain parameter values



Ptempest



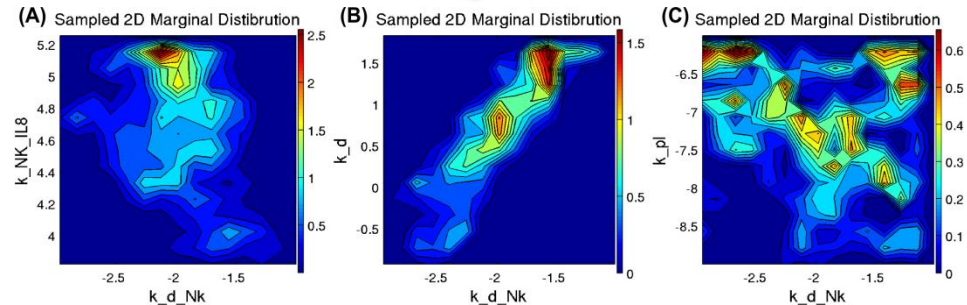
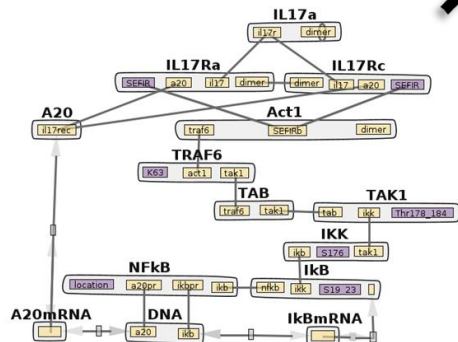
Experimental Data

ptempest

Parallel tempering for Bayesian parameter estimation of dynamical systems

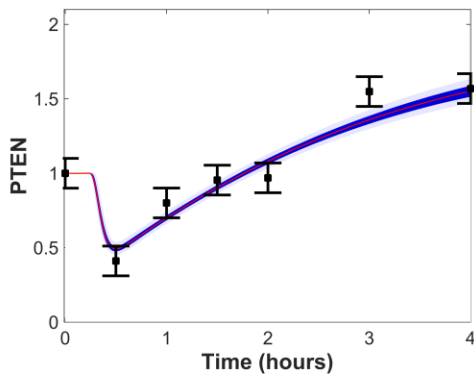
Best fit parameter ensembles

BioNetGen Model

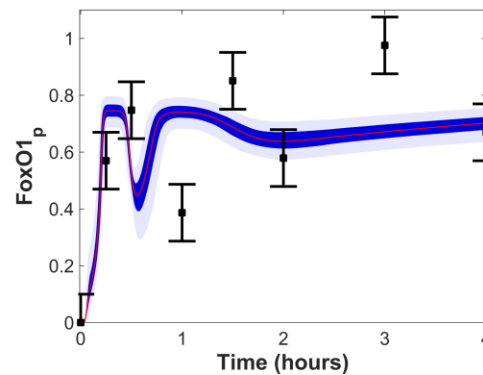
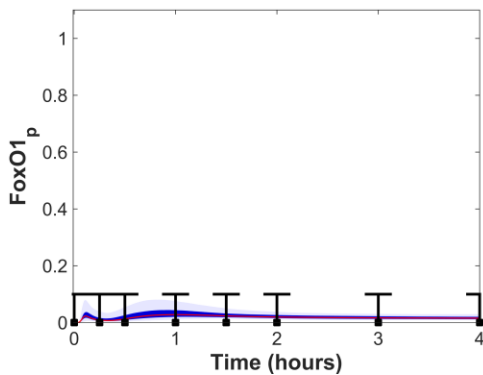
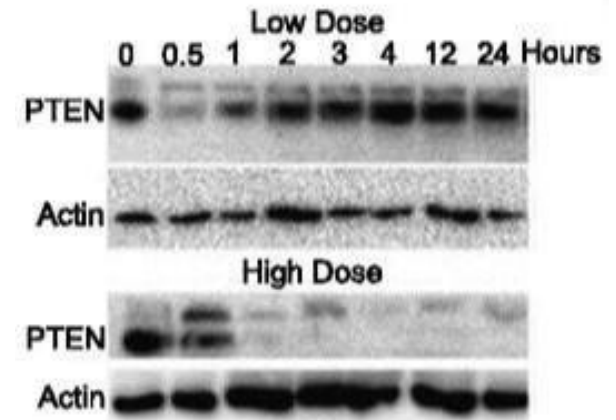
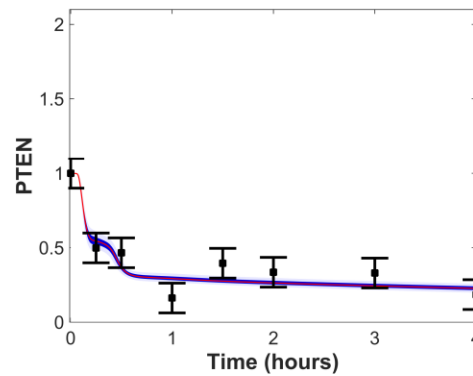


Simulations capture key differences between high and low dose stimulation

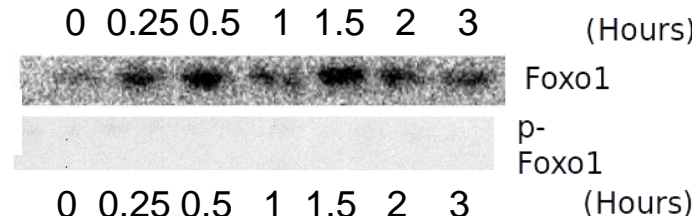
Low Dose



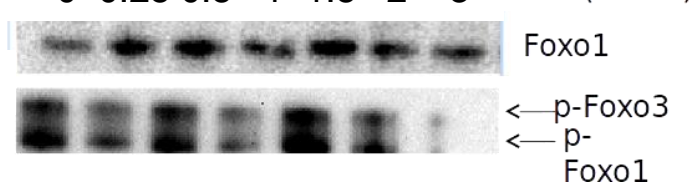
High Dose



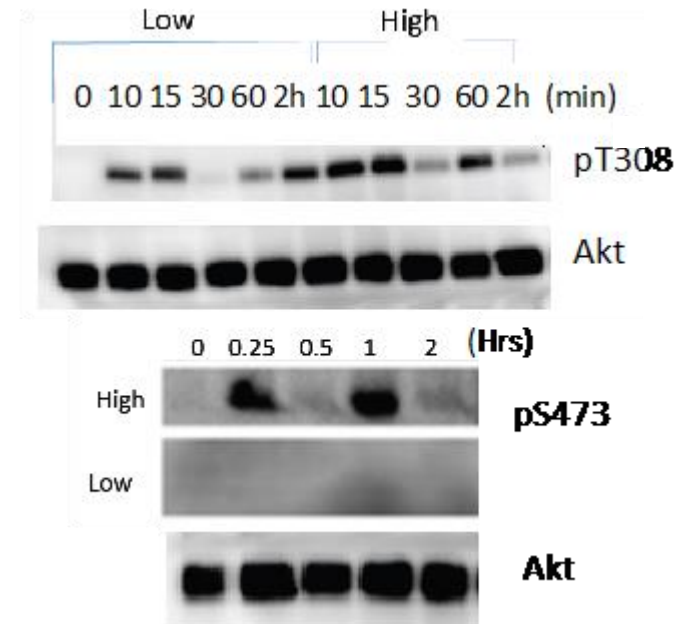
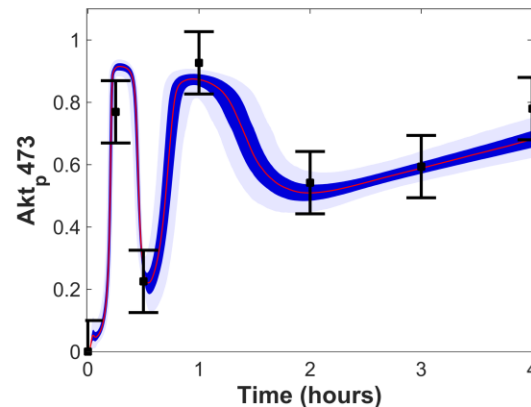
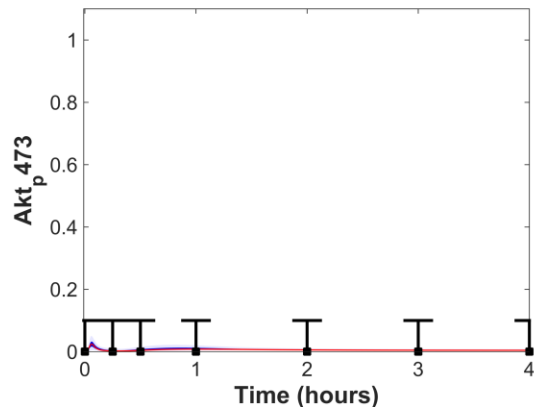
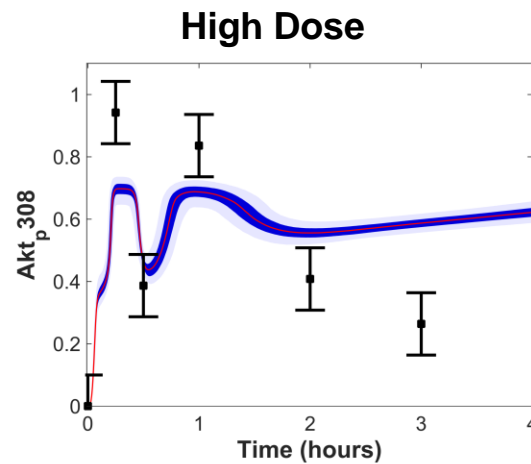
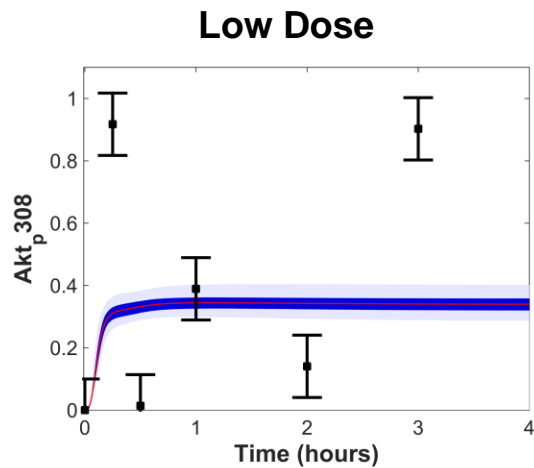
Low Dose



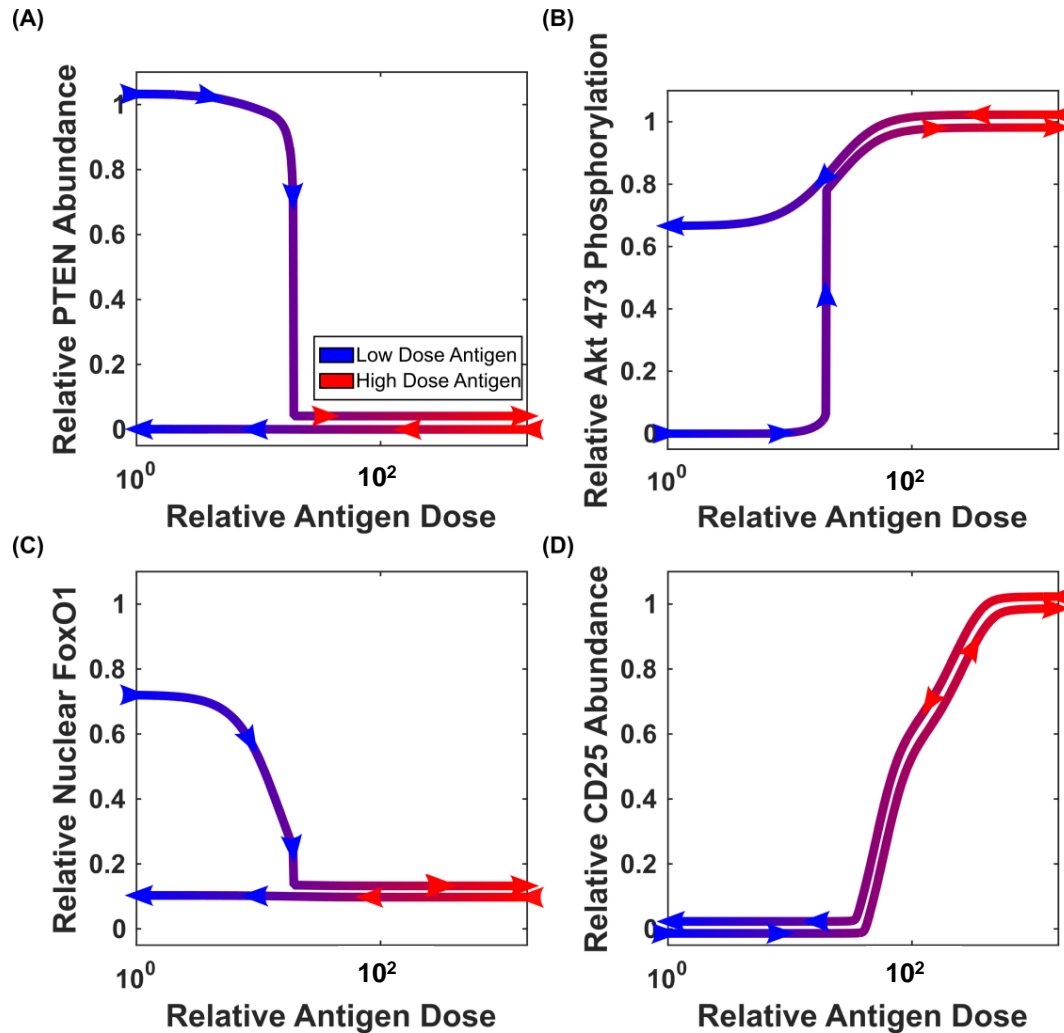
High Dose



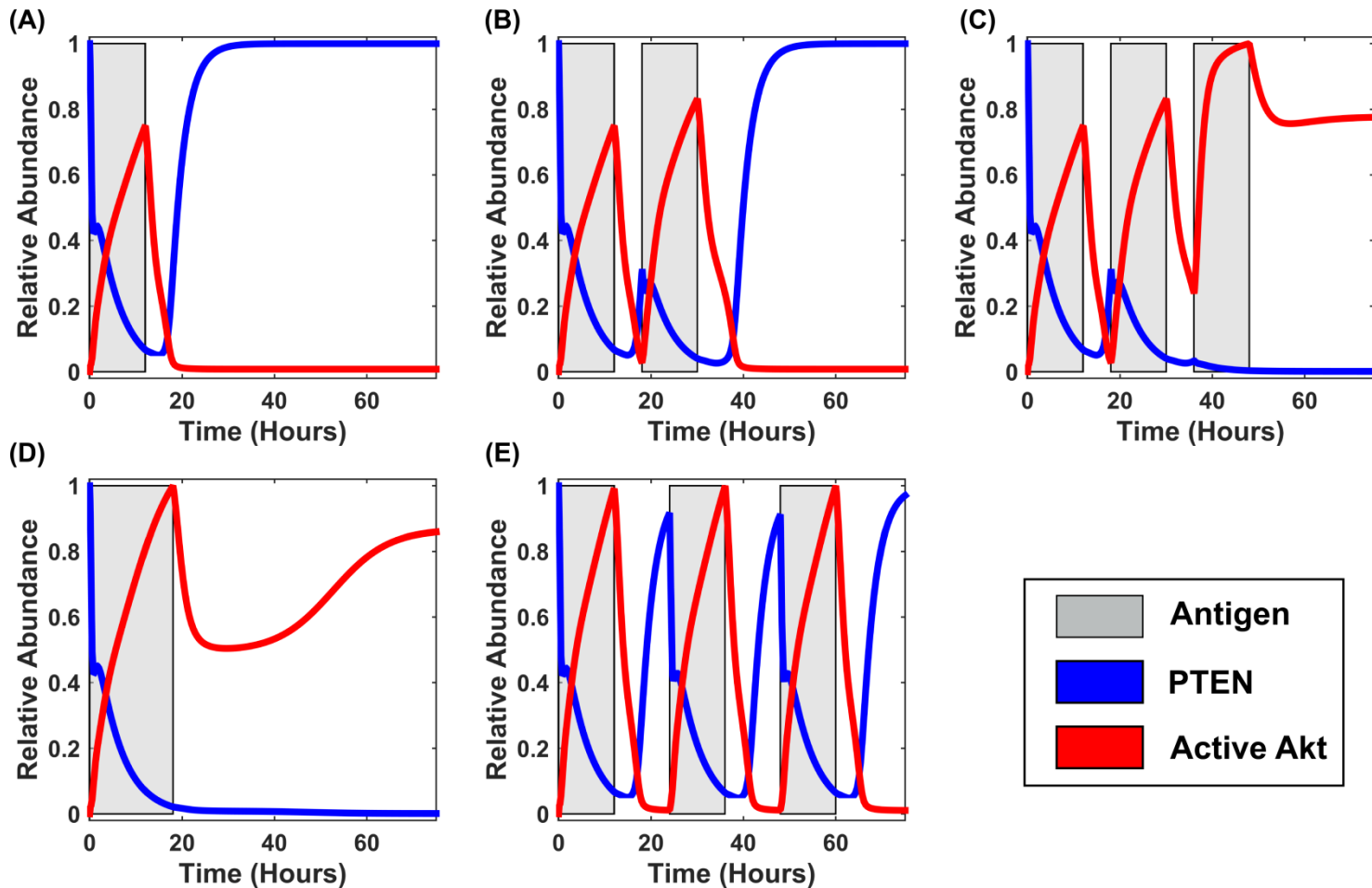
Simulations capture key differences between high and low dose stimulation



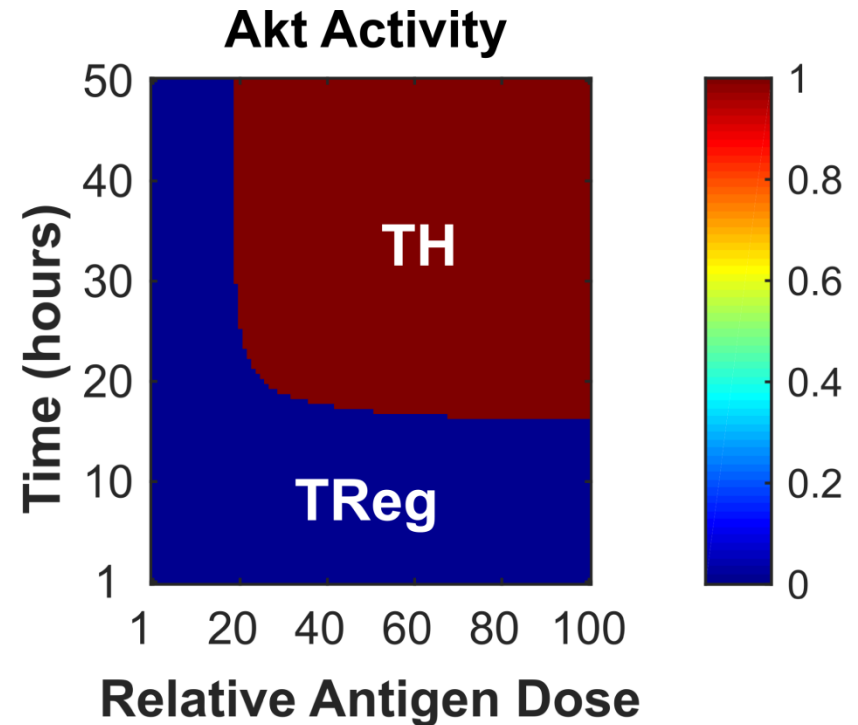
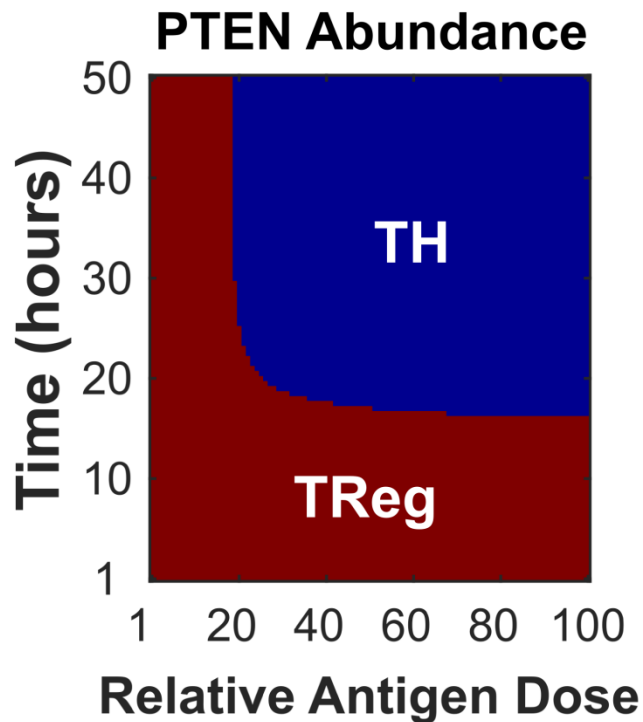
Sharp thresholds on antigen dose govern PTEN, Akt, and FoxO1 activity



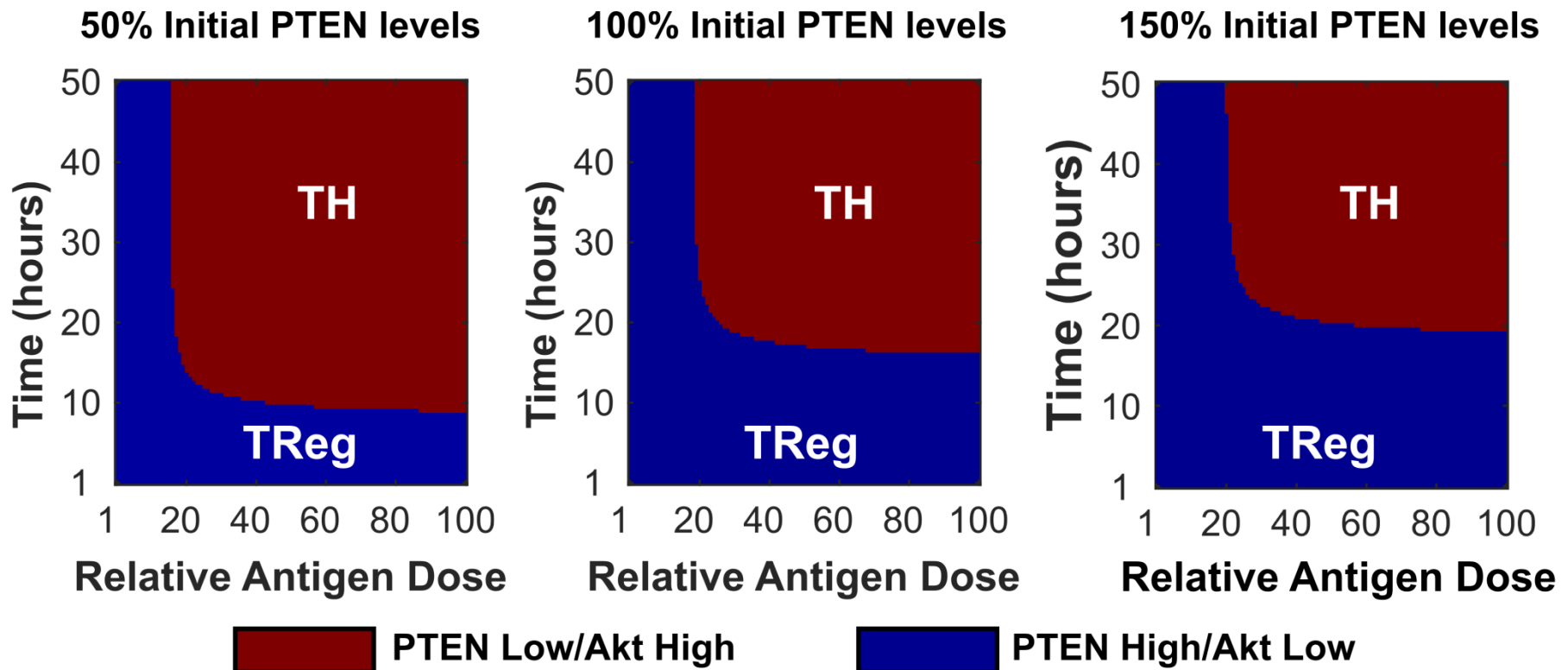
A minimum duration of stimulation is required to remove PTEN



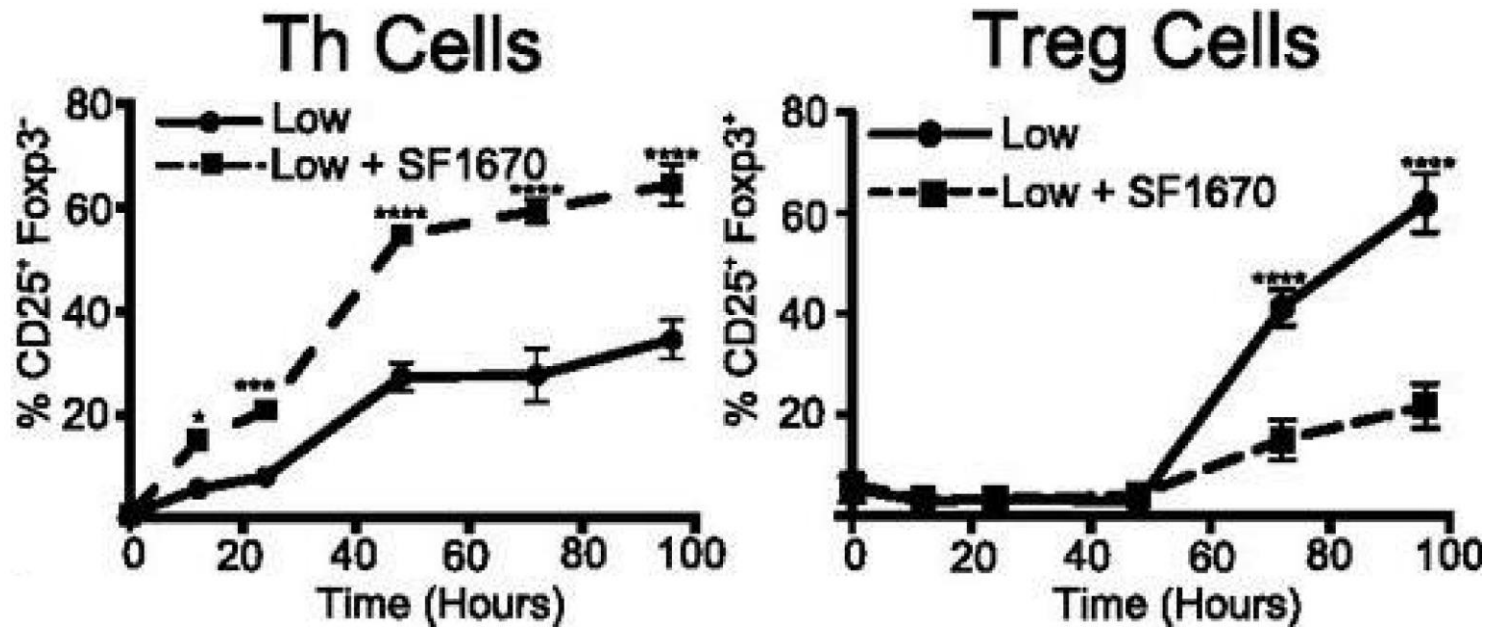
Dose and time thresholds define stimulation necessary to reduce PTEN and activate Akt



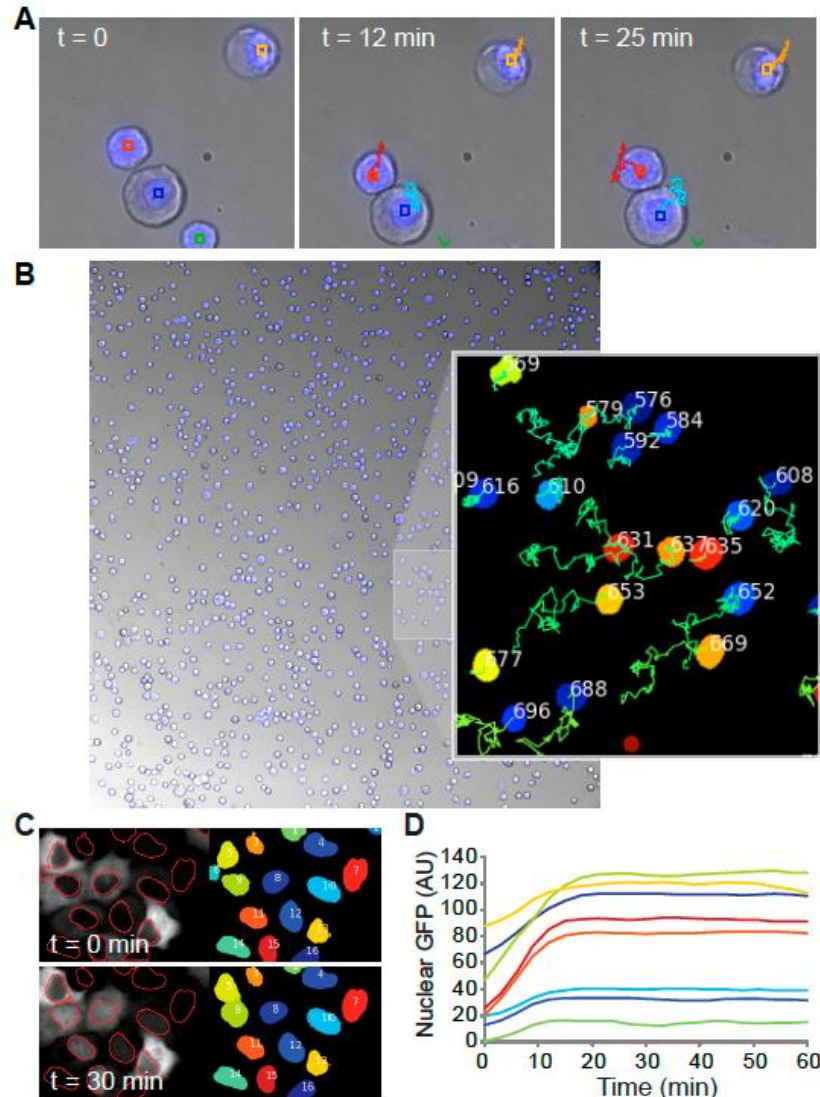
Varying initial concentrations of PTEN shifts the threshold



PTEN inhibitor SF1670 changes T cell populations

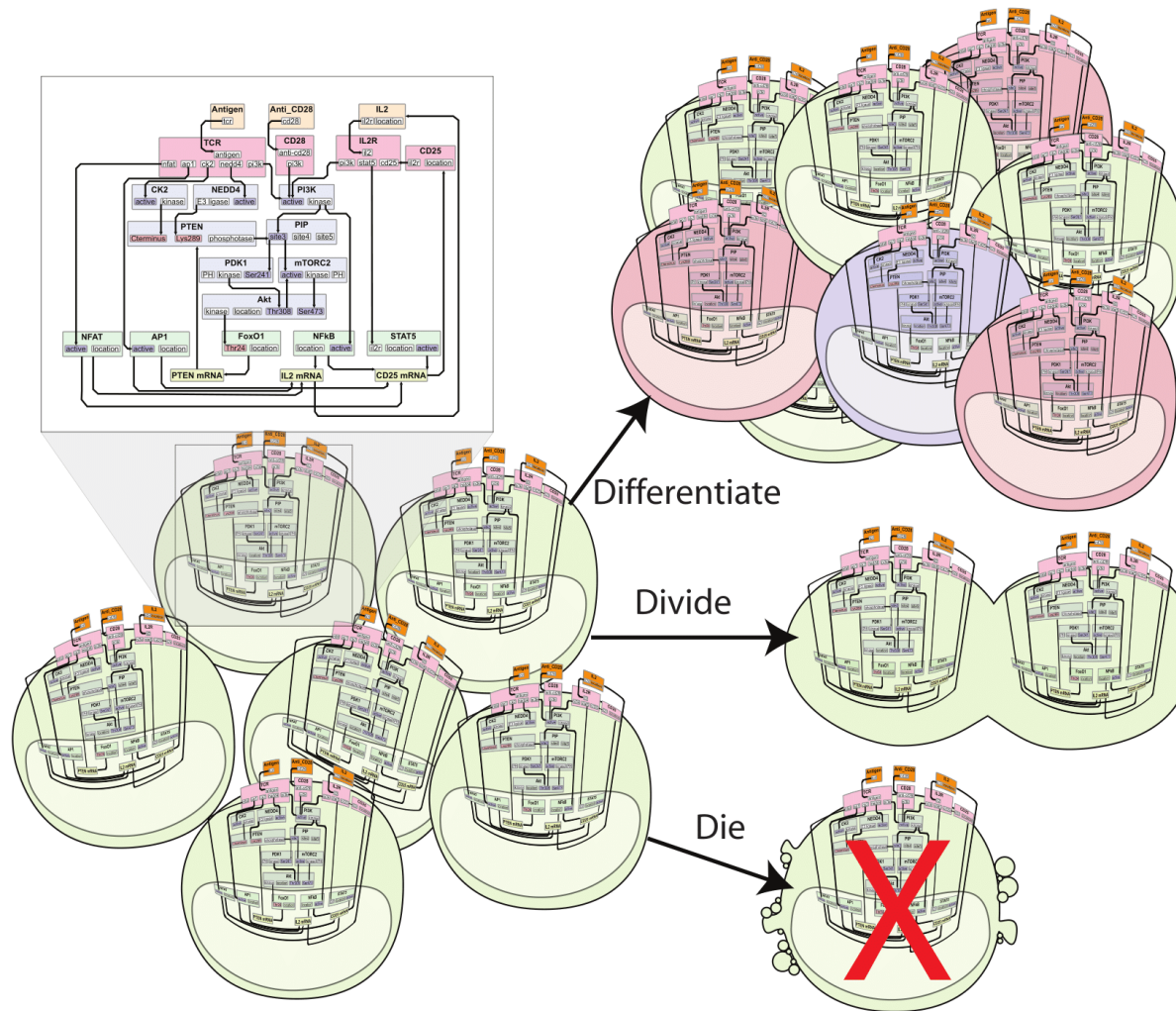


Live cell imaging can be used to validate model predictions



Courtesy of Dr. Robin Lee

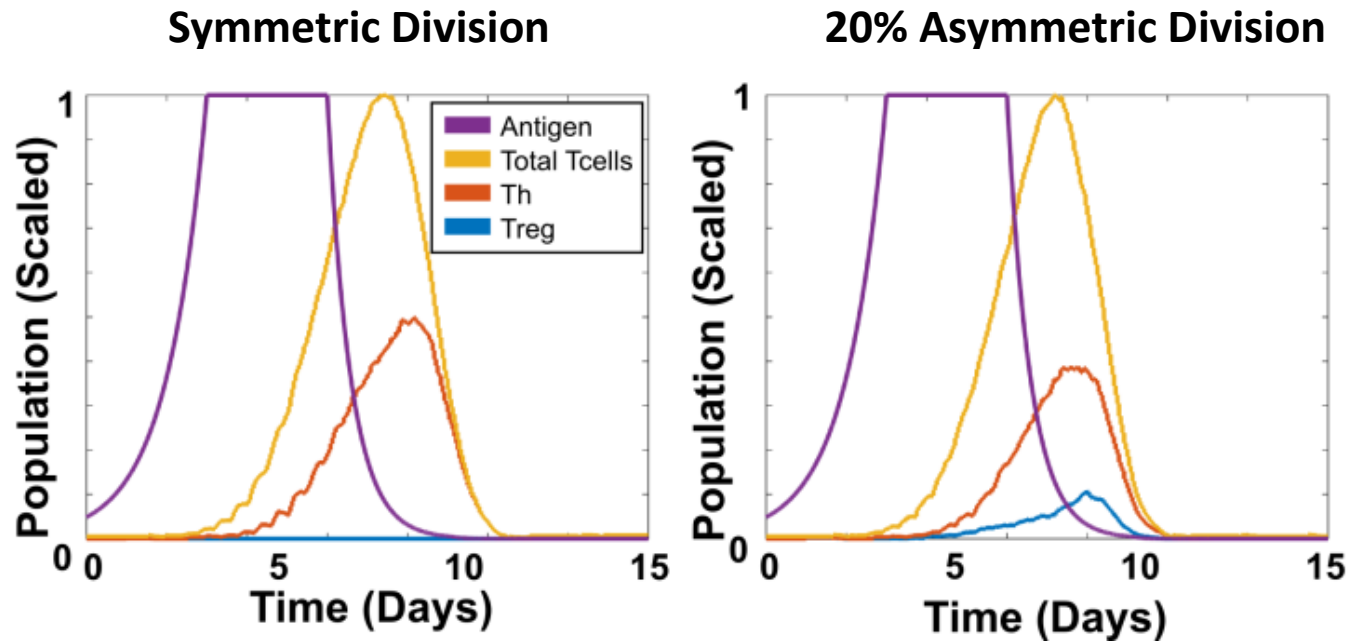
Encoding a RBM as a population model



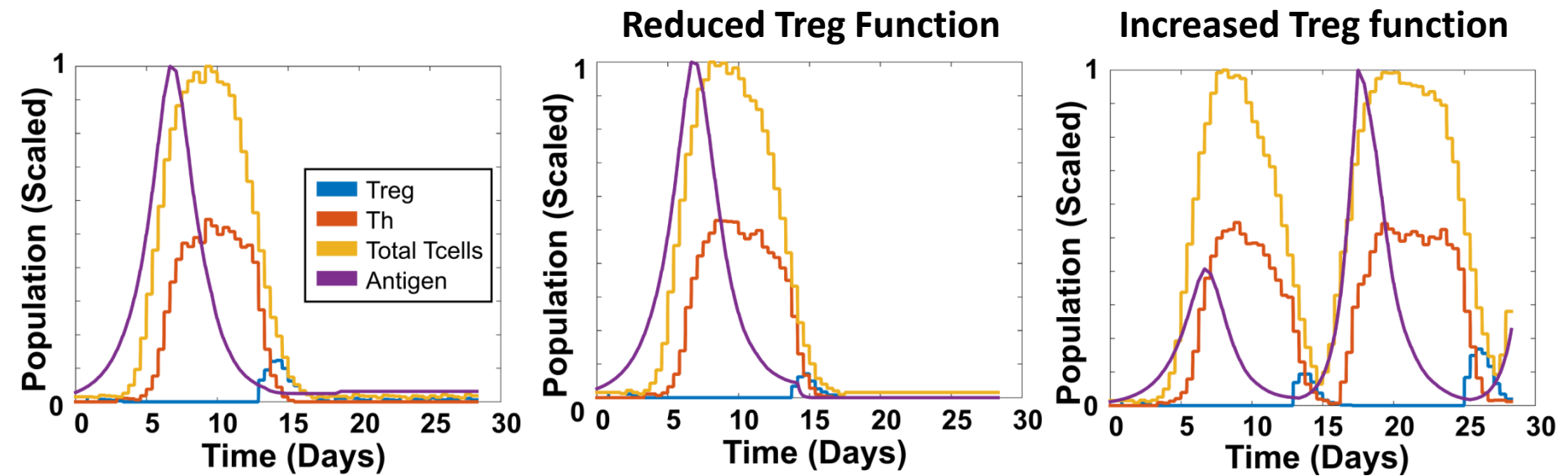
Populations model details

- T cells modeled as RBMs simulated independently
- Identical network architecture, heterogeneous initial conditions
- Communicate via shared IL-2 pool
- Simulated in 30 minute blocks
- Differentiate based on thresholds on total Akt activity
- Divide based on IL-2 signaling
- Die based on individual cell lifetime

Asymmetric T cell division allows for the emergence of a Treg population



Tregs alter the trajectory of disease clearance



Key extensions of the population model

- Fine tune asymmetric cell division
- More detailed differentiation
 - FOXP3, T-bet
- Include additional cell types
 - DCs, macrophages, CD8+ T cells, memory T cells
- Environment: Cytokines, spatial effects

Conclusions

- A novel Akt-FoxO1-PTEN positive feedback loop gives rise to bistability in PTEN/Akt activity
- Thresholds in both the strength and duration of TCR activation control commitment to two steady states
- Perturbing the system to shift this threshold could tune T cell population sizes and alter immune responses

Acknowledgements

- Faeder Lab
 - Dr. Justin Hogg
 - Dr. Natasa Miskov-Zivanov
- Morel Lab
 - Dr. Bill Hawse
 - Dr. Michael Turner
 - Ashley Menk
- Dr. Robin Lee
- Dr. Larry Kane
- NIH P41GM103712
- NIH T32 AI089443