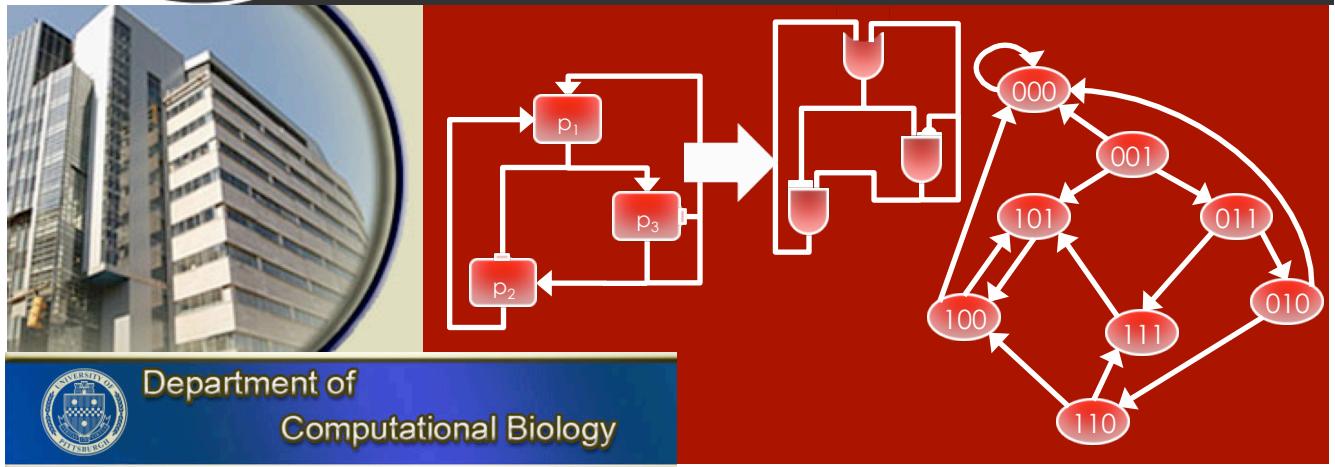


Virtual PI  
Meeting

April 2012



Computational M<sub>odeling</sub> and A<sub>nalysis</sub> for C<sub>omplex</sub> S<sub>ystems</sub>



# Timing Matters in T Cell Differentiation

Natasa Miskov-Zivanov  
University of Pittsburgh

# Acknowledgements



## ■ Faeder Lab:

- Department of Computational and Systems Biology, School of Medicine, University of Pittsburgh
  - John Sekar, James Faeder

## ■ Morel Lab:

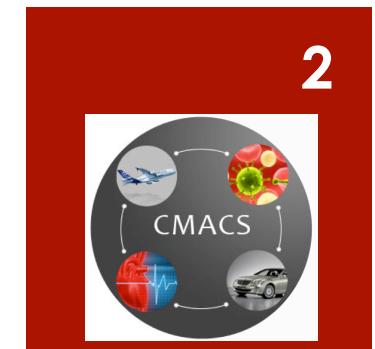
- Department of Immunology, School of Medicine, University of Pittsburgh
  - Michael Turner, Penelope Morel

## ■ Clarke Lab:

- Computer Science Department, Carnegie Mellon University
  - Paolo Zuliani, Haijun Gong, Edmund Clarke
  - Deepa Sathaye, Alexander Moser

## ■ Funding:

- NSF (Expeditions in Computing)
- NIH

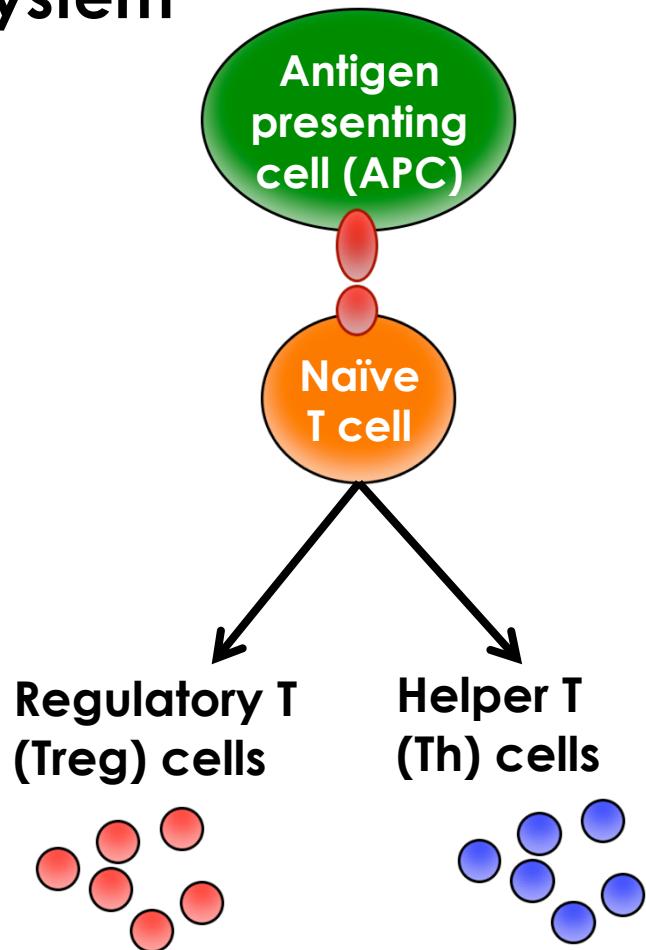


2

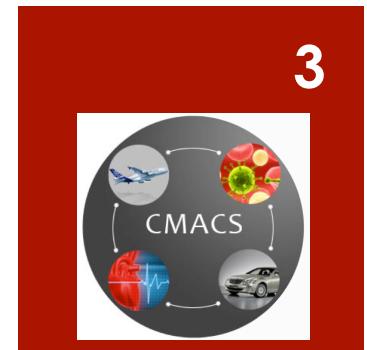
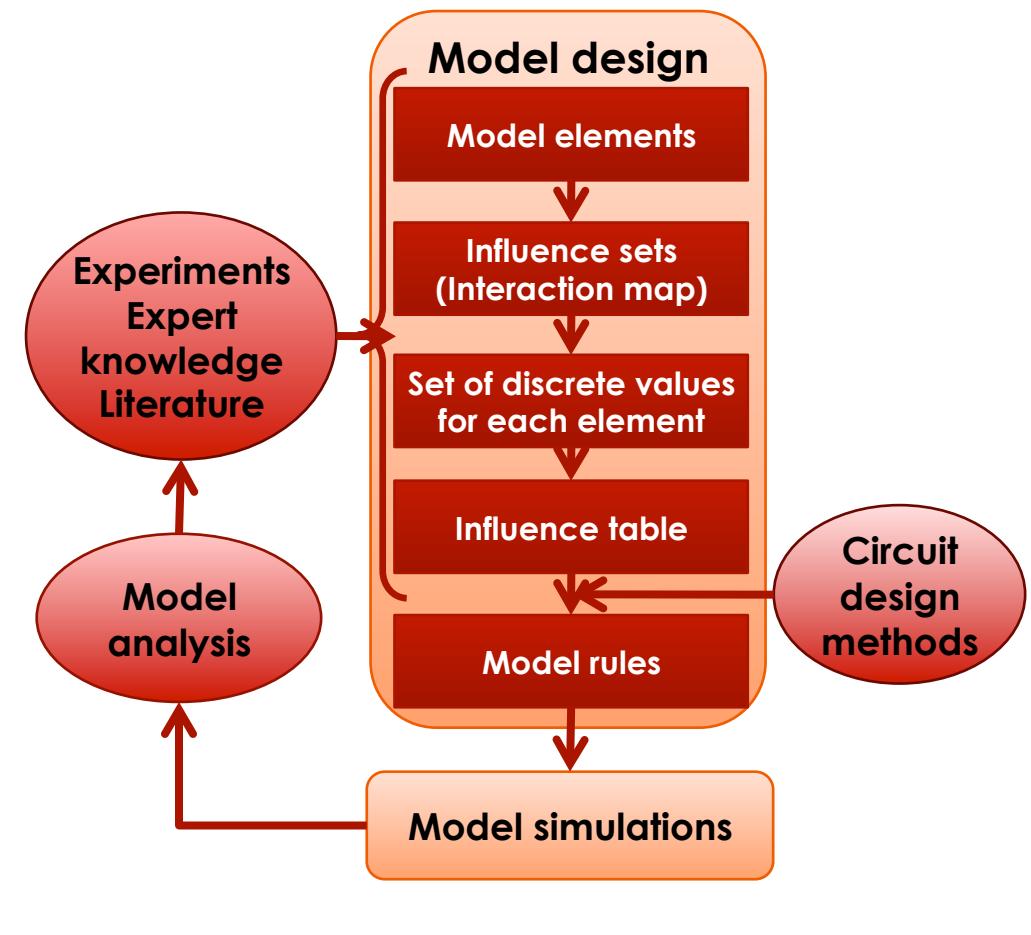
# Outline

3

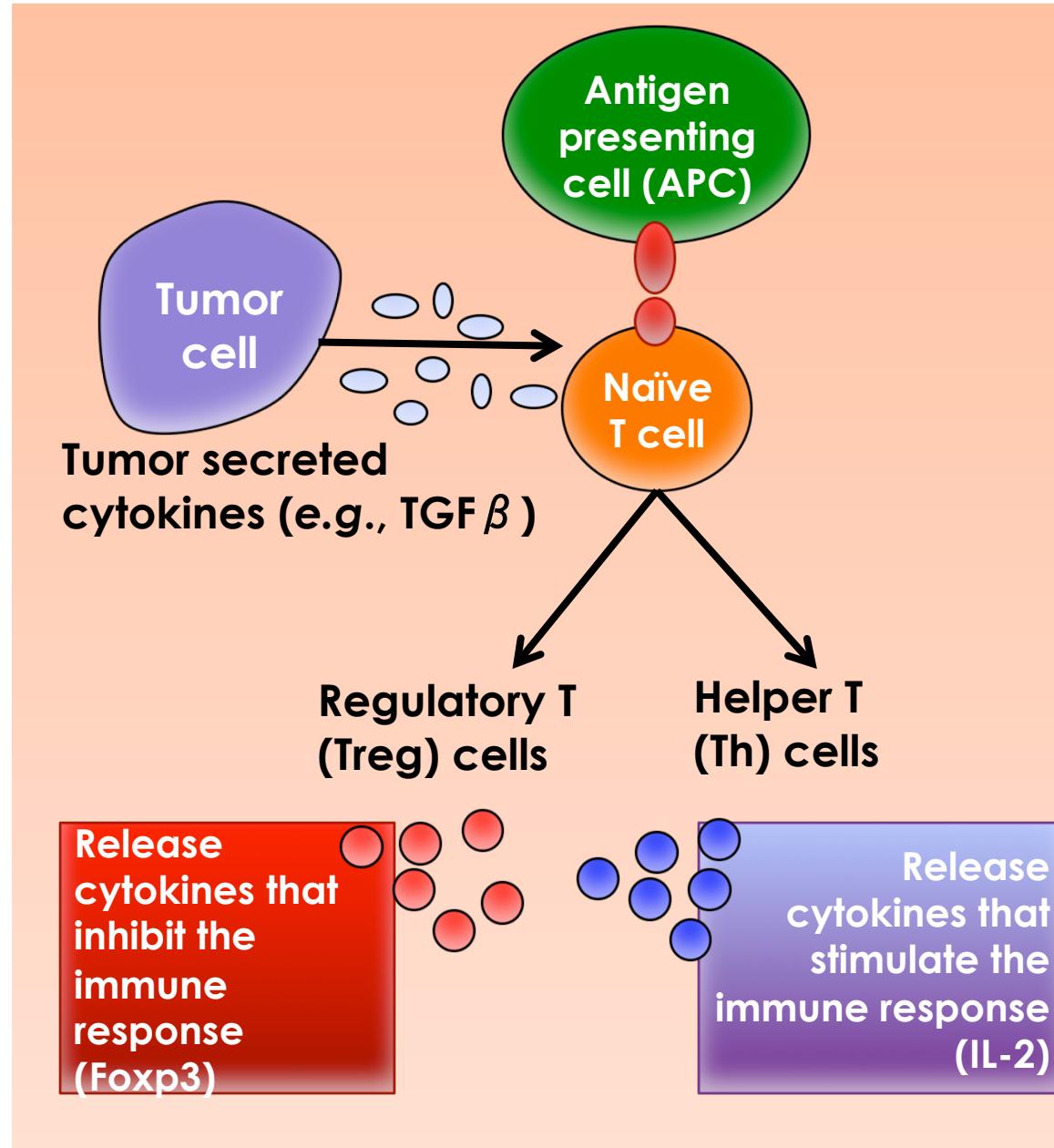
## System



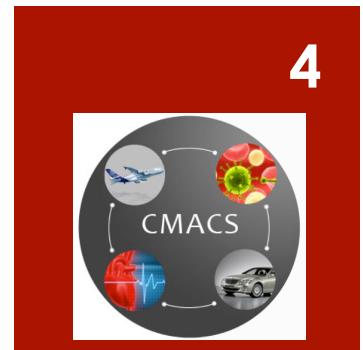
## Methodology



# T cell differentiation



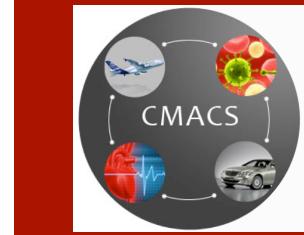
4



- T cell subpopulation ratios are critical for numerous immune and auto-immune pathologies
- Determinants of the peripheral T cell differentiation are not completely understood

# Questions to address

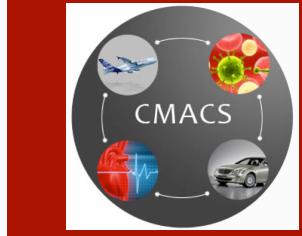
5



- How can we predict the antigen dose that will induce Treg versus Th?
- Are there signaling cascades in T cells that are critical in this cell fate decision?
- Can we use modeling to identify the critical factors?
- Many clinical trials involving DC vaccines do not take antigen dose into account
- Could also be important for the ex vivo expansion of Treg for therapeutic purposes

# Modeling goals

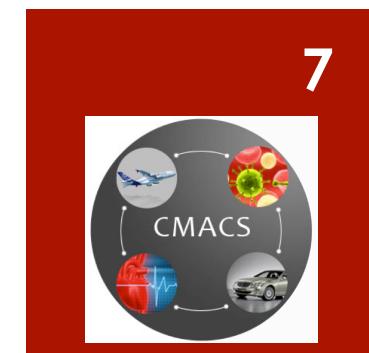
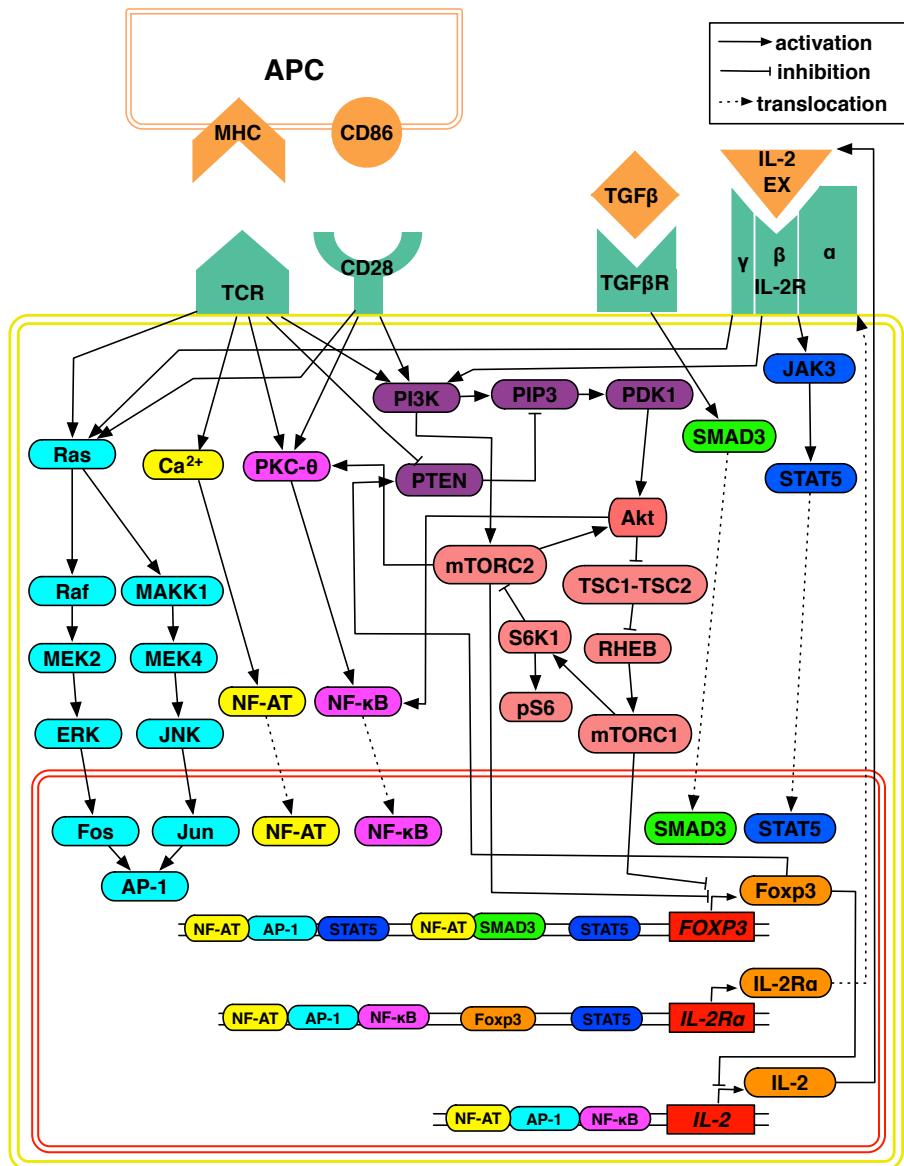
6



- Determine whether known mechanisms are *sufficient* to explain experimental observations
- Suggest additional experiments to identify missing mechanisms and clarify areas of *uncertainty*
- Identify early markers of the response

# Network model

7



## Receptors:

- T cell receptor (TCR)
- Co-stimulation through CD28
- IL-2 receptor (IL-2R)
- TGF $\beta$  receptor (TGF $\beta$  R)

## Transcription factors:

- AP-1, NFAT, NF $\kappa$ B, SMAD3, STAT5

## Genes:

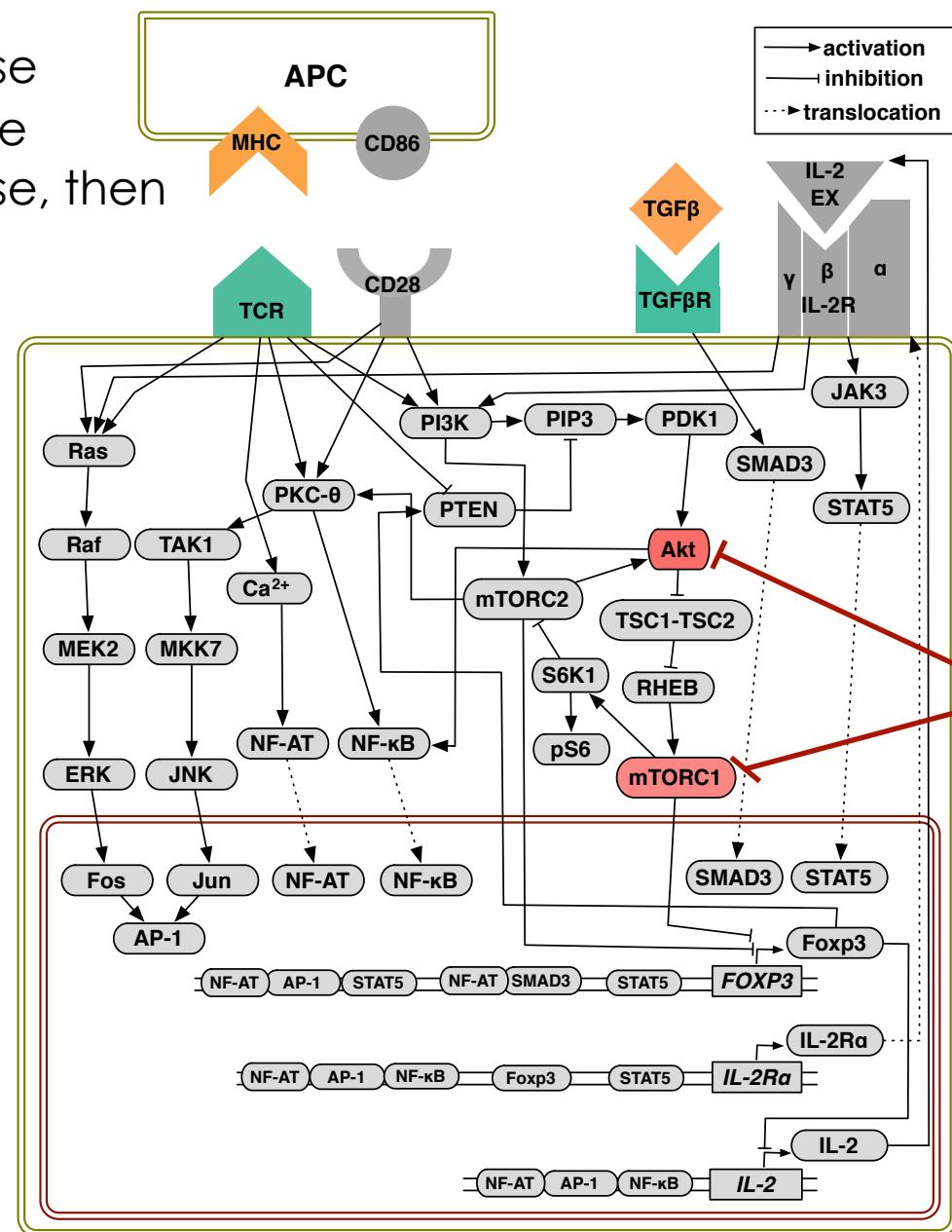
- IL-2, CD25, Foxp3

## Other important elements:

- PTEN, PI3K, PIP3, PDK1,
- Akt, mTORC1, mTORC2, TSC1-TSC2, Rheb, S6K1, pS6

# Five scenarios

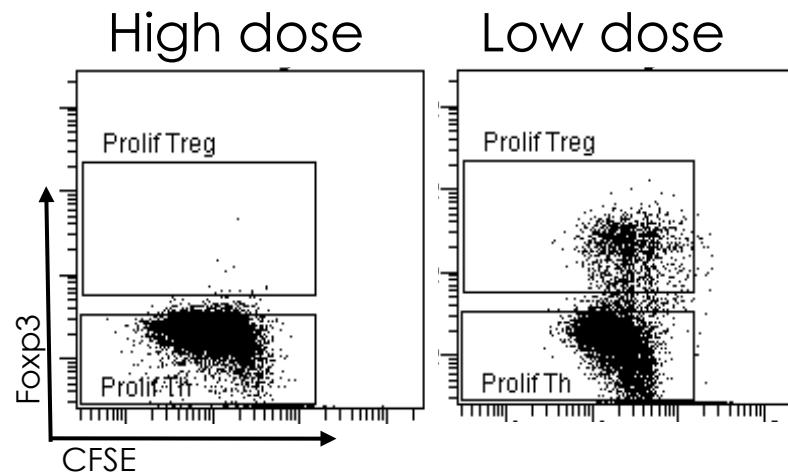
1. High antigen dose
2. Low antigen dose
3. High antigen dose, then removed



4. High antigen dose and  $TGF\beta$
5. High antigen dose, then inhibitors added

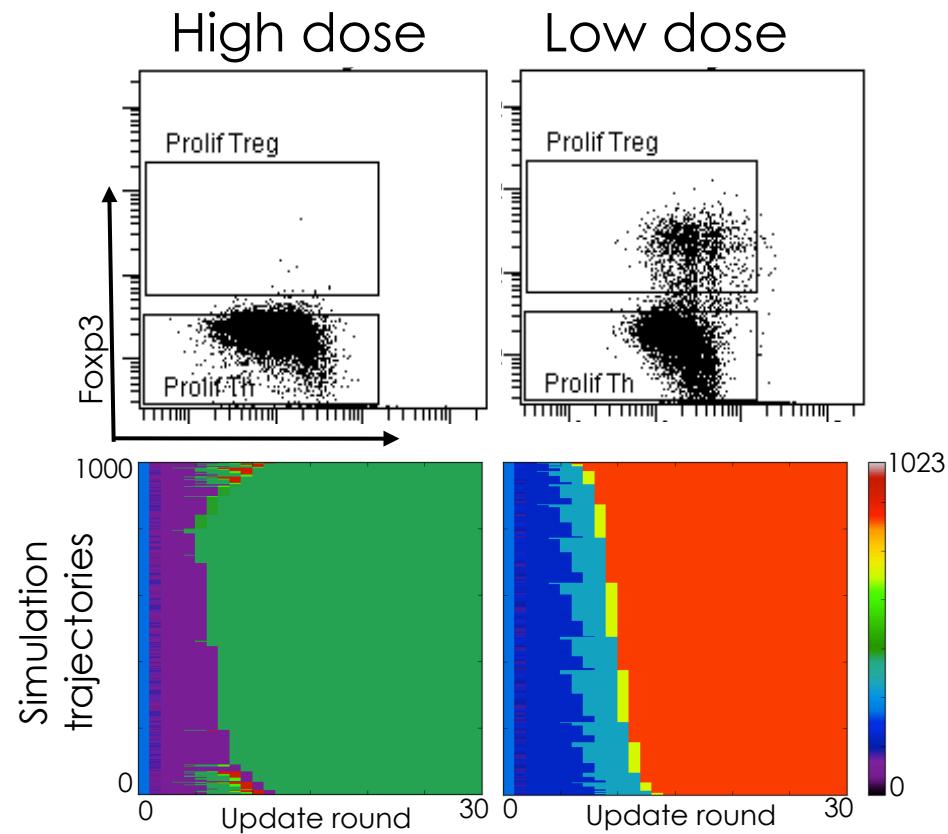
# Scenarios 1 and 2: High and Low antigen dose

9



# Scenarios 1 and 2: High and Low antigen dose

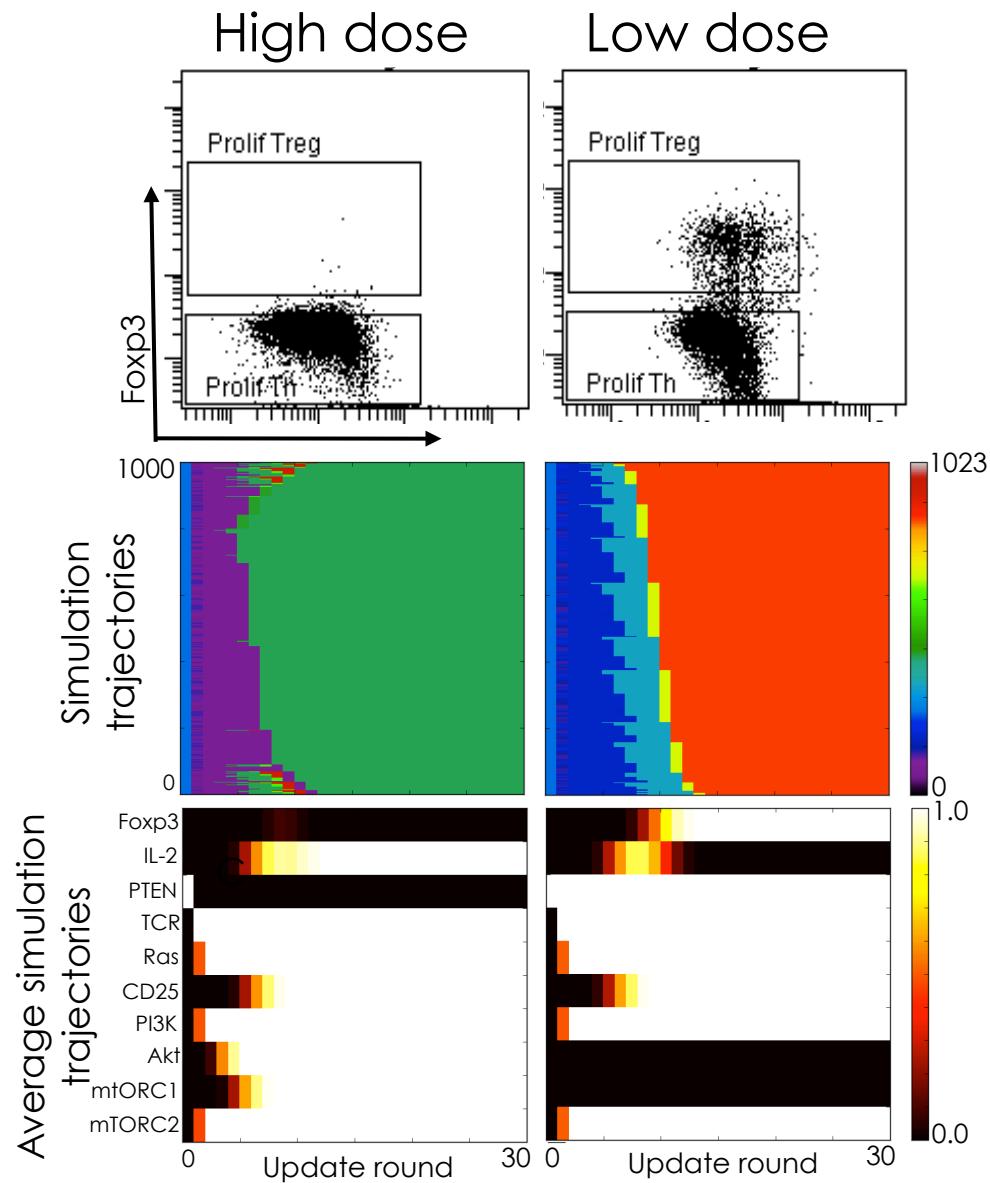
10



Source: N. Miskov-Zivanov et al., in preparation.

# Scenarios 1 and 2: High and Low antigen dose

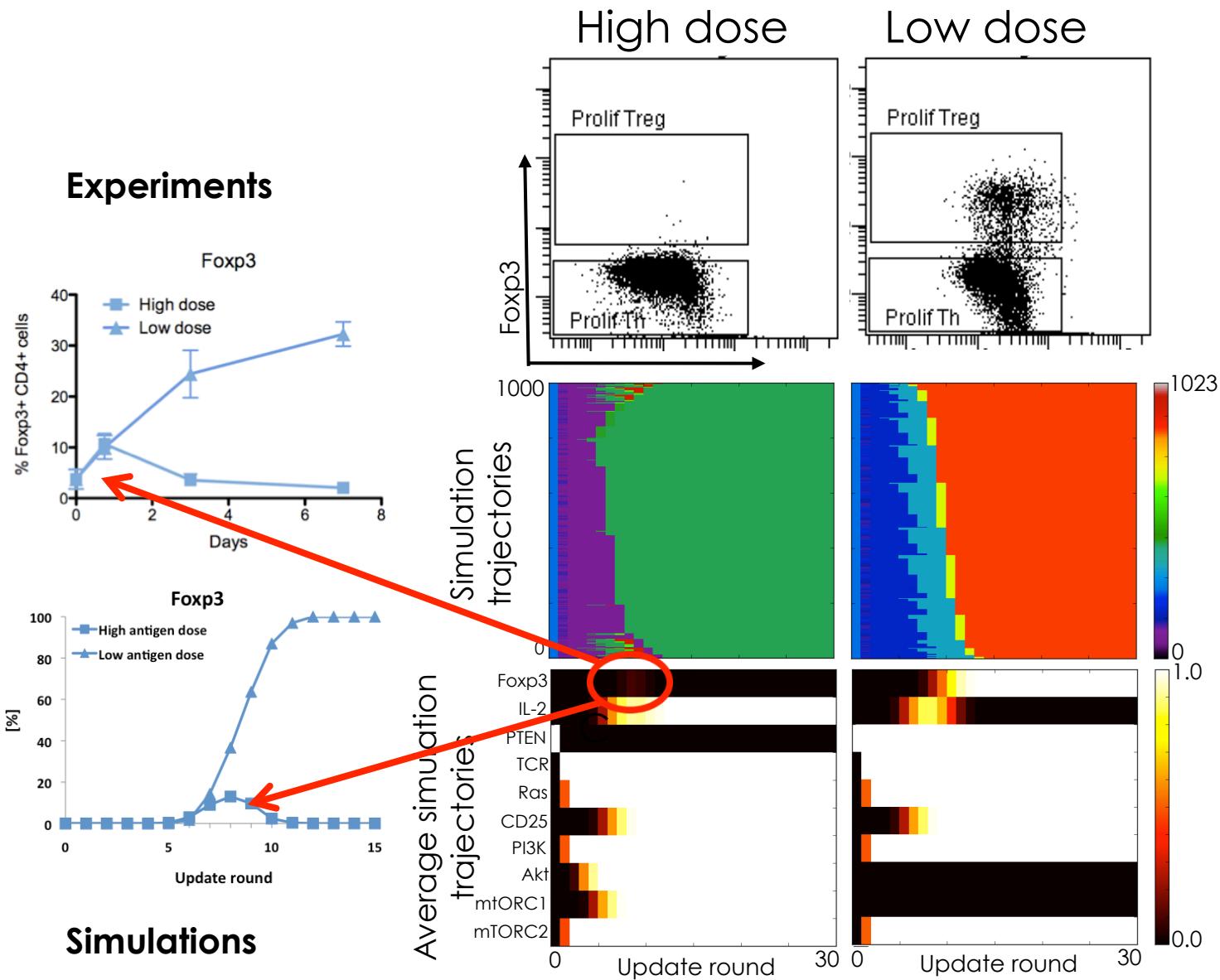
11



Source: N. Miskov-Zivanov et al., in preparation.

# Scenarios 1 and 2: High and Low antigen dose

12

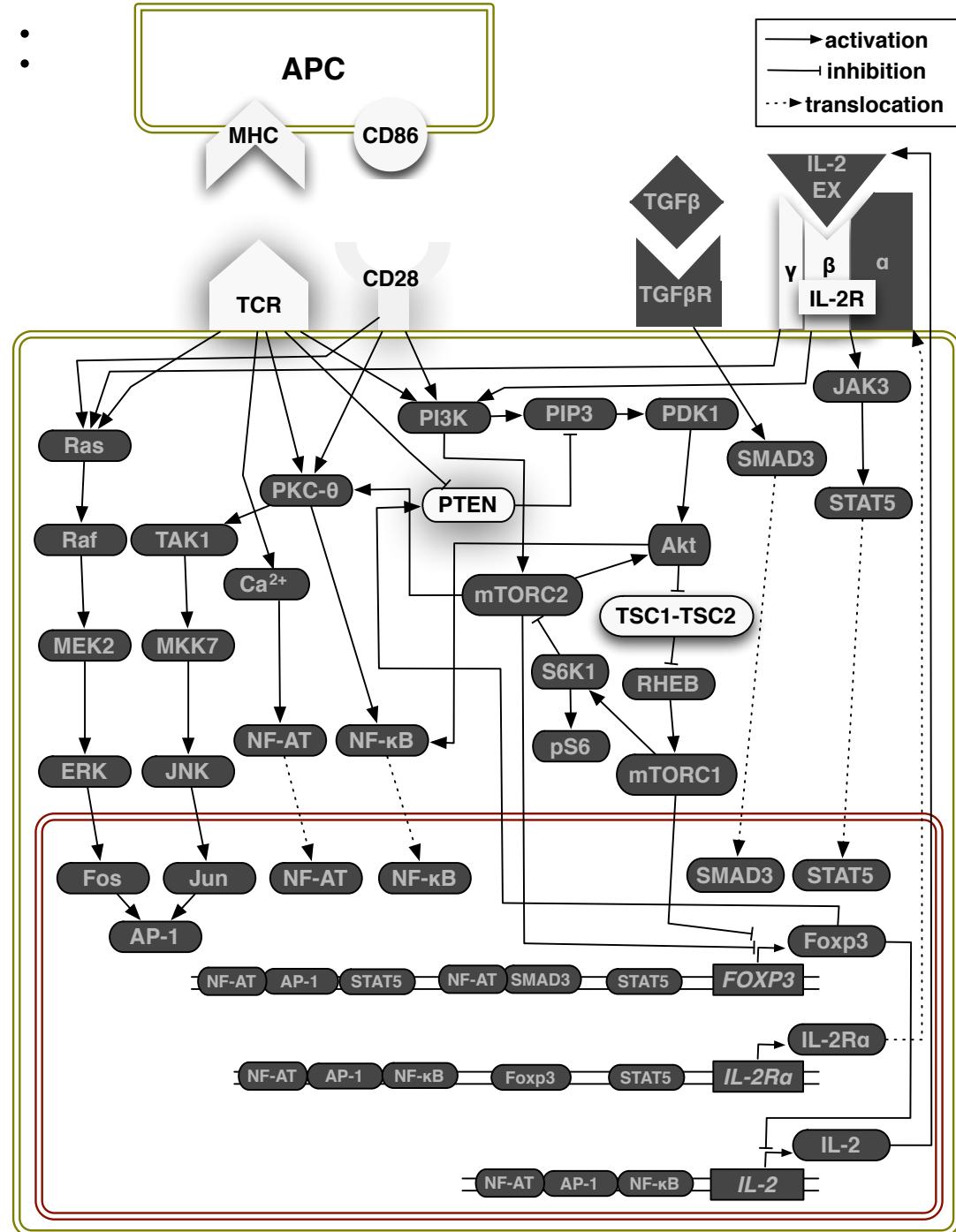


Source: N. Miskov-Zivanov et al., in preparation.

# Scenario 1: High antigen dose

13

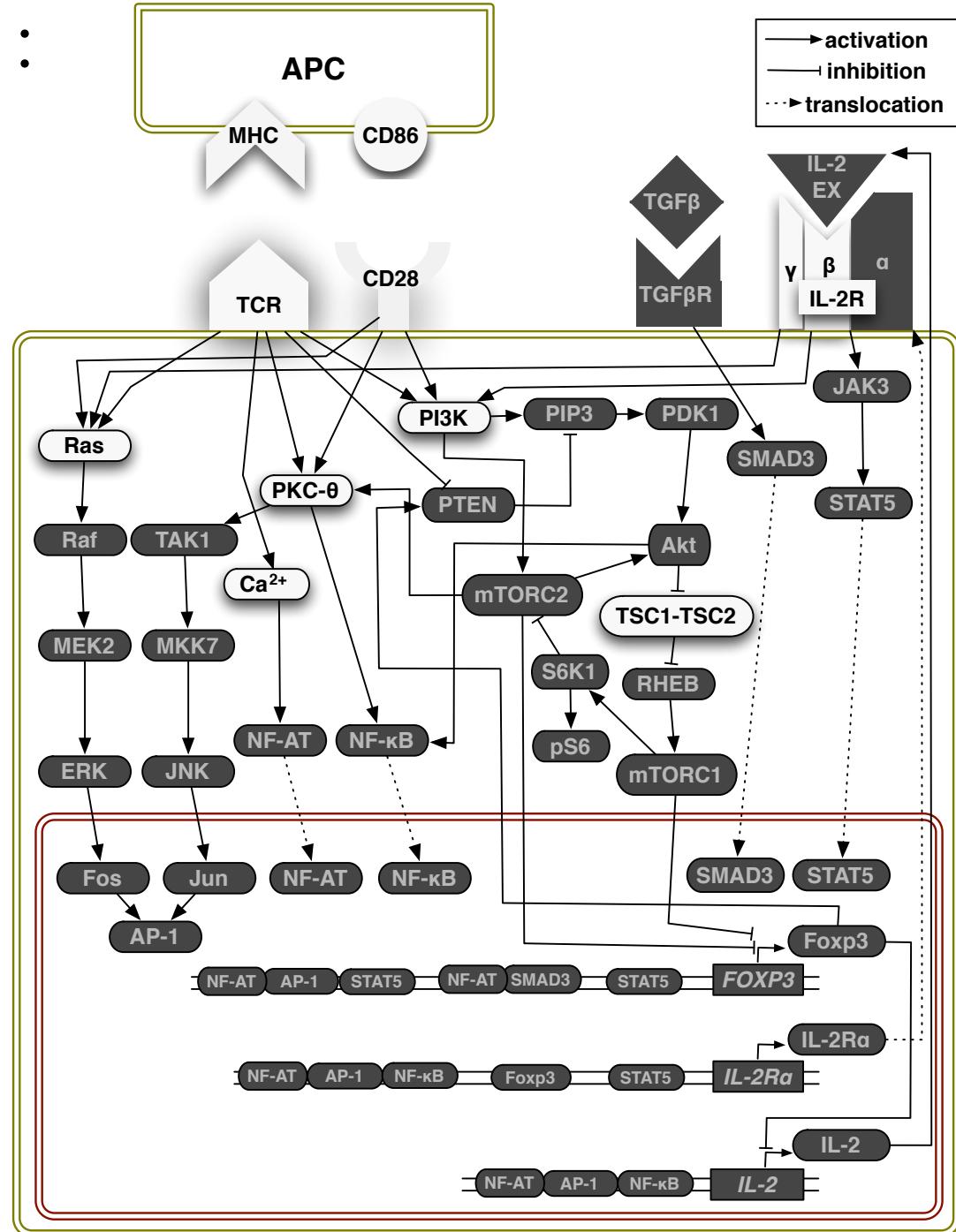
	value = ON (1)
	value = OFF (0)



# Scenario 1: High antigen dose

14

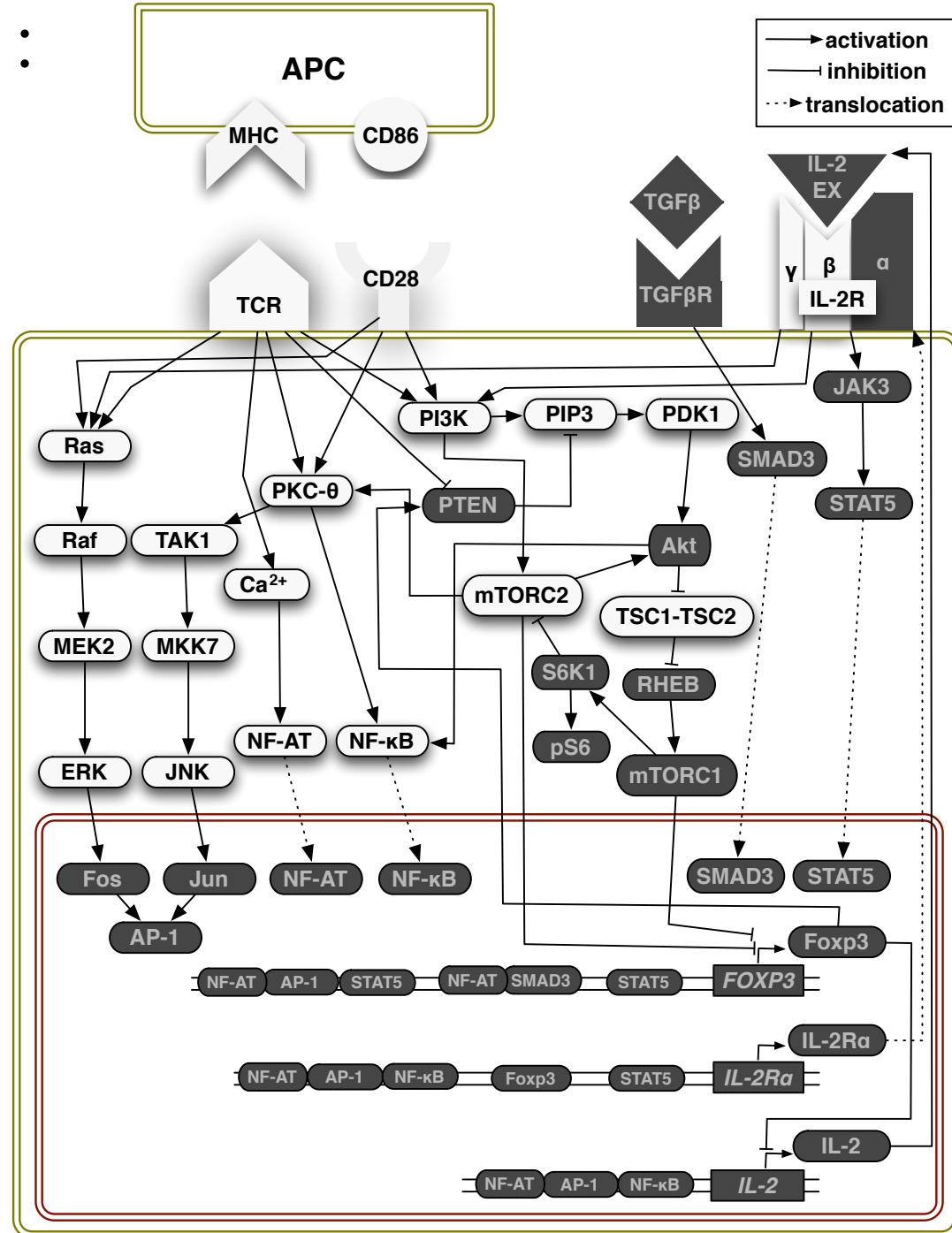
	value = ON (1)
	value = OFF (0)



# Scenario 1: High antigen dose

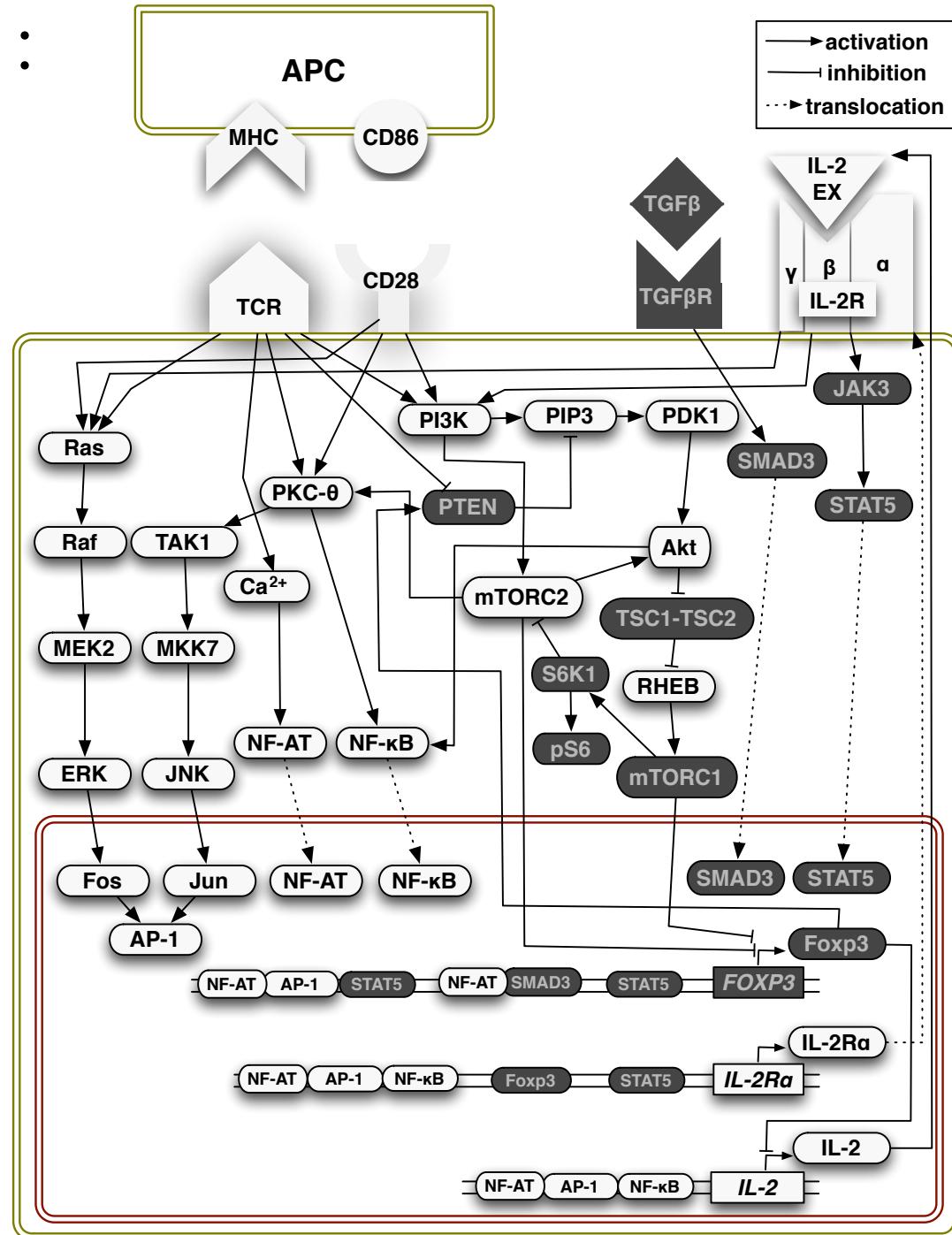
15

	value = ON (1)
■	value = OFF (0)



# Scenario 1: High antigen dose

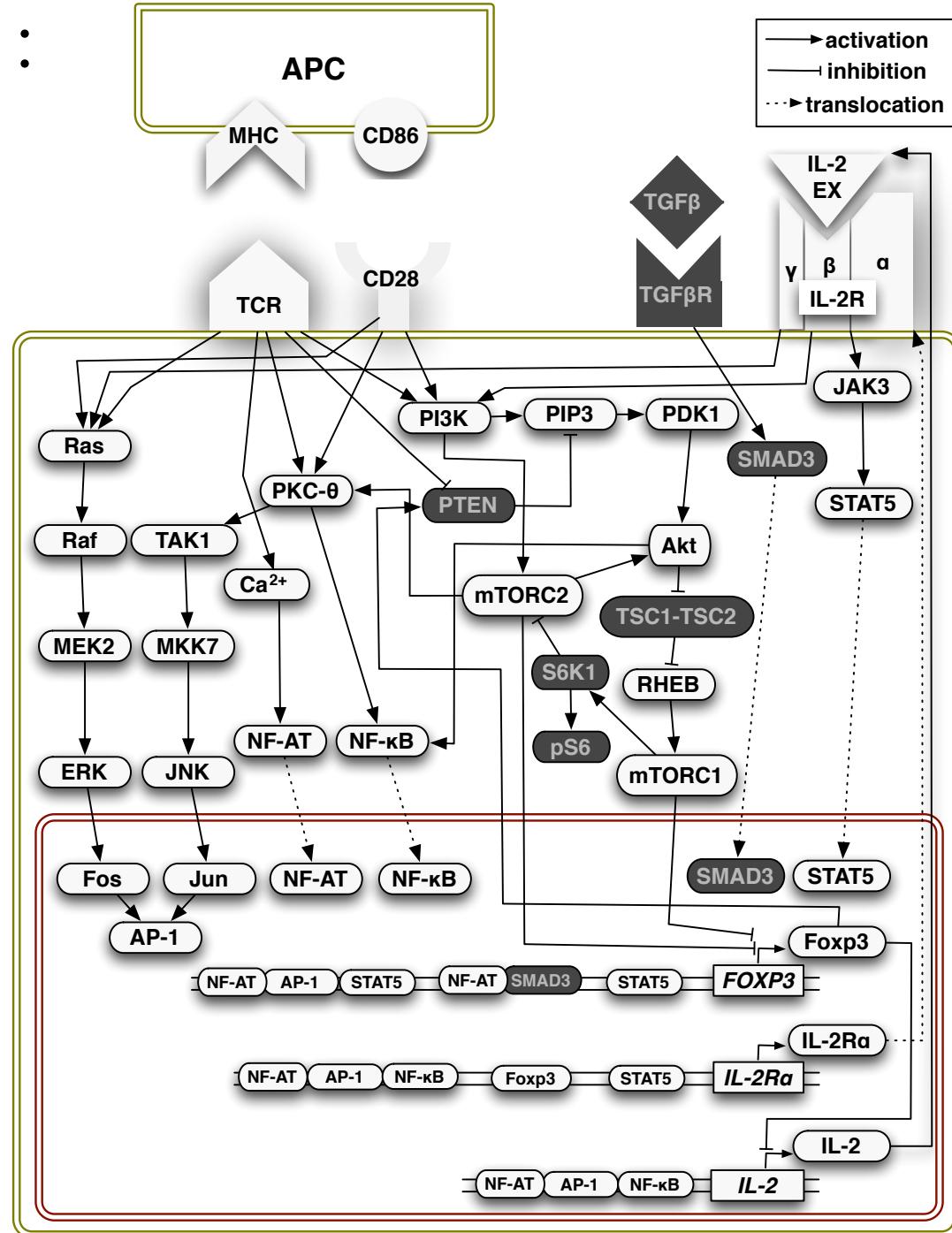
■ value = ON (1)  
■ value = OFF (0)



# Scenario 1: High antigen dose

17

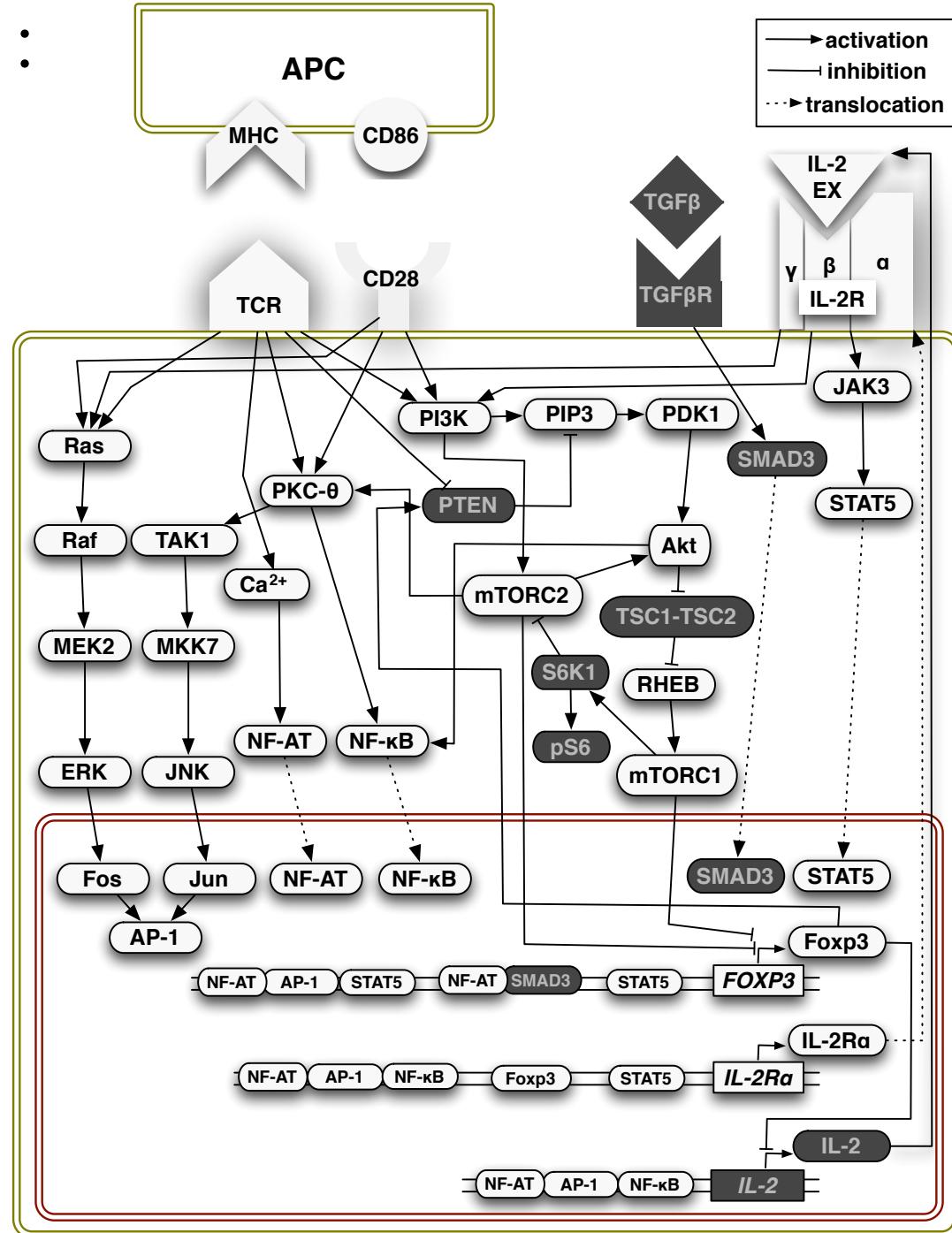
<span style="background-color: black; width: 10px; height: 10px;"></span>	value = ON (1)
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# Scenario 1: High antigen dose

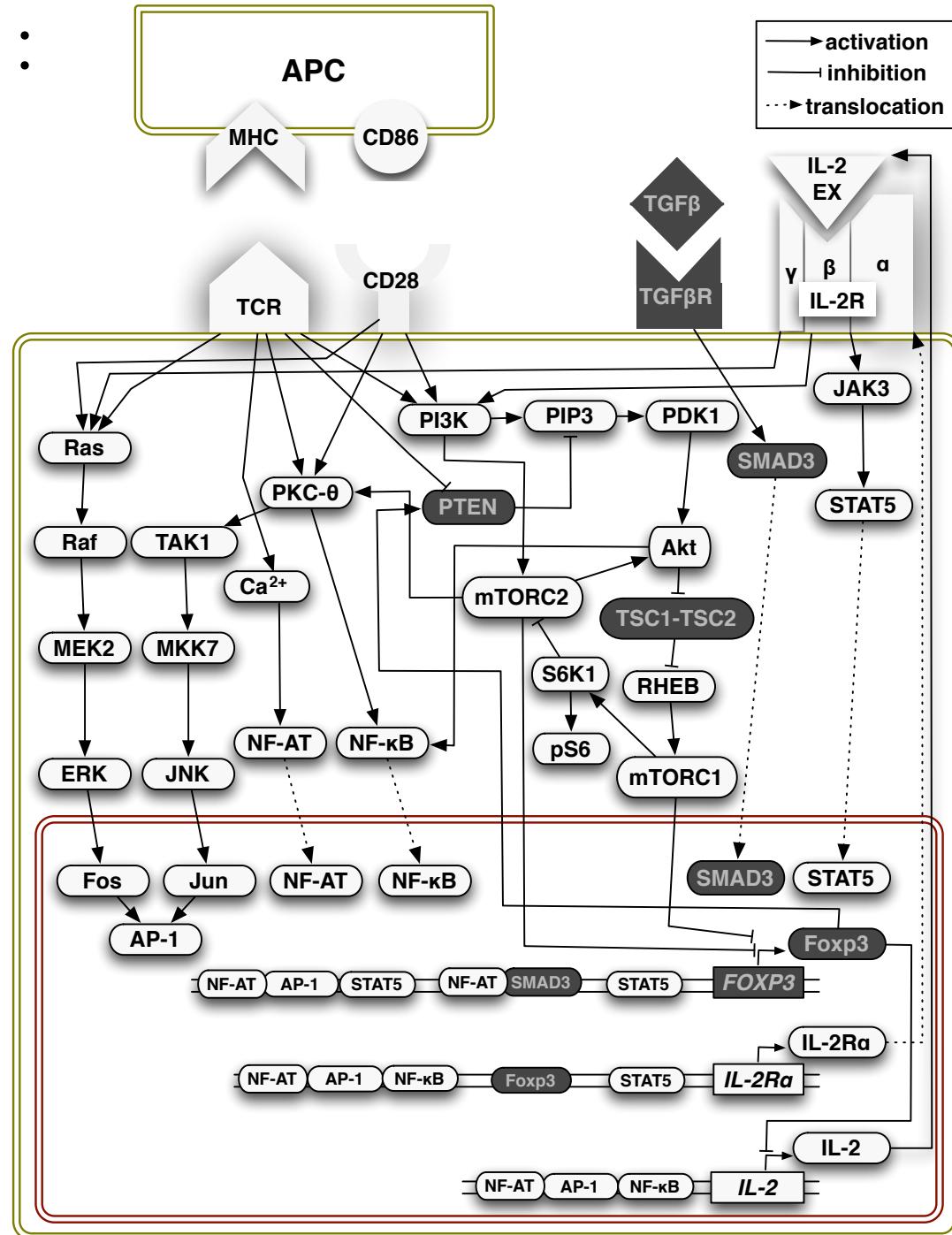
18

<input checked="" type="checkbox"/>	value = ON (1)
<input type="checkbox"/>	value = OFF (0)



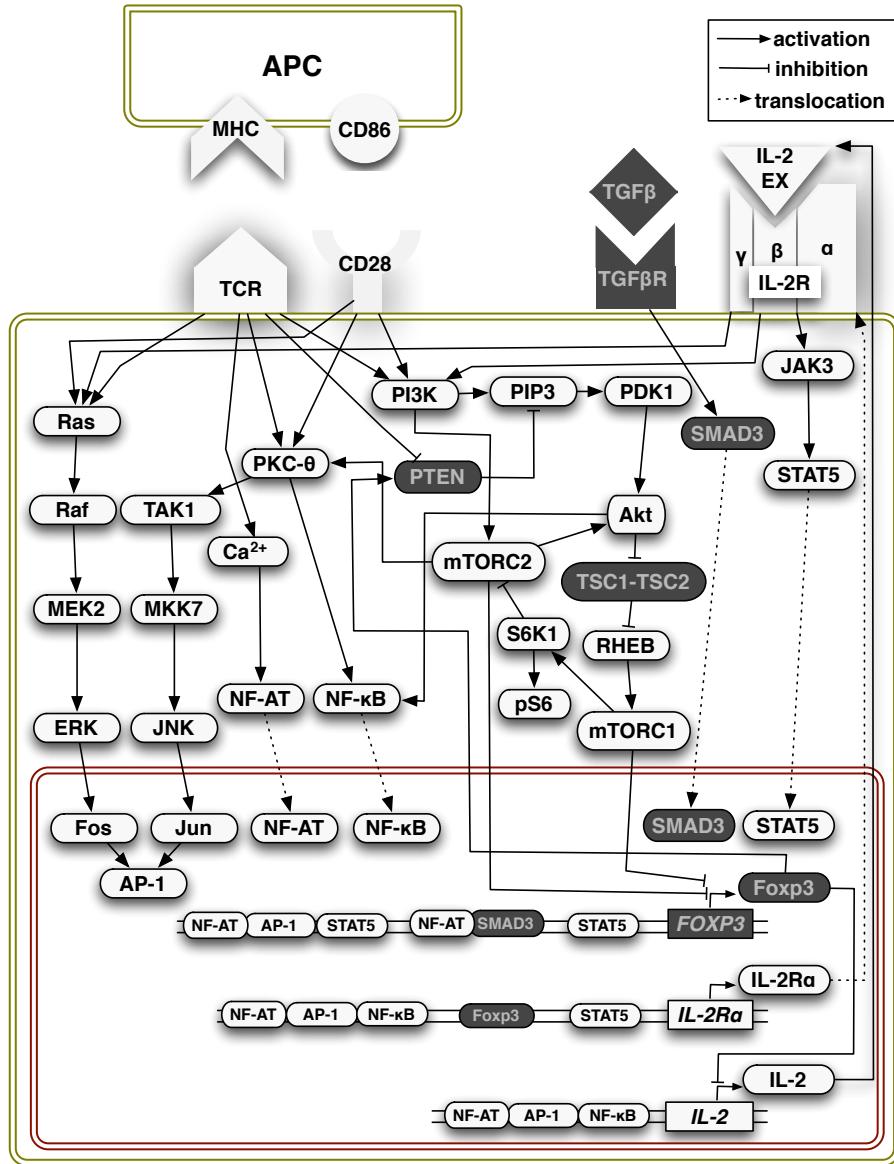
# Scenario 1: High antigen dose

■ value = ON (1)  
■ value = OFF (0)

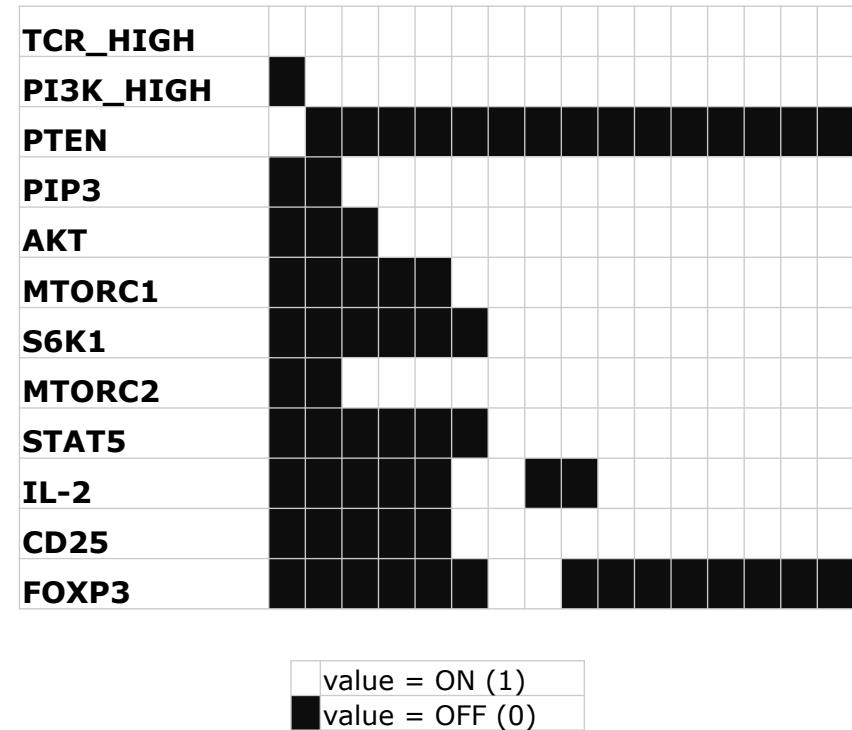


# Scenario 1: High antigen dose trajectory

20

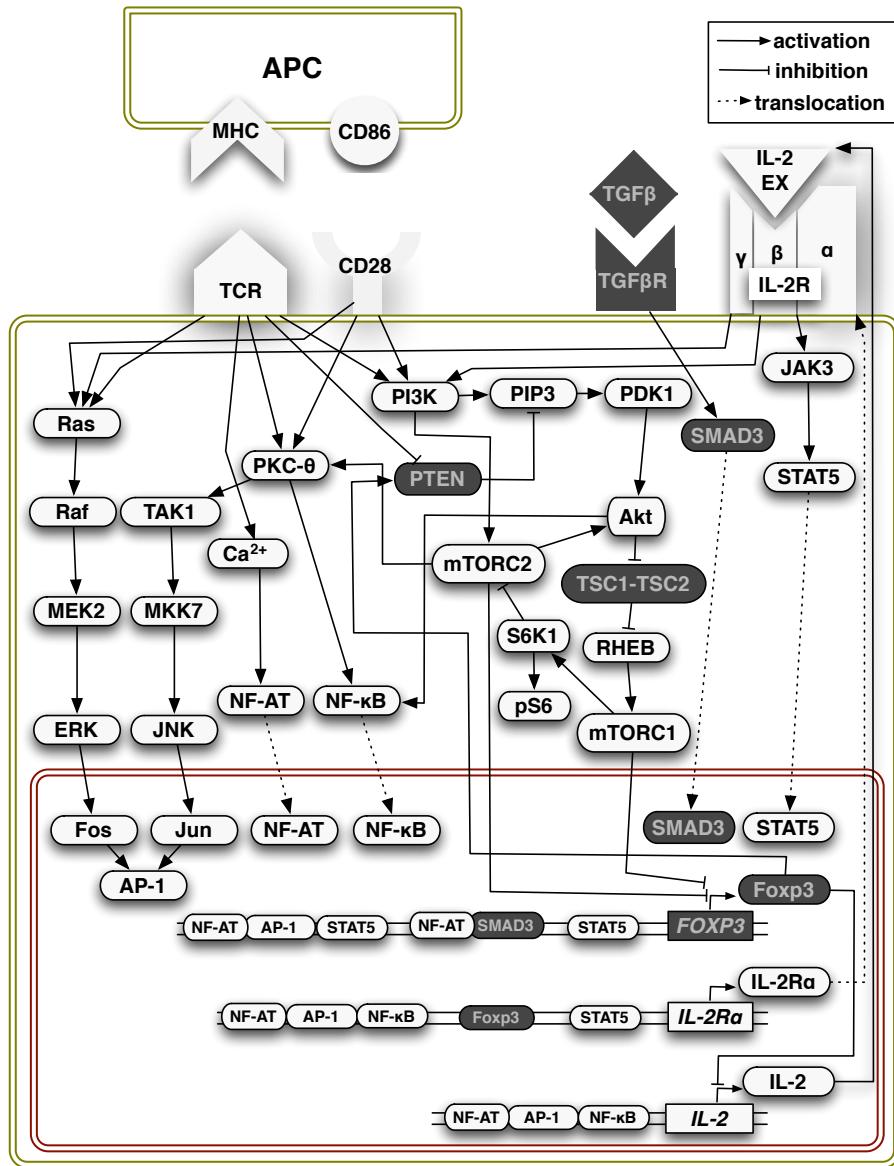


## Trajectory example

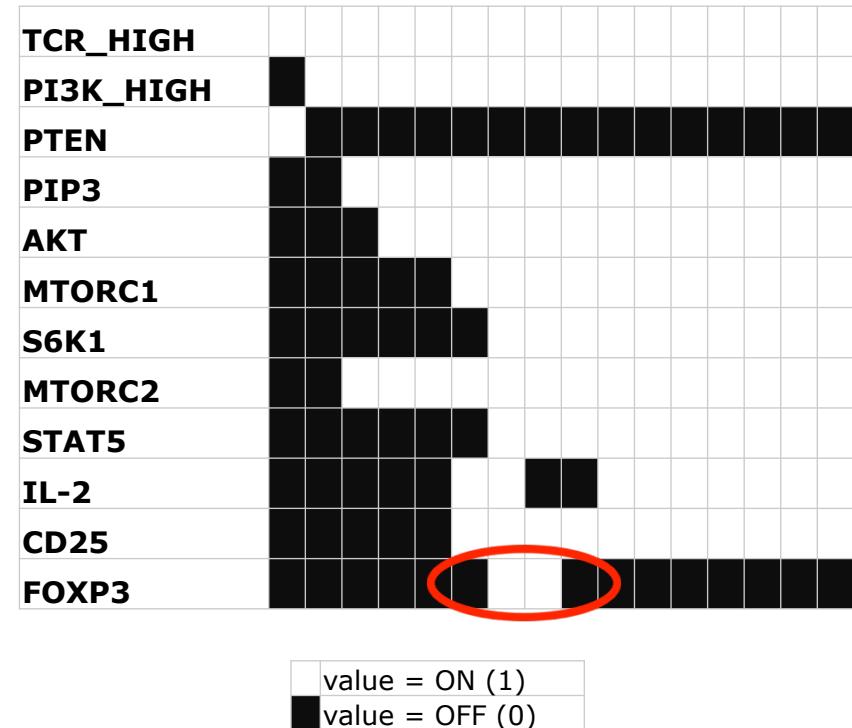


# Scenario 1: High antigen dose trajectory

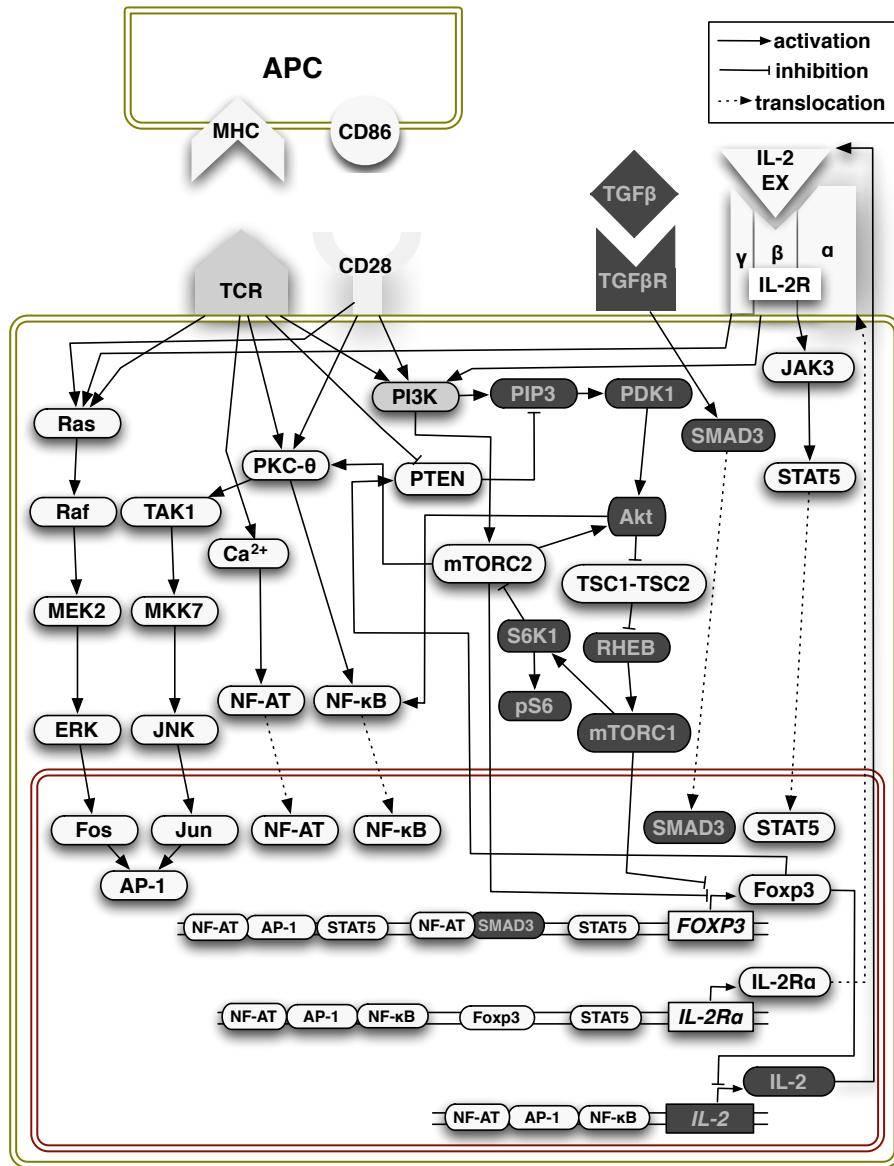
21



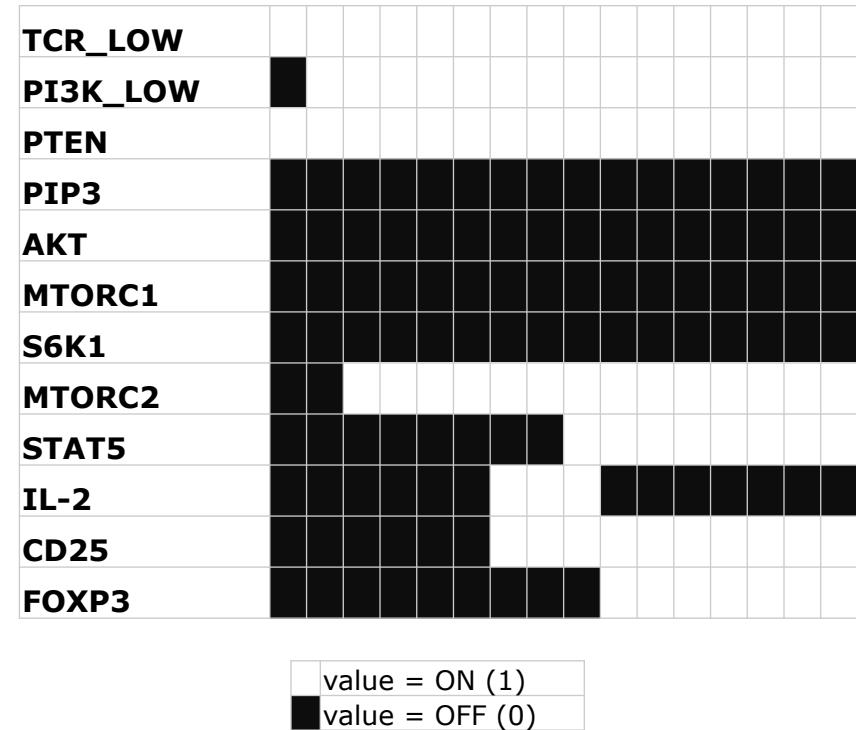
## Trajectory example



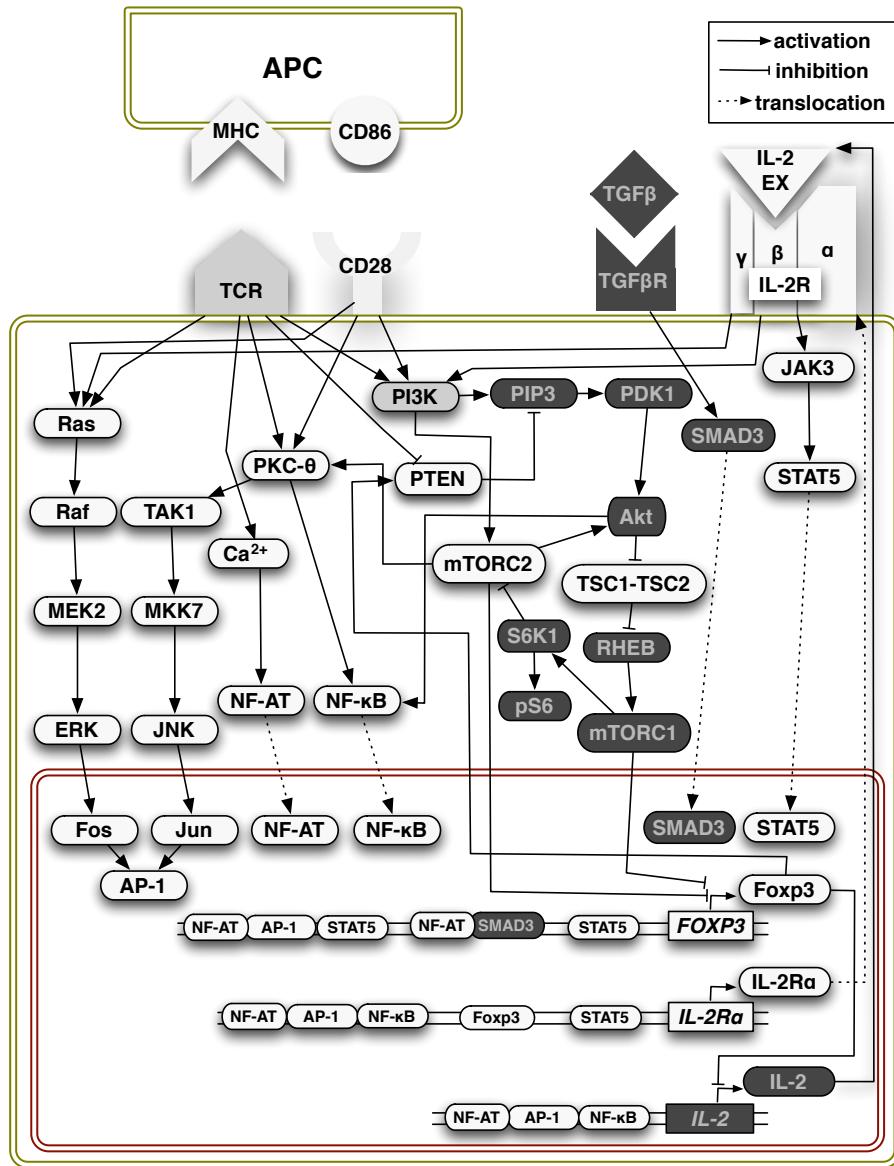
# Scenario 2: Low antigen dose trajectory



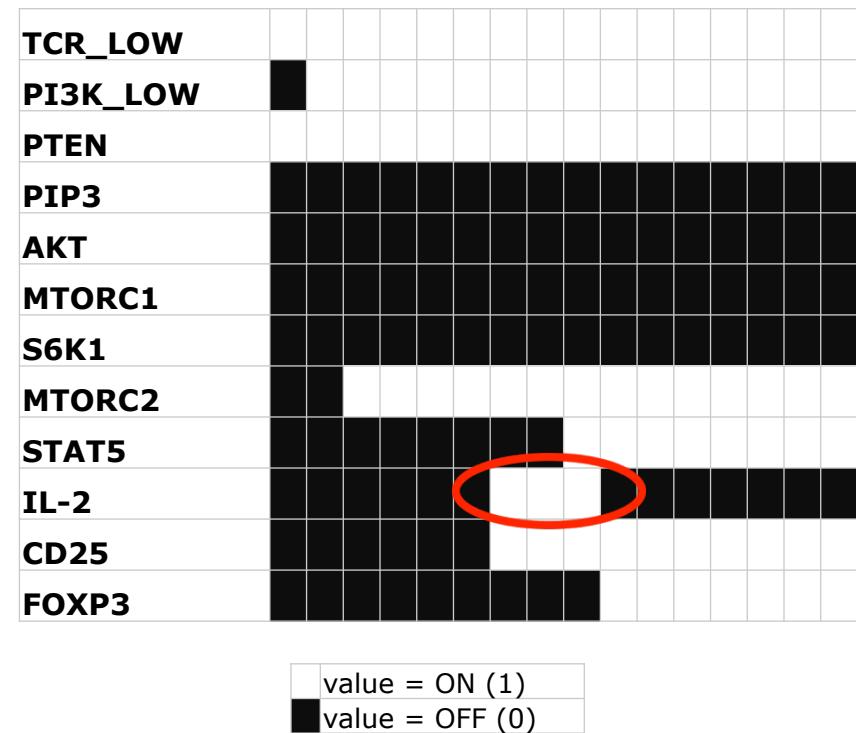
## Trajectory example



# Scenario 2: Low antigen dose trajectory

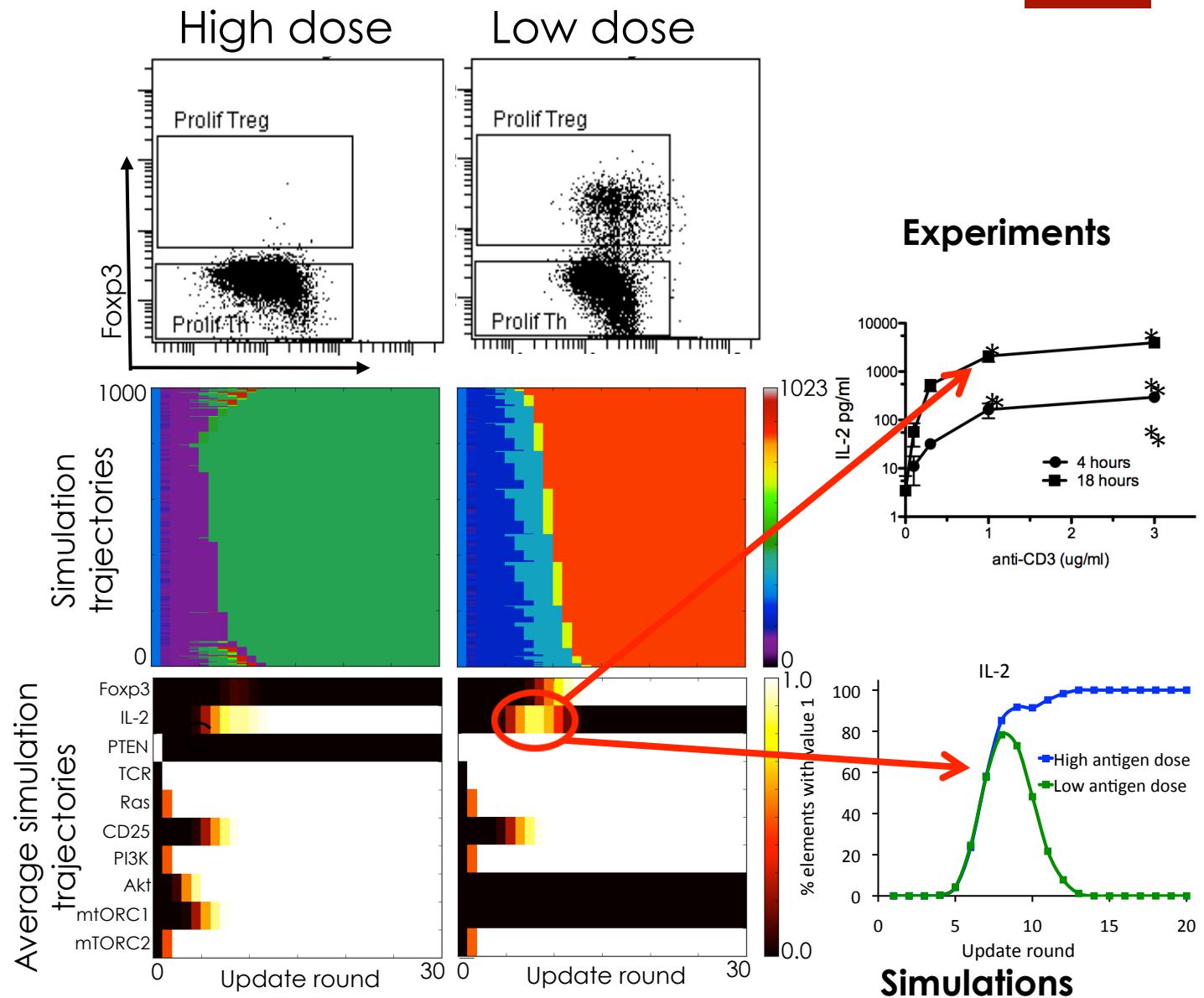


## Trajectory example



# Scenarios 1 and 2: High and Low antigen dose

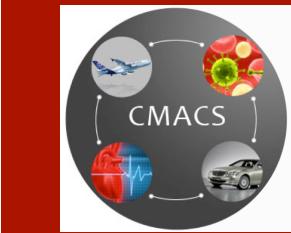
24



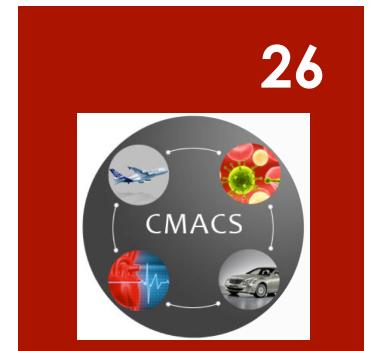
Source: N. Miskov-Zivanov et al., in preparation.

# Model does not capture low dose scenario

25

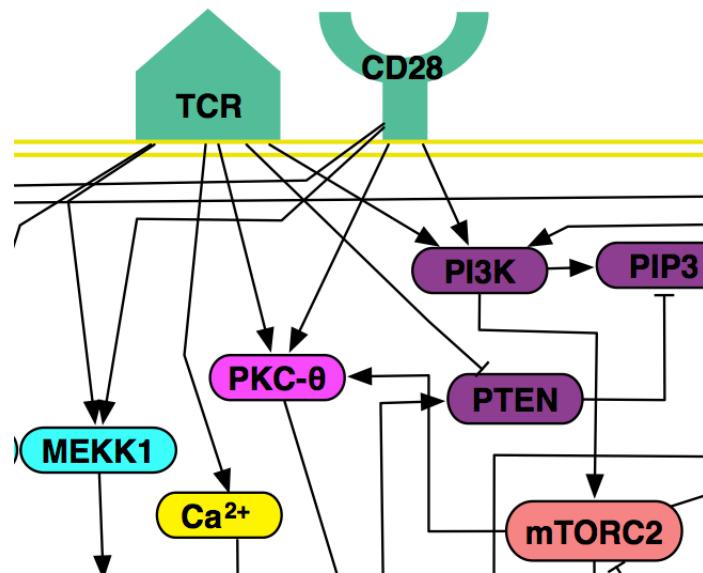


- Model simulations of low antigen dose result in 100%  $\text{Foxp3}^+$  cells, in experiments no more than 50%  $\text{Foxp3}^+$  cells



# Model does not capture low dose scenario

- Model simulations of low antigen dose result in 100% Foxp3+ cells, in experiments no more than 50% Foxp3+ cells



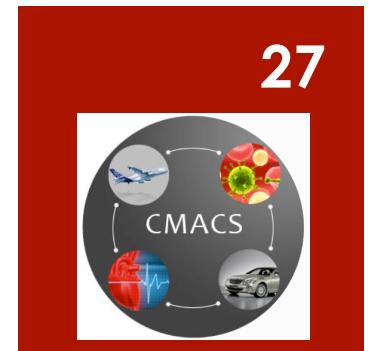
Low dose antigen is modeled as a change in rules:

$\text{PKCTHETA}^* = \text{TCR\_HIGH} \text{ or } (\text{TCR\_LOW} \text{ and } \text{CD28} \text{ and } \text{mTORC2})$

$\text{PI3K\_LOW}^* = (\text{TCR\_LOW} \text{ and } \text{CD28}) \text{ or } (\text{PI3K\_LOW} \text{ and } \text{IL2\_EX} \text{ and } \text{IL2R})$

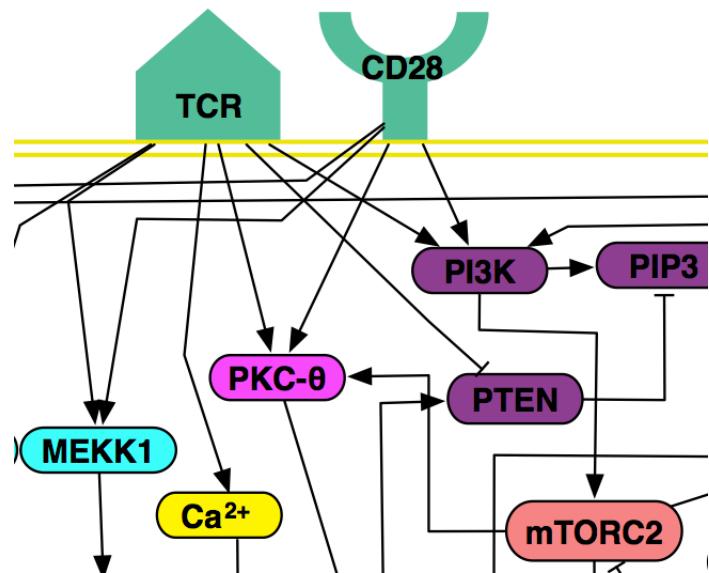
$\text{PI3K\_HIGH}^* = (\text{TCR\_HIGH} \text{ and } \text{CD28}) \text{ or } (\text{PI3K\_HIGH} \text{ and } \text{IL2\_EX} \text{ and } \text{IL2R})$

$\text{PTEN}^* = (\text{not TCR\_HIGH} \text{ and } \text{PTEN}) \text{ or } (\text{not TCR\_HIGH} \text{ and } \text{FOXP3})$



# Model does not capture low dose scenario

- Model simulations of low antigen dose result in 100% Foxp3+ cells, in experiments no more than 50% Foxp3+ cells



Low dose antigen is modeled as a change in rules:

$\text{PKCTHETA}^* = \text{TCR\_HIGH} \text{ or } (\text{TCR\_LOW} \text{ and } \text{CD28} \text{ and } \text{MTORC2})$

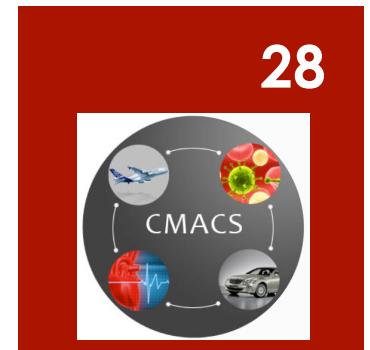
$\text{PI3K\_LOW}^* = (\text{TCR\_LOW} \text{ and } \text{CD28}) \text{ or } (\text{PI3K\_LOW} \text{ and } \text{IL2\_EX} \text{ and } \text{IL2R})$

$\text{PI3K\_HIGH}^* = (\text{TCR\_HIGH} \text{ and } \text{CD28}) \text{ or } (\text{PI3K\_HIGH} \text{ and } \text{IL2\_EX} \text{ and } \text{IL2R})$

$\text{PTEN}^* = (\text{not TCR\_HIGH and PTEN}) \text{ or } (\text{not TCR\_HIGH and FOXP3})$



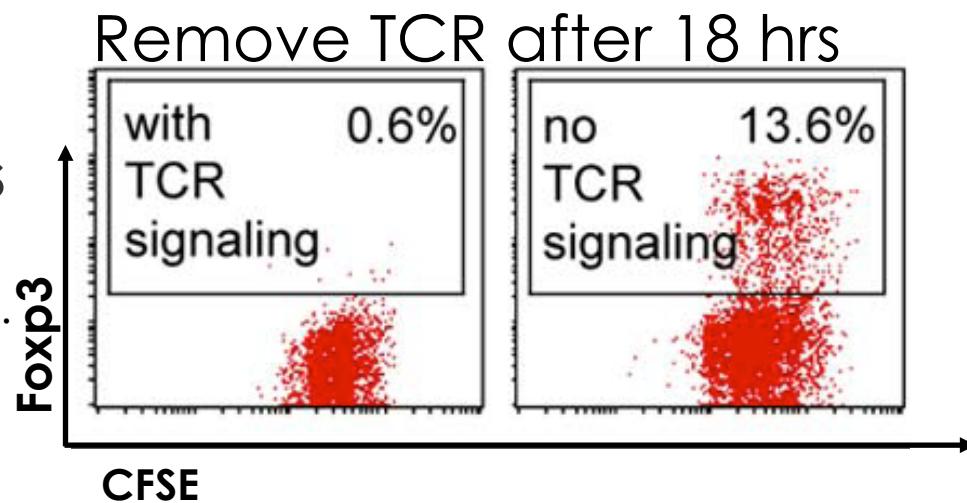
**A more dynamic analysis of TCR signal strength necessary: duration of stimulation**



# Analysis of duration of stimulation

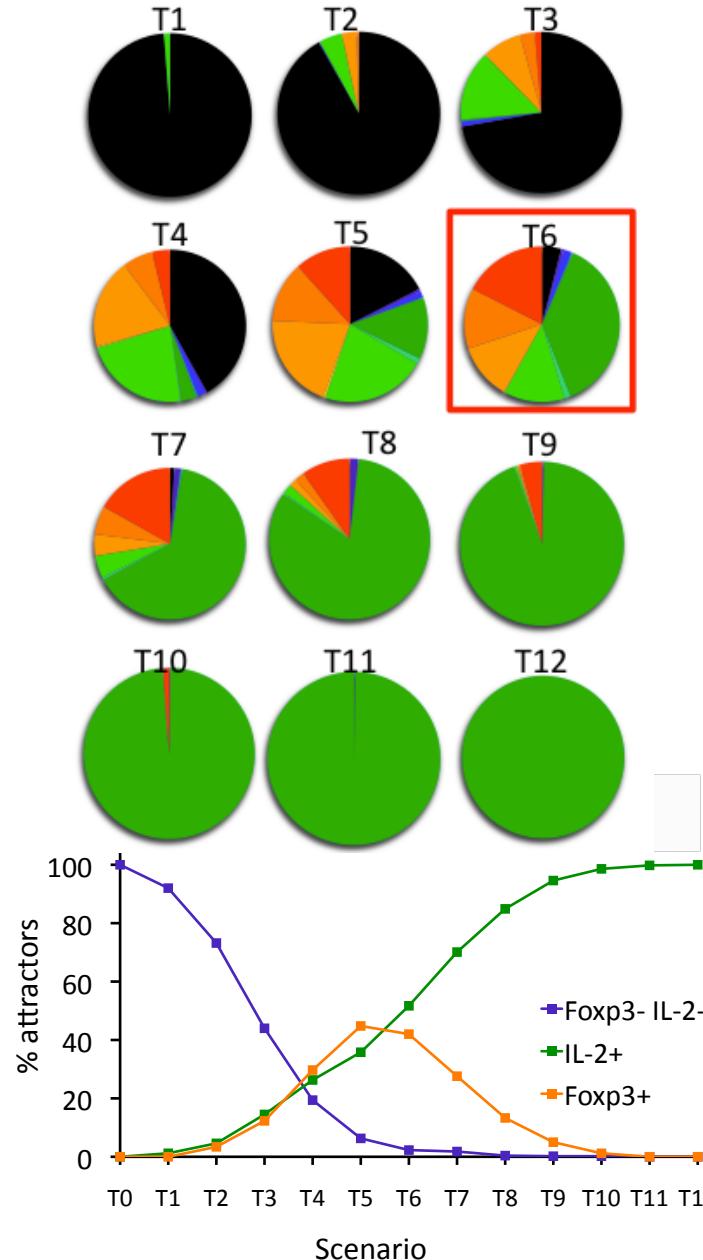
## Experiments

Source: Sauer et al.,  
PNAS 105:7797, 2008.



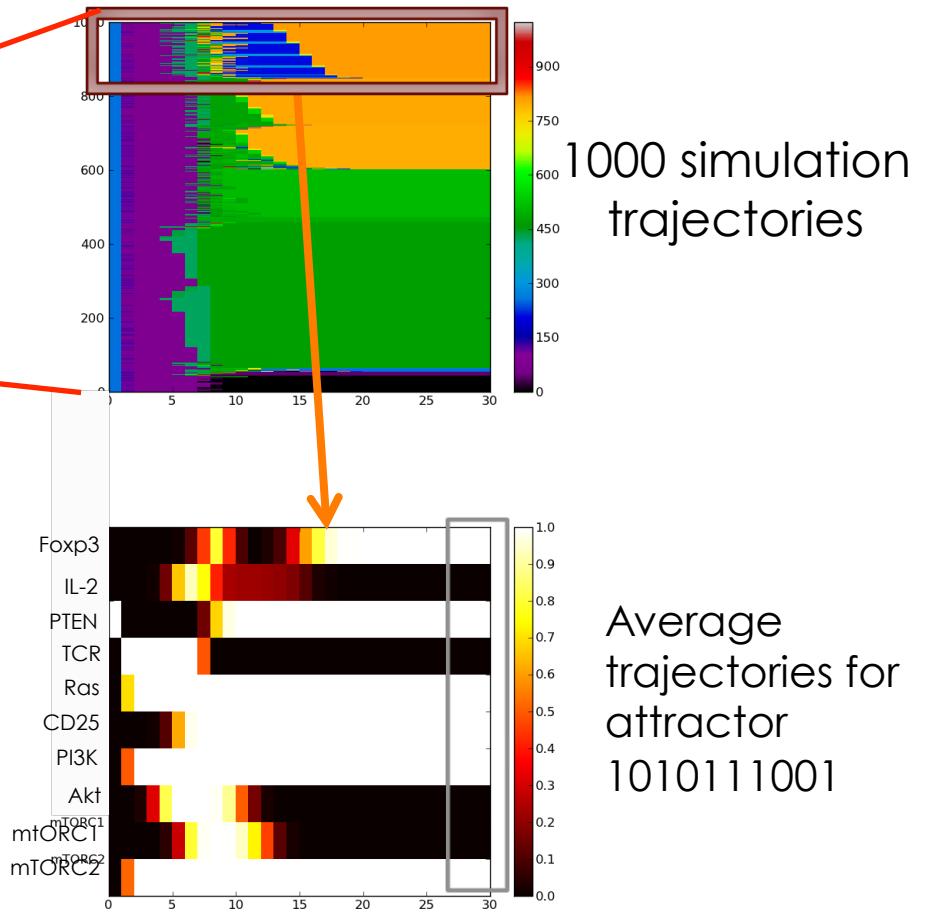
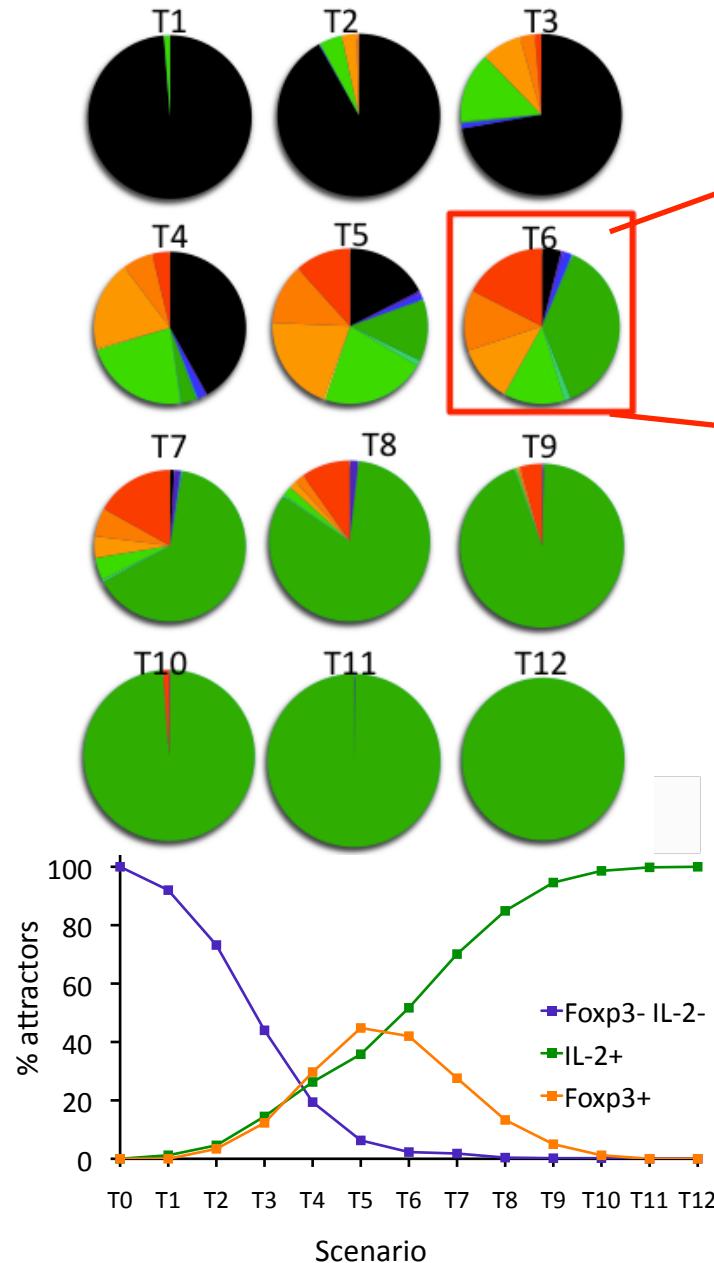
# Scenario 3:

## Antigen removal at rounds 1-12 (T1-T12)



Attractors	T6											No removal	
	A1	A2	A3	A4	A5	A6	A7	A8	A9	A10	A11	HD	LD
Foxp3													
IL-2													
PTEN													
TCR													
Ras													
CD25													
PI3K													
Akt													
mTORC1													
mTORC2													
Attractor size	40	6	17	3	374	13	127	1	118	126	175	1000	1000

# Scenario 3: Antigen removal at rounds 1-12 (T1-T12)

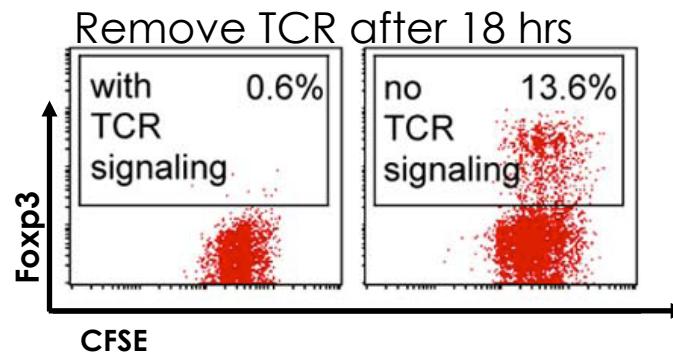


Average  
trajectories for  
attractor  
1010111001

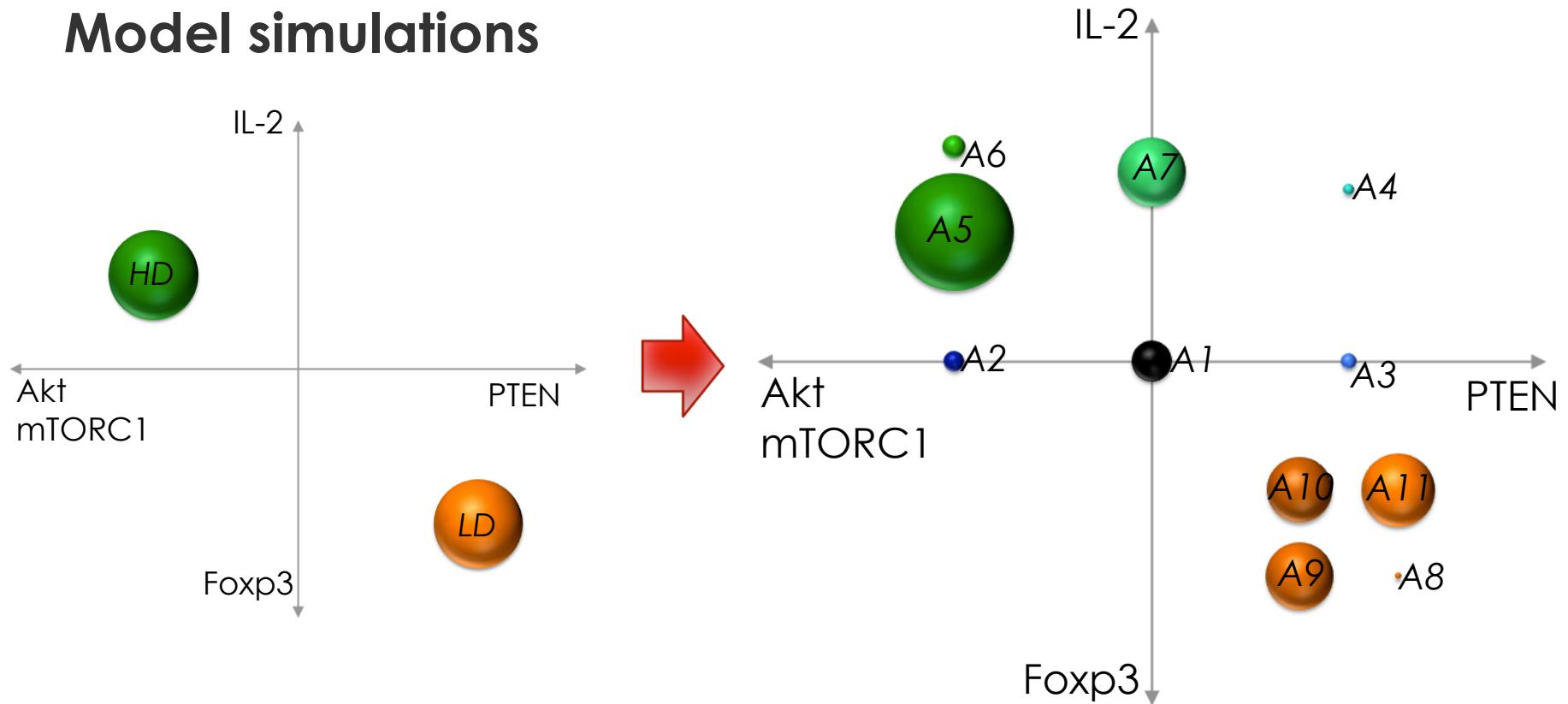
# Scenario 3: Antigen removal at round 6 (T6)

## Experiments

Source: Sauer et al., PNAS 105:7797, 2008.



## Model simulations

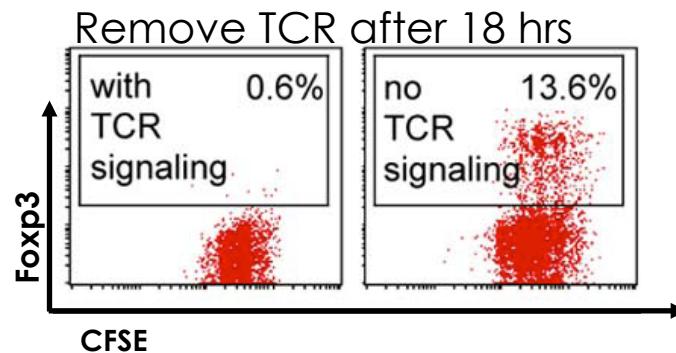


# Scenario 3: Antigen removal at round 6 (T6)

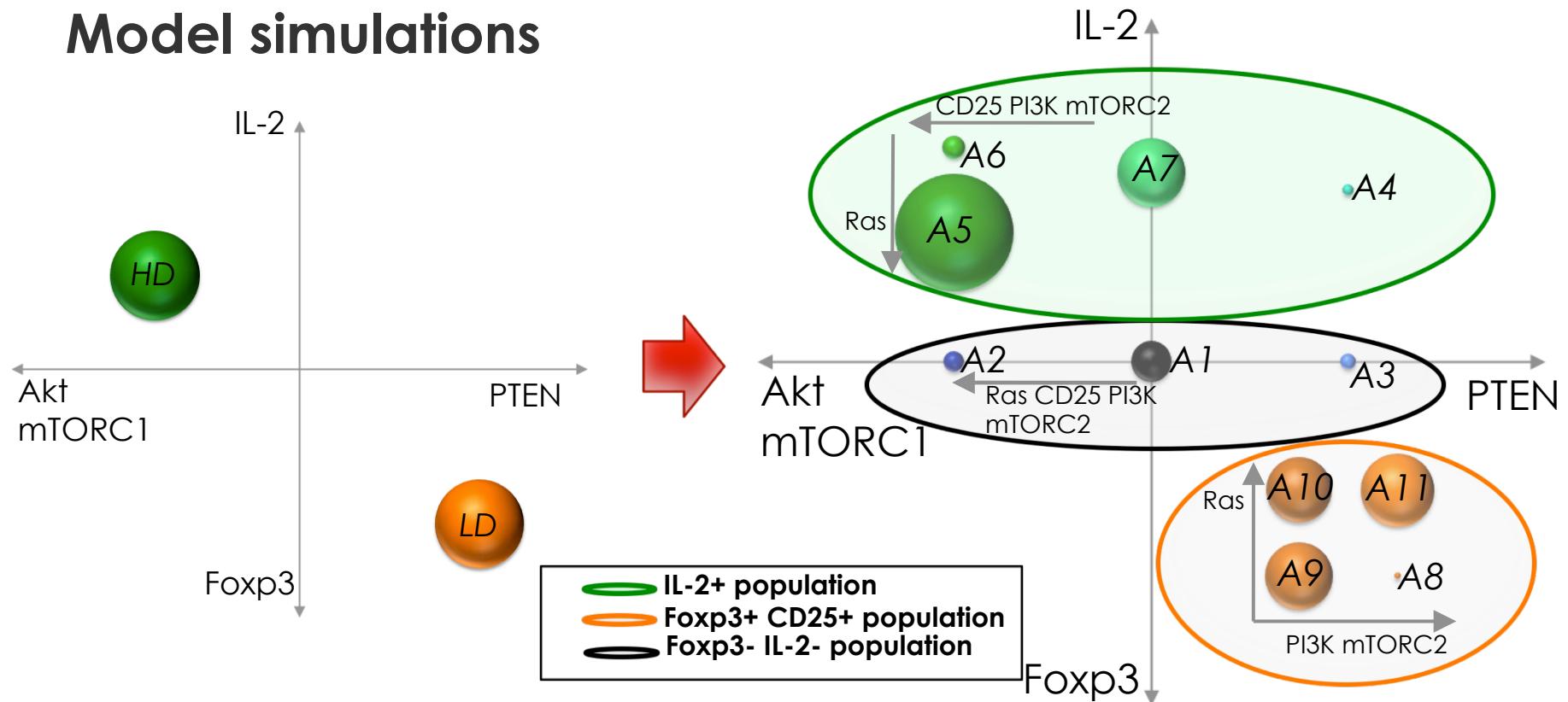
32

## Experiments

Source: Sauer et al.,  
PNAS 105:7797, 2008.

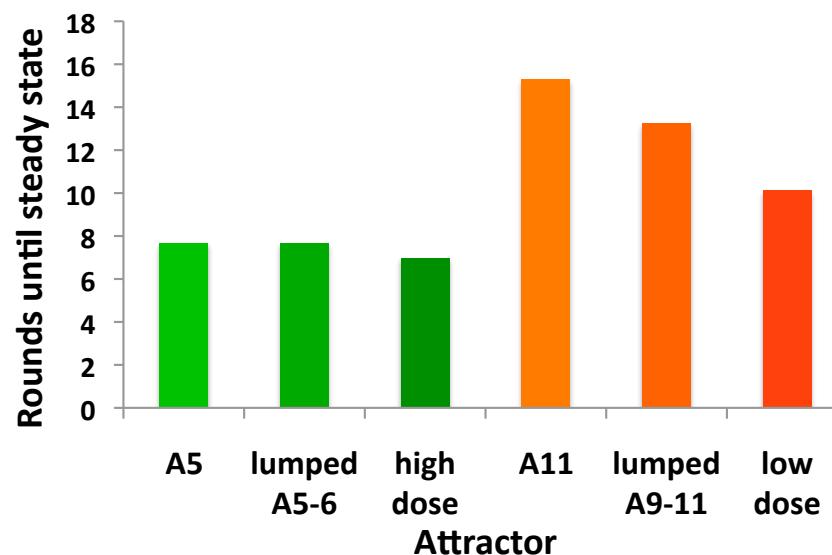
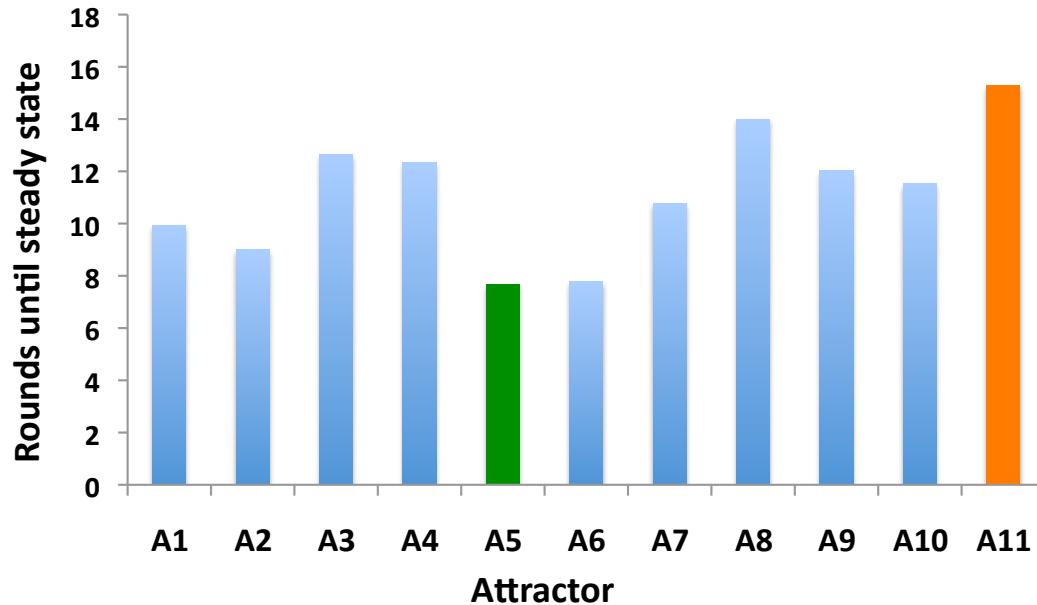


## Model simulations

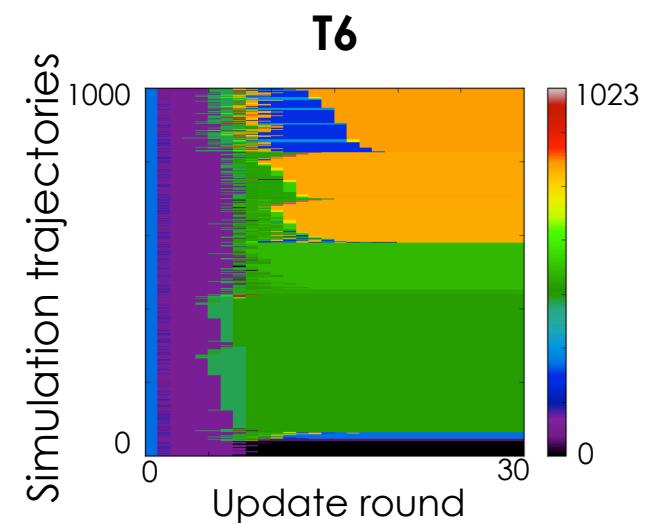


# Time to reach steady state (T6, HD, LD)

33



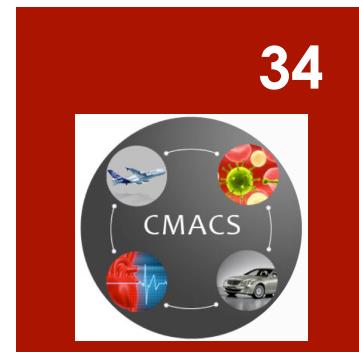
- Treg cells take longer to differentiate than Th cells



# Model checking

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- SPIN provides yes/no answers

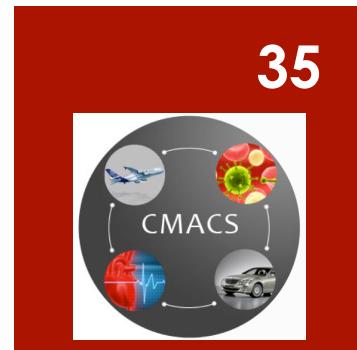


SPIN					
High dose			Low dose		
Specification	LTL Formula	Verified	Specification	LTL Formula	Verified
Does Foxp3 become false forever?	$!(<>[] !foxp3)$	Yes	Does Foxp3 become true forever?	$!(<>[] foxp3)$	Yes
Does ps6 become true forever?	$!(<>[] ps6)$	Yes	Does pS6 stay false forever?	$!([!] !ps6)$	Yes
Does PIP3 become true forever?	$!(<>[] pip3)$	Yes	Does IL-2 become true but eventually become false forever?	$!(<> il2 \&& <> [] !il2)$	Yes
Does Akt become true forever?	$!(<>[] akt)$	Yes	Is PTEN always true?	$!([!] pten)$	Yes
Does mtTORC1 become true forever?	$!(<>[] mtorc1)$	Yes	Does mTORC become true forever?	$!(<>[] mtorc)$	Yes
Does S6K1 become true forever?	$!(<>[] s6k1)$	Yes	Does CD25 become true forever?	$!(<>[] cd25)$	Yes
Does STAT5 become true forever?	$!(<>[] stat5)$	Yes	Does STAT5 become true forever?	$!(<>[] stat5)$	Yes
Does CD25 become true forever?	$!(<>[] cd25)$	Yes	<b>High dose + TGFβ</b>		
Does IL-2 become true forever?	$!(<>[] il2)$	Yes	Does IL-2 become true forever?	$!(<>[] il2)$	Yes
Does PTEN become true forever?	$!(<>[] pten)$	Yes	Does PTEN become false forever?	$!(<>[] !pten)$	Yes

# Probabilistic model checking

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- PRISM allows for analyzing transient behavior



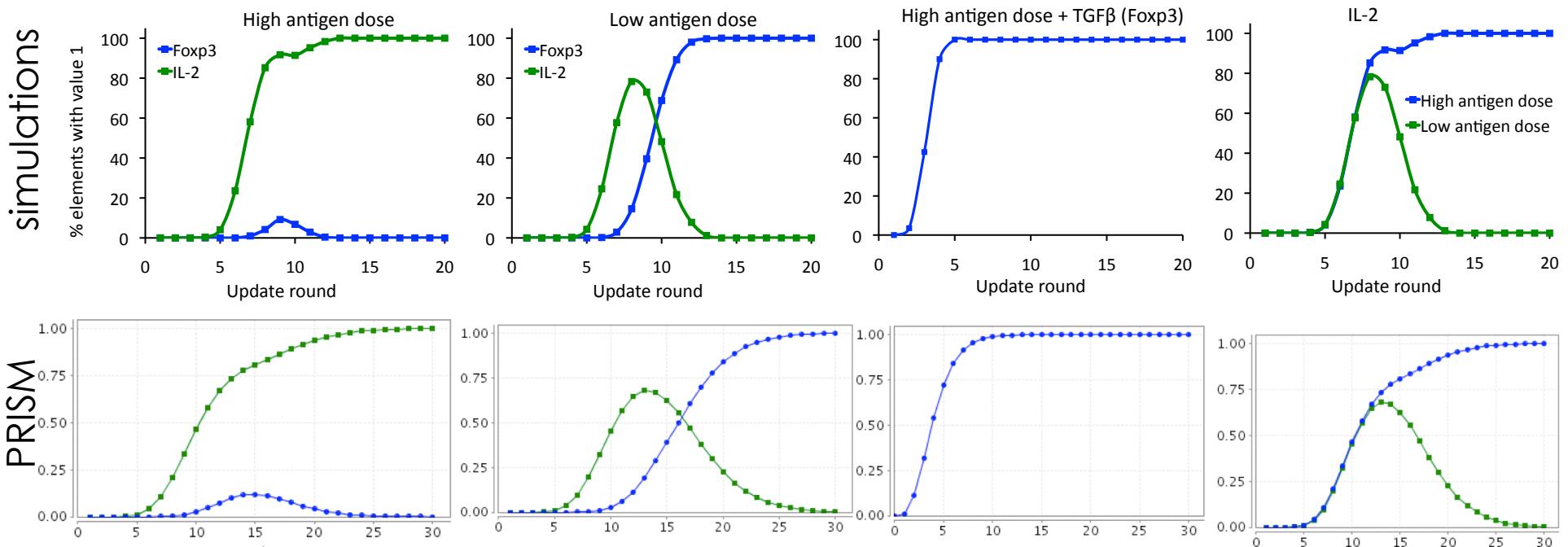
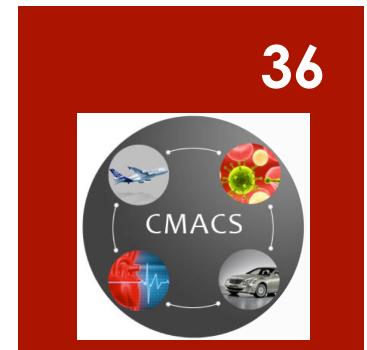
PRISM					
High dose			Low dose		
Specification	LTL Formula	Prob.	Specification	LTL Formula	Prob.
Does Foxp3 eventually become false forever?	$P=? [FG!foxp3] ]$	1	Does pS6 stay true?	$P=? [G ps6]$	0
What is the probability that Foxp3 never becomes true?	$P=? [G!foxp3]$	0.765098	Does mTORC2 ever get to true?	$P=? [F mtorc2]$	1
Does ps6 become true forever?	$P=? [F G ps6] ]$	1	Does PTEN ever get to false?	$P=? [ F !pten ]$	0
Are IL-2 and PTEN ever both true?	$P=? [F((pten) & (il2))]$	0.000468	High dose + TGFβ		
What is the probability that IL-2 is false before Foxp3 becomes true	$P=? [ (!il2)U(foxp3) ]$	0	Does IL-2 become true?	$P=? [ F il2 ]$	0.019584
PRISM – behavior over time					
What is the behavior of Foxp3 over time?	$P=? [G[t,t] foxp3]$	Figure	What is the behavior of IL-2 over time?	$P=? [G[t,t] il2]$	Figure

Deepa Sathaye, Alexander Moser

# Probabilistic model checking

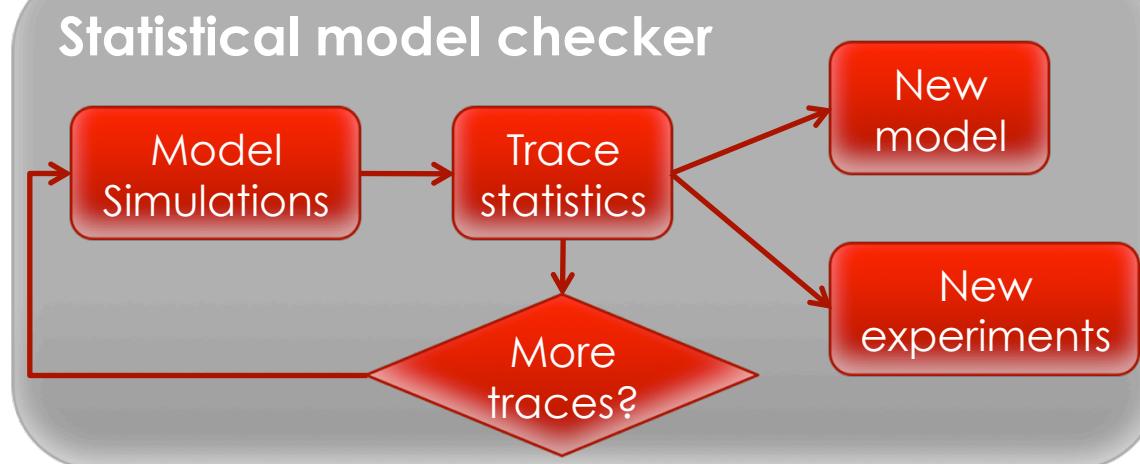
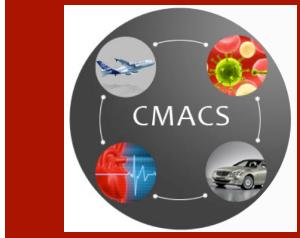
36

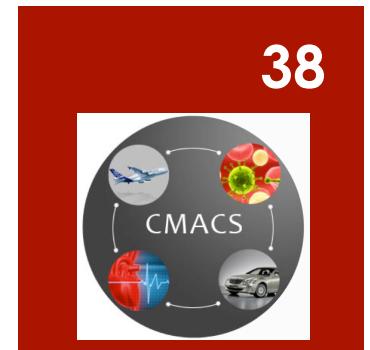
- PRISM allows for analyzing transient behavior



# Statistical model checking

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# Statistical model checking

- Low antigen dose scenario:

## 1. Does IL-2 always go to 1?

Property:  $F[20] (IL2 == 1)$

Test: BEST 0.001 0.999

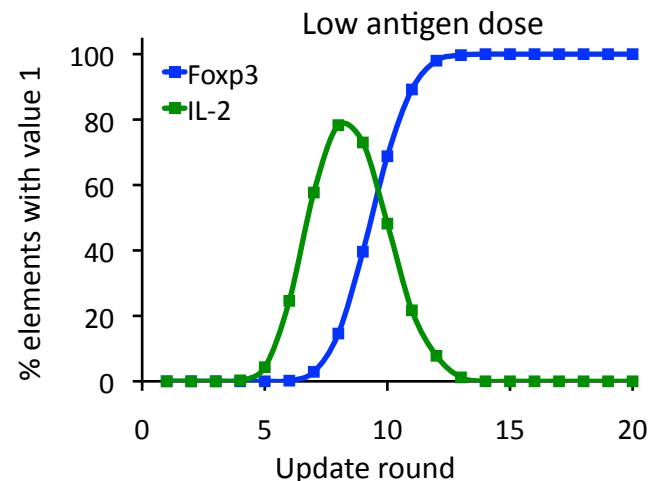
Result: estimated probability close to 1

## 2. Probability that IL-2 stays at 0 before Foxp3 becomes 1?

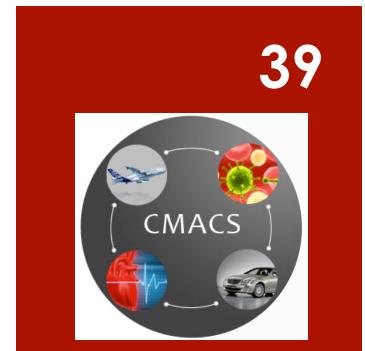
Property:  $(IL2 == 0) \cup [15] (FOXP3 == 1)$

Test: BEST 0.0001 0.999

Result: estimated probability = 0.00147  
**rare event**

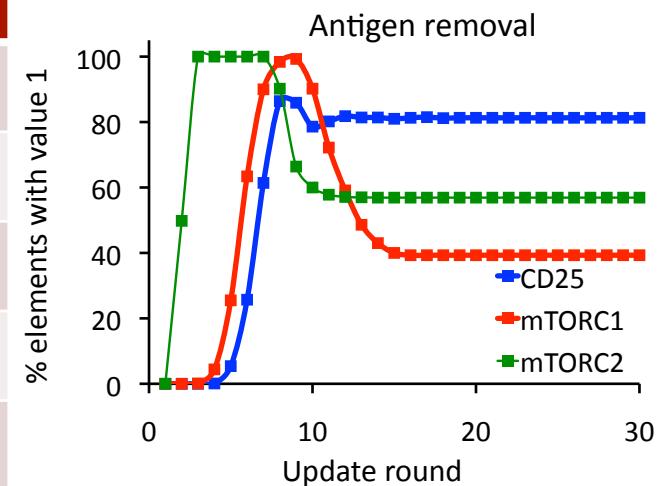


# Statistical model checking



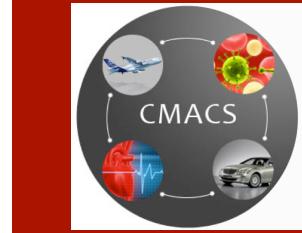
- High antigen dose + antigen removal scenario:
  - Studies of relative timing on mTOR vs. CD25/STAT5 pathway

	Property	Probability estimate and sample size	Elapsed time [s]
1	$G^7 \sim (\text{MTORC1} = 1 \& \text{MTORC2} = 1)$	estimate = 0.0188048 samples = 200,160	1,946
2	$F^7 (\text{MTORC1} = 1 \& \text{MTORC2} = 1)$	estimate = 0.980884 samples = 2,352	23
3	$F^{10} (\text{MTORC1} = 1 \& \text{MTORC2} = 1 \& \text{CD25} = 0 \& (F^{18} (\text{CD25} = 1)))$	estimate = 0.60104 samples = 25,968	253
4	$F^{28} (\text{MTORC1} == 1 \& \text{MTORC2} == 1 \& \text{CD25} == 0 \& (F^1 (\text{CD25} == 1)))$	estimate = 0.592195 samples = 26,160	254
5	$F^{10} (\text{MTORC1} = 1 \& \text{MTORC2} = 1 \& \text{CD25} = 0 \& (F^1 (G^{17} (\text{CD25} = 1))))$	estimate = 0.39669 samples = 25,920	254

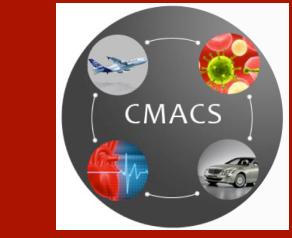


# Conclusion

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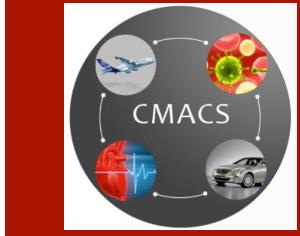
- **Logical modeling approach allows development of comprehensive models of cell fate**
  - Model of peripheral T cell differentiation recapitulates a wide range of experimental observations
  - Circuit analysis reveals key elements of the mechanism for Foxp3 expression
  - Timing is critical for Treg differentiation:
    - Treg cells take longer to differentiate than Th cells
    - Race between Foxp3 activating and inhibiting pathways
    - Feedback between Foxp3 and PTEN



# Conclusion

## ■ Model checking

- Allows for more efficient studies of the model
- Probabilistic model checking:
  - Provides transient results that match simulations
- Statistical model checking:
  - Further analysis of transient behavior
  - Provides insights into timing relationships between elements



# Next steps

- Analyze different removal scenarios using model checking
- Expansion of the model (keep up with fast pace of developments in the field)
- Develop a model for several cell types
- Develop population models that embed intracellular circuitry



Computational M<sub>odeling</sub> and A<sub>nalysis</sub> for C<sub>omplex</sub> S<sub>ystems</sub>

Thank you!