

The Fifth Annual **q-bio**  
**Conference on Cellular  
Information Processing**



**The Seventh q-bio Conference Invited Speakers for 2013**

[Nancy L. Allbritton](#), University of North Carolina

[Naama Barkai](#), Weizmann Institute of Science

[Sydney Brenner](#), Salk Institute (Opening Banquet Talk)

[Leah Edelstein-Keshet](#), University of British Columbia

[Hana El-Samad](#), University of California, San Francisco

[Jim Haseloff](#), University of Cambridge

[Suckjoon Jun](#), University of California, San Diego

[Marc W. Kirschner](#), Harvard Medical School (Closing Banquet Talk)

[Jennifer Lippincott-Schwartz](#), National Institutes of Health

[Zaida \(Zan\) Luthey-Schulten](#), University of Illinois, Urbana-Champaign

[Rama Ranganathan](#), University of Texas Southwestern Medical Center at  
Dallas

[Peter K. Sorger](#), Harvard Medical School

[Erik Winfree](#), California Institute of Technology

[Lani Wu](#), University of Texas Southwestern Medical Center at Dallas

[http://www.q-bio.org/wiki/The\\_Seventh\\_q-bio\\_Conference](http://www.q-bio.org/wiki/The_Seventh_q-bio_Conference)

# The Seventh Annual q-bio Summer School

Two Great Campuses (July 21 - August 2, 2013):

St. John's College  
(Santa Fe, New Mexico, USA)

University of California  
(San Diego, California, USA)

Converging at:

The q-bio Student Symposium  
(St. John's College, Santa Fe,  
New Mexico, USA, August 5-6, 2013)

The Seventh Annual q-bio Conference  
(Santa Fe, New Mexico, USA  
August 7-10, 2013)

- \* **Biomolecular Simulations (Santa Fe, NM)**
- \* **Cancer (Santa Fe, NM)**
- \* **Viral Dynamics (Santa Fe, NM)**
- \* **Computational Neuroscience (San Diego, CA)**
- \* **Stochastic Gene Regulation (Santa Fe, NM)**
- \* **Cell Signaling (Santa Fe, NM)**
- \* **Synthetic Biology (San Diego, CA)**



[http://q-bio.org/wiki/The\\_Seventh\\_q-bio\\_Summer\\_School](http://q-bio.org/wiki/The_Seventh_q-bio_Summer_School)

# Combining quantitative experiments and modeling to understand kinetics of the T cell response

Anton Zilman, Vitaly Ganusov and Alan Perelson  
*Los Alamos National Laboratory*  
*University of Toronto*



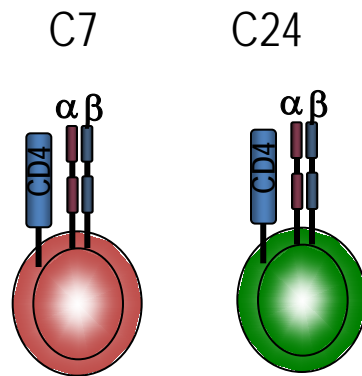
Physics  
UNIVERSITY OF TORONTO

Alena Gallegos and Eric Pamer  
*Memorial Sloan-Kettering Cancer Center*



# Model system to study CD4 T cell response to infection

2 TCR tg mice lines



ANTIGEN: ESAT-6

Infecing Bacteria

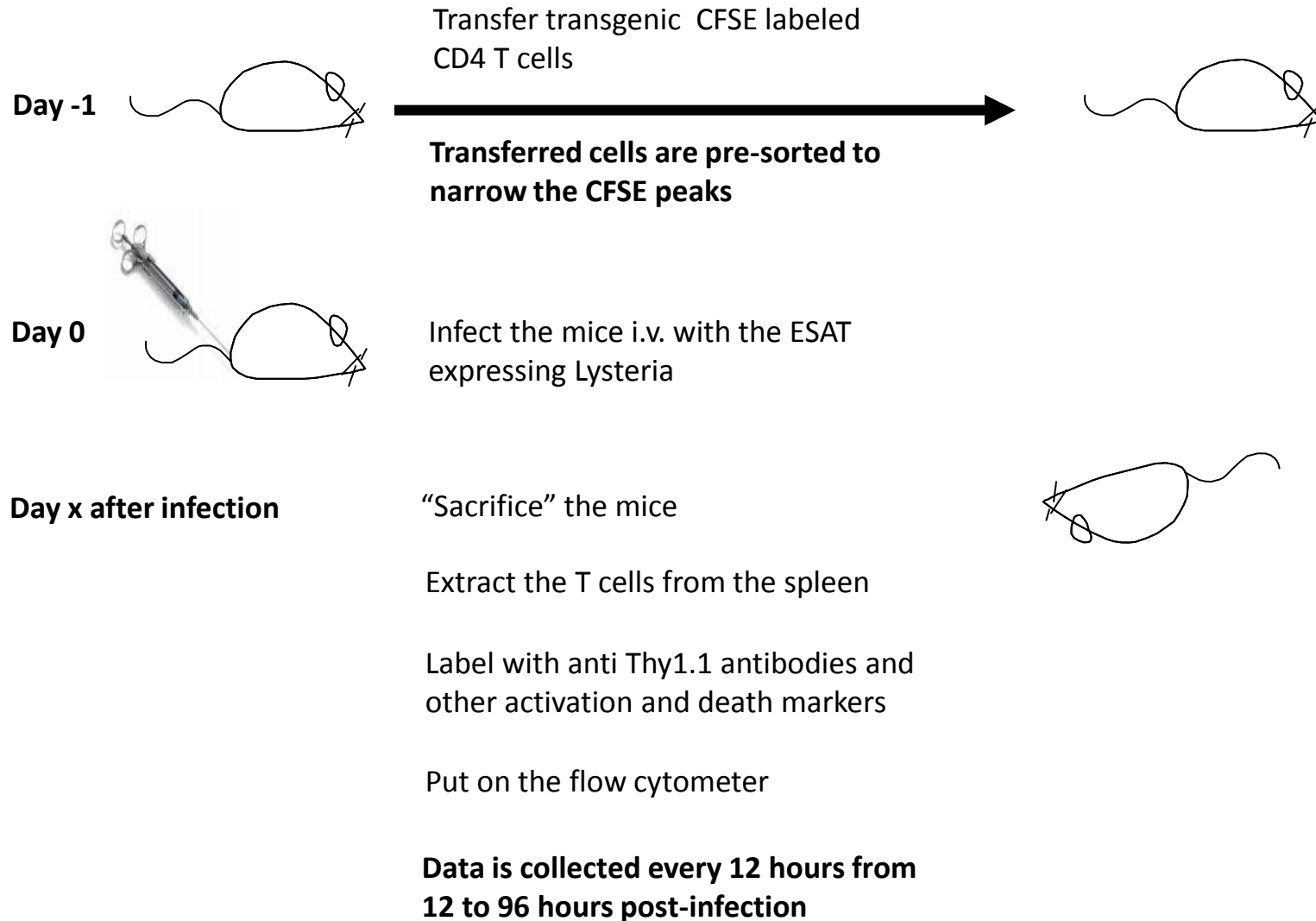
Expresses ESAT-6

*Listeria monocytogenes*



# Experimental procedure

Transgenic mouse on B6 Thy 1.1 background:  
CD4 T cells specific for ESAT (TB antigen)

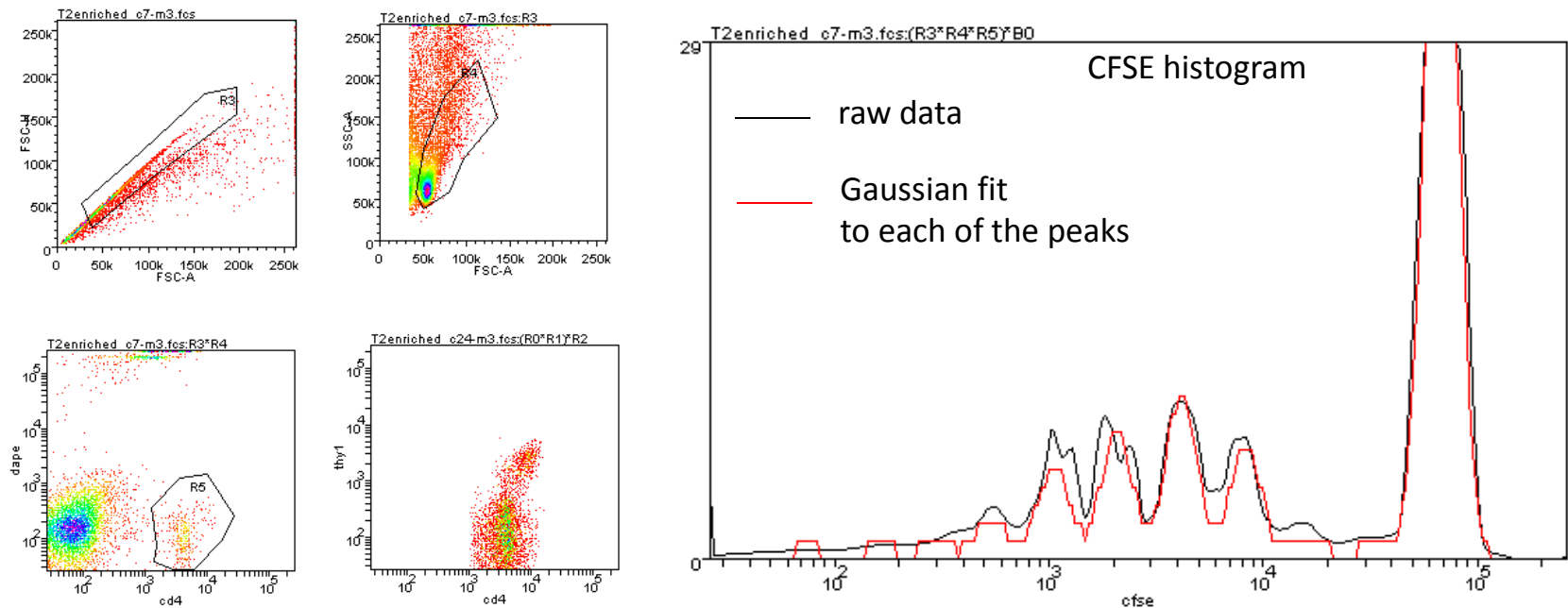


# Early proliferation kinetics: CFSE profiles

Numbers of cells in different division classes at time  $t$  are extracted from the CFSE profiles measured in cell transfer experiments

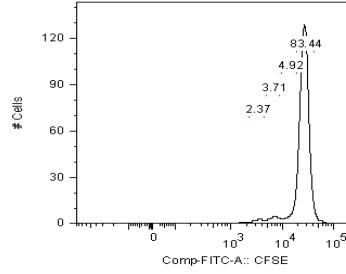
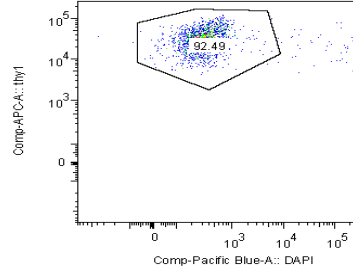
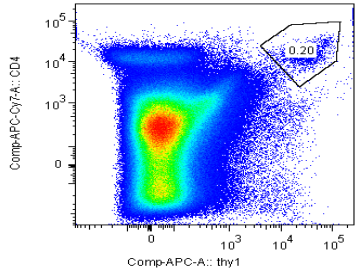
Numbers of cells in different division classes at time  $t$  are then used as input to the mathematical model

## Data fitting: example

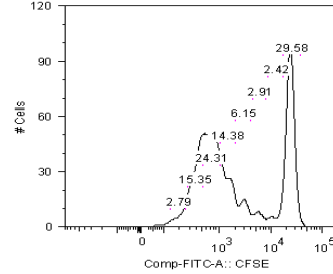
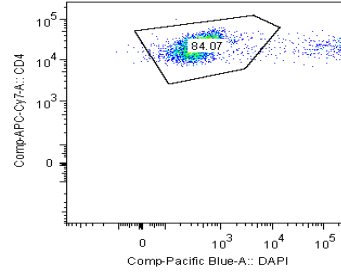
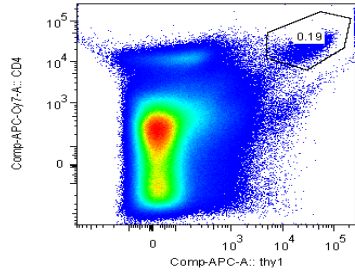


# Data analysis

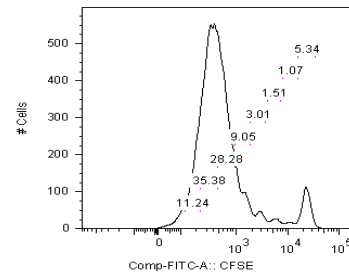
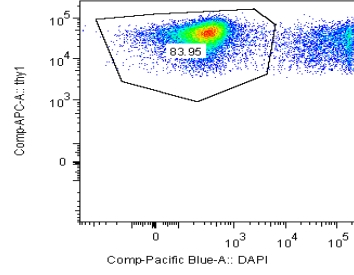
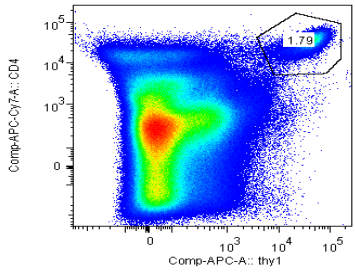
48 hrs



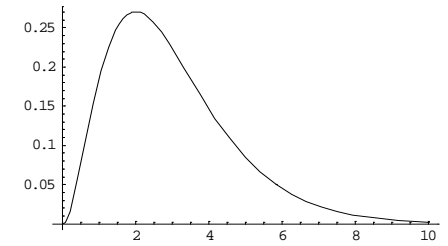
72 hrs



84 hrs

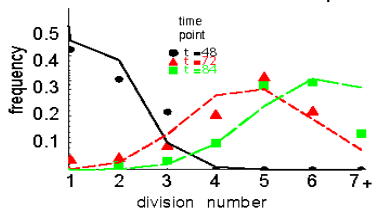


Model assumptions:  
the distribution of the  
inter-division times is  
a gamma function  
(similar to log-normal)

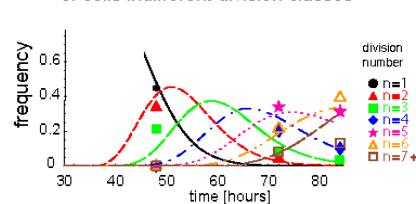


(results are relatively  
insensitive to the  
precise choice)

Frequencies of cells in different division classet at three time points



Estimated time course of frequencies of cells indifferent division classes



## Fit results

initial lag 25 hrs

mean time to first division 33.2 hrs

mean subsequent division time 9.3 hrs

# Results

Model parameters:

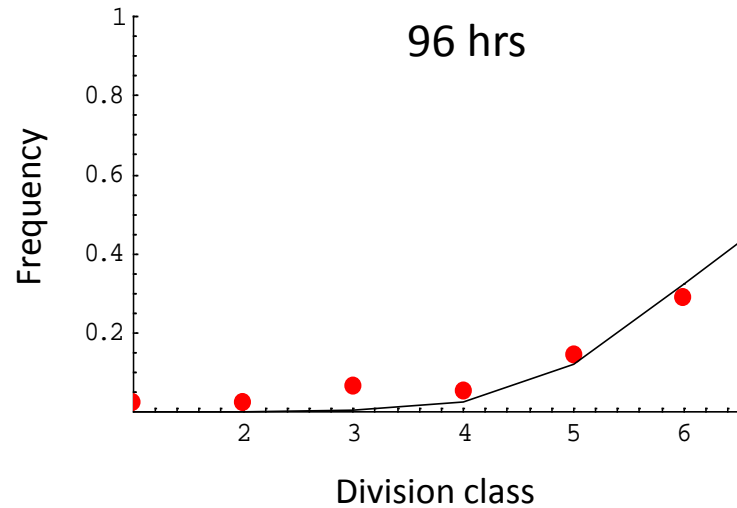
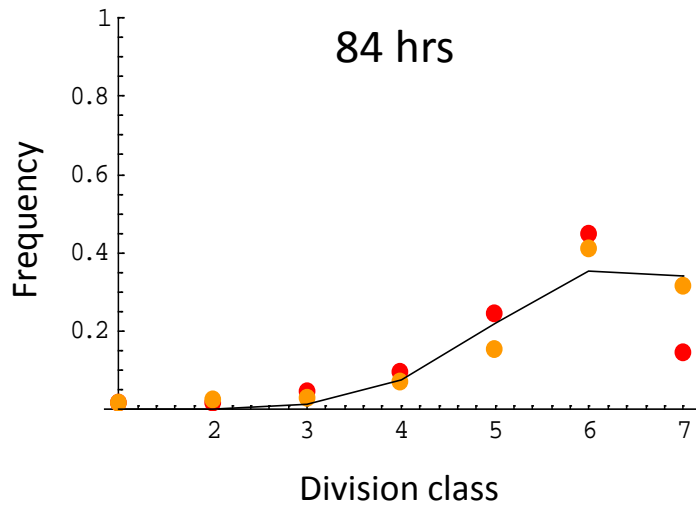
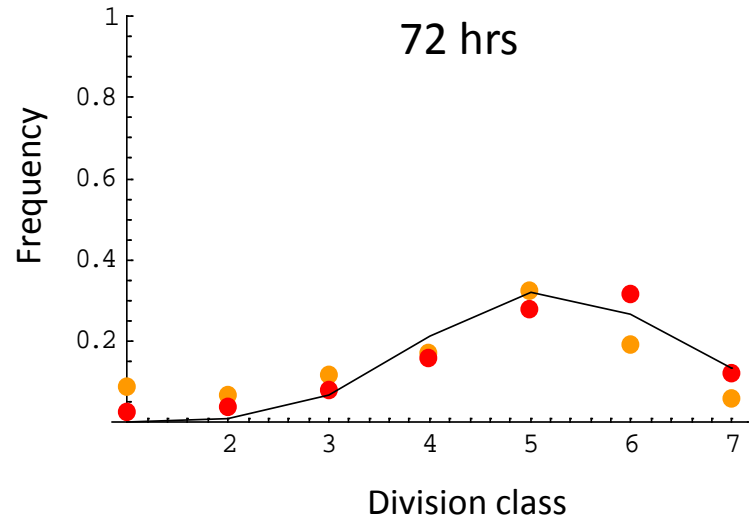
Inter-division time distribution:

$$P(t) = \frac{1}{2} b^3 t^2 e^{-bt}$$

Activation lag: 25 hrs

Mean inter-division time: 8 hrs

- Clone 7
- Clone 24
- model



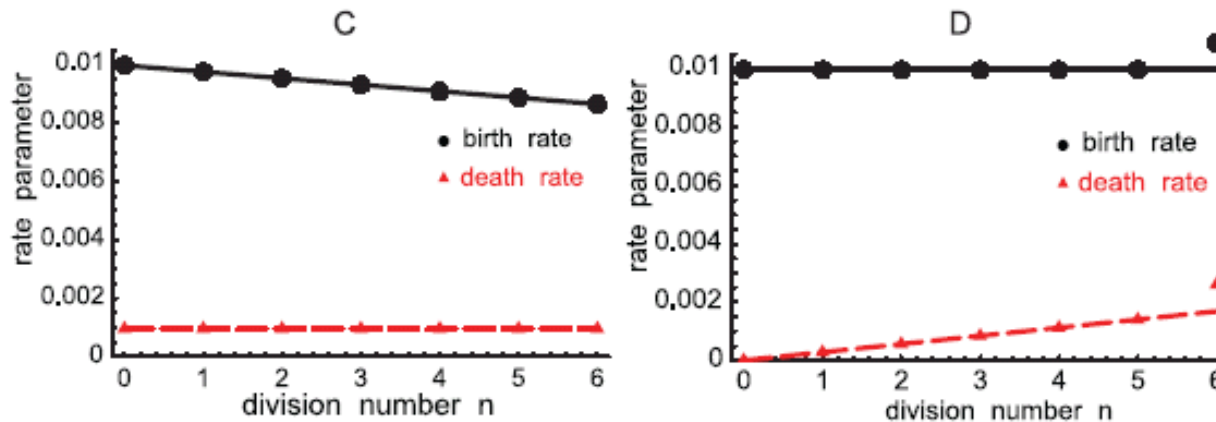
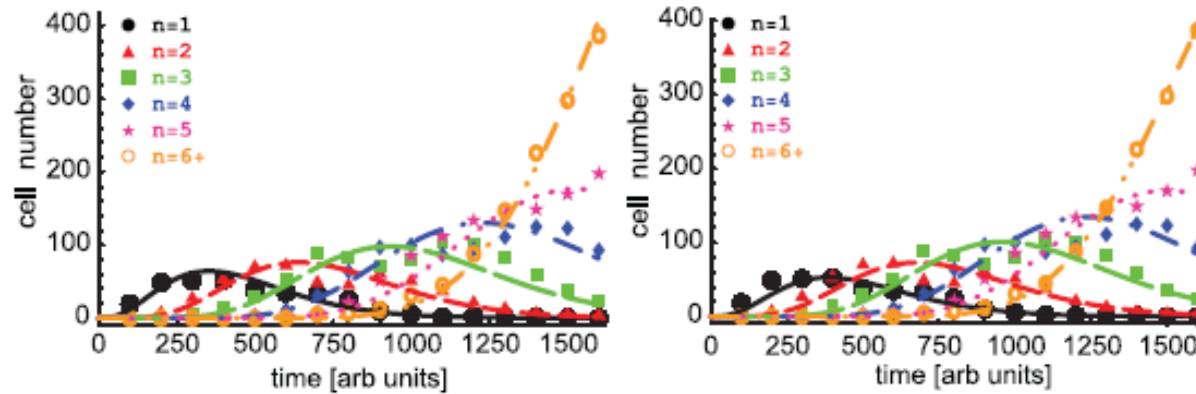


## Parameter sensitivity analysis: fitting same data with models with different distributions

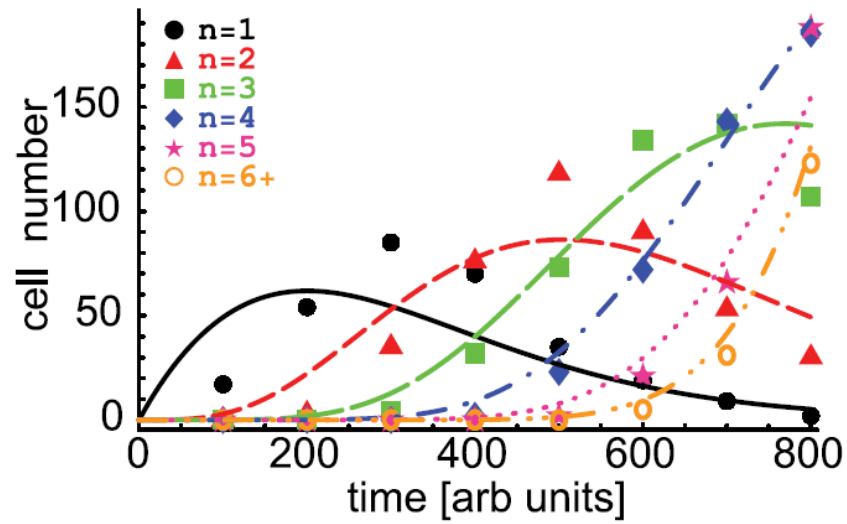
**Table 1.** Estimates of the parameters providing the best fit to the simulated and experimental data.

	Simulated data		Experimental data	
	Actual	Estimated	Estimated gamma	Estimated SM
$T_0, h$	66.7	$75.5 \pm 0.4$	$50.6 \pm 0.6$	$63.7 \pm 0.9$
$T, h$	20	$19.3 \pm 0.4$	$16.2 \pm 0.2$	$13.55 \pm 0.53$
$\tau, h$	0	$54.6 \pm 0.3$	$33.2 \pm 0.8$	$21.25 \pm 1.62$
$N_0$ cells	100	$105.9 \pm 12.8$	$(0.54 \pm 0.05) \times 10^4$	$(0.50 \pm 0.07) \times 10^4$
$d, h^{-1}$	0.01	$0.007 \pm 0.002$	$0.024 \pm 0.002$	$0.02 \pm 0.005$

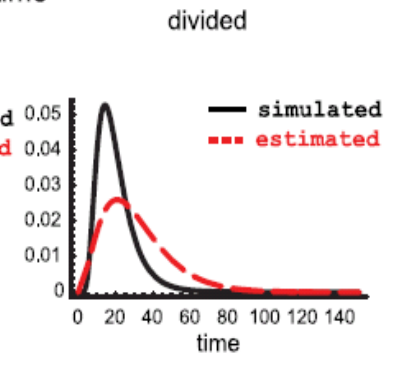
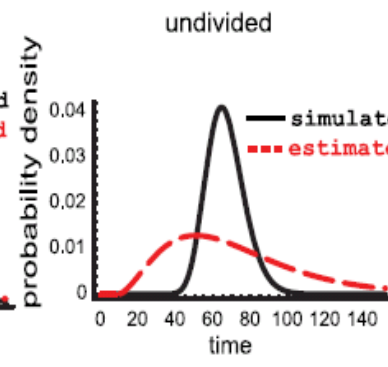
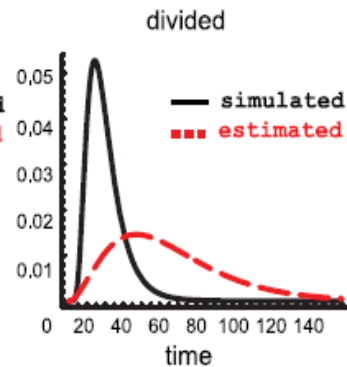
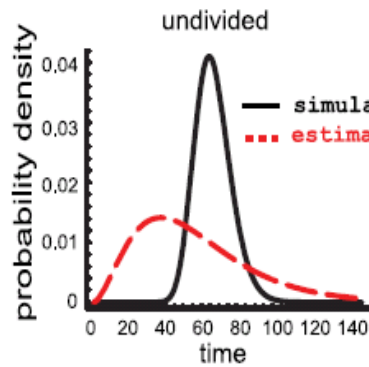
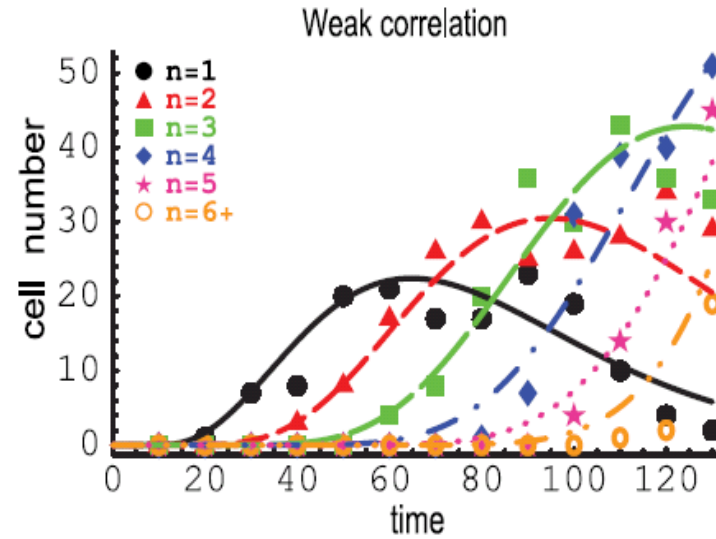
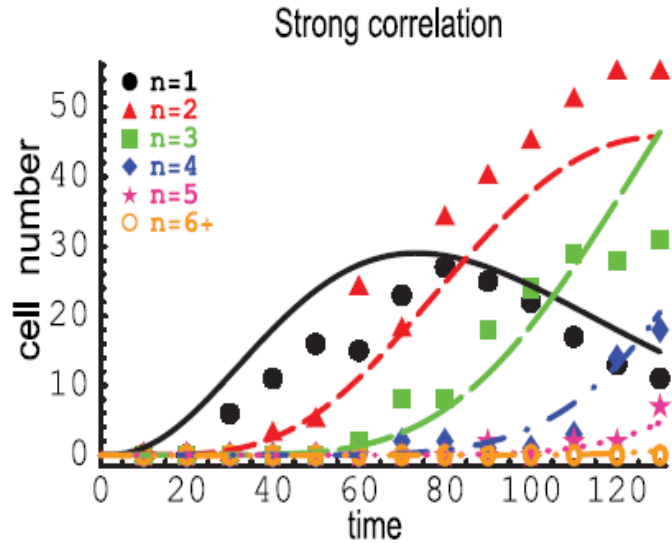
## More parameter sensitivity analysis: division-linked births vs. division-linked deaths



## More parameter sensitivity analysis: division-linked births vs. time-linked birth



# More parameter sensitivity analysis: mother-daughter correlations



## Some lessons and questions

In vivo quantification of early kinetics of T cell response is feasible

Comparisons of actual numbers obtained using different models are likely meaningless

How many features can be reliably estimated without over-fitting?

What is model accuracy??