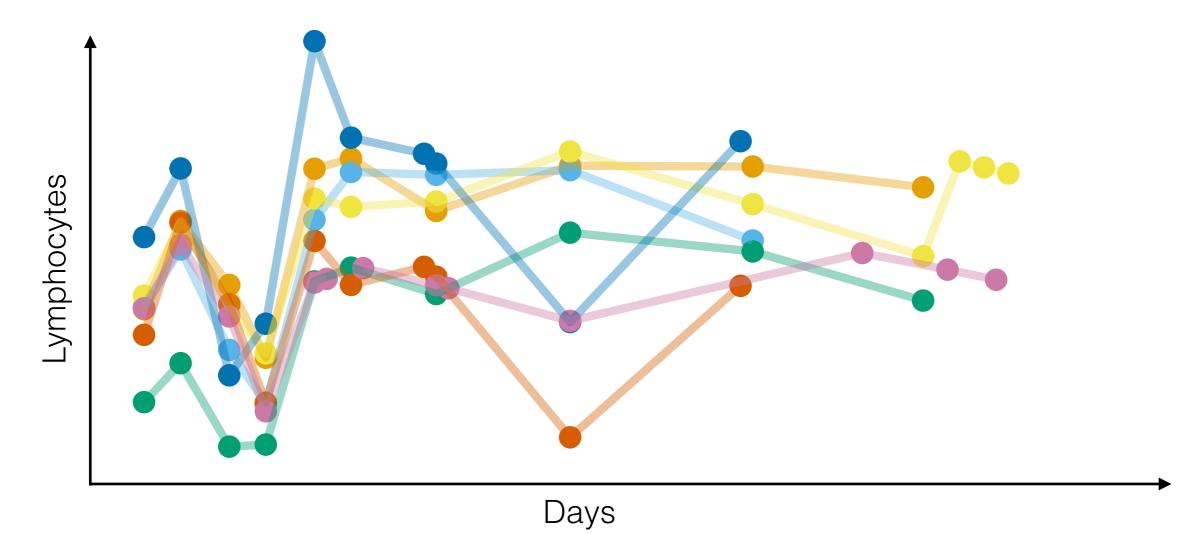
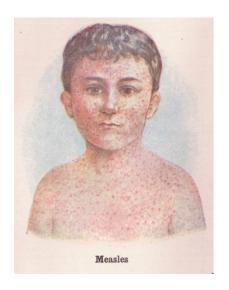
# Understanding the measles paradox: modeling host-parasite predatory feedbacks

Sinead Morris
Princeton University
semorris@princeton.edu
https://sineadmorris.github.io



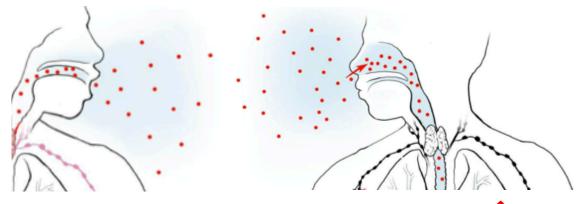
## Background



serious respiratory disease



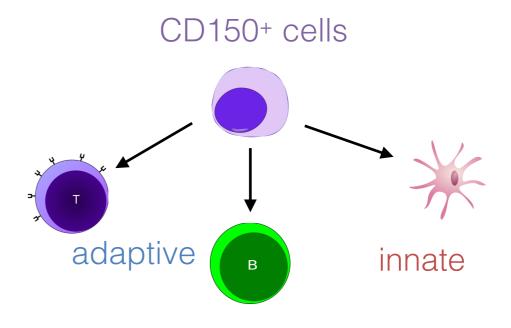
180,000 annual cases



classic respiratory infection

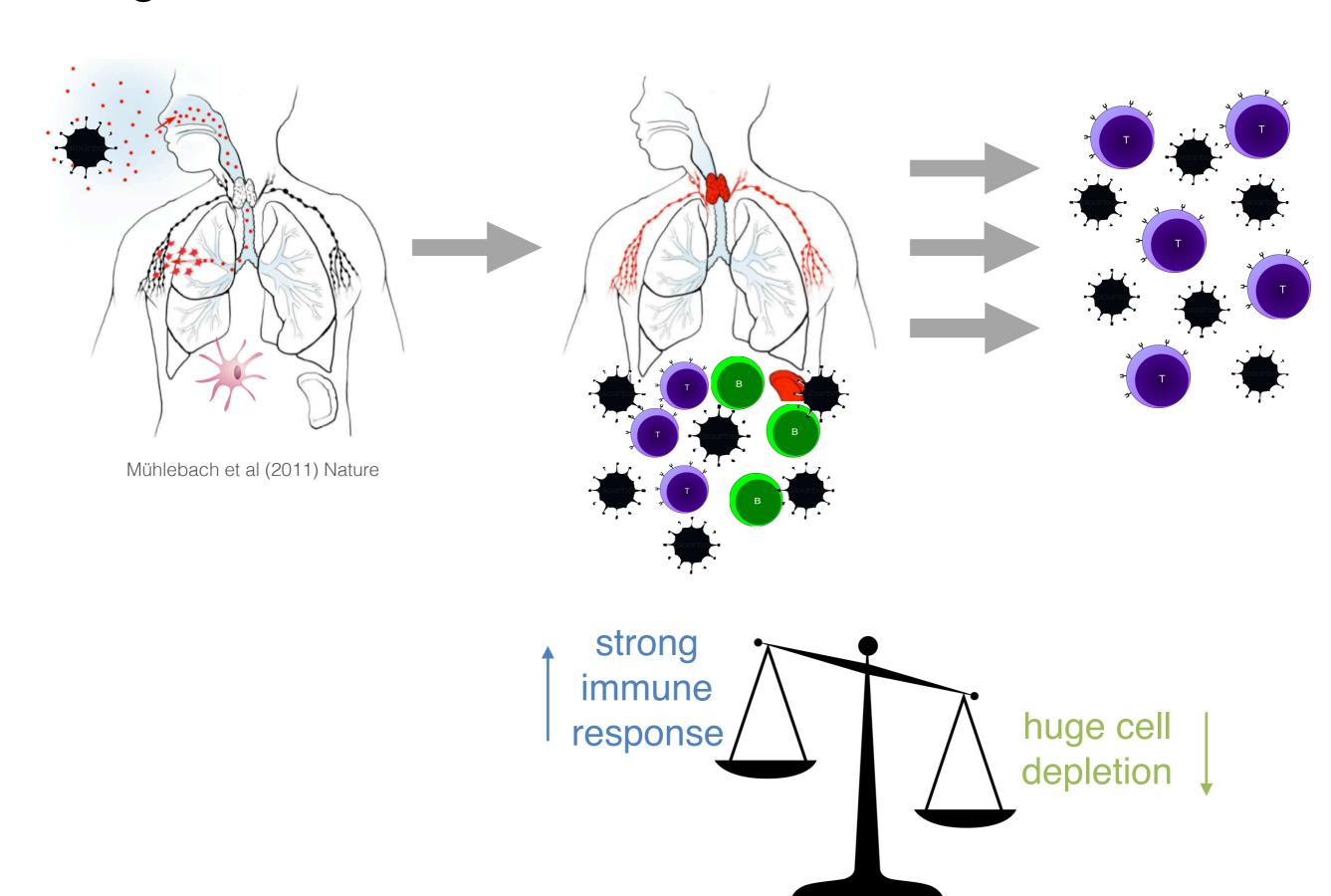






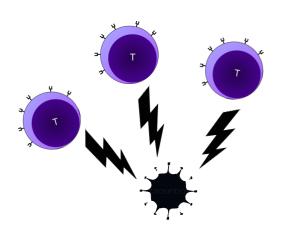
de Swart et al (2007) PLoS Pathogens

## Background

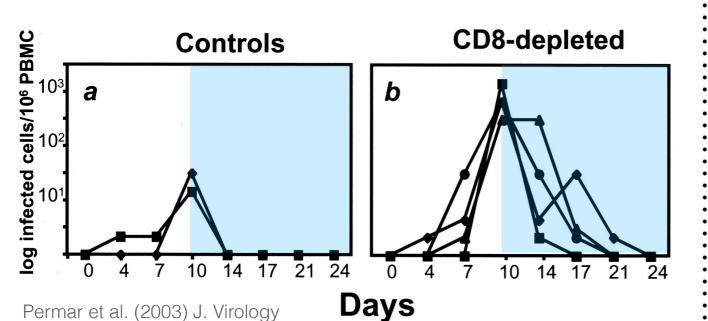


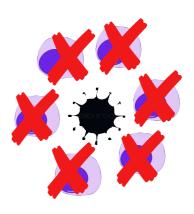
#### "Measles paradox"



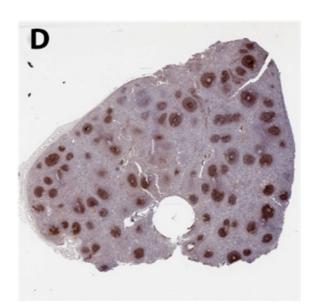


active suppression of viral growth





target cell limitation



Laksono et al. (2016) Viruses

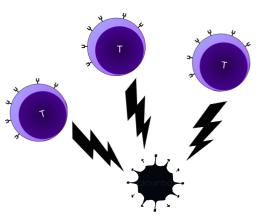
CDV: 100% mortality



Williams et al (1985) J. Wildlife Dis. Ludlow et al (2012) J. Virology

#### "Measles paradox"

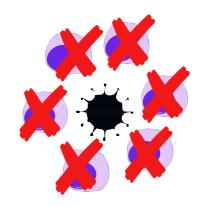




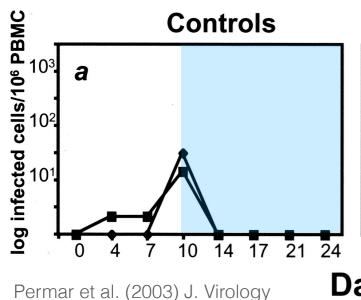
active suppression of viral growth

#### Aims

- within-host model of predatory feedbacks
- 2. identify drivers of viral clearance

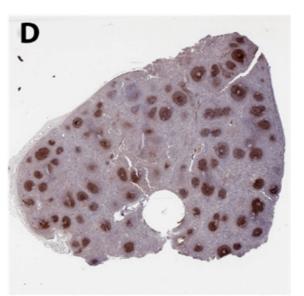


target cell limitation



**CD8-depleted b**0 4 7 10 14 17 21 24

Days Laksono et al. (2016) Viruses



CDV: 100% mortality



Williams et al (1985) J. Wildlife Dis. Ludlow et al (2012) J. Virology

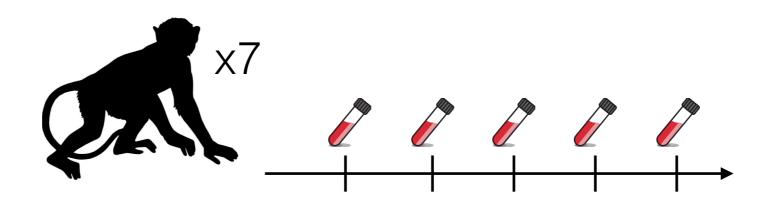


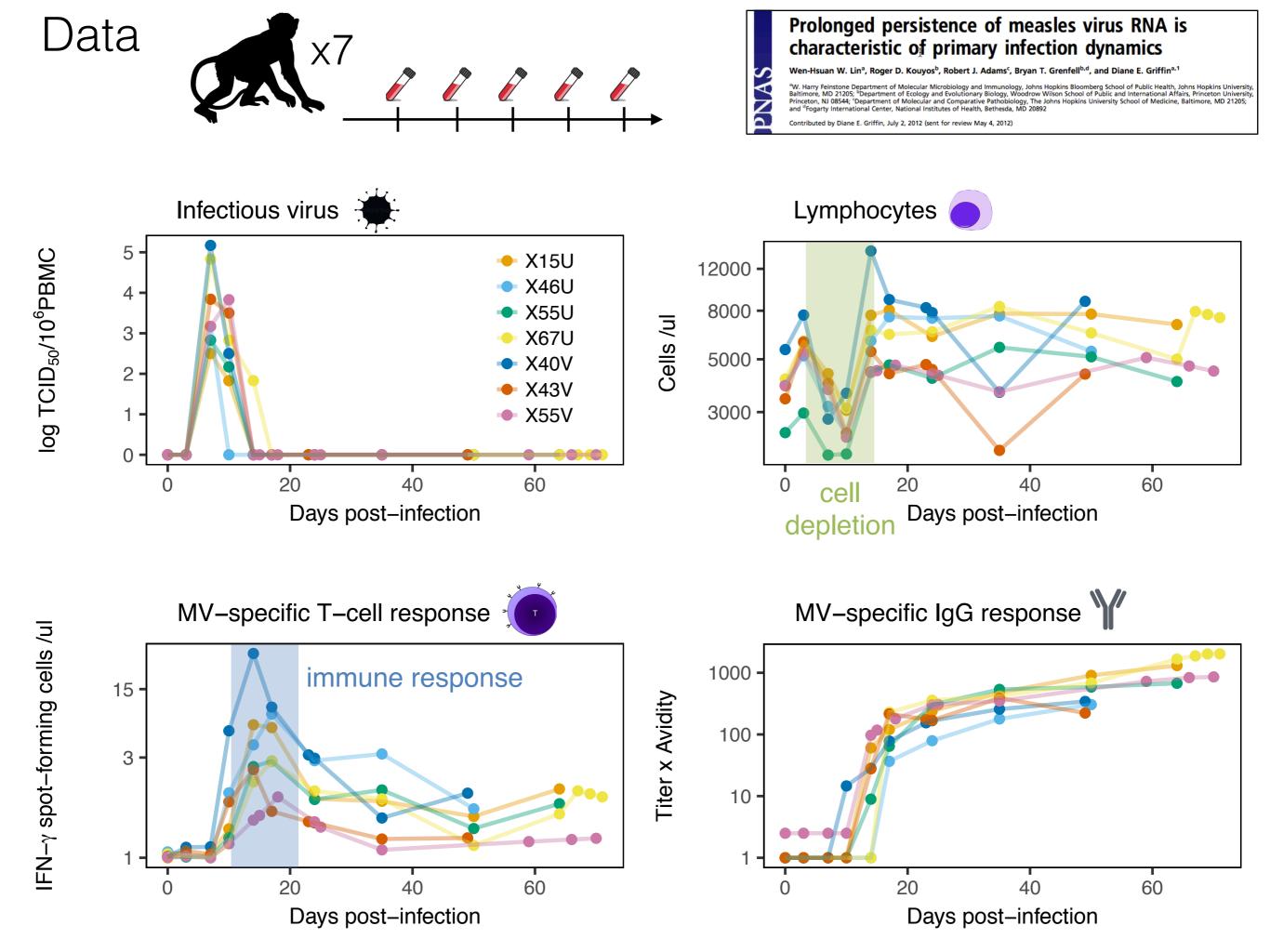
## Prolonged persistence of measles virus RNA is characteristic of primary infection dynamics

Wen-Hsuan W. Lina, Roger D. Kouyosb, Robert J. Adamsc, Bryan T. Grenfellb,d, and Diane E. Griffina,1

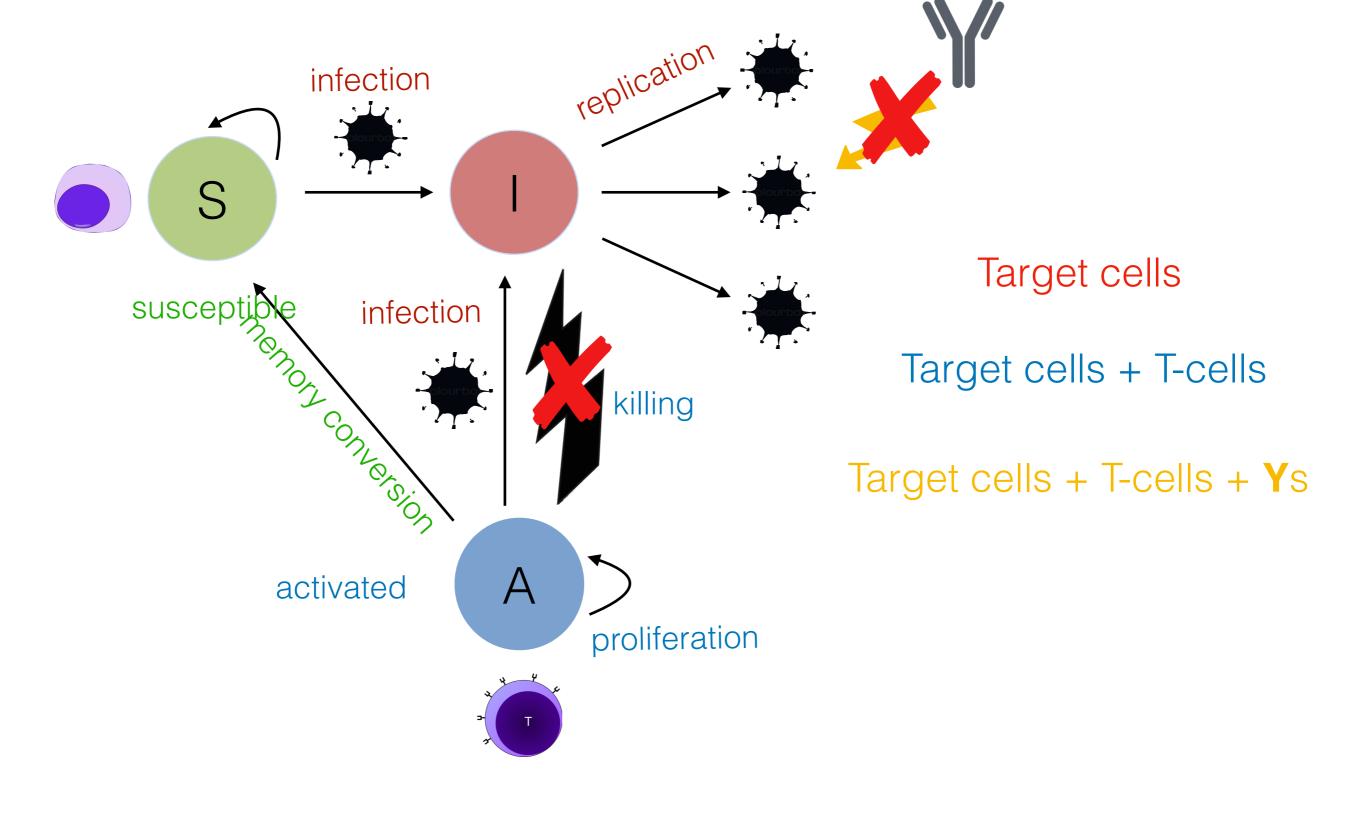
<sup>a</sup>W. Harry Feinstone Department of Molecular Microbiology and Immunology, Johns Hopkins Bloomberg School of Public Health, Johns Hopkins University, Baltimore, MD 21205; <sup>b</sup>Department of Ecology and Evolutionary Biology, Woodrow Wilson School of Public and International Affairs, Princeton University, Princeton, NJ 08544; <sup>c</sup>Department of Molecular and Comparative Pathobiology, The Johns Hopkins University School of Medicine, Baltimore, MD 21205; and <sup>d</sup>Fogarty International Center, National Institutes of Health, Bethesda, MD 20892

Contributed by Diane E. Griffin, July 2, 2012 (sent for review May 4, 2012)

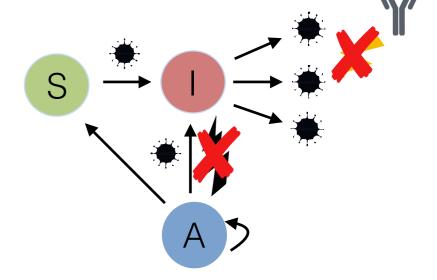


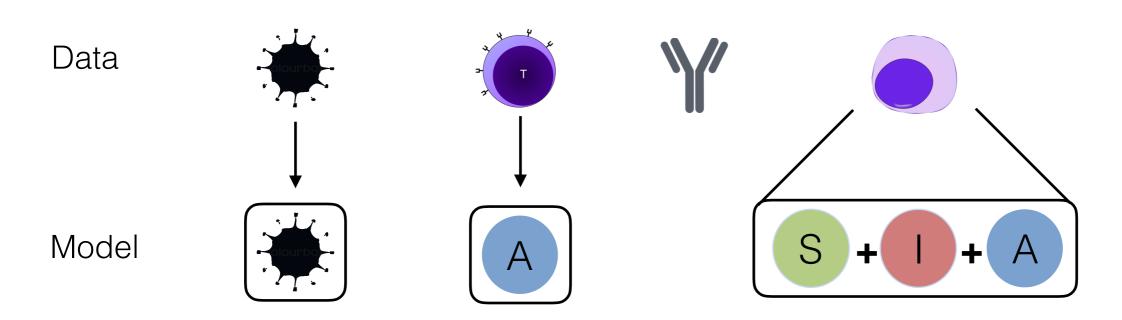


#### Model



#### Model

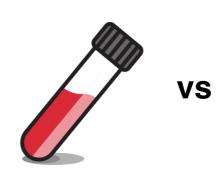


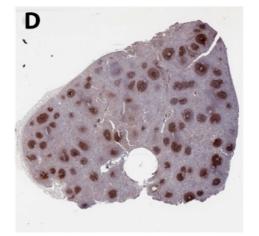


#### Caveats

Parameter specification

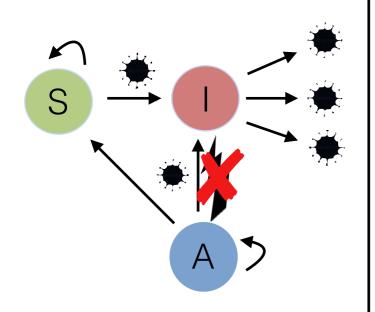
Data from blood, not lymphoid tissues



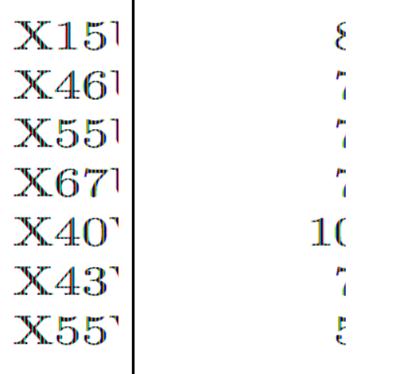


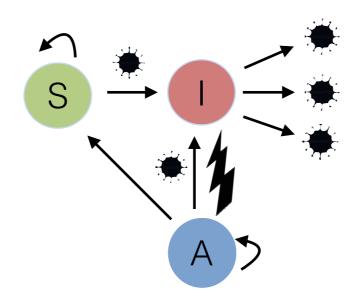
Laksono et al. (2016)

#### Results: AIC

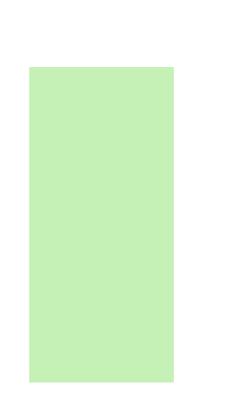


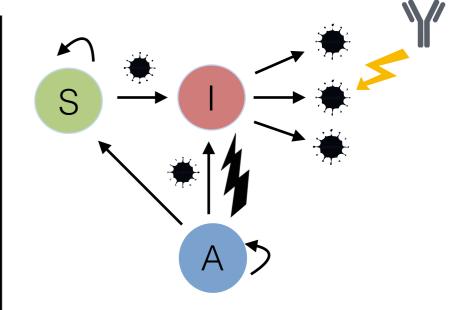






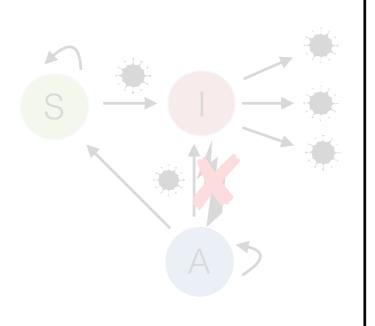
Target cells + T-cells



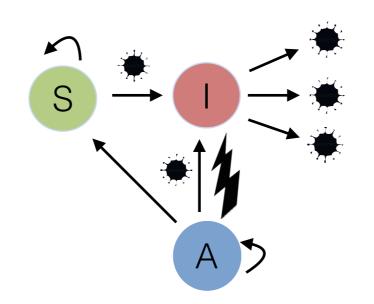


Target cells + T-cells + Ys

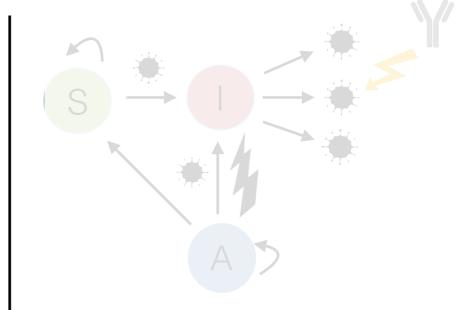
#### Results: AIC



Target cells

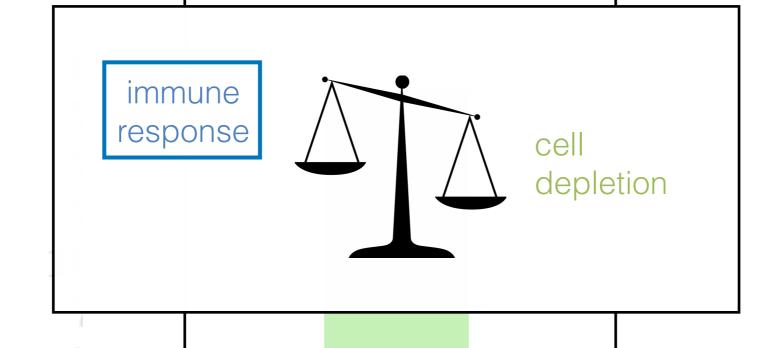


Target cells + T-cells

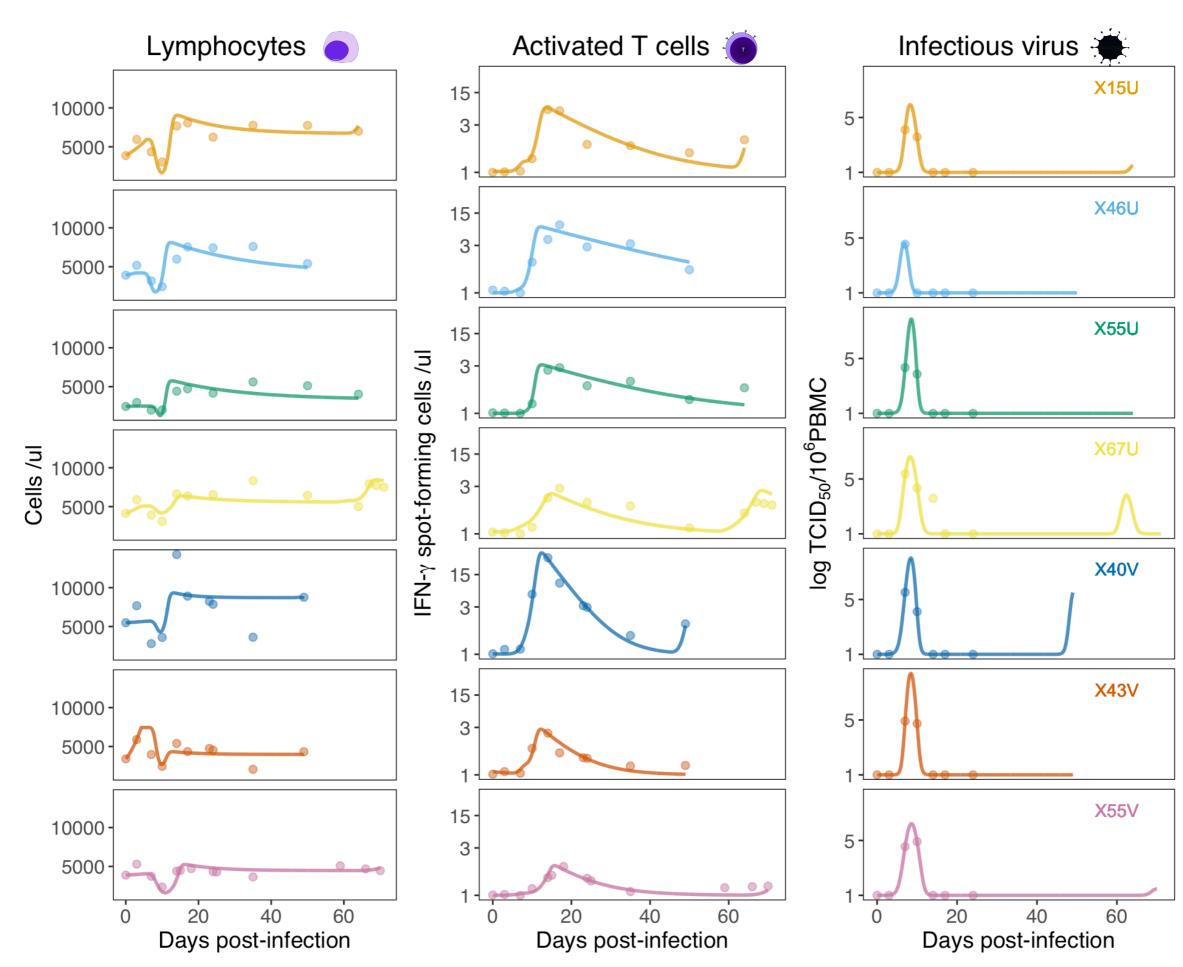


Target cells + T-cells + Ys

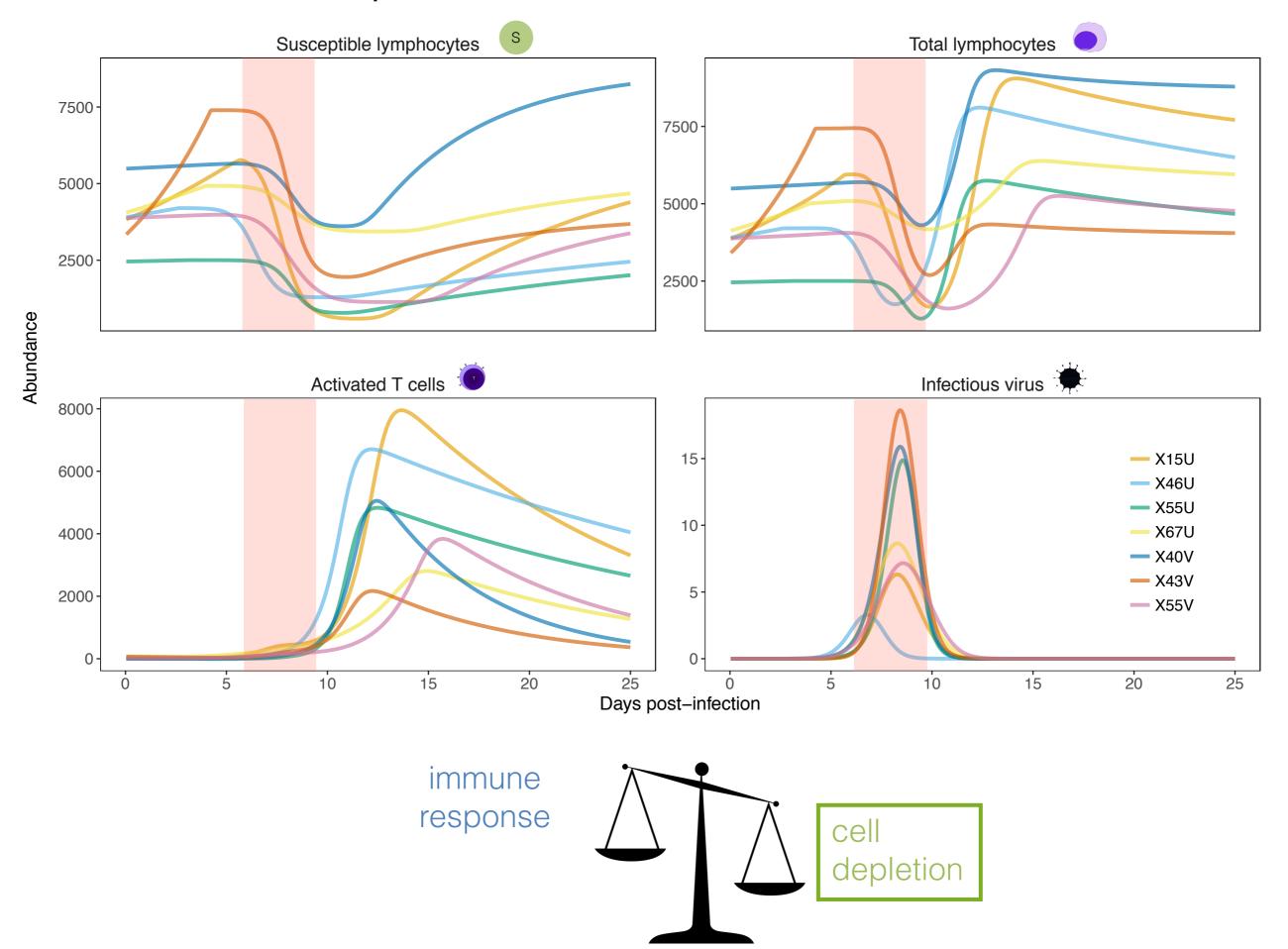
X15 X46 X55 X67 X40 X43 X55



#### Results: model fits



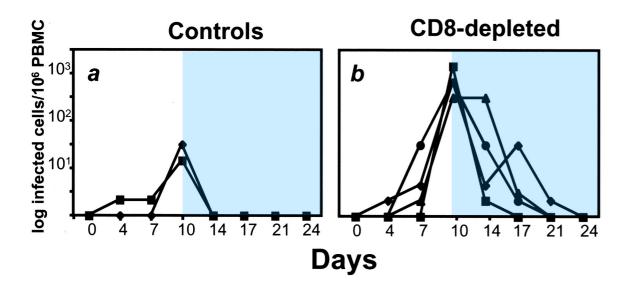
## Results: model predictions

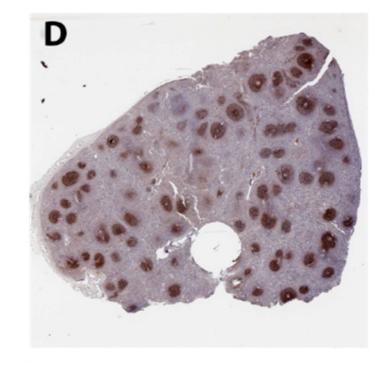


1



2



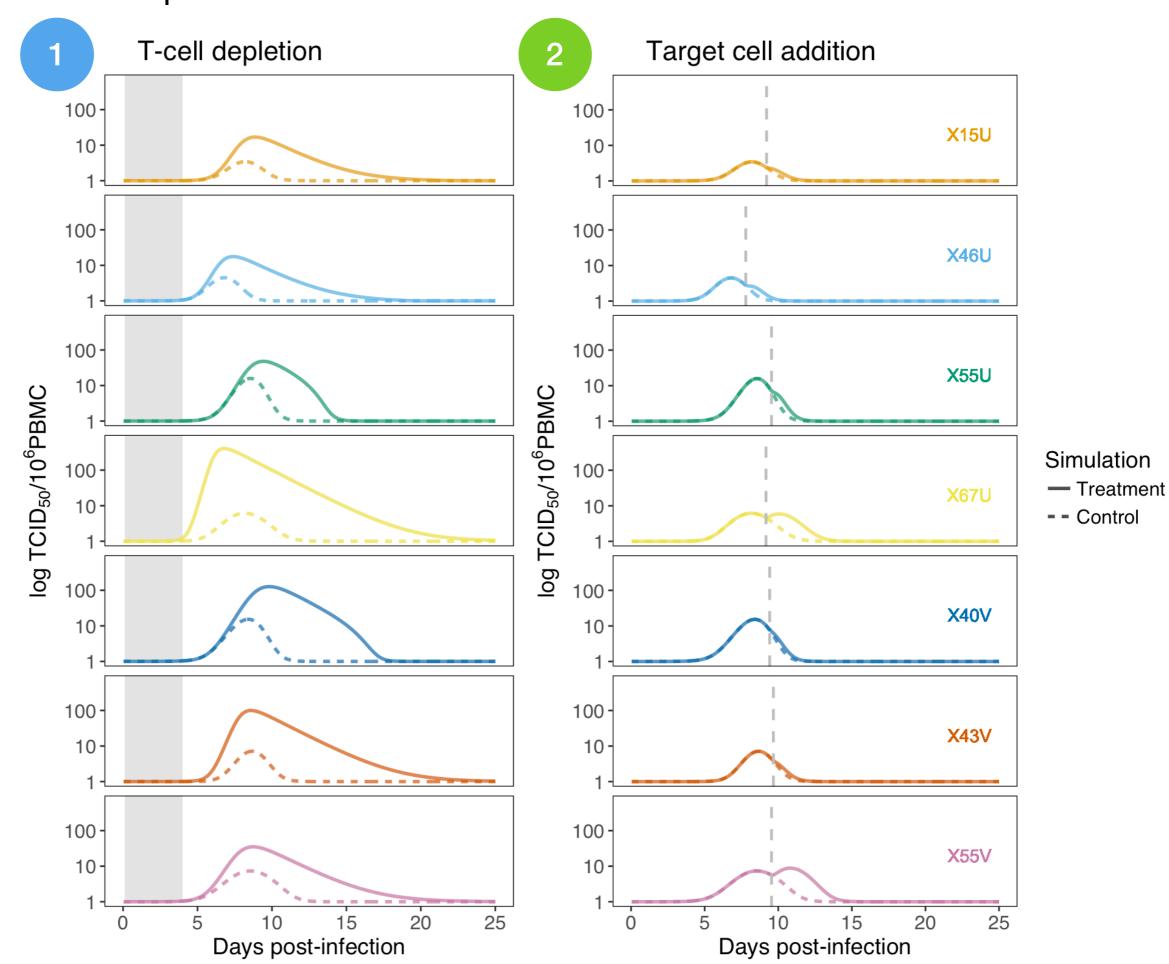


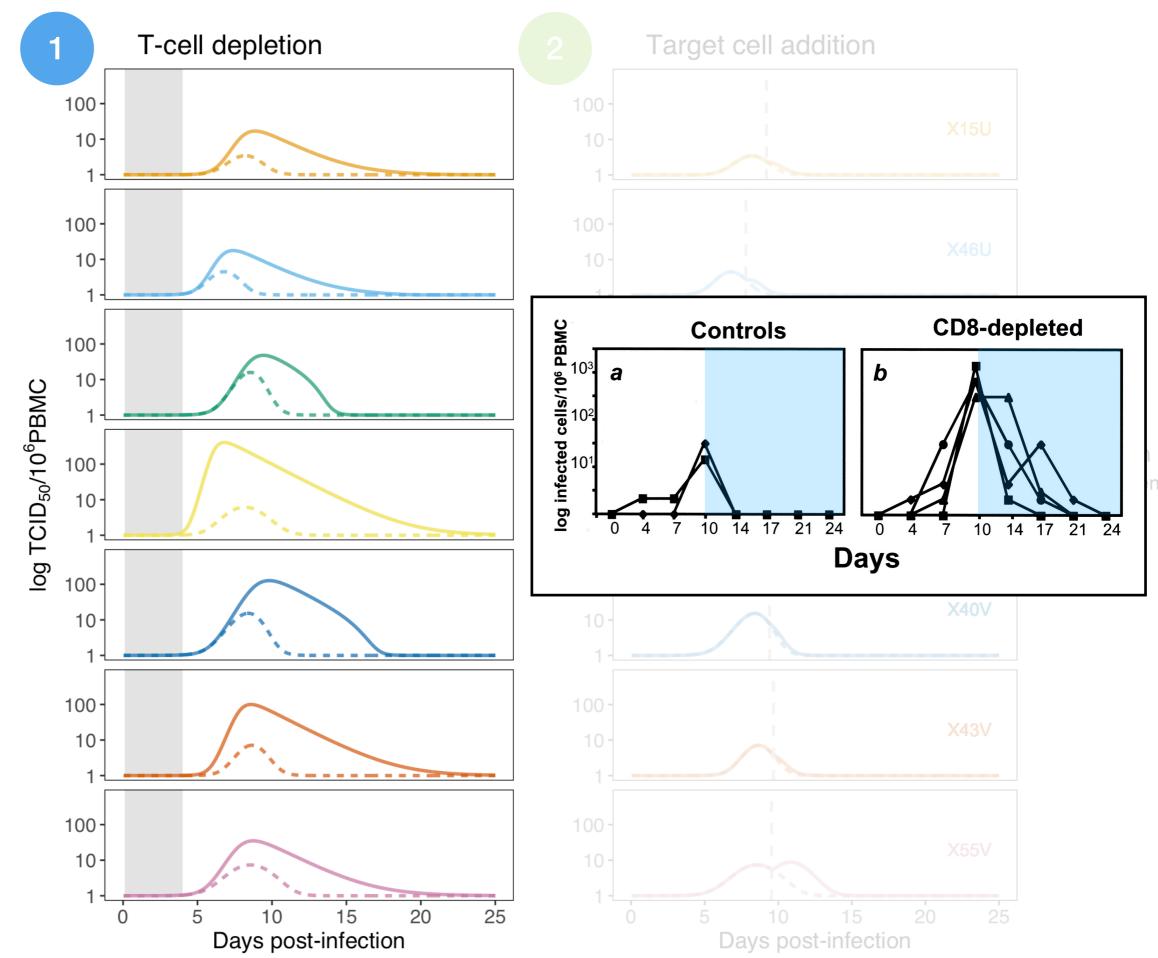
- t = 0: deplete T-cells
- *t* < 4d: suppress activation/ proliferation

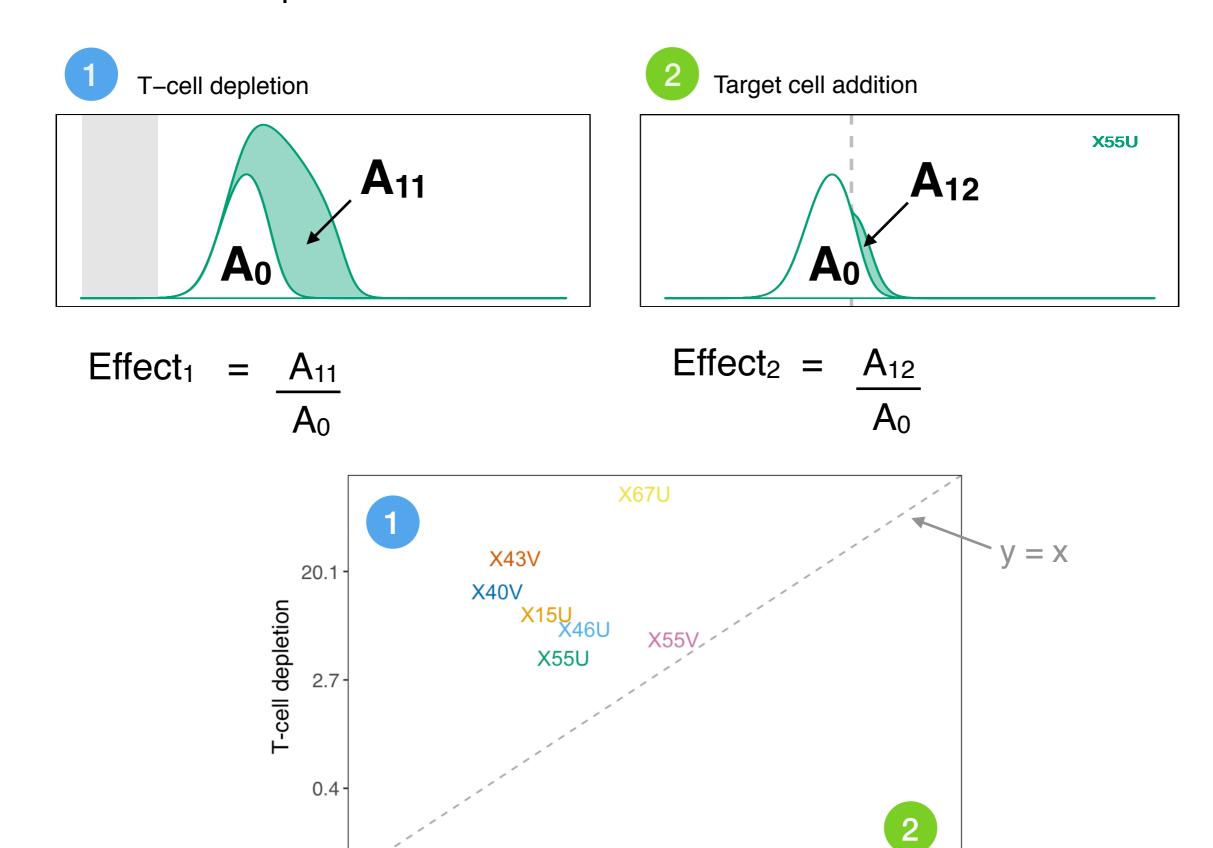
peak + 1d: add new S cells

Is viral clearance delayed?

Does viral load resurge?







2.7

Target cell addition

20.1

0.4

#### Extension to other systems

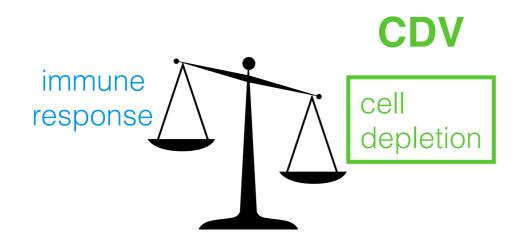
#### **Measles**

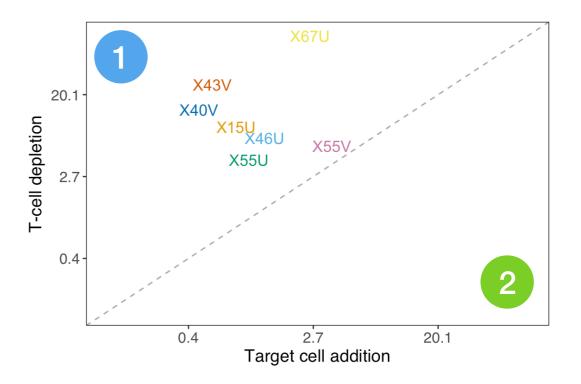




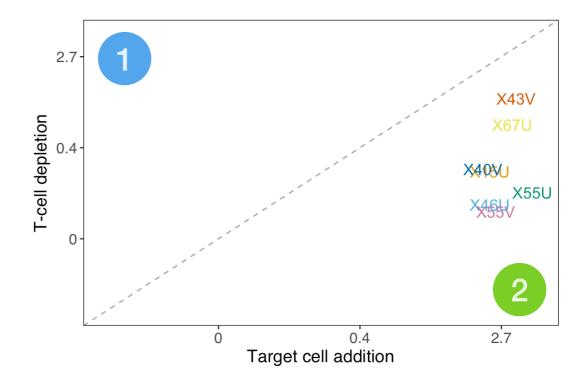
Rik de Swart, Erasmus MC







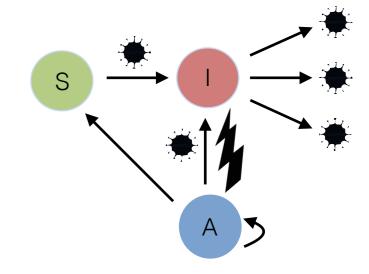


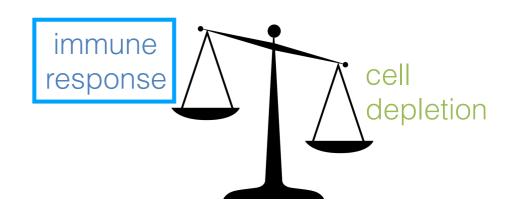


#### Conclusions

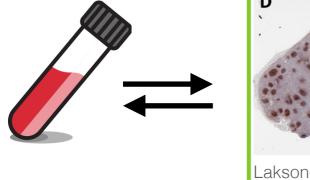
within-host model of predatory feedbacks

2. identify drivers of viral clearance





#### **Next steps**









#### Thanks



Bryan Grenfell
Princeton University



Diane Griffin Johns Hopkins



Ashley Nelson Johns Hopkins



Rik de Swart Erasmus MC

#### And:

Andrew Yates, Columbia University
Michael Mina, Harvard Medical School
Rory de Vries, Erasmus MC
Wen-Hsuan Lin, Columbia University
Roger Kouyos, University Hospital Zurich

#### PhD committee:

Jessica Metcalf, Princeton University Andrea Graham, Princeton University Cécile Viboud, Fogarty International Center



