

# Life Data Epidemiology

*Lect 21: projects*

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# Material

- Keeling, Matt J.; Rohani, Pejman, Modeling infectious diseases in humans and animals.  
Princeton University Press, 2008
- Wallinga, Lipsitch, How generation intervals shape the relationship between growth rates and reproductive numbers Proc. R. Soc B (2007) 274, 599
- Grassly, N., Fraser, C. Mathematical models of infectious disease transmission. Nat Rev Microbiol 6, 477-487 (2008)
- R. Pastor-Satorras, C. Castellano, P. Van Mieghem and A. Vespignani. Epidemic processes in complex networks.  
Rev. Mod. Phys. 87, 925 (2015) (<https://arxiv.org/abs/1408.2701>)
- Marc Barthélemy, Alain Barrat, Romualdo Pastor-Satorras, Alessandro Vespignani, Dynamical patterns of epidemic outbreaks in complex heterogeneous networks, Journal of Theoretical Biology 235 (2005) 275-288 (arXiv:cond-mat/0410330)
- Naoki Masuda and Petter Holme, Predicting and controlling infectious disease epidemics using temporal networks, F1000Prime Rep. 5, 6 (2013).
- Petter Holme and Jari Saramäki, Temporal networks, Phys. Rep. 519, 97-125 (2012).
- Perra, N., Gonçalves, B., Pastor-Satorras, R. et al. Activity driven modeling of time varying networks. Sci Rep 2, 469 (2012). <https://doi.org/10.1038/srep00469> (+ Supplementary Material)

# Exam

## **Rules written test:**

- 6 questions choose 4 (and not more!)
- For each question the answer must stay in 2 pages maximum (i.e. one A4 paper both side)
- Time: 2 hours

## **Rules projects:**

- groups of maximum 3 persons
- 20 minute presentation (slides recommended) + questions
- final score: kind of average between written test and project with more weight on the project

# Project Discussion

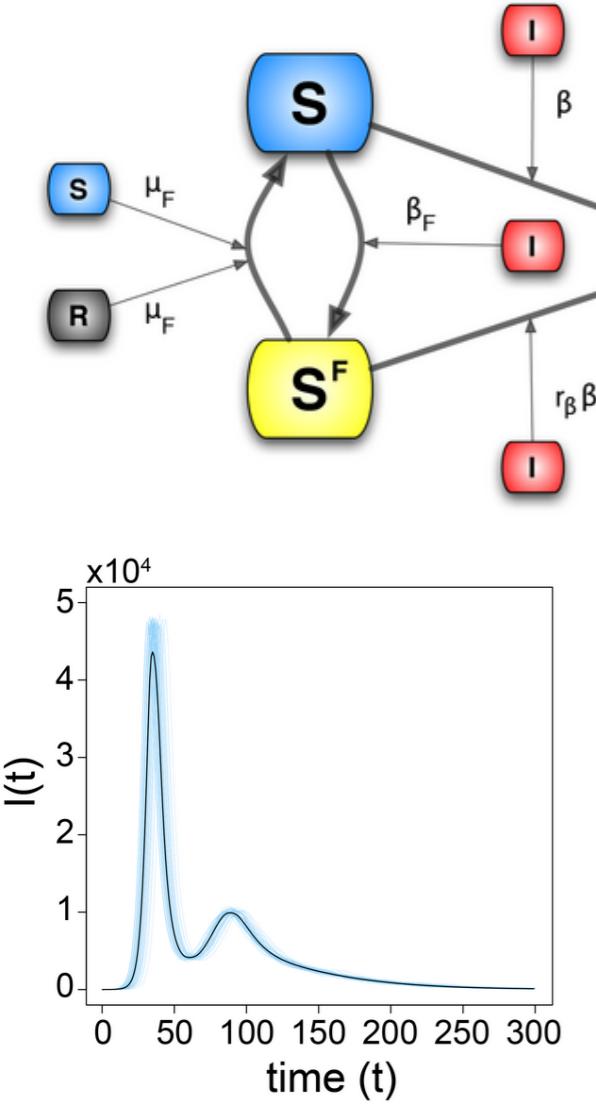
- Background
- Goal of the study
- Methods
- Results
- Interpretation of the results, Conclusions, and Discussion

**The talk need to stay within 20 minutes!**

(It means 18 slides maximum)

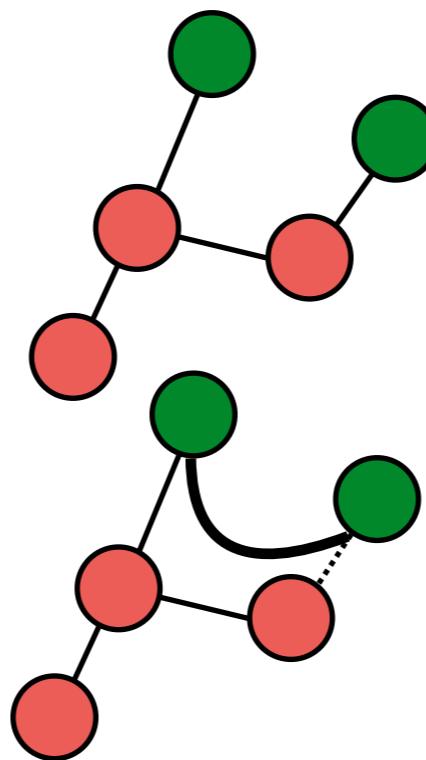
# project 1: behavioural adaption to epidemics

Compartmental models  
with fear



[Perra, et al PLOS ONE 2011]

adaptive networks

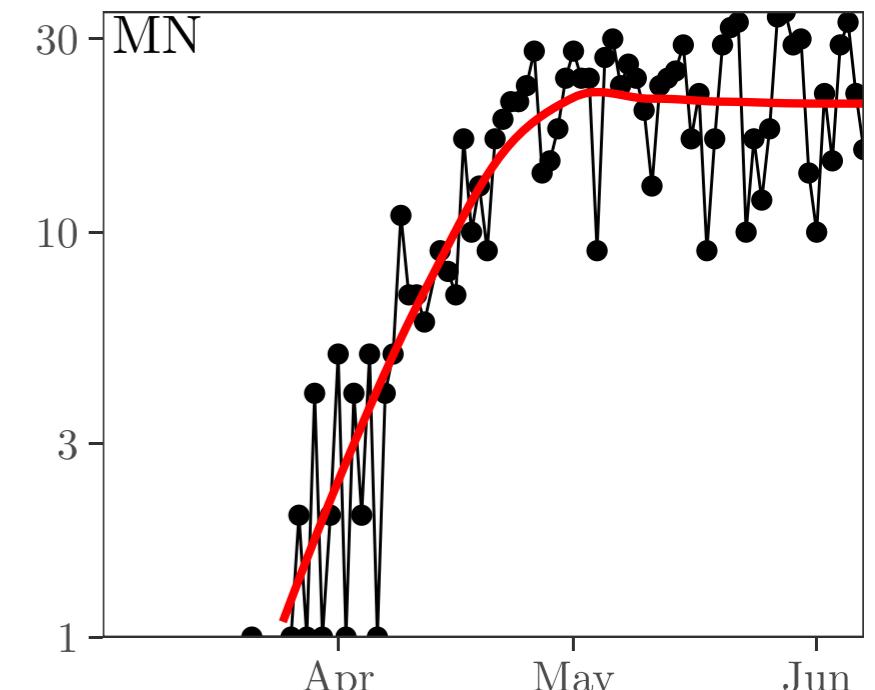


[Shaw, Schwartz, PRE 2008]

**model fear:**

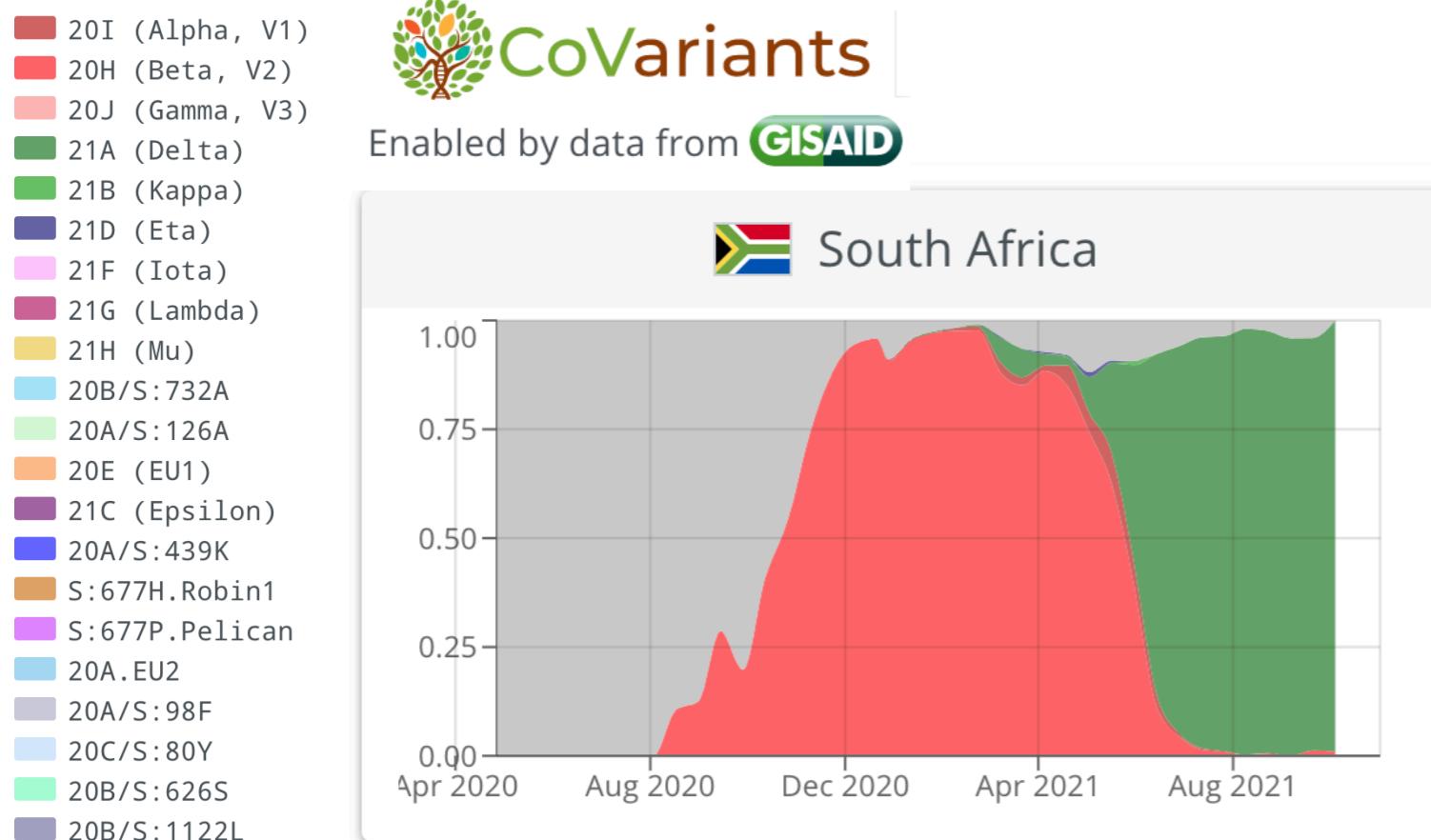
how does it impact the epidemic dynamics? Can we quantify its effect on the COVID-19 epidemic?

fear explains the plateau observed in the COVID-19 epidemic



[Weitz, et al PNAS 2020]

# project 2: interaction between SARS-CoV2 variants of concern



## Input data:

- frequency of variants by week and country: cov-spectrum.org;
- covid-19 incidence data by country: ourworldindata.org; coronavirus.jhu.edu
- human behavior data: <https://www.google.com/covid19/mobility>; <https://www.bsg.ox.ac.uk/research/covid-19-government-response-tracker>

## Papers:

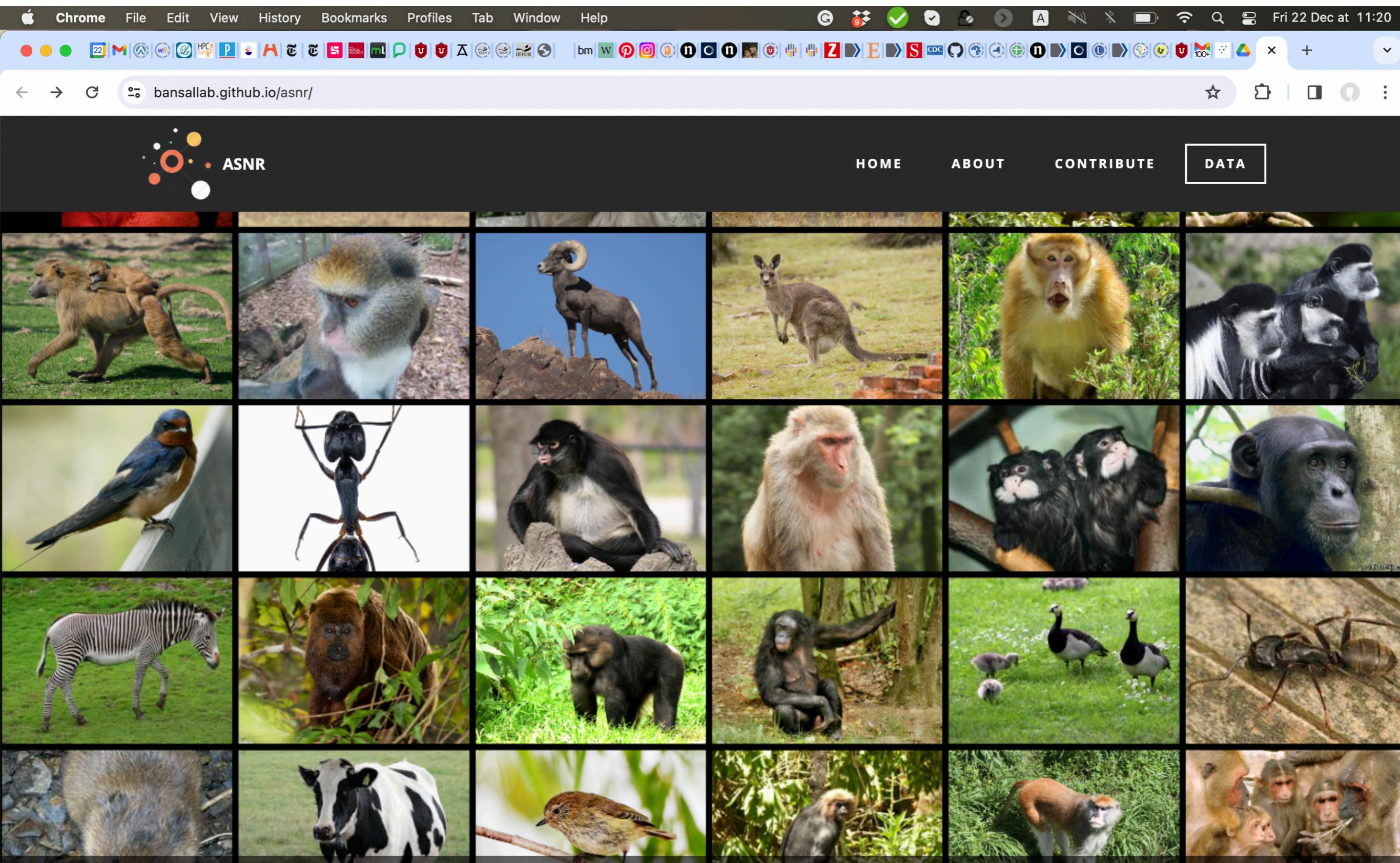
- Toranj Simin, et al, medRxiv 2025, <https://doi.org/10.1101/2025.11.07.25339691>

- $S$  : selection coefficient
- $V(t)$  : incidence of new variant at time  $t$
- $W(t)$ : incidence of resident strain at time  $t$

$$s = \frac{\ln\left(\frac{V(T)}{W(T)}\right) - \ln\left(\frac{V(0)}{W(0)}\right)}{T} \quad p(t) = \frac{V(t)}{V(t) + W(t)} = \frac{1}{1 + ae^{-St}}$$

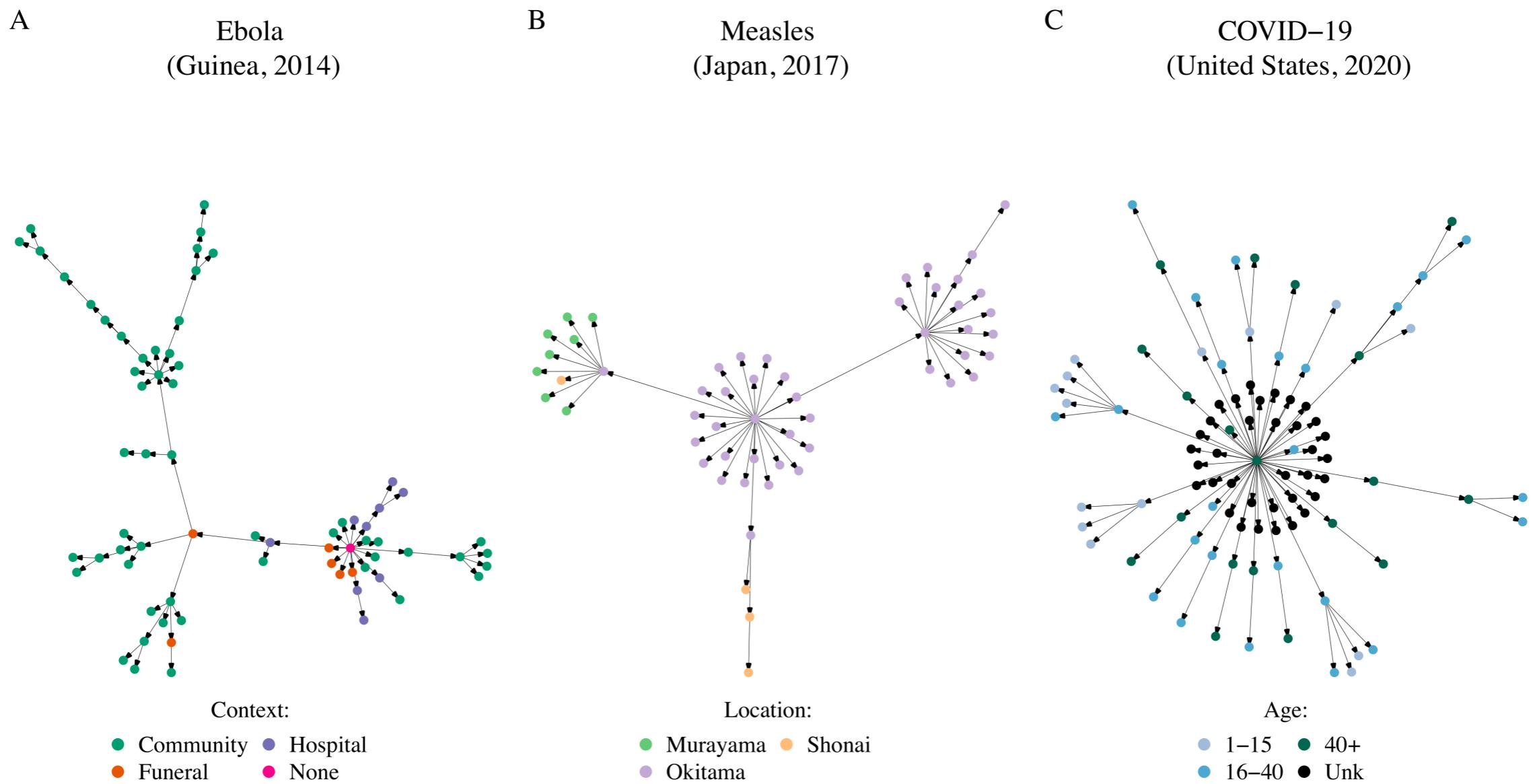
# project 3: let's put it in perspective - comparing epidemic spread across animal species

A screenshot of a web browser showing a grid of animal images. The browser interface includes a top navigation bar with tabs like Chrome, File, Edit, View, History, Bookmarks, Profiles, Tab, Window, Help, and a search bar containing the URL [bansallab.github.io/asnr/](https://bansallab.github.io/asnr/). Below the navigation bar is a dark header with the ASNR logo, HOME, ABOUT, CONTRIBUTE, and DATA buttons. The main content area is a 5x6 grid of animal photographs. The animals shown include various primates (baboons, monkeys, chimpanzees), a goat, a kangaroo, a zebra, a cow, a bird, and several insects (ants). The images are arranged in five rows and six columns.



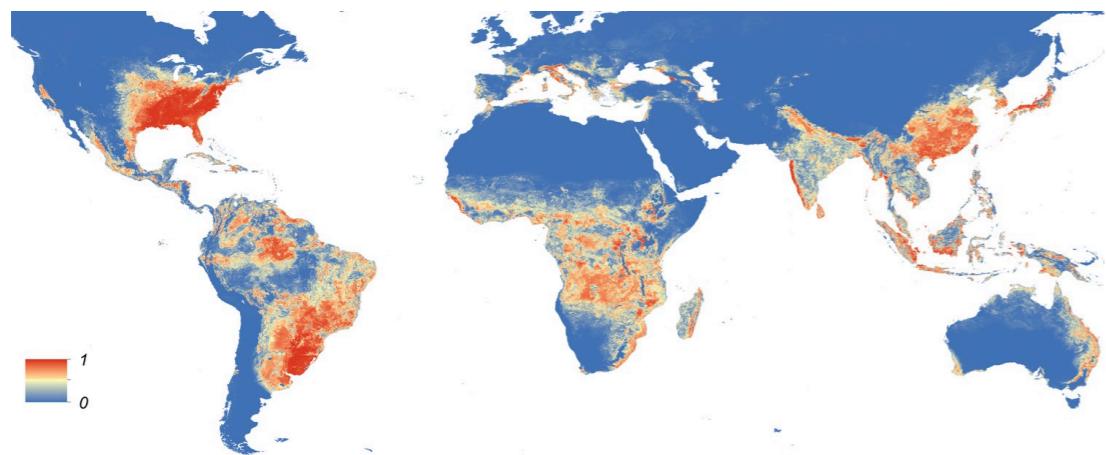
# project 4: transmission trees and super-spreading events

- An open-access database of infectious disease transmission trees to explore superspreaders epidemiology, Taube et al PLOS Biology 2022 (<https://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.3001685>)
- Clustering and super-spreading potential of SARS-CoV-2 infections in Hong Kong, Adam et al Nature Medicine 2020 (<https://www.nature.com/articles/s41591-020-1092-0>)

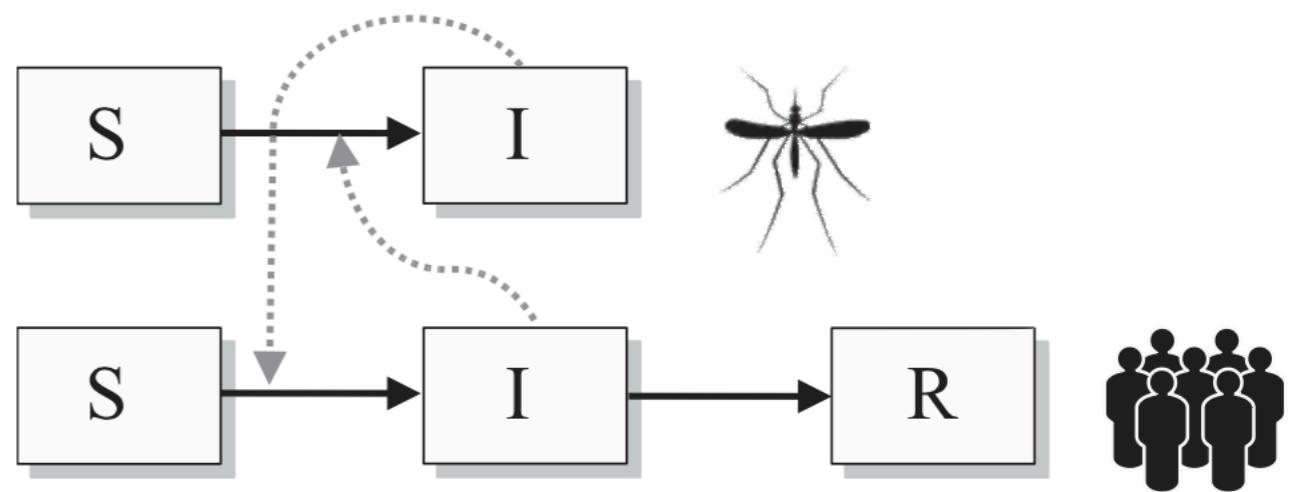


# project 5: vector-borne infections

- Vector-borne infections
- Zika, Chikungunya, Dengue



-The global compendium of *Aedes aegypti* and *Ae. albopictus* occurrence, Kraemer et al Scientific data 2015 <https://www.nature.com/articles/sdata201535>



-Keeling and Rohani book

Often only the human part is considered and the effect of mosquitos is collapsed in the delay from susceptible to infectious.

# project 6: networks are complex not only because they are heterogeneous

<https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1000736>

## Dynamics and Control of Diseases in Networks with Community Structure

Marcel Salathé , James H. Jones

Published: April 8, 2010 • <https://doi.org/10.1371/journal.pcbi.1000736>

Article	Authors	Metrics	Comments	Media Coverage
				

### Abstract

- Author Summary
- Introduction
- Results
- Discussion
- Methods
- Supporting Information
- Acknowledgments
- Author Contributions
- References

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### Reader Comments

### Abstract

The dynamics of infectious diseases spread via direct person-to-person transmission (such as influenza, smallpox, HIV/AIDS, etc.) depends on the underlying host contact network. Human contact networks exhibit strong community structure. Understanding how such community structure affects epidemics may provide insights for preventing the spread of disease between communities by changing the structure of the contact network through pharmaceutical or non-pharmaceutical interventions. We use empirical and simulated networks to investigate the spread of disease in networks with community structure. We find that community structure has a major impact on disease dynamics, and we show that in networks with strong community structure, immunization interventions targeted at individuals bridging communities are more effective than those simply targeting highly connected individuals. Because the structure of relevant contact networks is generally not known, and vaccine supply is often limited, there is great need for efficient vaccination algorithms that do not require full knowledge of the network. We developed an algorithm that acts only on locally available network information and is able to quickly identify targets for successful immunization intervention. The algorithm generally outperforms existing algorithms when vaccine supply is limited, particularly in networks with

# project 7: Exploring the impact of temporal network features

<http://www.sociopatterns.org/>



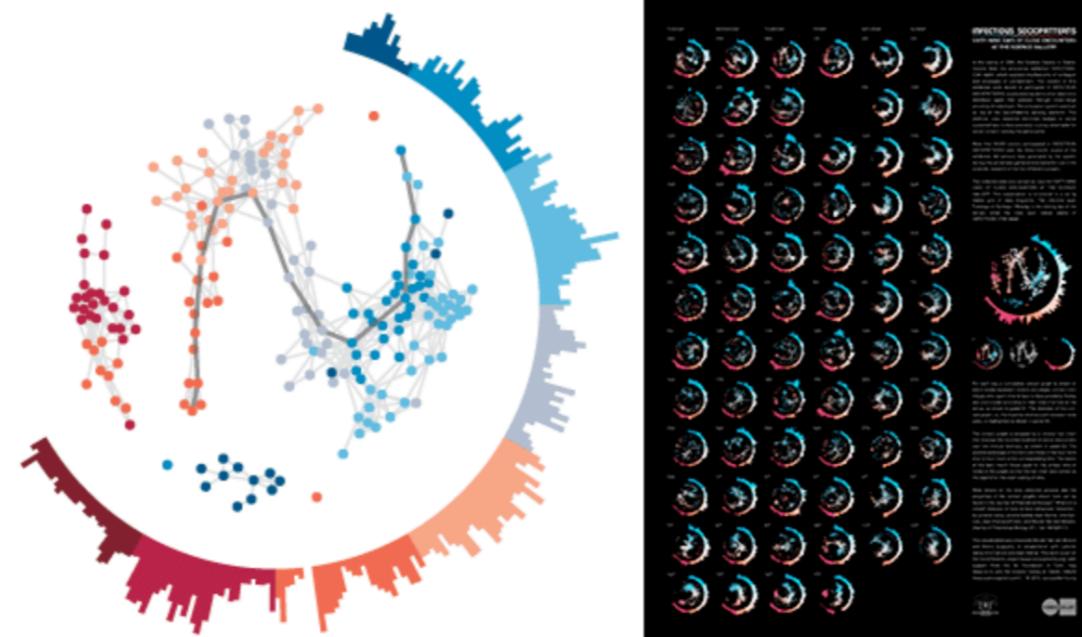
## WELCOME

SocioPatterns is an interdisciplinary research collaboration formed in 2008 that adopts a data-driven methodology to study social dynamics and human activity.

Since 2008, we have collected longitudinal data on the physical proximity and face-to-face contacts of individuals in numerous real-world environments, covering widely varying contexts across several countries: schools, museums, hospitals, etc. We use the data to study human behaviour and to develop agent-based models for the transmission of infectious diseases.

We make most of the collected data freely available to the scientific community.

## FEATURED: INFECTIOUS SOCIOPATTERNS POSTER



Left: One of the sixty-nine daily diagrams of contact activity. Right: Thumbnail of the poster with the complete visualization and accompanying text.

## NEWS

### New data sets published: co-presence and face-to-face contacts

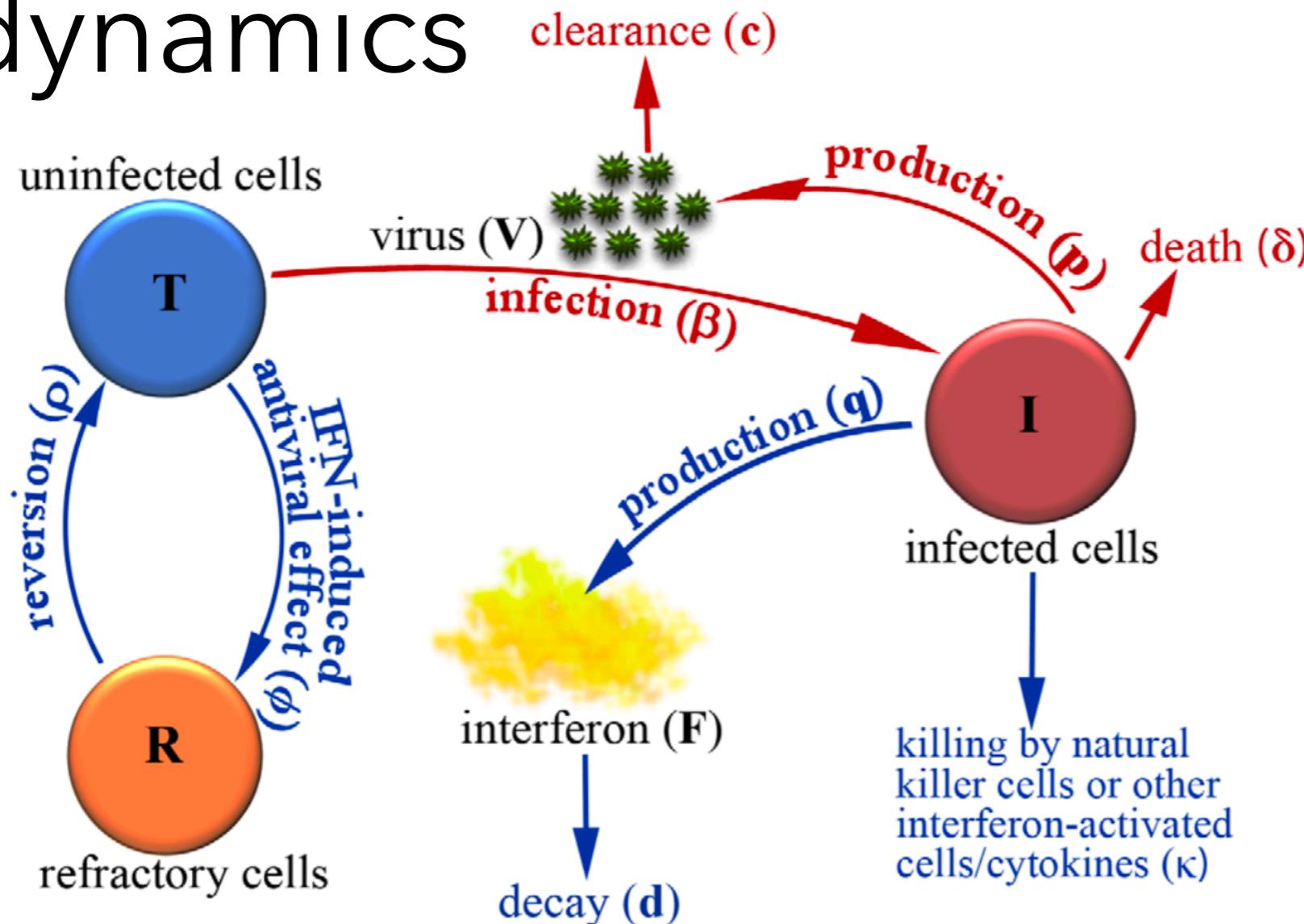
Through a publication in [EPJ Data Science](#), we have released several new data sets of different types. These datasets can be found on [Zenodo](#).

On the one hand, we have released new temporally resolved data on face-to-face interactions collected in

1. the SFHH scientific conference held in 2009, with more than 400 participants to the data collection, a data set that we have already used in several publications such as "[Simulation of an SEIR infectious disease model on the dynamic contact network of conference attendees](#)"
2. an office building (InVS, French Health observatory) in 2015 (following a first data collection performed in 2013, published [here](#)). This data set contains also metadata, i.e., to which department each individual belongs.

In addition, we release data sets describing the temporally resolved co-location of individuals, where co-location of two individuals at time  $t$  means that the same exact set of readers have received signals from both individuals at time  $t$ . Data can be found on our [website](#) or on [Zenodo](#).

# project 8: Modelling within host dynamics



-Pawelek KA, Huynh GT, Quinlivan M, Cullinane A, Rong L, et al. (2012) Modeling Within-Host Dynamics of Influenza Virus Infection Including Immune Responses. PLoS Comput Biol 8(6): e1002588. doi:10.1371/journal.pcbi.1002588

-Immunology for physicists, Alan S. Perelson and Gérard Weisbuch, Reviews of Modern Physics, 1997, <https://doi.org/10.1103/RevModPhys.69.1219>