Infectious diseases as complex systems

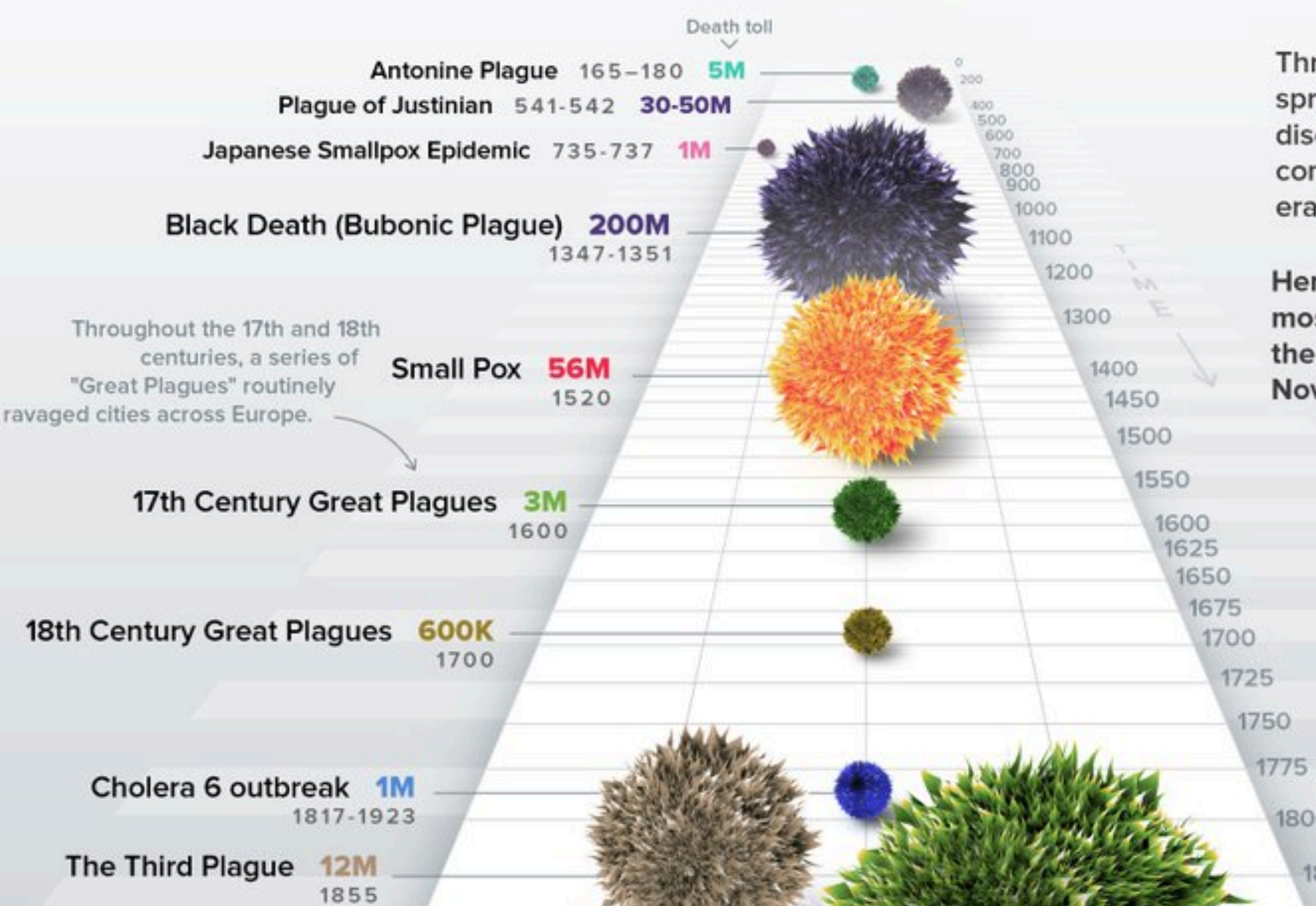
On the complex nature of viruses as fixed points and information processes

Francesco Sannino, 27 November 2023

ħQTC

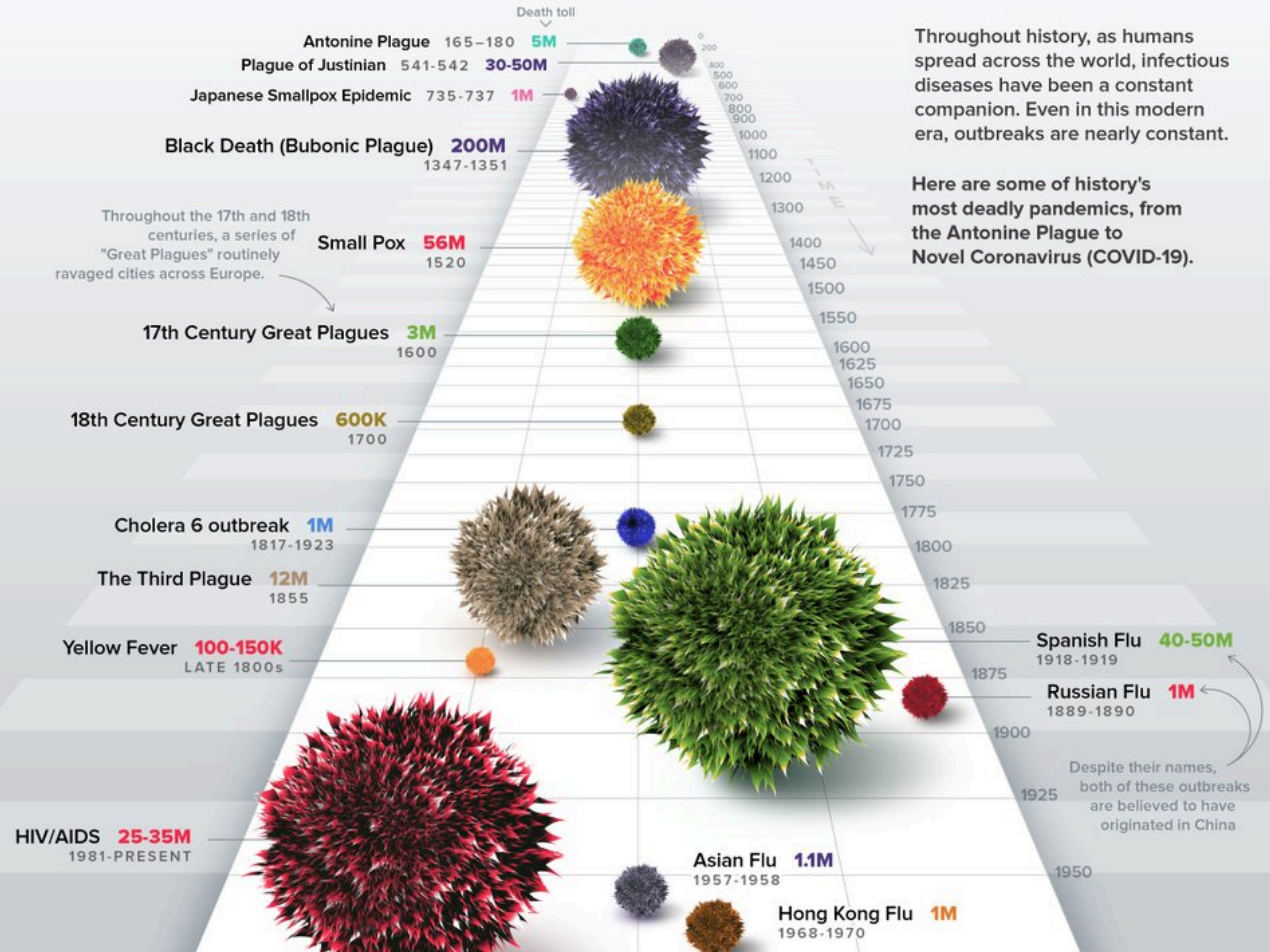
HISTORY OF **PANDEMICS**

Pan·dem·ic (of a disease) prevalent over a whole country or the world.



Throughout history, as humans spread across the world, infectious diseases have been a constant companion. Even in this modern era, outbreaks are nearly constant.

Here are some of history's most deadly pandemics, from the Antonine Plague to Novel Coronavirus (COVID-19).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Here are some of history's most deadly pandemics, from the Antonine Plague to Novel Coronavirus (COVID-19).
Death toll
Antonine Plague 165–180 5M
Plague of Justinian 541-542 30-50M
Japanese Smallpox Epidemic 735-737 1M
Black Death (Bubonic Plague) 200M 1347-1351
Throughout the 17th and 18th centuries, a series of "Great Plagues" routinely ravaged cities across Europe.
Small Pox 56M 1520
17th Century Great Plagues 3M 1600
18th Century Great Plagues 600K 1700
Cholera 6 outbreak 1M 1817-1923
The Third Plague 12M 1855
Yellow Fever 100-150K LATE 1800s
HIV/AIDS 25-35M 1981-PRESENT
Spanish Flu 40-50M 1918-1919
Russian Flu 1M 1889-1890
Despite their names, both of these outbreaks are believed to have originated in China
Asian Flu 1.1M 1957-1958
Hong Kong Flu 1M 1968-1970
TIME
0
200
400
500
600
700
800
900
1000
1100
1200
1300
1400
1450
1500
1550
1600
1625
1650
1675
1700
1725
1750
1775
1800
1825
1850
1875
1900
1925
1950

18th Century Great Plagues 600K
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LATE 1800s
HIV/AIDS 25-35M
1981-PRESENT
Spanish Flu 40-50M
1918-1919
Russian Flu 1M
1889-1890
Despite their names, both of these outbreaks are believed to have originated in China
Asian Flu 1.1M
1957-1958
Hong Kong Flu 1M
1968-1970
SARS 770
2002-2003
Swine Flu 200K
2009-2010
Ebola 1K
2014-2016
MERS 850
2015-PRESENT
Novel Coronavirus (COVID-19) 6.6 M
2019-PRESENT
1700
1725
1750
1775
1800
1825
1850
1875
1900
1925
1950
1975
2000
2025
December 2022

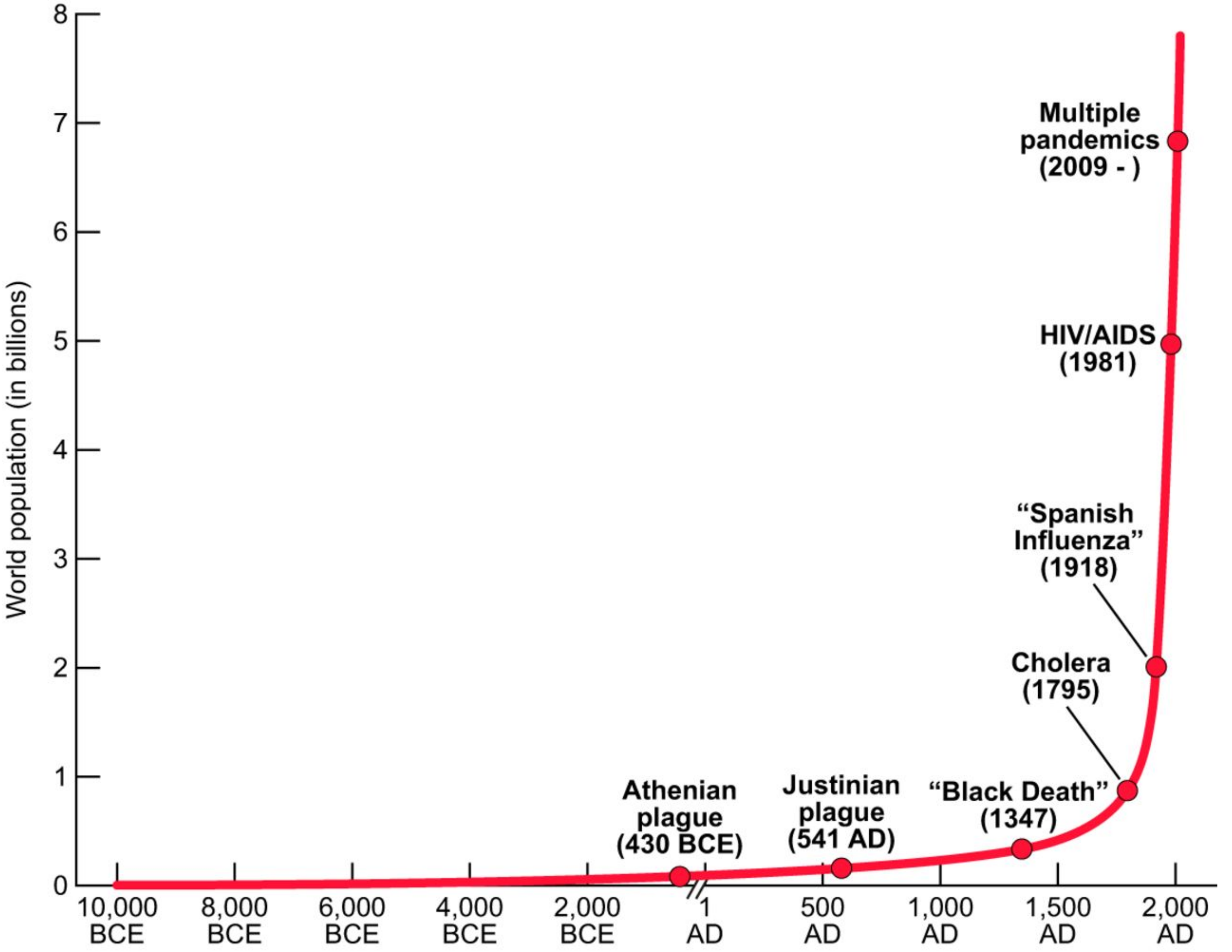
Pandemics

vs world population

Recurrent events

Increase with world population

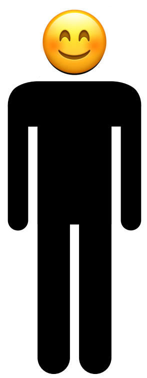
Spillover from wildlife to people



Epidemiology modeling

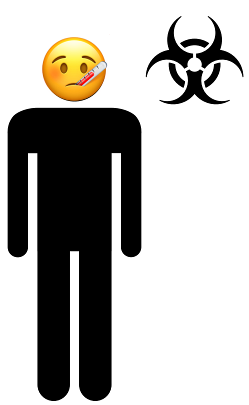
Compartmental models

Ross 1916
Ross, Hudson 1917
Kermack, McKendrick, 1927



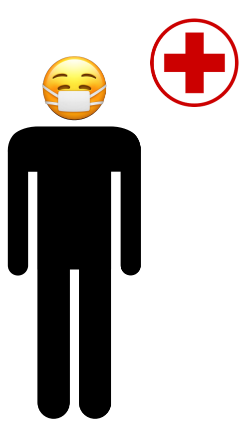
Susceptible: Not infectious, infectious in contact with disease

$S(t)$



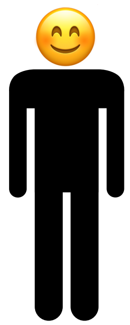
Infectious: Infected and can actively infect susceptible

$I(t)$



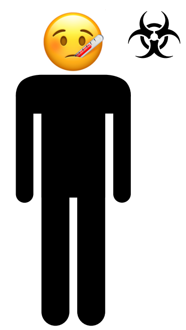
Removed: neither be infected or infect others

$R(t)$



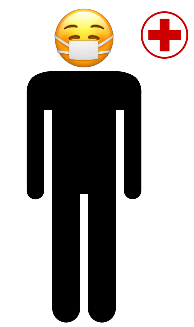
Infection rate

$\tilde{\gamma}$ constant



Removal rate

ϵ constant

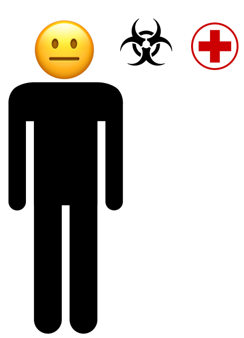


$$\frac{dS}{dt} = -\frac{\tilde{\gamma}}{N} S I$$

$$\frac{dI}{dt} = \frac{\tilde{\gamma}}{N} S I - \epsilon I$$

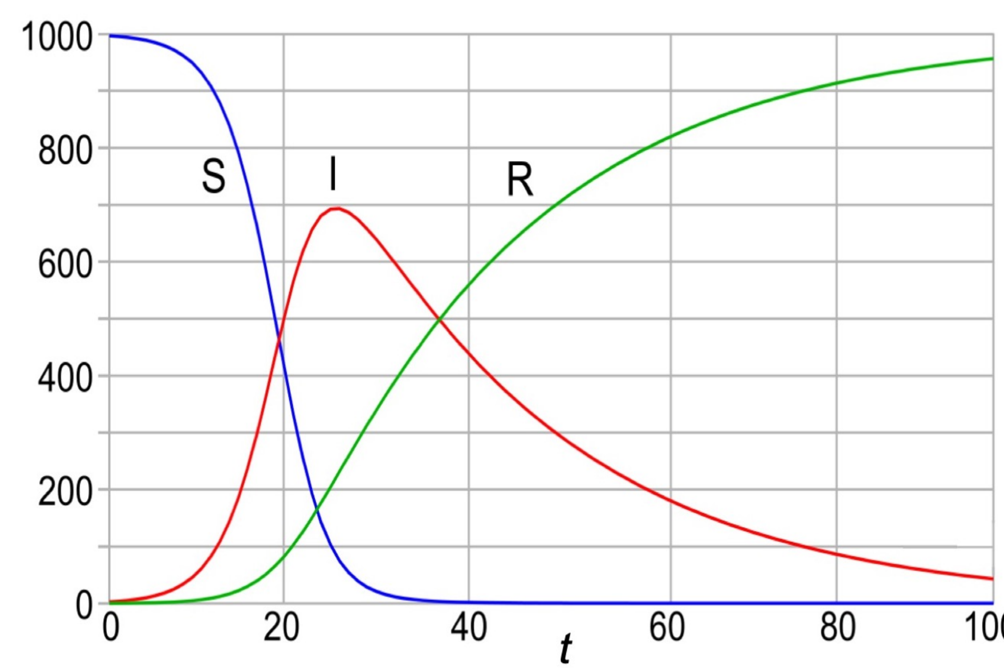
$$\frac{dR}{dt} = \epsilon I$$

Conservation law $S + I + R = N$



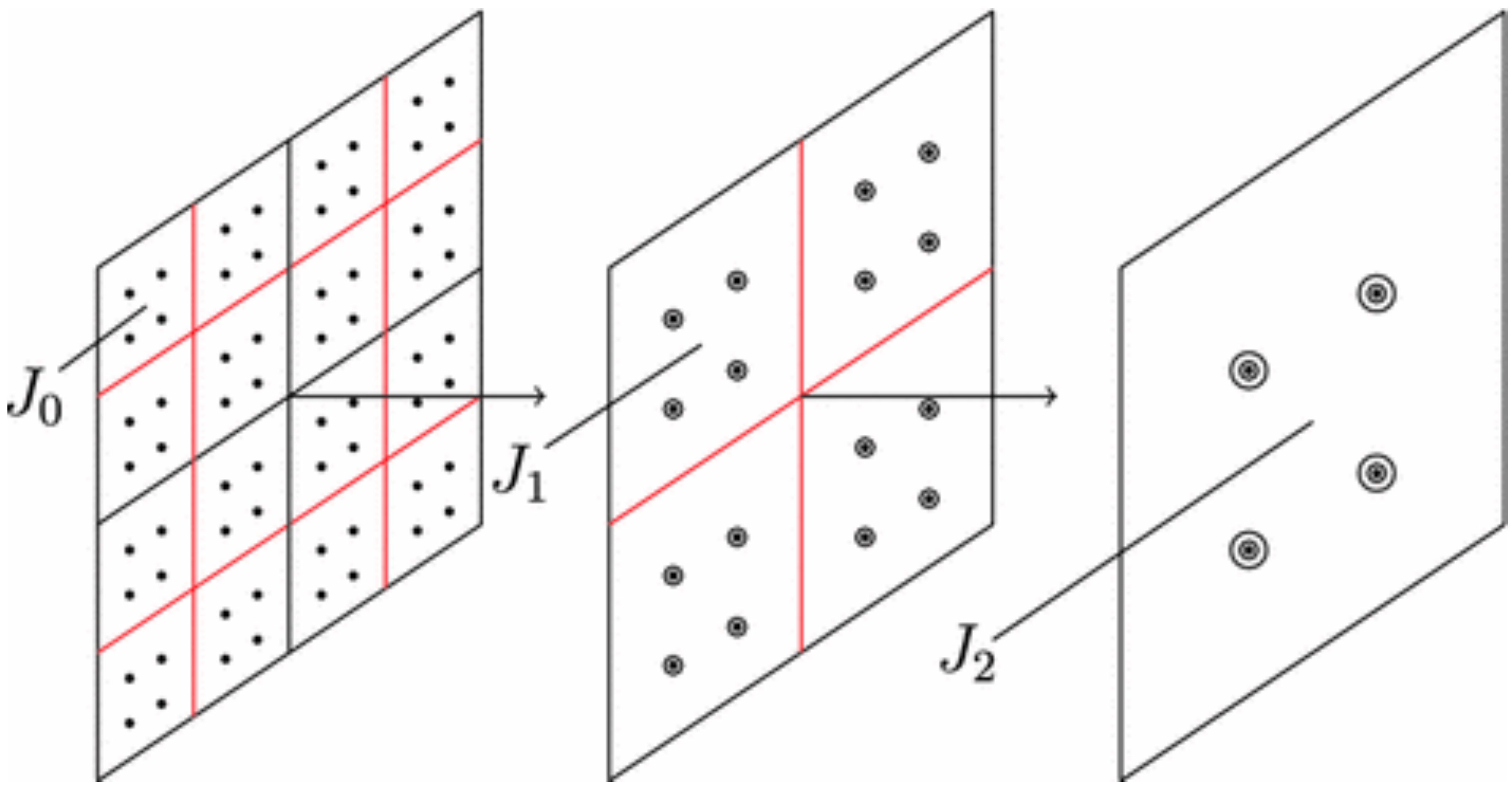
Cumulative number of infected

$$I_c \equiv I + R$$



Renormalization Group Idea

From complexity to simplicity



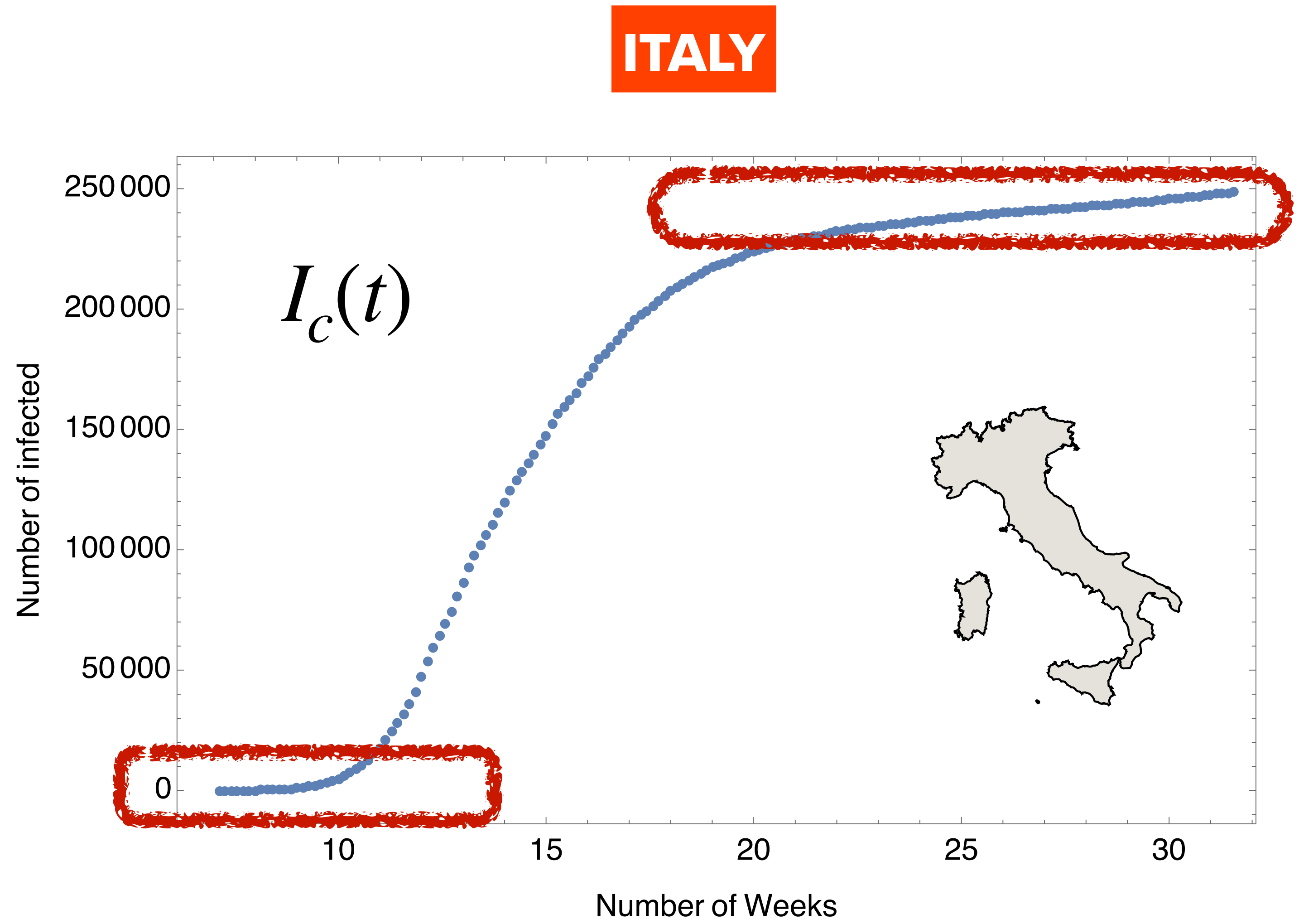
Epidemiological Renormalization Group

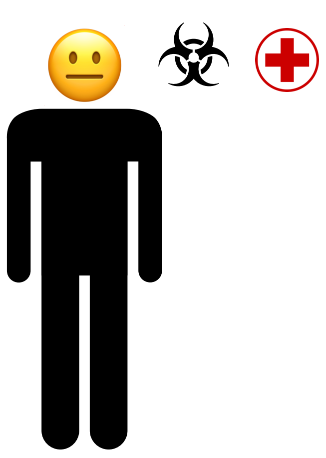
eRG

Early times invariance

Late time approx invariance

Approx time dilation symmetry





$$\alpha(t) = \ln I_c(t)$$

Renormalisation Group Approach to Pandemics...

M. Della Morte, D. Orlando and F. Sannino, Frontiers of Physics 8, 144

Epidemiological Renormalization Group

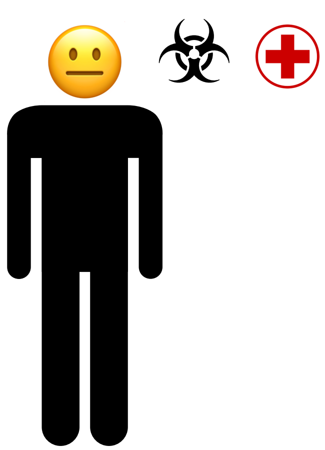
In a nutshell

Beta function effectively encodes underlying (pandemic) dynamics

$$-\beta(\alpha) \equiv \frac{d\alpha}{dt} = \gamma\alpha\left(1 - \frac{\alpha}{a}\right)$$

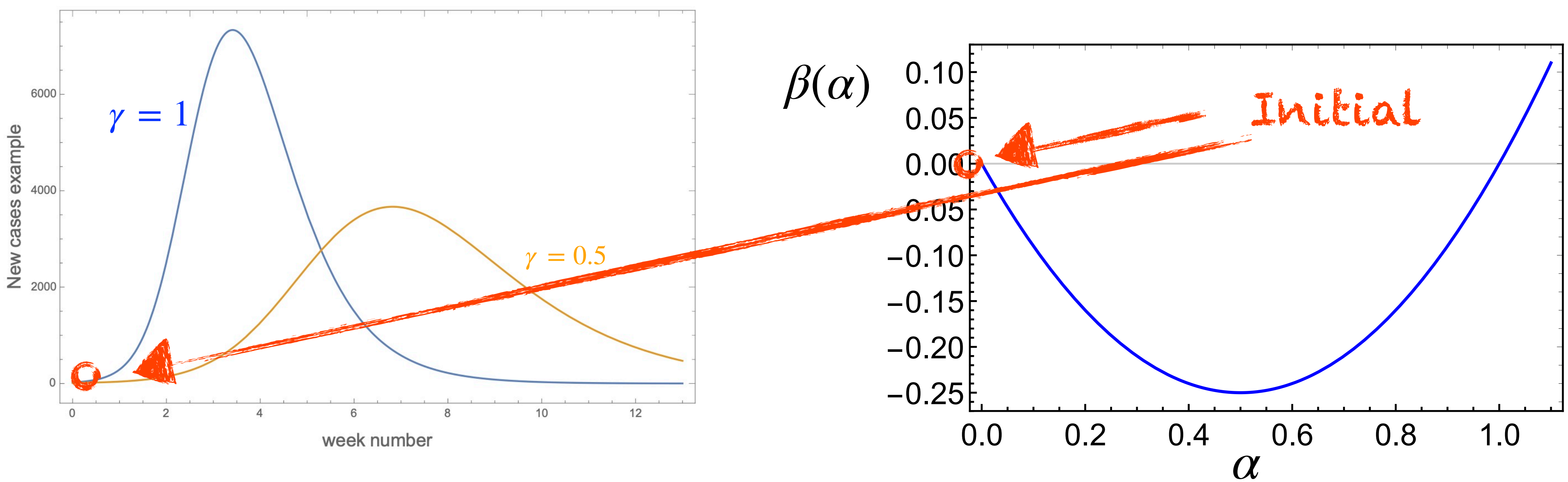
The zeros enforce time-scale invariance

The analytic solution is



$$\alpha(t) = \frac{a\, e^{\gamma\, t}}{b + e^{\gamma\, t}}$$

$$-\beta(\alpha) \equiv \frac{d\alpha}{dt} = \gamma\alpha\left(1-\frac{\alpha}{a}\right)$$



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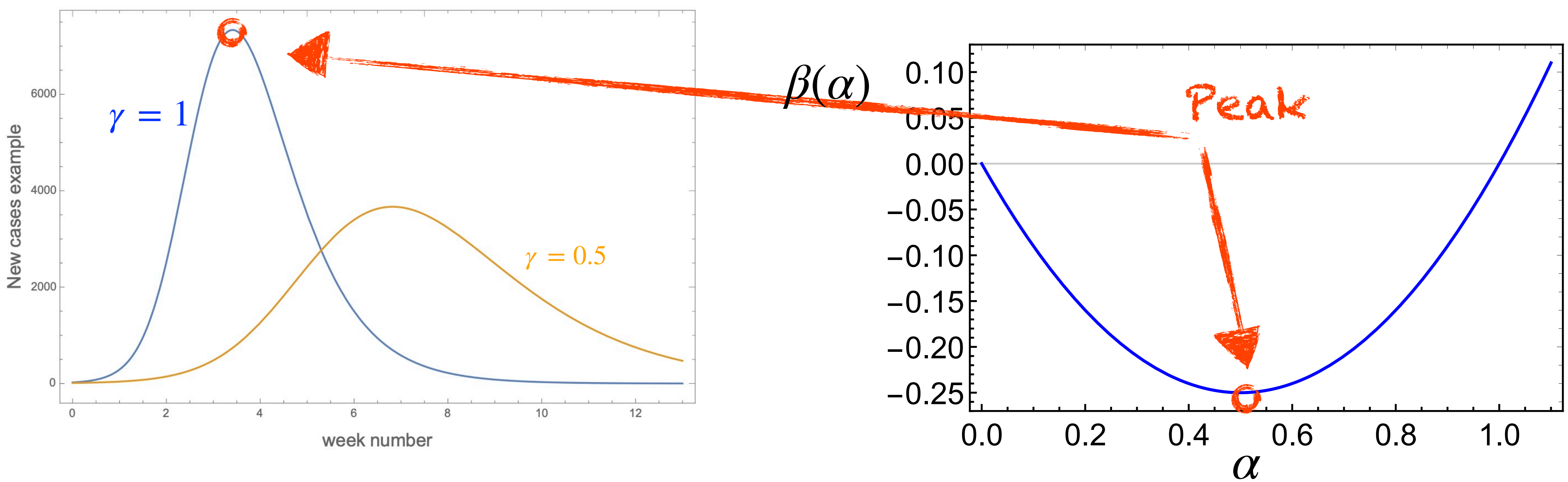

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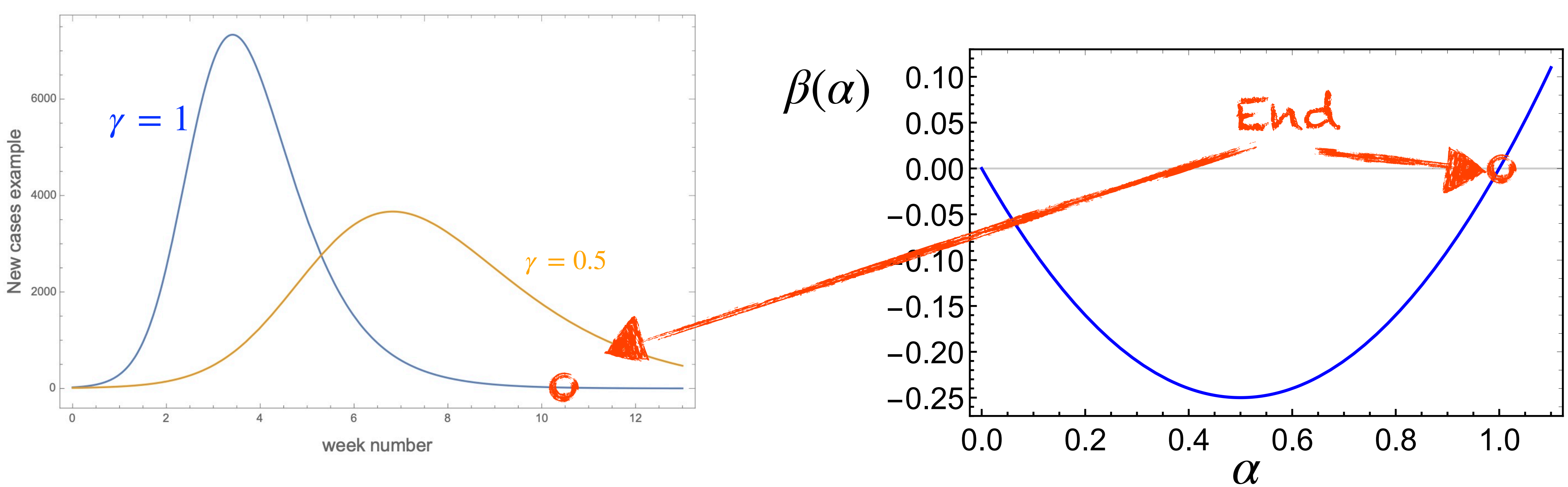
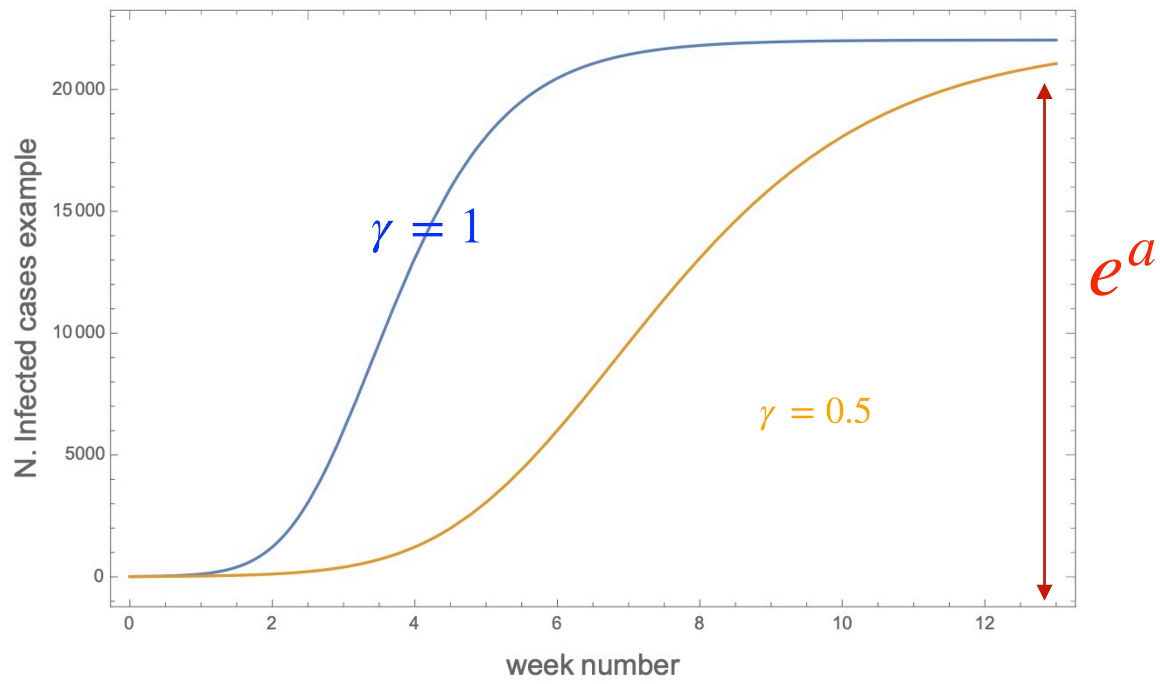
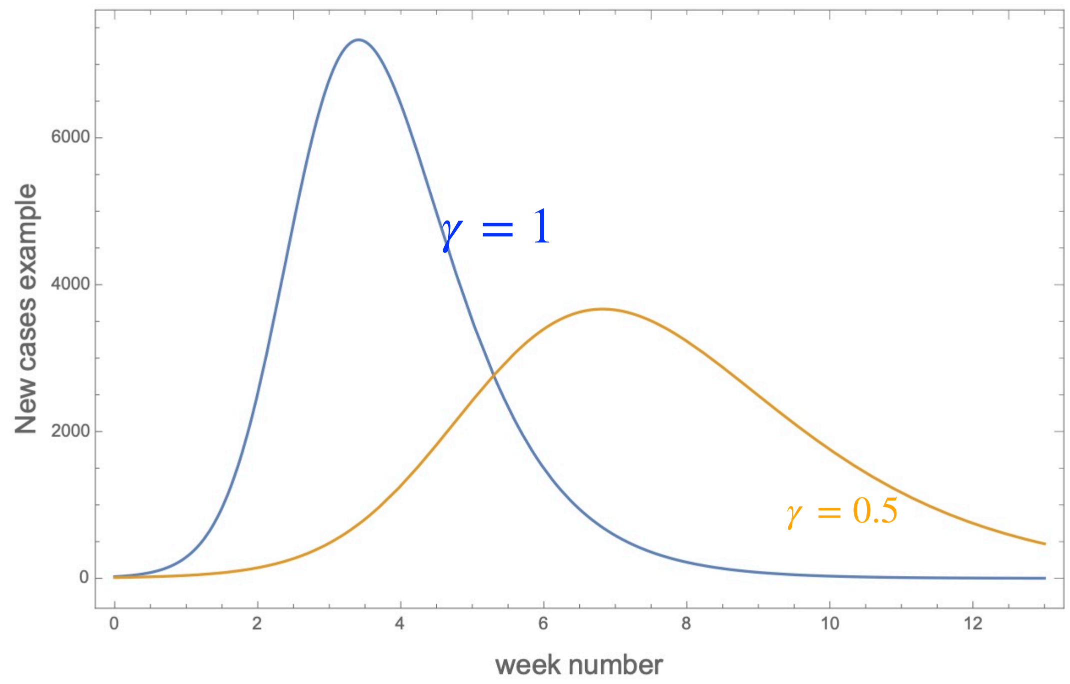


γ controls the infection rate and the flattening of the epidemic curve.

$$\alpha(t) = \frac{a\, e^{\gamma t}}{b + e^{\gamma t}}$$



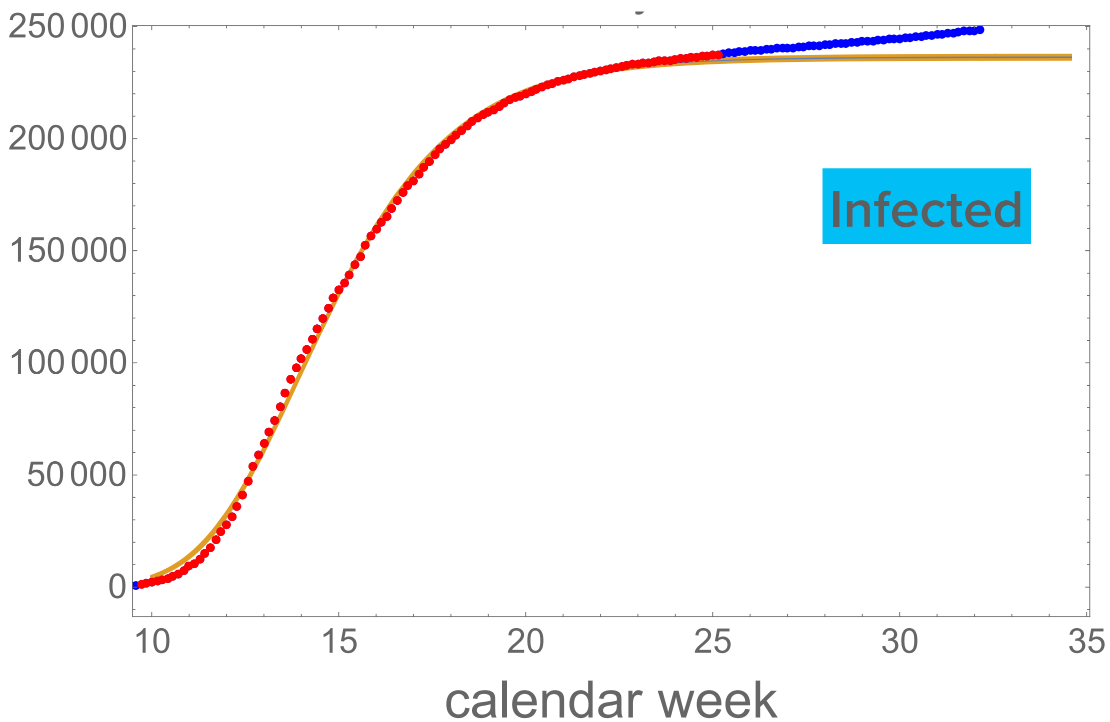


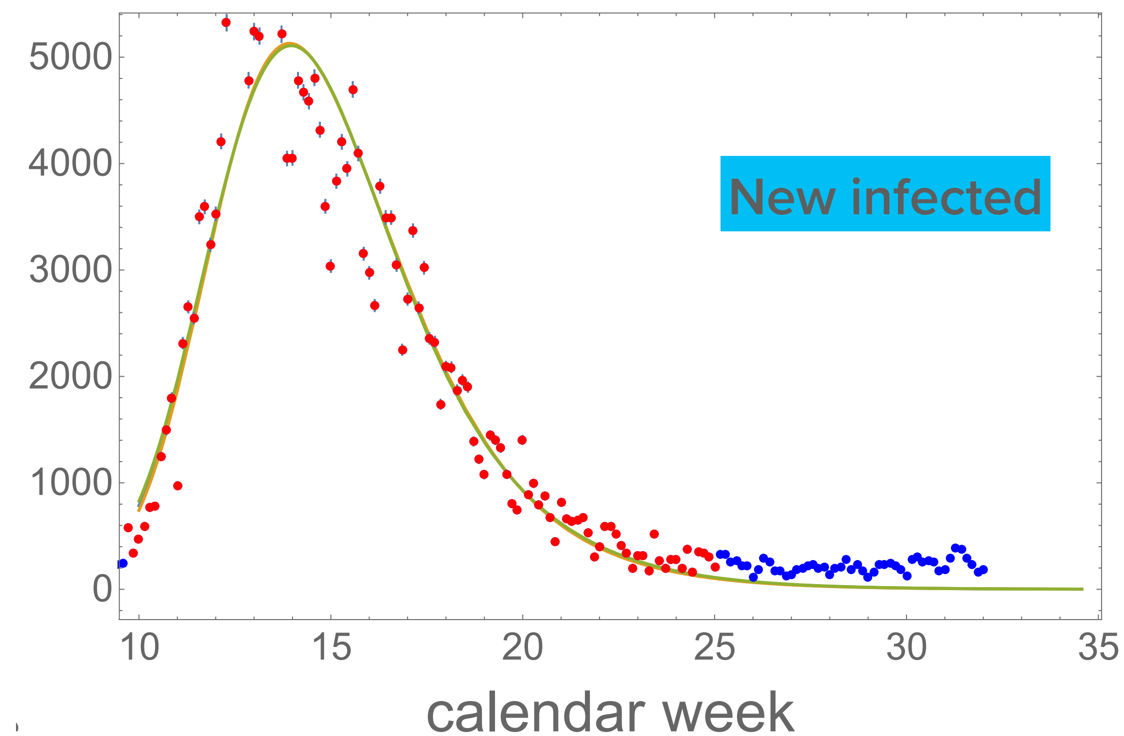
e^a is the total number of infected

b is a temporal shift

Time structure well reproduced

ITALY

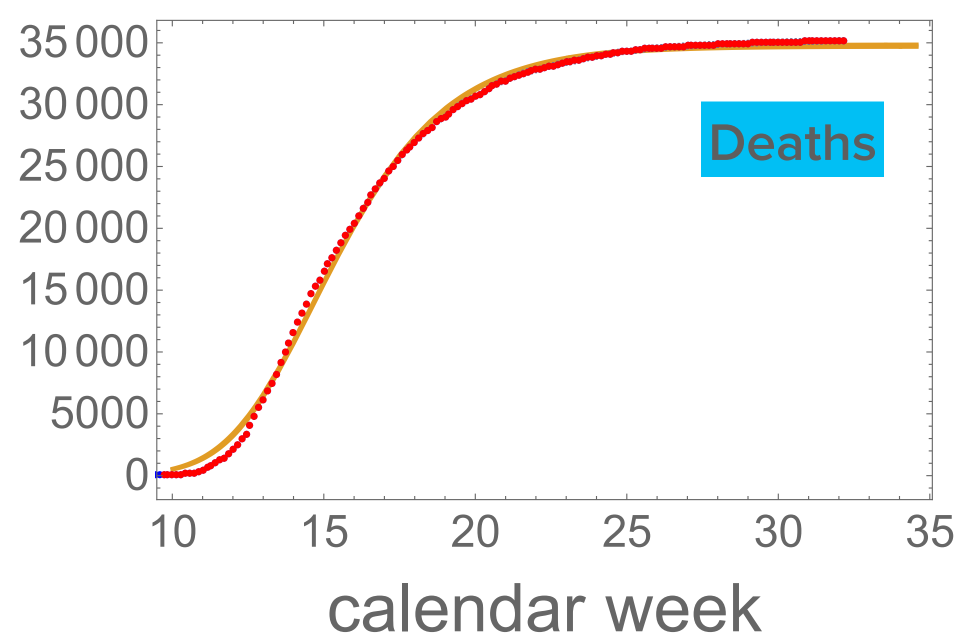




$a = 12.373 \pm 0.005$

$\gamma = 0.447 \pm 0.009$

$b = 41 \pm 5$



eRG vs SIR

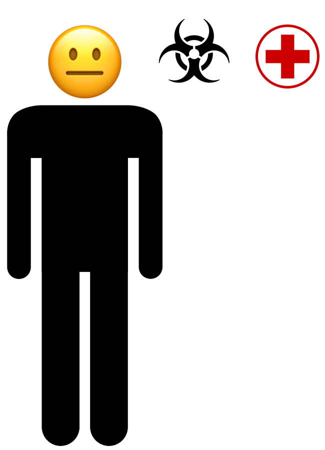
Time is key

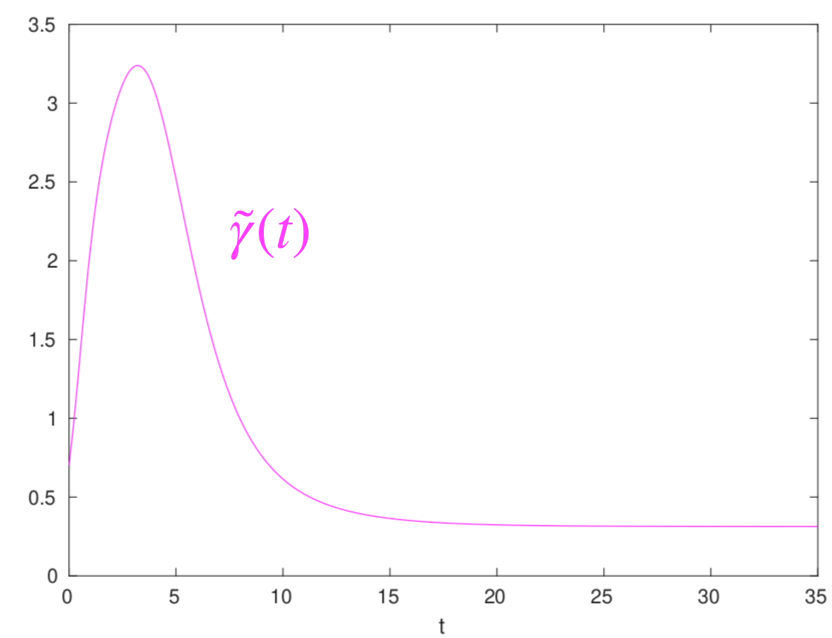
Standard SIR

$$\frac{dS}{dt} = -\tilde{\gamma} S \frac{I}{N} \qquad \frac{dI}{dt} = \tilde{\gamma} S \frac{I}{N} - \epsilon I \qquad \frac{dR}{dt} = \epsilon I \qquad S + I + R = N$$

$$I_{eRG} = I_c = I + R$$

eRG maps into a time-dependent SIR





RG approach to pandemics as a time-dependent SIR model
M. Della Morte and F. Sannino Front.in Phys. 8 (2021) 583

eRG

Advantages

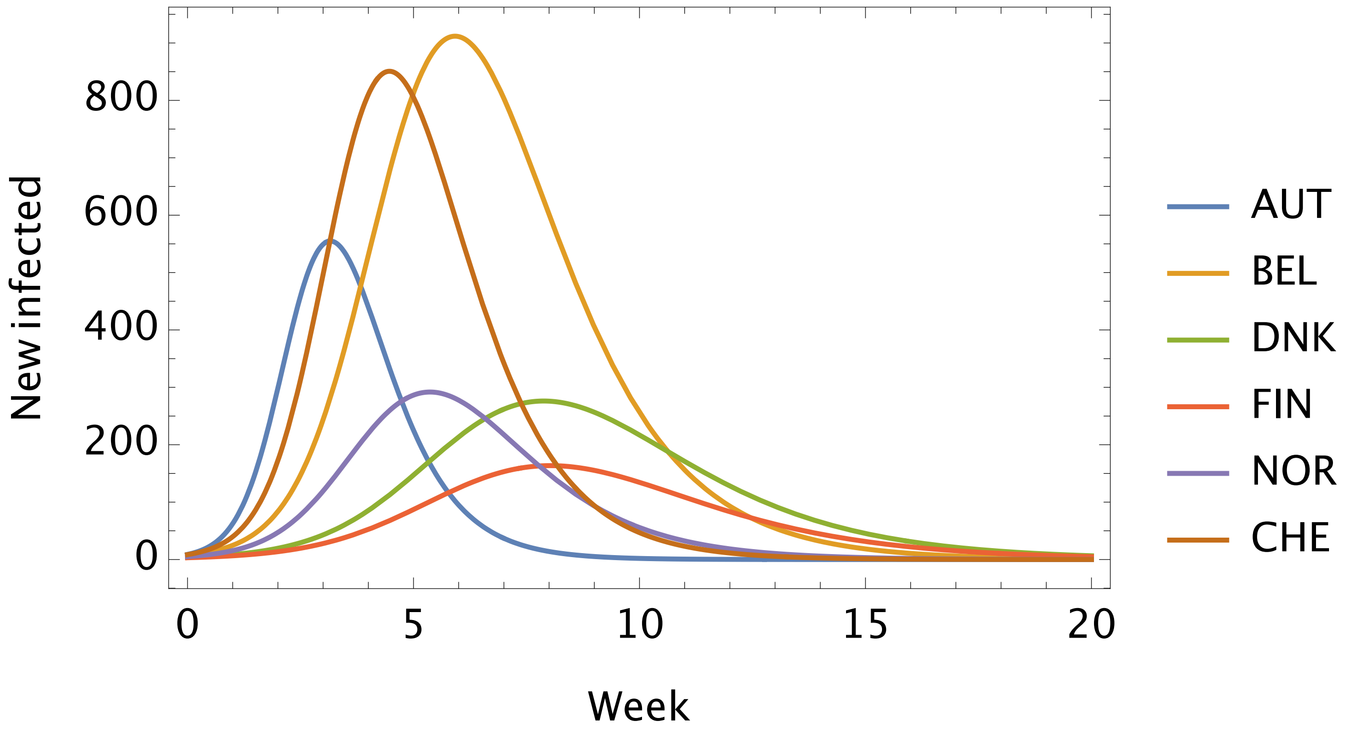
Analytic solutions

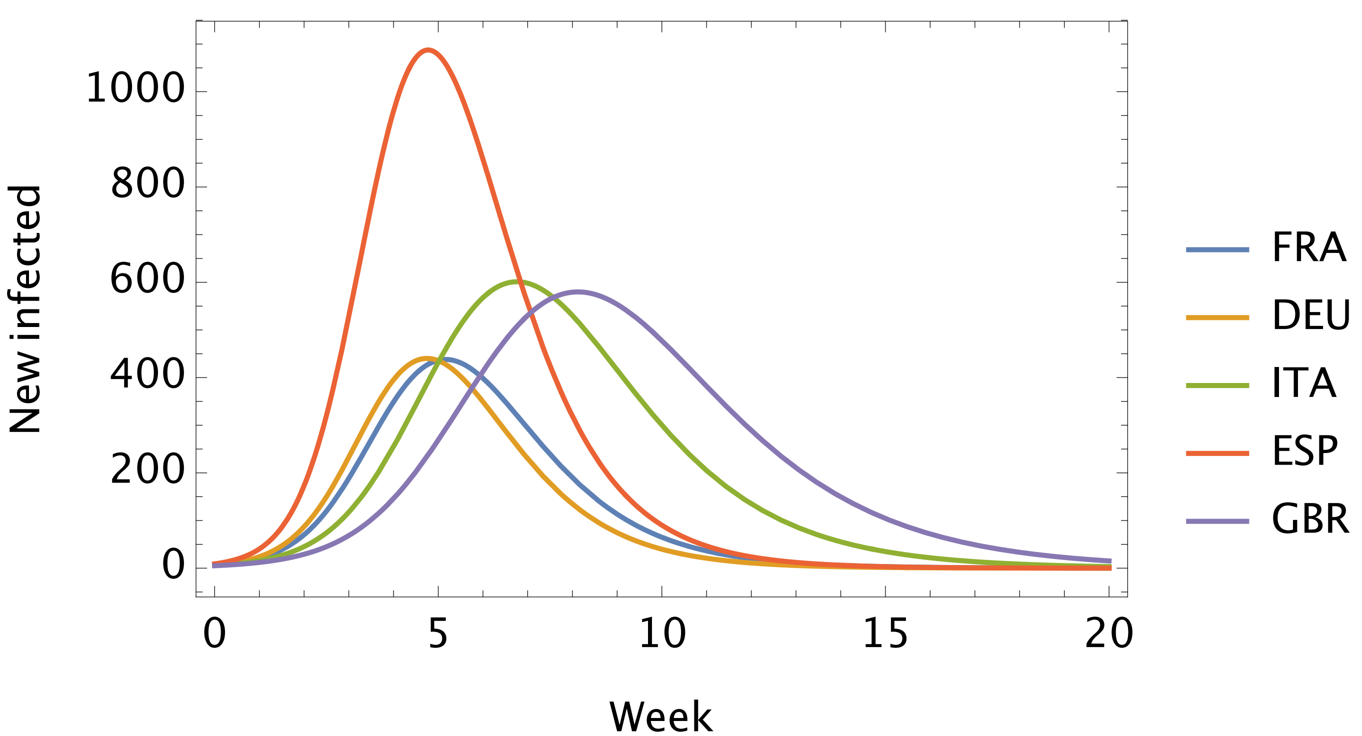
Symmetry powered

2 parameters per infected region

Overall time structure captured

Easily generalisable





What is the eRG good for?

THE HUMAN COST OF WAITING

nature
SCIENTIFIC REPORTS

Interplay of social distancing and border restrictions….

G. Cacciapaglia and F. Sannino Sci Rep 10, 15828 (2020)

WORLD-WIDE
PANDEMIC TEMPORAL PLAYBOOK

nature SCIENTIFIC REPORTS

Impact of US vaccination strategy on COVID-19 wave dynamics

C. Cot, G. Cacciapaglia, A.S. Islind, M. Oskarsdottir, F. Sannino Sci Rep

nature SCIENTIFIC REPORTS

Second wave COVID-19 pandemics in Europe:…..

G. Cacciapaglia, C. Cot and F. Sannino Sci Rep 10, 15514 (2020)

GOOGLE - APPLE MOBILITY DATA TO MEASURE SOCIAL DISTANCING IMPACT

nature SCIENTIFIC REPORTS

Mining Google and Apple mobility data…

G. Cacciapaglia, C. Cot and F. Sannino Sci Rep 11, 4150 (2021)

EPIDEMIOLOGICAL THEORY OF VARIANTS

[See Hohenegger]

Physica A: Statistical Mechanics and its Applications

Supports *open access*

Epidemiological theory virus variants

Cacciapaglia, Cot, Hoffer, Hohenegger, Sannino, Vatani

EARLY WARNING TOOL FOR VARIANTS OF INTEREST

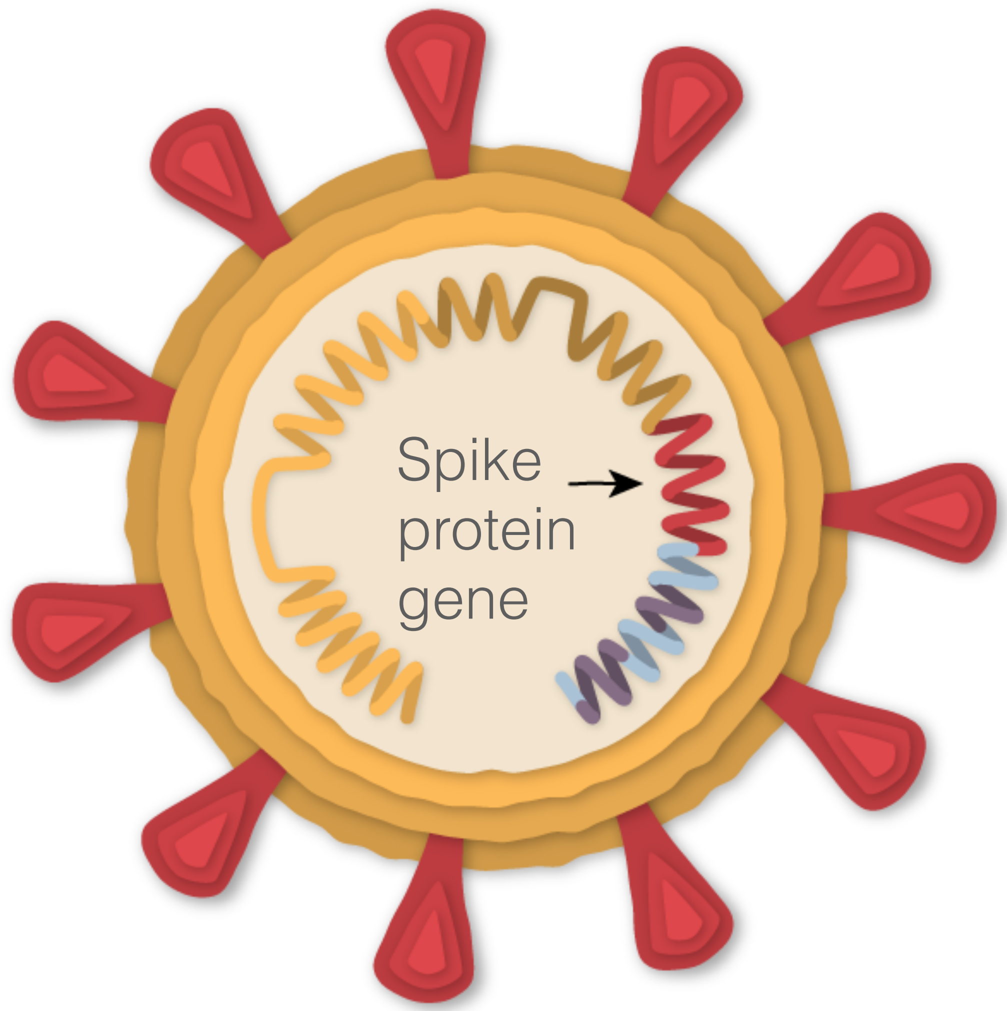
[See Conventi]

nature SCIENTIFIC REPORTS

Variant-driven multi-wave pattern of COVID-19 via ML ..

Cacciapaglia, Cimarelli, Chiusano, Conventi, Cot, Giannini, Hoffer, Hohenegger, Sannino, Vatani
Scientific Reports volume 12, Article number: 9275 (2022)

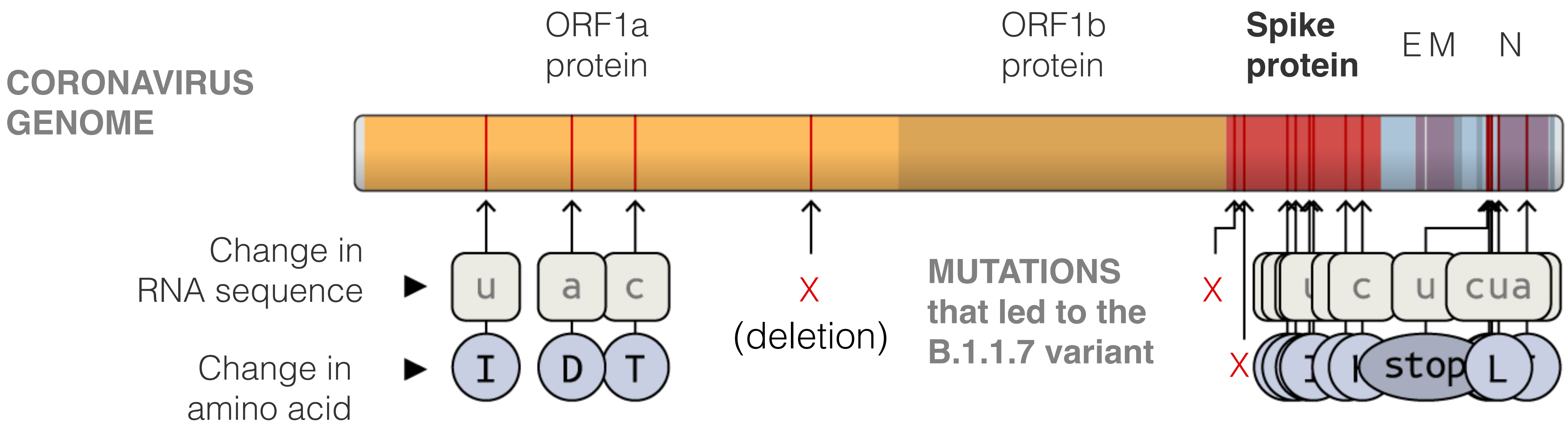
CORONAVIRUS



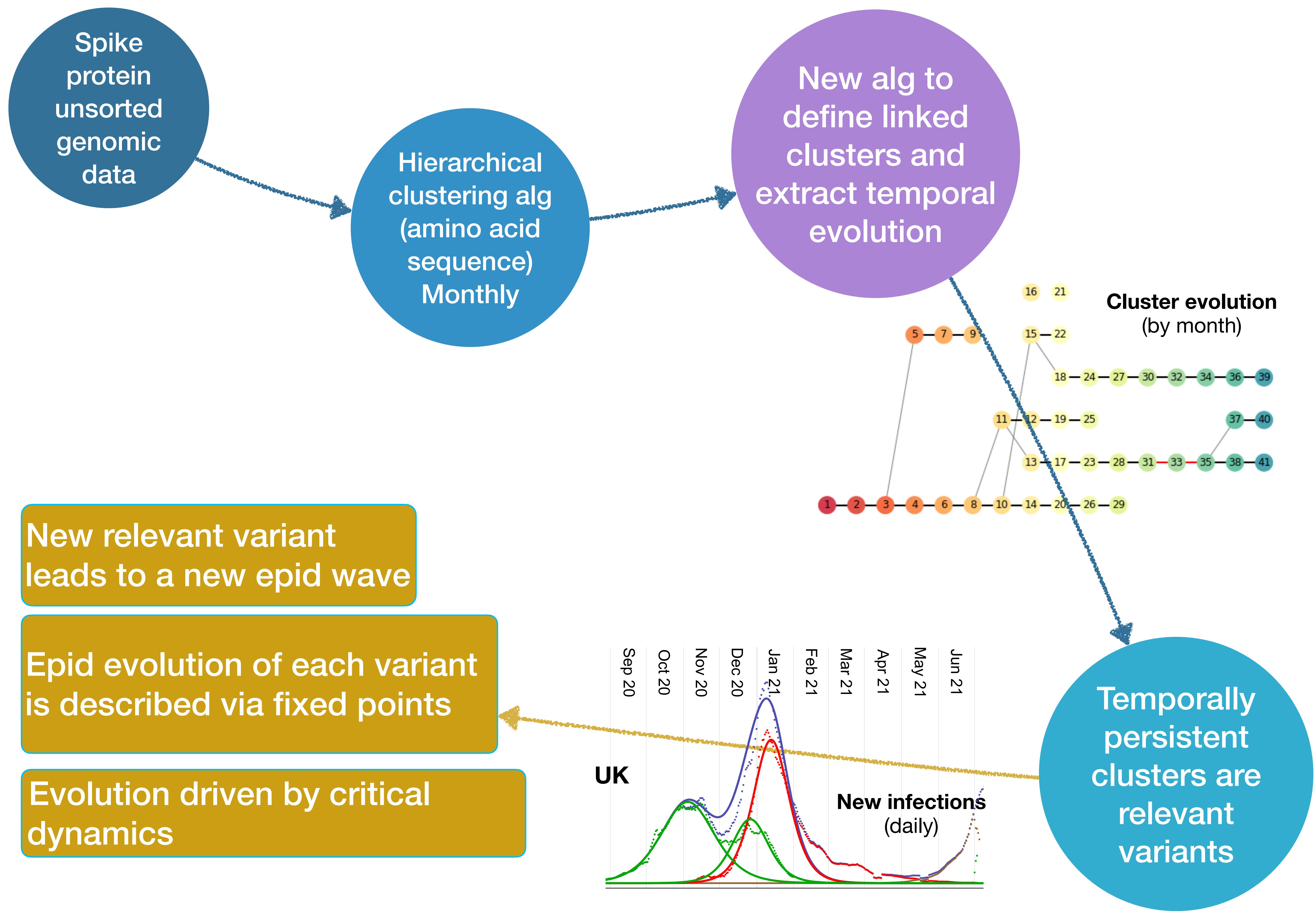
Spike latches onto and enter human cells

By Jonathan Corum | Source: Andrew Rambaut et al., Covid-19 Genomics Consortium U.K.

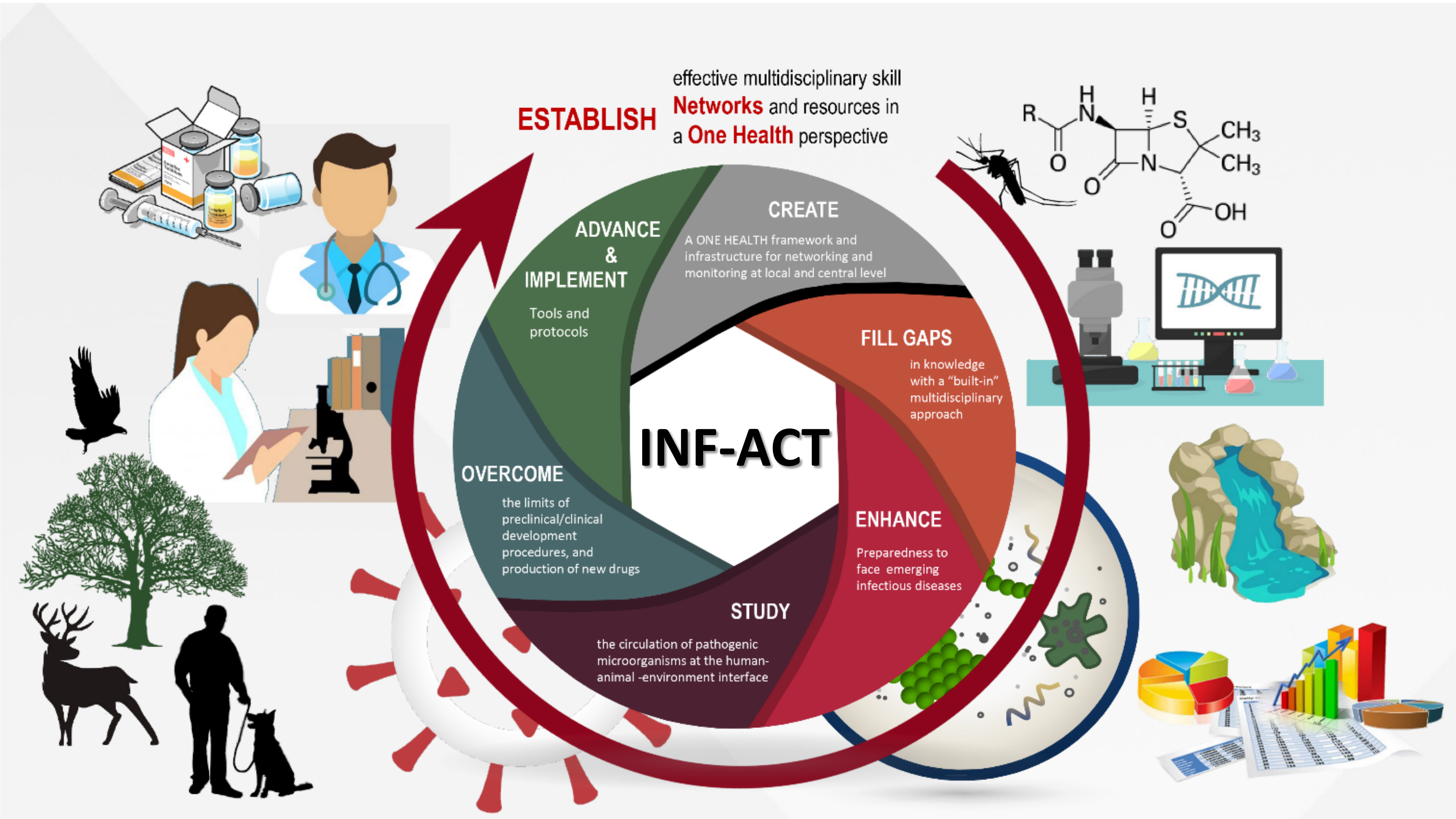
VARIANT OF CONCERN

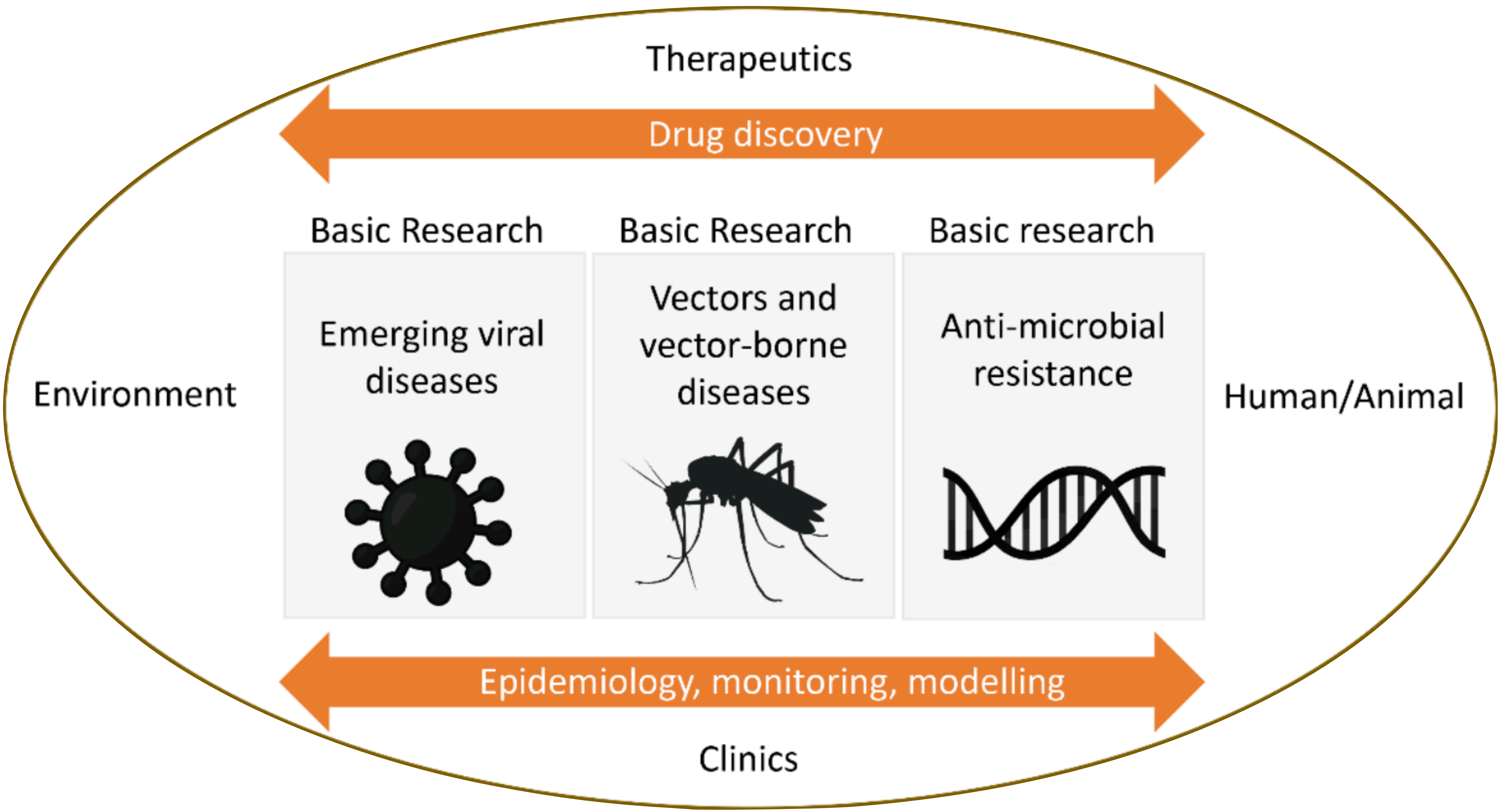


ByJonathan Corum | Source: Andrew Rambaut et al., Covid-19 Genomics Consortium U.K.


Spike protein unsorted genomic data
Hierarchical clustering alg (amino acid sequence) Monthly
New alg to define linked clusters and extract temporal evolution
Cluster evolution
(by month)
Temporally persistent clusters are relevant variants
Sep 20
Oct 20
Nov 20
Dec 20
Jan 21
Feb 21
Mar 21
Apr 21
May 21
Jun 21
UK
New infections
(daily)
New relevant variant leads to a new epid wave
Epid evolution of each variant is described via fixed points
Evolution driven by critical dynamics

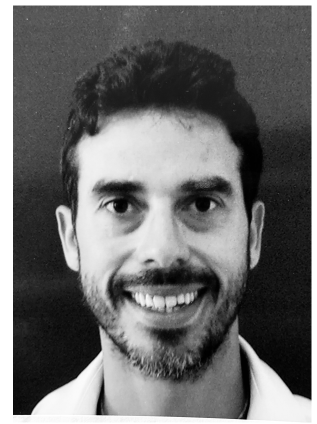
PNRR PE13: One Health Basic and Translational Research Actions addressing Unmet Needs on Emerging Infectious Diseases




Therapeutics
Drug discovery
Basic Research
Emerging viral diseases
Basic Research
Vectors and vector-borne diseases
Basic research
Anti-microbial resistance
Environment
Human/Animal
Epidemiology, monitoring, modelling
Clinics

Active INF-ACT epi-members





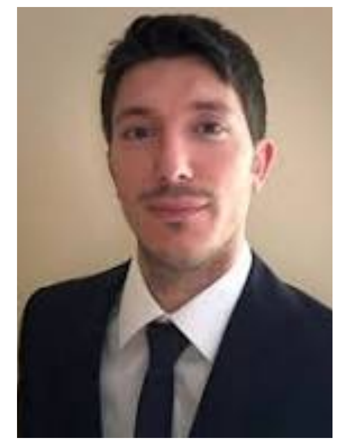




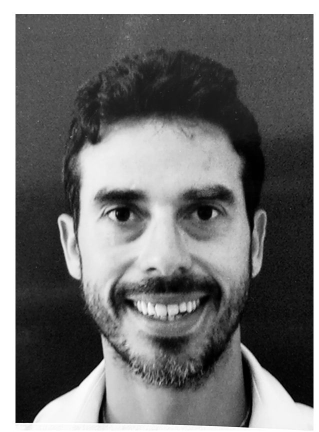
Active epi-members

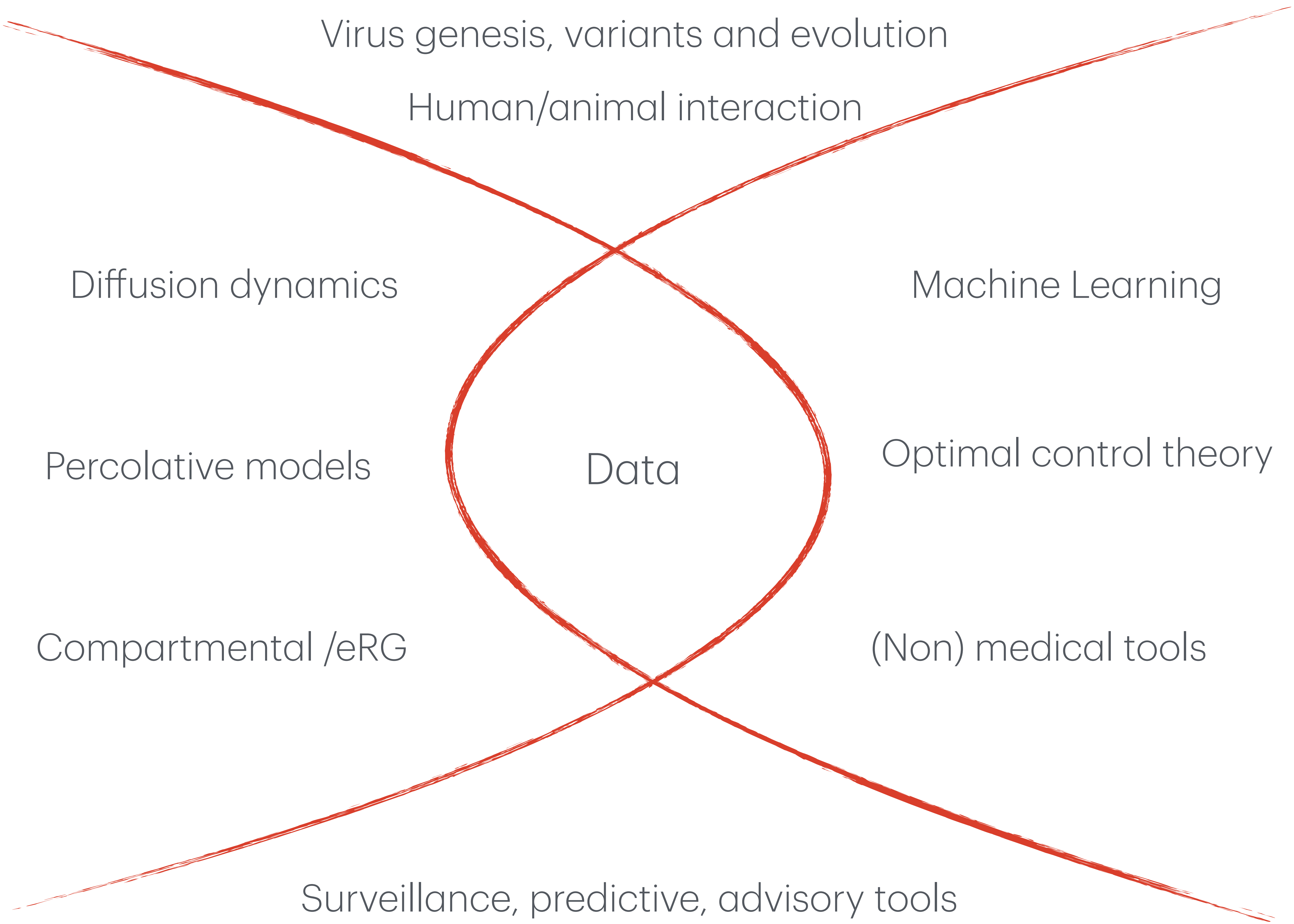









Virus genesis, variants and evolution
Human/animal interaction
Diffusion dynamics
Machine Learning
Percolative models
Data
Optimal control theory
Compartmental /eRG
(Non) medical tools
Surveillance, predictive, advisory tools

Thank you