

# Strain-space model for Sars-CoV-2

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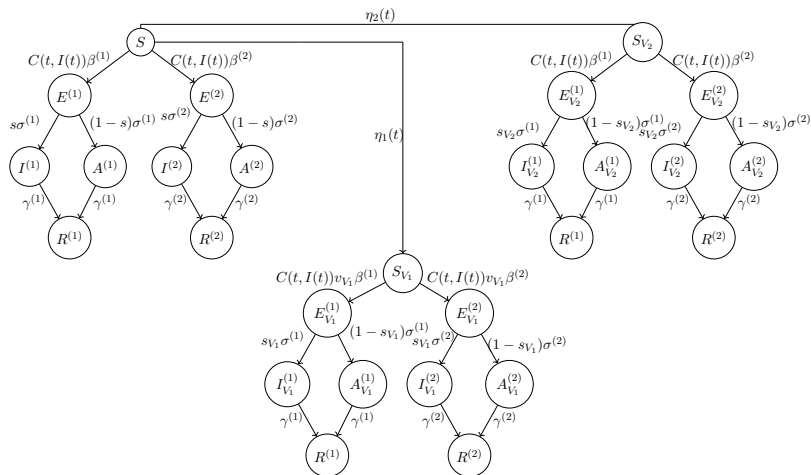
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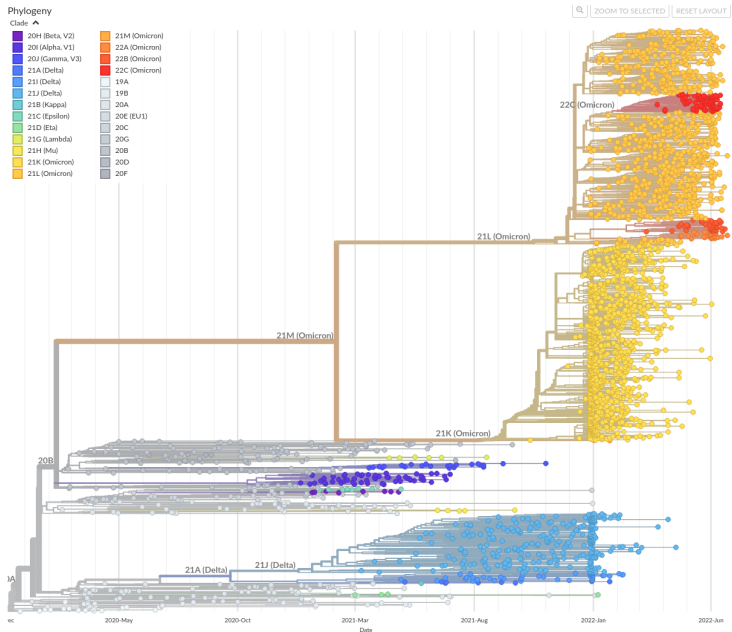
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July 6, 2022

# Modeling multiple infections is challenging



# How to incorporate more data?



# A useful approximation

RESEARCH ARTICLE | BIOLOGICAL SCIENCES

## Dynamics and selection of many-strain pathogens

Julia R. Gog and Bryan T. Grenfell [Authors Info & Affiliations](#)

December 12, 2002 | 99 (26) 17209–17214 | <https://doi.org/10.1073/pnas.252512799>

227 196

Abstract

Strain structure is of fundamental importance in the underlying dynamics of a number of pathogens. However, previous models have been too complex to accommodate many

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Abstract

Derivation of the Model

Application to Antigenic

J. Math. Biol. 44, 169–184 (2002)  
Digital Object Identifier (DOI):  
10.1007/s002850100120

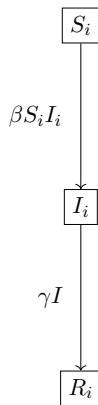
## Mathematical Biology

J.R. Gog · J. Swinton

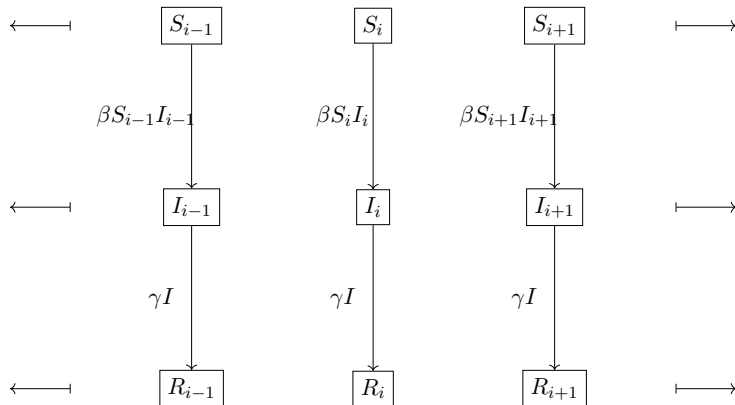
## A status-based approach to multiple strain dynamics

Received: 5 April 2000 / Revised version: 24 July 2001 /  
Published online: 8 February 2002 – © Springer-Verlag 2002

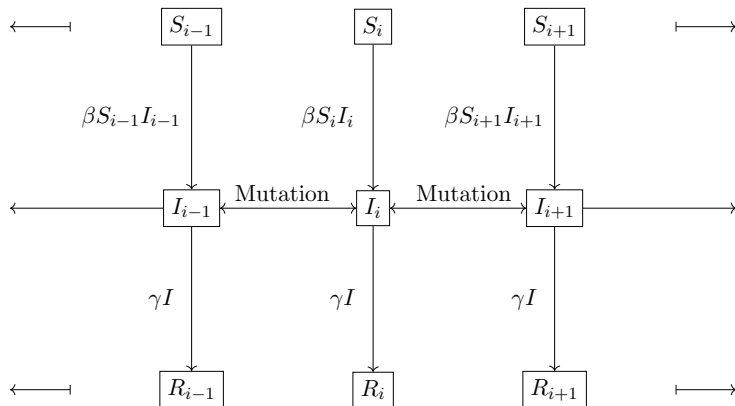
## Begin with simple SIR model



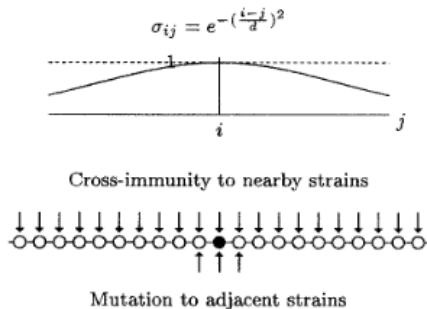
# Organize strains on a lattice



# Strains mutate into adjacent strains



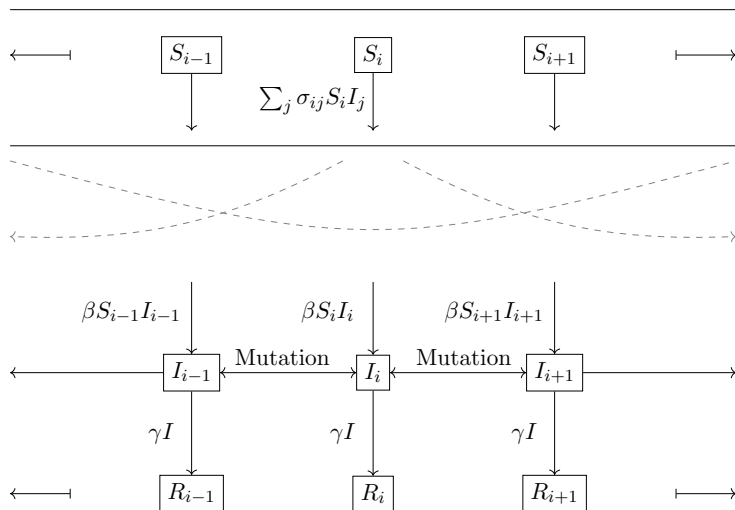
# Infections provide cross-immunity to nearby strains



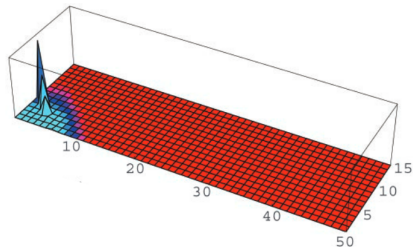
[Gog and Grenfell, 2002]



# Full strain lattice model in 1 dimension

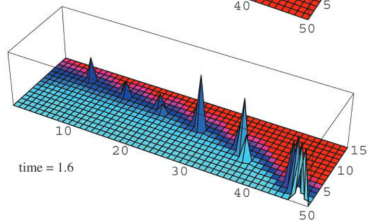
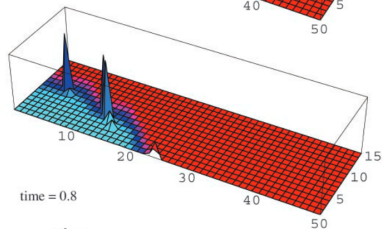
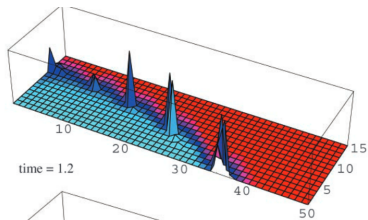
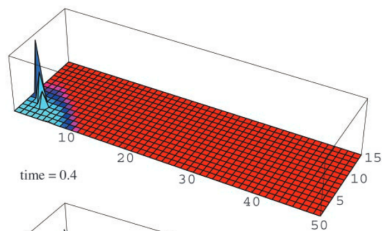


# Extending the strain lattice to 2 dimensions



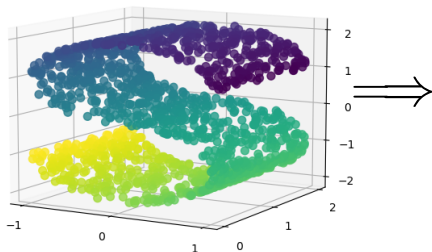
[Gog and Grenfell, 2002]

# Extending the strain lattice to 2 dimensions



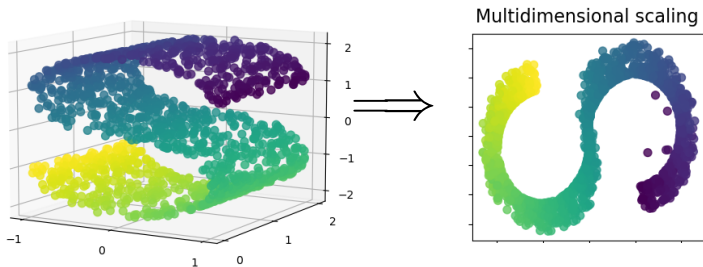
[Gog and Grenfell, 2002]

# Projecting to low dimensions while preserving distances



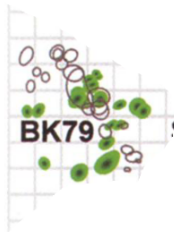
[Pedregosa et al., 2011]

# Projecting to low dimensions while preserving distances

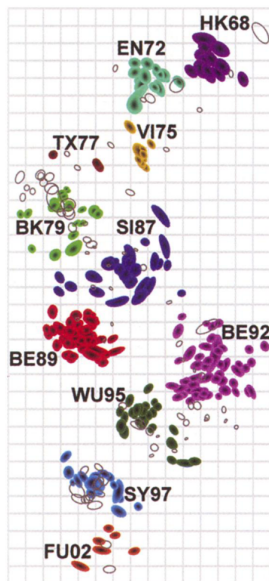


[Pedregosa et al., 2011]

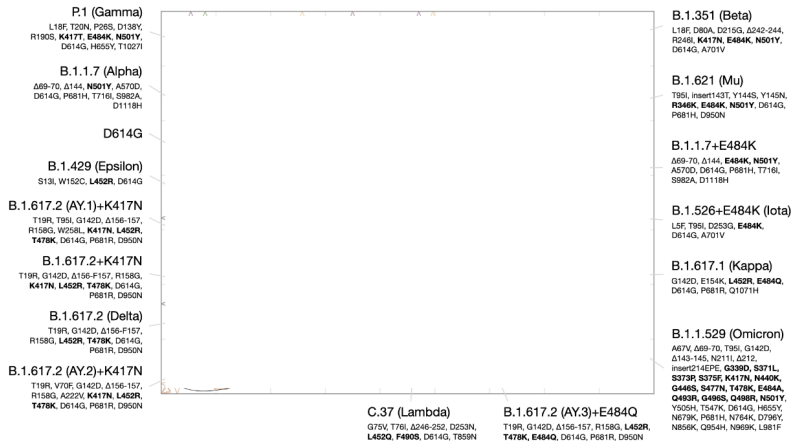
# Approximating genomic data in 2 dimesions



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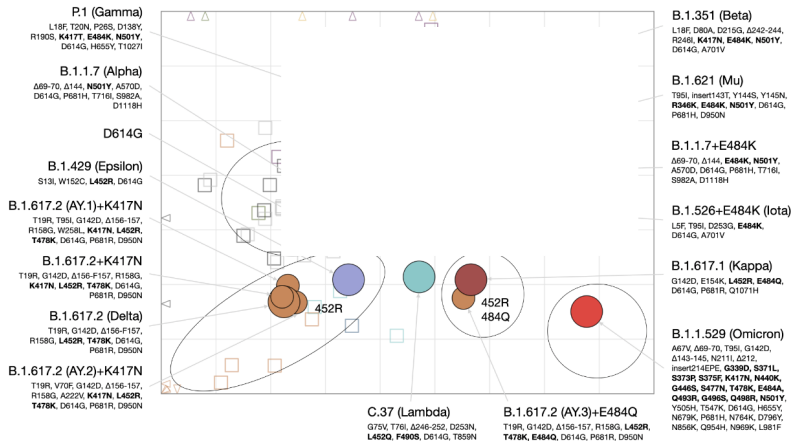
# Mapping SARS-CoV-2 in 2D



[Wilks et al., 2022]

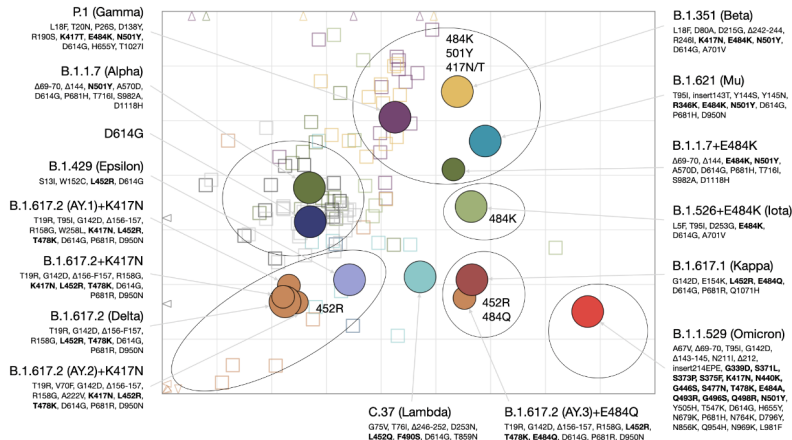


# Mapping SARS-CoV-2 in 2D



[Wilks et al., 2022]

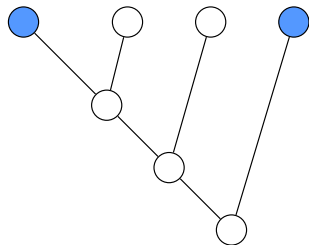
# Mapping SARS-CoV-2 in 2D



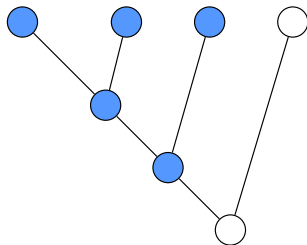
[Wilks et al., 2022]

# Methods of adding more genomes: homoplasious sites

Homoplasious trait

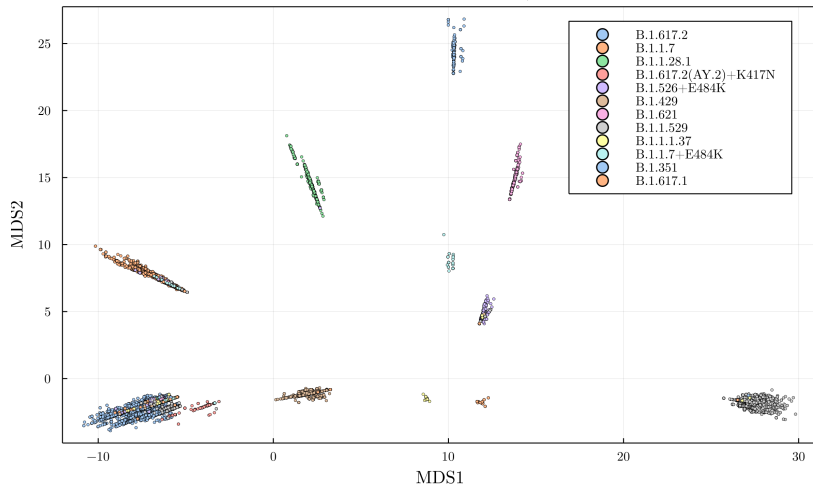


Homologous trait



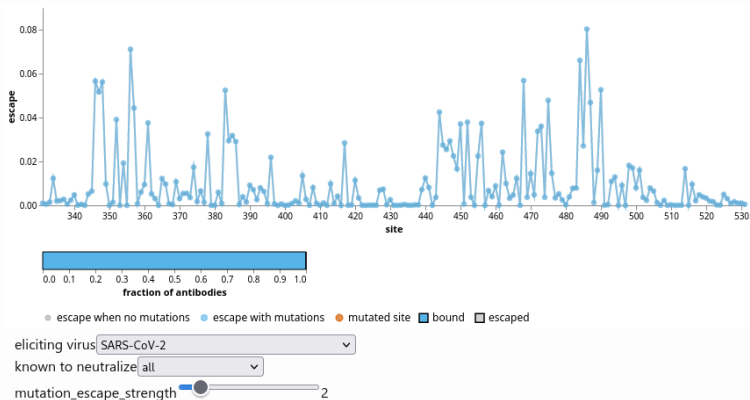
[Page and Holmes, 2009]

# Homoplasic mutations map



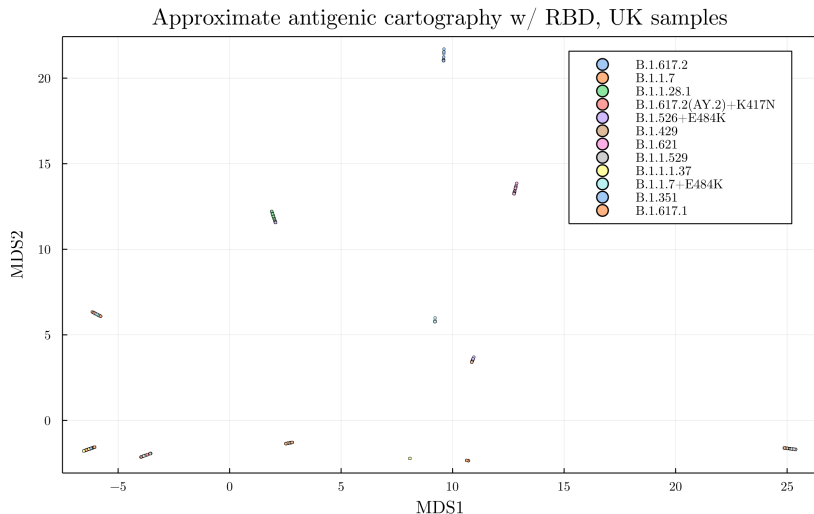
# Methods of adding more genomes: polyclonal antibody binding studies

## Escape calculator for SARS-CoV-2 RBD

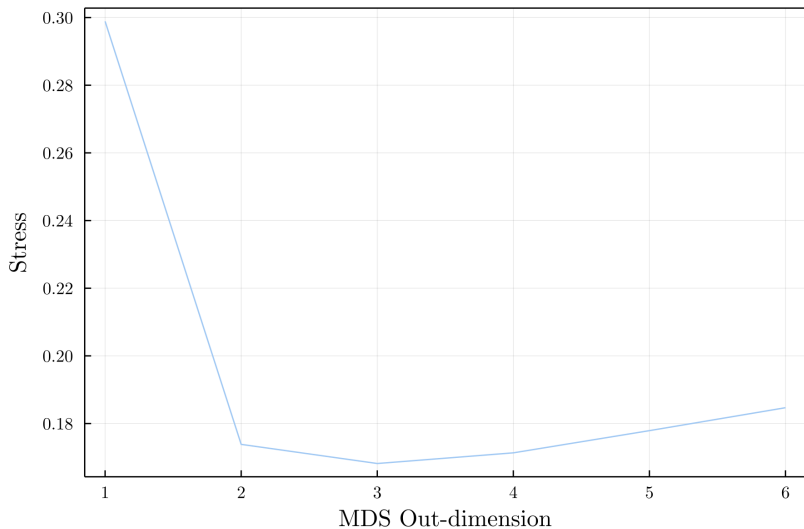


[Greaney et al., 2022]

# Antibody Binding map



# Evaluating the MDS approximation



## Model parameters/variables

Symbol	Description
$N$	Size of variant grid
$S_{ij}$	Population susceptible to variant $(i, j) \in [0, N]^2$
$I_{ij}$	Population infected by variant $(i, j) \in [0, N]^2$
$R_{ij}$	Recovered/Immune to variant $(i, j) \in [0, N]^2$
$\sigma_{ijkl}$	Probability that exposure to variant $(i, j)$ causes immunity to variant $(k, l)$
$\beta_{ij}$	Transmission rate of variant $(i, j)$
$v(t)$	vaccination rate at time $t$
$s(t)$	stringency at $t$
$\xi$	Recovery rate of all strains
$\gamma$	Rate of immunity loss of all strains

Table of symbols for Model 2



# Model Equations

$$\frac{S_{ij}}{dt} = - \sum_{kl} s(t) \beta_{kl} \sigma_{ijkl} S_{ij} I_{kl} + \gamma R_{ij} - V(t) S \quad (1)$$

$$\frac{I_{ij}(t)}{dt} = s(t) \beta_{ij} S_{ij} I_{ij} - \xi I_{ij} + M (-4I_{ij} + I_{i-1,j} + I_{i+1,j} + I_{i,j-1} + I_{i,j+1}) \quad (2)$$

$$\frac{R_{ij}(t)}{dt} = \xi I_{ij} - \gamma R_{ij} + V(t) S \quad (3)$$





Boundary conditions:  $I_{0,j} = 0, I_{j,0} = 0, I_{N,j} = 0, I_{j,N} = 0$



Initial conditions computed from genomic data in GISAID

(gifs of model dynamics)

## Further work

- Estimating a nonlocal diffusion kernel
- Better model fitting
- Predicting vaccine targets

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# Mutation homoplasy

