Characterizing evolutionary dynamics on a broader scale: a strain-space model for SARS-CoV-2

Peter C. Jentsch, PhD [1,4] Finlay Maguire, PhD [3,5]
Samira Mubareka, MD, FRCPC [1,2]

[1]Sunnybrook Research Institute, Toronto, Canada

[2]University of Toronto, Toronto, Canada

[3]Dalhousie University, Halifax, Canada

[4]Simon Fraser University, Burnaby, Canada

[5]Shared Hospital Laboratory, Toronto, Canada

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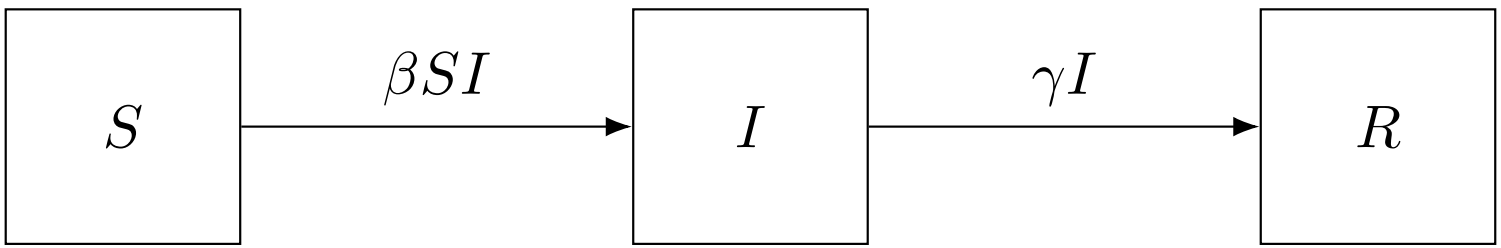
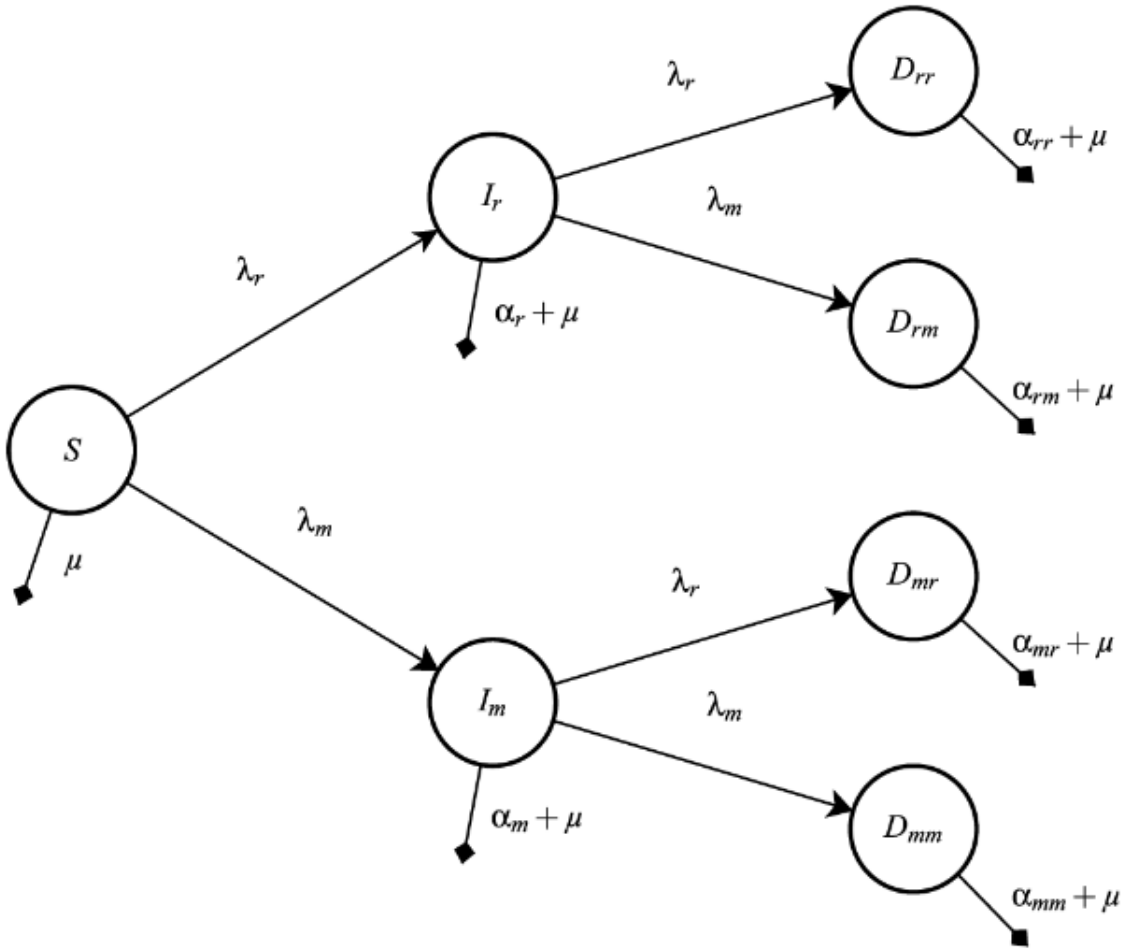
Infection spread with compartmental models

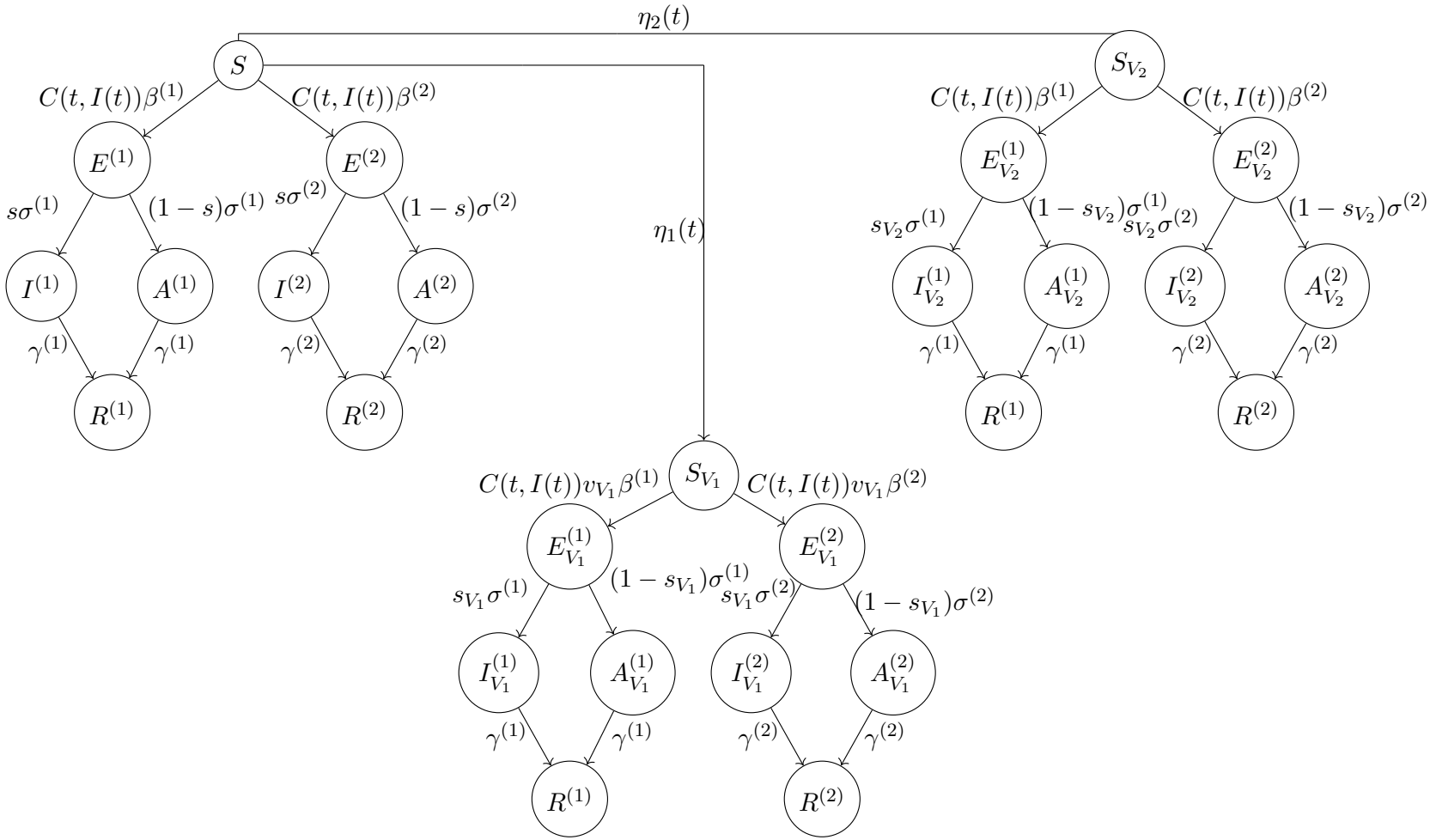


Modeling multiple infections is challenging

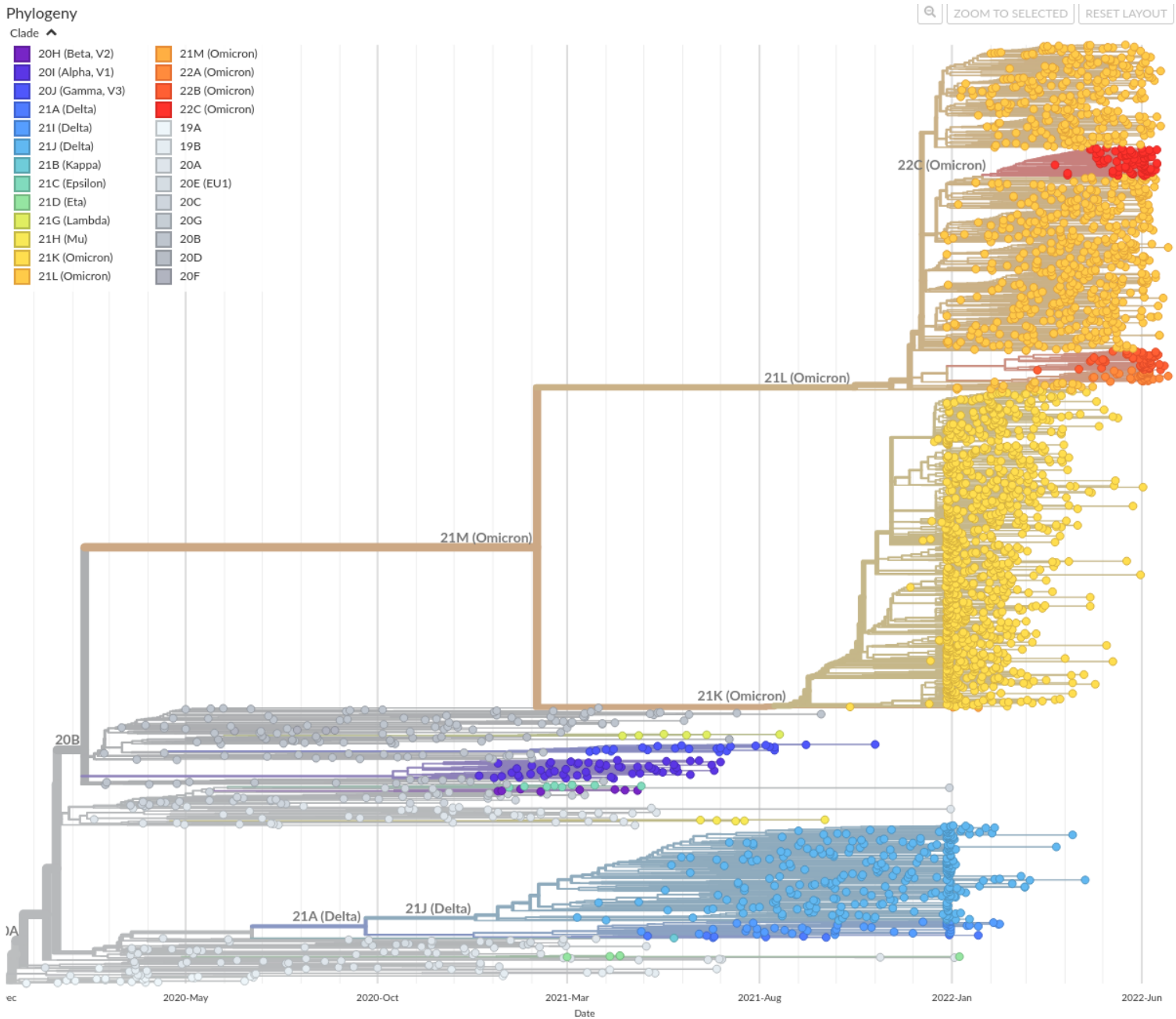


[Alizon and van Baalen, 2008]

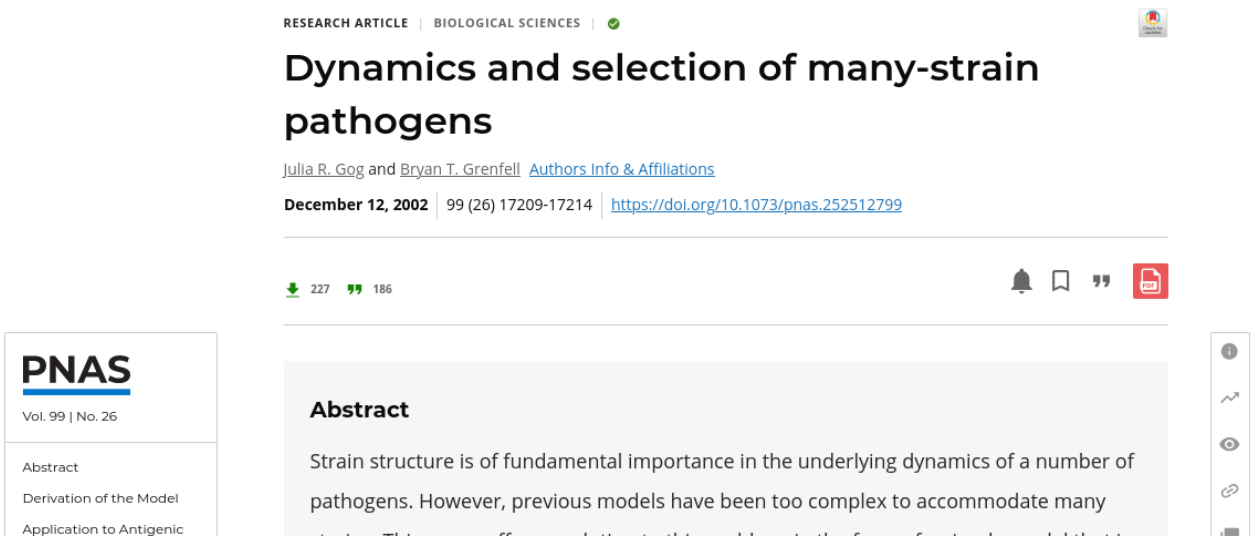
Complexity only increases with vaccination dynamics etc.



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

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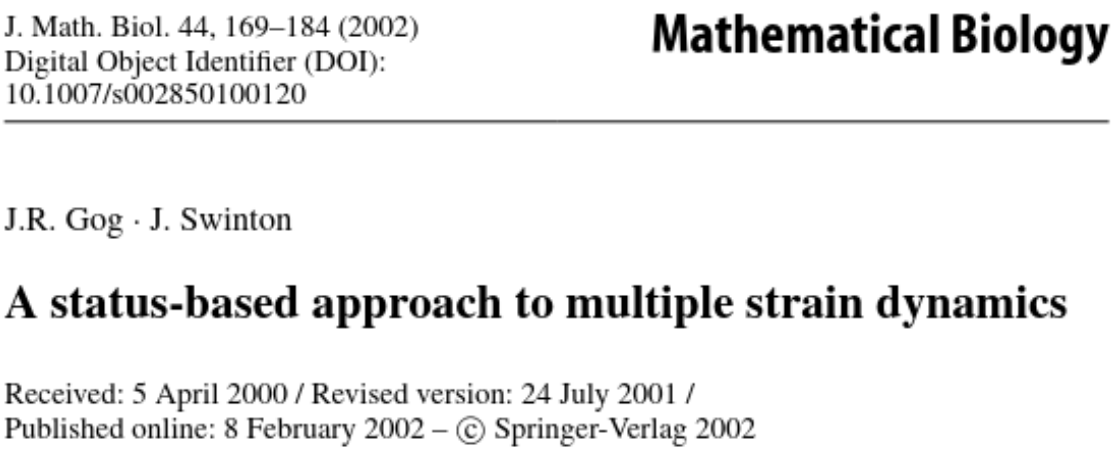
Abstract

Derivation of the Model

Application to Antigenic

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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Digital Object Identifier (DOI):
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Mathematical Biology

J.R. Gog · J. Swinton

A status-based approach to multiple strain dynamics

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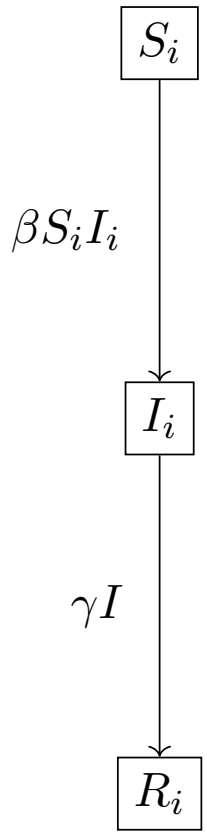
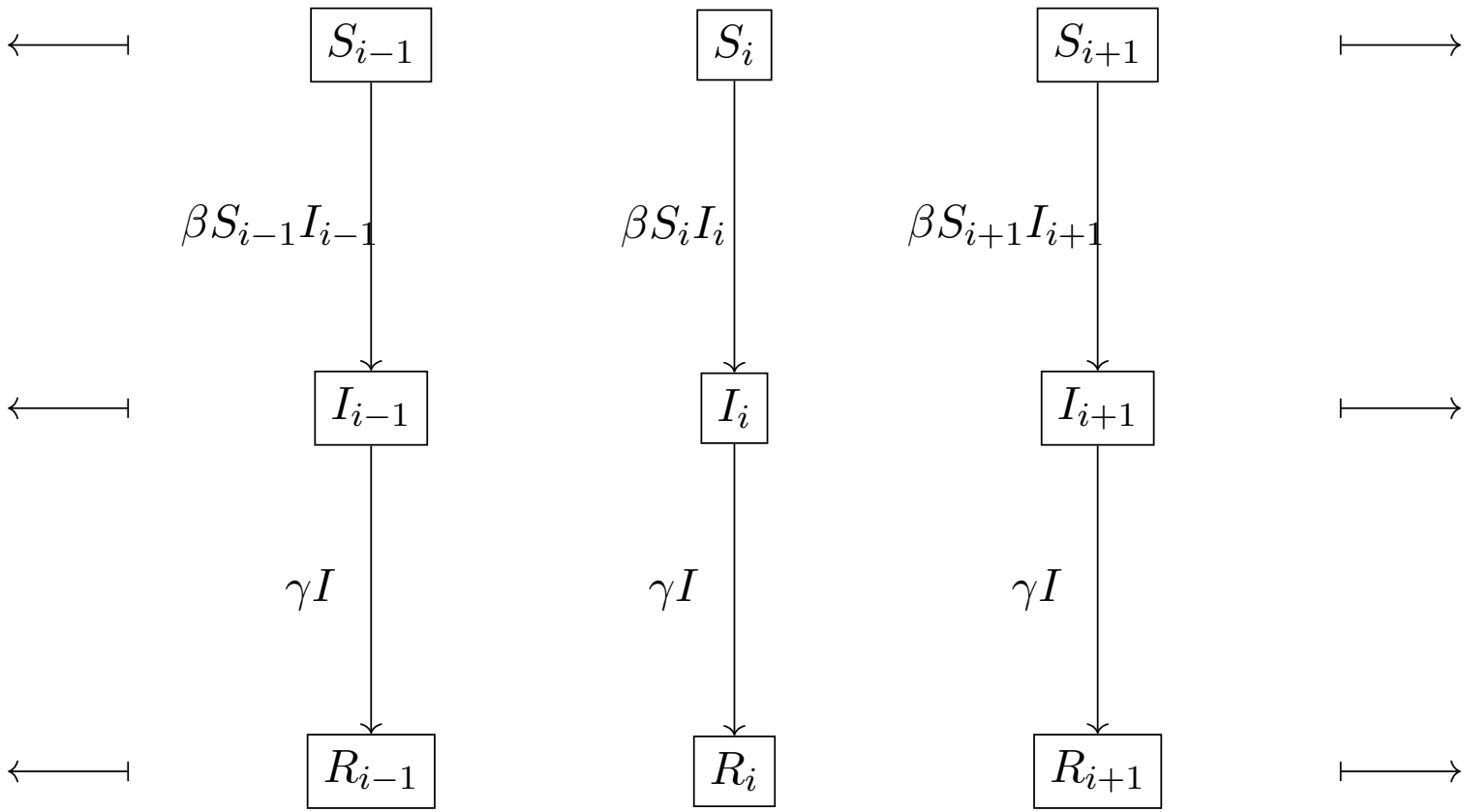
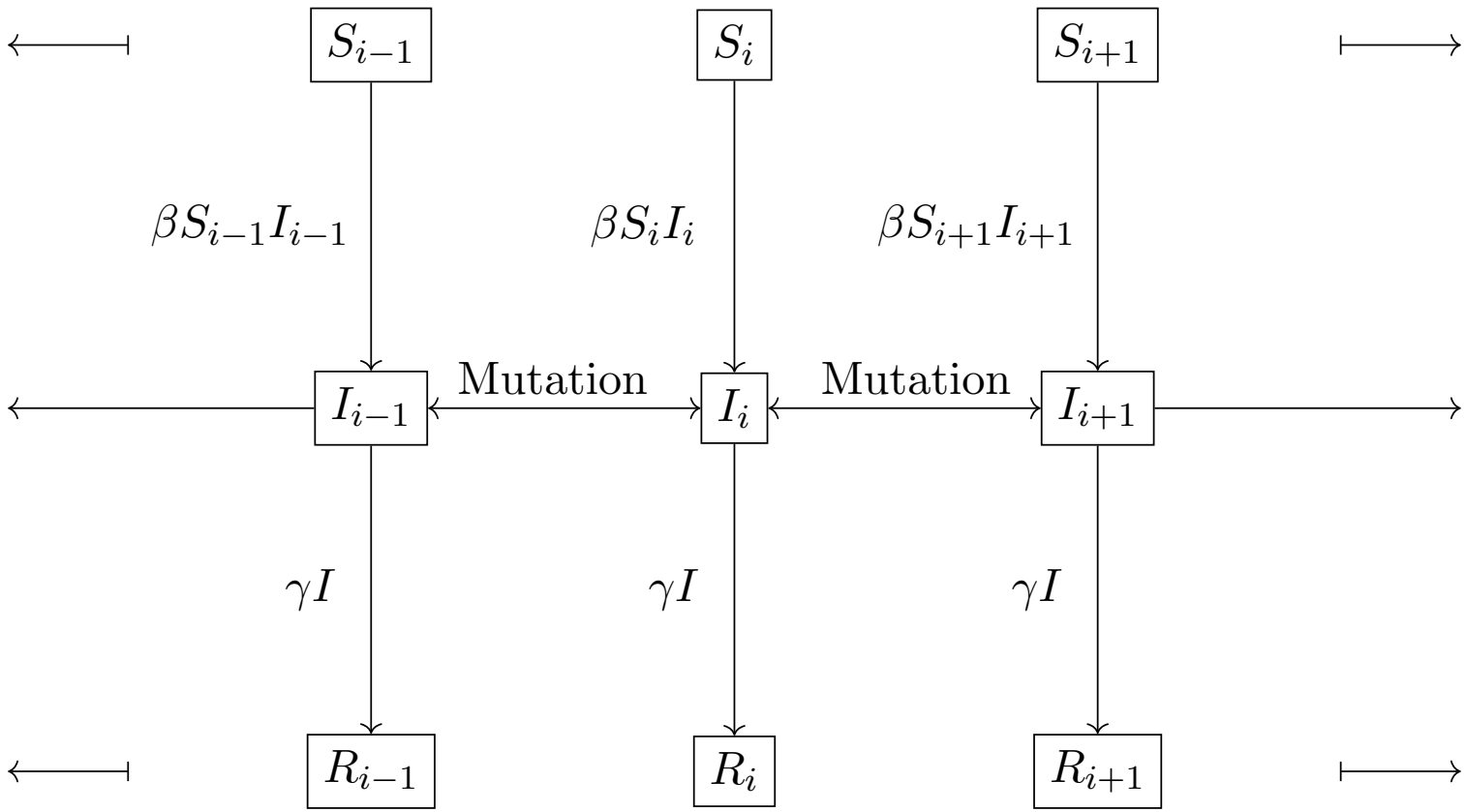
Begin with simple SIR model



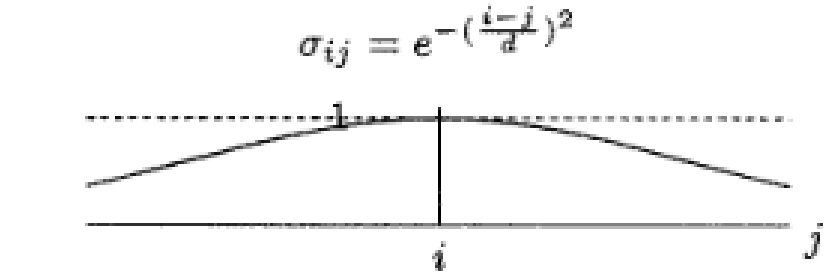
Organize strains on a lattice



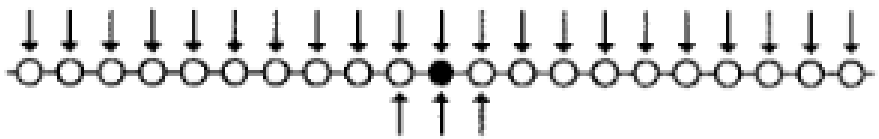
Strains mutate into adjacent strains



Infections provide cross-immunity to nearby strains



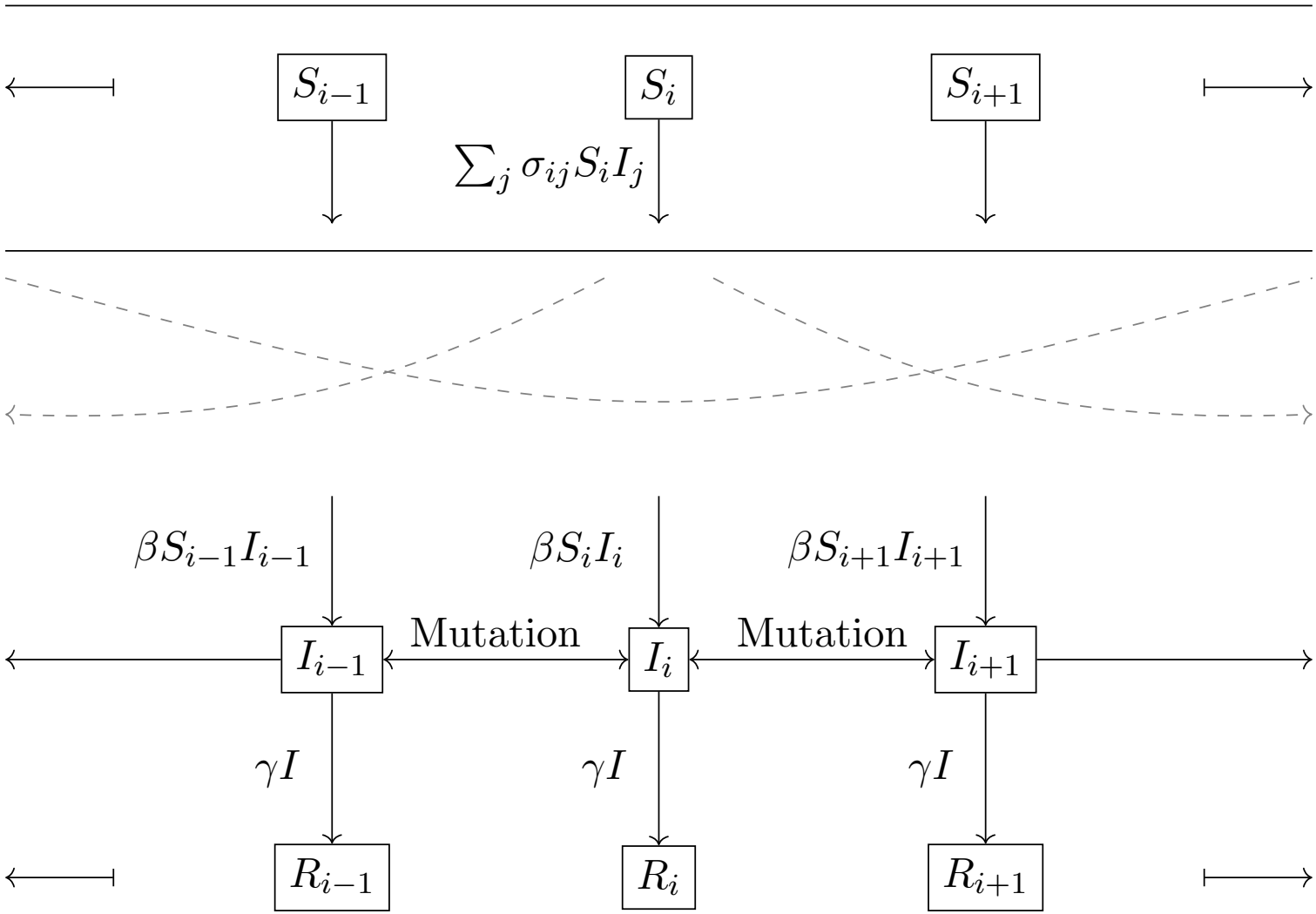
Cross-immunity to nearby strains



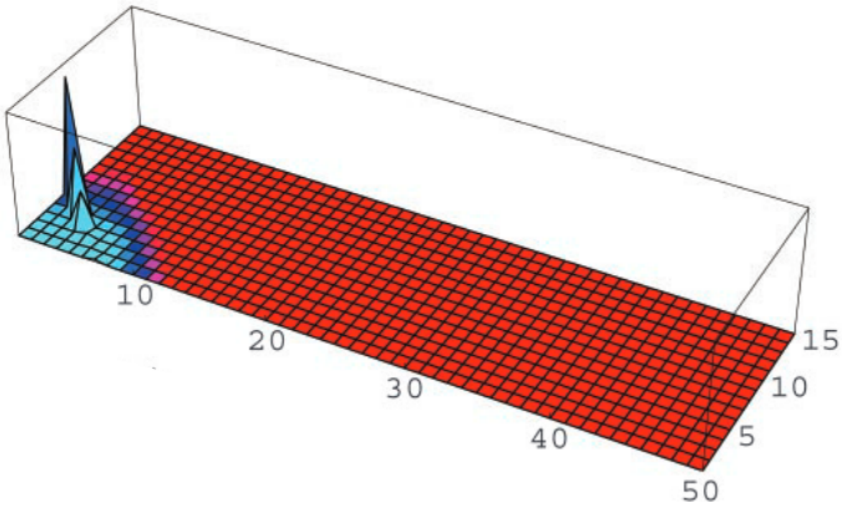
Mutation to adjacent strains

[Gog and Grenfell, 2002]

Full strain lattice model in 1 dimension

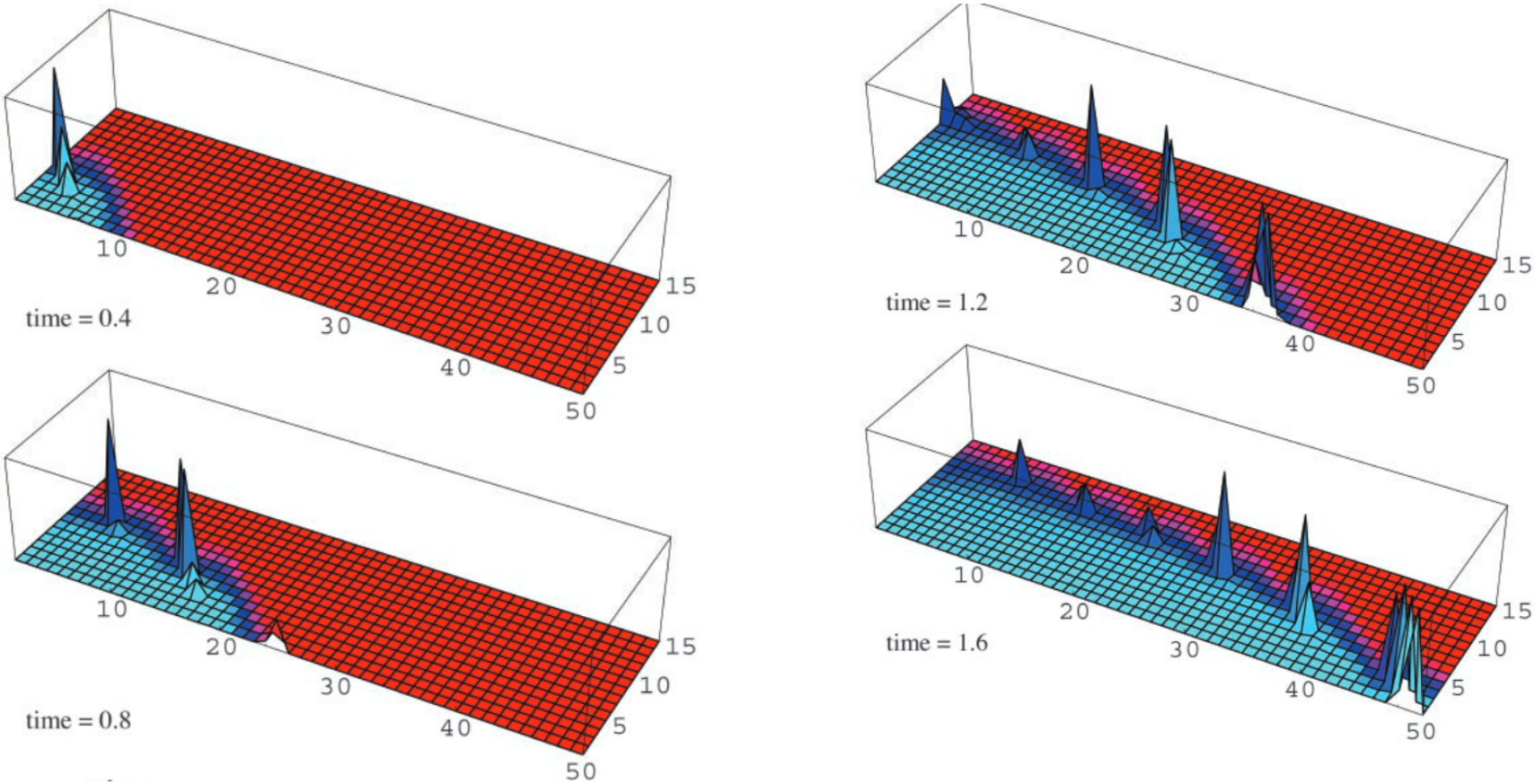


Extending the strain lattice to 2 dimensions



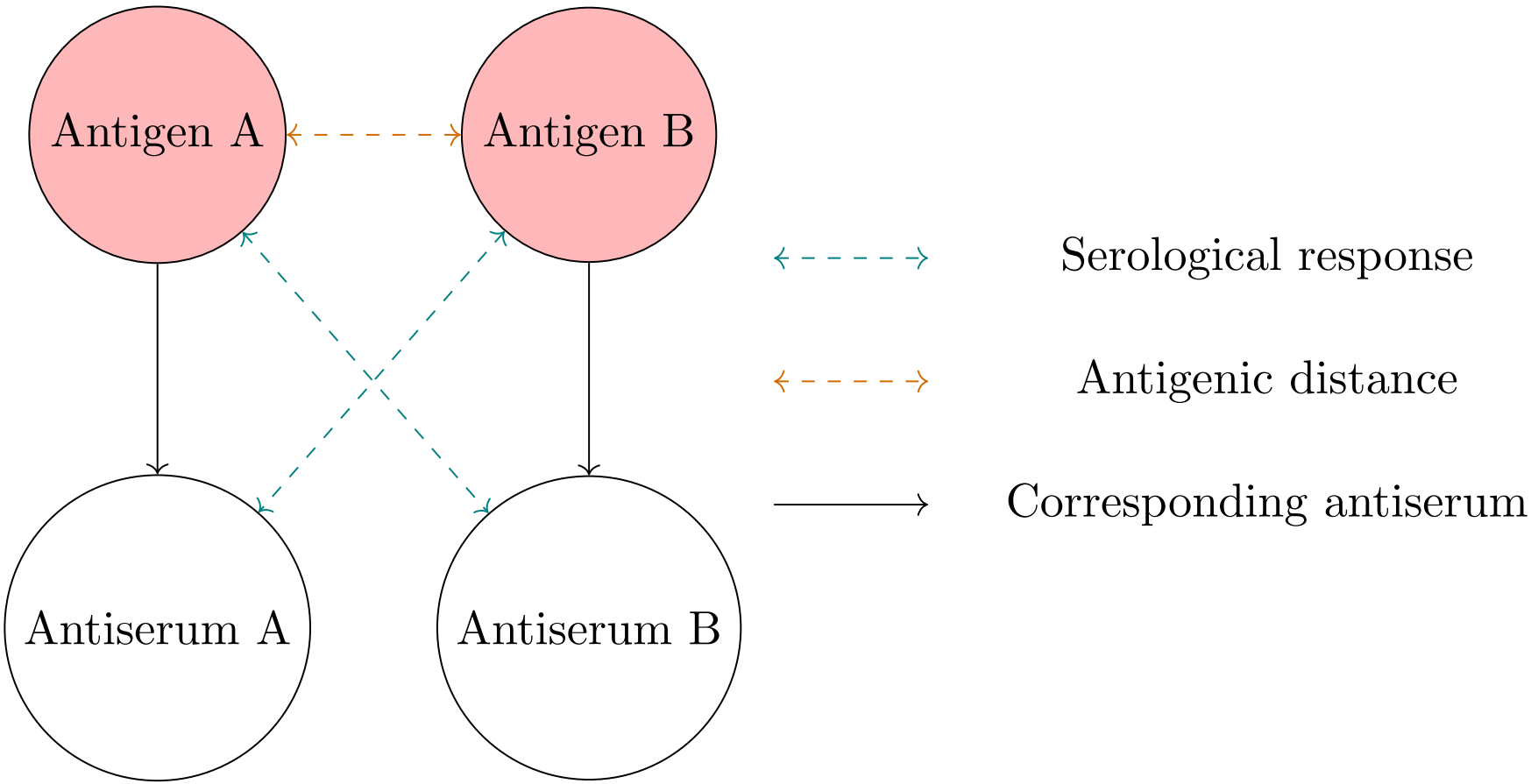
[Gog and Grenfell, 2002]

Extending the strain lattice to 2 dimensions

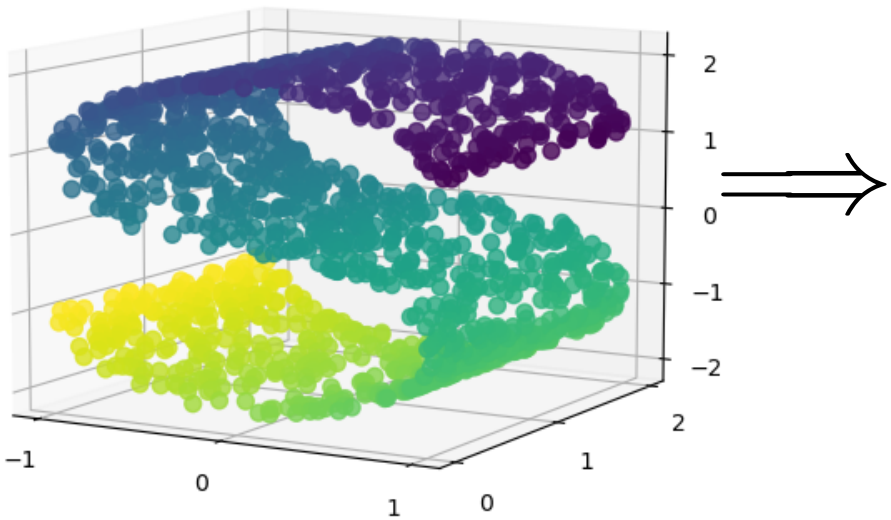


[Gog and Grenfell, 2002]

Quantifying antigenicity between viruses

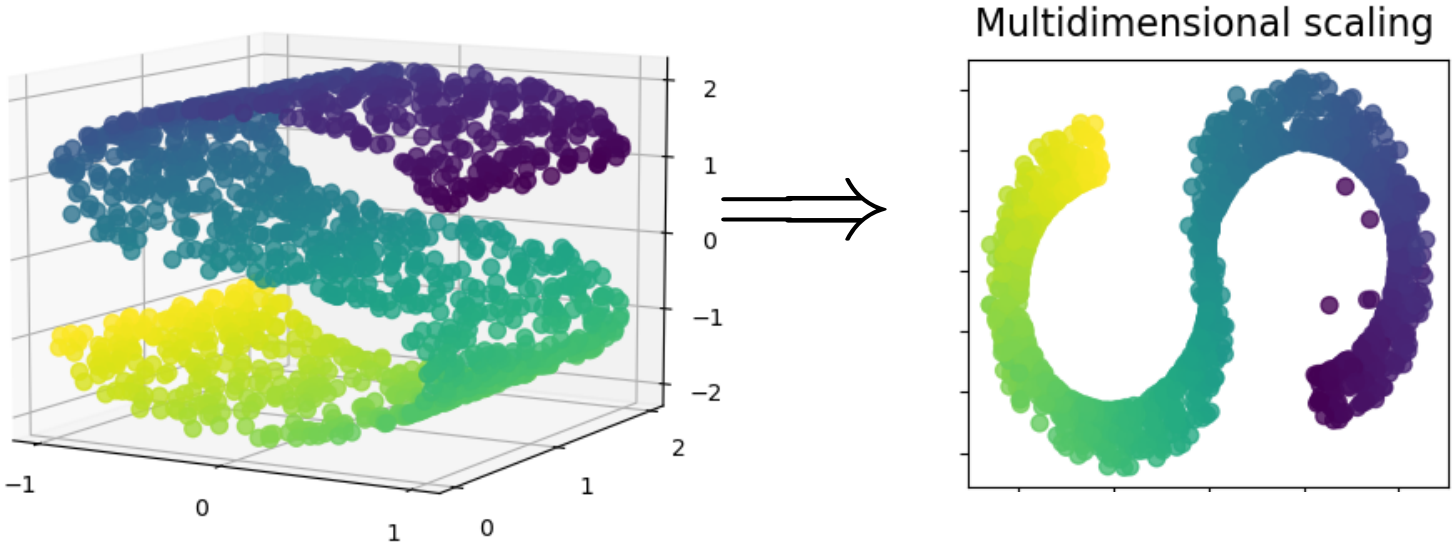


Projecting to low dimensions while preserving distances



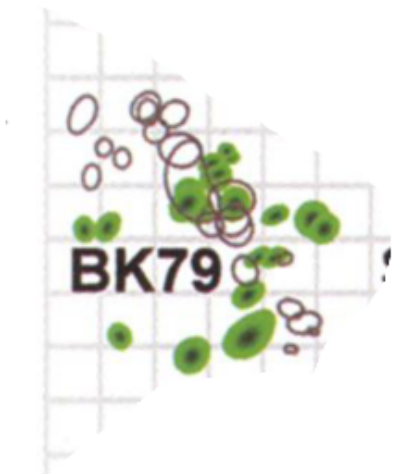
[Pedregosa et al., 2011]

Projecting to low dimensions while preserving distances

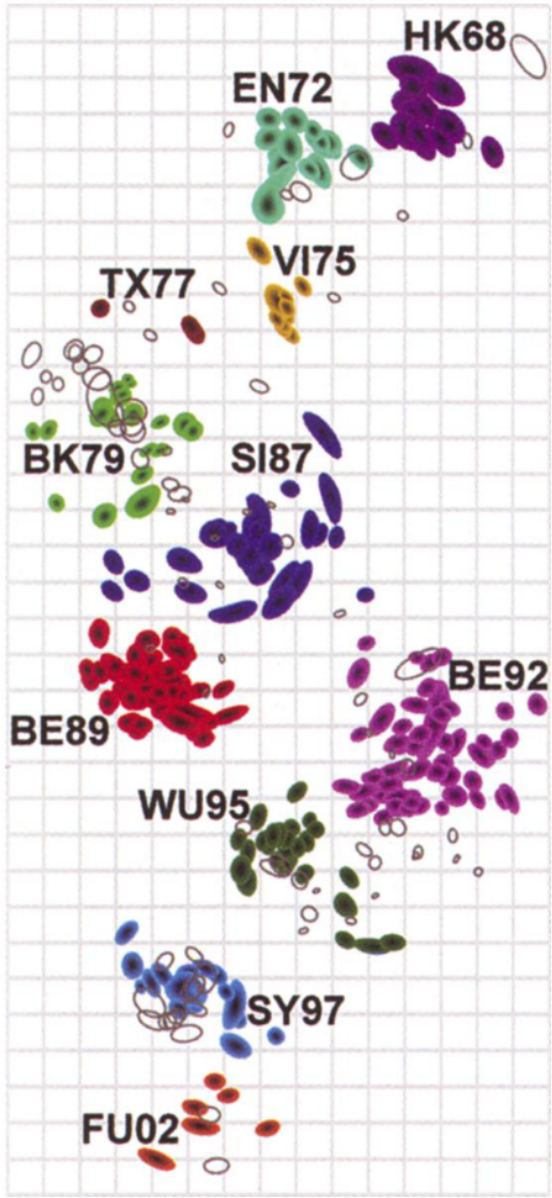


[Pedregosa et al., 2011]

Approximating genomic data in 2 dimesions

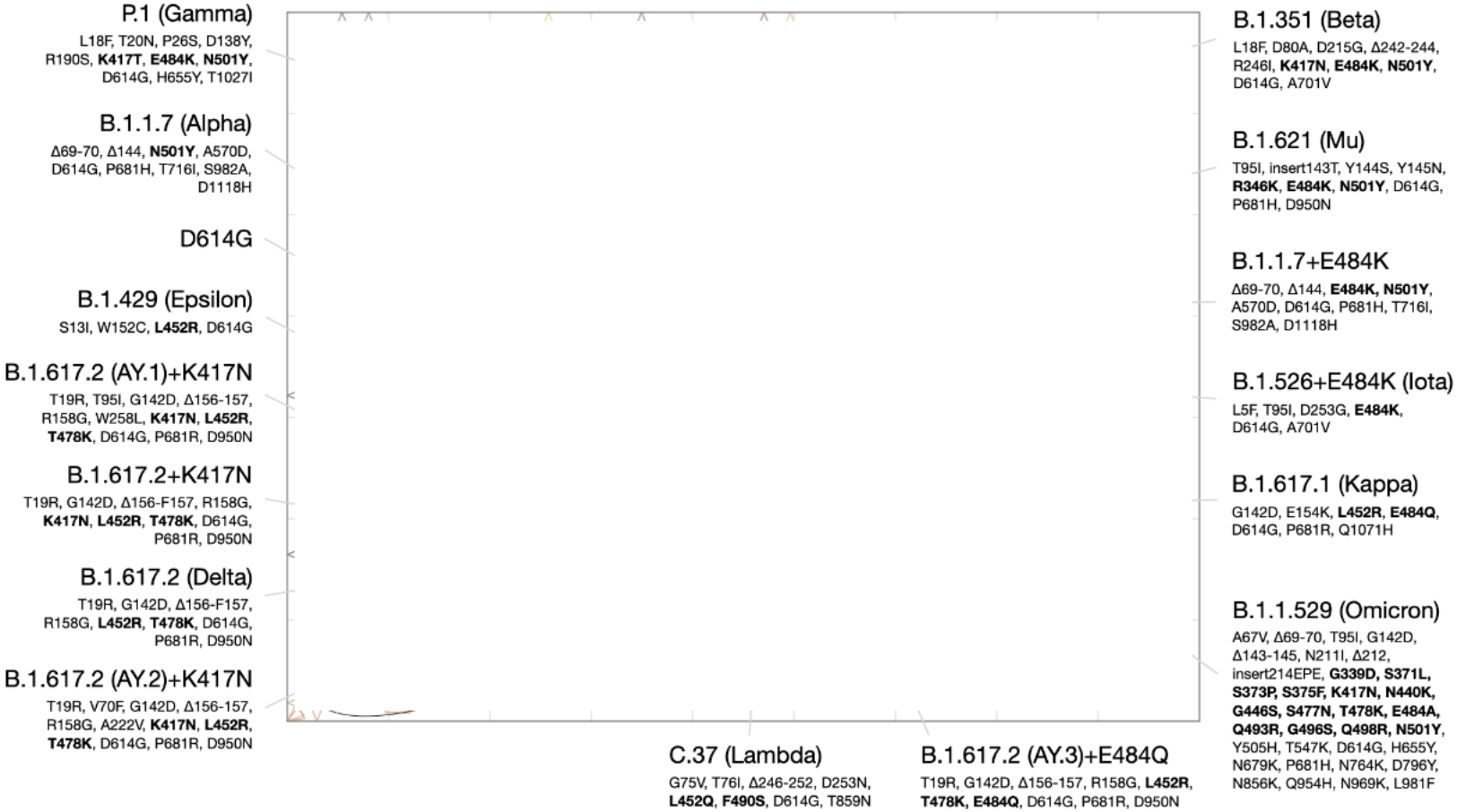


Approximating genomic data in 2 dimesions



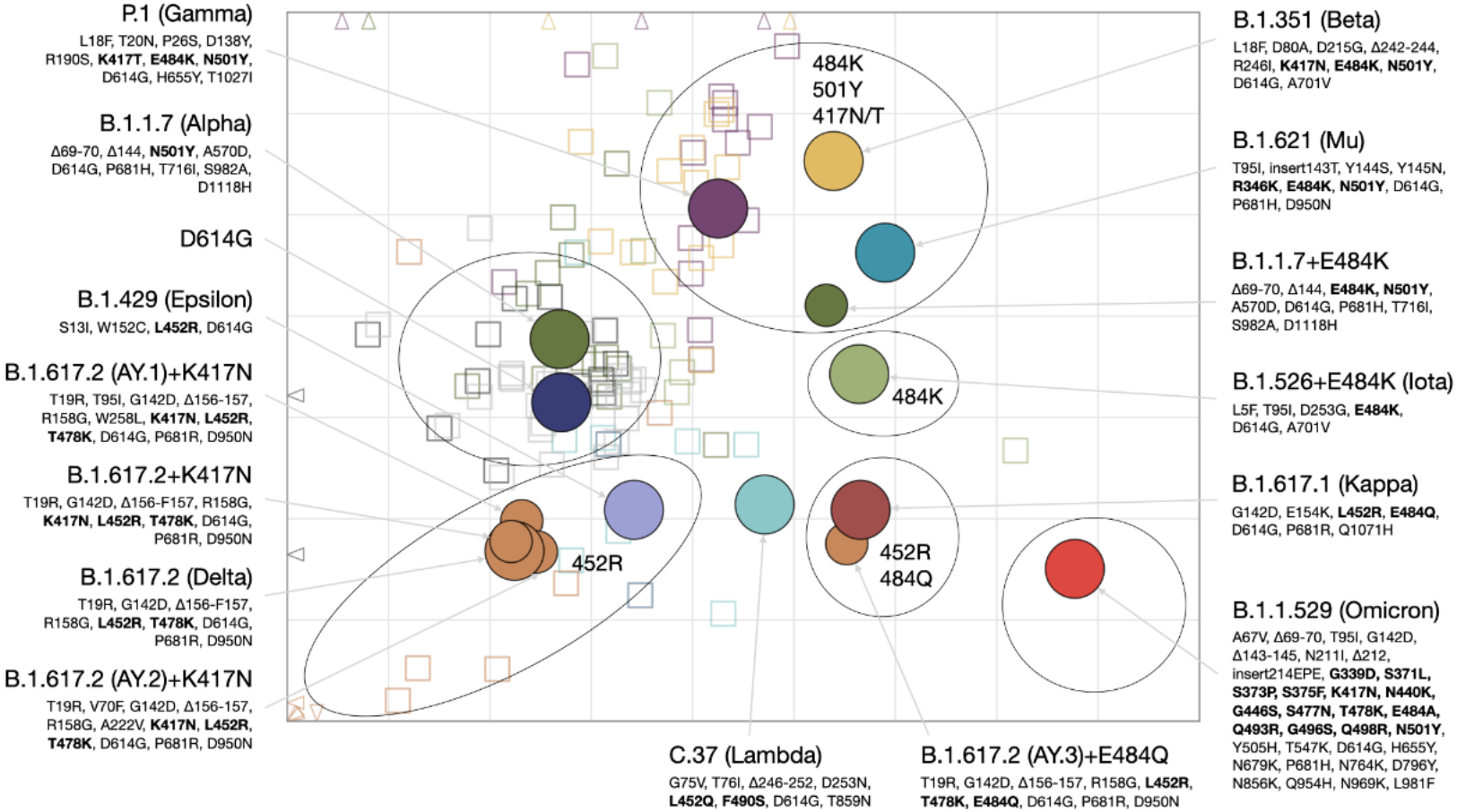
[Lapedes and Farber, 2001, Smith et al., 2004]

Mapping SARS-CoV-2 in 2D



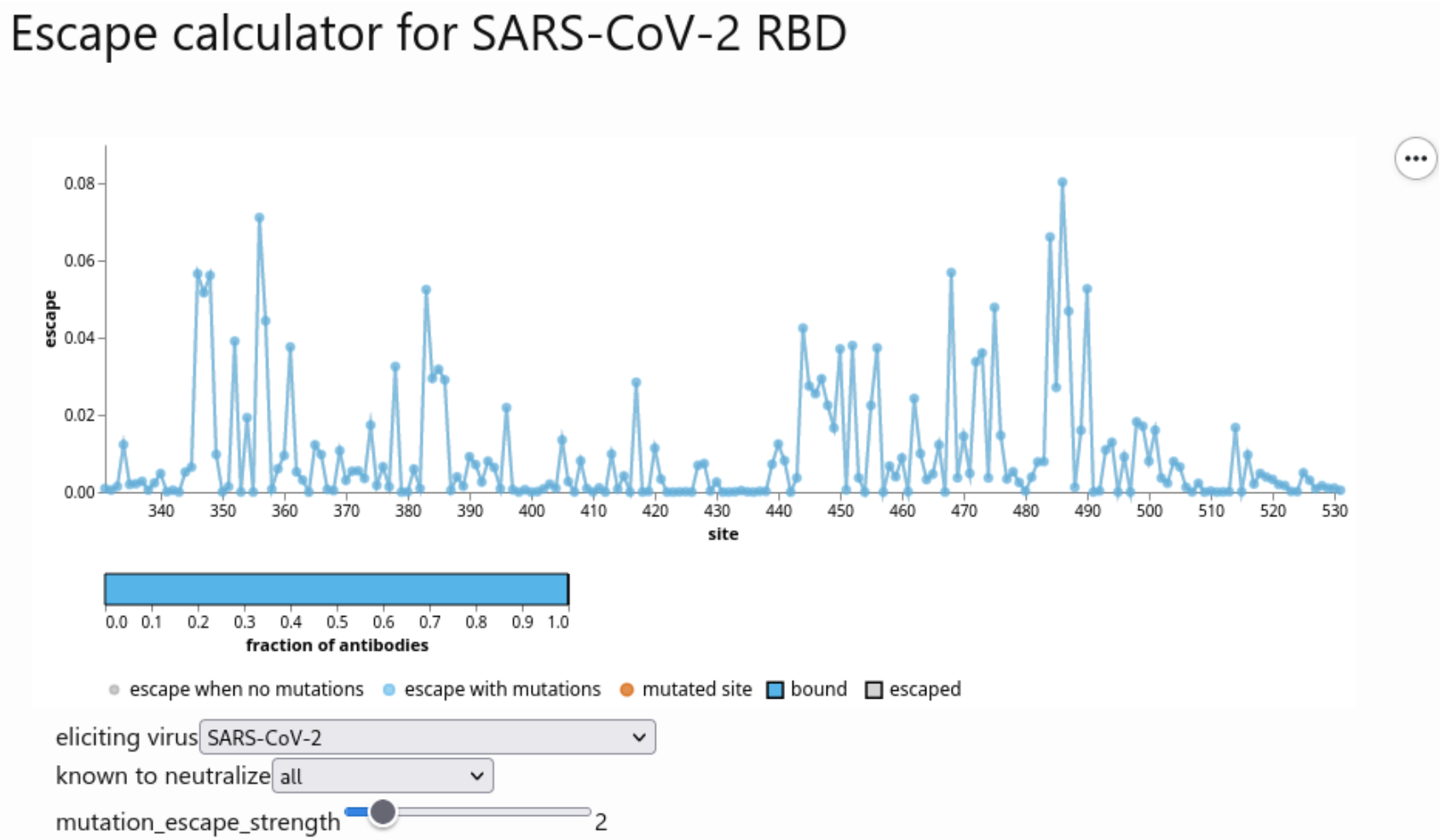
[Wilks et al., 2022]

Mapping SARS-CoV-2 in 2D



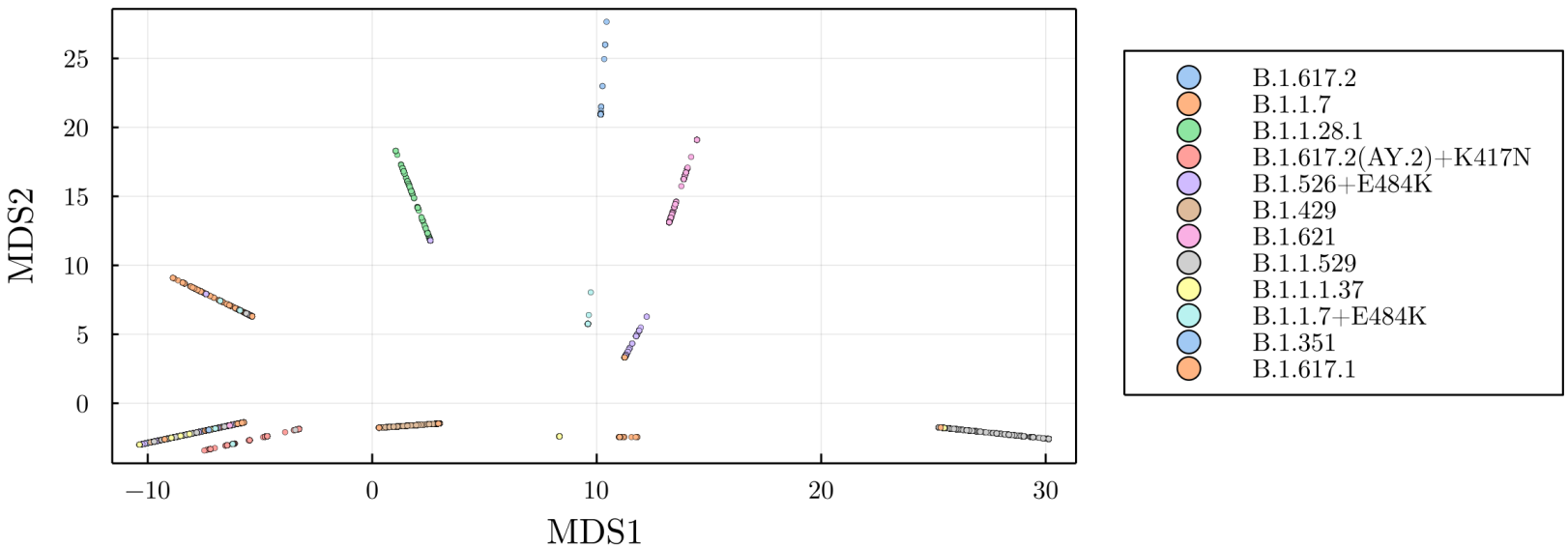
[Wilks et al., 2022]

Methods of adding more genomes: polyclonal antibody binding studies



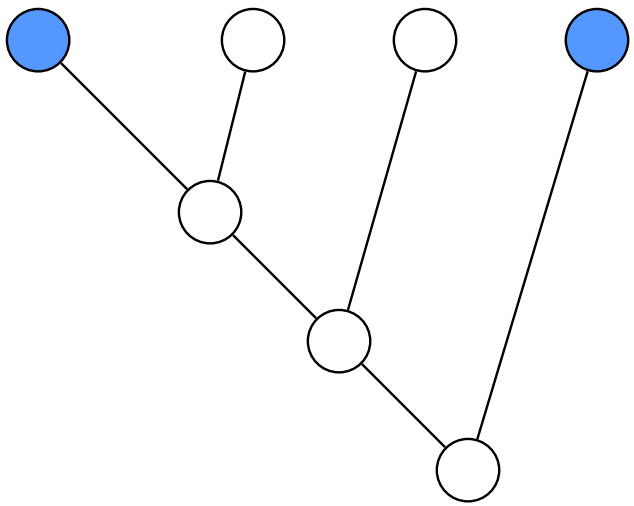
[Greaney et al., 2022]

Antibody Binding map

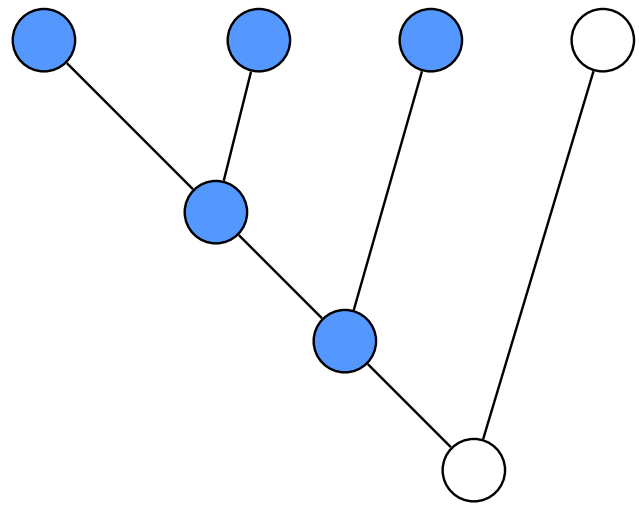


Methods of adding more genomes: homoplasic sites

Homoplasic trait

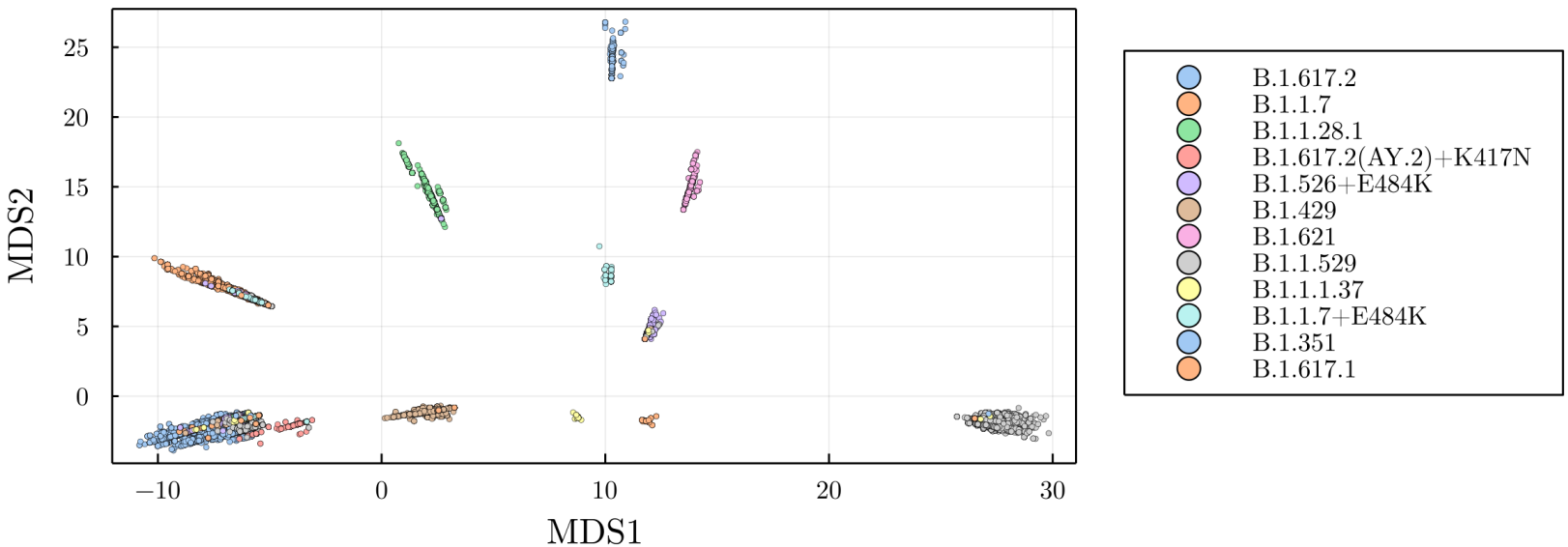


Homologic trait

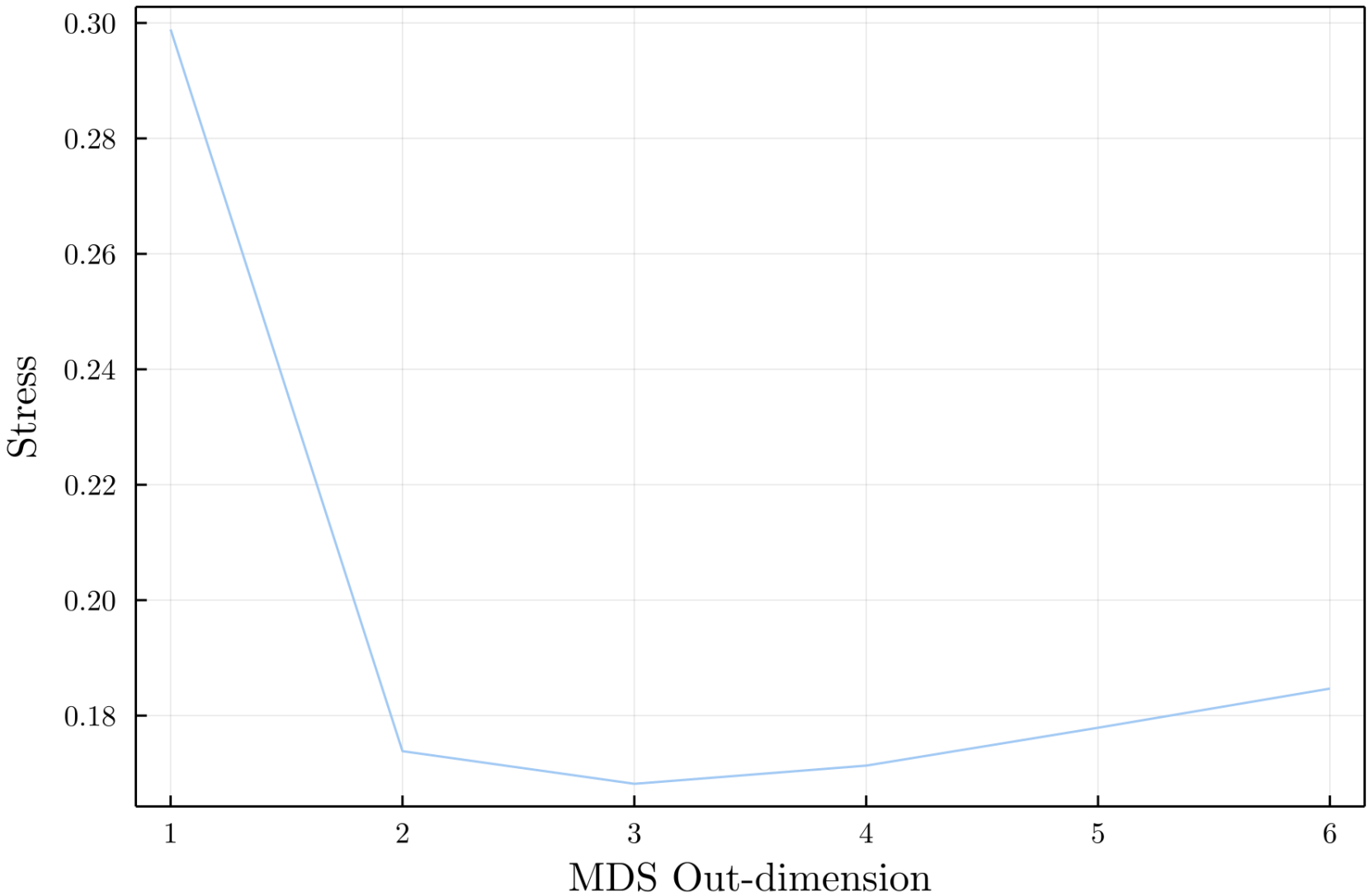


[Page and Holmes, 2009]

Homoplasic mutations 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 $(i, j) \in [0, N]^2$
σ_{ijkl}	Probability that exposure to variant (i, j) causes immunity to variant (k, l)
β_{ij}	Transmission rate of variant (i, j)
$v(t)$	vaccination rate at time t
$s(t)$	stringency at t
ξ	Recovery rate of all strains
γ	Rate of immunity loss of all strains

Table of symbols for Model 2

Model Equations

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

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

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

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

Model Dynamics

(gifs of model dynamics)

Further work

- Differentiate between antigenic and genomic space
  - $\rightarrow$ non-local diffusion
- Model fitting
- Applications
  - Simple inference on antigenic space
  - VoC-aware NPI usage and vaccination

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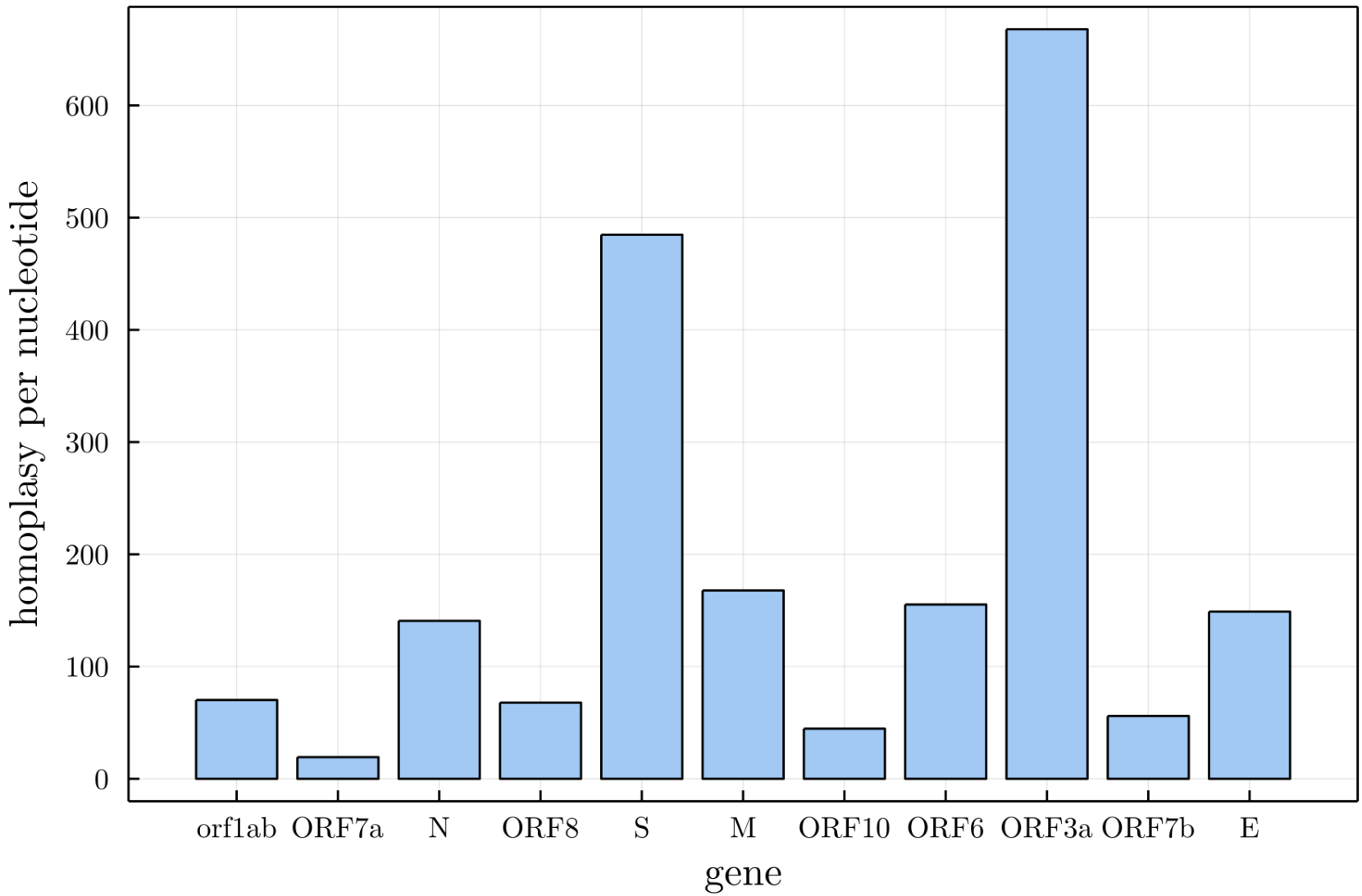
Mutation homoplasy