

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

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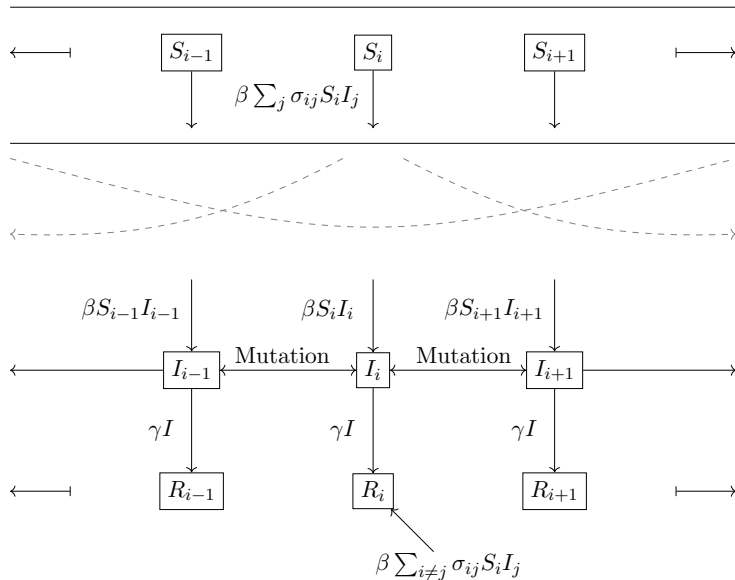
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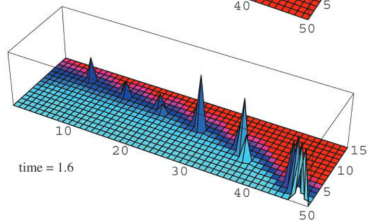
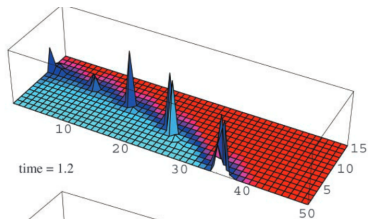
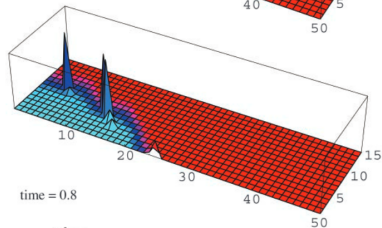
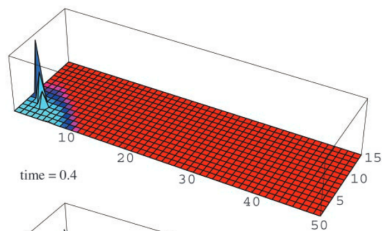
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Full strain lattice model in 1 dimension

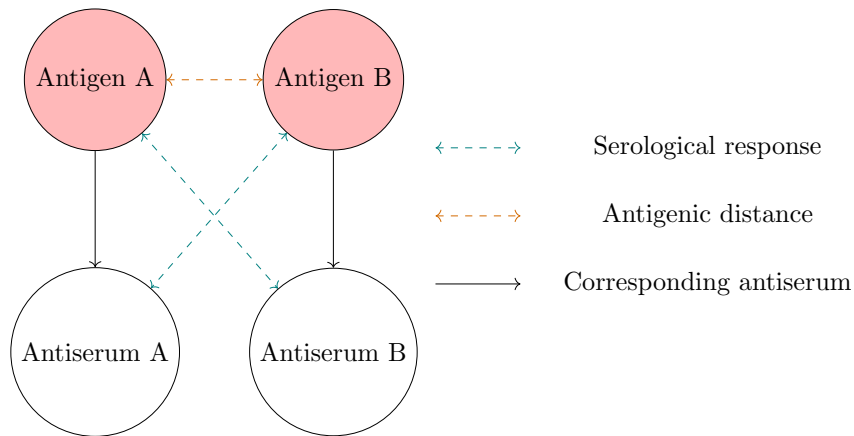


Extending the strain lattice to 2 dimensions



[Gog and Grenfell, 2002]

Quantifying antigenicity between viruses



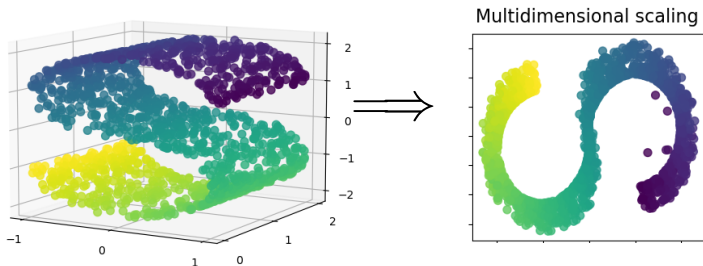
Projecting to low dimensions while preserving distances

Let D be the matrix of pairwise distances.

Multidimensional scaling finds $x_i \in \mathbb{R}^k$ to minimize

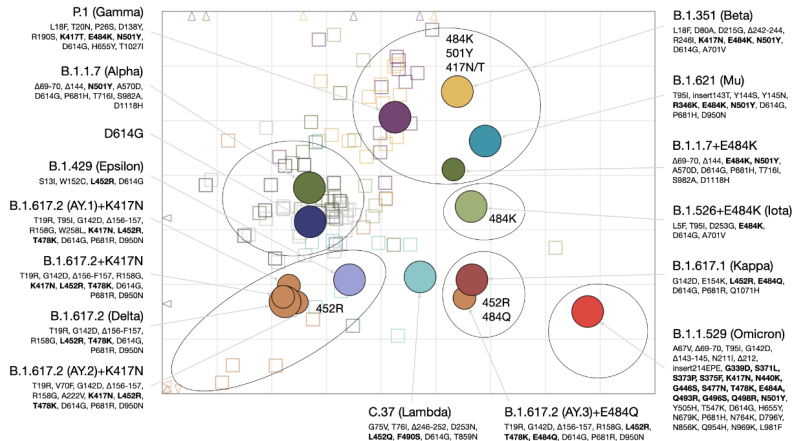
$$\text{STRESS}(x) = \sum_{i>j} (D_{ij} - \|x_i - x_j\|)^2$$

where k is small.



[Pedregosa et al., 2011]

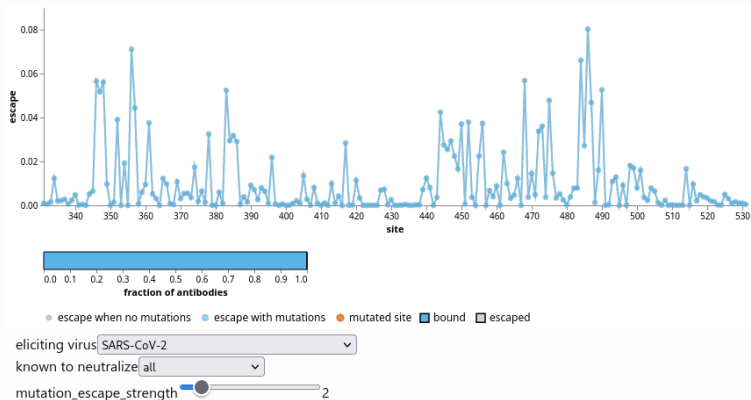
Mapping SARS-CoV-2 in 2D



[Wilks et al., 2022]

Methods of adding more genomes: polyclonal antibody binding studies

Escape calculator for SARS-CoV-2 RBD



[Greaney et al., 2022]

Interpolating more data into antigenic map

For each pair of genomes g_i and g_j ($i \neq j$)

1. Find the closest lineages in existing antigenic map to g_i , and g_j , and corresponding points x_i and x_j
- 2.
- 3.
- 4.

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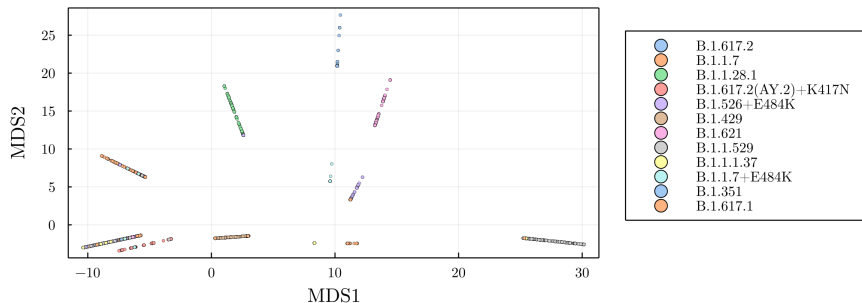
1. Find the closest lineages in existing antigenic map to g_i , and g_j , and corresponding points x_i and x_j
2. Determine difference in polyclonal binding affinity $B(g_i, g_j)$
3. Distance between g_i and g_j is $\|x_i - x_j\| + B(g_i, g_j)$
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Interpolating more data into antigenic map

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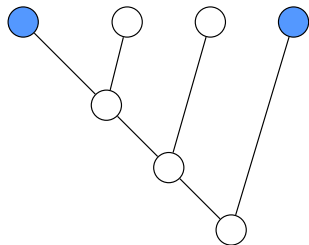
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3. Distance between g_i and g_j is $\|x_i - x_j\| + B(g_i, g_j)$
4. Use these distances as inputs to multidimensional scaling

Antibody Binding map

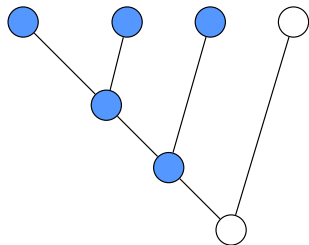


Methods of adding more genomes: homoplasious sites

Homoplasious mutation

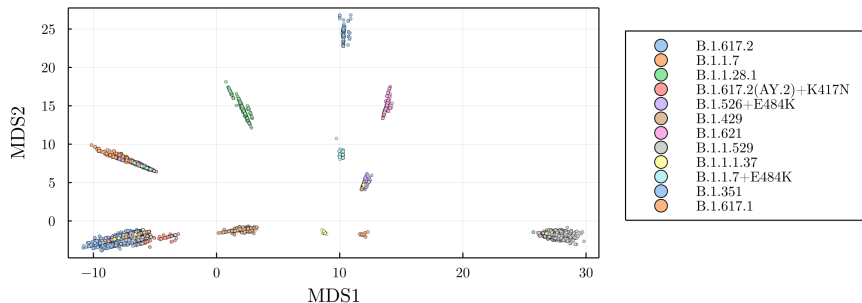


Homologous mutation



[Page and Holmes, 2009]

Homoplasic mutations map



Model parameters/variables

Symbol	Description
N	Size of variant grid
K	Total population
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 from variant $(i, j) \in [0, N]^2$
V_{ij}	Immune by vaccination to variant $(i, j) \in [0, N]^2$
σ_{ijkl}	Probability that exposure to variant (k, l) causes immunity to variant (i, j)
β_{ij}	Transmission rate of variant (i, j)
$v_{ij}(t)$	vaccination rate at time t against variant (i, j)
$s(t)$	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

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

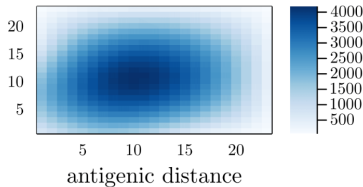
$$\frac{I_{ij}(t)}{dt} = s(t) \beta_{ij} S_{ij} I_{ij} - \xi I_{ij} + M (-4I_{ij} + I_{i-1,j} + I_{i+1,j} + I_{i,j-1} + I_{i,j+1}) \quad (2)$$

$$\frac{R_{ij}(t)}{dt} = \sum_{kl \neq ij} s(t) \beta_{kl} \sigma_{ijkl} S_{ij} I_{kl} + \xi I_{ij} - \gamma R_{ij} + v_{ij}(t)S \quad (3)$$

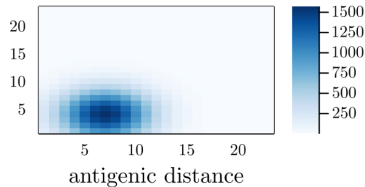
$$\frac{V_{ij}(t)}{dt} = v_{ij}(t)S - \gamma V_{ij} \quad (4)$$

Model Dynamics

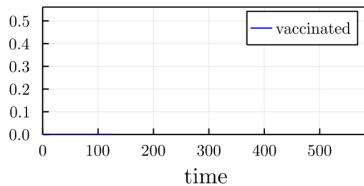
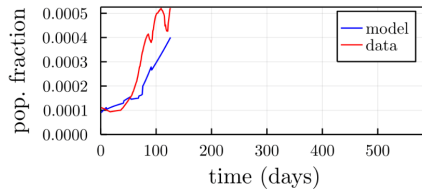
I



V



Incident (daily) cases



Case importation

- Evolution of Omicron represents a huge shift in antigenic space
- Intermediate steps not represented in data
- We can introduce omicron to solve this problem



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Mutation homoplasy

