Strain-space model for Sars-CoV-2

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- Dynamic model of Sars-CoV-2 evolution, representing antigenic diversity on a lattice (as in e.g. [Gog and Grenfell, 2002, Kryazhimskiy et al., 2007])
- Antigenically distinct variants of the virus are mapped to 2D grid, distance between variants corresponds to the proportional reduction in maximum serum viral titre [Wilks et al., 2022, van der Straten et al., 2022]

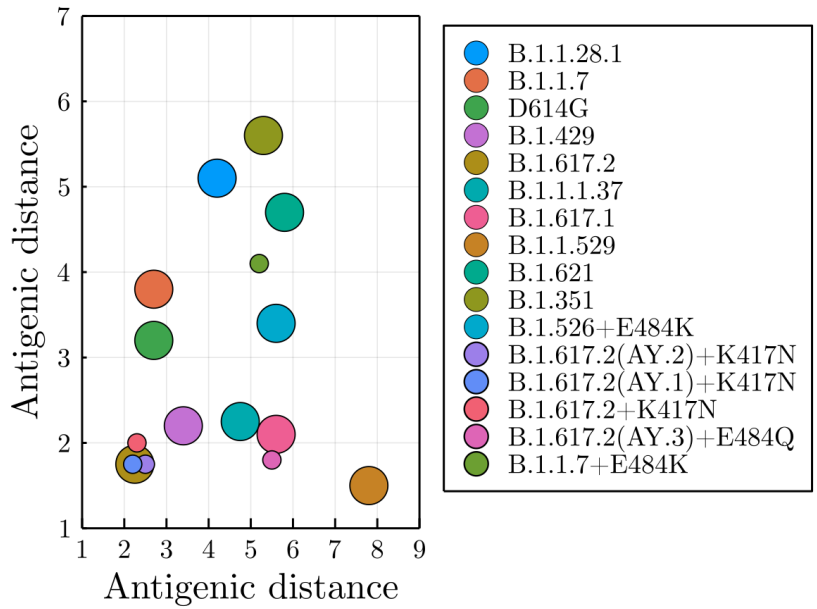

Figure: Antigenic cartography of Sars-CoV-2, reproduced from [Wilks et al., 2022], Fig. 2

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)
ξ	Recovery rate of all strains
γ	Rate of immunity loss of all strains

Table: Table of symbols for Model 2

In practice, we assume σ_{ijkl} is just a 2-D gaussian distribution parameterized by the distance between (i, j) and (k, l).

Model Equations

$$\frac{S_{ij}}{dt} = -\sum_{kl} \beta_{kl}\sigma_{ijkl}S_{ij}I_{kl} + \gamma R_{ij} \tag{1}$$

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

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

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

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