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

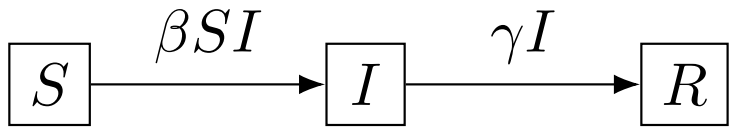
[3]Dalhousie University, Halifax, Canada

[4]Simon Fraser University, Burnaby, Canada

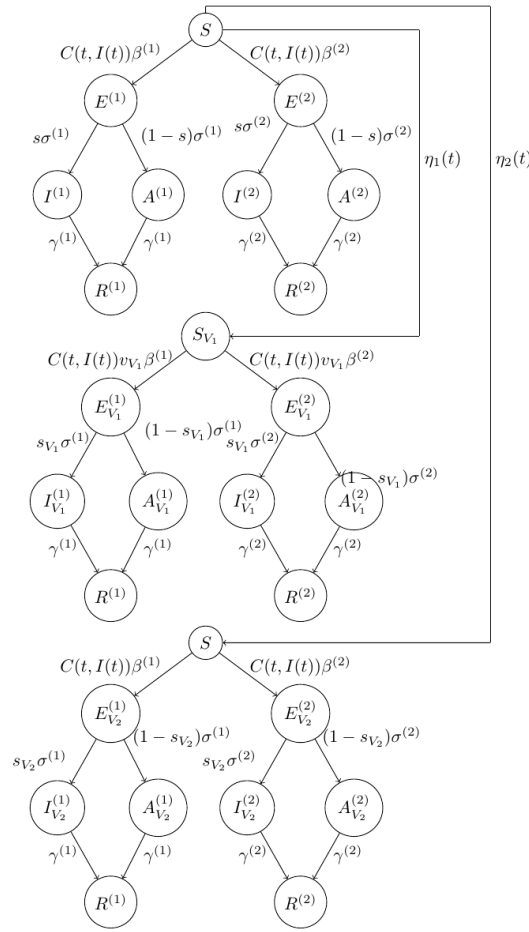
[5]Shared Hospital Laboratory, Toronto, Canada

June 30, 2022

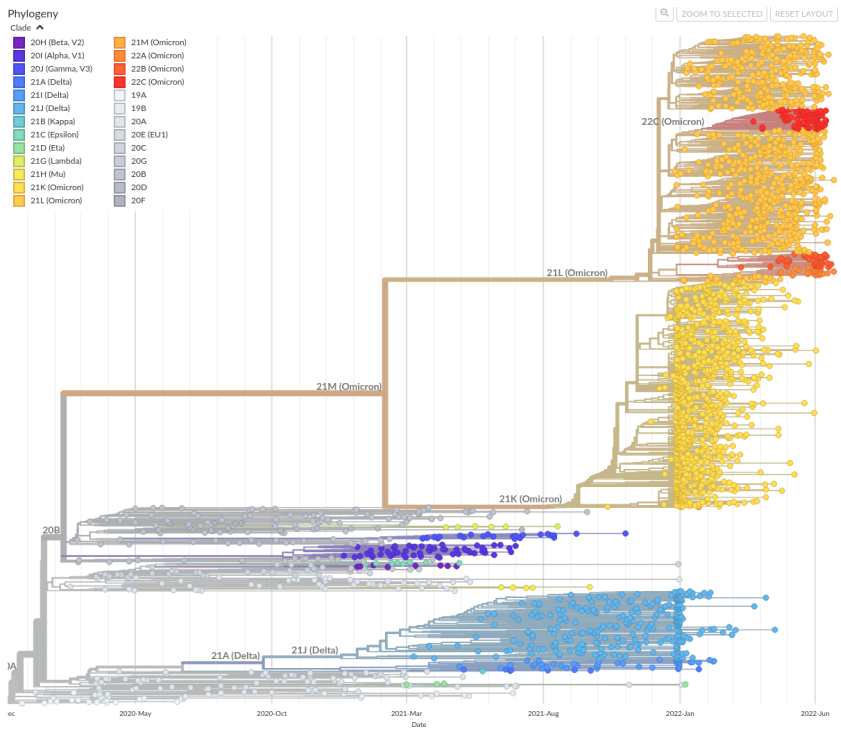
- Infection spread is often modelled using compartmental models
- Represent subsets of a host population and rates of movement between them

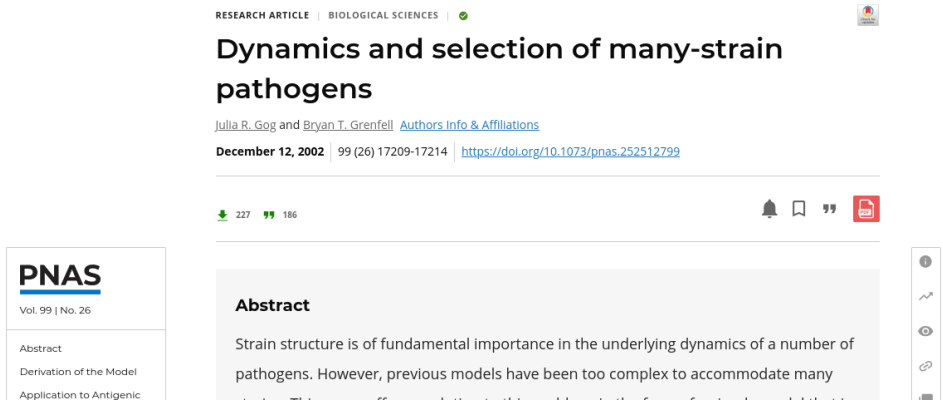


- Multiple infections (e.g. competing VoCs) can be represented as more compartments
- Work on multiple infections is usually here due to lack of data, increasing complexity



This only represents a tiny amount of the genomic data we have for Sars-CoV-2!





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

227 186

PNAS

Vol. 99 | No. 26

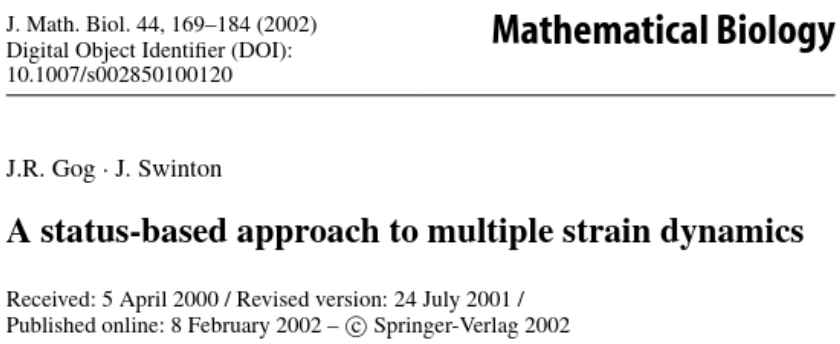
Abstract

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



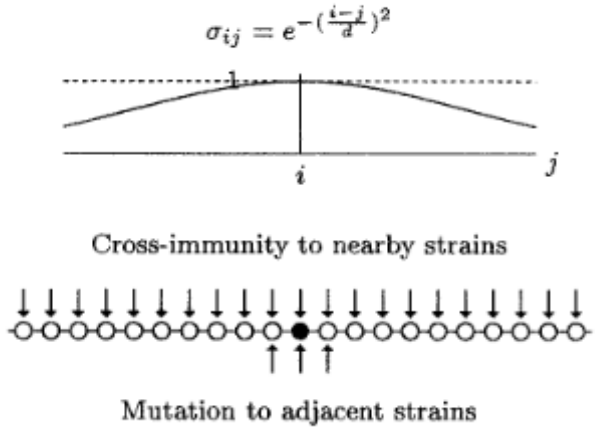
J. Math. Biol. 44, 169–184 (2002)
Digital Object Identifier (DOI):
10.1007/s002850100120

Mathematical Biology

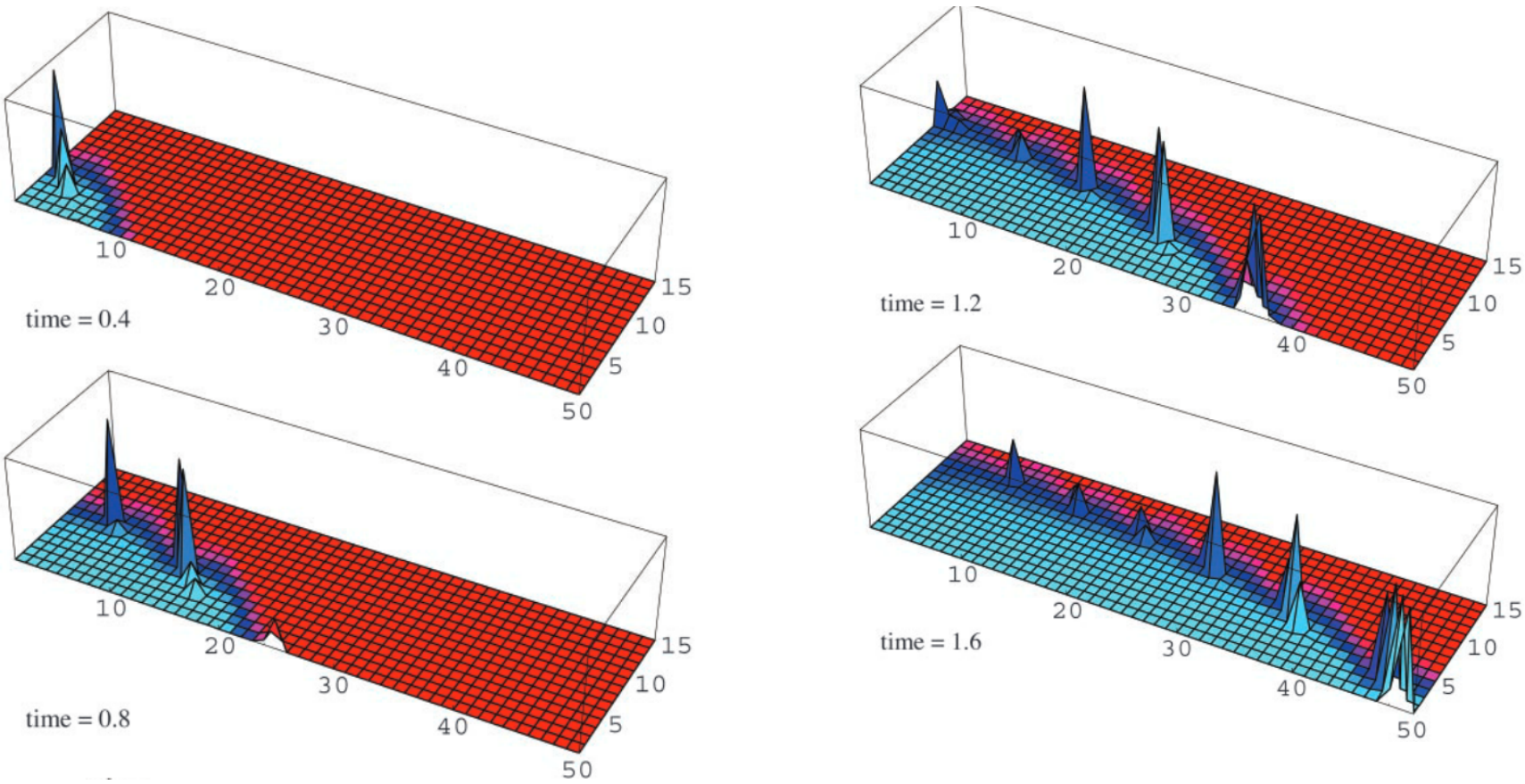
J.R. Gog · J. Swinton

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



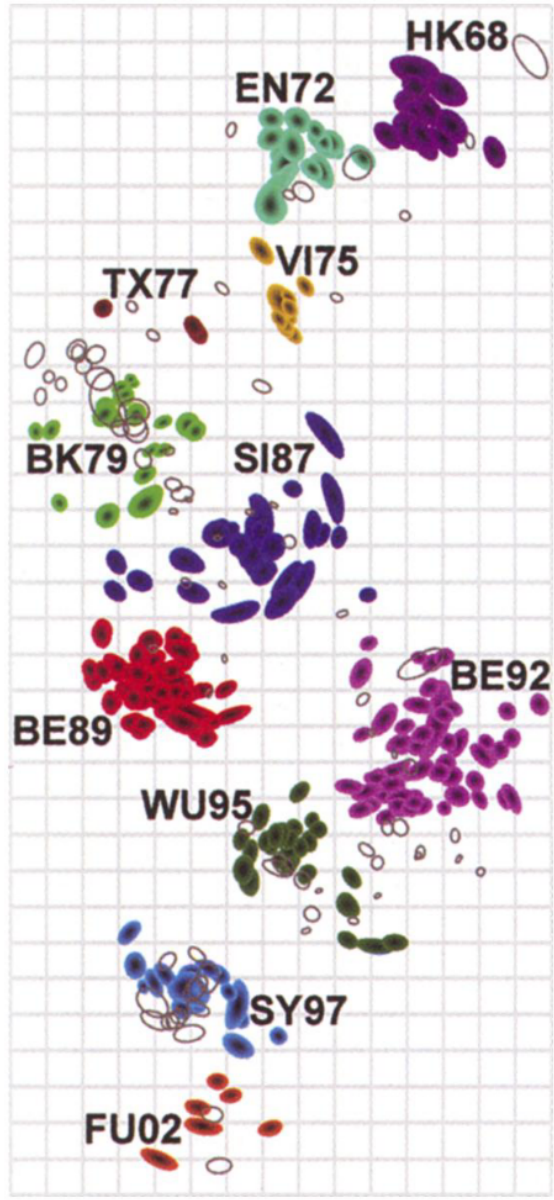
[Gog and Grenfell, 2002]



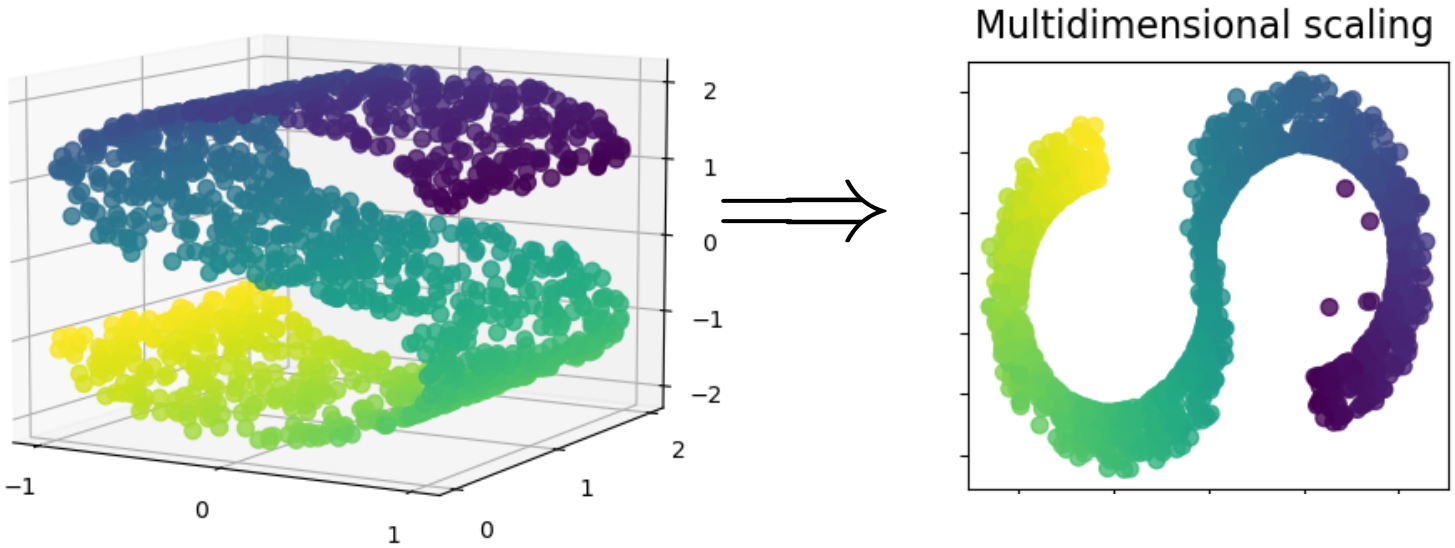
[Gog and Grenfell, 2002]

Antigenic cartography

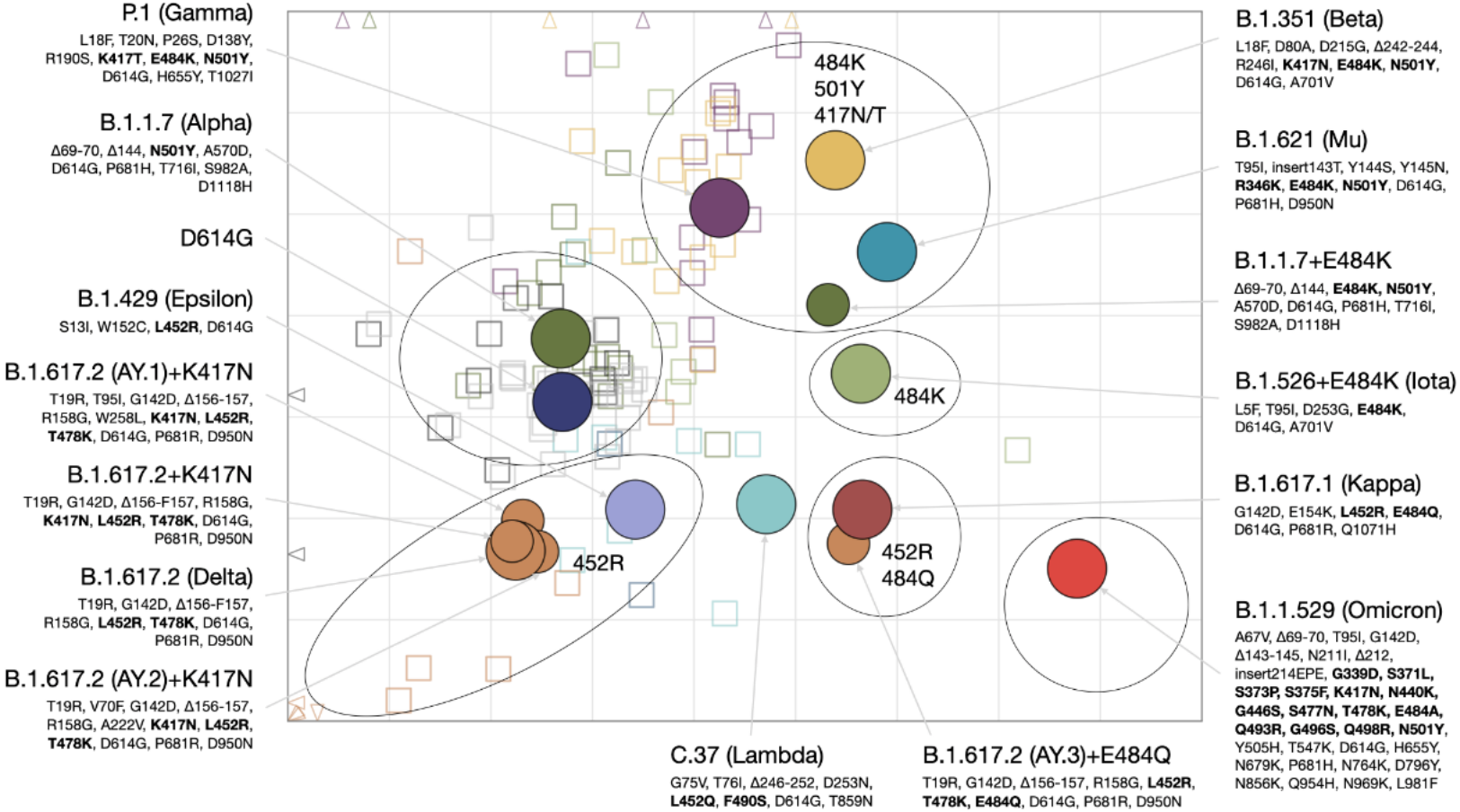
Technique developed to visualize the antigenic drift of influenza A (H3N2)



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



[Pedregosa et al., 2011]



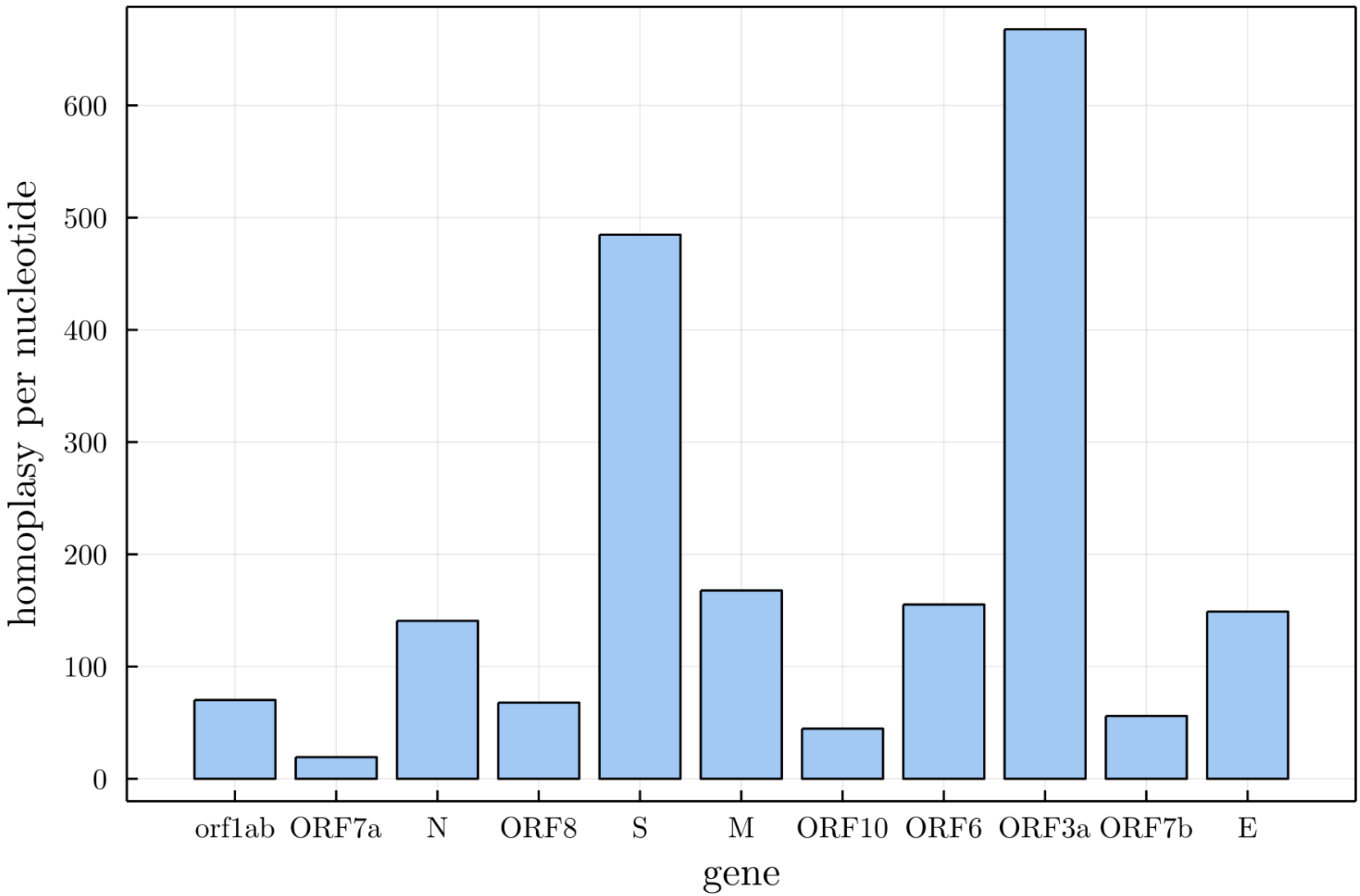
[Wilks et al., 2022]

These results suggest that 2 dimensions might be an adequate approximation to the full space!

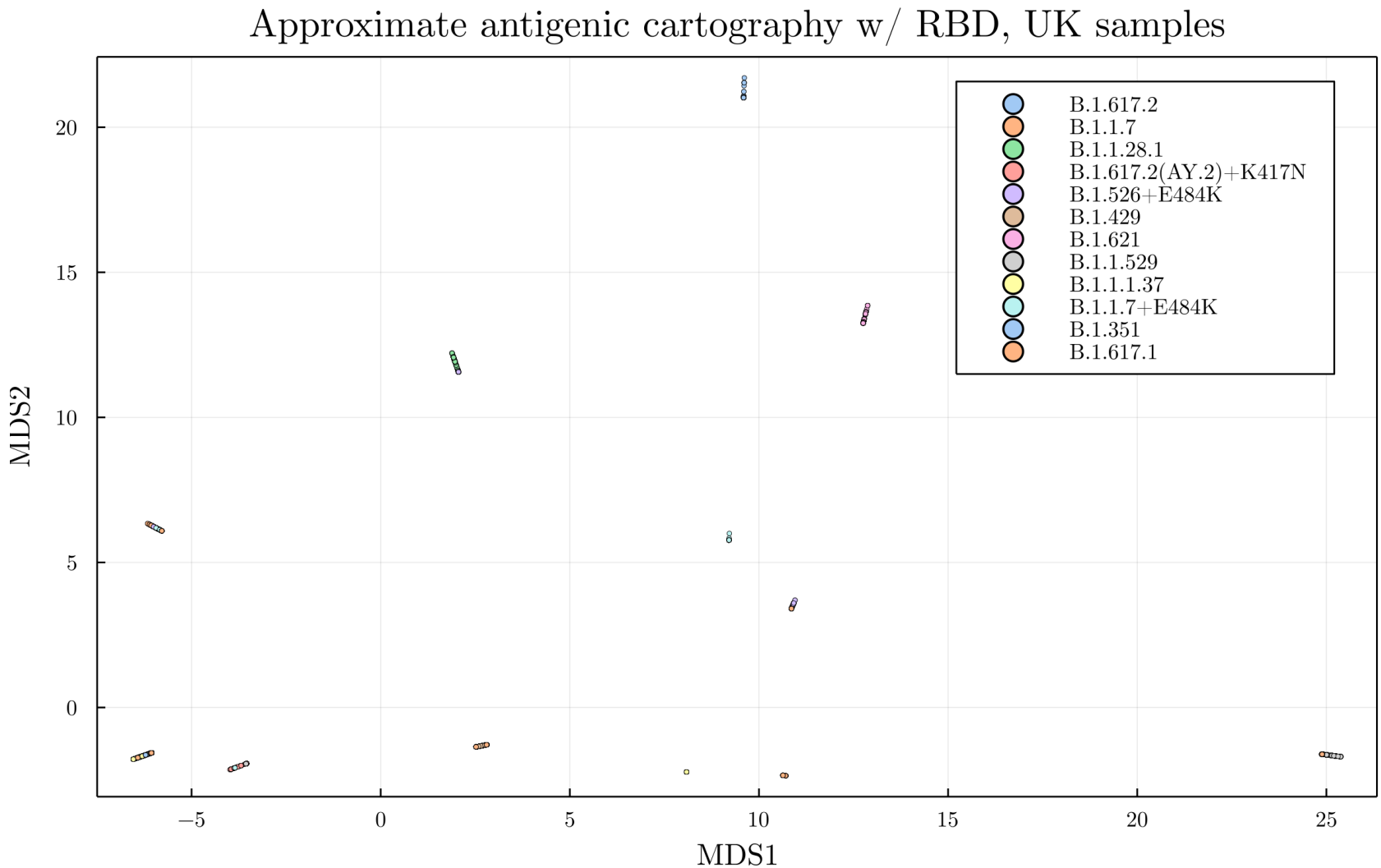
Incorporating more data

- A huge amount of genomic data is available
- Assign each sample to its closest lineage in the map from [Wilks et al., 2022]
- Two methods to further differentiate genomes: homoplasic mutations or antibody binding

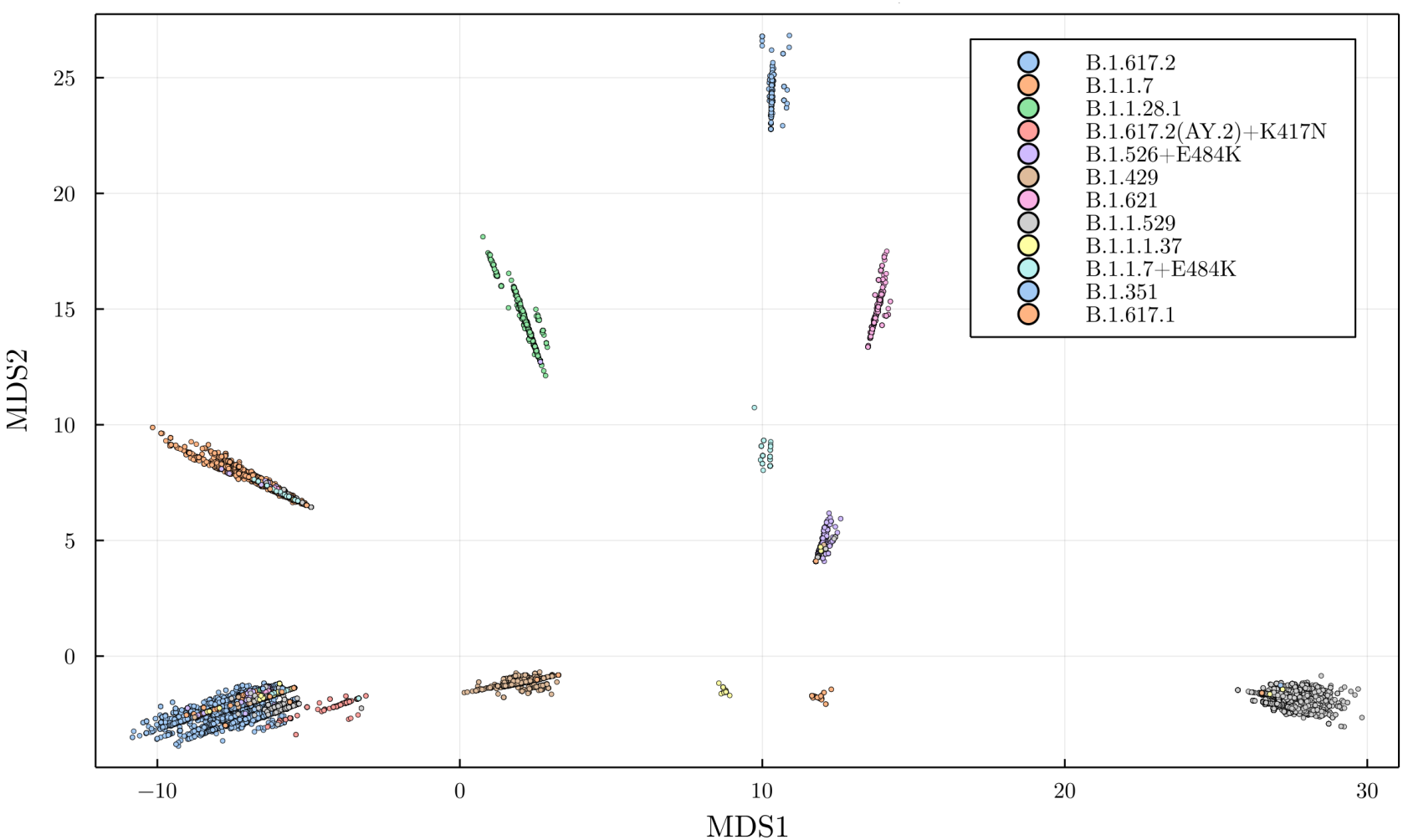
Mutation homoplasy



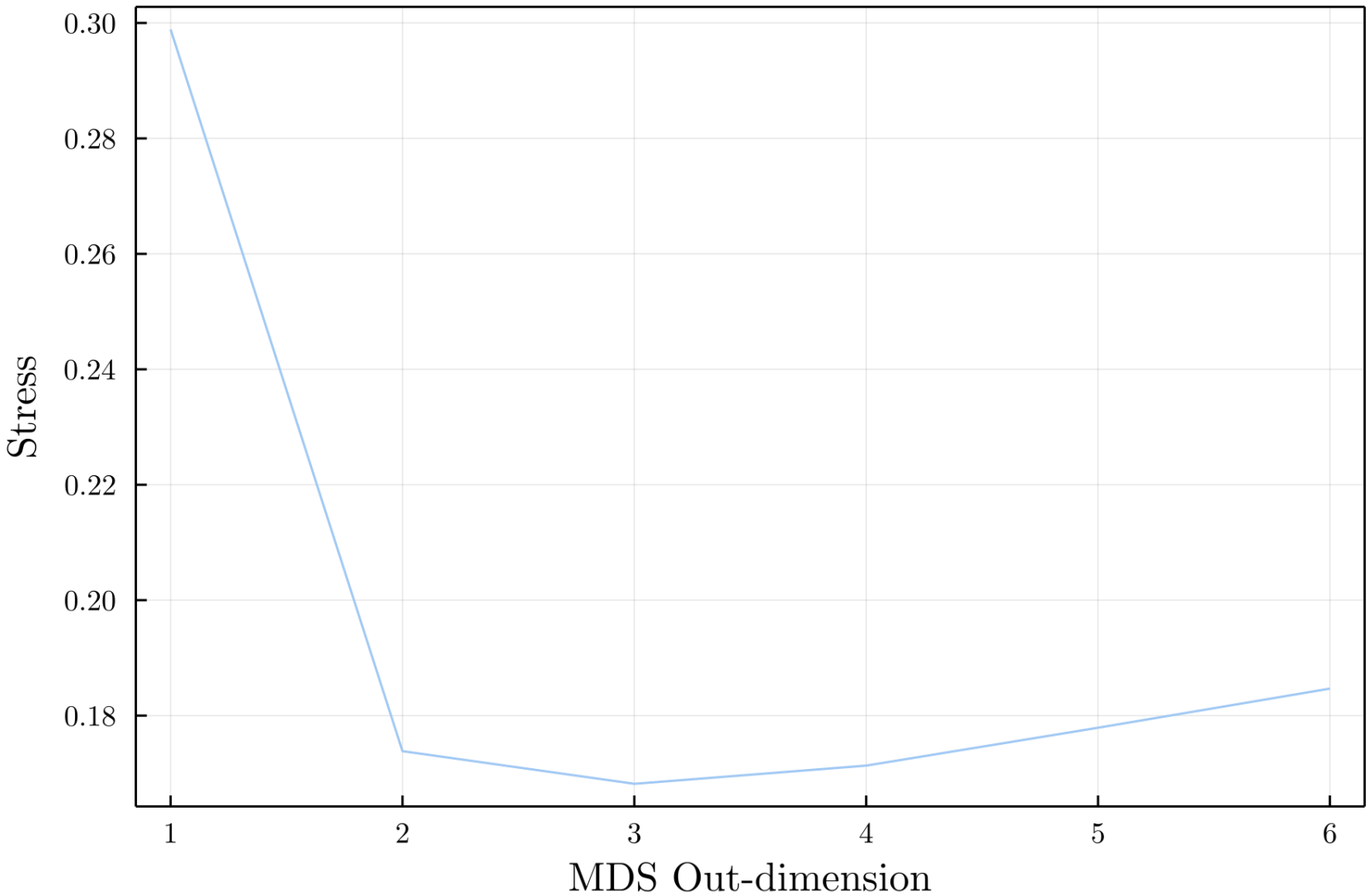
Antibody Binding map



Homoplasic mutations map



Evaluating the MDS approximation



(animation of kernel 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

(gifs of model dynamics)

Further work

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


Gog, J. R. and Grenfell, B. T. (2002).
Dynamics and selection of many-strain pathogens.
Proceedings of the National Academy of Sciences, 99(26):17209–17214.


Lapedes, A. and Farber, R. (2001).
The Geometry of Shape Space: Application to Influenza.
Journal of Theoretical Biology, 212(1):57–69.


Pedregosa, F., Varoquaux, G., Gramfort, A., Michel, V., Thirion, B., Grisel, O., Blondel, M., Prettenhofer, P., Weiss, R., Dubourg, V., Vanderplas, J., Passos, A., Cournapeau, D., Brucher, M., Perrot, M., and Duchesnay, E. (2011).
Scikit-learn: Machine learning in Python.
Journal of Machine Learning Research, 12:2825–2830.

Smith, D. J., Lapedes, A. S., de Jong, J. C., Bestebroer, T. M., Rimmelzwaan, G. F., Osterhaus, A. D. M. E., and Fouchier, R. A. M. (2004).
Mapping the Antigenic and Genetic Evolution of Influenza Virus.
Science, 305(5682):371–376.

Wilks, S. H., Mühlemann, B., Shen, X., Türeli, S., LeGresley, E. B., Netzl, A., Caniza, M. A., Chacaltana-Huarcaya, J. N., Daniell, X., Datto, M. B., Denny, T. N., Drosten, C., Fouchier, R. A. M., Garcia, P. J., Halfmann, P. J., Jassem, A., Jones, T. C., Kawaoka, Y., Krammer, F., McDanal, C., Pajon, R., Simon, V., Stockwell, M., Tang, H., van Bakel, H., Webby, R., Montefiori, D. C., and Smith, D. J. (2022).
Mapping SARS-CoV-2 antigenic relationships and serological responses.
Preprint, Immunology.