The Effect of Influenza Receptor Binding Avidity on Antigenic Drift

Shiny app description

Shiny app details

Author: James Hay Last edited: 03/09/2015 Title: Antigenic Drift Plotter

Description: Dynamically plots the all plots related to the antigenic drift and binding avidity sim-

ulation. The side bar allows all model parameter to be adjusted in real time.

Dependencies: Developed under R 3.2.1; ggplot2; gridExtra; shiny

Use: This is a shiny app. Once the shiny library (and all other dependencies) have been installed, the app can be run in R with the following commands:

library(shiny) runApp()

Note that the working directory must be set to the directory that contains this file.

Model Equations

Probability of Evading Immune System:

$$f(k, V_i) = [1 - e^{-p(V_i + q)}]^{rk - \delta_{ji}}$$
(1)

Probability of Successful Replication Within Host:

$$g(V_i) = e^{-aV_i^b} (2)$$

Probability of Successful Within Host Infection:

$$\phi(H_k, V_i) = f(k, V_i) \cdot g(V) = [1 - e^{-p(V_i + q)}]^{rk - \delta_{ji}} \cdot e^{-aV_i^b}$$
(3)

Within Host Reproductive Number:

$$R_{in} = n \cdot \phi(H_k, V_i) \tag{4}$$

Infectiousness:

$$\rho = 1 - \left(\frac{1}{R_{in}}\right)^{-v} = 1 - \left(\frac{1}{\phi(H_k, V_i)}\right)^{-nv} \tag{5}$$

Transmission Rate:

$$\beta = c \cdot \rho \tag{6}$$

Parameter Descriptions

- 1. p: parameter to control degree by which changes in binding a vidity affect probability of escape from immune response
- 2. r: parameter to control degree by which previous exposure reduce probability of immune escape
- 3. b: parameter to control the shape of the relationship between probability of successful replication and changes in binding avidity
- 4. a: controls rate of changes of relationship between probability of successful replication and change in binding avidity
- 5. c: per day contact rate
- 6. n: number of offspring per virus replication event
- 7. v: number of virions initially transmitted
- 8. q: parameter to control the shape of the relationship between binding avidity and immune escape (shift on the x-axis)
- 9. δ : constant antigenic distance between two viruses