**\*\*Be sure to put these files in the same directory and that that directory is the “working directory” for R, or else you will not be able to source files from one another\*\***

**finding slopes.R**

This file enters the viral load data for each patient and plots them over time. All of the patients are plotted on one graph using ggplot2. Then, the patients that responded to the antibody are used to find the slopes of their viral decay. Exponential decay functions are fit to each responding patient, and the fits and the data are then graphed, displaying the viral decay rates.

**finding ADCC hill slope.R**

This file enters 3 data points (1 at EC50 and 1 on either side of it) from ADCC dose response curves (from Bruel paper) and does a linear fit to find the hill slope for ADCC. This process was given for two different viruses, NLAD8 and NL4.3, because two different dose response curves were shown in the paper.

**fitting Ab curve.R**

This file enters the antibody data for each patient and plots them over time. I then fit a biphasic exponential decay to each set of antibody concentration data and graph the fit and the data. Then I collect the parameters for each patient’s antibody concentration decay and calculate the averages for each parameter.

**getdata SIV.R**

This file does all of the calculations necessary to examine virus and treatment over time. It calculates: antibody concentration, IIP, IAP, fu, fa, susceptible cells, infected cells, virus, and effective reproductive number. The default parameters and antibody potency measurements are the viral parameters from the Stafford paper and in vitro measurements for potency (from various papers, see “Sources” file for more information). These defaults can be changed to see how viral load and other measurements would be affected. This file is not intended to be run on its own, but rather with the client program: “SIV grapher.R”, which sources this file.

**SIV grapher.R**

This file sources “getdata SIV.R” and coordinates the calculations and graphs them. You may customize the time period you are looking at and the time of antibody infusion at the beginning of the file. All data is retrieved from the sourced file and is compiled into a data frame. Various results are then plotted.

**dose response curves.R**

This file plots dose-response curves for neutralization and ADCC given an IC50’s for each mechanism, and hill slopes for each mechanism.

**fit only ADCC.R**

This file first sources the patients’ viral load and antibody concentration data and then runs fitting algorithms (from the package “nloptr”) to fit parameters (alpha, deltas, pi, EC50, and h) to the patients’ data, assuming that ONLY ADCC is operational. Beta and deltai are fixed to .0001 and 1, respectively (this is the only way to create a comparison of antibody potency, because these two parameters are affected by the antibody). S0 and I0 are calculated from the equilibrium equations, using the parameters. C is calculated from the equilibrium equation for V, using pi, V, and I0. The fit is first run using a global optimization algorithm and initial parameter guesses, then using a global optimization algorithm and parameters resulting from the 1st fit, and lastly using a local optimization algorithm and parameters resulting from the 2nd fit.

**fit only NAB.R**

This file first sources the patients’ viral load and antibody concentration data and then runs fitting algorithms (from the package “nloptr”) to fit parameters (alpha, deltas, pi, IC50, and m) to the patients’ data, assuming that ONLY NAB is operational. Beta and deltai are fixed to .0001 and 1, respectively (this is the only way to create a comparison of antibody potency, because these two parameters are affected by the antibody). S0 and I0 are calculated from the equilibrium equations, using the parameters. C is calculated from the equilibrium equation for V, using pi, V, and I0. The fit is first run using a global optimization algorithm and initial parameter guesses, then using a global optimization algorithm and parameters resulting from the 1st fit, and lastly using a local optimization algorithm and parameters resulting from the 2nd fit.

**fit both NAB and ADCC.R**

This file first sources the patients’ viral load and antibody concentration data and then runs fitting algorithms (from the package “nloptr”) to fit parameters (alpha, deltas, pi, IC50, EC50, m, and h) to the patients’ data, assuming that BOTH ADCC AND NAB are operational. Beta and deltai are fixed to .0001 and 1, respectively (this is the only way to create a comparison of antibody potency, because these two parameters are affected by the antibody). S0 and I0 are calculated from the equilibrium equations, using the parameters. C is calculated from the equilibrium equation for V, using pi, V, and I0. The fit is first run using a global optimization algorithm and initial parameter guesses, then using a global optimization algorithm and parameters resulting from the 1st fit, and lastly using a local optimization algorithm and parameters resulting from the 2nd fit.

**plot fits.R**

This file coordinates the 3 fitting files, “fit only ADCC.R”, “fit only NAB.R”, and “fit both NAB and ADCC.R”. It retrieves the final parameter fits (after an initial global fit with guesses, second global fit using parameters from 1st fit, and lastly a local fit using parameters from the 2nd fit) for each patient in each scenario (only ADCC, only NAB, and both NAB and ADCC). The fits and data are plotted.