**Parameters are not consistent within each patient**

New approach to fixing this issue:

Fit viral kinetic parameters (alpha, deltas, beta, deltai, pi, c) to each patient’s rebound data to determine the values. Evaluate which of these viral kinetic parameters can be eliminated from the fitting process (pegged).

Then, using each patient’s individual viral kinetic parameters, use the entire data set to fit to the antibody potency measurements.

Previous idea:

The parameter fits for different scenarios, but for the same patient, yield different viral kinetic parameters. This cannot be true, so we need to find a way to standardize alpha, deltas, pi, c, S0, and I0 across the scenarios for each patient. One way to do this would be to simply use the parameters from the fit in which BOTH mechanisms are at work, and re run all of the fits, ONLY fitting to the antibody parameters. Once all of the other parameters are the same, we can actually compare between scenarios for each patient.

**Figure ideas**

Here are some ideas I had for figures (not necessarily in this order):

1. Raw patient viral load data
2. Model schema
3. Viral load during therapeutic VRC01 treatment simulation with IN VITRO measurements
4. Simulations with different VRC01 mechanisms (NAB, ADCC, & both)
5. Panel of fits to patients’ viral decay rates
6. Panel of fits to patients’ antibody decay rates
7. Panel of each patient’s viral load, with three fits shown: ADCC, NAB, and both
8. 3 plots of each parameter (1 for ADCC, 1 for NAB, and 1 for both) showing all of the patients’ values for the given parameter
9. Table with patients’ parameter values
10. Effective reproductive number using average patient potency results for 3 different scenarios
11. Sensitivity analysis for parameters

**Improving the model**

A couple of things to consider adding to the model:

1. Stochasticity
2. Escape mutations

**Data to get**

We should get patient viral load and antibody concentration data from the Lynch paper. Also, the dose-response ADCC data from the Bruel paper would be useful to more accurately calculate an in vitro hill slope for ADCC.