

Summary

Each viral property, e.g. IFN α 2 IC₅₀ or Env/RT ratios, was modeled using a Bayesian hierarchical model. The model is based on a linear regression estimating the differences between donor plasma viruses and viruses from donor genital fluid or recipient viruses along with the effects of clade and IFN α 2- and IFN β -selection. Unlike a normal linear regression, this model allows accounting for 1) nested measurements within transmission pairs, 2) multiple transmissions from a single donor, 3) heteroscedasticity among virus populations, 4) censored data where we only know that a measurement is less than a given value.

These hierarchical models are based on the assumption that observations within a single patient-fluid-treatment are independent and identically normally distributed with mean and variance drawn from common population-level distributions. Estimates of the population-level distributions can then be used to infer broader patterns in the data.

Methods

Data was first transformed as follows:

Variable	Transformation
Env/RT	log
Infectivity	log
Replicative capacity	log
IFN α 2 IC ₅₀	log
IFN β IC ₅₀	log
IFN α 2 Vres (pg/ml)	logit
IFN β Vres (pg/ml)	logit
p24 release with IFN α 2	logit
p24 release without IFN α 2	logit
Autologous IC ₅₀	log
Bnaber IC ₅₀	log

The i^{th} observation for each donor-recipient pair was then modeled as a normal distribution $N(\mu_i, \sigma_i^2)$ with mean μ_i :

$$\begin{aligned}
\mu_i = & \text{donor}_{\text{pair}_i} + \beta_{\text{recipient}, \text{pair}_i} \mathbb{1}(\text{recipient}_i) + \beta_{\text{genital}, \text{pair}_i} \mathbb{1}(\text{genital}_i) \\
& + \beta_{\text{clade}, \text{pair}_i} \mathbb{1}(\text{cladeB}_i) \mathbb{1}(\text{recipient}_i) + \beta_{\text{donorAlpha}, \text{pair}_i} \mathbb{1}(\text{donor}_i \& \text{alphaSelect}_i) \\
& + \beta_{\text{donorBeta}, \text{pair}_i} \mathbb{1}(\text{donor}_i \& \text{betaSelect}_i) + \beta_{\text{recipientAlpha}, \text{pair}_i} \mathbb{1}(\text{recipient}_i \& \text{alphaSelect}_i) \\
& + \beta_{\text{recipientBeta}, \text{pair}_i} \mathbb{1}(\text{recipient}_i \& \text{betaSelect}_i)
\end{aligned}$$

and variance σ_i^2 :

$$\sigma_i^2 = \begin{cases} \sigma_{\text{genital,pair}_i}^2 & \text{if genital}_i \\ \sigma_{\text{recipient,pair}_i}^2 & \text{if recipient}_i \\ \sigma_{\text{donorAlpha,pair}_i}^2 & \text{if donor}_i \& \text{alphaSelect}_i \\ \sigma_{\text{donorBeta,pair}_i}^2 & \text{if donor}_i \& \text{betaSelect}_i \\ \sigma_{\text{donor,pair}_i}^2 & \text{otherwise} \end{cases}$$

where pair_i indicates the pair identity of the i^{th} observation, donor_j is the estimated mean of untreated donor plasma viral isolates from pair j , $\mathbb{1}()$ is an indicator function that is 1 if True and 0 if False. The β are coefficients modeling the change expected for viruses in recipients, in donor genital samples, in recipients from HIV clade B and the effects of IFN α 2- or IFN β -selection on donor and recipient viruses. So for example, a donor plasma virus i from pair 2 would have mean $\mu_i = \text{donor}_2$ and an IFN α 2-selected recipient virus from pair 3 (which happened to be clade B) would have mean:

$$\mu_i = \text{donor}_3 + \beta_{\text{recipient},3} + \beta_{\text{clade},3} + \beta_{\text{recipientAlpha},3}$$

For a trio where one donor transmitted viruses to two separate recipients, recipient parameters were estimated independently for each recipient.

In Autologous and Bnaber IC₅₀, observations less than equal to 20 were censored at 20 (the maximum amount of plasma tolerated by the cells). To model this, the probability of these observations was considered to be:

$$p(\text{IC}_{50} = 20) = \int_{-\infty}^{\log(20)} N(\mu_i, \sigma_i^2)$$

Vres measurements were calculated as the amount of p24 released under maximum IFN dose divided by the released p24 without IFN as measured by ELISA. The limit of detection on these measurement was 0.1 so concentrations ≤ 0.1 were measured as 0.1. To account for this, the probability of these observations was considered to be:

$$p\left(\text{Vres} = \frac{0.1}{\text{Untreated p24}}\right) = \int_{-\infty}^{\log\left(\frac{0.1}{\text{Untreated p24}}\right)} N(\mu_i, \sigma_i^2)$$

The coefficients β for each pair j come from population-level normal hyperpriors:

$$\begin{aligned}
\text{donor}_j &\sim N(\mu_{\text{donor}}, \sigma_{\text{donor}}^2) \\
\beta_{\text{recipient},j} &\sim N(\mu_{\text{recipient}}, \sigma_{\text{recipient}}^2) \\
\beta_{\text{genital},j} &\sim N(\mu_{\text{genital}}, \sigma_{\text{genital}}^2) \\
\beta_{\text{clade},j} &\sim N(\mu_{\text{clade}}, \sigma_{\text{clade}}^2) \\
\beta_{\text{donorAlpha},j} &\sim N(\mu_{\text{donorAlpha}}, \sigma_{\text{donorAlpha}}^2) \\
\beta_{\text{donorBeta},j} &\sim N(\mu_{\text{donorBeta}}, \sigma_{\text{donorBeta}}^2) \\
\beta_{\text{recipientAlpha},j} &\sim N(\mu_{\text{recipientAlpha}}, \sigma_{\text{recipientAlpha}}^2) \\
\beta_{\text{recipientBeta},j} &\sim N(\mu_{\text{recipientBeta}}, \sigma_{\text{recipientBeta}}^2)
\end{aligned}$$

and coefficients σ from population-level normal hyperpriors:

$$\begin{aligned}
\sigma_{\text{donor},j} &\sim N(\theta_{\text{donor}}, \phi_{\text{donor}}^2) \\
\sigma_{\text{donorAlpha},j} &\sim N(\theta_{\text{donorAlpha}}, \phi_{\text{donorAlpha}}^2) \\
\sigma_{\text{donorBeta},j} &\sim N(\theta_{\text{donorBeta}}, \phi_{\text{donorBeta}}^2) \\
\sigma_{\text{recipient},j} &\sim N(\theta_{\text{recipient}}, \phi_{\text{recipient}}^2) \\
\sigma_{\text{genital},j} &\sim N(\theta_{\text{genital}}, \phi_{\text{genital}}^2)
\end{aligned}$$

The effect hyperparameters $\mu_{\text{recipient}}, \mu_{\text{genital}}, \mu_{\text{clade}}, \mu_{\text{donorAlpha}}, \mu_{\text{donorBeta}}, \mu_{\text{recipientAlpha}}$ and $\mu_{\text{recipientBeta}}$ were all given a flat prior probability. The variance parameters $\sigma_{\text{donor}}, \sigma_{\text{recipient}}, \sigma_{\text{genital}}, \sigma_{\text{clade}}, \sigma_{\text{donorAlpha}}, \sigma_{\text{donorBeta}}, \sigma_{\text{recipientAlpha}}, \sigma_{\text{recipientBeta}}, \phi_{\text{donor}}, \phi_{\text{donorAlpha}}, \phi_{\text{donorBeta}}, \phi_{\text{recipient}}, \phi_{\text{genital}}, \theta_{\text{donor}}, \theta_{\text{donorAlpha}}, \theta_{\text{donorBeta}}, \theta_{\text{recipient}}$ and θ_{genital} were given a prior of Gamma(1,2) reflecting prior knowledge that the standard deviation in these assays was unlikely to be greater than several logs.

Plots and statistics are based on the estimated posterior probabilities of the population-level effects $\mu_{\text{recipient}}, \mu_{\text{genital}}, \mu_{\text{clade}}, \mu_{\text{donorAlpha}}, \mu_{\text{donorBeta}}, \mu_{\text{recipientAlpha}}$ and $\mu_{\text{recipientBeta}}$.

Markov Chain Monte Carlo sampling of the posterior probability distributions of the models was implemented in Stan using the R package `rstan` and run in 50 chains with each having a 50,000 iteration burnin and 50,000 iterations of sampling every 25th iteration. Code is available at:

<https://github.com/sherrillmix/hivPair/blob/master/bayesIC50.R>.

Comparison