## Appendix: Estimating Mean Stage Residency Times and Dropout Probabilities

The queueing model of the continuum of care requires estimating two quantities for each stage: the mean residency time (denoted by *E*(*T*)) and the dropout probability (denoted by *p*). Letting subscript *i* denote stage *i*, the expected number of individuals in stage *i*, *E*(*X*i), is given by

where  is the aggregate rate of new HIV infections, believed to equal roughly 50,000 per year.1

Data from the CDC report residency times until progression to the next treatment stage or censoring for the diagnosed HIV+, linked to care, and retained in care stages as defined in the main paper. Censoring occurs to the end of data recording, and reflects two possibilities: either an individual truly remains in the treatment stage in question and has simply not yet progressed as of the end of the study, or an individual previously dropped out of the treatment cascade (or will in the future). To model these events for a given treatment stage, let *Y* denote the latent time from stage entry until progression to the next treatment stage, and *Z* denote the latent time from stage entry until dropout. The mean stage residency time is then given by

while the dropout probability is given by Pr{*Y* > *Z*}, that is, individuals dropout of the cascade if their latent time to progression exceeds their latent time to dropout. We assume that the latent variables *Y* and *Z* are statistically independent.

Suppose that an individual who enters a cascade stage at time 0 is observed to progress to the next treatment stage between times *t – 1* and *t* where time is measured in months (the CDC data discretize residency times to one month intervals). The probability of observing this event is given by

where *fY*(*u*) and *SZ*(*u*) = Pr{*Z* > *u*} are the probability density function of the latent progression time *Y* and the survivor function of the latent time to dropout *Z*. Alternatively, suppose that an individual is censored at the end of time *t* from stage entry. As censoring could be due to dropout at any time between 0 and *t*, or to progression or dropout that will occur beyond time *t*, the probability of observing a censoring event is given by

where *fZ*(*u*) and *SY*(*u*) = Pr{*Y* > *u*} are the probability density function of the latent time to dropout *Z* and the survivor function of the latent progression time *Y*. The CDC data provide, for each stage, the numbers of individuals *nt* and *ct* who were observed to have progressed between times *t – 1* and *t* or were censored at time *t*, respectively (again time is measured in months). The overall log-likelihood function for these data is therefore given by

where  is the censoring date.

To proceed further requires specific models for the probability distributions of the latent random times to progression *Y* and dropout *Z*. As stated in the main text, two models were pursued, an exponential model and a Weibull model. We utilized a Weibull model because it is a flexible model that allows for constant, increasing or decreasing hazards as revealed by the data (which also explains why the Weibull is commonly used in survival analysis). We also examined exponential and hyper-exponential survival distributions in the course of this research, but the Weibull was a better fit to the data in each case. The queueing model requires estimates of the mean time spent in each stage, not the entire distribution of waiting time. Given that the observable data requires a rather complex likelihood function due to the impossibility of exactly determining the timing of dropout, and given that a fully nonparametric formulation would not allow estimation of mean stage times due to data censoring, we settled on the Weibull as the best approach for our purposes. We did address goodness-of-fit indirectly by showing that in all cases, the Weibull provides a closer fit to the data than the simpler exponential model.

The exponential model specifies that *Y* and *Z* follow independent exponential distributions with rates  and  respectively, thus for the exponential model:

Substituting these expressions into the formulas for and enables evaluation of the overall log-likelihood log to estimate the parameters  and . Maximum likelihood estimates were obtained by maximizing the resulting log-likelihood with respect to the parameters  and using the Excel Solver, while standard errors were obtained via the delta method.15 Under the exponential model, the mean residency time is given by

while the dropout probability is given by

These formulas were used to produce the estimates corresponding to the exponential model in Table 1 in the main text.

The Weibull model specifies that *Y* and *Z* follow independent Weibull distributions with proportional hazards. The required density and survivor distributions are given by:

Maximum likelihood estimates were obtained by maximizing the resulting log-likelihood with respect to the parameters , and , while standard errors were obtained via the delta method.15 Under the Weibull model, the mean residency time is given by

while the dropout probability is given by

These formulas were used to produce the estimates corresponding to the Weibull model in Table 1 in the main text.

For the final stage in the continuum, viral suppression, data were obtained from NA-ACCORD describing the time from initial viral suppression until detectable viral load or censoring. As the only stage parameter required to estimate the expected number of individuals virally suppressed is the mean residency time, we directly estimated this for the exponential and Weibull models by setting  (for the exponential model) and (for the Weibull model) equal to zero.

**Table S1.** Estimated Expected Stage Occupancy Times and Dropout Fractions in the HIV Continuum of Care

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Model** | | **Chi-square** |
| **Stage** | ***Exponential*** | ***Weibull*** |
| Diagnosed (before 1st CD4/VL test) |  |  |  |
| ***Mean Time in Stage in months*** | 3.1 | 3.1 |  |
| *95% Confidence Interval* | 3.11-3.15 | 2.98-3.24 |  |
| ***Dropout Fraction*** | 0.083 | 0.079 |  |
| *95% Confidence Interval* | 0.067-0.098 | 0.074-0.083 |  |
| *Log Likelihoods* | -31077 | -27267 | 7620 |
|  |  |  |  |
| Linked to Care (before 2nd CD4/VL test) |  |  |  |
| ***Mean Time in Stage in months*** | 3.7 | 3.6 |  |
| *95% Confidence Interval* | 3.58-3.72 | 3.55-3.73 |  |
| ***Dropout Fraction*** | 0.058 | 0.056 |  |
| *95% Confidence Interval* | 0.054-0.062 | 0.052-0.060 |  |
| *Log Likelihoods* | -29635 | -28857 | 1556 |
|  |  |  |  |
| Engaged in Care (before undetectable VL test) | |  |  |
| ***Mean Time in Stage in months*** | 9.1 | 14.6 |  |
| *95% Confidence Interval* | 8.91-9.35 | 13.32-15.86 |  |
| ***Dropout Fraction*** | 0.17 | 0.094 |  |
| *95% Confidence Interval* | 0.16-0.18 | 0.078-0.11 |  |
| *Log Likelihoods* | -33747 | -33078 | 1340 |
|  |  |  |  |
| VL Suppressed to Unsuppressed (length of viral suppression) | |  |  |
| ***Mean Time in Stage in months*** | 71.5 | 36.6 |  |
| *95% Confidence Interval* | 68.44-74.61 | 35.58-37.57 |  |
| *Log Likelihoods* | -11346 | -10733 | 1228 |