

Viral load criteria and threshold optimization to improve HIV incidence assay characteristics

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Objective: Assays for classifying HIV infections as ‘recent’ or ‘nonrecent’ for incidence surveillance fail to simultaneously achieve large mean durations of ‘recent’ infection (MDRIs) and low ‘false-recent’ rates (FRRs), particularly in virally suppressed persons. The potential for optimizing recent infection testing algorithms (RITAs), by introducing viral load criteria and tuning thresholds used to dichotomize quantitative measures, is explored.

Design: The Consortium for the Evaluation and Performance of HIV Incidence Assays characterized over 2000 possible RITAs constructed from seven assays (Limiting Antigen, BED, Less-sensitive Vitros, Vitros Avidity, BioRad Avidity, Architect Avidity, and Geenius) applied to 2500 diverse specimens.

Methods: MDRIs were estimated using regression, and FRRs as observed ‘recent’ proportions, in various specimen sets. Context-specific FRRs were estimated for hypothetical scenarios. FRRs were made directly comparable by constructing RITAs with the same MDRI through the tuning of thresholds. RITA utility was summarized by the precision of incidence estimation.

Results: All assays produce high FRRs among treated patients and elite controllers (10–80%). Viral load testing reduces FRRs, but diminishes MDRIs. Context-specific FRRs vary substantially by scenario – BioRad Avidity and Limiting Antigen provided the lowest FRRs and highest incidence precision in scenarios considered.

Conclusion: The introduction of a low viral load threshold provides crucial improvements in RITAs. However, it does not eliminate nonzero FRRs, and MDRIs must be consistently estimated. The tuning of thresholds is essential for comparing and optimizing the use of assays. The translation of directly measured FRRs into context-specific FRRs critically affects their magnitudes and our understanding of the utility of assays.

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Introduction

The reliable measurement of HIV incidence is essential for monitoring the epidemic, and targeting and assessing interventions. However, traditional methods for estimating incidence often require cumbersome and costly longitudinal studies or multiple studies over time, or they rely on highly uncertain model inputs. Consequently, over the last 20 years, there has been much discourse on the estimation of HIV incidence from a single cross-sectional survey and a few well estimable parameters [1–13]. This has been made possible by the advent of *incidence assays*, or, more generally, potentially complex multicomponent *recent infection testing algorithms* (RITAs), which are used to classify the HIV infections detected in the incidence survey as ‘recently’ or ‘nonrecently’ acquired.

In 2011, inconsistent methodologies led to the establishment of an independent body: the Consortium for the Evaluation and Performance of HIV Incidence Assays (CEPHIA), funded by the Bill & Melinda Gates Foundation, was tasked to coordinate efforts and conduct independent evaluations of RITAs [14]. Recent work by CEPHIA [12] indicates that currently prominent incidence assays, applied according to developers’ previously published guidelines, fail to meet the requirements outlined in a widely referenced Target Product Profile [10,15]. The Target Product Profile calls simultaneously for a sufficiently enduring state of ‘recent infection’ – averaging more than 6 months – and low probability of (false) ‘recent’ results at large times post infection – ideally zero, but definitely below 2% [16,17]. The analyses showed that the assays produced extremely high false-recent rates (10–80%) in virally suppressed antiretroviral-treated patients and elite controllers [12]. These findings led to questions about the potential for optimizing the design of RITAs that utilize these immunoassays, including through the introduction of viral load criteria, as investigated in this work.

Results are provided below for the five incidence immunoassays previously described [12] – namely, Limiting Antigen (LAG) [18,19], BED [20,21], Detuned or Less-sensitive Vitros [22], Vitros Avidity [22], and BioRad Avidity [23] – as well as the two immunoassays that have subsequently completed a full CEPHIA evaluation – Architect Avidity [24,25] and Geenius [26,27].

In this analysis, each RITA utilizes a single incidence immunoassay and, potentially, a viral load measure. As before, an immunoassay measurement *below* some chosen immunoassay threshold is interpreted as indicative of ‘recent’ infection, although this threshold is now allowed

to vary. If supplemental viral load testing is included, the viral load measurement must *additionally* be *above* the chosen viral load threshold to confirm the ‘recent’ result (which is otherwise changed to ‘nonrecent’).

Two test characteristics are required to translate the incidence survey data, namely counts of HIV-negative, ‘recently’ infected HIV-positive and ‘nonrecently’ infected HIV-positive patients, into incidence estimates [11]:

- The Mean Duration of ‘Recent’ Infection (MDRI) is the average time spent ‘recently’ infected within some time T after infection.
- The False-Recent Rate (FRR) is the context-specific probability that an individual who is infected for longer than T will produce a ‘recent’ result.

Increasing the postinfection time cutoff T , which allows for consistent definitions of the MDRI and FRR, will generally appear to improve test performance – by increasing the MDRI and typically decreasing the FRR. However, a large T presents a number of limitations, including that the measured incidence represents an incidence averaged far into the past, and the MDRI becomes difficult to estimate and prone to varying by time and place [11].

In this analysis, the test characteristics of the RITAs are estimated for each of a number of subpopulations. Different RITAs are constructed by varying the immunoassay thresholds and viral load thresholds, and considering a few values for the cutoff T . For a RITA to be of utility for incidence estimation, its MDRI should be large and FRR small, preferably zero [10,15–17]. To illustrate the context dependence of the FRR, demonstrative FRRs are calculated in hypothetical scenarios. A balanced comparison of the assays’ FRRs is obtained by selecting immunoassay thresholds so that all RITAs produce a similar MDRI.

Summary figures and tables of data and results are provided below, and a more exhaustive collection of analysis outputs is provided in Supplemental Digital Content 1 and 2 (SDC 1, <http://links.lww.com/QAD/A957> and SDC 2, <http://links.lww.com/QAD/A958>).

Methods

The specimen set

The CEPHIA specimen repository, previously described [12], currently includes over 25 000 HIV-1 positive

specimens (about 12 000 of which are plasma) drawn from approximately 3000 well characterized patients. In this work, RITAs were assessed using a carefully selected subset of 2500 plasma specimens, termed the 'Evaluation Panel'. In this panel, each of 928 patients contribute one to 13 specimens drawn at different times after infection, and patients are from the USA (52%), Zambia (20%), Rwanda (11%), Uganda (8%), Brazil (3%), South Africa (3%), and Kenya (3%). Viral load data was provided by the contributing studies for 1995 of the specimens.

Laboratory procedures

All incidence immunoassays were applied independently in CEPHIA laboratories (at Blood Systems Research Institute, San Francisco and Public Health England, London) using standard operating procedures. The laboratory technicians were trained by the developers and blinded to the specimen background information, and controls were tested regularly to ensure stability of the assays and procedures. Testing protocols are available on the CEPHIA website [14].

Five assays have been previously summarized [12]: LAG aims to describe the avidity of HIV antibodies through a normalized optical density (ODn) [18,19]; BED captures the relative amount of immunoglobulin G that is specific to HIV, also as an ODn [20,21]; less-sensitive Vitros quantifies the level of HIV antibodies as a signal-to-cutoff value [22]; and Vitros Avidity [22] and BioRad Avidity [23] each measure antibody avidity as an avidity index, reported as a percentage.

The Architect Avidity and Geenius assays, which have not been described in previous CEPHIA reports, are summarized below.

Architect Avidity is based on a modification of the ARCHITECT HIV Ag/Ab Combo assay (Abbott Diagnostics, Wiesbaden, Germany) [24,25], which is a chemiluminescent microparticle immunoassay for the detection of p24 antigens and HIV-1/2 antibodies. Each specimen is tested in the presence and absence of a chaotropic agent (guanidine), and the ratio of the reactivity (treated to untreated) produces an avidity index, with measurements below 80% conventionally interpreted as representing 'recent' infection.

The Geenius HIV 1/2 Supplemental Assay (Bio-Rad Laboratories, Inc., Hercules, California, USA) is an immunochromatographic assay in the form of a rapid test [26,27]. The amount of HIV antibody that is specific to each of a number of antigens – namely gp36 and gp140 for HIV-2; and p31, gp160, p24, and gp41 for HIV-1 – is reported as a band intensity. For 'recent' infection testing, the developer proposes the use of a single summary quantitative measure, equal to the sum of the intensities for p31, gp160 and gp41, divided by the intensity for the control line. Referred to as the Geenius Index, Geenius

Index values below 1.5 are then interpreted as indicating 'recent' infection.

Tunable recent infection testing algorithms parameters

In this analysis, a RITA consists of a single incidence immunoassay and a viral load measure: 'recent' infection is identified by both the immunoassay measurement being *below* the (tunable) immunoassay threshold *and* the viral load measurement being *above* the (tunable) viral load threshold (effectively set to 0 in the case of no viral load criteria).

Each RITA is defined by specifying which of the seven incidence immunoassays is used and selecting values for the three tunable parameters – the immunoassay threshold, viral load threshold, and time cutoff T . As the cutoff T is not viewed as a parameter that would be finely tuned in practice, values of 1, 2 and 3 years were considered. For each immunoassay, a large number of immunoassay thresholds were investigated, and viral load thresholds of 0, 75, 250, 400, 1000 and 2000 copies/ml were used, allowing MDRI estimates to range from about a month to one and a half years and accommodating the varying limits of detection on viral load assays that may be used in practice.

Data analysis: data preparation

CEPHIA repository and assay results data are stored in a MySQL relational database, and the analysis was performed in Matlab (R2014b, the MathWork Inc., Natick, Massachusetts, USA).

In this analysis, a patient is considered to be 'detectably infected' if testing positive on an HIV viral lysate-based western blot assay. For each of the 56% of patients with sufficient data (521 patients), the patient's testing history was used to obtain the estimated (earliest) date of detectable infection (EDDI). These patients had recorded dates of last HIV-negative and first HIV-positive diagnoses, at most 120 days apart, together with data on the types of diagnostic tests used. The EDDI was obtained using published delays between earliest detections of HIV by different diagnostic tests [28,29]. A total of 5% of these patients also have recorded acute retroviral syndrome onset dates, which were instead used to obtain the EDDIs (refer to Methods in [12]). Field application requires adjustment of test characteristic estimates, most notably the MDRI estimates, according to the specific diagnostic protocol used (in this analysis, a western blot assay is considered to be used).

Data analysis: estimation of mean durations of 'recent' infection and false-recent rates in subpopulations

The test characteristics were evaluated in each of a number of subpopulations – created by stratifying by treatment history, subtype (based on country when not

assay-confirmed), time since infection, viral load, and CD4⁺ T-cell count. The Study of the Consequences of the Protease Inhibitor Era (SCOPE) [30], which contributed specimens to the Evaluation Panel, purposefully recruited patients who are virally suppressed in the absence of treatment, and these elite controllers were analysed separately.

The MDRI was estimated by fitting a binomial regression model to the probability of testing 'recent', accounting for the patient-level clustering of data in the bootstrap construction of the 95% confidence intervals [12]. In addition to the primary parametric form of the model, two alternative forms were also fitted by way of a sensitivity analysis. In the primary analysis, all data points beyond $(1 + 1/12) \times T$ after infection were discarded before model fitting, although a data exclusion cutoff of $2 \times T$ was also considered in the sensitivity analysis.

A proxy FRR was estimated as the proportion of patients infected for longer than T who test 'recent', using the majority classification for patients with multiple results, and reporting Clopper-Pearson 95% confidence intervals.

Data analysis: context-specific false-recent rates and recent infection testing algorithm performance

The FRRs estimated directly from the repository specimens do not represent any particular population-level FRR, which would depend in detail on the population's demographic and epidemiological history. To illustrate this context dependence, FRRs were estimated for some demonstrative hypothetical scenarios, as outlined in detail in SDC 1, <http://links.lww.com/QAD/A957>. Furthermore, to allow for a fair comparison of the different assays within a scenario, immunoassay thresholds were chosen so that the MDRI estimates for all RITAs were equal to some chosen value and then the corresponding context-dependent FRRs calculated. In a chosen scenario, for any specific MDRI value, the incidence assay with the lowest FRR provides the best RITA.

Such an analysis falls short of indicating which assay and immunoassay threshold is optimal – where one could naturally define optimal as providing the most precise incidence estimation [16,17]. Such an optimization warrants extensive additional analysis; in this work, the utility and potential of the RITAs are reported as the precision of the incidence estimator in chosen scenarios.

In summary of the methodology, scenarios were defined by specifying: the percentage of the long-infected population on treatment, termed the treatment coverage, c ; the average time, in years, since infection in the untreated long-infected population at the time of the survey, m ; and the viral load threshold used in the RITA (the time cutoff T equals 2 years). For each scenario, for

each of the seven incidence assays, for each chosen MDRI value (ranging from 50 to 400 days, and obtained by appropriately selecting the immunoassay threshold): a context-specific FRR was then calculated as a weighted average of the FRR among treated patients (measured directly from the CEPHIA specimens) and FRR among untreated patients (estimated by combining CEPHIA data with the times since infection existing in the hypothetical population) – see SDC 1, <http://links.lww.com/QAD/A957> for further details.

The context-specific precision of the incidence estimator was then calculated, assuming exactly known RITA characteristics, an incidence survey size of 4000 patients, and specifying HIV incidence and prevalence values for the scenarios. The precision of the incidence estimator was calculated using the Delta method, shown to be highly accurate for this application in [11]. The precision is reported as two metrics: the relative standard error (RSE) of the incidence estimator; and the probability of obtaining an incidence estimate that lies within 0.5%, in absolute terms, of the true incidence. Lower RSEs and higher probabilities represent more reliable incidence estimation.

Owing to the relatively simple scenario constructions (see SDC 1, <http://links.lww.com/QAD/A957>), uncertainties around estimates have not been formally quantified, and results should not be over interpreted. The scenarios, inspired by knowledge of real-world settings, are described alongside the results below.

Results

The data for Architect Avidity and Geenius are presented in Fig. 1; 40 and 53%, respectively, of the specimens drawn within 6 months of infection are already 'nonrecent', suggesting more transient states of 'recent' infection compared with the five previously reported assays [12] (at published immunoassay thresholds). Treated patients and SCOPE elite controllers again notably contribute 'false-recent' results.

Tables 1 and 2 provide estimated test characteristics for each assay, for selected subpopulations and a few demonstrative values of the tunable RITA parameters. Results for all values of tunable parameters and subpopulations considered, as well as the MDRI sensitivity analyses, are provided in SDC 2, <http://links.lww.com/QAD/A958>.

For $T=2$ years, the MDRI estimates reduce by 3–11% when introducing a viral load threshold of 75 copies/ml, and by 13–35% for a viral load threshold of 1000 copies/ml. However, FRR estimates for the 'nonchallenge' subpopulation are barely impacted by the introduction of any viral load criteria. By repository design, the

‘challenge’ specimens from treated patients and elite controllers have undetectable, rather than just low, viral loads, and therefore there is a dramatic drop in FRRs to zero using a viral load threshold of 75 copies/ml. These MDRI and FRR results together suggest that the optimal viral load threshold is one that is very low, as the primary reduction in the FRR is already seen, and any further increases in the threshold simply diminish the MDRI.

When considering the postinfection time cutoff T , the ‘nonchallenge’ FRR estimates decrease substantially moving from 1 to 2 years, with marginal benefit obtained from further increases in T . The remainder of the analysis and interpretation considers a cutoff T of 2 years, as proposed in earlier CEPHIA reports [12].

The results in Tables 1 and 2 highlight how differently the developer immunoassay thresholds have been selected, in terms of the resulting test characteristics. For example, the MDRI and ‘nonchallenge’ FRR estimates for Architect Avidity are 122 days and 1.5%, respectively, whereas they are much larger for Less-sensitive Vitros at 288 days and 12.4%, respectively (for a viral load threshold of 75 copies/ml) – leading to seemingly very differently behaving incidence assays. However, by increasing the Architect Avidity immunoassay threshold and/or decreasing the Less-sensitive Vitros threshold appropriately, one can obtain almost identical test characteristics for the two assays (see SDC 2, <http://links.lww.com/QAD/A958>).

Figure 2 shows rough context-specific FRR estimates, as a function of the MDRI (encoding immunoassay threshold), for hypothetical Scenarios a–f. Additional scenarios are presented in SDC 1, <http://links.lww.com/QAD/A957>. The assays performing the best, that is, providing the lowest lines, vary by scenario and even MDRI value.

Scenarios a and b, in which there is neither treatment nor viral load criteria, illustrate how the ‘nonchallenge’ FRR estimated directly from a sample of specimens does not necessarily represent any real-world population, and specimen data needs to be weighted by the times since infection expected in the population. For example, at the developer BioRad Avidity immunoassay threshold, the FRR estimate decreases from 7.1 (Table 2) to 0.8% (Scenario a) or 2.2% (Scenario b).

Scenarios c and d, in which treatment is introduced but there is still no viral load criteria, illustrate the escalation in the overall FRR through viral suppression in the population. Different assays become the frontrunners in different scenarios, but none would be of utility at high treatment coverage rates.

Scenarios e and f which additionally introduce viral load criteria, illustrate how the FRR is then driven down. Paradoxically, a higher treatment coverage produces a lower overall FRR because the FRR among treated

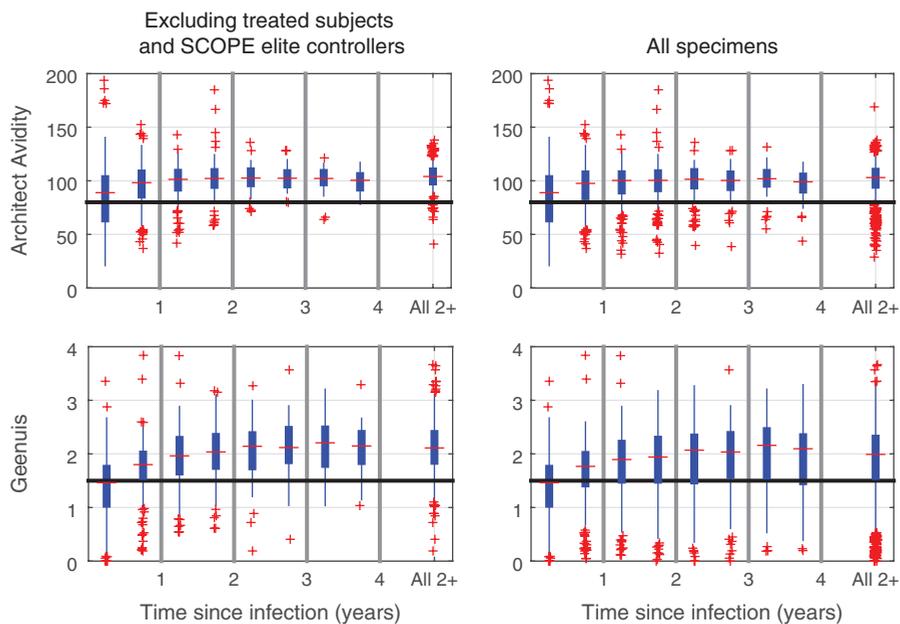


Fig. 1. Architect Avidity and Geenius Incidence Assay Results over Time since Infection. Box-and-whisker plots of assay measurements for each 6-month interval after infection until 4 years, and then for specimens drawn more than 2 years after infection. Left plots exclude treated patients and SCOPE elite controllers. For each interval, the box and dividing line capture the central 50% and median of the measurements, respectively; whiskers and crosses extend out to the remaining data points and outliers respectively (40–1000 data points per time interval). Based on developers’ guidelines, measurements below the horizontal lines indicate ‘recent’ infections. SCOPE, Study of the Consequences of the Protease Inhibitor Era.

Table 1. Estimated Mean Duration of Recent Infection and 95% confidence interval (days) for each assay – for demonstrative incidence immunoassay thresholds, viral load thresholds, and values of T ; excluding treated patients and SCOPE elite controllers.

Assay (unit of measurement)	Immunoassay threshold	$T^a = 2$ years			$T = 1$ year	$T = 3$ years
		No viral load	Viral load threshold ^b = 75	Viral load threshold = 1000	Viral load threshold = 75	
LA _g (OD _n)	0.75	97 (82–115)	88 (74–104)	71 (58–85)	82 (69–95)	88 (74–105)
	1.5*	184 (161–208)	173 (151–195)	141 (123–160)	150 (134–166)	176 (153–200)
	3	405 (373–436)	390 (360–420)	346 (316–376)	269 (251–286)	453 (410–497)
BED (OD _n)	0.4	172 (149–195)	159 (138–181)	129 (112–147)	138 (122–154)	173 (146–202)
	0.8*	300 (270–329)	286 (257–314)	245 (219–272)	220 (202–238)	332 (292–375)
	1.2	408 (377–440)	393 (362–425)	350 (319–382)	270 (252–287)	464 (417–513)
Less-sensitive Vitros (signal-to-cutoff)	10	186 (159–215)	175 (149–202)	141 (118–167)	125 (108–143)	220 (178–265)
	20*	302 (270–335)	288 (256–319)	246 (217–278)	197 (178–217)	364 (313–416)
	30	405 (370–439)	390 (355–424)	345 (311–380)	253 (234–271)	504 (448–560)
Vitros Avidity (avidity index as %)	40	127 (106–149)	119 (99–141)	93 (76–111)	89 (75–103)	138 (109–169)
	60*	282 (250–313)	268 (238–299)	228 (199–258)	193 (174–213)	324 (279–373)
	70	399 (366–431)	384 (352–417)	339 (307–372)	255 (237–273)	478 (427–531)
BioRad Avidity (avidity index as %)	10	129 (113–146)	124 (109–140)	111 (95–127)	111 (97–124)	133 (114–153)
	30*	293 (263–323)	280 (252–309)	248 (221–277)	216 (198–235)	310 (274–347)
	60	414 (382–445)	400 (369–432)	356 (326–389)	279 (263–296)	467 (423–514)
Architect Avidity (avidity index as %)	70	88 (69–109)	83 (64–103)	75 (57–96)	70 (56–85)	86 (65–109)
	80*	128 (106–152)	122 (100–146)	109 (89–133)	100 (84–118)	130 (104–158)
	100	389 (356–423)	375 (342–408)	328 (294–361)	226 (206–247)	507 (457–556)
Geenius (Geenius index)	1.25	110 (88–134)	97 (78–118)	72 (57–88)	73 (59–88)	110 (88–134)
	1.5*	179 (154–205)	163 (141–186)	129 (110–148)	123 (107–140)	201 (174–229)
	1.75	327 (299–355)	311 (285–338)	267 (241–293)	212 (195–229)	390 (355–426)

LA_g, Limiting Antigen; OD_n, normalized optical density.

*Threshold based on developer guidelines.

^aNumber of patients (number of data points) used in estimation: 283 (627) for $T = 1$ year, 397 (965) for $T = 2$ years, and 408 (1187) for $T = 3$ years.

^bMeasured in copies/ml.

patients, who are all virally suppressed by sample design, is 0%.

Table 3 provides the context-specific FRRs for selected values of the MDRI, together with immunoassay thresholds and the implied precision of incidence estimation, for Scenarios I to III. Scenario I captures a recent outbreak of HIV; Scenario II, a sustained epidemic with some treatment; and Scenario III, declining incidence and high treatment coverage.

Discussion

As highlighted by earlier work by CEPHIA and other groups [6–8,10,12,31,32], incidence immunoassays used in stand-alone form fail to simultaneously achieve usefully large MDRI and consistently low FRRs, and produce high FRRs in virally suppressed subpopulations. Also, previously proposed assay thresholds, for distinguishing ‘recent’ from ‘nonrecent’ HIV infections, may be significantly suboptimal; and there is a need to choose an appropriate postinfection time cutoff T which completes the definition of the required test characteristics.

The work, therefore, investigated the characteristics of RITAs that identify ‘recent’ infection by an immunoassay measurement below an immunoassay threshold and viral load measurement above a viral load threshold, for a

number of values of the tunable parameters. Each of the first seven assays that have completed a full CEPHIA evaluation were presented, namely LA_g, BED, Less-sensitive Vitros, Vitros Avidity, BioRad Avidity, Architect Avidity and Geenius. To demonstrate the context dependence of FRRs and directly compare the assays, results were also presented as context-specific FRR estimates, for each of a number of hypothetical scenarios, with immunoassay thresholds chosen so that all RITAs have the same MDRI. The context-dependent RITA performance, as measured by the precision of incidence estimation, was also shown.

Results highlight that the inclusion of viral load measurements is essential for moving the current incidence assays into regimes of utility. The viral load threshold should be low, as further increasing the threshold reduces the MDRI with little impact on the FRR. In practice, the minimum viral loads that are detectable by available assays would likely drive the choice of viral load threshold. The reduction in MDRI from viral load criteria also highlights the importance of estimating the MDRI consistently with the RITA design – a point sometimes missed in the focus on FRR reduction. Although the introduction of viral load criteria, by repository design, produces a zero FRR in the virally suppressed subpopulations, nonzero FRRs persist in the remaining subpopulations, even at high viral load thresholds.

Table 2. Estimated False-Recent Rate and 95% confidence interval (%) for each assay – for demonstrative incidence immunoassay thresholds, viral load thresholds, and values of *T*; for different subpopulations.

Assay (unit)	Immunoassay threshold	Subgroup ^b	<i>T</i> ^a = 2 years			<i>T</i> = 1 year	<i>T</i> = 3 years
			No viral load	Viral load threshold ^c = 75	Viral load threshold = 1000	Viral load threshold = 75	
LA _g (OD _n)	1.5*	Not Tx/EC	1.5 (0.3–4.4)	1.5 (0.3–4.4)	1.5 (0.3–4.4)	4.7 (2.7–7.5)	1.7 (0.2–5.8)
		Tx	58.8 (49.2–68.0)	0 ^d	0	0	0
		EC	14.3 (4.0–32.7)	0	0	0	0
BED (OD _n)	0.8*	Not Tx/EC	14.4 (9.8–20.1)	13.6 (9.2–19.2)	12.4 (8.1–17.8)	24.4 (19.9–29.4)	7.0 (3.2–13.1)
		Tx	65.9 (56.4–74.6)	8.3 (4.9–13.1)	7.6 (4.3–12.2)	13.4 (9.9–17.5)	5.4 (2.1–11.0)
		EC	21.4 (8.3–41.0)	0	0	0	0
Less-sensitive Vitros (signal-to-cutoff)	20*	Not Tx/EC	14.4 (9.8–20.1)	13.6 (9.2–19.2)	12.6 (8.3–18.1)	23.5 (19.0–28.4)	9.5 (4.9–16.2)
		Tx	76.1 (67.2–83.6)	12.4 (8.1–17.8)	10.6 (6.7–15.8)	16.7 (12.9–21.2)	10.3 (5.5–17.2)
		EC	46.4 (27.5–66.1)	0	0	0	0
Vitros Avidity (avidity index as %)	60*	Not Tx/EC	21.2 (15.7–27.6)	20.5 (15.1–26.8)	17.9 (12.9–24.0)	27.0 (22.3–32.1)	17.8 (11.4–25.8)
		Tx	9.8 (6.1–14.9)	9.1 (5.5–14.0)	8.1 (4.7–12.8)	13.3 (9.8–17.4)	10.3 (5.5–17.2)
		EC	72.6 (63.4–80.5)	0	0	0	0
BioRad Avidity (avidity index as %)	30*	Not Tx/EC	32.1 (15.9–52.4)	16.7 (11.8–22.6)	14.1 (9.6–19.8)	24.7 (20.2–29.7)	15.7 (9.7–23.4)
		Tx	17.4 (12.4–23.4)	6.6 (3.5–11.0)	6.6 (3.5–11.0)	11.9 (8.6–15.9)	3.3 (0.9–8.2)
		EC	42.4 (33.1–52.1)	0	0	0	0
Architect Avidity (avidity index as %)	80*	Not Tx/EC	10.7 (2.3–28.2)	17.4 (12.4–23.4)	16.9 (12.0–22.9)	25.6 (21.0–30.7)	13.2 (7.8–20.6)
		Tx	1.5 (0.3–4.4)	1.5 (0.3–4.4)	1.5 (0.3–4.4)	2.6 (1.1–4.9)	2.9 (0.7–7.7)
		EC	33.6 (25.0–43.1)	0	0	0	0
Geenius (Geenius index)	1.5*	Not Tx/EC	33.3 (26.8–40.4)	32.1 (25.6–39.1)	30.6 (24.2–37.5)	34.6 (29.5–40.0)	34.3 (25.9–43.5)
		Tx	6.1 (3.2–10.3)	5.1 (2.4–9.1)	5.1 (2.4–9.1)	6.5 (4.1–9.7)	7.0 (3.2–13.1)
		EC	66.4 (56.9–75.0)	0	0	0	0
	1.75	Not Tx/EC	33.9 (17.2–54.2)	12.9 (8.6–18.4)	11.4 (7.3–16.6)	17.0 (13.1–21.5)	11.6 (6.5–18.7)

EC, elite controller; LA_g, Limiting Antigen; OD_n, normalized optical density; Tx, treated.

*Threshold based on developer guidelines.

^aNumber of patients (number of data points) used in estimation: 332 (873) for subgroup ‘Not Tx/EC’, 140 (247) for ‘Tx’ 28 (86) for ‘EC’ for *T* = 1 year; 198 (448), 112 (185) and 28 (82), respectively, for *T* = 2 years; 121 (226), 91 (144), and 28 (72), respectively, for *T* = 3 years.

^b‘Not Tx/EC’: excludes treated patients and SCOPE elite controllers; ‘Tx’: patients have had at least 3 months of uninterrupted treatment; ‘EC’: contains elite controllers identified in the SCOPE cohort.

^cMeasured in copies/ml.

^dFRRs among ‘Tx’ and ‘EC’ subgroups are zero, by repository design, once a viral load threshold is introduced.

Large values of the postinfection time cutoff *T* generally appear to improve test performance, but present a number of practical limitations. For current incidence assays, a default value for *T* of 2 years appears reasonable, subject to review in the light of data on any specific RITA.

Although published studies of incidence assays suggest that they have very different characteristics, this analysis shows that sensible tuning of immunoassay thresholds, away from previous developer recommendations, reveals relatively similar performance of the assays.

The context-specific FRRs, when constructing the RITAs to have similar MDRIs, and precision of incidence estimation, suggest that BioRad Avidity and LA_g appear to be the frontrunners, although performance is context dependent and other assays can follow closely.

Although a general approach for better understanding the characteristics and utility of assays in the real world is presented in this work, in the analysis of real cross-sectional data obtained at substantial cost, more sophistication should be applied in blending available data into context-specific FRRs with a credible uncertainty estimate. Additionally, data on subpopulations currently not in the CEPHIA repository – such as treated patients who are not yet, or failing to remain, virally suppressed – should be considered.

Numerous such details remain to be further explored – including test refinements from possible combinations of serological or other markers in addition to viral load. This is part of ongoing work within and beyond CEPHIA [33,34].

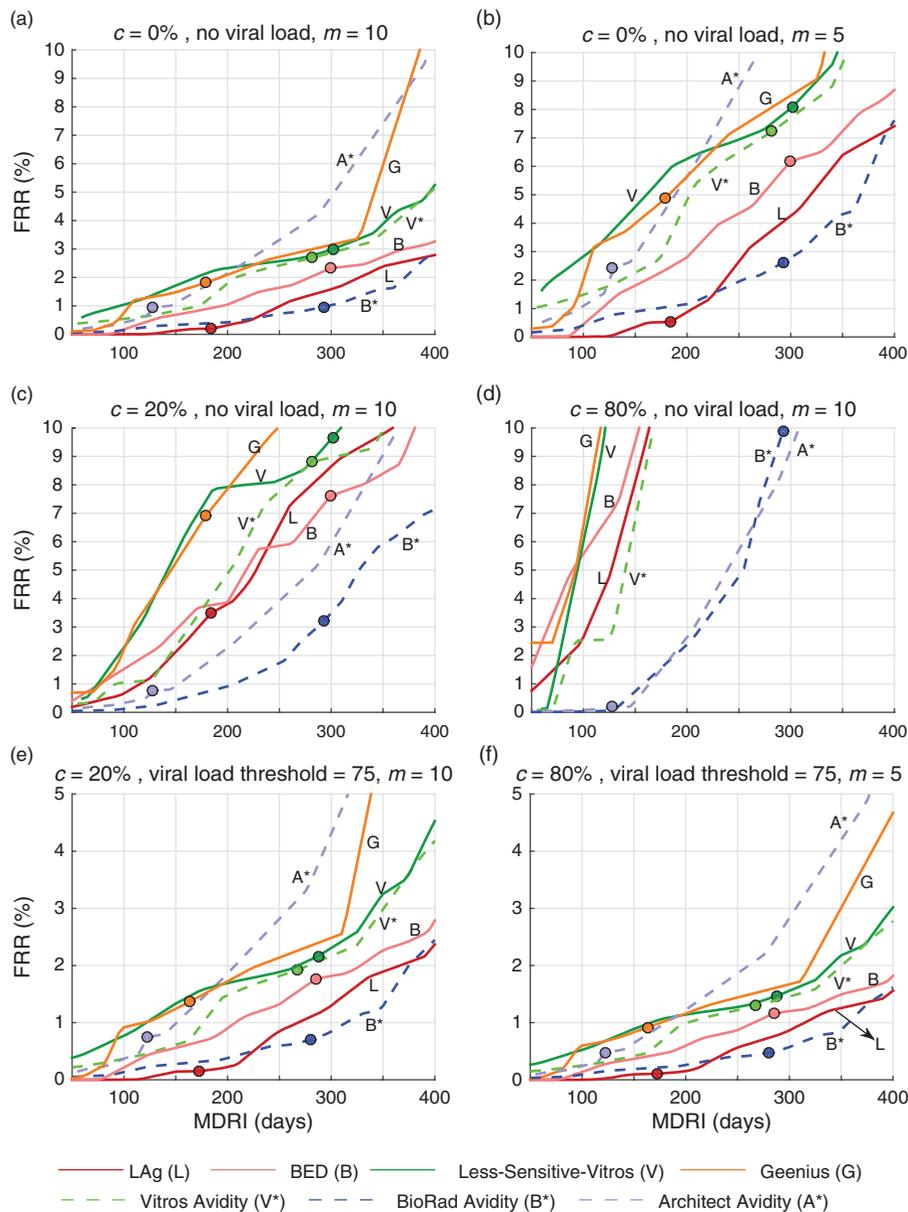


Fig. 2. Context-specific FRR, by MDRI value, per assay, for Scenarios a - f. Each scenario has the specified: treatment coverage c , viral load threshold used in the RITA (copies/ml), and mean years since infection in the untreated population m . The circles correspond to developers' proposed immunoassay thresholds. FRR, False-Recent Rate; MDRI, Mean Duration of Recent Infection; RITA, recent infection testing algorithm.

The importance of viral load as a marker of HIV infection is not just limited to its use in incidence estimation. The greater care required in the handling of specimens for reliable viral load determination, and the increased need for well preserved specimens in advanced studies, such as next generation sequencing, reinforces that specimens should be processed quickly after collection and stored appropriately.

Although this surveillance approach offers solutions to some of the obstacles posed by traditional incidence estimation methods, this work highlights that there

remains a number of conceptual complexities and nuances to be understood by users. Further promise of this approach arises from the potential use of these assays to both diagnosis HIV infection as well as provide information on the staging of infection, using the same specimen.

In conclusion, (1) viral load testing provides a crucial advance in the performance of currently available RITAs, but this does *not* eliminate the nonzero FRRs and the MDRI must be estimated consistently with the RITA design. (2) Tuning of thresholds is essential for the

Table 3. Context-specific False-Recent Rates and precision of incidence estimation, for demonstrative Mean Duration of Recent Infection values (with corresponding immunoassay thresholds), per assay, in hypothetical Scenarios I-III.

MDRI	Assay	Scenario I: no treatment, no viral load, mean time infected $m = 5$ years, incidence = 3% per person year, prevalence = 12%					Scenario II: treatment coverage $c = 20\%$, viral load threshold = 75 copies/ml, mean time infected $m = 10$ years, incidence = 2% per person year, prevalence = 20%					Scenario III: treatment coverage $c = 80\%$, viral load threshold = 75 copies/ml, mean time infected $m = 5$ years, incidence = 1% per person year, prevalence = 40%				
		Immunoassay threshold	FRR (%)	RSE (%) ^a	Within 0.5% (%) ^b	Immunoassay threshold	FRR (%)	RSE (%) ^a	Within 0.5% (%) ^b	Immunoassay threshold	FRR (%)	RSE (%) ^a	Within 0.5% (%) ^b			
200	LAG	1.7	0.9	13.8	77.1	1.9	0.2	17.4	84.8	1.9	0.2	30.2	90.2			
	BED	0.5	2.8	15.3	72.5	0.5	0.9	18.8	81.5	0.5	0.6	36.7	82.7			
	Less-sensitive Vitros	11.3	6.3	18.5	63.4	12.5	1.7	20.5	77.7	12.5	1.1	43.8	74.6			
	Vitros Avidity	49.0	4.8	17.0	67.3	50.9	1.5	20.0	78.8	50.9	1.0	41.9	76.7			
	BioRad Avidity	14.7	1.2	14.0	76.5	15.6	0.4	17.8	84.1	15.6	0.3	31.8	88.4			
	Architect Avidity	89.6	5.6	17.8	65.1	90.3	1.9	20.9	76.9	90.3	1.2	44.8	73.5			
300	Geenius	1.5	5.6	17.8	65.0	1.6	1.7	20.6	77.6	1.6	1.2	44.0	74.4			
	LAG	2.5	4.3	12.4	82.2	2.5	1.3	15.3	89.8	2.5	0.9	29.7	90.8			
	BED	0.8	6.2	13.2	79.5	0.8	1.8	15.9	88.5	0.8	1.2	32.1	88.0			
	Less-sensitive Vitros	19.9	8.0	14.0	76.6	20.8	2.3	16.4	87.3	20.8	1.6	34.6	85.2			
	Vitros Avidity	61.6	7.7	13.8	77.1	62.8	2.2	16.2	87.6	62.8	1.5	33.9	86.0			
	BioRad Avidity	32.0	2.8	11.8	84.2	35.7	0.8	14.8	90.9	35.7	0.6	27.5	93.1			
Architect Avidity	95.6	12.8	16.7	68.3	96.2	4.3	18.6	82.1	96.2	2.8	42.7	75.8				
	Geenius	1.7	8.5	14.2	75.9	1.7	2.5	16.6	86.8	1.7	1.7	35.4	84.3			

FRR, false-recent rate; MDRI, mean duration of 'recent' infection; RSE, relative standard error.

^aThe SD of the incidence estimator divided by its mean.

^bThe probability of a single incidence estimate lying within 0.5% (in absolute terms) of the true incidence value.

balanced comparison of assays and the optimization of RITA performance. (3) The translation of FRR estimates, measured directly from samples of specimens, into context-specific FRR estimates greatly changes their magnitudes and is critical for the application of the assays.

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Conflicts of interest

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References

1. Brookmeyer R, Quinn TC. **Estimation of current human immunodeficiency virus incidence rates from a cross-sectional survey using early diagnostic tests.** *Am J Epidemiol* 1995; **141**:166-172.
2. Janssen RS, Satten GA, Stramer SL, Rawal BD, O'Brien TR, Weiblen BJ, et al. **New testing strategy to detect early HIV-1 infection for use in incidence estimates and for clinical and prevention purposes.** *JAMA* 1998; **280**:42-48.
3. Kaplan EH, Brookmeyer R. **Snapshot estimators of recent HIV incidence rates.** *Oper Res* 1999; **47**:29-37.
4. McDougal JS, Parekh BS, Peterson ML, Branson BM, Dobbs T, Ackers M, et al. **Comparison of HIV type 1 incidence observed during longitudinal follow-up with incidence estimated by cross-sectional analysis using the BED capture enzyme immunoassay.** *AIDS Res Hum Retroviruses* 2006; **22**:945-952.
5. Hargrove JW, Humphrey JH, Mutasa K, Parekh BS, McDougal JS, Ntozini R, et al. **Improved HIV-1 incidence estimates using the BED capture enzyme immunoassay.** *AIDS* 2008; **22**:511-518.

6. Murphy G, Parry JV. **Assays for the detection of recent infections with human immunodeficiency virus type 1.** *Euro Surveill* 2008; **13**:4–10.
7. Busch MP, Pilcher CD, Mastro TD, Kaldor J, Vercauteren G, Rodriguez W, *et al.* **Beyond detuning: 10 years of progress and new challenges in the development and application of assays for HIV incidence estimation.** *AIDS* 2010; **24**:2763–2771.
8. Mastro TD, Kim AA, Hallett T, Rehle T, Welte A, Laeyendecker O, *et al.* **Estimating HIV incidence in populations using tests for recent infection: issues, challenges and the way forward.** *J HIV AIDS Surveill Epidemiol* 2010; **2**:1–14.
9. McWalter TA, Welte A. **Relating recent infection prevalence to incidence with a sub-population of assay nonprogressors.** *J Math Biol* 2010; **60**:687–710.
10. Incidence Assay Critical Path Working Group. **More and better information to tackle HIV epidemics: towards improved HIV incidence assays.** *PLoS Med* 2011; **8**:e1001045.
11. Kassanjee R, McWalter TA, Barnighausen T, Welte A. **A new general biomarker-based incidence estimator.** *Epidemiology* 2012; **23**:721–728.
12. Kassanjee R, Pilcher CD, Keating SM, Facente SN, McKinney E, Price MA, *et al.* **Independent assessment of candidate HIV incidence assays on specimens in the CEPHIA repository.** *AIDS* 2014; **28**:2439–2449.
13. Hargrove J, van Schalkwyk C, Eastwood H. **BED estimates of HIV incidence: resolving the differences, making things simpler.** *PLoS One* 2012; **7**:e29736.
14. The Consortium for the Evaluation and Performance of HIV Incidence Assays (CEPHIA). <http://www.incidence-estimation.com/page/cephia> [Accessed 3 April 2016].
15. Bill & Melinda Gates Foundation Letters of Inquiry (LOI): New biomarkers for HIV incidence measurement. <https://docs.gatesfoundation.org/Documents/hiv-incidence-rules-and-guidelines.pdf> [Accessed 3 April 2016].
16. Welte A, McWalter TA, Laeyendecker O, Hallett TB. **Using tests for recent infection to estimate incidence: problems and prospects for HIV.** *Euro Surveill* 2010; **15**:pii=19589.
17. Kassanjee R, McWalter TA, Welte A. **Defining optimality of a test for recent infection for HIV incidence surveillance.** *AIDS Res Hum Retroviruses* 2014; **30**:45–49.
18. Duong YT, Qiu M, De AK, Jackson K, Dobbs T, Kim AA, *et al.* **Detection of recent HIV-1 infection using a new limiting-antigen avidity assay: potential for HIV-1 incidence estimates and avidity maturation studies.** *PLoS One* 2012; **7**:e33328.
19. Sedia Biosciences Corporation. Sedia HIV-1 LAg-Avidity EIA: single well avidity enzyme immunoassay for detection of recent HIV-1 infection using liquid serum or plasma, Cat. No. 1002, 2014. www.sediabio.com/LiteratureRetrieve.aspx?ID=127076 [Accessed 3 April 2016].
20. Parekh BS, Kennedy MS, Dobbs T, Pau CP, Byers R, Green T, *et al.* **Quantitative detection of increasing HIV type 1 antibodies after seroconversion: a simple assay for detecting recent HIV infection and estimating incidence.** *AIDS Res Hum Retroviruses* 2002; **18**:295–307.
21. Sedia Biosciences Corporation. Sedia BED HIV-1 Incidence EIA: enzyme immunoassay for population estimates of HIV-1 incidence, Cat. No. 1000, 2014. <http://www.sediabio.com/LiteratureRetrieve.aspx?ID=127077> [Accessed 3 April 2016].
22. Keating SM, Hanson D, Lebedeva M, Laeyendecker O, Ali-Napo NL, Owen SM, *et al.* **Lower-sensitivity and avidity modifications of the vitros anti-HIV 1+2 assay for detection of recent HIV infections and incidence estimation.** *J Clin Microbiol* 2012; **50**:3968–3976.
23. Masciotra S, Dobbs T, Candal D, Hanson D, Delaney K, Rudolph D. **Antibody avidity-based assay for identifying recent HIV-1 infections based on genetic systems 1/2 Plus O EIA [Abstract Abstract 937]** *17th Conference on Retroviruses and Opportunistic Infections.* San Francisco, CA. 2010
24. Suligoi B, Rodella A, Raimondo M, Regine V, Terlenghi L, Manca N, *et al.* **Avidity Index for anti-HIV antibodies: comparison between third- and fourth-generation automated immunoassays.** *J Clin Microbiol* 2011; **49**:2610–2613.
25. Abbott Laboratories. ARCHITECT HIV Ag/Ab Combo Reagent Insert, 2014. <http://www.fda.gov/downloads/BiologicsBloodVaccines/.../UCM216309.p> [Accessed 3 April 2016].
26. Montesinos I, Eykmans J, Delforge ML. **Evaluation of the bio-rad genius HIV-1/2 test as a confirmatory assay.** *J Clin Virol* 2014; **60**:399–401.
27. Bio-Rad Laboratories. Genius™ HIV 1/2 Supplemental Assay Instructions For Use, 2014. <http://www.fda.gov/downloads/BiologicsBloodVaccines/BloodBloodProducts/ApprovedProducts/PremarketApprovalsPMAs/UCM420735.pdf> [Accessed 3 April 2016].
28. Fiebig EW, Wright DJ, Rawal BD, Garrett PE, Schumacher RT, Peddada L, *et al.* **Dynamics of HIV viremia and antibody seroconversion in plasma donors: implications for diagnosis and staging of primary HIV infection.** *AIDS* 2003; **17**:1871–1879.
29. Masciotra S, McDougal JS, Feldman J, Sprinkle P, Wesolowski L, Owen SM. **Evaluation of an alternative HIV diagnostic algorithm using specimens from seroconversion panels and persons with established HIV infections.** *J Clin Virol* 2011; **52** (Suppl 1):S17–S22.
30. Hunt PW, Brenchley J, Sinclair E, McCune JM, Roland M, Page-Shafer K, *et al.* **Relationship between T cell activation and CD4+ T cell count in HIV-seropositive individuals with undetectable plasma HIV RNA levels in the absence of therapy.** *J Infect Dis* 2008; **197**:126–133.
31. Laeyendecker O, Brookmeyer R, Oliver AE, Mullis CE, Eaton KP, Mueller AC, *et al.* **Factors associated with incorrect identification of recent HIV infection using the BED capture immunoassay.** *AIDS Res Hum Retroviruses* 2012; **28**:816–822.
32. Longosz AF, Mehta SH, Kirk GD, Margolick JB, Brown J, Quinn TC, *et al.* **Incorrect identification of recent HIV infection in adults in the United States using a limiting-antigen avidity assay.** *AIDS* 2014; **28**:1227–1232.
33. Brookmeyer R, Konikoff J, Laeyendecker O, Eshleman SH. **Estimation of HIV incidence using multiple biomarkers.** *Am J Epidemiol* 2013; **177**:264–272.
34. Laeyendecker O, Piwovar-Manning E, Fiamma A, Kulich M, Donnell D, Bassuk D, *et al.* **Estimation of HIV incidence in a large, community-based, randomized clinical trial: NIMH Project Accept (HIV Prevention Trials Network 043).** *PLoS One* 2013; **8**:e68349.