Comparative Analysis of HIV Estimation Methods and Results in Locations with Case Reports and High-Quality Vital Registration Data

Austin Carter

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Committee:

Laura Dwyer-Lindgren, Chair

Jeffrey Eaton

Haidong Wang

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Abstract

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Austin Carter

Chair of the Supervisory Committee:
Laura Dwyer-Lindgren, Assistant Professor
Department of Global Health

This thesis provides an overview of HIV burden estimation methods and results in high-income locations with high-quality vital registration data and case reports. In addition, it presents an investigation of the sensitivity of estimates to variation in model specification and input parameters. The study compared estimates of HIV burden from bespoke models in Australia, the Netherlands, and the United States to estimates produced using models developed by the Joint United Nations Programme on HIV/AIDS (UNAIDS) and the Institute for Health Metrics and Evaluation (IHME). The sensitivity of the results produced with the IHME model to differences in input parameter estimates from UNAIDS and IHME was investigated by conducting a Shapley decomposition. The decomposition breaks down the individual contributions of differences in a set of input parameters to variation in modeled estimates by averaging across multiple model runs with permutations of the input parameters. Upon comparison, the overall estimates from each model exhibited substantial heterogeneity, revealing the strengths and weaknesses of each modeling strategy in fitting to particular types of input data. From the decomposition analysis, antiretroviral therapy and disease progression parameters stood out as the largest contributors to variation between estimates from the IHME model, with one of the these two parameters explaining the majority of variation eight of the nine location-statistic

combinations evaluated. This study indicates the importance of pursuing harmony in modelling strategies in order to provide a coherent understanding of trends in HIV burden in high-income countries. In addition, future investigation of available data for better estimation of ART coverage may reduce some of the observed variation in modeled estimates.

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Acknowledgements

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1. Introduction

Accurate health statistics enable the development of effective health policy and resource allocation. When HIV/AIDS was first identified as a novel pathogen, very little data existed to support confident estimation of the scale and growth of the epidemic[1], delaying widespread recognition of HIV as a global health crisis. A number of modeling approaches have since emerged to leverage available data sources[2,3], which vary substantially across regions and are improving in quality over time.

In most high-income countries, reported HIV/AIDS diagnoses and recorded AIDS deaths serve as the primary data sources for monitoring the burden of HIV.[4–8] In contrast, countries with the greatest burden of HIV generally lack high-quality cause of death data and systems for registering new cases, and cross-sectional prevalence data from nationally representative surveys anchor most estimation methods.[9,10] The substantial difference in modeling strategies motivates an isolated investigation of the methods and results used in high-income countries.

Currently employed methods for estimating HIV burden in locations with case reports and high-quality vital registration data vary dramatically. Some models only incorporate case report data, bypassing the need to model post-diagnosis disease progression and mortality.[4,8,11,12] These approaches are generally employed in bespoke country models, where capacity to employ researchers and access to detailed data allows for location-specific models to be developed. In addition, generalized models for high-income settings have been developed, including a model supported by the European Centre for Disease Prevention and Control (ECDC). [13] Furthermore, institutions like the Joint United Nations Programme on HIV/AIDS (UNAIDS)[14] and the Institute for Health Metrics and Evaluation (IHME)[10] produce estimates for all countries, necessitating model strategies that can be employed broadly[10,14]. Within country experts produce estimate for UNAIDS in a piece of software called Spectrum which contains the Case Surveillance and Vital Registration (CSAVR) model. Estimates from IHME are produced for Global Burden of Disease (GBD) publications, and the model used to produce estimates in high-income locations uses a method called the cohort incidence bias adjustment (CIBA). Both the CSAVR and CIBA models are used to produce estimates for this analysis.

After a thorough review of available literature, I was unable to find a comprehensive comparison of methods and results from different models for HIV/AIDS burden estimation in high-income locations. Further, the sensitivity of these models to variation in input parameters has not been systematically investigated. Understanding the sources and impact of these differences will improve our understanding of current estimates and offer guidance into top priorities for data collection and model specification for countries which are increasing the quality of their surveillance and vital registration data. Given data

availability and documentation, I isolated my analysis to Australia, the Netherlands, and the United States.

The goals of this study are to describe the range of models currently in use for producing HIV burden estimates in locations with high-quality vital registration data and case reports, as well as to investigate the sensitivity of these estimates to model specification and variation of input parameters. Here I isolate my investigation to a subset of input parameters that differ between UNAIDS and IHME in and effort to address one of the multiple factors contributing to differences in estimates. In order to achieve these goal, this study consists of the following aims:

1. To present, in detail, the input data and range of estimation methods used to estimate HIV burden in Australia, the Netherlands, and the United States.
2. To produce estimates using CSAVR and CIBA and summarize the results in comparison to estimates from bespoke models.
3. To assess the sensitivity of incidence estimates from CIBA to variation in parameters describing disease progression, probability of death, and treatment coverage.

2. Data

2.1. Input Data

There are three primary data sources: case reports, vital registration (VR) death data, and cohort studies. Case report and VR provide directly observed information about the burden of HIV in a given country, while cohort studies provide information on the natural history of HIV (not specific to a particular country), including HIV-specific mortality in the presence and absence of treatment and disease progression measured through decline in the number of CD4 cells circulating in an infected individual's blood.

Case report data are required notifications of new HIV/AIDS diagnoses[15], catalogued in a central registry. These reports often include information about the demographics of the diagnosed individual, transmission category (e.g. men who have sex with men, female sex worker), and some measure clinical status. Measures of clinical status are usually either CD4 count or the stage of the infection (primary HIV infection, asymptomatic HIV, symptomatic HIV, or AIDS) at the time of diagnosis. Changes in diagnostic tools and frequency of HIV testing over time produce some challenges for integrating a full time series of case reports into a model. Data on the total number of diagnosed PLHIV are maintained by connected deaths due to HIV to reported cases.

Vital registration systems are a government's records of its citizens' births and deaths, most often including the cause of death[16]. Misclassified and under-reported AIDS deaths[17,18] necessitate methods for redistribution of deaths from other causes[19]. These methods detect abnormal increases in deaths due to causes often incorrectly coded as the cause of death instead of HIV.

Cohort studies are prospective longitudinal studies which enroll PLHIV and observe changes in their health over time. Concerted Action on Seroconversion to AIDS and Death in Europe (CASCADE)[22] cohort data are used to estimate the time from seroconversion to various CD4 count levels and probability of death in the absence of treatment. Similarly, data from the Antiretroviral Therapy Cohort Collaboration (ART-CC)[23] are used to estimate mortality rates for individuals on treatment.

2.2. Estimated input parameters

Both the CSAVR and CIBA models rely on a population projection model which simulates an age- and sex-stratified population while introducing dynamics that mimic that the natural history of HIV. The population projection model is included in the Spectrum software[20], and IHME replicated the model in Python to generate HIV burden estimates for their GBD study[21]. While a number of unique features have been introduced to the Spectrum and GBD models over time, they share a common set of inputs and

outputs, enabling investigation of how some of the assumed parameters of the models impact estimates. I refer to the parameters that I compare in this analysis as transition parameters, because they describe the rate at which individuals change states within the model. Below I describe how these parameters were estimated by UNAIDS and GBD for input into CSAVR and CIBA.

2.2.1. Off-ART mortality and disease progression

2.2.1.1. Spectrum Default

Off-ART mortality and disease progression were estimated simultaneously by fitting to cohort data on survival from the ALPHA network (Analysis of Longitudinal Population-based HIV data in Africa), which includes individuals who were monitored while not receiving ART.[24] Although ALPHA network data is from Sub-Saharan Africa, estimates of age-specific survival from the data closely match survival observed in European data. [25] Constraints were placed on the estimated parameters, including decline in CD4 count being a linear function of CD4 count and mortality patterns matching the ALPHA network patterns by age.[20]

2.2.1.2. GBD

Off-ART mortality and disease progression were also estimated simultaneously in the GBD by optimizing the fit to cohort survival from a group of 13 cohorts identified through a literature search.[26] A mixed-effects model described the logit of the conditional probability of death as a linear function of age, time since seroconversion, and a study random effect. Mortality rates were constrained to increase as function of decline in CD4 count.

2.2.2. On-ART mortality

2.2.2.1. Spectrum Default

UNAIDS recently updated their on-ART mortality parameters to change over time to account for recent improvements in ART. A Poisson mixed effects model was fit to ART-CC data, stratified by age, sex, CD4, duration on treatment, and calendar year[27].

2.2.2.2. GBD

Probabilities of death for individuals receiving ART were derived from cohort data attained through collaboration with the ART-CC[28]. Estimated probabilities were adjusted for loss to follow up (LTFU) using a modified version of a technique developed by Verguet et al., which estimates death in LTFU as a function of proportion LTFU[26].

2.2.3. ART coverage

2.2.3.1. Spectrum Default

Countries input counts of the number of people receiving treatment[20]. In the Netherlands, these are numbers are likely an accurate representation of ART coverage, as the government keeps track of all PLHIV on treatment through the ATHENA cohort[29]. In Australia, the number of people on ART were estimated through a 10% sample of Pharmaceutical Benefits Scheme (PBS) patient level prescription claims data along with an adjustment made for temporary residents using data obtained from National Association of People with HIV Australia (NAPWHA) on individuals receiving care through compassionate access schemes[30]. The total number on treatment was split into sex-specific numbers using proportions from the Australian HIV Observational Database Temporary Access Study (ATRAS). For the United States, there is not any centralized data on treatment, and so some amount of experimentation was done to identify a plausible coverage rate that contributed to a good fit to other input data.

2.2.3.2. GBD

In the context of limited data availability for ART coverage, GBD applied an assumption about the scale-up and level of coverage across all high-income locations. From 1996 to 1997, the GBD assumes an increase from 0% to 75% coverage among eligible individuals, and 90% coverage among eligible individuals for all later years. These assumptions about treatment scale-up were partially validated through assessing the fit of GBD HIV mortality estimates to vital registration data during and immediately after the introduction of treatment.

2.2.4. Other parameters

For the purposes of this decomposition, I sought alignment in all other inputs into both of the models. Specifically, I utilized Spectrum default parameters and input data, which include vital rates from World Population Prospects 2017[31] for population projection. As a single exception from the standard set of Spectrum inputs, I included a full time-series of HIV mortality, estimated from vital registration data using space-time Gaussian process regression[26]. CIBA relies on a full time-series of mortality data, and adjustments made to raw vital registration data for the GBD improve the accuracy of GBD's HIV mortality estimates[19].

3. Methods

3.1. Model Descriptions

Model	Countries	Primary Input Data	Diagnoses Rate	Transition Parameters	Functional form for Incidence
CDC	USA	Diagnoses by CD4	Backcast diagnoses and estimate delay weight	Disease progression	None
ECDC	Netherlands Australia	Diagnoses by CD4	Piecewise linear function by time and infection stage	Off-ART Mortality Disease progression	B-Splines M-Splines
CSAVR	USA Netherlands Australia	Deaths Diagnoses Median CD4 at diagnosis Total diagnosed PLHIV	Function of median CD4 and mortality (cdf of gamma)	Off-ART Mortality Disease progression ART Coverage On-ART Mortality	Logistic Double-Logistic Segmented polynomials
CIBA	USA Netherlands Australia	Deaths	Fixed	Off-ART Mortality Disease progression ART Coverage On-ART Mortality	None

Table 1: Models used for HIV burden estimation in Australia, the Netherlands, and the United States

3.1.1. Bespoke Country Models

3.1.1.1. CDC (United States)

The CDC uses reported diagnoses and the first CD4 count value recorded after diagnosis as the primary inputs to their model for estimating HIV incidence (see Table 1). As an extension of the “back calculation” model first developed in the late 1980’s, the current methods utilize a CD4 depletion model to estimate the lag between initial infection and diagnosis[4,11]. The intuition behind this model is that there

is a consistent relationship between an individual's CD4 count and the amount of time since they were infected – the assumed functional form is a linear relationship between the square root of CD4 count and time. The CDC stratifies CD4 depletion rates by transmission category, age group, and sex and fits to data from the CASCADE cohort. To account for undiagnosed individuals, the CDC weights a given diagnosis by the inverse of the probability that the individual would have been diagnosed during the years of observation. These probabilities are estimated with historical reporting data using similar methods to those used to account for reporting delays[32].

3.1.1.2. ECDC (The Netherlands and Australia)

The ECDC tool for HIV burden estimation defines a functional form for incidence and describes the progression of HIV through various stages, including declining CD4 count, death, and diagnosis[33]. Disease progression and mortality in the absence of ART are taken as inputs, while incidence and diagnoses rates for various CD4 count groups are estimated by the model. Incidence is parameterized using B-splines or M-splines which allow for significant flexibility in trends over time. In addition, diagnoses rates are approximated using a piecewise linear function over time with different slopes for different time intervals. Reported deaths and new infections are assumed to follow either a Poisson or negative-binomial distribution, and parameters are estimated through maximum likelihood estimation with confidence intervals generated through bootstrapping. While originally developed for the Netherlands, a number of European countries, as well as Australia, have begun to use the ECDC tool for their official estimates.

3.1.2. CSAVR (Spectrum)

The CSAVR tool[14] leverages the complete population projection model utilized in the Spectrum software[20]. A full set of vital rates, including starting population, fertility, mortality, and migration, are used to project a population over time. Parameters for HIV progression and mortality are also incorporated to model differences in mortality among HIV positive individuals. As input data, the model takes in treatment statistics, case reports, median CD4 count at diagnosis, total diagnosed individuals, and HIV deaths. By modeling the full progression of the disease, the model can be fit simultaneously to incidence and mortality data. Incidence can be parameterized as following a logistic function, a double-logistic function, or a B-spline with a variable number of knots. The rate of diagnosis is constrained to be proportionate to the mortality rate using a cumulative gamma function whose parameters are estimated as part of the model fitting process. Maximum likelihood or minimum chi-square estimation can be used to identify the optimal parameters. I produced estimates in the CSAVR tool using Spectrum software, version 5.67. As input data, I collaborated with UNAIDS to gain access to data assembled by within-country experts.

3.1.3. CIBA (GBD)

The cohort incidence bias adjustment (CIBA) method[34] developed for the GBD utilizes the same Spectrum population projection tool, but tracks deaths by incidence cohort to determine an annual adjustment to incidence that improves model fit to mortality data. The philosophy behind CIBA is that the best source of data for inference about HIV/AIDS burden in high-income countries is mortality data, and therefore the method leans entirely upon mortality data to produce estimates for other measures of the epidemic. The process involves conducting an initial run of the model to extract distribution of deaths for each cohort as well as mortality estimates for comparison to vital registration data. The incidence rate in each year is adjusted according to an average of the bias of the initial mortality estimates in future years weighted by the proportion of the cohort dying in each year.

3.2. Decomposition of Variation in Estimated Parameters

3.2.1. Shapley decomposition

In order to summarize the relative contribution of differences in each input parameter to HIV incidence estimates, I applied a Shapley decomposition to a number of scenarios.[35,36] The included scenarios are permutations of Spectrum defaults and GBD estimates for: 1) Off-ART mortality 2) Disease progression 3) On-ART mortality and 4) ART coverage. These necessitated 16 (2^4) scenarios to be run through CIBA. For example, if 0 indicates the Spectrum default parameter and 1 indicates the GBD parameter for each of my four parameters of interest, the 16 scenarios are 0000, 1000, 0100, 0010, 0001, 1100, 1010, 1001, 0110, 0101, 0011, 1110, 1101, 1011, 0111, and 1111. For a given parameter, an average of the difference in estimates across the eight pairs of scenarios where the remaining three parameters were the same was calculated. For example, the contribution of differences in the off-ART mortality parameter can be calculate by taking the average of the difference between the following pairs of parameter combinations where only the first parameter varies: (0000, 1000), (0100, 1100), (0010, 1010), (0001, 1001), (0110, 1110), (0011, 1011), (0101, 1101), (0111, 1111). The summary statistics used to compare each of the pairs were 1) new HIV infections in 2017; 2) cumulative new HIV infections; and 3) new HIV infections in the year with the greatest difference in incidence rates.

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4. Results

4.1. Model Comparison

4.1.1. Australia

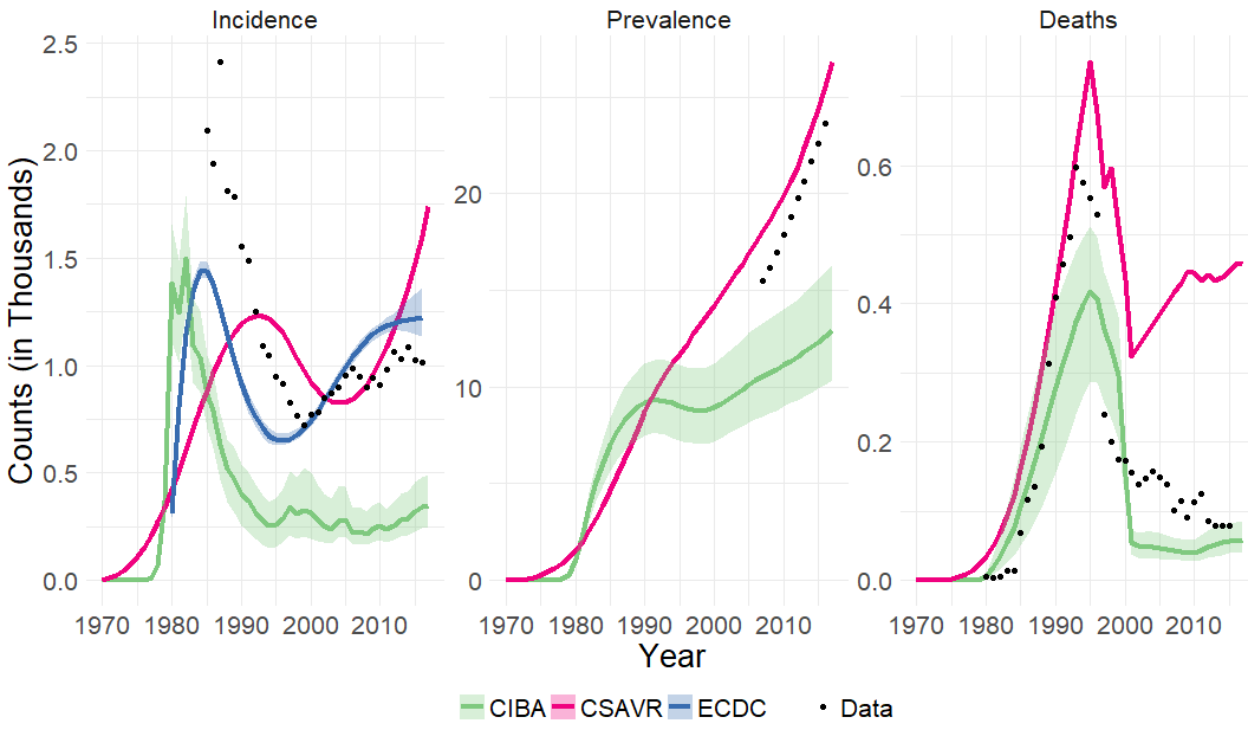

Figure 1: HIV Burden Estimates for Australia

CSAVR estimates for Australia estimates were produced using a spline with three knots for incidence and used maximum likelihood estimation (MLE). In general, I tried to use these specifications because of the flexibility of the three knot spline balanced with the speed of convergence from estimating less parameters than in the case of more knots. I was not able to test sensitivity to the use of minimum chi-square optimization instead of the default method of using MLE. For incidence estimates, CSAVR results exhibit a later peak than the other estimates (see Fig. 1), as well as a large second increase in new infections in recent years. GBD incidence estimates exhibit a single peak and are much lower than CSAVR and ECDC in recent years. ECDC estimates appear to fit diagnoses data the best, with an initial peak, followed by an increase of the last two decades. CSAVR estimates much higher prevalence than GBD, fitting to data on total diagnosed individuals much better than CIBA. In contrast, CIBA produces a better fit to mortality data, although it appears to overestimate the decline in mortality associated with the

introduction of ART in the late 1990's. CSAVR drastically overestimates mortality data and estimates increasing mortality despite a consistent decline in the data.

4.1.2. The Netherlands

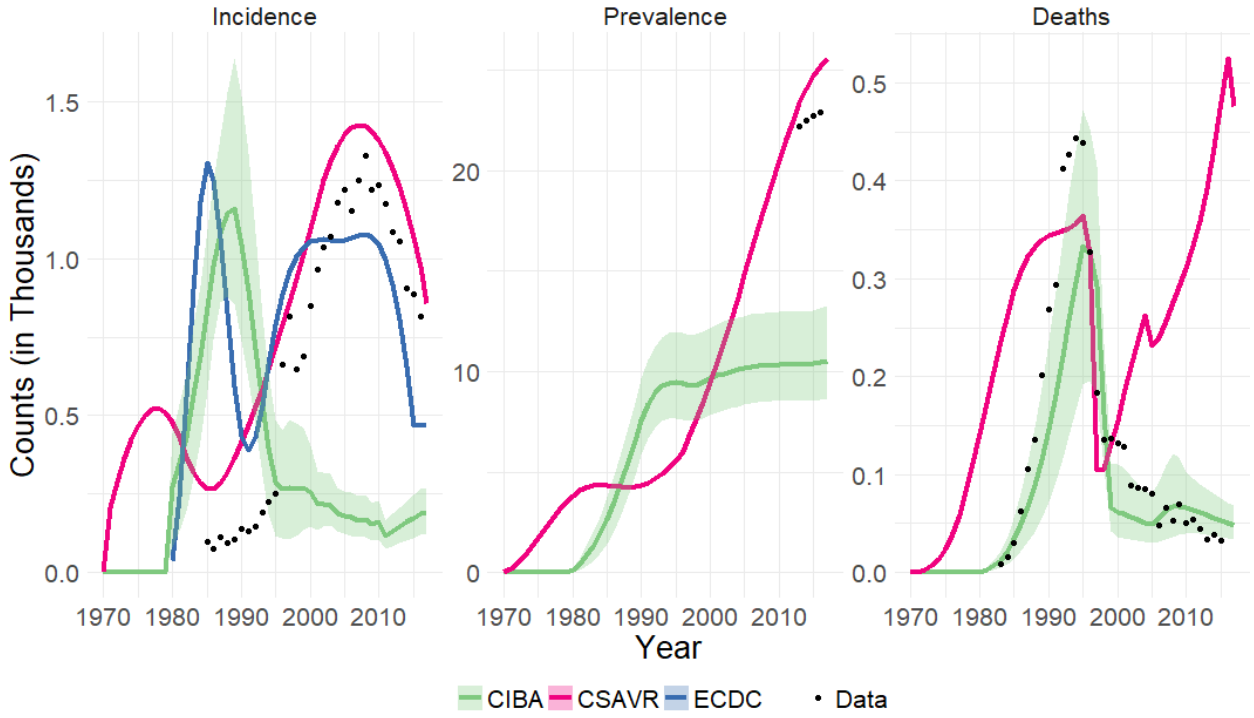

Figure 2: HIV Burden Estimates for the Netherlands

CSAVR estimates for the Netherlands estimates were produced using a spline with 3 knots for incidence and used maximum likelihood estimation. CSAVR estimates a small early peak in incidence followed by a late peak that aligns well with diagnoses data. CIBA produces an early peak in incidence (see Fig. 2), but fails to capture the second peak, likely because the recent incidence peak is not yet evidenced by mortality data. ECDC estimates a peak in the mid-1980's which is larger than CSAVR or CIBA, followed by a second peak that is smaller than CSAVR but much larger than CIBA. Again, CSAVR produces a better fit to total diagnosed data while CIBA estimates trends in HIV deaths that better align with mortality data. CIBA underestimates prevalence while CSAVR overestimates mortality.

4.1.3. United States

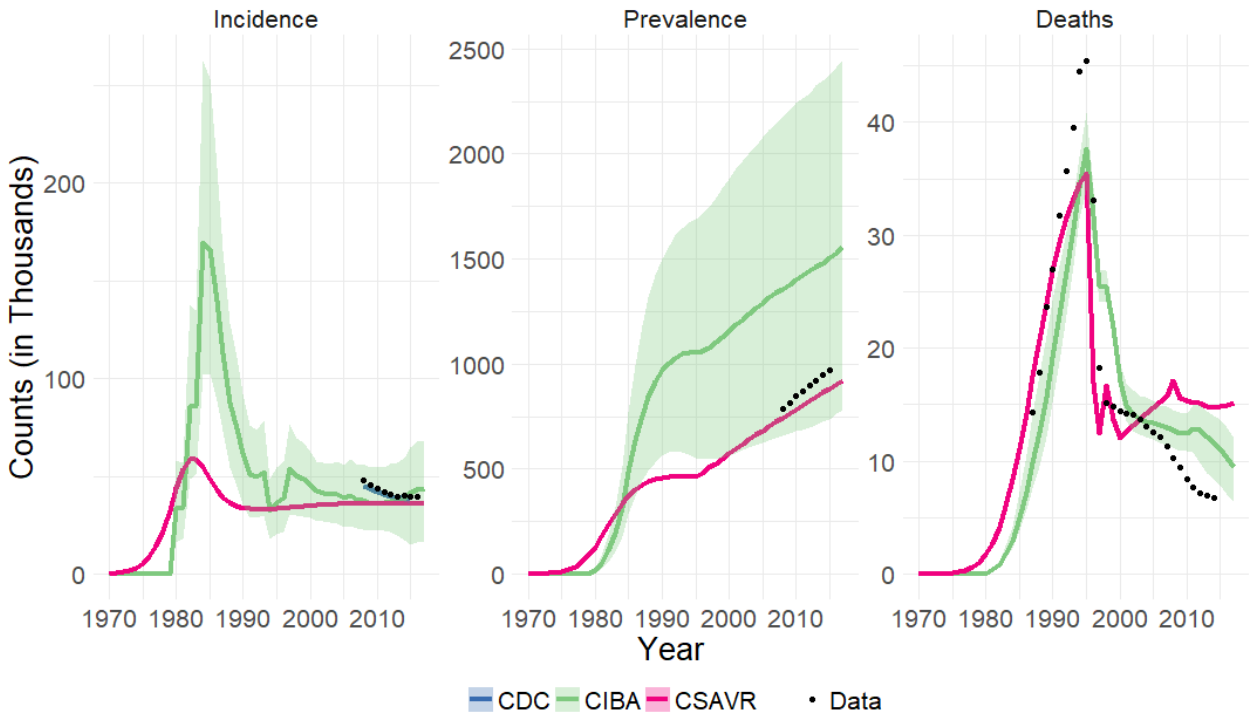

Figure 3: HIV Burden Estimates for the United States

United States estimates were produced in CSAVR using a double-logistic function for incidence and used maximum likelihood estimation. The choice of the double-logistic function occurred after failing to produce a plausible fit using the spline specification. The CDC estimates of incidence are nearly identical to the case report data, although they do not estimate a full time-series so I could not compare estimates from early in the epidemic. As seen in Fig. 3, CSAVR and CIBA produce fairly consistent incidence estimates, although the peak in incidence estimated by CIBA is much larger than CSAVR estimates. CIBA prevalence estimates are larger than those from CSAVR despite, and the mortality estimates from the two models are similar, although CIBA produces a better fit to mortality data in recent years.

4.2. Decomposition Analysis

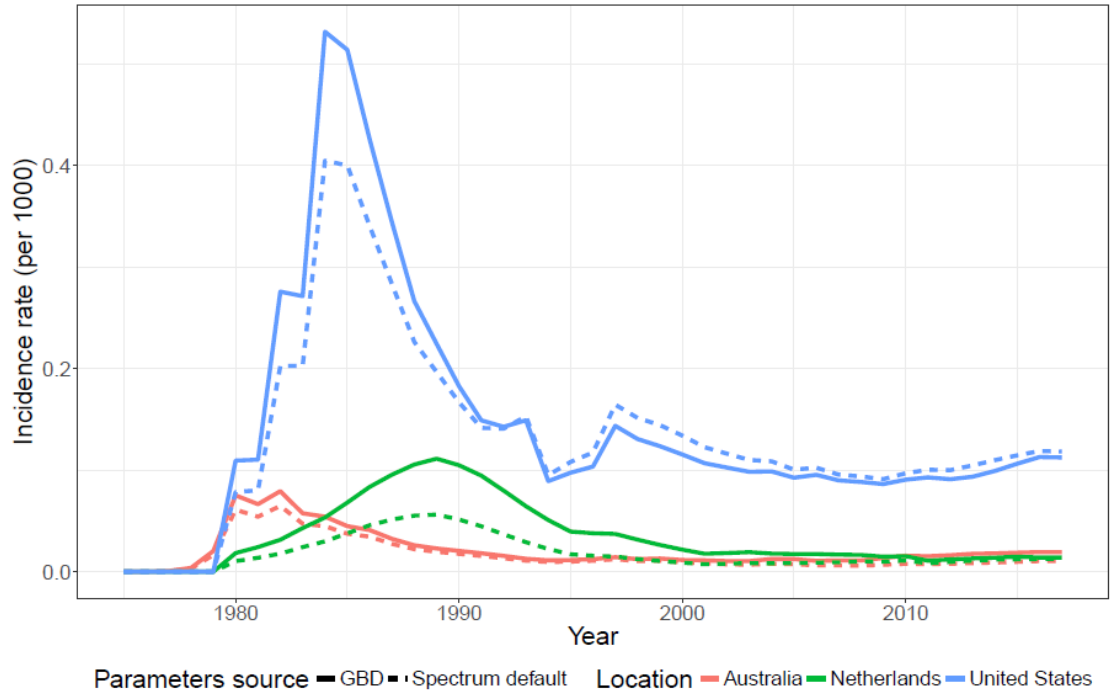

Figure 4: CIBA estimated incidence rates utilizing Spectrum default parameters and GBD parameters, subset to 1975-2017

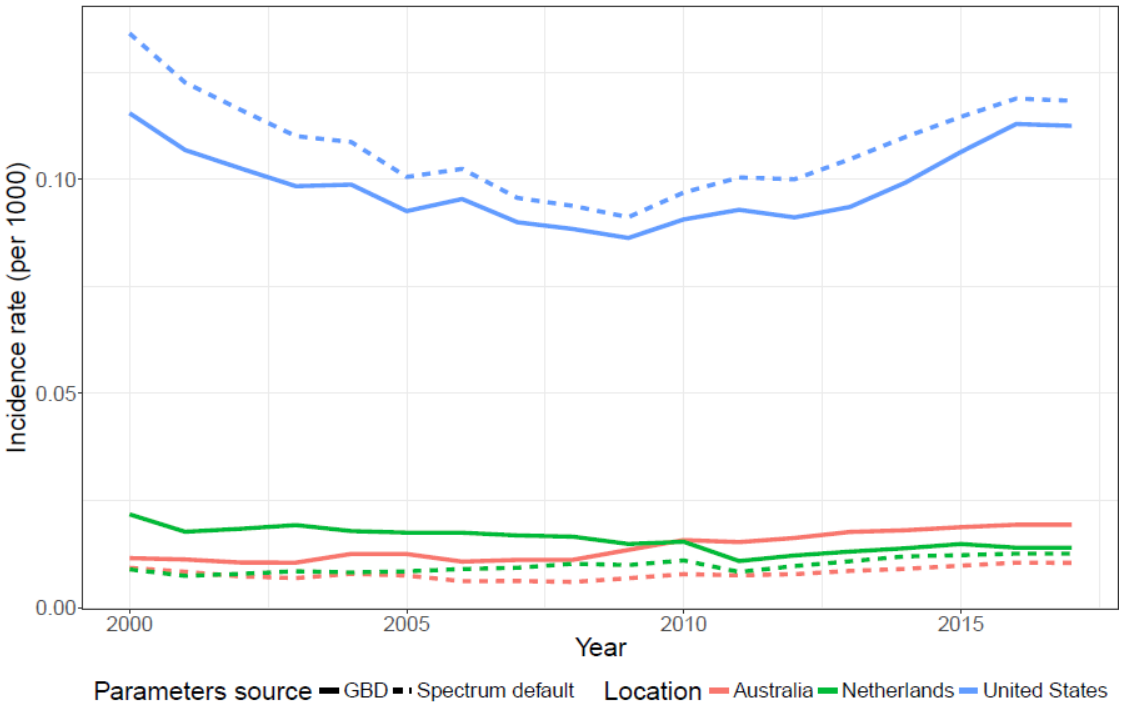

Figure 5: CIBA estimated incidence rates utilizing Spectrum default parameters and GBD parameters, subset to 2000-2017

Fig. 4 and Fig. 5 show estimates from CIBA using a full set of Spectrum default parameters and GBD parameters. While it appears that variation in transition parameters explain only a small portion of the differences between CSAVR and CIBA estimates, there do appear to be important difference in the estimated peak in incidence, as well as levels of incidence in recent years, as seen. As Table 2 shows, the GBD and Spectrum estimates vary substantially across locations and measures of incidence.

Location (year of greatest difference)	**Cumulative new HIV infections**	**New HIV infections in 2017**	**New HIV infections in year of greatest absolute difference in rate space**
Australia (1982)	4341.3 (35.8%)	233.9 (85.5%)	214.3 (22.4%)
The Netherlands (1989)	10983.1 (91.3%)	24.9 (10.9%)	816.6 (97.8%)
USA (1984)	89071.1 (5.6%)	-2052.7 (-5.0%)	31579.4 (31.4%)

Table 2: Statistics summarizing the absolute (GBD – Spectrum) and relative ((GBD-Spectrum) / Spectrum) difference in CIBA estimates with Spectrum default parameters and GBD parameters.

4.2.1. Australia

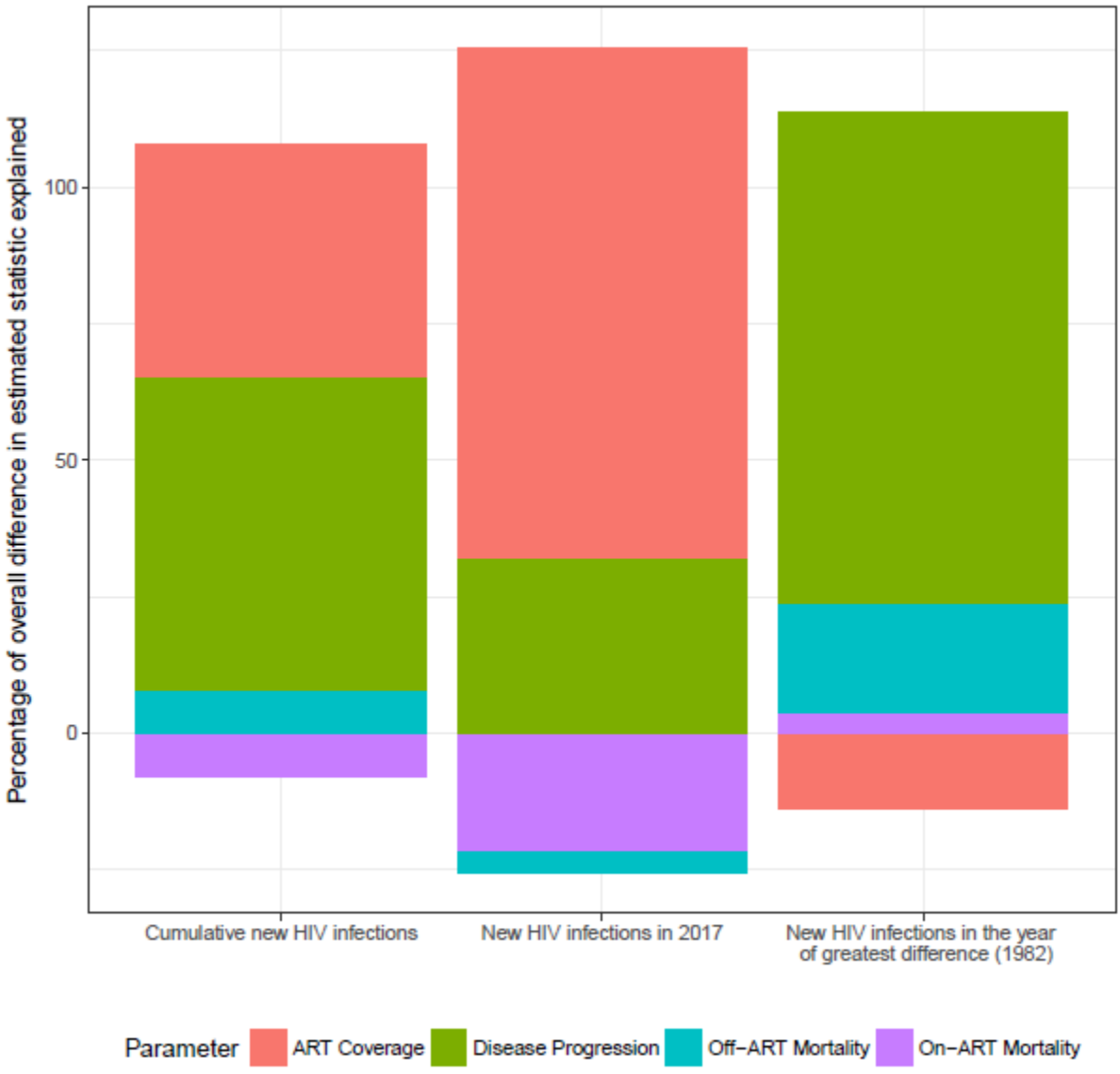

Figure 6: Decomposition of estimate differences attributable to each parameter in Australia

After decomposing the contributions of each parameter to differences in CIBA estimates, as showing in Fig. 6, it appears that ART coverage and disease progression have the largest impact across all statistics in Australia, while the two mortality parameters explain a smaller proportion. For cumulative new infections, differences due to on-ART mortality and off-ART morality parameters largely cancelled each other out, while disease progression explained the majority of the difference. With respect to estimated new HIV infections in 2017, ART coverage was the primary source of variation, while both on-ART mortality and off-ART mortality moved estimates the opposite direction of the overall difference. New HIV infections in 1982 differed primarily as a function of disease progression.

4.2.2. The Netherlands

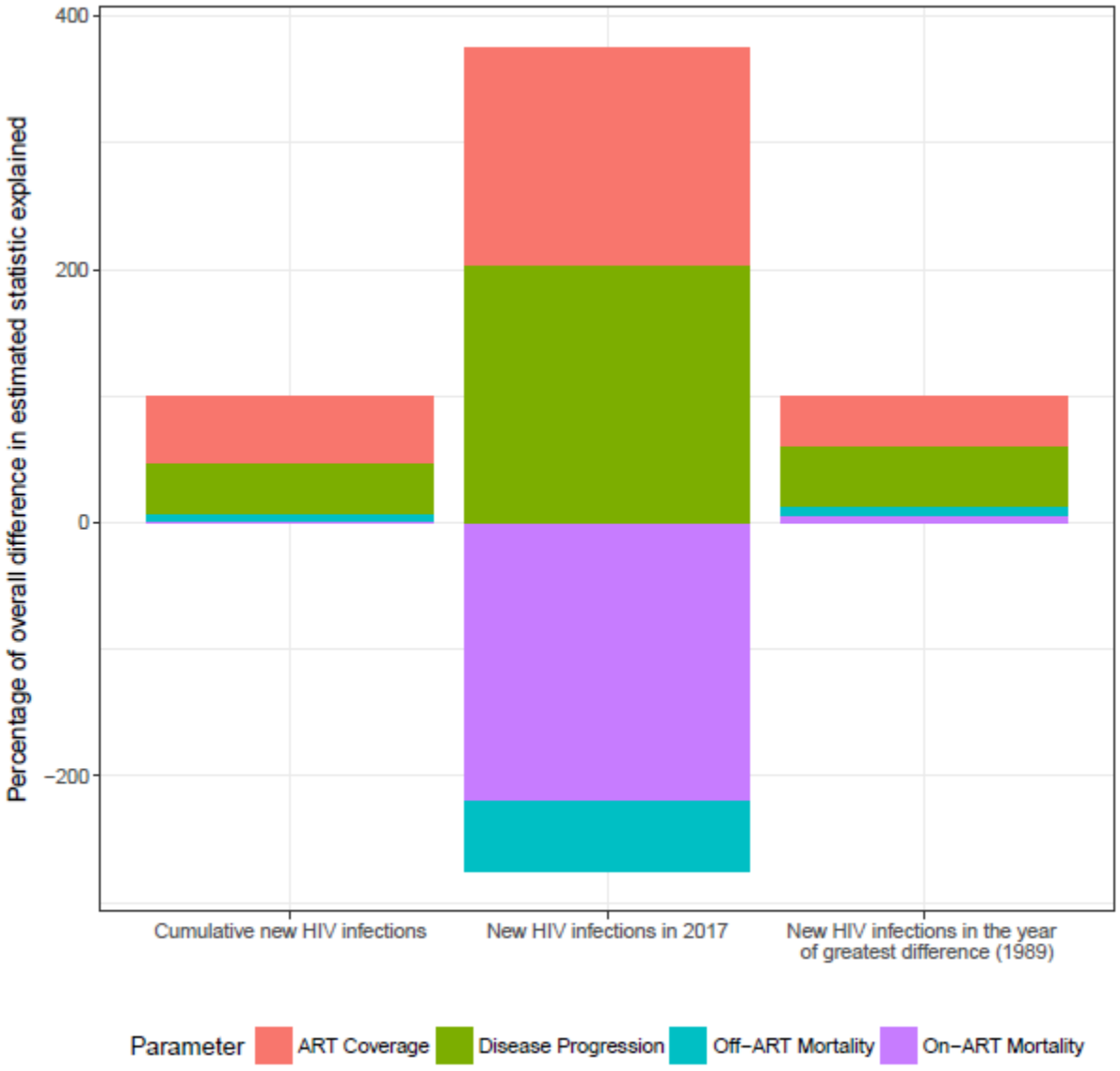

Figure 7: Decomposition of estimate differences attributable to each parameter in the Netherlands

In the Netherlands, ART coverage and disease progression were again the primary contributors to variation in CIBA estimates (see Fig. 7), although the parameters had large antagonistic impacts on estimates of new HIV infections in 2017. For cumulative new HIV infections and new HIV infections in 1989, ART coverage and disease progression explained the majority of variation with similar proportions explained between the two. There was very little overall variation in new HIV infections estimates in 2017 in the Netherlands, which may be the reason for the substantial heterogeneity in the direction parameter contributions to differences in the estimates.

4.2.3. United States

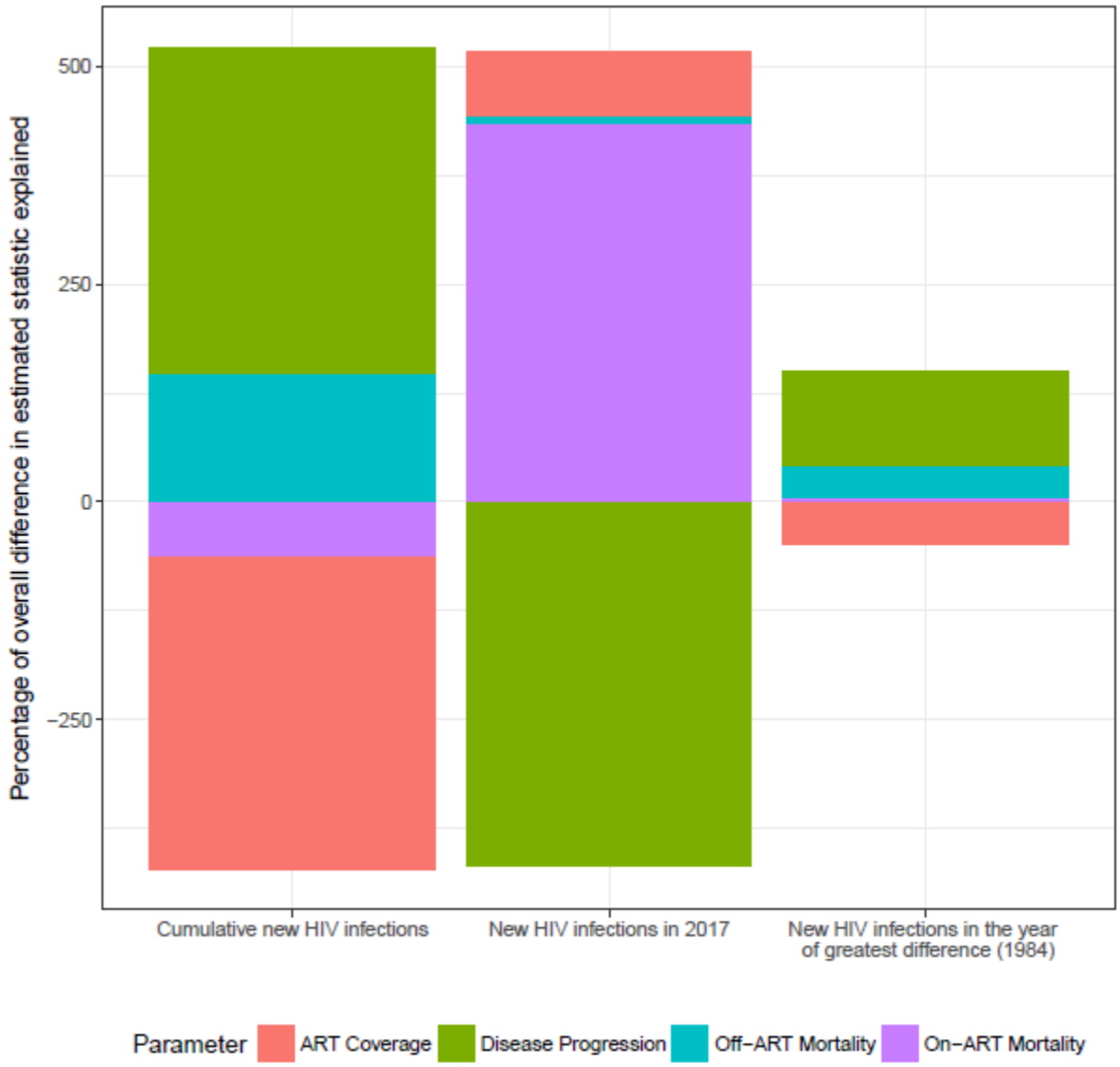

Figure 8: Decomposition of estimate differences attributable to each parameter in the United States

In the United States, ART coverage, disease progression, and on-ART mortality each explain a substantial proportion of the variation in one or more measures of incidence (see Fig. 8). For cumulative new HIV infections, ART coverage and disease progression have a large antagonistic relationship, with disease progression explaining variation in the same direction as the overall difference. For new HIV infections in 2017, disease progression again explains a large proportion of the variation, but here is pushing estimates the opposite direction of the overall difference and the antagonistic relationship is with on-ART mortality. ART coverage and disease progression explain the majority of variation in the year of greatest difference, and the magnitude of variation in the direction of the difference produced by each parameter is smaller than for the other two statistics.

5. Discussion

5.1. Model comparison

There is substantial variation in the estimates produced by each of the models. In terms of incidence estimates, the bespoke models produced close fits to diagnoses data, particularly in the case of the CDC model. Given the reliance of these models on case reports as the primary data source, the quality of the fit makes sense. For the CSAVR and CIBA estimates, it is clear that CIBA is constructed to best fit mortality data, while CSAVR strikes a compromise between all data sources. One major takeaway from the CIBA and CSAVR results is that there appears to be difficulty accurately representing the life course of HIV within the population projection model. The results highlight that when producing a good fit to case report data, it is difficult to accurately estimates mortality, and vice versa. This points to a need to examine opportunities to augment the population projection model to incorporate additional aspects of the natural history of HIV which are currently not being modelled, like the impact of the introduction of ART on mortality rates in the untreated population.

5.2. Decomposition analysis

While differences in transition parameters only explain a small amount of the total variation in estimates from CSAVR and CIBA, it is valuable to understand what parameters might be of greatest importance for future investigation. In general, ART coverage and disease progression were the most important factors in estimate differences, although on-ART mortality played an important role in recent years in the United States. The fact that difference in parameters impact estimates in opposing directions in a number of statistics imply that there are complex interactions between the parameters within the model.

5.3. Strengths and limitations

This study represents a novel contribution to the literature related to estimation of HIV burden in locations with high-quality vital registration data and case reports. Coordination with the UNAIDS Reference Group on Estimates, Modelling and Projections enabled access to country data and assisted in the establishment of connections with country experts to clarify methods and data idiosyncrasies. The simplicity of the decomposition allowed for an interpretable presentation of answers to the difficult question of why models produce different results

One limitation of the study is the small number of locations for which the decomposition analysis was conducted. Looking at trends in the amount variation explained by each parameter across all high-income locations would have given strength to the implications of the study on prior parameters for further investigation. In addition, the study was limited by only conducting the decomposition in CIBA.

In further analysis it would be worthwhile to conduct the same decomposition analysis in CSAVR. This would assist in understanding if priorities in harmonizing parameter estimates align between the two models. In addition, the same analysis in CSAVR would allow for assessment of how differences in the underlying model compare to the impact of difference in input parameters.

5.4. Implications

Based on substantial variation in the results from each of the modeling approaches, it appears that there are number of steps that need to be taken in order to achieve harmony in estimates. The poor fits obtained from CIBA to diagnoses data and CSAVR to deaths data indicate that there is work to be done in producing an accurate complete natural history model for HIV, which is what CSAVR and CIBA intend to do. Future work on these models will need to resolve the apparent discrepancy between data and estimates. The critical role of ART coverage in explaining differences CIBA estimates points to the need for efforts to resolve how ART coverage rates will be established in locations where it is difficult to estimate the number of PLHIV on treatment. This analysis offers insight for countries that are improving their vital registration and surveillance systems on the data and methods that might be incorporated into future modelling strategies.

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7. Appendix

Location	Statistic	Parameter	Proportion of total difference explained by parameter (%)	Difference from parameter	Total Difference
Australia	Cumulative new HIV infections	On-ART Mortality	-7.8	-339.7	4341.3
Australia	Cumulative new HIV infections	Off-ART Mortality	8.0	346.2	4341.3
Australia	Cumulative new HIV infections	Disease Progression	57.2	2484.9	4341.3
Australia	Cumulative new HIV infections	ART Coverage	42.6	1849.8	4341.3
Australia	New HIV infections in 2017	On-ART Mortality	-21.6	-50.5	233.9
Australia	New HIV infections in 2017	Off-ART Mortality	-3.8	-9.0	233.9
Australia	New HIV infections in 2017	Disease Progression	32.3	75.5	233.9
Australia	New HIV infections in 2017	ART Coverage	93.1	217.9	233.9
Australia	New HIV infections in the year of greatest difference (1982)	On-ART Mortality	3.7	7.9	214.3
Australia	New HIV infections in the year of greatest difference (1982)	Off-ART Mortality	20.1	43.2	214.3
Australia	New HIV infections in the year of greatest difference (1982)	Disease Progression	89.9	192.7	214.3
Australia	New HIV infections in the year of greatest difference (1982)	ART Coverage	-13.8	-29.5	214.3
Netherlands	Cumulative new HIV infections	On-ART Mortality	1.3	142.7	10983.1
Netherlands	Cumulative new HIV infections	Off-ART Mortality	5.8	639.8	10983.1

Netherlands	Cumulative new HIV infections	Disease Progression	39.7	4360.7	10983.1
Netherlands	Cumulative new HIV infections	ART Coverage	53.2	5839.8	10983.1
Netherlands	New HIV infections in 2017	On-ART Mortality	-220.2	-54.7	24.9
Netherlands	New HIV infections in 2017	Off-ART Mortality	-54.6	-13.6	24.9
Netherlands	New HIV infections in 2017	Disease Progression	203.3	50.5	24.9
Netherlands	New HIV infections in 2017	ART Coverage	171.5	42.6	24.9
Netherlands	New HIV infections in the year of greatest difference (1989)	On-ART Mortality	5.4	44.4	816.6
Netherlands	New HIV infections in the year of greatest difference (1989)	Off-ART Mortality	8.2	66.9	816.6
Netherlands	New HIV infections in the year of greatest difference (1989)	Disease Progression	47.4	387.4	816.6
Netherlands	New HIV infections in the year of greatest difference (1989)	ART Coverage	38.9	317.9	816.6
United States	Cumulative new HIV infections	On-ART Mortality	-63.5	-56599.4	89071.1
United States	Cumulative new HIV infections	Off-ART Mortality	147.4	131301.5	89071.1
United States	Cumulative new HIV infections	Disease Progression	374.3	333381.4	89071.1
United States	Cumulative new HIV infections	ART Coverage	-358.2	-319012.3	89071.1
United States	New HIV infections in 2017	On-ART Mortality	435.0	-8928.4	-2052.7
United States	New HIV infections in 2017	Off-ART Mortality	10.0	-204.5	-2052.7
United States	New HIV infections in 2017	Disease Progression	-418.6	8591.7	-2052.7

United States	New HIV infections in 2017	ART Coverage	73.6	-1511.5	-2052.7
United States	New HIV infections in the year of greatest difference (1984)	On-ART Mortality	4.9	1532.9	31579.4
United States	New HIV infections in the year of greatest difference (1984)	Off-ART Mortality	37.5	11849.9	31579.4
United States	New HIV infections in the year of greatest difference (1984)	Disease Progression	106.8	33717.1	31579.4
United States	New HIV infections in the year of greatest difference (1984)	ART Coverage	-49.1	-15520.5	31579.4

Table 3: Complete CIBA decomposition results