

# HIV.LifeTables 1.0:

## R package: HIV Prevalence-Calibrated Model Life Tables for Countries with Generalized HIV Epidemics

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# 1 Package Overview

`HIV.LifeTables` provides functions to estimate a complete set of mortality rates as a function of demographic and epidemiological inputs.<sup>1</sup> The demographic input can be either life expectancy at birth ( $e_0$ ),  ${}_5q_0$  alone, or  ${}_5q_0$  with  ${}_{45}q_{15}$ . The epidemiological input must include HIV prevalence and can optionally include adult antiretroviral therapy (ART) coverage and child ART coverage (i.e. prevalence alone, prevalence with adult ART, or prevalence with adult ART coverage and child ART coverage).<sup>2</sup>

## 1.1 Required packages

`HIV.LifeTables` requires the `bayesPop` package and installs it when this package is loaded.

## 1.2 Model Calibration

The package has a number of functions that execute the mechanics of the model (e.g. `hiv.mortmod()`, `mortmod.e0()`). Those mechanics work with a set of fixed model parameters based on some model calibration.

By default, the package functions access an R workspace in the ‘data’ folder of this package that contains fixed model parameters from calibrating the model with 5-year (1970-2010) mortality data from the *World Population Prospects 2012* with standard age groups (0, 1-4, 5-9, 10-14, ..., 100+) and epidemiological data (i.e. prevalence, ART coverage) from UNAIDS 2012 revision. The epidemiological data come in 1-year format so the mid-period (1973, 1978, 1983, ..., 2003, 2008) estimate is used for each 5-year period in the mortality data. While this is the default calibration, a function is included in this package for easily recalibrating the model (estimating new fixed parameters), `hiv.mlt.recal()`. See section 5 for further details on recalibration.

# 2 Installing and loading the package

The package is a local source package and can be installed from the R console with

```
install.packages("HIV.LifeTables_1.0.tar.gz", repos=NULL, type="source")
```

Once the package is installed, one can load it and see the help files with

```
library(HIV.LifeTables)
?HIV.LifeTables
```

---

<sup>1</sup>Sharrow DJ, Clark SJ, Raftery AE (2014) Modeling Age-Specific Mortality for Countries with Generalized HIV Epidemics. *PLoS ONE* 9(5): e96447. doi:10.1371/journal.pone.0096447

<sup>2</sup>Due to the limited variation in ART coverage, using adult or child ART coverage as an input is not recommended at this time. Future calibrations with sufficient effect of ART coverage may change this.

### 3 Producing a complete set of mortality rates using `hiv.mortmod()`

The primary function is `hiv.mortmod()`. The function can be evaluated three ways:

1. with prevalence and life expectancy at birth ( $e_0$ )
2. with prevalence and  ${}_5q_0$
3. with prevalence and  ${}_5q_0$  and  ${}_{45}q_{15}$

`hiv.mortmod()` simply aggregates three smaller functions presented in section 4. This function (as well as the smaller individual functions that it aggregates) also have additional functionality to include adult ART or adult ART with child ART in any of the three combinations of inputs above. The fixed model parameters are estimated by region (African vs. non-African) and sex, so the user must also supply an indication for each of these. `hiv.mortmod` takes as arguments:

`e0` life expectancy at birth

`child.mort` child mortality expressed as the probability a new born will die before reaching age 5 ( ${}_5q_0$ )

`adult.mort` adult mortality expressed as the probability a 15-year-old will die before reaching age 60 ( ${}_{45}q_{15}$ )

`prev` HIV prevalence expressed as a percentage; prevalence is the only required epidemiological input

`child.art` Child ART coverage expressed a percentage; optional; if `child.art=NULL` this input is ignored

`adult.art` Adult ART coverage expressed a percentage; optional; if `adult.art=NULL` this input is ignored

`model` Indicates which mortality indicators will be used as inputs expressed as an integer of `model=1` for models based on prevalence and  $e_0$ , `model=2` for models based on prevalence and  ${}_5q_0$ , or `model=3` for models based on prevalence,  ${}_5q_0$ , and  ${}_{45}q_{15}$

`region` A region expressed as an integer of either `region=1` for African models or `region=0` for all other countries

`sex` The sex of the desired life table expressed as an integer of either `sex=1` for female or `sex=0` for male

`lt` If `lt=TRUE` a life table will be calculated based on the estimated mortality rates

**opt** If **opt=TRUE**, the model will produce output  ${}_nm_x$  that will closely approximate the the input mortality indicator(s).

**recal** Defaults to **recal=NULL**. **recal=NULL** uses the model calibration (fixed parameters) saved in the workspace in the ‘data’ folder of this package. This argument could also be set to a character string indicating a different workspace (including file path if not in the working directory) from which to take the fixed parameters. The function **hiv.mlt.recal()** will recalibrate the fixed model parameters and save a workspace that can be used for this argument.

## 3.1 Example usage

### 3.1.1 Example usage with prevalence and $e_0$

- To obtain a mortality rate schedule for Africa, female, at  $e_0 = 63$  and HIV prevalence of 5%

```
> hiv.mortmod(prev=5, e0=63, model=1, region=1, sex=1)
[1] 0.056431283 0.006159641 0.002016322 0.001276233 0.001833200
[6] 0.002762606 0.003943120 0.004875801 0.005835859 0.006529953
[11] 0.007572941 0.009627145 0.012961508 0.019424509 0.030206215
[16] 0.048908085 0.078776842 0.128094506 0.196629924 0.287481141
[21] 0.395360972 0.527321956
```

- One can calculate a life table as well by setting **lt=TRUE**.

```
> hiv.mortmod(prev=5, e0=63, model=1, region=1, sex=1, lt=TRUE)
  age      Lx      lx      qx      ax      mx
1   0 0.957374019 1.000000000 0.054025844 0.2110076 0.056431283
2   1 3.725073097 0.945974156 0.015791241 1.4363373 0.006159641
3   5 4.588940053 0.923029044 0.010024368 2.1678606 0.002016322
4  10 4.554219954 0.913776262 0.006360687 2.4775054 0.001276233
5  15 4.520404665 0.907964017 0.009126802 2.6570687 0.001833200
6  20 4.469417068 0.899677209 0.013724075 2.6538090 0.002762606
7  25 4.395231393 0.887329971 0.019531547 2.6101414 0.003943120
8  30 4.299090591 0.869999045 0.024093718 2.5715190 0.004875801
9  35 4.185314878 0.849037534 0.028767758 2.5486993 0.005835859
10 40 4.057896364 0.824612627 0.032133724 2.5406793 0.006529953
11 45 3.918322295 0.798114753 0.037179144 2.5650953 0.007572941
12 50 3.755151571 0.768441530 0.047045075 2.5919023 0.009627145
13 55 3.551846788 0.732290140 0.062867554 2.6192362 0.012961508
14 60 3.280607249 0.686252850 0.092858172 2.6357955 0.019424509
15 65 2.904654287 0.622528665 0.140939070 2.6294469 0.030206215
16 70 2.392825596 0.534790054 0.218830768 2.5978105 0.048908085
```

```

17 75 1.749318937 0.417761536 0.329867185 2.5364702 0.078776842
18 80 1.052457260 0.279955714 0.481554710 2.4236998 0.128094506
19 85 0.471543070 0.145141721 0.638820301 2.2587687 0.196629924
20 90 0.141754705 0.052422243 0.777376200 2.0465967 0.287481141
21 95 0.025773019 0.011670439 0.873115904 1.8027176 0.395360972
22 100 0.002808139 0.001480793 1.000000000 NA 0.527321956

```

		Tx	ex
1	63.000024996	63.000025	
2	62.042650977	65.585989	
3	58.317577880	63.180653	
4	53.728637827	58.798461	
5	49.174417873	54.158994	
6	44.654013209	49.633372	
7	40.184596141	45.287094	
8	35.789364748	41.137246	
9	31.490274156	37.089378	
10	27.304959278	33.112468	
11	23.247062914	29.127469	
12	19.328740619	25.153170	
13	15.573589048	21.266965	
14	12.021742261	17.517949	
15	8.741135011	14.041337	
16	5.836480725	10.913593	
17	3.443655129	8.243112	
18	1.694336192	6.052158	
19	0.641878932	4.422429	
20	0.170335862	3.249305	
21	0.028581158	2.449022	
22	0.002808139	NA	

- Add adult ART coverage (disclaimer: This example is meant to show how ART coverage should be inputted but use of ART as an input is not recommended at this time.) Note: child ART coverage cannot be included alone. It must be in conjunction with adult ART as there is no calibrated model that includes child ART without adult ART.

```

> hiv.mortmod(prev=5, e0=63, model=1, region=1, sex=1, adult.art=50)
[1] 0.055756466 0.006002478 0.001986208 0.001262138 0.001810221
[6] 0.002783200 0.004080051 0.005090316 0.006097145 0.006740618
[11] 0.007731598 0.009704862 0.012957110 0.019292443 0.029915022
[16] 0.048333514 0.077792638 0.126470810 0.194332353 0.284457031
[21] 0.392397874 0.524690203

```

### 3.1.2 Example usage with prevalence and ${}_5q_0$

- A complete set of mortality rates using  ${}_5q_0$  and prevalence for non-Africa, male, at  ${}_5q_0 = 0.05$  and HIV prevalence of 1.5%

```
> hiv.mortmod(prev=1.5, child.mort=0.05, model=2, region=0, sex=0)
[1] 0.0447983665 0.0018029610 0.0009026468 0.0006763805 0.0013237526
[6] 0.0022823726 0.0030373516 0.0038381385 0.0049509038 0.0063580329
[11] 0.0083191050 0.0113633040 0.0159100860 0.0235698766 0.0351276568
[16] 0.0530027294 0.0805299945 0.1233851745 0.1841218658 0.2639821682
[21] 0.3596483841 0.4729958846
```

### 3.1.3 Example usage with prevalence and ${}_5q_0$ and ${}_{45}q_{15}$

- A complete set of mortality rates using  ${}_5q_0$ ,  ${}_{45}q_{15}$ , and prevalence for Africa, female, at  ${}_5q_0 = 0.08$ ,  ${}_{45}q_{15} = 0.30$  and HIV prevalence of 10%

```
> hiv.mortmod(prev=10, child.mort=0.08, adult.mort=0.30, model=3,
  region=1, sex=1)
[1] 0.064926118 0.004901531 0.002929449 0.001891969 0.002770987
[6] 0.004558057 0.006500086 0.008331982 0.010498182 0.011853281
[11] 0.013286954 0.015594547 0.019823386 0.028203241 0.041449113
[16] 0.062659262 0.095972905 0.147877179 0.221743981 0.318160086
[21] 0.434185793 0.563457164
```

## 4 Individual functions

`hiv.mortmod()` simply aggregates three simpler functions that produce a set of mortality rates based on one of the three potential sets of inputs described at the beginning of section 3. These simpler functions are demonstrated below and only produce a set of age-specific mortality rates. They take as arguments many of the same arguments described for `hiv.mortmod()` but without a life table option or `model`.

### 4.1 `mortmod.e0()`

This function estimates a complete set of mortality rates from HIV prevalence and life expectancy at birth. It is equivalent to `model=1` in the function `hiv.mortmod`.

Note: The life expectancy/prevalence model also includes the optional argument `determ`. `determ=TRUE` will simply return the deterministic model output. `determ=FALSE` adds a random deviation to each age-specific mortality rate. The deviations are drawn from a normal distribution with `mean=0`. The standard deviation is age-specific and is the standard deviation from the distribution of residuals at each each age after fitting the calibration data with the deterministic model. This functionality is only available in the  $e_0$ /prevalence model and typically impacts mortality rates at older ages more substantially.

The following produces a set of mortality rates for Africa, female, at  $e_0 = 55$  and HIV prevalence of 5%.

```
> mortmod.e0(e0=55, prev=5, region=1, sex=1)
[1] 0.085358145 0.012025401 0.003919436 0.002405483 0.003190014
[6] 0.004637624 0.006491922 0.007799719 0.009038966 0.009672068
[11] 0.010654579 0.013084898 0.017168914 0.025369953 0.038876866
[16] 0.061931690 0.097777021 0.155581686 0.234021970 0.335026906
[21] 0.450606499 0.587951319
```

With optional addition of adult ART coverage of 60% (`adult.art=60`)...

```
> mortmod.e0(e0=55, prev=5, region=1, sex=1, adult.art=60)
[1] 0.083995541 0.011619134 0.003841503 0.002369980 0.003136666
[6] 0.004682577 0.006790590 0.008255375 0.009576436 0.010085170
[11] 0.010948903 0.013222455 0.017158151 0.025137552 0.038375034
[16] 0.060960205 0.096147212 0.152951015 0.230370506 0.330313997
[21] 0.446065051 0.583968767
```

## 4.2 `mortmod.5q0()`

This function estimates a complete set of mortality rates from HIV prevalence and child mortality expressed as the probability a newborn will die before reaching age 5. It is equivalent to `model=2` in the function `hiv.mortmod`. The following produces a set of mortality rates for non-Africa, male, at  ${}_5q_0 = 0.05$  and HIV prevalence of 6%.

```
> mortmod.5q0(child.mort=0.05, prev=6, region=0, sex=0)
[1] 0.0450384808 0.0017431217 0.0008920605 0.0006213013 0.0010355987
[6] 0.0019446833 0.0034173987 0.0049365381 0.0067658203 0.0075197720
[11] 0.0082177974 0.0092418803 0.0116731286 0.0168854173 0.0254537663
[16] 0.0388070302 0.0605564207 0.0956537864 0.1479823471 0.2198475212
[21] 0.3164959088 0.4307884331
```

## 4.3 `mortmod.45q15()`

This function estimates a complete set of mortality rates from HIV prevalence, child mortality expressed as the probability a newborn will die before reaching age 5, and adult mortality expressed as the probability a 15-year-old will die before reaching age 60. It is equivalent to `model=3` in the function `hiv.mortmod`. The following produces a set of mortality rates for Africa, female, at  ${}_5q_0 = 0.08$ ,  ${}_{45}q_{15} = 0.30$  and HIV prevalence of 2.5%.

```
> mortmod.45q15(child.mort=0.08, adult.mort=0.30, prev=2.5,
  region=1, sex=1)
[1] 0.064127520 0.005076481 0.003295629 0.002142907 0.003300101
[6] 0.005209334 0.006529226 0.007856514 0.009601735 0.011511711
[11] 0.013906757 0.017750354 0.023613891 0.034085201 0.050116383
[16] 0.076065211 0.116107780 0.177890465 0.264265757 0.375142304
[21] 0.500790831 0.640608521
```



## 5 Recalibrating HIV.LifeTables

As mentioned in section 1.2, there is a default model calibration (fixed parameters) in the ‘data’ folder of this package based on mortality data from WPP 2012 and prevalence/ART data from UNAIDS 2012 revision, but it is possible to recalibrate this model with different data. The function for this task is `hiv.mlt.recal()`. This function takes sex-age-specific mortality and epidemiological data of corresponding periods and recalibrates (estimates a new set of fixed parameters for) the HIV MLT model. The new calibration is saved in an R workspace that can be input as an argument to the functions described already, which work the same way with the new calibration. This function takes as arguments:

- mx.m** A tab delimited text file of age-specific mortality rates for males readable with `read.table()`. The file must have columns titles: “country” (a string for country name); “country\_code” - a numeric for the UN country code; “age” - a numeric indicating age groups; then column names for each period in the calibration dataset. Five year intervals should be “1975-1980”, “1980-1985”, etc. Single year intervals should be “1980”, “1981”, etc.
- mx.f** A tab delimited text file of age-specific mortality rates for females readable with `read.table()`. The file must have columns titles: “country” (a string for country name); “country\_code” - a numeric for the UN country code; “age” - a numeric indicating age groups; then column names for each period in the calibration dataset. Five year intervals should be “1975-1980”, “1980-1985”, etc. Single year intervals should be “1980”, “1981”, etc.
- prev** A tab delimited text file of HIV prevalence rates readable with `read.table()`. The file must have column titles: “country” - a string for country name; “country\_code” - a numeric for the UN country code; then column names for each period in the calibration dataset. Even if **mx.f** and **mx.m** are in 5-year intervals, this data can be 1-year and the argument `midperiod` will indicate which column should be associated with which 5-year period of mx data. If mx data is 1-year and prevalence data is as well, set `midperiod` to the 1-year intervals.
- c.art** A tab delimited text file of child ART coverage rates readable with `read.table()`. The file must have column titles: “country” - a string for country name; “country\_code” - a numeric for the UN country code; then column names for each period in the calibration dataset. Even if **mx.f** and **mx.m** are in 5-year intervals, this data can be 1-year and the argument `midperiod` will indicate which column should be associated with which 5-year period of mx data. If mx data is 1-year and prevalence data is as well, set `midperiod` to the 1-year intervals.
- a.art** A tab delimited text file of adult ART coverage rates readable with `read.table()`. The file must have column titles: “country” - a string for country name; “country\_code” - a

numeric for the UN country code; then column names for each period in the calibration dataset. Even if `mx.f` and `mx.m` are in 5-year intervals, this data can be 1-year and the argument `midperiod` will indicate which column should be associated with which 5-year period of `mx` data. If `mx` data is 1-year and prevalence data is as well, set `midperiod` to the 1-year intervals.

**ages** A numeric vector indicating the beginning age of age intervals of the `mx` data (i.e. 5-year age intervals with childhood ages broken into two groups would be `ages=c(0,1,seq(5,100,5))`). Age intervals must match values in ‘ages’ column from `mx` input data.

**la.countries** A character vector of non-African countries in the calibration dataset. Separate models are calibrated for countries in Africa and countries not in Africa. This argument identifies those countries during calibration.

**midperiod** A numeric vector to indicate which columns of the prevalence, adult ART, and child ART inputs should be used for calibration. If mortality data are in greater than 1-year intervals (e.g. 5-year intervals) but epidemiological data are in 1-year intervals, `midperiod` tells the function which periods in the epidemiological data should correspond to the multi-year periods in mortality data. If `mx` data are 1-year and epidemiological data are also 1-year, set `midperiod` to the 1-year periods from the calibration datasets.

**determ** `determ=FALSE` will calculate the standard deviation of the distribution of residuals at each age after fitting the input data with the calibrated model. These standard deviations can be used to add random noise to the mortality rate schedule by simulating a random deviation for each age from a normal distribution with mean=0 and the standard deviation for a specific age to be added (or subtracted in the case of a negative deviation) to the predicted mortality rate at a given age. `determ=TRUE` will set both the mean and standard deviation to 0, so no deviation will be added—the result being just the deterministic model output. This functionality is only available for the model predicting mortality rates as a function of life expectancy and HIV prevalence, `mortmod.e0`.

**save.output** A character string giving the name of the output workspace file. If NULL, no output workspace is saved.

## 5.1 Example usage for `hiv.mlt.recal()`

### 5.1.1 Example A (GBD 2013 and UNAIDS 2014)

The following shows how to recalibrate the HIV MLT model with 1-year mortality data from the Global Burden of Disease (GBD) Study 2013<sup>3</sup> from 1990-2013 and 1-year prevalence and

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<sup>3</sup>Global Burden of Disease Study 2013. Global Burden of Disease Study 2013 (GBD 2013) Age-Sex Specific All-Cause and Cause-Specific Mortality 1990-2013. Seattle, United States: Institute for Health

ART data from UNAIDS 2014 revision.

1. First read in the new data. Note that we have created a vector for ages up to 80+ as those are the ages in the GBD data. We have also created a vector for midperiod that indicates each single year prevalence/ART period has a corresponding period in the mortality data. Screen shots of the data files are available in figure 1 for reference.

```
## GBD 2013 and UNAIDS 2014
#1. ages
ages.gbd <- c(0,1,seq(5,80,5))

#2. prevalence
prev.2014 <- read.table("UNAIDS2014/HIV_PrevalenceRate.txt", header=T)

#3a. ART (adult)
aart.2014 <- read.table("UNAIDS2014/ART_CoverageAdult.txt", header=T)

#3b. ART (child)
cart.2014 <- read.table("UNAIDS2014/ART_CoverageChild.txt", header=T)

#4. nmx
mxF.gbd <- read.table("GBD2013/mxF.txt", header=T)
mxM.gbd <- read.table("GBD2013/mxM.txt", header=T)

#5. non-African countries
# create vector to indicate which rows in the mortality and
# epidemiological data are the non-African and African Countries
la.countries=c("Bahamas", "Belize", "Cambodia", "Dominican Republic",
"Estonia", "Guyana", "Haiti", "Honduras", "Jamaica", "Panama",
"Russian Federation", "Suriname", "Thailand", "Trinidad and Tobago",
"Ukraine")

#6. midperiod
midperiod.gbd=seq(1990,2013,1)

recal.gbd <- hiv.mlt.recal.un(ages=ages.gbd, mx.m=mxM.gbd, mx.f=mxF.gbd,
```

---

Metrics and Evaluation (IHME), 2014.

```
prev=prev.2014, c.art=cart.2014, a.art=aart.2014, midperiod=midperiod.gbd,
save.output="Ws-models-gbd.RData")
```

The function saves the new fixed parameters in the output R workspace and returns several fixed parameters of the model:

```
> str(recal.gbd)
List of 9
 $ svd.comps   : num [1:36, 1:3] -0.0989 -0.1746 -0.2265 -0.2358 -0.2224 ...
 $ weights     : num [1:1296, 1:11] -0.0486 -0.0469 -0.0503 -0.0622 -0.0512 ...
 $ params.a.m  : num [1:7, 1:9, 1:3] 8.568 0.344 NA NA NA ...
 .. attr(*, "dimnames")=List of 3
 .. ..$ : chr [1:7] "Intercept" "e0" "5q0" "45q15" ...
 .. ..$ : chr [1:9] "mod1" "mod2" "mod3" "mod4" ...
 .. ..$ : chr [1:3] "co1" "co2" "co3"
 $ params.a.f  : num [1:7, 1:9, 1:3] 9.014 0.317 NA NA NA ...
 .. attr(*, "dimnames")=List of 3
 .. ..$ : chr [1:7] "Intercept" "e0" "5q0" "45q15" ...
 .. ..$ : chr [1:9] "mod1" "mod2" "mod3" "mod4" ...
 .. ..$ : chr [1:3] "co1" "co2" "co3"
 $ params.na.m : num [1:7, 1:9, 1:3] 5.465 0.403 NA NA NA ...
 .. attr(*, "dimnames")=List of 3
 .. ..$ : chr [1:7] "Intercept" "e0" "5q0" "45q15" ...
 .. ..$ : chr [1:9] "mod1" "mod2" "mod3" "mod4" ...
 .. ..$ : chr [1:3] "co1" "co2" "co3"
 $ params.na.f : num [1:7, 1:9, 1:3] 5.421 0.371 NA NA NA ...
 .. attr(*, "dimnames")=List of 3
 .. ..$ : chr [1:7] "Intercept" "e0" "5q0" "45q15" ...
 .. ..$ : chr [1:9] "mod1" "mod2" "mod3" "mod4" ...
 .. ..$ : chr [1:3] "co1" "co2" "co3"
 $ params.a    : num [1:7, 1:9, 1:3] 8.089 0.343 NA NA NA ...
 .. attr(*, "dimnames")=List of 3
 .. ..$ : chr [1:7] "Intercept" "e0" "5q0" "45q15" ...
 .. ..$ : chr [1:9] "mod1" "mod2" "mod3" "mod4" ...
 .. ..$ : chr [1:3] "co1" "co2" "co3"
 $ params.na   : num [1:7, 1:9, 1:3] 4.023 0.407 NA NA NA ...
 .. attr(*, "dimnames")=List of 3
 .. ..$ : chr [1:7] "Intercept" "e0" "5q0" "45q15" ...
 .. ..$ : chr [1:9] "mod1" "mod2" "mod3" "mod4" ...
 .. ..$ : chr [1:3] "co1" "co2" "co3"
 $ input.epi   : 'data.frame': 1296 obs. of 6 variables:
 ..$ country    : Factor w/ 54 levels "Angola","Bahamas",...: 1 1 1 1 1 ...
 ..$ country_code: int [1:1296] 24 24 24 24 24 24 24 24 24 24 ...
```

```
..$ midperiod : num [1:1296] 1990 1991 1992 1993 1994 ...  
..$ prev      : num [1:1296] 0.234 0.376 0.539 0.719 0.909 ...  
..$ aart      : num [1:1296] 0 0 0 0 0 0 0 0 0 0 ...  
..$ cart      : num [1:1296] 0 0 0 0 0 0 0 0 0 0 ...
```

3. We can now use the saved output workspace, “Ws-models-gbd.RData”, as an input to the other functions in the package to obtain predicted mortality rates based on the new calibration. Here’s an example using the same inputs as the first usage example in section 3.1.1.

```
> hiv.mortmod(prev=5, e0=63, model=1, region=1, sex=1,
  recal="Ws-models-gbd.RData")
[1] 0.0553307119 0.0067525992 0.0014117048 0.0009708096 0.0013930695
[6] 0.0026738842 0.0039836771 0.0049489976 0.0058585205 0.0066056108
[11] 0.0079300969 0.0104071995 0.0140582614 0.0212239174 0.0317502817
[16] 0.0497779600 0.0760247987 0.1605567797
```

Or the equivalent with one of the individual functions...

```
> mortmod.e0(e0=63, prev=5, region=1, sex=1, recal="Ws-models-gbd.RData")
[1] 0.0553307119 0.0067525992 0.0014117048 0.0009708096 0.0013930695
[6] 0.0026738842 0.0039836771 0.0049489976 0.0058585205 0.0066056108
[11] 0.0079300969 0.0104071995 0.0140582614 0.0212239174 0.0317502817
[16] 0.0497779600 0.0760247987 0.1605567797
```

- Note that the estimates themselves are slightly different than the example in 3.1.1 due to the calibration with GBD 2013 and UNAIDS 2014 instead of the default WPP 2012 and UNAIDS 2012 but also that there are now mortality rates for ages 0, 1-4, 5-9, ..., 80+ since those are the available ages in the GBD mortality data.

### 5.1.2 Example B (WPP 2012 and UNAIDS 2014)

Example A showed recalibration with 1-year mortality data and 1-year epidemiological data. The following shows recalibration with 5-year mortality data from WPP 2012 and 1-year epidemiological data from UNAIDS 2014.

1. Get the WPP 2012 mortality data and set up necessary input objects. Note the change in `midperiod` because we now have 5-year mortality data and we want to use the midperiod prevalence and ART estimates for each 5-year mortality period. Also note we have different age groups because the WPP mortality data have an open age interval of 100+.

```
ages.wpp <- c(0,1,seq(5,100,5)) ## default input
midperiod.wpp <- seq(1973,2008,5)

mxF.wpp <- read.table("WPP2012/mxF.txt", header=T)
mxM.wpp <- read.table("WPP2012/mxM.txt", header=T)
```

2. Use function to recalibrate

```
recal.wpp <- hiv.mlt.recal(ages=ages.wpp, mx.m=mxM.wpp, mx.f=mxF.wpp,  
  prev=prev.2014, c.art=cart.2014, a.art=aart.2014, midperiod=midperiod.wpp,  
  save.output="Ws-models-wpp.RData")
```

3. Now use the new recalibration as input to existing functions. Again, let's use our previous example input but with this new calibration.

```
> mortmod.e0(e0=63, prev=5, region=1, sex=1, recal="Ws-models-wpp.RData")  
[1] 0.054036718 0.005368370 0.001796151 0.001178111 0.001794567  
[6] 0.002601860 0.003468100 0.004257403 0.005192161 0.006207310  
[11] 0.007704441 0.010334768 0.014370155 0.021807695 0.033979221  
[16] 0.055002491 0.088557834 0.143875168 0.220240813 0.321816568  
[21] 0.441739615 0.589489063
```

- Again the estimates themselves are slightly different with this calibration and we now have ages groups up to 100+.

[illegible]

(a) Adult ART coverage .txt file cropped screenshot

		HM_Predictions.txt																																	
"country"	"country_code"	'1976'	'1971'	'1972'	'1973'	'1974'	'1975'	'1976'	'1977'	'1978'	'1979'	'1980'	'1981'	'1982'	'1983'	'1984'	'1985'	'1986'	'1987'	'1988'	'1989'	'1990'	'1991'	'1992'	'1993'	'1994'	'1995'	'1996'	'1997'	'1998'	'1999'	'2000'	'2001'		
"Angola"	24	0	0	0	0	0	0.00006	0.00051	0.00029	0.00051	0.00084	0.00132	0.00202	0.00444	0.00849	0.01558	0.02887	0.05202	0.09103	0.14617	0.23405	0.35753	0.55985	0.71883	0.9937	1.1	1.29	1.48	1.56	1.67	1.74	1.78	1.83	1.1	
"Argentina"	133	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Armenia"	24	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Belize"	24	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Benin"	204	0	0	0	0	0	0.00120	0.00129	0.00045	0.00185	0.00166	0.00244	0.00311	0.00424	0.00608	0.00913	0.0146	0.02380	0.0365	0.05991	0.1457	0.22544	0.33447	0.47593	0.64846	0.80861	1.02	1.2	1.35	1.45	1.52	1.54	1.59	1.63	1.69
"Bhutan"	24	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Burkina Faso"	154	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Cameroon"	116	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Canada"	24	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Central African Republic"	140	0	0	0	0	0	0.01250	0.01744	0.024	0.023	0.030	0.04612	0.06228	0.0805	0.117	0.16084	0.22217	0.3083	0.4282	0.56305	0.75378	0.99981	1.3	1.675	2.499	2.96	3.43	3.89	4.29	4.63	4.93	5.11	5.26	5.33	5.5
"Chad"	148	0	0	0	0	0	0.00347	0.00921	0.0153	0.023	0.0326	0.0516	0.07933	0.12212	0.1883	0.2858	0.425	0.612	0.858	1.2	1.78	2.58	3.78	5.48	7.98	11.2	15.6	20.8	26.8	33.6	41.1	49.1	57.1	65.1	
"Chile"	148	0	0	0	0	0	0.00948	0.0181	0.02769	0.0348	0.0567	0.0885	0.13685	0.20183	0.28607	0.3912	0.514	0.6496	0.7939	0.9385	1.08	1.25	1.42	1.6	1.8	2.02	2.25	2.48	2.72	2.98	3.18	3.37	3.53	3.69	3.9
"China"	24	0	0	0	0	0	0.01620	0.0293	0.0517	0.078	0.108	0.142	0.180	0.222	0.266	0.312	0.36	0.408	0.456	0.504	0.552	0.6	0.648	0.696	0.744	0.792	0.84	0.888	0.936	0.984	1.032	1.08	1.128	1.176	
"Cote d'Ivoire"	204	0	0	0	0	0	0.00653	0.0123	0.0242	0.0448	0.0825	0.1416	0.2314	0.3615	0.5318	0.77432	1.08	1.45	2.32	2.83	3.37	3.94	4.5	5.04	5.54	5.98	6.37	6.67	6.84	6.89	6.82	6.63	6.34	5.9	
"Democratic Republic of the Congo"	140	0	0	0	0	0	0.2818	0.4497	0.688	1.1294	0.1519	0.4714	0.2503	0.4133	0.5938	0.6889	0.7499	0.7858	0.8122	0.8353	0.8622	0.87189	0.8838	0.8548	0.8499	0.8299	0.7496	0.6287	0.5065	0.3215	0.73619	0.9437	1.28	1.59	1.9
"Dominican Republic"	242	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Dominican Republic"	214	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Ecuador"	24	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Eritrea"	232	0	0	0	0	0	0.00213	0.00234	0.00254	0.00372	0.005	0.00671	0.00988	0.01422	0.0218	0.03385	0.051	0.0894	0.12886	0.19589	0.28809	0.40377	0.53771	0.67161	0.81296	0.954	1.1	1.25	1.4	1.56	1.72	1.84	1.97	2.1	
"Ethiopia"	232	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Ethiopia"	232	0	0	0	0	0	0.00034	0.0009	0.0015	0.00383	0.00631	0.0116	0.0209	0.03591	0.06482	0.0898	0.15789	0.24131	0.37971	0.524	0.708	1.21	1.6	2.08	2.73	3.21	3.62	3.93	4.1	4.14	4.06	3.87	3.6	3.3	
"Gabon"	206	0	0	0	0	0	0.0159	0.0175	0.0229	0.0326	0.0477	0.0633	0.0830	0.1074	0.13798	0.17599	0.2253	0.2924	0.371	0.4696	0.4305	0.4388	1.1	1.41	1.29	2.82	3.37	3.95	4.5	5.4	5.73	5.91	5.97	5.5	
"Ghana"	270	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Ghana"	270	0	0	0	0	0	0.00526	0.01294	0.01668	0.0279	0.03586	0.04474	0.0572	0.07378	0.1146	0.1585	0.2259	0.30989	0.39685	0.5178	0.65178	0.812	0.9984	1.2	1.41	1.63	1.82	1.99	2.13	2.22	2.27	2.28	2.26	2.21	2.13
"Guinea"	224	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Guinea-Bissau"	224	0	0	0	0	0	0.00983	0.01337	0.0138	0.01662	0.02284	0.03433	0.0545	0.08399	0.13848	0.22681	0.3755	0.45939	0.6084	0.72688	0.87884	0.97494	1.0937	1.28	1.49	1.69	1.82	1.94	2.04	2.1	2.16	2.2	2.26	2.3	
"Guyana"	328	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Honduras"	24	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Honduras"	24	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Honduras"	24	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Honduras"	24	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Honduras"	24	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
"Honduras"	24	0	0	0	0	0	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000										

(b) Prevalence .txt file cropped screenshot

[illegible]

(c) Mortality .txt file cropped screenshot

Figure 1: Screenshots of the various data inputs to `hiv.mlt.recal()`



## 6 Weight ( $\omega$ ) regressions

This model expresses a set of mortality rates as a weighted combination of three age-varying components obtained from a Singular Value Decomposition. The weights are the effective parameters in the model and are modeled themselves as a function of either prevalence and life expectancy at birth, or prevalence and  ${}_5q_0$ , or prevalence,  ${}_5q_0$ , and  ${}_5q_0$ . Both the age-varying components and the models used to estimate the weights can be found in the “data” folder of the package or in the recalibrated saved and printed output from `hiv.mlt.recal()`.