HIV.LifeTables 0.1:
A Package for use of HIV calibrated Model Life Tables for Countries with Generalized Epidemics

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1   Package Overview

HIV.LifeTables provides functions to estimate a complete set of mortality rates as a function of HIV prevalence and one of the following mortality indicators: life expectancy at birth (e_0), child mortality ($_5q_0$), or child mortality with adult mortality ($_{45}q_{15}$).

1.1   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_0.1.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
```

2   Producing a complete set of mortality rates using `hiv.mortmod`

The primary function is `hiv.mortmod`. The function can be evaluated three ways: with prevalence and life expectancy at birth, with prevalence and child mortality, or with prevalence, child mortality, and adult mortality. The function also uses different models for African and non-African countries (Bahamas, Belize, Guyana, Haiti, Jamaica) and for males and females. This function also has the option of producing a life table based on the estimated mortality rates. It takes as arguments:

     prev HIV prevalence expressed as a percentage

     e0 life expectancy at birth

child.mort child mortality expressed as the probability of death between age 0 and 5 ($_5q_0$)

adult.mort adult mortality expressed as the probability of death between age 15 and 60 ($_{45}q_{15}$)

     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 child mortality, or `model=3` for models based on prevalence, child mortality, and adult mortality

     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 (The user can supply their own $_na_x$ values or the default is half the length of the age interval except at the youngest ages.)

opt If `opt=TRUE`, the model will produce output $_nm_x$ that will match the the input mortality indicator(s).

2.1 Example usage

- 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]  0.059886927 0.007030778 0.002051046 0.001165340 0.001637792
 [6]  0.003105215 0.004777112 0.005900426 0.006271064 0.006223325
[11]  0.006490759 0.007852528 0.010989756 0.017037184 0.027739636
[16]  0.045931223 0.075528092 0.120927924 0.186566772 0.274437414
[21]  0.381615656 0.505724588
```

- One can calculate a life table as well by setting `lt=TRUE` this time for Africa, males, at $e_0 = 55$ and HIV prevalence of 8%.

```
> hiv.mortmod(prev=8, e0=55, model=1, region=1, sex=0, lt=TRUE)
$e0
   ex
54.23

$lt.5q0
[1] 0.13098

$lt.45q15
[1] 0.3640926

$lt
      Age nax         nmx          nqx         npx    ndx     lx     nLx
 [1,]   0 2.5 0.083577133 0.095556660 0.9044433   9556 100000 114334
 [2,]   1 2.5 0.009938262 0.039169137 0.9608309   3542  90444 356463
 [3,]   5 2.5 0.003195222 0.015849502 0.9841505   1378  86902 431065
 [4,]  10 2.5 0.001960565 0.009755013 0.9902450    834  85524 425535
 [5,]  15 2.5 0.002572152 0.012778589 0.9872214   1082  84690 420745
```

```
 [6,]  20 2.5 0.004357272 0.021551597 0.9784484  1802 83608 413535
 [7,]  25 2.5 0.006637043 0.032643574 0.9673564  2670 81806 402355
 [8,]  30 2.5 0.008840107 0.043244813 0.9567552  3423 79136 387122
 [9,]  35 2.5 0.010591498 0.051591415 0.9484086  3906 75713 368800
[10,]  40 2.5 0.011677925 0.056733309 0.9432667  4074 71807 348850
[11,]  45 2.5 0.012629470 0.061214583 0.9387854  4146 67733 328300
[12,]  50 2.5 0.014565819 0.070270238 0.9297298  4468 63587 306765
[13,]  55 2.5 0.018638077 0.089041479 0.9109585  5264 59119 282435
[14,]  60 2.5 0.026536234 0.124426634 0.8755734  6701 53855 252522
[15,]  65 2.5 0.040160166 0.182479784 0.8175202  8605 47154 214258
[16,]  70 2.5 0.063169662 0.272771154 0.7272288 10515 38549 166458
[17,]  75 2.5 0.099419708 0.398140907 0.6018591 11161 28034 112268
[18,]  80 2.5 0.152542418 0.552147357 0.4478526  9317 16873  61072
[19,]  85 2.5 0.226097822 0.722244397 0.2777556  5457  7556  24138
[20,]  90 2.5 0.320843505 0.890189071 0.1098109  1869  2099   5822
[21,]  95 2.5 0.432807798 1.000000000 0.0000000   230   230    531
           Tx    ex
 [1,] 5423373 54.23
 [2,] 5309039 58.70
 [3,] 4952576 56.99
 [4,] 4521511 52.87
 [5,] 4095976 48.36
 [6,] 3675231 43.96
 [7,] 3261696 39.87
 [8,] 2859341 36.13
 [9,] 2472219 32.65
[10,] 2103419 29.29
[11,] 1754569 25.90
[12,] 1426269 22.43
[13,] 1119504 18.94
[14,]  837069 15.54
[15,]  584546 12.40
[16,]  370289  9.61
[17,]  203831  7.27
[18,]   91564  5.43
[19,]   30491  4.04
[20,]    6354  3.03
[21,]     531  2.31
```

- A complete set of mortality rates using child mortality and prevalence for non-Africa, male, at $_5q_0 = 0.10$ and HIV prevalence of 1.5%

```
> hiv.mortmod(prev=1.5, child.mort=0.10, model=2, region=0, sex=0, lt=FALSE)
 [1] 0.0781124841 0.0072497168 0.0015664801 0.0009867883 0.0015737551
 [6] 0.0025674605 0.0035340808 0.0043980923 0.0053331007 0.0064266446
[11] 0.0080245458 0.0108790242 0.0158187906 0.0241353517 0.0375845333
[16] 0.0598774582 0.0950131783 0.1466799421 0.2182931727 0.3104665451
[21] 0.4191927637 0.5418424915
```

- A complete set of mortality rates using child mortality, adult mortality, and prevalence for Africa, female, at $_5q_0 = 0.15$, $_{45}q_{15} = 0.30$ and HIV prevalence of 2.5%

```
> hiv.mortmod(prev=2.5, child.mort=0.15, adult.mort=0.30, model=3, region=1,
sex=1)
 [1] 0.101441832 0.015866436 0.004516126 0.002516932 0.003054113
 [6] 0.004431973 0.005750258 0.006741688 0.007439870 0.008004072
[11] 0.008981754 0.011242938 0.015672013 0.023726604 0.037601326
[16] 0.060435787 0.096389614 0.149601174 0.223753365 0.319473695
[21] 0.432284898 0.558026904
```

3   Individual functions

`hiv.mortmod` simply aggregates simpler functions that produce a set of mortality rates based on one of the three potential sets of inputs. These simpler functions are demonstrated below.

3.1   `mortmod.e0`

This function estimates a complete set of mortality rates from HIV prevalence and life expectancy. It is equivalent to `model=1` in the function `hiv.mortmod`. 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]  0.086751577 0.012558998 0.004022234 0.002271267 0.002890524
 [6]  0.004950952 0.007225248 0.008795135 0.009387003 0.009360933
[11]  0.009681353 0.011460632 0.015617940 0.023546823 0.037312174
[16]  0.060090127 0.096173138 0.150040181 0.225950452 0.325236126
[21]  0.443934501 0.578734660
```

3.2   `mortmod.5q0`

This function estimates a complete set of mortality rates from HIV prevalence and child mortality expressed as a probability of death between age 0 and 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 $_5q_0 == 0.10$ and HIV prevalence of 2.5%.

```
> mortmod.5q0(child.mort=0.10, prev=2.5, region=0, sex=0)
 [1]  0.0789786729 0.0070606306 0.0014548463 0.0009460926 0.0014720469
 [6]  0.0025387880 0.0038224330 0.0050611170 0.0061880673 0.0071990337
[11]  0.0084910754 0.0109027230 0.0153097118 0.0230898050 0.0359261172
[16]  0.0572684713 0.0910451083 0.1409780888 0.2106777406 0.3011543960
[21]  0.4089067514 0.5319490030
```

3.3   `mortmod.45q15`

This function estimates a complete set of mortality rates from HIV prevalence, child mortality expressed as a probability of death between age 0 and 5, and adult mortality expressed as a probability of death between 15 and 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] 0.055360877 0.007199649 0.003154139 0.001793273 0.002414553
 [6] 0.004276607 0.006308256 0.007688125 0.008228049 0.008293882
[11] 0.008755352 0.010611621 0.014745698 0.022590936 0.036314702
[16] 0.059322229 0.096238097 0.152059321 0.231641600 0.336775814
[21] 0.463481433 0.608437701
```

4   Weight (ω) 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 child mortality, or prevalence, child mortality, and adult mortality. Both the age-varying components and the models used to estimate the weights can be found in the workspace, HIV-MLTs-obs.RData in the "data" folder of the package.