# Package 'HIV.LifeTables'

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**Type** Package

**Title** HIV calibrated model life tables for countries with generalized HIV epidemics

**Version** 0.1

**Date** 2012-12-04

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**Description** The functions in this package produce a complete set of mortality rates as a function of a combination of HIV prevalence and either life expectancy at birth (e0), child mortality (5q0), or child mortality with adult mortality (45q15)

**License** Unlimited

**LazyData** yes

**LazyLoad** yes

**Depends** R (>= 2.10)

**NeedsCompilation** no

**Repository** CRAN

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## R topics documented:

HIV.LifeTables-package

*HIV calibrated model life tables for countries with generalized HIV epidemics*

## Description

The functions in this package produce a complete set of mortality rates as a function of a combination of HIV prevalence and either life expectancy at birth (e0), child mortality alone (5q0), or child mortality with adult mortality (45q15)

## Details

| | |
|---|---|
| Package: | HIV.LifeTables |
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The central function is `hiv.mortmod` which takes prevalence and some mortality indicator (e0, 5q0 alone, or 5q0 with 45q15) to produce set of mortality rates. The user also needs to select a region (Africa or Caribbean) and sex. `hiv.mortmod` will also produce a life table based on the estimated mortality rates. `mortmod.e0`, `mortmod.5q0`, and `mortmod.45q15` produce mortality rates for the various input combinations.

## Author(s)

David J Sharrow
Maintainer: Dave Sharrow <dsharrow@uw.edu>

## References

Sharrow, David J., Samuel J. Clark, Adrian E. Raftery. 2013 "Modeling Age-Specific Mortality for Countries with a Generalized HIV Epidemic" http://www.iussp.org/en/event/17/programme/paper/3284

## Examples

```
## produces a life table and mortality rates at 1.5% prevalence,
## life expectancy of 60, for Africa Females
hiv.mortmod(prev=1.5, e0=60, model=1, region=1, sex=1, lt=TRUE)
```

`hiv.mortmod` *HIV calibrated model life tables for countries with generalized HIV epidemics*

## Description

This function produces a complete set of mortality rates for ages 0, 1-4, 5-9, 10-14, ...,100+ and life table given a region, sex, and set of inputs which must include HIV prevalence and one of the following mortality indicators: life expectancy at birth (e0), child mortality alone (5q0), or child mortality with adult mortality (45q15)

## Usage

```
hiv.mortmod(prev=NULL, e0=NULL, child.mort = NULL, adult.mort = NULL, model = 1,
region = 1, sex = 1, lt = FALSE, nax=NULL, opt=TRUE)
```

## Arguments

| | |
|---|---|
| `prev` | HIV prevalence expressed as a percentage |
| `e0` | Life expectancy at birth (used only if model=1) |
| `child.mort` | Probability of death between age 0 and 5, 5q0 (used only if model=2 or model=3) |
| `adult.mort` | Probability of death between age 15 and 60, 45q15 (used only if model=3) |
| `model` | An interger to indicate which inputs will be used on the model. 1 for life expectancy, 2 for child mortality alone, 3 for child mortality with adult mortality |
| `region` | An integer to indicate which regional model to use. 1 for Africa, 0 for Caribbean or Latin American |
| `sex` | An interger to indicate the sex of the desired life table. 1 for female, 0 for male |
| `lt` | Logical. If TRUE a life table is calculated based on the estimated mortality rates. The user can supply nax values. Otherwise, the assumption of half the length of the age interval is used for nax values. |
| `nax` | If lt=TRUE, the user can supply a set of nax values |
| `opt` | If model=1, opt=TRUE will use a value for the weight for the first SVD component that produces a set of age-specific mortality rates that produce a life exepctancy at birth that matches the input life exepctancy. |

## Value

| | |
|---|---|
| `nmx` | The estimated nmx values produced by the model |
| `lt` | If `lt=TRUE` A life table with age intervals matching those of the nmx schedule on which the table is built and with columns for age, nax, nmx, nqx, npx, ndx, lx, nLx, Tx, and ex. |
| `lt.5q0` | If `lt=TRUE` The probability of death between birth and age 5 |
| `lt.45q15` | If `lt=TRUE` The probability of death between age 15 and 60 |

## Note

If `lt=TRUE`, it is possible that the life table contains fewer age groups than the 22 in the estimated mortality rates if the mortality rates are high enough to kill off all people before the final age group, 100+.

## Author(s)

David J Sharrow

## See Also

`mortmod.e0`, `mortmod.5q0`, `mortmod.45q15`

## Examples

```
## a life table at 1.5 percent prevalence, life expectancy of 60, for Africa Females
hiv.mortmod(prev=1.5, e0=60, model=1, region=1, sex=1, lt=TRUE)

## a set of mortality rates at 2.5 percent prevalence, life expectancy of 53,
## for Caribbean Males
hiv.mortmod(prev=2.5, e0=53, model=1, region=0, sex=0, lt=FALSE)
```

---

# mortmod.45q15 — *Age-specific mortality rate model as a function of HIV prevalence, child mortality (5q0), and adult mortality (45q15)*

---

## Description

This function produces a complete set of mortality rates for ages 0, 1-4, 5-9, 10-14, ...,100+ given a region, sex, HIV prevalence, child mortality (5q0), and adult mortality (45q15)

## Usage

```
mortmod.45q15(child.mort, adult.mort, prev, region = 1, sex = 1, opt=TRUE)
```

## Arguments

| | |
|---|---|
| `child.mort` | Probability of death between age 0 and 5, 5q0 |
| `adult.mort` | Probability of death between age 15 and 60, 45q15 |
| `prev` | HIV prevalence expressed as a percentage |
| `region` | An integer to indicate which regional model to use. 1 for Africa, 0 for Caribbean or Latin American |
| `sex` | An interger to indicate the sex of the desired life table. 1 for female, 0 for male |
| `opt` | If opt=TRUE, the model will use a value for the weight for the first SVD component that produces a set of age-specific mortality rates that produce a 45q15 that matches the input 45q15. The model will also adjust the first two (childhood) mortality rates (1q0, 4q1) in a proportional way so as to match the input 5q0. |

## Value

A set of mortality rates for ages 0, 1-4, 5-9, 10-14, ...,100+

## Author(s)

David J Sharrow

## See Also

hiv.mortmod

## Examples

```
mortmod.45q15(child.mort=0.06, adult.mort=0.20, prev=2.5)
```

---

`mortmod.5q0` *Age-specific mortality rate model as a function of HIV prevalence and child mortality (5q0)*

---

## Description

This function produces a complete set of mortality rates for ages 0, 1-4, 5-9, 10-14, ...,100+ given a region, sex, HIV prevalence and child mortality alone (5q0)

## Usage

```
mortmod.5q0(child.mort, prev, region = 1, sex = 1, opt=TRUE)
```

## Arguments

| | |
|---|---|
| `child.mort` | Probability of death between age 0 and 5, 5q0 |
| `prev` | HIV prevalence expressed as a percentage |
| `region` | An integer to indicate which regional model to use. 1 for Africa, 0 for Caribbean or Latin American |
| `sex` | An interger to indicate the sex of the desired life table. 1 for female, 0 for male |
| `opt` | If opt=TRUE, the model adjusts the first two (childhood) mortality rates (1q0, 4q1) in a proportional way so as to match the input 5q0. |

## Value

A set of mortality rates for ages 0, 1-4, 5-9, 10-14, ...,100+

## Author(s)

David J Sharrow

## See Also

hiv.mortmod

## Examples

```
mortmod.5q0(child.mort=0.06, prev=2.5)
```

---

`mortmod.e0` *Age-specific mortality rate model as a function of HIV prevalence and life expectancy at birth (e0)*

---

## Description

This function produces a complete set of mortality rates for ages 0, 1-4, 5-9, 10-14, ...,100+ given a region, sex, HIV prevalence and life expectancy at birth (e0)

## Usage

```
mortmod.e0(e0, prev, region = 1, sex = 1, opt=TRUE)
```

## Arguments

| | |
|---|---|
| `e0` | Life exepctancy at birth |
| `prev` | HIV prevalence expressed as a percentage |
| `region` | An integer to indicate which regional model to use. 1 for Africa, 0 for Caribbean or Latin American |
| `sex` | An interger to indicate the sex of the desired life table. 1 for female, 0 for male |
| `opt` | opt=TRUE will use a value for the weight for the first SVD component that produces a set of age-specific mortality rates that produce a life expectancy at birth that matches the input life expectancy. |

## Value

A set of mortality rates for ages 0, 1-4, 5-9, 10-14, ...,100+

## Author(s)

David J Sharrow

## See Also

hiv.mortmod

## Examples

```
mortmod.e0(e0=55, prev=2.5)
```

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