

# Package: eppasm (via r-universe)

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**Title** Age-structured EPP Model for HIV Epidemic Estimates

**Version** 0.7.6

**Description** What the package does (one paragraph).

**Depends** R (>= 3.1.0),

**Imports** abind (>= 1.4), anclik, binom, epp (>= 0.4.1), fastmatch (>= 1.1), mvtnorm, plyr, readxl, reshape2, vroom, xml2

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**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**Suggests** testthat, knitr, rmarkdown, covr

**VignetteBuilder** knitr

**URL** <https://github.com/mrc-ide/eppasm>

**BugReports** <https://github.com/mrc-ide/eppasm/issues>

**RoxygenNote** 7.2.3

**Repository** <https://mrc-ide.r-universe.dev>

**RemoteUrl** <https://github.com/mrc-ide/eppasm>

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---

agemx.spec	<i>Age-specific mortality</i>
------------	-------------------------------

---

**Description**

Calculate all-cause mortality rate by single year of age and sex from a spec object.

**Usage**

```
## S3 method for class 'spec'
agemx(mod, nonhiv = FALSE)
```

**Arguments**

mod                    output of simmod of class [spec](#).

**Details**

Mortality in year Y is calculated as the number of deaths occurring from the mid-year of year Y-1 to mid-year Y, divided by the population size at the mid-year of year Y-1. !!! NOTE: This might be different from the calculation in Spectrum. Should confirm this with John Stover.

**Value**

3-dimensional array of mortality by age, sex, and year.

---

agepregartcov	<i>Age-specific ART coverage among pregnant women</i>
---------------	---

---

**Description**

Age-specific ART coverage among pregnant women

**Usage**

```
agepregartcov(
  mod,
  fp,
  aidx = 3:9 * 5 - fp$ss$AGE_START + 1L,
  yidx = 1:fp$ss$PROJ_YEARS,
  agspan = 5,
  expand = FALSE
)
```

**Arguments**

expand	whether to expand aidx, yidx, sidx, and agspan
--------	--

---

agepregprev	<i>Age-specific prevalence among pregnant women</i>
-------------	---

---

**Description**

Age-specific prevalence among pregnant women

**Usage**

```
agepregprev(
  mod,
  fp,
  aidx = 3:9 * 5 - fp$ss$AGE_START + 1L,
  yidx = 1:fp$ss$PROJ_YEARS,
  agspan = 5,
  expand = FALSE
)
```

**Arguments**

expand                    whether to expand aidx, yidx, sidx, and agspan

---

ageprev                    *Prevalence by arbitrary age groups*

---

**Description**

Prevalence by arbitrary age groups

**Usage**

```
ageprev(
  mod,
  aidx = NULL,
  sidx = NULL,
  yidx = NULL,
  agspan = 5,
  expand = FALSE,
  VERSION = "C"
)
```

**Arguments**

sidx                    sex (1 = Male, 2 = Female, 0 = Both) Notes: Assumes that AGE\_START is 15 and single year of age.

---

ancsite\_pred\_df            *Prepare design matrix indices for ANC prevalence predictions*

---

**Description**

Prepare design matrix indices for ANC prevalence predictions

**Usage**

```
ancsite_pred_df(ancsite_df, fp)
```

**Arguments**

ancsite\_df            data.frame of site-level ANC design for predictions  
fp                    fixed parameter input list

### Examples

```
pjnz <- system.file("extdata/testpjnz", "Botswana2017.PJNZ", package="eppasm")
bw <- prepare_spec_fit(pjnz, proj.end=2021.5)

bw_u_ancsite <- attr(bw$Urban, "eppd")$ancsitedat
fp <- attr(bw$Urban, "specfp")

ancsite_pred_df(bw_u_ancsite, fp)
```

---

calc\_infections\_eppspectrum  
*Annualized number of new infections*

---

### Description

Annualized number of new infections

### Usage

```
calc_infections_eppspectrum(fp, pop, hivpop, artpop, i, ii, r_ts)
```

---

create\_spectrum\_fixpar  
*Create simulation inputs fixed parameters*

---

### Description

Create simulation inputs fixed parameters

### Usage

```
create_spectrum_fixpar(
  projp,
  demp,
  hiv_steps_per_year = 10L,
  proj_start = projp$yr_start,
  proj_end = projp$yr_end,
  AGE_START = 15L,
  relinfectART = projp$relinfectART,
  time_epi_start = projp$t0,
  popadjust = FALSE,
  targetpop = demp$basepop,
  artelig200adj = TRUE,
```

```

  who34percelig = 0,
  frr_art6mos = projp$frr_art6mos,
  frr_art1yr = projp$frr_art6mos,
  projection_period = NULL,
  art_dropout_recover_cd4 = NULL
)

```

### Details

If argument 'projection\_period = NULL', R determines the projection period based on the Spectrum version number. For version  $\leq 6.19$ , projection period is "midyear", and for version  $\geq 6.20$ , projection period is "calendar".

---

get_proj_years	<i>Get vector of years spanned by projections</i>
----------------	---

---

### Description

Get vector of years spanned by projections

### Usage

```
get_proj_years(ss)
```

---

hivpop_singleage	<i>Convert aggregate HIV population to single year</i>
------------------	--

---

### Description

EPP-ASM tracks the CD4 distribution and ART duration of the HIV population by coarse age groups '15-16, 17-19, 20-24, ..., 45-49, 50+' for computational efficiency.

### Usage

```
hivpop_singleage(mod, ss)
```

### Arguments

mod	EPP-ASM model output of class 'spec'
ss	Model state space inputs

### Details

'hivpop\_singleage' converts the coarse age group CD4 distribution and ART coverage to single year of age counts assuming uniform proportions in each category within coarse age groups.

**Examples**

```

pjnz <- system.file("extdata/testpjnz", "Botswana2018.PJNZ", package="eppasm")
fp <- prepare_directincid(pjnz)
mod <- simmod(fp)
hivp1 <- hivpop_singleage(mod, fp$ss)

```

imis

*Incremental Mixture Importance Sampling (IMIS)***Description**

Implements IMIS algorithm with optional optimization step (Raftery and Bao 2010).

**Usage**

```

imis(
  B0,
  B,
  B_re,
  number_k,
  opt_k = NULL,
  fp,
  likdat,
  prior = eppasm::prior,
  likelihood = eppasm::likelihood,
  sample_prior = eppasm::sample.prior,
  dsamp = eppasm::dsamp,
  save_all = FALSE
)

```

**Arguments**

B0	number of initial samples to draw
B	number of samples at each IMIS iteration
B_re	number of resamples
number_k	maximum number of iterations
opt_k	vector of iterations at which to use optimization step to identify new mixture component
fp	fixed model parameters
likdat	likelihood data
prior	function to calculate prior density for matrix of parameter inputs
likelihood	function to calculate likelihood for matrix of parameter inputs
sample_prior	function to draw an initial sample of parameter inputs

dsamp            function to calculate density for initial sampling distribution (may be equal to prior)

save\_all        logical whether to save all sampled parameters

**Value**

list with items resample, stat, and center

---

incid                            *Incidence rate among adults age 15-49 years*

---

**Description**

Incidence rate among adults age 15-49 years

**Usage**

```
incid(mod, ...)
```

**Arguments**

mod                    model output

**Details**

This returns incidence rate calculated as the number of infections during the projection period divided by the number susceptible at the mid-point of the projection period. This is the default incidence calculation for Spectrum version  $\geq 6.2$ . For Spectrum versions  $\leq 6.19$  incidence was calculated as number of infections divided by susceptible population at the start of the projection year.

---

incid15to49\_eppinput\_specres  
*Incidence rate age 15-49 using previous-year susceptible population*

---

**Description**

Return HIV incidence calculated as number of infections among age 15-49 population divided by susceptible population at the start of the projection year. This was the standard HIV incidence calculation reported by Spectrum up to version  $\leq 6.19$ . From Spectrum version  $\geq 6.2$ , the incidence rate is reported divided by the projection period population.

**Usage**

```
incid15to49_eppinput_specres(x)
```

**Arguments**

x                    'specres' object created by 'read\_hivproj\_output()'.



---

ll_ancsite_conditional	<i>Pointwise likelihood for site-level ANC observations given site-level effects</i>
------------------------	--

---

**Description**

Pointwise likelihood for site-level ANC observations given site-level effects

**Usage**

```
ll_ancsite_conditional(mod, fp, newdata, b_site)
```

---

ll_hhsage	<i>Log likelihood for age-specific household survey prevalence</i>
-----------	--

---

**Description**

Log likelihood for age-specific household survey prevalence

**Usage**

```
ll_hhsage(mod, fp, dat, pointwise = FALSE)
```

---

ll_hhsage_binom	<i>Log likelihood for age-specific household survey prevalence using binomial approximation</i>
-----------------	---

---

**Description**

Log likelihood for age-specific household survey prevalence using binomial approximation

**Usage**

```
ll_hhsage_binom(mod, fp, dat, pointwise = FALSE)
```

---

ll_hhsartcov	<i>Log likelihood for age-specific household survey prevalence</i>
--------------	--

---

**Description**

Log likelihood for age-specific household survey prevalence

**Usage**

```
ll_hhsartcov(mod, fp, dat, pointwise = FALSE)
```

---

ll_hhsincid	<i>Log-likelihood for direct incidence estimate from household survey</i>
-------------	---

---

**Description**

Calculate log-likelihood for nationally representative incidence estimates from a household survey. Currently implements likelihood for a log-transformed direct incidence estimate and standard error. Needs to be updated to handle incidence assay outputs.

**Usage**

```
ll_hhsincid(mod, fp, hhsincid.dat)
```

**Arguments**

mod	model output, object of class 'spec'.
hhsincid.dat	prepared household survey incidence estimates (see perp

---

melt_ancsite_data	<i>Melt ANC-SS and site-level ANC-RT to long dataset</i>
-------------------	--

---

**Description**

Melt ANC-SS and site-level ANC-RT to long dataset

**Usage**

```
melt_ancsite_data(eppd)
```

---

mod_dimnames	<i>Add dimnames to spec model output</i>
--------------	--

---

**Description**

'mod\_dimnames' assigns dimnames to spec model outputs.

**Usage**

```
mod_dimnames(mod, ss)
```

**Arguments**

mod	EPP-ASM model output of class 'spec'
ss	Model state space inputs

**Value**

EPP-ASM model output with labelled dimensions

**Examples**

```
pjnz <- system.file("extdata/testpjnz", "Botswana2018.PJNZ", package="eppasm")
fp <- prepare_directincid(pjnz)
mod <- simmod(fp)
```

---

natagemx.spec	<i>Non-HIV age-specific mortality</i>
---------------	---------------------------------------

---

**Description**

Calculate all-cause mortality rate by single year of age and sex from a spec object.

**Usage**

```
## S3 method for class 'spec'
natagemx(mod)
```

**Arguments**

mod	output of simmod of class <a href="#">spec</a> .
-----	--

**Details**

Mortality in year Y is calculated as the number of non-HIV deaths occurring from the mid-year of year Y-1 to mid-year Y, divided by the population size at the mid-year of year Y-1. !!! NOTE: This might be different from the calculation in Spectrum. Should confirm this with John Stover.

**Value**

3-dimensional array of mortality by age, sex, and year.

---

```
prepare_ancsite_likdat
```

*Prepare site-level ANC prevalence data for EPP random-effects likelihood*

---

**Description**

Prepare site-level ANC prevalence data for EPP random-effects likelihood

**Usage**

```
prepare_ancsite_likdat(ancsitedat, fp)
```

**Arguments**

ancsitedat	data.frame of site-level ANC data
fp	fixed parameter input list, including state space

---

```
prepare_directincid Prepare direct incidence input EPP simulation
```

---

**Description**

Prepare direct incidence input EPP simulation

**Usage**

```
prepare_directincid(pjnz, method = "directincid_hts")
```

**Arguments**

method	Method for intercalating new infections. Either "directincid_ann" for annual new infections or "directincid_hts" for new infections each HIV time step.
--------	---

---

```
prepare_hhsageprev_likdat
    Prepare age-specific HH survey prevalence likelihood data
```

---

**Description**

Prepare age-specific HH survey prevalence likelihood data

**Usage**

```
prepare_hhsageprev_likdat(hhsage, fp)
```

---

```
prepare_hhsartcov_likdat
    ## Household survey ART coverage likelihood
```

---

**Description**

## Household survey ART coverage likelihood

**Usage**

```
prepare_hhsartcov_likdat(hhsartcov, fp)
```

---

```
prepare_hhsincid_likdat
    Prepare household survey incidence likelihood data
```

---

**Description**

Prepare household survey incidence likelihood data

**Usage**

```
prepare_hhsincid_likdat(hhsincid, fp)
```

---

```
prepare_rhybrid      Setup the r-hybrid model
```

---

**Description**

Setup the r-hybrid model

**Usage**

```
prepare_rhybrid(  
  fp,  
  tsEpidemicStart = fp$ss$time_epi_start + 0.5,  
  rw_start = fp$rw_start,  
  rw_trans = fp$rw_trans,  
  rw_dk = fp$rw_dk  
)
```

**Arguments**

fp	model parameters object
tsEpidemicStart	time step at which epidemic is seeded
rw_start	time when random walk starts
rw_trans	number of years to transition from logistic differences to RW differences. If NULL, defaults to 5 steps

---

```
prepare_spec_fit      Prepare fit by EPP regions
```

---

**Description**

Prepare fit by EPP regions

**Usage**

```
prepare_spec_fit(  
  pjnz,  
  proj.end = 2016.5,  
  popadjust = NULL,  
  popupdate = TRUE,  
  use_ep5 = FALSE  
)
```

**Arguments**

pjnz	file path to Spectrum PJNZ file.
proj.end	end year for projection.
popupdate	logical should target population be updated to match age-specific population size from DP file and %Urban from EPP XML.

---

read_csavr_data	<i>Read CSAVR input data</i>
-----------------	------------------------------

---

**Description**

Read CSAVR input data

**Usage**

```
read_csavr_data(pjnz)
```

**Arguments**

pjnz	file path to Spectrum PJNZ file.
------	----------------------------------

---

read_dp	<i>Read Spectrum internal files file from PJNZ</i>
---------	--

---

**Description**

Read Spectrum internal files file from PJNZ

**Usage**

```
read_dp(pjnz, use_ep5 = FALSE)
```

**Arguments**

pjnz	file path to Spectrum PJNZ file.
------	----------------------------------

---

read_incid_input	<i>Read annual incidence input</i>
------------------	------------------------------------

---

**Description**

Read annual incidence input

**Usage**

```
read_incid_input(pjnz)
```

**Arguments**

pjnz	file path to Spectrum PJNZ file.
------	----------------------------------

---

read_pop1	<i>Read Spectrum _pop1.xlsx export file</i>
-----------	---

---

**Description**

Spectrum has a debug mode option to output a file recording the entire state space when a model simulation is computed. This function parse the \*\_pop1.xlsx file into long-format data.frame.

**Usage**

```
read_pop1(pop1file, country, years = 2000:2021)
```

**Arguments**

pop1file	path to *_pop1.xlsx export file
country	string giving the identifying country / region name to be added as a column in the output file
years	integer vector of years to extract

**Details**

TODO: tidy up the dependencies in this function: reshape, pryr, readxl.

TODO: Insert instructions for how to enter Spectrum debug mode.

‘years’ must be in the file as sheets, but this is not currently checked. It will fail hard. Inserting a check for this would make it fail softer.

**Value**

A data.frame consisting of pop1 file in long format



---

sample\_ancsite\_pred     *Sample posterior predictions for site-level ANC observations*

---

**Description**

Sample posterior predictions for site-level ANC observations

**Usage**

```
sample_ancsite_pred(mod, fp, newdata, b_site)
```

---

sample\_b\_site     *Sample from posterior ditribution for ANC site level random effects*

---

**Description**

Sample from posterior ditribution for ANC site level random effects

**Usage**

```
sample_b_site(mod, fp, dat, resid = TRUE)
```

---

sample\_invgamma\_post     *Sample from conditional posterior distribution for variance parameter*

---

**Description**

Sample from conditional posterior distribution for variance parameter

**Usage**

```
sample_invgamma_post(x, prior_shape, prior_rate)
```

---

simmod	<i>Simulate model</i>
--------	-----------------------

---

**Description**

Simulate model

**Usage**

```
simmod(fp, ...)
```

**Arguments**

fp	fixed parameter input object
...	Arguments to be passed to methods

---

spec_add_dimnames	<i>Add dimnames to EPP-ASM model output</i>
-------------------	---

---

**Description**

Add dimnames to EPP-ASM model output

**Usage**

```
spec_add_dimnames(mod, fp)
```

**Arguments**

mod	output from 'simmod()'
fp	fixed parameters input to 'simmod()'

**Value**

Input 'mod' object with dimnames applied to arrays.

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