

# Package ‘HPbayes’

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**Type** Package

**Title** Heligman Pollard mortality model parameter estimation using  
Bayesian Melding with Incremental Mixture Importance Sampling

**Depends** MASS, mvtnorm, corpcor, numDeriv, stats, boot

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**Description** This package provides all the functions necessary to estimate the 8 parameters of the Heligman Pollard mortality model using a Bayesian Melding procedure with IMIS as well as to convert those parameters into age-specific probabilities of death and a corresponding life table

**License** Unlimited

**LazyLoad** yes

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## R topics documented:

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HPbayes-package	<i>Heligman Pollard mortality model parameter estimation using Bayesian Melding with Incremental Mixture Importance Sampling</i>
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## Description

This package provides all the functions necessary to estimate the 8 parameters of the Heligman-Pollard mortality model using Bayesian Melding with IMIS and optimization. Functions are also provided to estimate the model using maximum likelihood and to plot the results of either ML or BM with IMIS.

## Details

Package:	HPbayes
Type:	Package
Version:	1.0
Date:	2009-05-06
License:	
LazyLoad:	yes

[hp.bm.imis](#) is the most central function in the package. This single function combines all the necessary functions to execute the parameter estimation via Bayesian Melding using Incremental Mixture Importance Sampling with optimization. Once the parameter estimates are obtained [hp.nqx](#) can be used to convert the parameter estimates into probabilities of death for all  $x > 0$ . Likewise, [hp.lifetab](#) will convert the parameter estimates into a life table with age groups selected by the user. Plotting functions include [hpbayes.plot](#), which will plot the resulting output from the deterministic model along with confidence intervals, and [postpri.plot](#), which will plot the resulting posterior parameter distributions along with the prior for each.

## Author(s)

Dave Sharrow with code from Jason Thomas

Maintainer: Dave Sharrow <dsharrow@u.washington.edu>

## References

- Heligman, Larry and John H. Pollard. 1980 "The Age Pattern of Mortality." *Journal of the Institute of Actuaries* **107**:49–80.
- Poole, David and Adrian Raftery. 2000. "Inference for Deterministic Simulation Models: The Bayesian Melding Approach." *Journal of the American Statistical Association* **95**:1244–1255.
- Raftery, Adrian and Le Bao. 2009. "Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling." Technical Report 560, Department of Statistics, University of Washington.

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dens.prior	<i>Density of the prior</i>
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---

## Description

This function calculates the density of the prior distribution for the eight parameters of the Heligman Pollard model. The density is calculated using a uniform distribution. The lower bounds all default to 0 except parameter F, which has a default lower bound of 15. The upper bounds default to A-0.15, B-1, C-1, D-0.25, E-15, F-55, G-0.1, F-1.25.

## Usage

```
dens.prior(x, pri.lo = c(0, 0, 0, 0, 0, 15, 0, 0),
  pri.hi = c(0.15, 1, 1, 0.25, 15, 55, 0.1, 1.25))
```

## Arguments

- |        |   |
|--------|---|
| x      | A 1 x 8 vector or n x 8 matrix containing values for the eight Heligman-Pollard Parameters  |
| pri.lo | A vector giving the lower bounds of the uniform prior. Defaults to 0 for all parameters except F which has a default lower bound of 15. |
| pri.hi | A vector giving the upper bounds of the uniform prior. Defaults to A-0.15, B-1, C-1, D-0.25, E-15, F-55, G-0.1, F-1.25.                 |

## Value

A scalar describing the density of the prior distribution

## Examples

```
#Generate a prior distribution
pri.lo = c(0, 0, 0, 0, 0, 15, 0, 0)
pri.hi = c(0.15, 1, 1, 0.25, 15, 55, 0.1, 1.25)
B0 <- 8000
```

```

q0 <- cbind(runif(B0, pri.lo[1], pri.hi[1]),
runif(B0, pri.lo[2], pri.hi[2]),
runif(B0, pri.lo[3], pri.hi[3]),
runif(B0, pri.lo[4], pri.hi[4]),
runif(B0, pri.lo[5], pri.hi[5]),
runif(B0, pri.lo[6], pri.hi[6]),
runif(B0, pri.lo[7], pri.hi[7]),
runif(B0, pri.lo[8], pri.hi[8]))

density <- dens.prior(x=q0)

```

---

entropy.wts

*Entropy of the rescaled weights relative to uniformity*


---

### Description

Performance measure for the IMIS algorithm that calculates the entropy of the importance weights relative to uniformity.

### Usage

```
entropy.wts(w)
```

### Arguments

**w** A vector of importance weights corresponding to each row of the mixture of the prior and multivariate gaussian draws

### Value

Vector of entropy values relative to uniformity for a vector of weights

### Note

For use in the function `final.resamp` from the package HPbayes

### References

Raftery, Adrian and Le Bao. 2009. "Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling." Technical Report 560, Department of Statistics, University of Washington.

Poole, David and Adrian Raftery. 2000. "Inference for Deterministic Simulation Models: The Bayesian Melding Approach." *Journal of the American Statistical Association* **95**:1244–1255.

**Examples**

```
#Generate a vector of weights#
wts <- runif(100, 0, .99)
entropy.wts(w=wts)
```

---

expt.upts

*Expected number of unique inputs after the final IMIS re-sample*


---

**Description**

Performance measure for the IMIS algorithm that calculates the expected number of unique points after re-sampling

**Usage**

```
expt.upts(w, m)
```

**Arguments**

w                    A vector of importance weights corresponding to each row of the mixture of the prior and multivariate gaussian distributions

m                    The final re-sample size

**Value**

A scalar describing the number of unique points from the final re-sample

**Note**

For use in the function [final.resamp](#)

**References**

Raftery, Adrian and Le Bao. 2009. "Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling." Technical Report 560, Department of Statistics, University of Washington.

**Examples**

```
#Generate a vector of weights#
wts <- runif(100, 0, .99)
expt.upts(wts, m = 3000)
```

---

final.resamp

*Final re-sampling step in Bayesian Melding using IMIS*


---

### Description

Performs the final re-sampling step in the Bayesian Melding with IMIS procedure for the eight Heligman-Pollard parameters.

### Usage

```
final.resamp(K, B1, H.new, H.k, log.like, d.keep, prior, h.mu, h.sig,
            nrisk, ndeath, B = 400, theta.dim = 8, age = c(1e-05, 1,
            seq(5, 100, 5)))
```

### Arguments

K	The number of iterations of the importance sampling stage
B1	sample size at the importance sampling stage multiplied by the number of local optimums
H.new	A matrix with dimensions (B*d.keep) x 8 containing the B*d.keep inputs drawn from the multivariate gaussians
H.k	A matrix containing the prior plus new inputs from the multivariate gaussians
log.like	A vector of log-likelihoods corresponding to each row of H.k
d.keep	The number of local optimums found in the optimizer step
prior	A matrix containing the prior
h.mu	A d.keep x 8 matrix containing the results of the optimizer step
h.sig	An array containing the covariance matrix for each row of h.mu
nrisk	A vector containing the number of persons at risk in each age group
ndeath	A vector containing the number of deaths in each age group
B	sample size at the importance sampling stage
theta.dim	The number of columns of the prior matrix
age	A vector containing the ages at which each age interval begins

### Details

The function, hp.bm.imis, will perform this along with all other steps in a single function

**Value**

H.new	A B x theta.dim matrix containing the posterior distribution for each parameter
vwts	A vector containing the variance of the rescaled weights at each IMIS iteration
ewts	A vector containing the entropy of the rescaled weights at each IMIS iteration
mwt.s	A vector containing the maximum of the rescaled weights at each IMIS iteration
nup	A vector containing the expected number of unique points at each IMIS iteration
frac.up	A vector containing the proportion of unique points in the final resample at each IMIS iteration
wts.k	A vector containing the importance weights for the final iteration
mwt.case	The maximum weight value and associated case

**References**

Raftery, Adrian and Le Bao. 2009. "Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling." Technical Report 560, Department of Statistics, University of Washington.

Poole, David and Adrian Raftery. 2000. "Inference for Deterministic Simulation Models: The Bayesian Melding Approach." *Journal of the American Statistical Association* **95**:1244–1255.

Heligman, Larry and John H. Pollard. 1980 "The Age Pattern of Mortality." *Journal of the Institute of Actuaries* **107**:49–80.

**See Also**

[loop.optim](#), [samp.postopt](#), [like.resamp](#), [hp.bm.imis](#), [entropy.wts](#), [expt.upts](#), [var.rwts](#)

**Examples**

```
## Not run:
data(HPprior)
lx
dx
summary(q0)
age

opt.result <- loop.optim(prior = q0, nrisk=lx, ndeath=dx)
opt.mu.d <- opt.result$opt.mu.d
opt.cov.d <- opt.result$opt.cov.d
theta.new <- opt.result$theta.new
d.keep <- opt.result$d.keep
log.like.0 <- opt.result$log.like.0
wts.0 <- opt.result$wts.0
samp.po <- samp.postopt(opt.cov.d = opt.cov.d, opt.mu.d = opt.mu.d,
  prior = q0, d.keep = d.keep)
H.k <- samp.po$H.k
H.new <- samp.po$H.new
B1 <- samp.po$B1
```

```

ll.postopt <- like.resamp(K = 10, log.like.0 = log.like.0,
  opt.cov.d = opt.cov.d, opt.mu.d = opt.mu.d, d.keep = d.keep)
h.mu <- ll.postopt$h.mu
h.sig <- ll.postopt$h.sig
log.like <- ll.postopt$log.like
K <- ll.postopt$K
result <- final.resamp(K = K, B1 = B1, H.new = H.new, H.k = H.k,
  log.like = log.like, d.keep = d.keep, prior = q0,
  h.mu = h.mu, h.sig = h.sig, nrisk=lx, ndeath=dx, age=age)

## End(Not run)

```

---

hp.bm.imis

*Heligman-Pollard parameter estimator using Bayesian Melding with  
Incremental Mixture Importance Sampling*


---

## Description

Runs all the necessary functions to estimate the eight Heligman-Pollard parameters in one step via Bayesian Melding with IMIS and optimization. In this order and with the proper arguments imputed the functions run are `loop.optim`, `samp.postopt`, `like.resamp`, `final.resamp`.

## Usage

```

hp.bm.imis(prior, nrisk, ndeath, K, d = 10,
  B = 400, age = c(1e-05, 1, seq(5, 100, 5)), CI=95)

```

## Arguments

prior	A matrix with dimensions 8000 x theta.dim containing the prior distribution for each Heligman-Pollard parameter
nrisk	A vector containing the total number of individuals at risk of death in each age group. Length should equal the length of age
ndeath	A vector containing the total number of deaths in each age group. Length should equal the length of age
K	The number of IMIS iterations
d	The number of optimizer iterations
B	The sample size at each importance sampling iteration
age	A vector of the ages at which the probabilities of death will be calculated
CI	Defines the width of the credible interval (Defaults to 95 percent). A summary table is printed with the median estimate and lower and upper confidence bounds. Setting CI=95 prints a table with the first column representing the 2.5th percentile for each parameter distribution, the second column represents the median value for each parameter distribution and the third column represents the 97.5th percentile for each parameter distribution.



**Value**

out	A summary table of the results with the median parameter values in the middle column, the lower bound results in the left column, and upper bound result in the right column
H.final	A $B \times \text{theta.dim}$ matrix containing the posterior distribution for each parameter
h.mu	The sets of parameters found in the optimizer step
h.sig	The covariance matrix for each set of parameters in h.mu
log.like	A vector of likelihoods for the prior plus resamples
log.like.0	A vector of the likelihoods for the prior
wts.0	A vector of importance weights for each set of parameters in the prior
d.keep	The number of optimizer runs where the likelihood exceeded the maximum likelihood of the prior
vwts	A vector containing the variance of the rescaled weights at each IMIS iteration
ewts	A vector containing the entropy of the rescaled weights at each IMIS iteration
mwt	A vector containing the maximum of the rescaled weights at each IMIS iteration
mwt.case	The maximum weight and associated case
nup	A vector containing the expected number of unique points at each IMIS iteration
frac.up	A vector containing the proportion of unique points in the final resample at each IMIS iteration
wts.k	A vector containing the importance weights for the final IMIS iteration

**Note**

Because there are multiple sampling steps sometimes with upper and lower bound restrictions, this function can take several minutes to run depending on the sample size, K

**References**

- Heligman, Larry and John H. Pollard. 1980 "The Age Pattern of Mortality." *Journal of the Institute of Actuaries* **107**:49–80.
- Poole, David and Adrian Raftery. 2000. "Inference for Deterministic Simulation Models: The Bayesian Melding Approach." *Journal of the American Statistical Association* **95**:1244–1255.
- Raftery, Adrian and Le Bao. 2009. "Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling." Technical Report 560, Department of Statistics, University of Washington.

**See Also**

[loop.optim](#), [samp.postopt](#), [like.resamp](#), [final.resamp](#)

## Examples

```
##a prior##
## Not run: data(HPprior)
q0 <- HPprior
##number of deaths in each age group##
dx <- c(68, 47, 16, 10, 13, 29, 92, 151, 188, 179, 156, 155, 147, 150,
122, 106, 88, 113, 63, 38, 32, 8)
##number at risk in each age group##
lx <- c(1974, 1906, 1860, 1844, 1834, 1823, 1793, 1700, 1549, 1361,
1181, 1025, 870, 721, 571, 450, 344, 256, 142, 79, 41, 8)
result <- hp.bm.imis(prior=q0, K=10, nrisk=lx, ndeath=dx)
## End(Not run)
```

---

hp.lifetab

*Heligman-Pollard life table conversion*

---

## Description

Generates a life table from the age-specific probabilities of death resulting from the estimation of the eight parameters of the Heligman-Pollard mortality model

## Usage

```
hp.lifetab(hpp, nax, age = seq(0, 85, 1), l0 = 1e+05,
with.CI=FALSE, CI=95)
```

## Arguments

hpp	A vector of length 8 containing the Heligman-Pollard model parameter values
nax	A vector of equal length to age containing the appropriate nax values for each age interval in the life table
age	A vector containing the ages at which to estimate the life table columns
l0	The radix of the life table (Defaults to 100,000)
with.CI	Logical. If TRUE, produces two additional life tables each generated from the lower CI bound values of nqx and the upper bound values of nqx respectively
CI	Defines the width of the confidence interval. A value of CI=95 creates a 95 percent confidence interval with the upper bound defined as the 97.5th percentile nqx value for each age and the lower bound defined as the 2.5th percentile.

**Value**

A life table containing the columns "Age" (the starting age of the interval), "nax" (the set of nax values passed as an argument), "nqx" (the age-specific probabilities of dying in the interval  $x$  to  $x+n$ ), "np $x$ " (the probability of surviving the interval age  $x$  to  $x+n$  or  $1-np_x$ ), "nd $x$ " (the number of deaths in the interval), "l $x$ " (the number of persons who have survived up to age  $x$ ), "nL $x$ " (the total number of person years lived within the interval  $x$  to  $x+n$ ), "T $x$ " (the total number of person years left to live above age  $x+n$ ), "ex" (life expectancy at age  $x$ ).

**References**

Heligman, Larry and John H. Pollard. 1980 "The Age Pattern of Mortality." *Journal of the Institute of Actuaries* **107**:49–80.

**Examples**

```
##requires a set of Heligman-Pollard parameters##
theta <- cbind(0.06008, 0.31087, 0.34431, 0.00698,
              1.98569, 26.71071, 0.00022, 1.08800)
age <- seq(0, 85, 1)
nax <- rep(.5, length(age))
HP.lt <- hp.lifetab(hpp=theta, nax=nax)
```

---

hp.nqx	<i>Heligman-Pollard parameter conversion to age-specific probabilities of death</i>
--------	---

---

**Description**

Converts a set of Heligman-Pollard mortality model parameters into age-specific probabilities of death

**Usage**

```
hp.nqx(H.out, age = seq(0, 85, 1))
```

**Arguments**

H.out	A vector of length eight containing the values for the eight parameters of the model
age	A vector containing the ages at which the probability of death will be calculated

**Value**

Set of age specific probabilities of death equal to the length of age

## References

Heligman, Larry and John H. Pollard. 1980 "The Age Pattern of Mortality." *Journal of the Institute of Actuaries* **107**:49–80.

## See Also

[hp.lifetab](#)

## Examples

```
theta <- cbind(0.06008, 0.31087, 0.34431, 0.00698,
              1.98569, 26.71071, 0.00022, 1.08800)
nqx <- hp.nqx(H.out=theta)
```

---

hpbayes.plot	<i>Bayesian Melding posterior Heligman-Pollard parameter distribution plot</i>
--------------	--

---

## Description

This function converts the posterior Heligman-Pollard parameter distribution resulting from a Bayesian Melding procedure to probabilities of death over a specified age range. In addition, this function also calculates and plots a CI over the specified age range. The user can also elect to plot the data (ndeath/nrisk) from which the model was estimated.

## Usage

```
hpbayes.plot(..., nrisk = NULL, ndeath = NULL, age, hpp,
             yrange = c(0, 0.8), xrange = c(0, 85), log = FALSE, plotdata = FALSE,
             plotpost= TRUE, data.type="b", post.type="l",
             line.col=c("grey", "blue", "red", "dark green"), CI=95)
```

## Arguments

...	Arguments to be passes to <a href="#">par</a>
nrisk	A vector containing the number of persons at risk at age x
ndeath	A vector containing the number of deaths at age x
age	A vector containing the ages at which the probabilities of death will be calculated and plotted
hpp	A matrix containing the posterior distribution of Heligman-Pollard parameters resulting from the Bayesian Melding procedure
yrange	Same as ylim in <code>plot()</code>
xrange	Same as xlim in <code>plot()</code>

log	Logical. If TRUE the data will be converted and plotted on the log scale
plotdata	Logical. If TRUE the data (ndeath/nrisk) will be plotted as well.
plotpost	Logical. If TRUE the posterior output will be plotted.
data.type	Same as type in plot.
post.type	Same as type in plot. Defines the "type" for plotting the posterior age-specific probabilities of death
line.col	A vector of length four containing either numbers or strings describing the colors of the plot. In order, the vector elements control the color of the posterior output lines (defaults to "grey"), the color of the median line representing the median probability of death at each age (defaults to "blue"), the color of the two lines representing the upper and lower credible interval bounds (defaults to "red"), and the final element in this vector controls the color of the data points if they are plotted (defaults to "dark green").
CI	Defines the width of the credible interval if plotted (defaults to 95 percent). Setting CI=95 for example will plot two lines representing the upper and lower bounds of the confidence interval with the upper bound line representing the 97.5th percentile for each age and the lower bound representing the 2.5th percentile for each age.

### Details

If plotdata is TRUE, the user will need to supply the persons at risk at each age  $x$  and the number of deaths at age  $x$  with the arguments nrisk and ndeath respectively.

### Value

A plot depicting the posterior distribution of probabilities of death calculated from the posterior parameter distribution resulting from the Bayesian Melding procedure (see [hp.bm.imis](#))

### Note

Likely used to plot the H.final return from [hp.bm.imis](#)

### References

Heligman, Larry and John H. Pollard. 1980 "The Age Pattern of Mortality." *Journal of the Institute of Actuaries* **107**:49–80.

### See Also

[hp.nqx](#), [hp.bm.imis](#)

### Examples

```
#load a prior, age, nrisk and ndeath#
```

```

data(HPprior)

result <- hp.bm.imis(prior=q0, K=10, age=age, nrisk=lx, ndeath=dx)
H.final <- result$H.final

hpbayes.plot(nrisk=lx, ndeath=dx, age=age, hpp=H.final, plotdata=TRUE)
hpbayes.plot(age=age, hpp=H.final)

```

---

HPprior *prior, age groups, lx and dx values*

---

### Description

This data set contains 4 objects,  $q_0$ , age,  $lx$  and  $dx$ .  $q_0$  is a prior distribution for the eight Heligman-Pollard parameters. It was formed using `prior.form()`. age is a vector providing age groups (0-1, 1-4, 5-9, 10-14,...,100+) which matches the length of  $lx$  and  $dx$ .  $lx$  is a vector of persons at risk in the age groups described in age.  $dx$  is a vector containing the corresponding deaths in the age groups in age.

### Usage

```
data(HPprior)
```

### Format

Four objects:  $q_0$  (a matrix with 8000 rows and 8 columns), age (a vector of length 22),  $lx$  (a vector of length 22),  $dx$  (a vector of length 22)

---

like.resamp *Local Optimimums and Covariance from the optimizer step*

---

### Description

Defines some necessary arguments for the function `final.resamp`. Removes NAs from the `opt.mu.d` and `opt.cov.d` matrixes.

### Usage

```
like.resamp(K, log.like.0, opt.cov.d, opt.mu.d, d.keep,
d = 10, theta.dim = 8)
```

**Arguments**

K	Number of iterations at the importance sampling stage
log.like.0	A vector containing the likelihoods for each row of the prior
opt.cov.d	Covariance matrixes for the local optimums
opt.mu.d	A d x 8 matrix containing the local optimums (sets of parameters from the optimizer step)
d.keep	Number of local optimums found in the optimizer step
d	A scalar defining the number of optimizer iterations. Defaults to 10
theta.dim	Number of columns in the prior matrix

**Value**

h.mu	A d.keep x 8 matrix containing the local optimum results
h.sig	An array with theta.dim x theta.dim x (K+d.keep) dimensions containing the covariance matrix for each local optimum
log.like	A vector of likelihoods for each row of H.k

**Note**

Typically for use immediately before running [final.resamp](#) or within the function [hp.bm.imis](#)

**References**

- Poole, David and Adrian Raftery. 2000. "Inference for Deterministic Simulation Models: The Bayesian Melding Approach." *Journal of the American Statistical Association* **95**:1244–1255.
- Raftery, Adrian and Le Bao. 2009. "Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling." Technical Report 560, Department of Statistics, University of Washington.

**See Also**

[final.resamp](#), [hp.bm.imis](#)

---

ll.binom

*Binomial likelihood*


---

**Description**

Calculates a log likelihood from a binomial distribution

**Usage**

```
ll.binom(x, n, p)
```

**Arguments**

x	Same as x from dbinom - successes
n	Same as size from dbinom - trials
p	Same as prob from dbinom - observed probability

**Value**

Log-Likelihood based on a binomial distribution

**References**

R Development Core Team. 2009. "R: A Language and Environment for Statistical Computing" *R Foundation for Statistical Computing* Vienna, Austria.

**See Also**

[dbinom](#)

**Examples**

```
ll.binom(x=1, n=2, p=0.5)
```

---

loop.optim	<i>Optimizer step for estimating the Heligman-Pollard Parameters using the Bayesian Melding with IMIS-opt procedure</i>
------------	---

---

**Description**

Performs the optimizer step in the IMIS procedure for the eight Heligman-Pollard parameters

**Usage**

```
loop.optim(prior, nrisk, ndeath, d = 10, theta.dim = 8,
age = c(1e-05, 1, seq(5, 100, 5)))
```

**Arguments**

prior	A matrix containing the prior
nrisk	A vector containing the number of persons at risk in each age group
ndeath	A vector containing the number of deaths in each age group
d	Number of optimizer iterations
theta.dim	Number of columns of the prior (This should be 8 if estimating all parameters. Functionality for estimation a limited number of parameters does not exist yet.)
age	A vector containing the ages at which each age interval begins



**Value**

opt.mu.d	A matrix containing the local optimums resulting from the optimizer step. Each local optimum contains a set of 8 parameter values.
opt.cov.d	A array containing the covariance matrix for each of the local optimums
d.keep	The number of local optimums found whose likelihood is greater than the maximum likelihood from the prior
theta.new	The set of parameters from the prior with the greatest weight as calculated with prior.likewts
log.like.0	A vector containing a likelihood for each row of the prior
wts.0	A vector containing an importance weight for each row of the prior

**Warning**

If the likelihood for the initial local maximum does not exceed the highest likelihood from the prior, a warning will be issued.

**Note**

Occasionally, this step fails to produce an initial local maximum that exceeds the highest likelihood of the prior and a warning is issued. Usually drawing a new prior or selecting a different algorithm solves this problem.

**References**

Poole, David and Adrian Raftery. 2000. "Inference for Deterministic Simulation Models: The Bayesian Melding Approach." *Journal of the American Statistical Association* **95**:1244–1255.

Raftery, Adrian and Le Bao. 2009. "Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling." Technical Report 560, Department of Statistics, University of Washington.

**See Also**

[hp.bm.imis](#)

**Examples**

```
#Generate a prior and numbers of death and persons at risk#
## Not run: q0 <- prior.form()
lx <- c(1974, 1906, 1860, 1844, 1834, 1823, 1793, 1700, 1549, 1361,
1181, 1025, 870, 721, 571, 450, 344, 256, 142, 79, 41, 8)
dx <- c(68, 47, 16, 10, 13, 29, 92, 151, 188, 179, 156, 155, 147, 150,
122, 106, 88, 113, 63, 38, 32, 8)
opt.result <- loop.optim(prior=q0, nrisk=lx, ndeath=dx)
## End(Not run)
```

---

mod8p	<i>Heligman-Pollard parameter conversion to age-specific probabilities of death</i>
-------	---

---

**Description**

Calculates the age-specific probabilities of death using the Heligman-Pollard model

**Usage**

```
mod8p(theta, x)
```

**Arguments**

theta	A vector containing values for the 8 parameters of the Heligman-Pollard model
x	A vector containing the ages at which to calculate the probabilities of death

**Value**

A vector of probabilities of death at ages defined by x

**References**

Heligman, Larry and John H. Pollard. 1980 "The Age Pattern of Mortality." *Journal of the Institute of Actuaries* **107**:49–80.

**Examples**

```
theta <- c(0.06008, 0.31087, 0.34431, 0.00698,
          1.98569, 26.71071, 0.00022, 1.08800)
age <- c(0.00001, 1, seq(5, 85, 5))
result <- mod8p(theta=theta, x=age)
```

---

mp8.ll	<i>Binomial likelihood for a set of Heligman-Pollard Parameters</i>
--------	---

---

**Description**

Calculates the log-likelihood based on a binomial distribution of observing a set of age-specific probabilities of death resulting from a set of eight parameters of the Heligman-Pollard Model given a certain number of age-specific death counts and persons at risk

**Usage**

```
mp8.ll(theta, nrisk, ndeath, age = c(1e-05, 1, seq(5, 85, 5)))
```

**Arguments**

theta	A vector containing the values for the 8 Heligman-Pollard parameters
nrisk	A vector containing the number of persons at risk in each age group
ndeath	A vector containing the number of deaths in each age group
age	A vector containing the age values of which the probabilities of death resulting from the HP model are a function

**Value**

Log likelihood of observing the resulting probabilities of death calculated from the set of parameters, theta

**Note**

For use in the optimizer step of the IMIS procedure

**References**

Heligman, Larry and John H. Pollard. 1980 "The Age Pattern of Mortality." *Journal of the Institute of Actuaries* **107**:49–80.

**See Also**

[loop.optim](#), [hp.bm.imis](#)

**Examples**

```
##A set of parameters##
theta <- c(0.06008, 0.31087, 0.34431, 0.00698,
          1.98569, 26.71071, 0.00022, 1.08800)
##Deaths and persons at risk##
lx <- c(1974, 1906, 1860, 1844, 1834, 1823, 1793, 1700, 1549, 1361,
        1181, 1025, 870, 721, 571, 450, 344, 256, 142, 79, 41, 8)
dx <- c(68, 47, 16, 10, 13, 29, 92, 151, 188, 179, 156, 155, 147, 150,
        122, 106, 88, 113, 63, 38, 32, 8)
mp8.ll(theta=theta, nrisk=lx, ndeath=dx)
```

---

 postpri.plot

*Posterior/Prior Heligman-Pollard parameter distribution plot*


---

### Description

Produces an 8 panel plot of both the prior and posterior distribution for the eight parameters of the Heligman-Pollard model

### Usage

```
postpri.plot(..., prior, hpp, box = FALSE, type = "l",
  line.col = c("black", "red"), line.bound = TRUE,
  rowcol = c(2, 4))
```

### Arguments

...	Arguments to be passed to <a href="#">par</a>
prior	A $n \times 8$ matrix containing the prior distribution for each of eight Heligman-Pollard parameters (8 columns)
hpp	An matrix containing the posterior distribution for each of the eight Heligman-Pollard parameters
box	If TRUE, the plot will appear as box plots instead of Kernel density lines
type	Same as type in <a href="#">par</a> . Sets the line type when the plot is the Kernel density
line.col	The line color for the plot. The first argument is the color for the prior and the second is for the posterior.
line.bound	If TRUE, will plot a box representing the prior density
rowcol	A vector describing the number of rows and columns of the plot. These arguments are passed to <a href="#">mfrow</a> in <a href="#">par</a> .

### Value

A plot graphing the prior and posterior distribution of the Heligman Pollard parameters

### References

- Heligman, Larry and John H. Pollard. 1980 "The Age Pattern of Mortality." *Journal of the Institute of Actuaries* **107**:49–80.
- Poole, David and Adrian Raftery. 2000. "Inference for Deterministic Simulation Models: The Bayesian Melding Approach." *Journal of the American Statistical Association* **95**:1244–1255.
- Raftery, Adrian and Le Bao. 2009. "Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling." Technical Report 560, Department of Statistics, University of Washington.

**See Also**

[hp.bm.imis](#), [par](#), [density](#), [boxplot](#)

**Examples**

```
##load a prior distribution##
data(HPprior)
##obtain and posterior distribution##
result <- hp.bm.imis(prior=q0, K=10, nrisk=lx, ndeath=dx)

##plot them##
postpri.plot(prior=q0, hpp=result$H.final)
postpri.plot(prior=q0, hpp=result$H.final, box=TRUE)
```

---

pri.mle	<i>Heligman-Pollard parameter prior formation for use with Bayesian Melding using IMIS</i>
---------	--

---

**Description**

Forms a prior distribution (drawn from a uniform distribution) for each of the eight Heligman-Pollard parameters. First, using `optim()`, mle estimates of the parameters are fitted to the deaths and persons at risk supplied by the user. Once these estimates (returned as `mle`) and their standard errors (`se`) are obtained, 8000 (See documentation for [prior.form](#)) draws from a uniform distribution with bounds `mle[i] +/- senum*se` are taken to form a prior distribution for each parameter.

**Usage**

```
pri.mle(nrisk, ndeath, age = c(0, 1, seq(5, 100, 5)),
lo = c(1e-08, 1e-07, 1e-07, 1e-07, 1e-07, 15, 1e-07, 1),
hi = c(1, 1, 1, 0.5, 15, 55, 0.1, 1.5), senum = 15,
theta.test = c(0.06008, 0.31087, 0.34431, 0.00698, 1.98569,
26.71071, 0.00022, 1.088), opt.meth = "Nelder-Mead")
```

**Arguments**

nrisk	The number of persons at risk of death in each age group
ndeath	The number of deaths in each age group
age	A vector containing the ages at which probabilities of death are calculated
lo	If <code>opt.meth="L-BFGS"</code> , this vector contains the lower bounds in lower argument of <code>optim()</code> )
hi	If <code>opt.meth="L-BFGS"</code> , this vector contains the upper bounds in upper argument of <code>optim()</code> )
senum	The number of standard errors on each side of the mle estimate. This argument controls how wide or narrow the uniform distribution is from which the prior distribution will be drawn.

theta.test	Start values for optim. The defaults encompass the Brass standard (Rogers and McKnown 1989).
opt.meth	The same as method in optim().

### Details

Priors drawn with this function can be used with the function [hp.bm.imis](#) or other functions from the HPbayes package.

### Value

q0	A matrix containing the prior distribution with each column corresponding to one of the Heligman-Pollard parameters
mle	A vector containing the mle estimates. These define the center of each uniform from which the prior was drawn
se.out	A vector containing the standard error for each element of mle
pri.lo	The lower bounds on the uniform distributions from which the prior for each parameter is drawn
pri.hi	The upper bounds on the uniform distributions from which the prior for each parameter is drawn

### References

Heligman, Larry and John H. Pollard. 1980 "The Age Pattern of Mortality." *Journal of the Institute of Actuaries* **107**:49–80.

### See Also

[hp.bm.imis](#), [optim](#)

### Examples

```
data(HPprior) ##loads a vector of persons at risk (lx) and deaths (dx)
prior <- pri.mle(nrisk=lx, ndeath=dx)
summary(prior$q0)
```

---

prior.form

*Heligman-Pollard parameter prior formation*

---

### Description

Draws from a uniform distribution with bounds `pri.lo` and `pri.hi` to create the prior distribution of the Heligman-Pollard parameters necessary for the Bayesian Melding procedure

### Usage

```
prior.form(pri.lo = c(0, 0, 0, 0, 0, 15, 0, 0),
pri.hi = c(0.15, 1, 1, 0.25, 15, 55, 0.1, 1.25), theta.dim = 8)
```

**Arguments**

pri.lo	Lower bound of the uniform from which the prior is drawn. Defaults to pri.lo = c(0, 0, 0, 0, 0, 15, 0, 0)
pri.hi	Upper bound of the uniform from which the prior is drawn. Defaults to pri.hi = c(0.15, 1, 1, 0.25, 15, 55, 0.1, 1.25)
theta.dim	The number of parameters to be estimated. Defaults to 8

**Value**

A (1000\*theta.dim) x theta.dim matrix containing the 1000\*theta.dim sets of the Heligman-Pollard parameters drawn from a uniform distribution

**References**

Heligman, Larry and John H. Pollard. 1980 "The Age Pattern of Mortality." *Journal of the Institute of Actuaries* **107**:49–80.

Poole, David and Adrian Raftery. 2000. "Inference for Deterministic Simulation Models: The Bayesian Melding Approach." *Journal of the American Statistical Association* **95**:1244–1255.

Raftery, Adrian and Le Bao. 2009. "Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling." Technical Report 560, Department of Statistics, University of Washington.

**Examples**

```
q0 <- prior.form()
```

---

prior.likewts                      *Prior likelihoods and weights*

---

**Description**

Calculates the log-likelihood and importance weight for each set (i.e. each row) of Heligman-Pollard parameters in the prior

**Usage**

```
prior.likewts(prior, nrisk, ndeath, theta.dim = 8,
age = c(1e-05, 1, seq(5, 100, 5)))
```

**Arguments**

prior	A (theta.dim*1000) x theta.dim matrix containing the prior distribution
nrisk	A vector containing the number of persons at risk in each age group
ndeath	A vector containing the number of deaths in each age group
theta.dim	Number of columns of the prior matrix. Defaults to 8
age	A vector containing the ages at which each age interval begins

**Value**

wts.0	A vector containing an importance weight for each set of parameters from the prior
log.ilke.0	A vector containing a log likelihood for each set of parameters from the prior

**Note**

Used in the [loop.optim](#) function

**References**

Heligman, Larry and John H. Pollard. 1980 "The Age Pattern of Mortality." *Journal of the Institute of Actuaries* **107**:49–80.

Poole, David and Adrian Raftery. 2000. "Inference for Deterministic Simulation Models: The Bayesian Melding Approach." *Journal of the American Statistical Association* **95**:1244–1255.

Raftery, Adrian and Le Bao. 2009. "Estimating and Projecting Trends in HIV/AIDS Gen-eralized Epidemics Using Incremental Mixture Importance Sampling." Technical Report 560, Department of Statistics, University of Washington.

**See Also**

[loop.optim](#), [hp.bm.imis](#)

**Examples**

```
lx <- c(1974, 1906, 1860, 1844, 1834, 1823, 1793, 1700, 1549, 1361,
1181, 1025, 870, 721, 571, 450, 344, 256, 142, 79, 41, 8)
dx <- c(68, 47, 16, 10, 13, 29, 92, 151, 188, 179, 156, 155, 147, 150,
122, 106, 88, 113, 63, 38, 32, 8)
age <- c(1e-05, 1, seq(5, 85, 5))
q0 <- prior.form()
result <- prior.likewts(prior=q0, nrisk=lx, ndeath=dx, age=age)
summary(result$wts.0)
summary(result$log.like.0)
```



---

samp.postopt                      *Multivariate Gaussian Sampling for Heligman-Pollard model estimated via Bayesian Melding*

---

### Description

Samples the eight Heligman-Pollard parameters from the mvnorm distribution for each run of optimizer step where the likelihood for that run exceeds the maximum likelihood from the prior

### Usage

```
samp.postopt(opt.cov.d, opt.mu.d, d.keep, prior, B = 400,
             B0 = 8000, d = 10)
```

### Arguments

opt.cov.d	An array containing a covariance matrix for each run of optimizer where the likelihood for that run exceeds the maximum likelihood from the prior
opt.mu.d	A matrix containing the results of the optimizer step
d.keep	Number of runs of optimizer where the likelihood for that run exceeds the maximum likelihood from the prior
prior	A matrix containing the prior distribution (see prior.form and prior.mle)
B	sample size at the importance sampling stage
B0	Sample size of the prior. This is equal to theta.dim*1000
d	Number of optimizer iterations

### Details

For use within the function [hp.bm.imis](#)

### Value

H.k	The prior plus new samples
H.new	The new samples from the multivariate normal
B1	The number of new samples - should be equal to B*d.keep

### References

Heligman, Larry and John H. Pollard. 1980 "The Age Pattern of Mortality." *Journal of the Institute of Actuaries* **107**:49–80.

Poole, David and Adrian Raftery. 2000. "Inference for Deterministic Simulation Models: The Bayesian Melding Approach." *Journal of the American Statistical Association* **95**:1244–1255.

Raftery, Adrian and Le Bao. 2009. "Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling." Technical Report 560, Department of Statistics, University of Washington.

**See Also**

hp.bm.imis

**Examples**

```
## Not run: data(HPprior)
q0 <- HPprior
lx <- c(1974, 1906, 1860, 1844, 1834, 1823, 1793, 1700, 1549, 1361,
1181, 1025, 870, 721, 571, 450, 344, 256, 142, 79, 41, 8)
dx <- c(68, 47, 16, 10, 13, 29, 92, 151, 188, 179, 156, 155, 147, 150,
122, 106, 88, 113, 63, 38, 32, 8)
opt.result <- loop.optim(prior = q0, nrisk=lx, ndeath=dx)
  opt.mu.d <- opt.result$opt.mu.d
  opt.cov.d <- opt.result$opt.cov.d
  theta.new <- opt.result$theta.new
  d.keep <- opt.result$d.keep
  log.like.0 <- opt.result$log.like.0
  wts.0 <- opt.result$log.like.0
samp.po <- samp.postopt(opt.cov.d = opt.cov.d, opt.mu.d = opt.mu.d,
  prior = q0, d.keep = d.keep)
## End(Not run)
```

var.rwts

*Variance of the rescaled weights when estimating the Heligman-Pollard parameters using Bayesian Melding with IMIS*

**Description**

Calculates the variance of the rescaled weights

**Usage**

var.rwts(w)

**Arguments**

w                    A vector of importance weights corresponding to each row of the mixture of the prior and multivariate gaussian draws

**Value**

A scalar representing the variance of the rescaled weights

**Note**Used in the [final.resamp](#) function

## References

Poole, David and Adrian Raftery. 2000. "Inference for Deterministic Simulation Models: The Bayesian Melding Approach." *Journal of the American Statistical Association* **95**:1244–1255.

Raftery, Adrian and Le Bao. 2009. "Estimating and Projecting Trends in HIV/AIDS Generalized Epidemics Using Incremental Mixture Importance Sampling." Technical Report 560, Department of Statistics, University of Washington.

## See Also

[final.resamp](#), [hp.bm.imis](#)

## Examples

```
#Generate a vector of weights#  
wts <- runif(100, 0, .99)  
var.rwts(wts)
```

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