

# Package ‘WARN’

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**Type** Package

**Title** Weaning Age Reconstruction with Nitrogen Isotope Analysis

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**Imports** graphics, grDevices, MASS, stats

**Description** This estimates precise weaning ages for a given skeletal population by analyzing the stable nitrogen isotope ratios of them. Bone collagen turnover rates estimated anew and the approximate Bayesian computation (ABC) were adopted in this package.

**Repository** CRAN

**License** GPL (>= 3)

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WARN-package

*Weaning Age Reconstruction with Nitrogen isotope analysis*

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## Description

WARN is a package to estimate precise weaning ages for a given skeletal population by analyzing the measured stable nitrogen isotope ratios (d15Ns) of them. Bone collagen turnover rates in non-adults estimated anew and the approximate Bayesian computation (ABC) were adopted in the model.

## Details

Package: WARN  
Type: Package  
Version: 1.2-4  
Date: 2019-10-18  
License: GPL (>= 3)

Function [warn](#) estimates the age at the start and end of weaning, enrichment of d15N through maternal to infant tissue, and d15N value of collagen synthesized entirely from weaning foods with their posterior probabilities. Other geochemical values that change with breastfeeding and weaning can also be analyzed (e.g., d18O, Sr/Ca, and Ba/Ca). The `warn` performs approximate Bayesian computation (ABC) for a given set of estimated ages and measured d15N of non-adults from the skeletal population. Function [warnCI](#) calculates credible intervals (CIs) of posterior probabilities under a given class "warn" object and a given threshold of CIs. Function [warnProb](#) calculate posterior probabilities under a given class "warn" object and given parameter ranges. This package adopts S3 class. The detail of mathematical models is described in Tsutaya and Yoneda (2013).

## Author(s)

Takumi Tsutaya <tsutayatakumi@gmail.com>

## References

Tsutaya, T., and Yoneda, M. (2013). Quantitative reconstruction of weaning ages in archaeological human populations using bone collagen nitrogen isotope ratios and approximate Bayesian computation. *PLoS ONE* **8**, e72327.

## See Also

[warn](#), [warnCI](#), [warnOptim](#), [warnProb](#)

## Examples

## See `?warn`, `?warnCI`, and `?warnProb` for examples.

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lerna	<i>Stable isotopic data of the Lerna population</i>
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**Description**

This data set gives the stable carbons and nitrogen isotope ratios of the 39 human bone samples from Middle Bronze Age (ca. 2100–1700 BC) Lerna, Greece reported in Triantaphyllou et al. (2008).

**Usage**

```
lerna
```

**Format**

lerna is a data frame with 39 individuals (rows) and 5 variables (columns) of ID (skeletal number), sex, estimated age at death, and carbon and nitrogen isotope ratios, named id, sex, age, d13C, and d15N, respectively. sex is a factor with levels f, m, and u, which corresponds to female, male, unknown, respectively. The estimated ages at death were midpoint values.

**Details**

See detail for Triantaphyllou et al. (2008).

**Source**

Triantaphyllou, S., Richards, M. P., Zerner, C., and Voutsaki, S. (2008). Isotopic dietary reconstruction of humans from Middle Bronze Age Lerna, Argolid, Greece. *J. Archaeol. Sci.* **35**, 3028–3034.

---

plot.warn	<i>Plot for posterior weaning parameters</i>
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---

**Description**

plot.warn is a plotting utility for quick visualization of the result of weaning age reconstruction from an object of class "warn". The measured and modeled bone collagen nitrogen isotope ratios (d15Ns) are plotted against estimated ages.

**Usage**

```
## S3 method for class 'warn'  
plot(x, hline.female = TRUE, hline.adult = FALSE,  
     adult.mean = NA, adult.sd = 0,  
     is.legend = TRUE, is.female = TRUE, plot = TRUE, ...)
```

**Arguments**

x	an object of class "warn" generated by <a href="#">warn</a> .
hline.female, hline.adult	logical; if TRUE, horizontal dotted lines indicating one standard deviation ranges of adult females and all adults are plotted on the figure; the default is TRUE for female and FALSE for adult.
adult.mean	the mean d15N of all adults, an optional single value.
adult.sd	the one standard deviation of all adult d15N, an optional single value. Utilized later in <a href="#">plot.warn</a> .
is.legend	logical; if TRUE (the default), legend is plotted on the figure.
is.female	logical; if TRUE (the default), female mean d15N is plotted on the figure.
plot	logical; if TRUE (the default), a figure is plotted, otherwise a list of d15N changes in modeled bone and modeled diet is returned.
...	additional arguments passed to <a href="#">plot</a> .

**Details**

The following three results on d15N are plotted against age, the original measured ratios of non-adult bone collagen (Measured d15N), modeled ratios of non-adult bone collagen (Modeled d15N), and modeled ratios of collagen synthesized entirely from consumed foods in the last half year (Modeled diet). These results are calculated in [warn](#). Mean d15Ns of adult females and all adults can also be plotted.

**References**

Tsutaya, T., and Yoneda, M. (2013). Quantitative reconstruction of weaning ages in archaeological human populations using bone collagen nitrogen isotope ratios and approximate Bayesian computation. *PLoS ONE* **8**, e72327.

**See Also**

[WARN](#), [warn](#), [warnCI](#), [warnProb](#), [summary.warn](#)

**Examples**

```
## See ?warn for examples.
```

---

plot.warnCI

*Plot for CI of posterior probabilities of weaning parameters*

---

**Description**

plot.warnCI is a plotting utility for quick visualization of credible interval (CI) of posterior probabilities of the weaning parameters from an object of class "warnCI". Results of kernel density estimation for the posteriors are plotted as a form of [contour](#) or one-dimensional distribution with CIs.

**Usage**

```
## S3 method for class 'warnCI'
plot(x, weaning.par = "age", ...)
```

**Arguments**

`x` an object of class "warnCI" generated by [warnCI](#).

`weaning.par` character for the intended weaning parameter. The allowed values are "age" (the default), "enrich", and "wnfood".

`...` additional arguments passed to [plot.warnProb](#).

**Details**

Values on the contour lines indicate relative probabilities based on that of the maximum density estimator.

**References**

Tsutaya, T., and Yoneda, M. (2013). Quantitative reconstruction of weaning ages in archaeological human populations using bone collagen nitrogen isotope ratios and approximate Bayesian computation. *PLoS ONE* **8**, e72327.

**See Also**

[WARN](#), [warn](#), [warnCI](#), [warnProb](#), [plot.warnProb](#)

**Examples**

```
## See ?warnCI for examples.
```

---

plot.warnProb	<i>Plot for probabilities of posterior weaning parameters</i>
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---

**Description**

`plot.warnProb` is a plotting utility for quick visualization of the posterior weaning parameters from an object of class "warnProb". Results of kernel density estimation for the posteriors are plotted as a form of [contour](#) with designated parameter ranges.

**Usage**

```
## S3 method for class 'warnProb'
plot(x, is.legend = TRUE, is.contour = TRUE,
     is.image = FALSE, is.prior = FALSE, ...)
```

## Arguments

x	an object of class "warnProb" generated by <a href="#">warnProb</a> .
is.legend	logical; if TRUE (the default), legend is plotted on the figure.
is.contour	logical; if TRUE (the default), contour lines corresponding to the probabilities are plotted with <a href="#">contour</a> . Only used if the intended weanig parameter is weaning ages (i.e., weaning.par = "age" in <a href="#">warnProb</a> ).
is.image	logical; if TRUE, grid of gray-scale rectangles with color strength corresponding to the probabilities is plotted with <a href="#">image</a> . The default is FALSE, and only used if the intended weanig parameter is weaning ages (i.e., weaning.par = "age" in <a href="#">warnProb</a> ).
is.prior	logical; if TRUE, prior density of the paramter is also plotted with dotted line. The default is FALSE, and only used if the intended weanig parameter is enrichment or weaning food (i.e., weaning.par = "enrich" or "wnfood" in <a href="#">warnProb</a> ).
...	additional arguments passed to <a href="#">plot</a> .

## Details

Values on the contour lines indicate relative probabilities based on that of the maximum density estimator.

## References

Tsutaya, T., and Yoneda, M. (2013). Quantitative reconstruction of weaning ages in archaeological human populations using bone collagen nitrogen isotope ratios and approximate Bayesian computation. *PLoS ONE* **8**, e72327.

## See Also

[WARN](#), [warn](#), [warnCI](#), [warnProb](#), [summary.warnProb](#)

## Examples

```
## See ?warnProb for examples.
```

---

summary.warn

*Summaries of posterior weaning parameters*

---

## Description

summary.warn calculates simple summaries of posterior samples for the four weaning parameters, which is the maximum density estimators and its marginal probabilities, a joint probability for the combination of the maximum density weaning ages, mean squared distance between the measured and modeled nitrogen isotope ratio (d15N), number of non-adult individuals used, and number of particles used in sequential Monte Carlo (SMC) sampling.

**Usage**

```
## S3 method for class 'warn'
summary(object, ...)
```

**Arguments**

object            an object of class "warn" generated by [warn](#).  
 ...                additional arguments affecting the summary produced.

**Value**

summary.warn returns a list containing following components and those succeeded from "warn":

call	the matched call.
mde	the maximum density estimators and the marginal probabilities.
prob.2d.age	the joint probability for the combination of the maximum density weaning ages.
dist.mde	the mean squared distance between the measured and modeled d15Ns.
individual	the number of non-adult individuals used.
particle	the number of particles used in SMC sampling.

**References**

Tsutaya, T., and Yoneda, M. (2013). Quantitative reconstruction of weaning ages in archaeological human populations using bone collagen nitrogen isotope ratios and approximate Bayesian computation. *PLoS ONE* **8**, e72327.

**See Also**

[WARN](#), [warn](#), [warnCI](#), [warnProb](#), [plot.warn](#)

**Examples**

```
## See ?warn for examples.
```

---

summary.warnProb	<i>Summaries of probabilities of posterior weaning parameters</i>
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**Description**

summary.warnProb calculates simple summaries of probabilities of posterior samples for the four weaning parameters, which is the intended weaning parameter, designated parameter range, and calculate posterior probability of the weaning parameter that ranges between the range.

**Usage**

```
## S3 method for class 'warnProb'
summary(object, ...)
```

**Arguments**

`object` an object of class "warnProb" generated by `warnProb`.  
`...` additional arguments affecting the summary produced.

**Value**

`summary.warnProb` returns a list containing following components and those succeeded from "warnProb":

`call` the matched call.  
`range` a vector giving the range of the intended weaning parameter.  
`probability` posterior probability of parameter in the designated range.  
`weaning.par` a character indicating the weaning parameter used.

**References**

Tsutaya, T., and Yoneda, M. (2013). Quantitative reconstruction of weaning ages in archaeological human populations using bone collagen nitrogen isotope ratios and approximate Bayesian computation. *PLoS ONE* **8**, e72327.

**See Also**

[WARN](#), [warn](#), [warnCI](#), [warnProb](#), [plot.warnProb](#)

**Examples**

```
## See ?warnProb for examples.
```

---

warn	<i>Weaning parameter estimation with approximate Bayesian computation</i>
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**Description**

`warn` estimates weaning parameters (i.e., weaning ages, enrichment factor, and nitrogen isotope ratio ( $\delta^{15}\text{N}$ ) of weaning food derived collagen) for a given skeletal population under the framework of approximate Bayesian computation (ABC).



**Usage**

```
## Default S3 method:
warn(age, d15N, female.mean, female.sd = NA,
     fraction = "collagen",
     prior = c(0.5, 3, 3, 3, 1.9, 0.9, female.mean, 3, 0, 1),
     num.particle = 10000, form = "parabolic",
     tolerances = c(2.0, 1.0, 0.5, 0.25, 0.125, 0.0625, 0))
```

**Arguments**

age	a vector of estimated ages in year of the non-adult skeletons. Ages greater than 10 years are not allowed.
d15N	a vector of bone collagen d15N of non-adult skeletons. Other geochemical values (e.g., d18O, Sr/Ca, and Ba/Ca) can be used with this argument.
female.mean	the mean d15N of the adult females, single value.
female.sd	the one standard deviation of adult female d15Ns, an optional single value. Utilized later in <a href="#">plot.warn</a> .
fraction	fraction of bone analyzed. The allowed values are collagen and mineral. The turnover rate specific to each fraction will be used.
prior	a vector of hyper parameter values for prior distributions of the weaning parameters and the individual error term. Mean and SD for t1 (age at the start of weaning), t2 (age at the end of weaning), enrichment of d15N, d15N of weaning food derived collagen, and sigma used in ABC-SMC, in sequence. The values are succeeded to mean and sd arguments of <a href="#">rnorm</a> . The default is <code>c(0.5, 3, 3, 3, 1.9, 0.9, female.mean, 3, 0, 1)</code> .
num.particle	number of particles in sequential Monte Carlo (SMC) sampling; defaults to 10000.
form	form of the model curve for the weaning process. The allowed values are "linear", "parabolic" (the default), "reverse", and "sigmoid".
tolerances	a vector of decreasing tolerances used in the SMC sampling. The default is <code>c(2.0, 1.0, 0.5, 0.25, 0.125, 0.0625, 0)</code> .

**Details**

The `warn` estimates the age at the start and end of weaning, enrichment of d15N through maternal to infant tissue, and d15N value of collagen synthesized entirely from weaning foods with their posterior probabilities. Other geochemical values that change with breastfeeding and weaning can also be analyzed (e.g., d18O, Sr/Ca, and Ba/Ca). Probabilities are estimated by SMC with partial rejection control, and the algorithm was derived from Sisson et al. (2007, 2009). The posterior probabilities are obtained as a result of kernel density estimation, a product of [kde2d](#) in **MASS** package for weaning ages, and [density](#) for enrichment and weaning foods. The model used to describe the change in d15N during weaning contains a new estimate of bone collagen turnover rates in non-adults, and is shown in Tsutaya and Yoneda (2013).

**Value**

warn returns an object of class "warn".

The function `summary` and `plot` are used to obtain and indicate a summary and figure of the results, respectively.

An object of class "warn" is a list containing at least the following components:

mde	the maximum density estimators and their marginal probabilities for the weaning parameters.
prob.2d.age	the joint probability for combination of the maximum density weaning ages.
dist.mde	the mean squared distance between the measured and modeled d15Ns of non-adults.
kde.age	two-dimensional kernel density estimates of the weaning ages. A product of <code>kde2d</code> in <b>MASS</b> package.
kde.enrich	kernel density estimates of the enrichment factor from mother to infant. A product of <code>density</code> .
kde.wnfood	kernel density estimates of the d15N of collagen synthesized entirely from weaning foods. A product of <code>density</code> .
posterior	a matrix of final particles in SMC sampling.
age	the non-adult ages used.
d15N	the measured d15Ns of non-adult bone collagen used.
female.mean	the mean d15N of adult females used.
female.sd	the one standard deviation of adult female d15Ns used.
fraction	the fraction of bone analyzed.
prior	a vector of the hyper parameter values for the prior distributions used.
particle	the number of particles used.
form	the form of the model curve used.
call	the matched call.

The band-width of kernel density estimation (i.e., `h` in `kde2d` and `bw` in `density`) is selected by SJ method, `width.SJ` in **MASS**, with "direct plug-in".

**Author(s)**

Takumi Tsutaya developed this model.

**References**

Sisson, S. A., Fan, Y., and Tanaka, M. M. (2007, 2009). Sequential Monte Carlo without likelihoods. *Proc. Natl. Acad. Sci.* **104**, 1760–1765.

Tsutaya, T., and Yoneda, M. (2013). Quantitative reconstruction of weaning ages in archaeological human populations using bone collagen nitrogen isotope ratios and approximate Bayesian computation. *PLoS ONE* **8**, e72327.

**See Also**

[WARN](#), [warnCI](#), [warnProb](#), [summary.warn](#), [plot.warn](#)

**Examples**

```
## Data from the Lerna population.
nonadult <- subset(lerna, lerna$age <= 10)
adult <- subset(lerna, lerna$age > 17)
female <- subset(adult, adult$sex == "f")

## Calculate maximum density estimators using ABC.
warn.lerna <- warn(
  age = nonadult$age,
  d15N = nonadult$d15N,
  female.mean = mean(female$d15N),
  num.particle = 500,
  female.sd = sd(female$d15N),
  prior = c(0.2, 0.2, 1.6, 0.2, 2.5, 0.2, 8.1, 0.2, 0, 0.7),
  tolerances = c(1.5, 0.7))

## Indicate summary.
summary(warn.lerna)

## Plot.
plot(warn.lerna)

## Plot with adult mean.
plot(warn.lerna,
  hline.adult = TRUE,
  adult.mean = mean(adult$d15N),
  adult.sd = sd(adult$d15N),
  is.female = FALSE)
```

---

warnCI

*Calculate credible intervals for posterior probability of the weaning parameters*

---

**Description**

warnCI calculate credible intervals (CIs) of posterior probabilities under a given class "warn" object and a given threshold of CIs.

**Usage**

```
## Default S3 method:
warnCI(object, threshold = 0.95)
```

**Arguments**

object	an object of class "warn".
threshold	numeric scalar or vector giving the threshold of CI for posterior probabilities of weaning ages, nitrogen isotope ratios (d15Ns) of enrichment factor, and d15Ns of collagen derived entirely from weaning foods. Minimum range with over $(\text{threshold} * 100)\%$ of summed posterior probability is calculated. If scalar is given, value is repeated. Values between 0 and 1 must be given.

**Details**

warnCI calculates minimum ranges with over  $(\text{threshold} * 100)\%$  of summed posterior probability of the weaning parameters. Posterior probabilities are represented as the product of kernel density estimation performed in [warn](#). CIs of weaning ages are obtained from two-dimensional probability distribution, and those of d15Ns of enrichment factor and collagen derived entirely from weaning foods are from one-dimensional. Posterior probability distributions with multiple notable peaks are not supported by warnCI.

**Value**

warnCI returns an object of [class](#) "warnCI" which is a subclass of "warn". The function [plot](#) is used to indicate figures of the results. An object of class "warnCI" has following list components in addition to those succeeded from "warn":

ci.age	a list containing the CIs for the combination of t1 and t2, and its summed posterior probability.
ci.enrich	a list containing the CI for the d15N-enrichment from mother to infant, and its summed posterior probability.
ci.wnfood	a list containing the CI for the d15N value of collagen derived entirely from weaning foods, and its summed posterior probability.
ci.threshold	a vector showing the thresholds used to calculate the CIs.

**Author(s)**

Takumi Tsutaya developed this model.

**References**

Tsutaya, T., and Yoneda, M. (2013). Quantitative reconstruction of weaning ages in archaeological human populations using bone collagen nitrogen isotope ratios and approximate Bayesian computation. *PLoS ONE* **8**, e72327.

**See Also**

[WARN](#), [warn](#), [warnProb](#), [plot.warnCI](#)

**Examples**

```

## Data from the Lerna population.
nonadult <- subset(lerna, lerna$age <= 10)
adult <- subset(lerna, lerna$age > 17)
female <- subset(adult, adult$sex == "f")

## Calculate maximum density estimators using ABC.
warn.lerna <- warn(
  age = nonadult$age,
  d15N = nonadult$d15N,
  female.mean = mean(female$d15N),
  num.particle = 500,
  female.sd = sd(female$d15N),
  prior = c(0.2, 0.2, 1.6, 0.2, 2.5, 0.2, 8.1, 0.2, 0, 0.7),
  tolerances = c(1.5, 0.7))

## Calculate over (>=) 50% CIs.
warn.lerna.50ci <- warnCI(warn.lerna, 0.50)

## Indicate result.
warn.lerna.50ci

## Plot.
plot(warn.lerna.50ci, "age")
plot(warn.lerna.50ci, "enrich")

```

---

warnOptim

*Optimize the weaning parameters*


---

**Description**

warnOptim optimizes the weaning parameters for a given skeletal population. This function can be preliminarily used in order to set efficient priors of the weaning parameters.

**Usage**

```

## Default S3 method:
warnOptim(age, d15N, female.mean,
  fraction = "collagen",
  par.initial = c(0.5, 3, 1.9, female.mean),
  form = "parabolic", ...)

```

**Arguments**

age                    a vector of estimated ages of non-adult skeletons. Ages greater than 10 years are not allowed.

d15N	a vector of bone collagen nitrogen isotope ratio (d15N) of non-adult skeletons. Other geochemical values (e.g., d18O, Sr/Ca, and Ba/Ca) can be used with this argument.
fraction	fraction of bone analyzed. The allowed values are collagen and mineral.
par.initial	a vector of the initial parameter values for optimization: t1, t2, enrichment, and weaning food, in sequence. The values are succeeded to the par arguments of <a href="#">optim</a> .
female.mean	the mean d15N (or other geochemical value) of adult females, single value.
form	form of the model curve for the weaning process. The allowed values are "linear", "parabolic" (the default), "reverse", and "sigmoid".
...	additional argunemts passed to <a href="#">optim</a> .

### Details

The `warnOptim` calculates the weaning parameters (i.e., weaning ages, enrichment factor, and d15N of bone collagen synthesized entirely from the weaning foods), which minimize the mean squared distance between the measured and modeled d15Ns using [optim](#). Result of this function is just a rough indication and initial parameter dependent, and can be preliminary used in order to set efficient priors of the weaning parameters.

### Value

`warnOptim` directly returns a result list of [optim](#).

### See Also

[WARN](#), [warn](#), [warnCI](#), [warnProb](#)

### Examples

```
## Data from the Lerna population.
nonadult <- subset(lerna, lerna$age <= 10)
adult <- subset(lerna, lerna$age > 17)
female <- subset(adult, adult$sex == "f")

## Simple optimization without probability.
(opt.lerna <- warnOptim(
  age = nonadult$age,
  d15N = nonadult$d15N,
  female.mean = mean(female$d15N),
  control = list(maxit = 10000, ndeps = 1e-2, reltol = 1e-7)))
```

---

warnProb

*Calculate posterior probability of the weaning parameters*


---

### Description

warnProb calculate posterior probabilities under a given class "warn" object and a given parameter range.

### Usage

```
## Default S3 method:
warnProb(object, weaning.par = "age", range.x, range.y = NA)
```

### Arguments

object	an object of class "warn".
weaning.par	character for the intended weanig parameter. The allowed values are "age" (the default), "enrich", and "wnfood".
range.x, range.y	numeric vectors of length 2, giving the range of the intended weanig parameters. For example, range.x corresponds to the age at the start of weaning if weaning.par = "age". range.y is used only if weaning.par = "age", and corresponds to the age at the end of weaning. Fractional point lower than e-002 is rounded.

### Details

warnProb calculates posterior probability of the weaning parameter that ranges between designated range. Parameter distribution is represented as the product of kernel density estimation performed in [warn](#). Weaning ages are estimated from two-dimensional probability distribution, and nitrogen isotope ratios (d15Ns) of enrichment factor and weaning food derived collagen are from one-dimensional.

### Value

warnProb returns an object of `class` "warnProb" which is a subclass of "warn". The functions [summary](#) and [plot](#) are used to obtain and indicate a summary and figure of the results, respectively. An object of class "warnProb" at least has following list components in addition to those succeeded from "warn":

probability	posterior probability of parameter that range between the designated range.
range	a vector giving the range of the intended weanig parameter.
weaning.par	a character indicating the weaning parameter used.

**Author(s)**

Takumi Tsutaya developed this model.

**References**

Tsutaya, T., and Yoneda, M. (2013). Quantitative reconstruction of weaning ages in archaeological human populations using bone collagen nitrogen isotope ratios and approximate Bayesian computation. *PLoS ONE* **8**, e72327.

**See Also**

[WARN](#), [warn](#), [warnCI](#), [summary.warnProb](#), [plot.warnProb](#)

**Examples**

```
## Data from the Lerna population.
nonadult <- subset(lerna, lerna$age <= 10)
adult <- subset(lerna, lerna$age > 17)
female <- subset(adult, adult$sex == "f")

## Calculate maximum density estimators using ABC.
warn.lerna <- warn(
  age = nonadult$age,
  d15N = nonadult$d15N,
  female.mean = mean(female$d15N),
  num.particle = 500,
  female.sd = sd(female$d15N),
  prior = c(0.2, 0.2, 1.6, 0.2, 2.5, 0.2, 8.1, 0.2, 0, 0.7),
  tolerances = c(1.5, 0.7))

## Calculate probabilities for a given parameter range.
warnprob.age <- warnProb(warn.lerna, "age", c(0.0, 1.1), c(0.8, 2.3))
warnprob.enrich <- warnProb(warn.lerna, "enrich", c(1.5, 3.5))
warnprob.wnfood <- warnProb(warn.lerna, "wnfood", c(7.3, 8.8))

## Indicate summary.
summary(warnprob.age)
summary(warnprob.enrich)

## Plot.
plot(warnprob.age)
plot(warnprob.wnfood)

## Plot with image.
plot(warnprob.age, is.image = TRUE)
```



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