Package 'nutriR'

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Type Package

Title Nutritional intake functions for R

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Description This package provides the subnational habitual intake distributions estimated in Passarelli et al. (in prep) as well as a number of functions for analyzing and using subnational intake distributions.

License GPL-3

Encoding UTF-8

LazyData true

Depends R (>= 2.10)

RoxygenNote 7.1.1

Suggests knitr,
rmarkdown

VignetteBuilder knitr

R topics documented:

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cv *Calculate the coefficient of variation (CV) of a habitual intake distribution*

Description

This function calculates the coefficient of variation (CV) of a habitual intake distribution. It handles gamma and log-normal distributions.

Usage

```
cv(shape = NULL, rate = NULL, meanlog = NULL, sdlog = NULL)
```

Arguments

shape	Shape parameter for gamma distribution
rate	Rate parameter for gamma distribution
meanlog	Mean parameter for gamma distribution
sdlog	Standard deviation parameter for gamma distribution

Value

The coefficient of variation (CV) of the distribution

Examples

```
cv(shape=1, rate=0.5)
cv(meanlog=3, sdlog=1)
```

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dists_full *Subnational habitual nutrient intake distributions*

Description

This dataset contains the subnational habitual nutrient intake distributions estimated by Passarelli et al. (in prep).

Usage

```
dists_full
```

Format

A data frame with the following attributes::

country Country name

iso3 ISO3 code for country

nutrient_type Type of nutrient (i.e., macronutrient, vitamin, element)

nutrient Nutrient name

nutrient_units Nutrient name and units

sex Sex (i.e., males, females, both)

age_group Age group (5-yr intervals)

sex_ear Sex used to assign EAR value

age_group_ear Age group used to assign EAR value

ear_units EAR units

ear_cv Recommended coefficient of variation (CV) for the EAR value

ear EAR value

ear_lact EAR value for lactating women

ear_preg EAR value for pregnant women

g_shape Shape parameter for a gamma-distributed intake distribution

g_rate Rate parameter for a gamma-distributed intake distribution

g_ks K-S goodness-of-fit for a gamma-distributed intake distribution

g_mu Mean of a gamma-distributed intake distribution

g_cv Coefficient of variation (CV) of a gamma-distributed intake distribution

g_var Variance a gamma-distributed intake distribution

g_skew Skewness of a gamma-distributed intake distribution

g_kurt Kurtosis of a gamma-distributed intake distribution

g_sev Summary exposure value (SEV) of a gamma-distributed intake distribution

ln_meanlog Meanlog parameter for a lognormally-distributed intake distribution

ln_sdlog Sdlog parameter for a lognormally-distributed intake distribution

ln_ks K-S goodness-of-fit for a lognormally-distributed intake distribution

ln_mu Mean of a lognormally-distributed intake distribution

ln_cv Coefficient of variation (CV) of a lognormally-distributed intake distribution

ln_var Variance a lognormally-distributed intake distribution

ln_skew Skewness of a lognormally-distributed intake distribution

ln_kurt Kurtosis of a lognormally-distributed intake distribution

ln_sev Summary exposure value (SEV) of a lognormally-distributed intake distribution

best_dist Best distribution based on the K-S goodness-of-fit statistic

mu Mean of the best intake distribution

cv Coefficient of variation (CV) of the best intake distribution

var Variance the best intake distribution

skew Skewness of the best intake distribution

kurt Kurtosis of the best intake distribution

sev Summary exposure value (SEV) of the best intake distribution

Source

Passarelli S, Free CM, Shepon A, Lee C, Moursi M, Cao L, Li Y, Crispim S, Schmidhuber J, Bromage S, Beal T, Golden CD (in prep) Global modeling of subnational habitual nutrient intake distributions. Near submission.

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dris   *Dietary Reference Intake (DRI) values*

Description

Dietary Reference Intake (DRIs) values from the Food and Nutrition Board of the National Academy of Sciences. The file includes DRIs for 42 nutrients and 22 life stage groups. The following DRI types are included in this dataset: Estimated Average Requirements (EARs), Adequate Intakes (AIs), Recommended Daily Averages (RDAs), and Upper Limits (ULs).

Usage

```
dris
```

Format

A data frame with the following attributes::

nutrient_type Type of nutrient (i.e., macronutrient, vitamin, element)

nutrient_units Nutrient name and units

nutrient Nutrient name

units Nutrient units (e.g., g/d, mg/d, µg/d)

sex_stage Sex and life stage (e.g., Infants, Women, Women (pregnant), Women (lactating))

sex Sex (i.e., males, females, both)

stage Life stage (i.e., infants, children, pregnancy, lactation, none)

age_range Age range

dri_type Dietary reference intake type (i.e., EAR, AI, RDA, UL)

value DRI value

footnote Footnote

Source

Food and Nutrition Board, National Academy of Sciences, Institute of Medicine (2020). Dietary Reference intakes: Estimated Average requirements and recommended intakes. Accessed at https://www.nal.usda.gov/sites/default/files/fnic_uploads//recommended_intakes_individuals.pdf.

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generate_dists	*Generate subnational nutrient intake distributions*

Description

This function generates data for plotting subnational nutrient intake distributions. It is provided a dataframe generated from the get_dists() function.

Usage

```
generate_dists(dists)
```

Arguments

dists   A data frame of nutrient distributions

Value

A dataframe

Examples

```
dists <- nutriR::get_dists(isos=c("USA", "BGD"), nutrients=c("Iron"), sexes="MF", ages=20:40)
dists_sim <- nutriR::generate_dists(dists)
```

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get_dists	*Get subnational nutrient intake distributions*

Description

This function retrieves the subnational nutrient intake distributions modelled by Passarreli et al. (in prep).

Usage

```
get_dists(nutrients = NULL, isos = NULL, sexes = NULL, ages = NULL)
```

Arguments

nutrients	A character vector of nutrients of interest (e.g., "Iron", "Calcium", etc.)
isos	A character vector of ISO3s of countries of interest (e.g., "USA")
sexes	A character string of sexes of interest (i.e., "M", "F", or "MF")
ages	A numeric vector of ages of interest (e.g., 10:50, 0:75, 55:90)

Value

A data frame with the parameters describing the requested subnational intake distributions

Examples

```
dists_all <- get_dists()
dists_usa <- get_dists(isos="USA")
dists_usa_iron <- get_dists(isos="USA", nutrients="Iron", sexes="MF")
dists_usa_iron_2040 <- get_dists(isos="USA", nutrients="Iron", sexes="MF", ages=20:40)
```

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kurtosis   *Calculate the kurtosis of a habitual intake distribution*

Description

This function calculates the kurtosis of a habitual intake distribution. It handles gamma and log-normal distributions.

Usage

```
kurtosis(shape = NULL, rate = NULL, meanlog, sdlog = NULL)
```

Arguments

shape	Shape parameter for gamma distribution
rate	Rate parameter for gamma distribution
meanlog	Mean parameter for gamma distribution
sdlog	Standard deviation parameter for gamma distribution

Value

The kurtosis of the distribution

Examples

```
kurtosis(shape=1, rate=0.5)
kurtosis(meanlog=3, sdlog=1)
```

---

mean_dist   *Calculate the mean of a habitual intake distribution*

Description

This function calculates the mean of a habitual intake distribution. It handles gamma and log-normal distributions.

Usage

```
mean_dist(shape = NULL, rate = NULL, meanlog = NULL, sdlog = NULL)
```

Arguments

shape	Shape parameter for gamma distribution
rate	Rate parameter for gamma distribution
meanlog	Mean parameter for gamma distribution
sdlog	Standard deviation parameter for gamma distribution

Value

The mean of the distribution

Examples

```
mean_dist(shape=1, rate=0.5)
mean_dist(meanlog=3, sdlog=1)
```

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overlap	*Calculate the percent overlap between two habitual intake distributions*

Description

This function calculates the percent overlap between two habitual intake distributions. It handles combinations of gamma and log-normal distributions. The percent overlap is calculated as the Bhattacharyya coefficient.

Usage

```
overlap(dist1, dist2, plot = F)
```

Arguments

dist1	List containing the named distribution parameters for distribution A
dist2	List containing the named distribution parameters for distribution B
plot	Boolean (TRUE/FALSE) indicating whether to plot the distributions and overlap

Value

The percent overlap in the two distributions

Examples

```
overlap(dist1=list(shape=2, rate=2), dist2=list(shape=2, rate=2), plot=T) # same distribution
overlap(dist1=list(shape=2, rate=2), dist2=list(shape=3, rate=2), plot=T) # slighly different
overlap(dist1=list(shape=2, rate=2), dist2=list(meanlog=0.5, sdlog=0.4), plot=T) # slightly different
overlap(dist1=list(meanlog=0.5, sdlog=0.4), dist2=list(shape=2, rate=2), plot=T) # slightly different
overlap(dist1=list(shape=2, rate=2), dist2=list(shape=15, rate=4), plot=T) # more different
overlap(dist1=list(shape=2, rate=2), dist2=list(shape=30, rate=4), plot=T) # very different
```

---

plot_dists   *Plot subnational nutrient intake distributions*

Description

This function prepares a quick plot comparing subnational nutrient intake distributions. It is provided a dataframe generated from the get_dists() function.

Usage

```
plot_dists(dists)
```

Arguments

dists   A data frame of nutrient distributions

Value

A plot

Examples

```
# A one nutrient example
dists_usa_iron <- get_dists(isos="USA", nutrients="Iron")
plot_dists(dists_usa_iron)

# A two nutrient example
dists_usa_iron_vitB <- get_dists(isos="USA", nutrients=c("Iron", "Vitamin B12"))
plot_dists(dists_usa_iron_vitB)

# A two nutrient-two country example
dists_usa_bgd_iron_vitB <- get_dists(isos=c("USA", "BGD"), nutrients=c("Iron", "Vitamin B12"))
plot_dists(dists_usa_bgd_iron_vitB)

# A whole countries data
dists_bfa <- get_dists(isos=c("BFA"))
plot_dists(dists_bfa)
```

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sev   *Calculate summary exposure value*

Description

This function calculates the summary exposure value (SEV), i.e., the percent deficiency, for a group based on its Estimated Average Requirement (EAR) and its habitual intake distribution. It uses the probability method. A CV of 0.25 is recommended for the EAR of Vitamin B12 and a CV of 0.10 is recommended for the EAR of all other nutrients.

Usage

```
sev(ear, cv, shape = NULL, rate = NULL, meanlog = NULL, sdlog = NULL, plot = F)
```

Arguments

ear	Estimated Average Requirement (EAR)
cv	Coefficient of variation (CV) of the EAR
shape	Shape parameter for gamma distribution
rate	Rate parameter for gamma distribution
meanlog	Mean parameter for gamma distribution
sdlog	Standard deviation parameter for gamma distribution
plot	Boolean (TRUE/FALSE) indicating whether to plot the distributions relative to the EAR

Value

The percent of a population deficient in a nutrient (SEV)

Examples

```
sev(ear=8.1, cv=0.1, shape=9.5, rate=1.3, plot=T)
sev(ear=8.1, cv=0.1, meanlog=1.9, sdlog=0.3, plot=T)
```

---

shift_dist	*Shift the mean of a habitual intake distribution*

Description

This function shifts the mean of a habitual intake distribution and provides the new parameters used to describe the shifted distribution.

Usage

```
shift_dist(
  shape = NULL,
  rate = NULL,
  meanlog = NULL,
  sdlog = NULL,
  by = NULL,
  to = NULL,
  plot = F
)
```

Arguments

shape	Shape parameter for gamma distribution
rate	Rate parameter for gamma distribution
meanlog	Mean parameter for gamma distribution
sdlog	Standard deviation parameter for gamma distribution
by	Amount to shift the current mean by
to	New mean to shift the current mean to
plot	Boolean (TRUE/FALSE) indicating whether to plot the current/shifted distributions

Value

A list with the parameters for the shifted distribution

Examples

```
# Shift gamma distribution by an amount (2 and -3)
shift_dist(shape=9.7, rate=1.25, by=2, plot=T)
shift_dist(shape=9.7, rate=1.25, by=-3, plot=T)

# Shift gamma distribution to a new mean (10 or 4)
shift_dist(shape=9.7, rate=1.25, to=10, plot=T)
shift_dist(shape=9.7, rate=1.25, to=4, plot=T)

# Shift log-normal distribution by an amount (10 and -5)
shift_dist(meanlog=3, sdlog=0.5, by=10, plot=T)
shift_dist(meanlog=3, sdlog=0.5, by=-5, plot=T)

# Shift log-normal distribution to a new mean (35 and 15)
shift_dist(meanlog=3, sdlog=0.5, to=35, plot=T)
shift_dist(meanlog=3, sdlog=0.5, to=15, plot=T)
```

---

skewness   *Calculate the skewness of a habitual intake distribution*

Description

This function calculates the skewness of a habitual intake distribution. It handles gamma and log-normal distributions.

Usage

```
skewness(shape = NULL, rate = NULL, meanlog, sdlog = NULL)
```

Arguments

shape	Shape parameter for gamma distribution
rate	Rate parameter for gamma distribution
meanlog	Mean parameter for gamma distribution
sdlog	Standard deviation parameter for gamma distribution

Value

The skewness of the distribution

Examples

```
skewness(shape=1, rate=0.5)
skewness(meanlog=3, sdlog=1)
```

---

variance   *Calculate the variance of a habitual intake distribution*

Description

This function calculates the variance of a habitual intake distribution. It handles gamma and log-normal distributions.

Usage

```
variance(shape = NULL, rate = NULL, meanlog = NULL, sdlog = NULL)
```

Arguments

shape	Shape parameter for gamma distribution
rate	Rate parameter for gamma distribution
meanlog	Mean parameter for gamma distribution
sdlog	Standard deviation parameter for gamma distribution

Value

The variance of the distribution

Examples

```
variance(shape=1, rate=0.5)
variance(meanlog=3, sdlog=1)
```

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