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Type Package

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Analysis of Wasting in R

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and prevalence analysis of wasting based on the Standardized
Monitoring and Assessment of Relief and Transition (SMART)
Methodology <<https://smartmethodology.org/>>, with application
in R.

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anthro.01	<i>A sample data of district level SMART surveys with location anonymised</i>
-----------	---

Description

anthro.01 is a two-stage cluster-based survey with probability of selection of clusters proportional to the size of the population. The survey employed the SMART methodology.

Usage

anthro.01

Format

A tibble of 1,191 rows and 11 columns.

Variable	Description
<i>area</i>	Survey location
<i>dos</i>	Survey date
<i>cluster</i>	Primary sampling unit
<i>team</i>	Enumerator IDs
<i>sex</i>	Sex; "m" = boys, "f" = girls
<i>dob</i>	Date of birth
<i>age</i>	Age in months, typically estimated using local event calendars
<i>weight</i>	Weight in kilograms
<i>height</i>	Height in centimetres
<i>oedema</i>	oedema; "n" = no oedema, "y" = with oedema
<i>muac</i>	Mid-upper arm circumference in millimetres

Source

Anonymous

Examples

anthro.01

anthro.02	<i>A sample of an already wrangled survey data</i>
-----------	--

Description

A household budget survey data conducted in Mozambique in 2019/2020, known as *IOF (Inquérito ao Orçamento Familiar* in Portuguese). *IOF* is a two-stage cluster-based survey, representative at province level (second administrative level), with probability of the selection of the clusters proportional to the size of the population. Its data collection spans for a period of 12 months.

Usage

anthro.02

Format

A tibble of 2,267 rows and 14 columns.

Variable	Description
<i>province</i>	The administrative unit level 1 where data was collected

<i>strata</i>	Rural or Urban
<i>cluster</i>	Primary sampling unit
<i>sex</i>	Sex; "m" = boys, "f" = girls
<i>age</i>	Calculated age in months with two decimal places
<i>weight</i>	Weight in kilograms
<i>height</i>	Height in centimetres
<i>oedema</i>	oedema; "n" = no oedema, "y" = with oedema
<i>muac</i>	Mid-upper arm circumference in millimetres
<i>wfactor</i>	Survey weights
<i>wfzh</i>	Weight-for-height z-scores with 3 decimal places
<i>flag_wfzh</i>	Flagged WFHZ value. 1 = flagged, 0 = not flagged
<i>mfaz</i>	MUAC-for-age z-scores with 3 decimal places
<i>flag_mfaz</i>	Flagged MFAZ value. 1 = flagged, 0 = not flagged

Source

Mozambique National Institute of Statistics. The data is publicly available at https://mozdata.ine.gov.mz/index.php/catalog/88#metadata-data_access. Data was wrangled using this package's wranglers. Details about survey design can be read from: <https://mozdata.ine.gov.mz/index.php/catalog/88#metadata-sampling>

Examples

anthro.02

anthro.03	<i>A sample data of district level SMART surveys conducted in Mozambique</i>
-----------	--

Description

anthro.03 contains survey data of four districts. Each district dataset presents distinct data quality scenarios that require a specific prevalence analysis approach. Data from two districts have a problematic WFHZ standard deviation. The data from the remaining two districts are all within range.

This sample data is useful to demonstrate the use of the prevalence functions on a multiple-domain survey data where there can be variations in the rating of acceptability of the standard deviation, hence requiring different analytical approach for each survey domain to ensure accurate estimation.

Usage

anthro.03

Format

A tibble of 943 x 9.

Variable	Description
<i>district</i>	Survey location
<i>cluster</i>	Primary sampling unit
<i>team</i>	Survey teams
<i>sex</i>	Sex; "m" = boys, "f" = girls
<i>age</i>	Calculated age in months with two decimal places
<i>weight</i>	Weight in kilograms
<i>height</i>	Height in centimetres
<i>oedema</i>	oedema; "n" = no oedema, "y" = with oedema
<i>muac</i>	Mid-upper arm circumference in millimetres

Source

Anonymous

Examples

anthro.03

anthro.04	<i>A sample data from a community-based sentinel site with location anonymised</i>
-----------	--

Description

Data herein was derived from population-based assessments in three locations (analysis unit). Each unit presents distinct scenarios that requires also-distinct handling during the prevalence analysis:

- *Unit A* has flawless data.
- *Unit B* has age-ratio-test results rated as problematic, with an observed proportion of children aged 24-59 months < 0.66.
- *Unit C* has age-ratio-test results rated as problematic, with an observed proportion of children aged 24-59 months >= 0.66.

This sample data is useful to demonstrate designed behaviours of MUAC-prevalence functions to dealing with certain-and-expected flaws in the data.

Usage

anthro.04

Format

A tibble of $2,192 \times 6$.

Variable	Description
<i>analysis_unit</i>	Location wherein the assessment was conducted
<i>cluster</i>	Primary sampling unit
<i>sex</i>	Sex; "1" = boys, "2" = girls
<i>age</i>	Calculated age in months
<i>muac</i>	Mid-upper arm circumference in millimetres
<i>oedema</i>	oedema; "n" = no oedema, "y" = yes oedema

Source

Anonymous

Examples

anthro.04

define_wasting	<i>Define wasting</i>
----------------	-----------------------

Description

Determine if a given observation in the dataset is wasted or not, and its respective form of wasting (global, severe or moderate) on the basis of z-scores of weight-for-height (WFHZ), muac-for-age (MFAZ), raw MUAC values and combined case-definition.

Usage

```
define_wasting(
  df,
  zscores = NULL,
  muac = NULL,
  oedema = NULL,
  .by = c("zscores", "muac", "combined")
)
```

Arguments

<i>df</i>	A tibble object. It must have been wrangled using this package's wrangling functions for WFHZ or MUAC, or both (for combined) as appropriate.
<i>zscores</i>	A vector of class double of WFHZ or MFAZ values.
<i>muac</i>	An integer or character vector of raw MUAC values in millimetres.

oedema	A character vector indicating oedema status. Default is NULL. Code values should be "y" for presence and "n" for absence of nutritional oedema.
.by	A choice of the criterion by which a case is to be defined. Choose "zscores" for WFHZ or MFAZ, "muac" for raw MUAC and "combined" for combined. Default value is "zscores".

Value

The tibble object `df` with additional columns named `gam`, `sam` and `mam`, each of class `numeric` containing coded values of either 1 (case) and 0 (not a case). If `.by = "combined"`, additional columns are named `cgam`, `csam` and `cmam`.

Examples

```
## Case-definition by z-scores ----
z <- anthro.02 |>
  define_wasting(
    zscores = wfhz,
    muac = NULL,
    oedema = oedema,
    .by = "zscores"
  )
head(z)

## Case-definition by MUAC ----
m <- anthro.02 |>
  define_wasting(
    zscores = NULL,
    muac = muac,
    oedema = oedema,
    .by = "muac"
  )
head(m)

## Case-definition by combined ----
c <- anthro.02 |>
  define_wasting(
    zscores = wfhz,
    muac = muac,
    oedema = oedema,
    .by = "combined"
  )
head(c)
```

Description

Identify outlier z-scores for weight-for-height (WFHZ) and MUAC-for-age (MFAZ) following the SMART methodology. The function can also be used to detect outliers for height-for-age (HFAZ) and weight-for-age (WFAZ) z-scores following the same approach.

For flagging z-scores, z-scores that deviate substantially from the sample's z-score mean are considered outliers and are unlikely to reflect accurate measurements. For raw MUAC, values that are less than 100 millimetres or greater than 200 millimetres are considered outliers as recommended by Bilukha & Kianian (2023). Including these values in the analysis could compromise the accuracy of the resulting estimates.

To remove outliers, their values are set to NA rather than removing the record from the dataset. This process is also called *censoring*. By assigning NA values to these outliers, they can be effectively removed during statistical operations with functions that allow for removal of NA values such as `mean()` for getting the mean value or `sd()` for getting the standard deviation.

Usage

```
flag_outliers(x, .from = c("zscores", "raw_muac"))

remove_flags(x, .from = c("zscores", "raw_muac"))
```

Arguments

<code>x</code>	A numeric vector of WFHZ, MFAZ, HFAZ, WFAZ or raw MUAC values. Raw MUAC values should be in millimetre units.
<code>.from</code>	Either "zscores" or "raw_muac" for type of data to flag outliers from.

Value

An vector of the same length as `x` of flagged records coded as 1 for a flagged record and 0 for a non-flagged record.

References

Bilukha, O., & Kianian, B. (2023). Considerations for assessment of measurement quality of mid-upper arm circumference data in anthropometric surveys and mass nutritional screenings conducted in humanitarian and refugee settings. *Maternal & Child Nutrition*, 19, e13478. Available at <https://onlinelibrary.wiley.com/doi/10.1111/mcn.13478>

SMART Initiative (2017). *Standardized Monitoring and Assessment for Relief and Transition*. Manual 2.0. Available at: <https://smartmethodology.org>.

Examples

```
## Sample data of raw MUAC values ----
x <- anthro.01$muac

## Apply the function with `.from` set to "raw_muac" ----
m <- flag_outliers(x, .from = "raw_muac")
head(m)
```

```
## Sample data of z-scores (be it WFHZ, MFAZ, HFAZ or WFAZ) ----
x <- anthro.02$mfaz

# Apply the function with `.from` set to "zscores" ----
z <- flag_outliers(x, .from = "zscores")
tail(z)

## With `.from` set to "zscores" ----
z <- remove_flags(
  x = wfhz.01$wfhz,
  .from = "zscores"
)

head(z)

## With `.from` set to "raw_muac" ----
m <- remove_flags(
  x = mfaz.01$muac,
  .from = "raw_muac"
)

tail(m)
```

get_age_months

Calculate child's age in months

Description

Calculate child's age in months based on the date of birth and the date of data collection.

Usage

```
get_age_months(dos, dob)
```

Arguments

dos	A Date vector of date of data collection.
dob	A Date vector of the child's date of birth.

Value

A numeric vector of child's age in months. Any value less than 6.0 and greater than or equal to 60.0 months are set to NA.

Examples

```
## Take two vectors of class "Date" ----
surv_date <- as.Date(
  c(
    "2024-01-05", "2024-01-05", "2024-01-05", "2024-01-08", "2024-01-08",
    "2024-01-08", "2024-01-10", "2024-01-10", "2024-01-10", "2024-01-11"
  )
)
bir_date <- as.Date(
  c(
    "2022-04-04", "2021-05-01", "2023-05-24", "2017-12-12", NA,
    "2020-12-12", "2022-04-04", "2021-05-01", "2023-05-24", "2020-12-12"
  )
)

## Apply the function ----
get_age_months(
  dos = surv_date,
  dob = bir_date
)
```

mfaz.01	<i>A sample mid-upper arm circumference (MUAC) screening data</i>
---------	---

Description

A sample mid-upper arm circumference (MUAC) screening data

Usage

mfaz.01

Format

A tibble with 661 rows and 4 columns.

Variable	Description
<i>sex</i>	Sex; "m" = boys, "f" = girls
<i>months</i>	Calculated age in months with two decimal places
<i>oedema</i>	oedema, "n" = no oedema, "y" = with oedema
<i>muac</i>	Mid-upper arm circumference in millimetres

Source

Anonymous

Examples

mfaz.01

mfaz.02	<i>A sample SMART survey data with mid-upper arm circumference measurements</i>
---------	---

Description

A sample SMART survey data with mid-upper arm circumference measurements

Usage

mfaz.02

Format

A tibble with 303 rows and 7 columns.

Variable	Description
<i>cluster</i>	Primary sampling unit
<i>sex</i>	Sex; "m" = boys, "f" = girls
<i>age</i>	Calculated age in months with two decimal places
<i>oedema</i>	oedema, "n" = no oedema, "y" = with oedema
<i>mfaz</i>	MUAC-for-age z-scores with 3 decimal places
<i>flag_mfaz</i>	Flagged MUAC-for-age z-score value. 1 = flagged, 0 = not flagged

Source

Anonymous

Examples

mfaz.02

`mw_check_ipcamn_ssreq` *Check whether sample size requirements for IPC Acute Malnutrition (IPC AMN) analysis are met*

Description

Data for estimating the prevalence of acute malnutrition used in the IPC AMN can come from different sources: surveys, screenings or community-based surveillance systems. The IPC has set minimum sample size requirements for each source. This function verifies whether these requirements are met.

Usage

```
mw_check_ipcamn_ssreq(
  df,
  cluster,
  .source = c("survey", "screening", "ssite"),
  ...
)
```

Arguments

<code>df</code>	A data.frame object to check.
<code>cluster</code>	A vector of class integer or character of unique cluster or screening or sentinel site identifiers. If a character vector, ensure that each unique name represents one location. If <code>cluster</code> is not of class integer or character, an error message will be returned indicating the type of mismatch.
<code>.source</code>	The source of evidence. A choice between "survey" for representative survey data at the area of analysis; "screening" for screening data; "ssite" for community-based sentinel site data. Default value is "survey".
<code>...</code>	A vector of class character, specifying the categories for which the analysis should be summarised for. Usually geographical areas. More than one vector can be specified.

Value

A summary tibble containing check results for:

- `n_clusters` - the total number of unique clusters or screening or site identifiers;
- `n_obs` - the corresponding total number of children in the dataset; and,
- `meet_ipc` - whether the IPC AMN requirements were met.

References

IPC Global Partners. 2021. *Integrated Food Security Phase Classification Technical Manual Version 3.1.Evidence and Standards for Better Food Security and Nutrition Decisions*. Rome. Available at: <https://www.ipcinfo.org/ipcinfo-website/resources/ipc-manual/en/>.

Examples

```
mw_check_ipcamn_ssreq(
  df = anthro.01,
  cluster = cluster,
  .source = "survey",
  area
)
```

```
mw_estimate_age_weighted_prev_muac
```

Estimate age-weighted prevalence of wasting by MUAC

Description

Estimates age-weighted prevalence of wasting using MUAC. Accepts age in months or in categories ('6–23', '24–59'). The default is age in months.

The prevalence is weighted as:

$$(prevalence_{6-23} + (2 \times prevalence_{24-59}))/3$$

Whilst the function is exported to users as a standalone, it is embedded into the following major MUAC prevalence functions of this package: [mw_estimate_prevalence_muac\(\)](#), [mw_estimate_prevalence_screening\(\)](#) and [mw_estimate_prevalence_screening2\(\)](#).

Usage

```
mw_estimate_age_weighted_prev_muac(
  df,
  muac,
  has_age = TRUE,
  age = NULL,
  age_cat = NULL,
  oedema = NULL,
  raw_muac = FALSE,
  ...
)
```

Arguments

df	A tibble object produced by mwana data wranglers.
muac	A numeric or integer vector of raw MUAC values. The measurement unit should be millimetres.
has_age	Logical. Specifies whether the input dataset provides age in months or in categories ('6–23', '24–59'). Defaults to TRUE when age is given in months.

age	A vector of class double of child's age in months. Defaults to NULL. Only use if has_age = TRUE, otherwise set it to NULL.
age_cat	A character vector of child's age in categories. Code values should be "6-23" and "24-59". Defaults to NULL. Only use it if has_age = FALSE.
oedema	A character vector for presence of nutritional oedema. Code values should be "y" for presence and "n" for absence. Defaults to NULL.
raw_muac	Logical. Whether outliers should be excluded based on the raw MUAC values or MFAZ. For the former, set it to TRUE, otherwise FALSE. Defaults to MFAZ.
...	A vector of class character, specifying the categories for which the analysis should be summarised for. Usually geographical areas. More than one vector can be specified.

Details

As a standalone function, the user must check data quality before calling the function.

Value

A summary tibble with wasting prevalence estimates, as given by the SMART updated MUAC tool (see references below).

References

SMART Initiative (no date). *Updated MUAC data collection tool*. Available at: <https://smartmethodology.org/survey-planning-tools/updated-muac-tool/>

Examples

```
## Example application when age is given in months ----
anthro.04 |>
  mw_wrangle_age(age = age) |>
  mw_wrangle_muac(
    muac = muac,
    .recode_muac = TRUE,
    .to = "cm",
    age = age,
    sex = sex,
    .recode_sex = FALSE
  ) |>
  transform(muac = recode_muac(muac, "mm")) |>
  mw_estimate_age_weighted_prev_muac(
    muac = muac,
    has_age = TRUE,
    age = age,
    age_cat = FALSE,
    oedema = oedema,
    raw_muac = FALSE,
    analysis_unit
  )
```

```
## Example application when age is given in categories ----
anthro.04 |>
  transform(age_cat = ifelse(age < 24, "6-23", "24-59")) |>
  mw_wrangle_muac(
    muac = muac,
    .recode_muac = FALSE,
    .to = "none",
    sex = sex,
    .recode_sex = FALSE
  ) |>
  mw_estimate_age_weighted_prev_muac(
    has_age = FALSE,
    age = NULL,
    age_cat = age_cat,
    oedema = oedema,
    raw_muac = TRUE
  )
```

mw_estimate_prevalence_combined

Estimate the prevalence of combined wasting

Description

Estimate the prevalence of wasting based on the combined case-definition of weight-for-height z-scores (WFHZ), MUAC and/or oedema. The function allows users to estimate prevalence in accordance with complex-sample design properties such as accounting for survey sample weights when needed or applicable.

The data quality is first assessed by calculating and rating the standard deviation (SD) of WFHZ. Then it calculates the observed proportion of children aged 24–59 months out of all children in the dataset. Next, it estimates the p-value for the difference between this observed proportion and the expected (0.66), and rates the result.

Prevalence is estimated only when the WFHZ SD is not problematic and the age ratio test is not problematic, or — if the age ratio test is problematic — the proportion of children aged 24–59 months is greater than or equal to 0.66.

Usage

```
mw_estimate_prevalence_combined(df, wt = NULL, oedema = NULL, ...)
```

Arguments

df A tibble object produced by sequential application of the [mw_wrangle_wfhz\(\)](#) and [mw_wrangle_muac\(\)](#). Note that MUAC values in df must be in millimetres unit after using [mw_wrangle_muac\(\)](#). In addition, df must have a variable called cluster, which contains the primary sampling unit identifiers.

wt	A vector of class double of the survey sampling weights. Default is NULL which assumes a self-weighted survey as is the case for a survey sample selected proportional to population size (i.e., SMART survey sample). Otherwise, a weighted analysis is implemented.
oedema	A character vector for presence of nutritional oedema coded as "y" for presence of nutritional oedema and "n" for absence of nutritional oedema. Default is NULL.
...	A vector of class character, specifying the categories for which the analysis should be summarised for. Usually geographical areas. More than one vector can be specified.

Details

A concept of *combined flags* is introduced in this function. Any observation that is flagged for either `flag_wfhz` or `flag_mfaz` is flagged under a new variable named `cflags` added to `df`. This ensures that all flagged observations from both WFHZ and MFAZ data are excluded from the prevalence analysis.

flag_wfhz	flag_mfaz	cflags
1	0	1
0	1	1
0	0	0

Value

A summary tibble for the descriptive statistics about combined wasting.

Examples

```
## When wt are set to NULL ----
mw_estimate_prevalence_combined(
  df = anthro.02,
  wt = NULL,
  oedema = oedema
)

## When `wt` is not set to NULL ----
mw_estimate_prevalence_combined(
  df = anthro.02,
  wt = wtfactor,
  oedema = oedema
)
```

mw_estimate_prevalence_mfaz

Estimate the prevalence of wasting based on z-scores of muac-for-age (MFAZ)

Description

Calculate the prevalence estimates of wasting based on z-scores of MUAC-for-age and/or bilateral oedema. The function allows users to estimate prevalence in accordance with complex sample design properties such as accounting for survey sample weights when needed or applicable. The quality of the data is first evaluated by calculating and rating the standard deviation of MFAZ. Standard approach to prevalence estimation is calculated only when the standard deviation of MFAZ is rated as not problematic. If the standard deviation is problematic, prevalence is estimated using the PROBIT estimator. Outliers are detected based on SMART flagging criteria. Identified outliers are then excluded before prevalence estimation is performed.

Usage

```
mw_estimate_prevalence_mfaz(df, wt = NULL, oedema = NULL, ...)
```

Arguments

df	A data.frame object that has been produced by the <code>mw_wrangle_age()</code> and <code>mw_wrangle_muac()</code> functions. The df should have a variable named cluster for the primary sampling unit identifiers.
wt	A vector of class double of the survey sampling weights. Default is NULL which assumes a self-weighted survey as is the case for a survey sample selected proportional to population size (i.e., SMART survey sample). Otherwise, a weighted analysis is implemented.
oedema	A character vector for presence of nutritional oedema coded as "y" for presence of nutritional oedema and "n" for absence of nutritional oedema. Default is NULL.
...	A vector of class character, specifying the categories for which the analysis should be summarised for. Usually geographical areas. More than one vector can be specified.

Value

A summary tibble for the descriptive statistics about wasting.

Examples

```
## Without grouping variables ----
anthro.04 |>
  mw_wrangle_age(age = age) |>
  mw_wrangle_muac(
    muac = muac,
```

```

    .recode_muac = TRUE,
    .to = "cm",
    age = age,
    sex = sex,
    .recode_sex = FALSE
  ) |>
  transform(muac = recode_muac(muac, "mm")) |>
  mw_estimate_prevalence_mfaz(
    wt = NULL,
    oedema = oedema,
    analysis_unit
  )

```

mw_estimate_prevalence_muac

Estimate the prevalence of wasting based on MUAC for survey data

Description

Estimate the prevalence of wasting based on MUAC and/or nutritional oedema. The function allows users to estimate prevalence in accordance with complex sample design properties, such as accounting for survey sample weights when needed or applicable.

It first evaluates the quality of the data to determine the appropriate prevalence-analysis flow to be employed. Quality is evaluated by estimating the observed proportion of children aged 24-59 months of the total children in the dataset, then it estimates the p-value for the difference between the above-mentioned category against the expected (0.66) and rates it.

If age ratio test is "problematic" and the proportion of children aged 24-59 months is < 0.66 , age-weighting approach is applied to prevalence estimation, to account for the over-representation of younger children in the sample; otherwise, a non-age-weighted prevalence is estimated.

Usage

```
mw_estimate_prevalence_muac(df, age, muac, wt = NULL, oedema = NULL, ...)
```

Arguments

df	A tibble object produced by <code>mw_wrangle_muac()</code> and <code>mw_wrangle_age()</code> functions. Note that MUAC values in df must be in millimetres after using <code>mw_wrangle_muac()</code> . Also, df must have a variable called cluster wherein the primary sampling unit identifiers are stored.
age	A vector of class double of child's age in months.
muac	A numeric or integer vector of raw MUAC values. The measurement unit should be millimetres.
wt	A vector of class double of the survey sampling weights. Default is NULL, which assumes a self-weighted survey, the case of SMART surveys. Otherwise, a weighted analysis is implemented.

oedema	A character vector for presence of nutritional oedema Code values should be "y" for presence and "n" for absence. Default is NULL.
...	A vector of class character, specifying the categories for which the analysis should be summarised for. Usually geographical areas. More than one vector can be specified.

Details

A typical user analysis workflow is expected to begin with data quality checks, followed by a thorough review, and only thereafter proceed to prevalence estimation. This sequence places the user in the strongest position to assess whether the resulting prevalence estimates are reliable.

Outliers are identified using SMART flagging criteria applied to MFAZ, and are excluded from the prevalence estimation.

Value

A summary tibble for the descriptive statistics about wasting based on MUAC, with confidence intervals.

References

SMART Initiative (no date). *Updated MUAC data collection tool*. Available at: <https://smartmethodology.org/survey-planning-tools/updated-muac-tool/>

See Also

[mw_estimate_age_weighted_prev_muac\(\)](#) [mw_estimate_prevalence_mfaz\(\)](#) [mw_estimate_prevalence_screening\(\)](#)

Examples

```
## Ungrouped analysis ----
anthro.04 |>
  mw_wrangle_age(age = age) |>
  mw_wrangle_muac(
    muac = muac,
    .recode_muac = TRUE,
    .to = "cm",
    age = age,
    sex = sex,
    .recode_sex = FALSE
  ) |>
  transform(muac = recode_muac(muac, "mm")) |>
  mw_estimate_prevalence_muac(
    muac = muac,
    age = age,
    wt = NULL,
    oedema = oedema,
    analysis_unit
  )
```

mw_estimate_prevalence_screening

Estimate the prevalence of wasting based on MUAC for non-survey data

Description

It is common to estimate prevalence of wasting from non-survey data, such as screenings or any other data derived from community-based surveillance systems. In such situations, the analysis usually consists only in estimating the point prevalence and the counts of positive cases, without necessarily estimating the uncertainty. This function serves this purpose.

It first evaluates the quality of the data to determine the appropriate prevalence-analysis flow to be employed. Quality is evaluated by estimating the observed proportion of children aged 24-59 months of the total children in the dataset, then it estimates the p-value for the difference between the above-mentioned category against the expected (0.66) and rates it.

If age ratio test is "problematic" and the proportion of children aged 24-59 months is < 0.66 , age-weighting approach is applied to prevalence estimation, to account for the over-representation of younger children in the sample; otherwise, a non-age-weighted prevalence is estimated.

Usage

```
mw_estimate_prevalence_screening(df, muac, age, oedema = NULL, ...)
```

```
mw_estimate_prevalence_screening2(df, age_cat, muac, oedema = NULL, ...)
```

Arguments

df	A tibble object produced by <code>mw_wrangle_muac()</code> and <code>mw_wrangle_age()</code> functions. Note that MUAC values in df must be in millimetres unit after using <code>mw_wrangle_muac()</code> . Also, df must have a variable called cluster wherein the primary sampling unit identifiers are stored.
muac	A numeric or integer vector of raw MUAC values. The measurement unit should be millimetres.
age	A vector of class double of child's age in months.
oedema	A character vector for presence of nutritional oedema. Code values should be "y" for presence and "n" for absence. Default is NULL.
...	A vector of class character, specifying the categories for which the analysis should be summarised for. Usually geographical areas. More than one vector can be specified.
age_cat	A character vector of child's age in categories. Code values should be "6-23" and "24-59".

Details

A typical user analysis workflow is expected to begin with data quality checks, followed by a thorough review, and only thereafter proceed to prevalence estimation. This sequence places the user in the strongest position to assess whether the resulting prevalence estimates are reliable.

In `mw_estimate_prevalence_screening()`, outliers are identified using SMART flagging criteria applied to MFAZ, whereas in `mw_estimate_prevalence_screening2()` are based on the raw MUAC values. In either functions, outliers are excluded from the prevalence estimation.

Value

A summary tibble for the descriptive statistics about wasting based on MUAC, with no confidence intervals.

References

SMART Initiative (no date). *Updated MUAC data collection tool*. Available at: <https://smartmethodology.org/survey-planning-tools/updated-muac-tool/>

See Also

`mw_estimate_prevalence_muac()`, `mw_estimate_age_weighted_prev_muac()`, `flag_outliers()` and `remove_flags()`.

Examples

```
mw_estimate_prevalence_screening(  
  df = anthro.02,  
  muac = muac,  
  age = age,  
  oedema = oedema,  
  province  
)  
  
## With `oedema` set to `NULL` ----  
mw_estimate_prevalence_screening(  
  df = anthro.02,  
  muac = muac,  
  age = age,  
  oedema = NULL,  
  province  
)  
  
## Specifying the grouping variables ----  
mw_estimate_prevalence_screening(  
  df = anthro.02,  
  muac = muac,  
  age = age,  
  oedema = NULL,  
  province  
)
```

```
anthro.01 |>
  mw_wrangle_muac(
    sex = sex,
    .recode_sex = TRUE,
    muac = muac
  ) |>
  transform(
    age_cat = ifelse(age < 24, "6-23", "24-59")
  ) |>
  mw_estimate_prevalence_screening2(
    age_cat = age_cat,
    muac = muac,
    oedema = oedema,
    area
  )
```

```
mw_estimate_prevalence_wfhz
```

Estimate the prevalence of wasting based on weight-for-height z-scores (WFHZ)

Description

Calculate the prevalence estimates of wasting based on z-scores of weight-for-height and/or nutritional oedema. The function allows users to estimate prevalence in accordance with complex sample design properties such as accounting for survey sample weights when needed or applicable. The quality of the data is first evaluated by calculating and rating the standard deviation of WFHZ. Standard approach to prevalence estimation is calculated only when the standard deviation of MFAZ is rated as not problematic. If the standard deviation is problematic, prevalence is estimated using the PROBIT estimator. Outliers are detected based on SMART flagging criteria. Identified outliers are then excluded before prevalence estimation is performed.

Usage

```
mw_estimate_prevalence_wfhz(df, wt = NULL, oedema = NULL, ...)
```

Arguments

df	A tibble object that has been produced by the <code>mw_wrangle_wfhz()</code> functions. The df should have a variable named cluster for the primary sampling unit identifiers.
wt	A vector of class double of the survey sampling weights. Default is NULL which assumes a self-weighted survey as is the case for a survey sample selected proportional to population size (i.e., SMART survey sample). Otherwise, a weighted analysis is implemented.

oedema	A character vector for presence of nutritional oedema coded as "y" for presence of nutritional oedema and "n" for absence of nutritional oedema. Default is NULL.
...	A vector of class character, specifying the categories for which the analysis should be summarised for. Usually geographical areas. More than one vector can be specified.

Value

A summary tibble for the descriptive statistics about wasting.

Examples

```
## When .by = NULL ----
### Start off by wrangling the data ----
data <- mw_wrangle_wfhz(
  df = anthro.03,
  sex = sex,
  weight = weight,
  height = height,
  .recode_sex = TRUE
)

### Now run the prevalence function ----
mw_estimate_prevalence_wfhz(
  df = data,
  wt = NULL,
  oedema = oedema
)

## Now when .by is not set to NULL ----
mw_estimate_prevalence_wfhz(
  df = data,
  wt = NULL,
  oedema = oedema,
  district
)

## When a weighted analysis is needed ----
mw_estimate_prevalence_wfhz(
  df = anthro.02,
  wt = wtfactor,
  oedema = oedema,
  province
)
```

mw_neat_output_mfaz	<i>Clean and format the output tibble returned from the MUAC-for-age z-score plausibility check</i>
---------------------	---

Description

Converts scientific notations to standard notations, rounds off values, and renames columns to meaningful names.

Usage

```
mw_neat_output_mfaz(df)
```

Arguments

df An `data.frame` object returned by `mw_plausibility_check_mfaz()` containing the summarized results to be formatted.

Value

A `data.frame` object of the same length and width as `df`, with column names and values formatted as appropriate.

Examples

```
## First wrangle age data ----
data <- mw_wrangle_age(
  df = anthro.01,
  dos = dos,
  dob = dob,
  age = age,
  .decimals = 2
)

## Then wrangle MUAC data ----
data_mfaz <- mw_wrangle_muac(
  df = data,
  sex = sex,
  age = age,
  muac = muac,
  .recode_sex = TRUE,
  .recode_muac = TRUE,
  .to = "cm"
)

## Then run plausibility check ----
pl <- mw_plausibility_check_mfaz(
  df = data_mfaz,
  flags = flag_mfaz,
```

```

    sex = sex,
    muac = muac,
    age = age,
    area
  )

  ## Now neat the output table ----
  mw_neat_output_mfaz(df = pl)

```

mw_neat_output_muac	<i>Clean and format the output tibble returned from the MUAC plausibility check</i>
---------------------	---

Description

Converts scientific notations to standard notations, rounds off values, and renames columns to meaningful names.

Usage

```
mw_neat_output_muac(df)
```

Arguments

df	A tibble object returned by the <code>mw_plausibility_check_muac()</code> function containing the summarized results to be formatted.
----	---

Value

A data.frame object of the same length and width as df, with column names and values formatted for clarity and readability.

Examples

```

## First wrangle MUAC data ----
df_muac <- mw_wrangle_muac(
  df = anthro.01,
  sex = sex,
  muac = muac,
  age = NULL,
  .recode_sex = TRUE,
  .recode_muac = FALSE,
  .to = "none"
)

## Then run the plausibility check ----
pl_muac <- mw_plausibility_check_muac(
  df = df_muac,

```

```

    flags = flag_muac,
    sex = sex,
    muac = muac
  )

  ## Neat the output table ----

  mw_neat_output_muac(df = pl_muac)

```

mw_neat_output_wfhz	<i>Clean and format the output tibble returned from the WFHZ plausibility check</i>
---------------------	---

Description

Converts scientific notations to standard notations, rounds off values, and renames columns to meaningful names.

Usage

```
mw_neat_output_wfhz(df)
```

Arguments

df	An tibble object returned by the mw_plausibility_check_wfhz() containing the summarized results to be formatted.
----	--

Value

A tibble object of the same length and width as df, with column names and values formatted for clarity and readability.

Examples

```

## First wrangle age data ----
data <- mw_wrangle_age(
  df = anthro.01,
  dos = dos,
  dob = dob,
  age = age,
  .decimals = 2
)

## Then wrangle WFHZ data ----
data_wfhz <- mw_wrangle_wfhz(
  df = data,
  sex = sex,
  weight = weight,

```

```

    height = height,
    .recode_sex = TRUE
  )

  ## Now run the plausibility check ----
  pl <- mw_plausibility_check_wfhz(
    df = data_wfhz,
    sex = sex,
    age = age,
    weight = weight,
    height = height,
    flags = flag_wfhz,
    area
  )

  ## Now neat the output table ----
  mw_neat_output_wfhz(df = pl)

```

mw_plausibility_check_mfaz

Check the plausibility and acceptability of MUAC-for-age z-score (MFAZ) data

Description

Check the overall plausibility and acceptability of MFAZ data through a structured test suite encompassing checks for sampling and measurement-related biases in the dataset. This test suite follows the recommendation made by Bilukha & Kianian (2023) on the plausibility of constructing a comprehensive plausibility check for MUAC data similar to weight-for-height z-score to evaluate its acceptability when age values are available in the dataset.

The function works on a `data.frame` returned from wrangling functions for age and for MUAC-for-age z-score data available from this package.

Usage

```
mw_plausibility_check_mfaz(df, sex, muac, age, flags, ...)
```

Arguments

<code>df</code>	A <code>data.frame</code> object to check.
<code>sex</code>	A numeric vector for child's sex with 1 = males and 2 = females.
<code>muac</code>	A numeric vector of child's MUAC in centimetres.
<code>age</code>	A vector of class <code>double</code> of child's age in months.
<code>flags</code>	A numeric vector of flagged records.
<code>...</code>	A vector of class <code>character</code> , specifying the categories for which the analysis should be summarised for. Usually geographical areas. More than one vector can be specified.

Details

Whilst the function uses the same checks and criteria as those for weight-for-height z-scores in the SMART plausibility check, the percent of flagged records is evaluated using different cut-off points, with a maximum acceptability of 2.0% as shown below:

Excellent	Good	Acceptable	Problematic
0.0 - 1.0	>1.0 - 1.5	>1.5 - 2.0	>2.0

Value

A single-row summary tibble with columns containing the plausibility check results. If ungrouped analysis, the output will consist of 17 columns and one row; otherwise, the number of columns will vary according to the number vectors specified, and the number of rows to the categories within the grouping variables.

References

Bilukha, O., & Kianian, B. (2023). Considerations for assessment of measurement quality of mid-upper arm circumference data in anthropometric surveys and mass nutritional screenings conducted in humanitarian and refugee settings. *Maternal & Child Nutrition*, 19, e13478. <https://onlinelibrary.wiley.com/doi/10.1111/mcn.13478>

SMART Initiative (2017). *Standardized Monitoring and Assessment for Relief and Transition*. Manual 2.0. Available at: <https://smartmethodology.org>.

See Also

`mw_wrangle_age()` `mw_wrangle_muac()` `mw_stattest_ageratio()` `flag_outliers()`

Examples

```
## First wrangle age data ----
data <- mw_wrangle_age(
  df = anthro.01,
  dos = dos,
  dob = dob,
  age = age,
  .decimals = 2
)

## Then wrangle MUAC data ----
data_muac <- mw_wrangle_muac(
  df = data,
  sex = sex,
  age = age,
  muac = muac,
  .recode_sex = TRUE,
  .recode_muac = TRUE,
  .to = "cm"
)
```

```
## And finally run plausibility check ----
mw_plausibility_check_mfaz(
  df = data_muac,
  flags = flag_mfaz,
  sex = sex,
  muac = muac,
  age = age,
  area, team
)
```

`mw_plausibility_check_muac`

Check the plausibility and acceptability of raw MUAC data

Description

Check the overall plausibility and acceptability of raw MUAC data through a structured test suite encompassing checks for sampling and measurement-related biases in the dataset. The test suite in this function follows the recommendation made by Bilukha & Kianian (2023).

Usage

`mw_plausibility_check_muac(df, sex, muac, flags, ...)`

Arguments

- `df` A `data.frame` object to check. It must have been wrangled using the `mw_wrangle_muac()` function.
- `sex` A numeric vector for child’s sex with 1 = males and 2 = females.
- `muac` A vector of class `double` of child’s MUAC in centimetres.
- `flags` A numeric vector of flagged records.
- `...` A vector of class `character`, specifying the categories for which the analysis should be summarised for. Usually geographical areas. More than one vector can be specified.

Details

Cut-off points used for the percent of flagged records:

Excellent	Good	Acceptable	Problematic
0.0 - 1.0	>1.0 - 1.5	>1.5 - 2.0	>2.0

Value

A single-row summary tibble with columns containing the plausibility check results. If ungrouped analysis, the output will consist of nine columns and one row; otherwise, the number of columns will vary according to the number vectors specified, and the number of rows to the categories within the grouping variables.

References

Bilukha, O., & Kianian, B. (2023). Considerations for assessment of measurement quality of mid-upper arm circumference data in anthropometric surveys and mass nutritional screenings conducted in humanitarian and refugee settings. *Maternal & Child Nutrition*, 19, e13478. <https://onlinelibrary.wiley.com/doi/10.1111/mcn.13478>

SMART Initiative (2017). *Standardized Monitoring and Assessment for Relief and Transition*. Manual 2.0. Available at: <https://smartmethodology.org>.

See Also

`mw_wrangle_muac()` `flag_outliers()`

Examples

```
## First wrangle MUAC data ----
df_muac <- mw_wrangle_muac(
  df = anthro.01,
  sex = sex,
  muac = muac,
  age = NULL,
  .recode_sex = TRUE,
  .recode_muac = FALSE,
  .to = "none"
)

## Then run the plausibility check ----
mw_plausibility_check_muac(
  df = df_muac,
  flags = flag_muac,
  sex = sex,
  muac = muac,
  area, team # group analysis by survey area and by survey team
)
```

`mw_plausibility_check_wfhz`

Check the plausibility and acceptability of weight-for-height z-score (WFHZ) data

Description

Check the overall plausibility and acceptability of WFHZ data through a structured test suite encompassing checks for sampling and measurement-related biases in the dataset. The test suite, including the criteria and corresponding rating of acceptability, follows the standards in the SMART plausibility check.

The function works on a data frame returned by this package's wrangling functions for age and for WFHZ data.

Usage

```
mw_plausibility_check_wfhz(df, sex, age, weight, height, flags, ...)
```

Arguments

df	A tibble object to check.
sex	A numeric vector for child's sex with 1 = males and 2 = females.
age	A vector of class double of child's age in months.
weight	A vector of class double of child's weight in kilograms.
height	A vector of class double of child's height in centimetres.
flags	A numeric vector of flagged records.
...	A vector of class character, specifying the categories for which the analysis should be summarised for. Usually geographical areas. More than one vector can be specified.

Value

A single-row summary tibble with columns containing the plausibility check results. If ungrouped analysis, the output will consist of 19 columns and one row; otherwise, the number of columns will vary according to the number vectors specified, and the number of rows to the categories within the grouping variables.

References

SMART Initiative (2017). *Standardized Monitoring and Assessment for Relief and Transition*. Manual 2.0. Available at: <https://smartmethodology.org>.

See Also

[mw_plausibility_check_mfaz\(\)](#) [mw_plausibility_check_muac\(\)](#) [mw_wrangle_age\(\)](#)

Examples

```
## First wrangle age data ----
data <- mw_wrangle_age(
  df = anthro.01,
  dos = dos,
  dob = dob,
  age = age,
```

```

    .decimals = 2
  )

  ## Then wrangle WFHZ data ----
  data_wfhz <- mw_wrangle_wfhz(
    df = data,
    sex = sex,
    weight = weight,
    height = height,
    .recode_sex = TRUE
  )

  ## Now run the plausibility check ----
  mw_plausibility_check_wfhz(
    df = data_wfhz,
    sex = sex,
    age = age,
    weight = weight,
    height = height,
    flags = flag_wfhz,
    area, team
  )

```

mw_stattest_ageratio	<i>Test for statistical difference between the proportion of children aged 24 to 59 months old over those aged 6 to 23 months old</i>
----------------------	---

Description

Calculate the observed age ratio of children aged 24 to 59 months old over those aged 6 to 23 months old and test if there is a statistically significant difference between the observed and the expected.

Usage

```

mw_stattest_ageratio(age, .expectedP = 0.66)

mw_stattest_ageratio2(age_cat, .expectedP = 0.66)

```

Arguments

age	A numeric vector of child's age in months.
.expectedP	The expected proportion of children aged 24 to 59 months old over those aged 6 to 23 months old. By default, this is expected to be 0.66.
age_cat	A character vector of child's age in categories. Code values should be "6-23" and "24-59".

Details

This function should be used specifically when assessing the quality of MUAC data. For age ratio test of children aged 6 to 29 months old over 30 to 59 months old, as performed in the SMART plausibility check, use `nipnTK::ageRatioTest()` instead.

Value

A list object with three elements: `p` for p-value of the difference between the observed and the expected proportion of children aged 24 to 59 months old over those aged 6 to 23 months old, `observedR` for the observed ratio, and `observedP` for the observed proportion.

References

SMART Initiative. *Updated MUAC data collection tool*. Available at: <https://smartmethodology.org/survey-planning-tools/updated-muac-tool/>

Examples

```
mwstattest_ageratio(
  age = anthro.02$age,
  .expectedP = 0.66
)

age <- ifelse(anthro.02$age < 24, "6-23", "24-59")

mwstattest_ageratio2(
  age = age,
  .expectedP = 0.66
)
```

mw_wrangle_age

Wrangle child's age

Description

Wrangle child's age for downstream analysis. This includes calculating age in months based on the date of data collection and the child's date of birth, and setting to NA the age values that are less than 6.0 and greater than or equal to 60.0 months old.

Usage

```
mw_wrangle_age(df, dos = NULL, dob = NULL, age, .decimals = 2)
```

Arguments

<code>df</code>	A <code>data.frame</code> object to wrangle age from.
<code>dos</code>	A Date vector of dates when data collection was conducted. Default is NULL.
<code>dob</code>	A Date vector of dates of birth of child. Default is NULL.
<code>age</code>	A numeric vector of child's age in months. In most cases this will be estimated using local event calendars or calculated age in months based on date of data collection and date of birth of child.
<code>.decimals</code>	The number of decimal places to round off age to. Default is 2.

Value

A tibble based on `df`. The variable `age` will be automatically filled in each row where age value was missing and both the child's date of birth and the date of data collection are available. Rows where age is less than 6.0 and greater than or equal to 60.0 months old will be set to NA. Additionally, a new variable named `age_days` of class double for calculated age of child in days is added to `df`.

Examples

```
## A sample data ----
df <- data.frame(
  surv_date = as.Date(c(
    "2023-01-01", "2023-01-01", "2023-01-01", "2023-01-01", "2023-01-01"
  )),
  birth_date = as.Date(c(
    "2019-01-01", NA, "2018-03-20", "2019-11-05", "2021-04-25"
  )),
  age = c(NA, 36, NA, NA, NA)
)

## Apply the function ----
mw_wrangle_age(
  df = df,
  dos = surv_date,
  dob = birth_date,
  age = age,
  .decimals = 3
)
```

mw_wrangle_muac

Wrangle MUAC data

Description

Calculate z-scores for MUAC-for-age (MFAZ) and identify outliers based on the SMART methodology. When age is not supplied, only outliers are detected from the raw MUAC values. The function only works after age has gone through `mw_wrangle_age()`.

Usage

```
mw_wrangle_muac(
  df,
  sex,
  muac,
  age = NULL,
  .recode_sex = TRUE,
  .recode_muac = TRUE,
  .to = c("cm", "mm", "none"),
  .decimals = 3
)
```

Arguments

<code>df</code>	A <code>data.frame</code> object to wrangle data from.
<code>sex</code>	A numeric or character vector of child's sex. Code values should only be 1 or "m" for males and 2 or "f" for females.
<code>muac</code>	A numeric vector of child's age in months.
<code>age</code>	A numeric vector of child's age in months. Default is <code>NULL</code> .
<code>.recode_sex</code>	Logical. Set to <code>TRUE</code> if the values for sex are not coded as 1 (for males) or 2 (for females). Otherwise, set to <code>FALSE</code> (default).
<code>.recode_muac</code>	Logical. Set to <code>TRUE</code> if the values for raw MUAC should be converted to either centimetres or millimetres. Otherwise, set to <code>FALSE</code> (default).
<code>.to</code>	A choice of the measuring unit to convert MUAC values into. Can be "cm" for centimetres, "mm" for millimetres, or "none" to leave as it is.
<code>.decimals</code>	The number of decimal places to use for z-score outputs. Default is 3.

Value

A tibble based on `df`. If `age = NULL`, `flag_muac` variable for detected MUAC outliers based on raw MUAC is added to `df`. Otherwise, variables named `mfaz` for child's MFAZ and `flag_mfaz` for detected outliers based on SMART guidelines are added to `df`.

References

Bilukha, O., & Kianian, B. (2023). Considerations for assessment of measurement quality of mid-upper arm circumference data in anthropometric surveys and mass nutritional screenings conducted in humanitarian and refugee settings. *Maternal & Child Nutrition*, 19, e13478. <https://onlinelibrary.wiley.com/doi/10.1111/mcn.13478>

SMART Initiative (2017). *Standardized Monitoring and Assessment for Relief and Transition*. Manual 2.0. Available at: <https://smartmethodology.org>.

See Also

`flag_outliers()` `remove_flags()` `mw_wrangle_age()`

Examples

```
## When age is available, wrangle it first before calling the function ----
w <- mw_wrangle_age(
  df = anthro.02,
  dos = NULL,
  dob = NULL,
  age = age,
  .decimals = 2
)

### Then apply the function to wrangle MUAC data ----
mw_wrangle_muac(
  df = w,
  sex = sex,
  age = age,
  muac = muac,
  .recode_sex = TRUE,
  .recode_muac = TRUE,
  .to = "cm",
  .decimals = 3
)

## When age is not available ----
mw_wrangle_muac(
  df = anthro.02,
  sex = sex,
  age = NULL,
  muac = muac,
  .recode_sex = TRUE,
  .recode_muac = TRUE,
  .to = "cm",
  .decimals = 3
)
```

mw_wrangle_wfhz

Wrangle weight-for-height data

Description

Calculate z-scores for weight-for-height (WFHZ) and identify outliers based on the SMART methodology.

Usage

```
mw_wrangle_wfhz(df, sex, weight, height, .recode_sex = TRUE, .decimals = 3)
```

Arguments

<code>df</code>	A <code>data.frame</code> object to wrangle data from.
<code>sex</code>	A numeric or character vector of child's sex. Code values should only be 1 or "m" for males and 2 or "f" for females.
<code>weight</code>	A vector of class <code>double</code> of child's weight in kilograms.
<code>height</code>	A vector of class <code>double</code> of child's height in centimetres.
<code>.recode_sex</code>	Logical. Set to <code>TRUE</code> if the values for sex are not coded as 1 (for males) or 2 (for females). Otherwise, set to <code>FALSE</code> (default).
<code>.decimals</code>	The number of decimal places to use for z-score outputs. Default is 3.

Value

A data frame based on `df` with new variables named `wfhz` for child's WFHZ and `flag_wfhz` for detected outliers added.

References

SMART Initiative (2017). *Standardized Monitoring and Assessment for Relief and Transition*. Manual 2.0. Available at: <https://smartmethodology.org>.

See Also

`flag_outliers()` `remove_flags()`

Examples

```
mw_wrangle_wfhz(
  df = anthro.01,
  sex = sex,
  weight = weight,
  height = height,
  .recode_sex = TRUE,
  .decimals = 2
)
```

recode_muac

Convert MUAC values to either centimetres or millimetres

Description

Convert MUAC values to either centimetres or millimetres

Usage

```
recode_muac(x, .to = c("cm", "mm"))
```

Arguments

<code>x</code>	A vector of raw MUAC values. The class can either be double or numeric or integer.
<code>.to</code>	Either "cm" (centimetres) or "mm" (millimetres) for the unit of measurement to convert MUAC values to.

Value

A numeric vector of the same length as `x` with values set to specified unit of measurement.

Examples

```
## Recode from millimetres to centimetres ----
muac_cm <- recode_muac(
  x = anthro.01$muac,
  .to = "cm"
)
head(muac_cm)

## Using the `muac_cm` object to recode it back to "mm" ----
muac_mm <- recode_muac(
  x = muac_cm,
  .to = "mm"
)
tail(muac_mm)
```

wfhz.01

A sample SMART survey data with weight-for-height z-score standard deviation rated as problematic

Description

A sample SMART survey data with weight-for-height z-score standard deviation rated as problematic

Usage

```
wfhz.01
```

Format

A tibble with 303 rows and 6 columns.

Variable	Description
<code>cluster</code>	Primary sampling unit
<code>sex</code>	Sex; "m" = boys, "f" = girls
<code>age</code>	Calculated age in months with two decimal places

<i>oedema</i>	oedema, "n" = no oedema, "y" = with oedema
<i>wfhz</i>	MUAC-for-age z-scores with 3 decimal places
<i>flag_wfhz</i>	Flagged weight-for-height z-score value; 1 = flagged, 0 = not flagged

Source

Anonymous

Examples

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