# Package: ipctools (via r-universe)

September 4, 2024

**Type** Package

**Title** Utilities to Support Integrated Food Security Phase
Classification (IPC) Data Analysis and Visualisation

**Version** 0.0.0.9000

**Description** The Integrated Food Security Phase Classification (IPC) is
a widely used tool for classifying and analysing the severity
and magnitude of food insecurity and malnutrition situations in
various countries and regions around the world. It provides a
common understanding of the food security situation and enables
decision-makers to take appropriate actions to mitigate and
respond to food crises. This package provides functions and
utilities that support IPC-related data analysis and
visualisation.

**License** GPL (>= 3)

**Depends** R (>= 2.10)

**Imports** dplyr, nipnTK, rlang

**Encoding** UTF-8

**LazyData** true

**Language** en-GB

**RoxygenNote** 7.3.1

**Roxygen** list(markdown = TRUE)

**URL** https://nutriverse.io/ipctools/,
https://github.com/nutriverse/ipctools,
http://nutriverse.io/ipctools/

**BugReports** https://github.com/nutriverse/ipctools/issues

**Suggests** covr, spelling, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**Repository** https://nutriverse.r-universe.dev

**RemoteUrl** https://github.com/nutriverse/ipctools

**RemoteRef** HEAD

**RemoteSha** 0553afc70dd982a9a7d8e69a9fb90580d24fac0c

# Contents

---

calculate_unweighted_prevalence

*Calculate wasting prevalence by MUAC*

---

## Description

Calculate wasting prevalence by MUAC

## Usage

```
calculate_unweighted_prevalence(
  muac,
  muac_units = c("mm", "cm"),
  oedema,
  oedema_recode = NULL,
  status = c("sam", "mam")
)

calculate_weighted_prevalence(
  age,
  sex,
  sex_recode = NULL,
  muac,
  muac_units = c("mm", "cm"),
  oedema,
  oedema_recode = NULL,
  status = c("sam", "mam")
)

ipc_calculate_prevalence(df, status = c("sam", "mam"))
```

## Arguments

muac            A numeric value or vector of numeric values for MUAC measurement of child.
                The expected values for MUAC are in millimetres. If units are different, use
                `muac_units` to specify which units are used.

| | |
|---|---|
| muac_units | A character value for units used for MUAC measurement. Currently accepts either "mm" for millimetres (default) or "cm" for centimetres. |
| oedema | A value or a vector of values for oedema status of child. The expected values for oedema is 1 = for presence of oedema and 2 for no oedema. If data values are different, use oedema_recode to map out the values to what is required. |
| oedema_recode | A vector of values with length of 2 with the first element for the value signifying presence of oedema and second element for the value signifying no oedema in the dataset. For example, if "y" is the value for presence of oedema and "n" is the value for no oedema, then specify c("y", "n"). If set to NULL (default), then the values c(1, 0) are used. |
| status | Which wasting anthropometric indicator to report. A choice between c("sam", "mam"). Default to "sam" |
| age | A numeric or integer value or vector of values for age of child. The age of child should be in months. |
| sex | A value or a vector of values for sex of child. The expected values for sex is 1 = males; 2 = females. If data values are different, use sex_recode to map out the values to what is required. |
| sex_recode | A vector of values with length of 2 with the first element for the value signifying males and second element for the value signifying females in the dataset. For example, if "m" is the value for males and "f" is the value for females, then specify c("m", "f"). If set to NULL (default), then the values c(1, 2) are used. |
| df | A data.frame for a MUAC dataset on which appropriate checks have been applied already produced via a call to ipc_muac_check() with the .summary argument set to FALSE. |

## Value

A single value, a vector of values, or a table providing a prevalence

## Examples

```
calculate_unweighted_prevalence(
  muac = muac_data$muac,
  oedema = muac_data$oedema,
  status = "sam"
)

ipc_muac_check(
  muac_data, age = "age", sex = "sex",
  muac = "muac", muac_units = "cm",
  oedema = "oedema", oedema_recode = c(1, 2),
  .summary = FALSE
) |>
ipc_calculate_prevalence()
```

---

check_missing_data *Check missing anthropometry data*

---

### Description

Check missing anthropometry data

### Usage

```
check_missing_data(df)
```

### Arguments

df                A data.frame with information on age, sex, oedema status, and MUAC of each
                  child that has been processed using `process_muac_data()`

### Value

A tibble summarising number and percent missing data for age, sex, oedema status, and MUAC for
the given df

### Examples

```
check_missing_data(muac_data)
```

---

classify_age_ratio *Classification functions that support the main functions for working
with MUAC datasets*

---

### Description

Classification functions that support the main functions for working with MUAC datasets

### Usage

```
classify_age_ratio(p)

classify_sex_ratio(p)

classify_sd(std_dev)

classify_quality(age_ratio_class, sex_ratio_class, std_dev_class, dps_class)

classify_acute_malnutrition(
  muac,
```

```
  muac_units = c("mm", "cm"),
  oedema,
  oedema_recode = NULL
)
```

## Arguments

| | |
|---|---|
| p | Numeric value for p-value of a statistical test used in the various checks applied. |
| std_dev | Numeric value for standard deviation (SD) of a measurement usually MUAC. |
| age_ratio_class | |
| | A character value or vector for classification based on the result of the age ratio test. |
| sex_ratio_class | |
| | A character value or vector for classification based on the sex ratio test. |
| std_dev_class | A character value for vector for classification based on standard deviation. |
| dps_class | A character value for vector for classification based on the digit preference score (DPS) |
| muac | A numeric value or vector of numeric values for MUAC measurement of child. The expected values for MUAC are in millimetres. If units are different, use muac_units to specify which units are used. |
| muac_units | A character value for units used for MUAC measurement. Currently accepts either "mm" for millimetres (default) or "cm" for centimetres. |
| oedema | A value or a vector of values for oedema status of child. The expected values for oedema is 1 = for presence of oedema and 2 for no oedema. If data values are different, use oedema_recode to map out the values to what is required. |
| oedema_recode | A vector of values with length of 2 with the first element for the value signifying presence of oedema and second element for the value signifying no oedema in the dataset. For example, if "y" is the value for presence of oedema and "n" is the value for no oedema, then specify c("y", "n"). If set to NULL (default), then the values c(1, 0) are used. |

## Value

A single value or a vector of values providing a classification

## Examples

```
age_ratio_p <- nipnTK::ageRatioTest(as.integer(!is.na(muac_data$age)))$p
classify_age_ratio(age_ratio_p)
```

---

ipc_muac_check                    *Perform MUAC check based on IPC and CDC recommendations*

---

### Description

Perform MUAC check based on IPC and CDC recommendations

### Usage

```
ipc_muac_check(
  df,
  age = "age",
  sex = "sex",
  sex_recode = NULL,
  muac = "muac",
  muac_units = c("mm", "cm"),
  oedema = "oedema",
  oedema_recode = NULL,
  .summary = TRUE,
  .list = TRUE
)

summarise_muac_check(df, .summary = TRUE, .list = TRUE)
```

### Arguments

| | |
|---|---|
| df | A data.frame with information on age, sex, oedema status, and MUAC of each child |
| age | A character value for name of variable in df for age of child. The age of child should be in months. |
| sex | A character value for name of variable in df for sex of child. The expected values for sex is 1 = males; 2 = females. If data values are different, use sex_recode to map out the values to what is required. |
| sex_recode | A vector of values with length of 2 with the first element for the value signifying males and second element for the value signifying females in the dataset. For example, if "m" is the value for males and "f" is the value for females, then specify c("m", "f"). If set to NULL (default), then the values c(1, 2) are used. |
| muac | A character value for name of variable in df for MUAC measurement of child. The expected values for MUAC are in millimetres. If units are different, use muac_units to specify which units are used. |
| muac_units | A character value for units used for MUAC measurement. Currently accepts either "mm" for millimetres (default) or "cm" for centimetres. |
| oedema | A character value for name of variable in df for oedema status of child. The expected values for oedema is 1 = for presence of oedema and 2 for no oedema. If data values are different, use oedema_recode to map out the values to what is required. If dataset does not have oedema values, set this to NULL. |

oedema_recode
A vector of values with length of 2 with the first element for the value signifying presence of oedema and second element for the value signifying no oedema in the dataset. For example, if "y" is the value for presence of oedema and "n" is the value for no oedema, then specify c("y", "n"). If set to NULL (default), then the values c(1, 0) are used.

.summary
Logical. Should output be a summary of all the checks performed on the MUAC dataset? If TRUE (default), output will be a single row data.frame with each column for each metric used to check MUAC dataset. If FALSE, a data.frame with same number of rows as df and columns for each metric used to check MUAC dataset is added to df. Setting .summary to FALSE is usually only used for when the output structure is required for further analysis (i.e., calculation of prevalence).

.list
Logical. Relevant only if .summary is TRUE. Should summary be given in list format? If TRUE (default), then the output is in list format otherwise a data.frame is provided.

### Value

A data.frame with a single row with each column for each metric used to check MUAC dataset if .summary is TRUE. If .summary is FALSE, a data.frame with same number of rows as df and columns for each metric used to check MUAC dataset is added to df.

### Examples

```
ipc_muac_check(df = muac_data, oedema_recode = c(1, 2), muac_units = "cm")
```

---

muac_data                 *Nutrition survey data with MUAC and oedema measurements and location information anonymised.*

---

### Description

Nutrition survey data with MUAC and oedema measurements and location information anonymised.

### Usage

```
muac_data
```

### Format

A data frame with 6 columns and 435 rows:

| Variable | Description |
|---|---|
| *state_name* | Name of state |
| *district_name* | Name of district |
| *age* | Age of child in months |

| | |
|---|---|
| *sex* | Sex of child. 1 = male; 2 = female |
| *muac* | Mid-upper arm circumference (MUAC) measurement in centimetres |
| *oedema* | Presence or absence of oedema. 1 = oedema; 2 = no oedema |

## Examples

```
muac_data
```

---

| process_muac_data | *Process MUAC data* |
|---|---|

---

## Description

Process MUAC data

## Usage

```
process_muac_data(
  df,
  age = "age",
  sex = "sex",
  sex_recode = NULL,
  muac = "muac",
  muac_units = c("mm", "cm"),
  oedema = "oedema",
  oedema_recode = NULL
)
```

## Arguments

| | |
|---|---|
| df | A data.frame with information on age, sex, oedema status, and MUAC of each child |
| age | A character value for name of variable in df for age of child. The age of child should be in months. |
| sex | A character value for name of variable in df for sex of child. The expected values for sex is 1 = males; 2 = females. If data values are different, use sex_recode to map out the values to what is required. |
| sex_recode | A vector of values with length of 2 with the first element for the value signifying males and second element for the value signifying females in the dataset. For example, if "m" is the value for males and "f" is the value for females, then specify c("m", "f"). If set to NULL (default), then the values c(1, 2) are used. |
| muac | A character value for name of variable in df for MUAC measurement of child. The expected values for MUAC are in millimetres. If units are different, use muac_units to specify which units are used. |

| | |
|---|---|
| muac_units | A character value for units used for MUAC measurement. Currently accepts either "mm" for millimetres (default) or "cm" for centimetres. |
| oedema | A character value for name of variable in df for oedema status of child. The expected values for oedema is 1 = for presence of oedema and 2 for no oedema. If data values are different, use oedema_recode to map out the values to what is required. If dataset does not have oedema values, set this to NULL. |
| oedema_recode | A vector of values with length of 2 with the first element for the value signifying presence of oedema and second element for the value signifying no oedema in the dataset. For example, if "y" is the value for presence of oedema and "n" is the value for no oedema, then specify c("y", "n"). If set to NULL (default), then the values c(1, 0) are used. |

## Value

An appropriately structured data.frame that can be passed on to other functions

## Examples

```
process_muac_data(muac_data)
```

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