Package: BRINDA (via r-universe)

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Type Package

Title Computation of BRINDA Adjusted Micronutrient Biomarkers for Inflammation

Version 0.1.5

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Description Inflammation can affect many micronutrient biomarkers and can thus lead to incorrect diagnosis of individuals and to over- or under-estimate the prevalence of deficiency in a population. Biomarkers Reflecting Inflammation and Nutritional Determinants of Anemia (BRINDA) is a multi-agency and multi-country partnership designed to improve the interpretation of nutrient biomarkers in settings of inflammation and to generate context-specific estimates of risk factors for anemia (Suchdev (2016) <doi:10.3945/an.115.010215>). In the past few years, BRINDA published a series of papers to provide guidance on how to adjust micronutrient biomarkers, retinol binding protein, serum retinol, serum ferritin by Namaste (2020), soluble transferrin receptor (sTfR), serum zinc, serum and Red Blood Cell (RBC) folate, and serum B-12, using inflammation markers, alpha-1-acid glycoprotein (AGP) and/or C-Reactive Protein (CRP) by Namaste (2020) <doi:10.1093/ajcn/nqaa141>, Rohner (2017) <doi:10.3945/ajcn.116.142232>, McDonald (2020) <doi:10.1093/ajcn/nqz304>, and Young (2020) <doi:10.1093/ajcn/nqz303>. The BRINDA inflammation adjustment method mainly focuses on Women of Reproductive Age (WRA) and Preschool-age Children (PSC); however, the general principle of the BRINDA method might apply to other population groups. The BRINDA R package is a user-friendly all-in-one R package that uses a series of functions to implement BRINDA adjustment method, as described above. The BRINDA R package will first carry out rigorous checks and provides users guidance to correct data or input errors (if they occur) prior to inflammation adjustments. After no errors are detected, the package implements the BRINDA inflammation adjustment for up to

five micronutrient biomarkers, namely retinol-binding-protein, serum retinol, serum ferritin, sTfR, and serum zinc (when appropriate), using inflammation indicators of AGP and/or CRP for various population groups. Of note, adjustment for serum and RBC folate and serum B-12 is not included in the R package, since evidence shows that no adjustment is needed for these micronutrient biomarkers in either WRA or PSC groups (Young (2020) <doi:10.1093/ajcn/nqz303>).

BugReports https://github.com/hanqiluo/BRINDA/issues

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URL https://github.com/hanqiluo/BRINDA

Depends R (>= 4.1.0)

Imports berryFunctions, data.table, dplyr, Hmisc, rlang

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

Encoding UTF-8

Language en-US

LazyData true

RoxygenNote 7.2.1

Repository https://hanqiluo.r-universe.dev

RemoteUrl https://github.com/hanqiluo/brinda

RemoteRef HEAD

RemoteSha 6c4aacf462665847ad4df80fe84953134953201f

Contents

BRINDA *Computation of BRINDA Adjusted Micronutrient Biomarkers for inflammation*

Description

Inflammation can affect many micronutrient biomarkers and can thus lead to incorrect diagnosis of individuals and to over- or under-estimate the prevalence of deficiency in a population. Biomarkers Reflecting Inflammation and Nutritional Determinants of Anemia (BRINDA) is a multi-agency and multi-country partnership designed to improve the interpretation of nutrient biomarkers in settings of inflammation and to generate context-specific estimates of risk factors for anemia (Suchdev (2016) <doi:10.3945/an.115.010215>). In the past few years, BRINDA published a series of papers to provide guidance on how to adjust micronutrient biomarkers, retinol binding protein, serum retinol, serum ferritin by Namaste (2020), soluble transferrin receptor (sTfR), serum zinc, serum and Red Blood Cell (RBC) folate, and serum B-12, using inflammation markers, alpha-1-acid glycoprotein (AGP) and/or C-Reactive Protein (CRP) by Namaste (2020) <doi:10.1093/ajcn/nqaa141>, Rohner (2017) <doi:10.3945/ajcn.116.142232>, McDonald (2020) <doi:10.1093/ajcn/nqz304>, and Young (2020) <doi:10.1093/ajcn/nqz303>. The BRINDA inflammation adjustment method mainly focuses on Women of Reproductive Age (WRA) and Preschool-age Children (PSC); however, the general principle of the BRINDA method might apply to other population groups. The BRINDA R package is a user-friendly all-in-one R package that uses a series of functions to implement BRINDA adjustment method, as described above. The BRINDA R package will first carry out rigorous checks and provides users guidance to correct data or input errors (if they occur) prior to inflammation adjustments. After no errors are detected, the package implements the BRINDA inflammation adjustment for up to five micronutrient biomarkers, namely retinol-binding-protein, serum retinol, serum ferritin, sTfR, and serum zinc (when appropriate), using inflammation indicators of AGP and/or CRP for various population groups. Of note, adjustment for serum and RBC folate and serum B-12 is not included in the R package, since evidence shows that no adjustment is needed for these micronutrient biomarkers in either WRA or PSC groups (Young (2020) <doi:10.1093/ajcn/nqz303>).

Usage

```
BRINDA(
  dataset,
  retinol_binding_protein_varname,
  retinol_varname,
  ferritin_varname,
  soluble_transferrin_receptor_varname,
  zinc_varname,
  crp_varname,
  agp_varname,
  population_group,
  crp_ref_value_manual = NULL,
  agp_ref_value_manual = NULL,
  output_format
)
```

Arguments

`dataset`	Enter the name of the dataset (should be already loaded in the R environment; micronutrient biomarkers should NOT be log-transformed).

`retinol_binding_protein_varname`
: Enter the variable name of retinol binding protein (if available) in your dataset. The variable can be in either international or conventional units. The adjusted values in the output dataset will be in the same unit as retinol binding protein variable in the input dataset.

`retinol_varname`
: Enter the variable name of serum/plasma retinol (if available) in your dataset. The variable can be in either international or conventional units. The adjusted values in the output dataset will be in the same unit as retinol variable in the input dataset.

`ferritin_varname`
: Enter the variable name of serum/plasma ferritin (if available) in your dataset. The variable can be in either international or conventional units. The adjusted values in the output dataset will be in the same unit as serum ferritin in the input dataset.

`soluble_transferrin_receptor_varname`
: Enter the variable name of serum/plasma soluble transferrin receptor (if available) in your dataset. The variable can be in either international or conventional units. The adjusted values in the output dataset will be in the same unit as soluble transferrin receptor in the input dataset.

`zinc_varname`
: Enter the variable name of serum/plasma zinc (if available) in your dataset. The variable can be in either international or conventional units. The adjusted values in the output dataset will be in the same unit as serum zinc in the input dataset.

`crp_varname`
: Enter the variable name of CRP (if available) in your dataset. Unit must be mg/L

`agp_varname`
: Enter the variable name of AGP (if available) in your dataset (unit must be g/L)

`population_group`
: Please write WRA, PSC, Other, or Manual. The BRINDA R package can only analyze one population group at one time. If users select WRA or PSC, external CRP/AGP reference values will be used If users select Other, the lowest decile of the CRP and AGP will be calculated and used as CRP and AGP reference values If users select Manual as the population group, users can define their own AGP and CRP reference values for the BRINDA adjustment.

`crp_ref_value_manual`
: Leave it empty if users select population_group as WRA, PSC, or Other. If users select population_group as Manual, and there is a CRP variable in the dataset, enter a user-specified CRP reference value

`agp_ref_value_manual`
: Leave it empty if users select population_group as WRA, PSC, or Other If users select population_group as Manual, and there is an AGP variable in the dataset, enter a user specified AGP reference value

`output_format`
: Please write FULL or SIMPLE (SIMPLE by default if users leave it empty). The SIMPLE output only provides users adjusted micronutrient biomarker values. The FULL output provides users all the intermediate parameters for the BRINDA adjustment, such as coefficients of log (AGP) and log (CRP) and associated standard errors and P values, in addition to adjusted micronutrient biomarker values.

Value

'brinda()' returns a data frame object that contains additional variables of adjusted micronutrient biomarkers (by default). If users specify output format = full, the output dataset will also include additional variables such as coefficients of regressions of micronutrient biomarkers on AGP and CRP, natural logs of AGP/CRP reference values.

Author(s)

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Examples

```
data(sample_data)

# Example 1
# Calculate BRINDA inflammation adjustment values for preschool-age children
# (Assuming the data set contains information of preschool-age children)

sample_data_adj <-
    BRINDA(dataset = sample_data,
       retinol_binding_protein_varname = rbp,
       retinol_varname = sr,
       ferritin_varname = sf,
       soluble_transferrin_receptor_varname = stfr,
       zinc_varname = zinc,
       crp_varname = crp,
       agp_varname = agp,
       population = Psc,
       crp_ref_value_manual = ,
       agp_ref_value_manual = ,
       output_format = )

# Example 2
# Calculate BRINDA inflammation adjustment values for non-pregnant women of
# reproductive age assuming the sample data set contains information of women
# of reproductive age).

sample_data_adj2 <-
    BRINDA(dataset = sample_data,
       retinol_binding_protein_varname = rbp,
       retinol_varname = sr,
       ferritin_varname = sf,
       soluble_transferrin_receptor_varname = stfr,
       zinc_varname = zinc,
       crp_varname = ,
       agp_varname = agp, population = WRA,
       crp_ref_value_manual = ,
       agp_ref_value_manual = ,
       output_format = )

# Example 3
# Calculate BRINDA inflammation adjustment values for other population assuming
```

```
# the study population is neither women of reproductive age nor preschool-age
# children

sample_data_adj3 <-
    BRINDA(dataset = sample_data,
       retinol_binding_protein_varname = rbp,
       retinol_varname = sr,
       ferritin_varname = sf,
       soluble_transferrin_receptor_varname = stfr,
       zinc_varname = zinc,
       crp_varname = crp,
       agp_varname = ,
       population = OTHER,
       crp_ref_value_manual = ,
       agp_ref_value_manual = ,
       output_format = FULL)

# Example 4
# Calculate BRINDA inflammation adjustment values for a population when users
# would like to apply user-defined CRP and AGP reference values

sample_data_adj4 <-
    BRINDA(dataset = sample_data,
       retinol_binding_protein_varname = rbp,
       retinol_varname = sr,
       ferritin_varname = sf,
       soluble_transferrin_receptor_varname = stfr,
       zinc_varname = zinc,
       crp_varname = crp,
       agp_varname = agp,
       population = MANUAL,
       crp_ref_value_manual = 0.2,
       agp_ref_value_manual = 1.4,
       output_format = FULL)
```

`sample_data` *Micronutrient biomarker dataset*

Description

A biomarker data set that was subset from a cross-sectional survey in Malawi. It provides de-identified information for serum ferritin, soluble transferrin receptor, retinol binding protein, retinol, zinc, C-reactive protein (CRP), Alpha1-acid glycoprotein (AGP) to illustrate the use of the package.

Usage

```
data(sample_data)
```

Format

An object of class `"data.frame"`

id Unique identification numbers

sf Serum ferritin, µg/l

stfr Soluble transferrin receptor, mg/L

rbp Retinol binding protein, µmol/L

sr Serum retinol, µmol/L

zinc Zinc, µg/L

crp C-reactive Protein, mg/L

agp Alpha1-acid glycoprotein, g/L

References

National Statistical Office (NSO), Community Health Sciences Unit (CHSU) [Malawi], Centers for Disease Control and Prevention (CDC), and Emory University. 2017. Malawi Micronutrient Survey 2015-16. Atlanta, GA, USA: NSO, CHSU, CDC, and Emory University

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