

# Package ‘BRINDA’

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**Type** Package

**Title** Biomarker Reflecting Inflammation and Nutrition Determinant of Anemia (BRINDA) Adjustment Method

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**Description** The BRINDA R package is a user-friendly all-in-one R package that uses a series of functions to implement BRINDA adjustment method.

**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  
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**R topics documented:**

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BRINDA	<i>Biomarker Reflecting Inflammation and Nutrition Determinant of Anemia (BRINDA) Adjustment Method</i>
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**Description**

The BRINDA R package is a user-friendly all-in-one R package that uses a series of functions to implement BRINDA adjustment method.

**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)

Hanqi Luo, O.Yaw Addo, Afrin Jahan

### Examples

```
data(sample_data)
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 = )
```

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sample\_data

*Micronutrient biomarker dataset*


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## 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

## Examples

```
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 = )
```