HOW TO APPLY THE BRINDA APPROACH TO YOUR DATA

Objective: To apply BRINDA regression inflammation correction (BRC) for <u>both</u> AGP & CRP on a given nutritional biomarker - for preschool children ages 6-59 months and non-pregnant women of reproductive age.
(*If you only have one inflammation biomarker (CRP or AGP) please contact us for assistance*).

<u>**Information needed to start:**</u>
1. Research dataset should include: ID, nutrition biomarker, inflammation (AGP/CRP) variables
2. Nutritional biomarker indicator cut-offs for deficiency (from literature)
3. Download the BRINDA Macro for preschool children and women of reproductive age from:
   http://www.brinda-nutrition.org/
   All sample code for the steps below are provided in the macro code.

<u>**How to apply macro to your data:**</u>

1. Create libname (can use search/replace to swap the libname in macro example with your working directory).
2. Specify the SAS macro fields and supply working directory for your research data
   a. Specify **brc sas** macro location directory on your computer
   b. Research data library directory i.e data you want to perform brc on is located
   c. Name of the research datafile in #2 above
   d. Label for your output
   e. ID - Identifier variable in your dataset
   f. CRP - Exact name of CRP variable in your dataset
   g. AGP - Exact name of AGP variable in your dataset
   h. Biomarker - Exact name of nutritional biomarker variable in your dataset you wish to brinda correct
   i. Outdata - Name of resultant dataset after brc (BRINDA regression correction)
3. Supply input code after each equal sign (=) in the macro call below (users can simply copy and paste directly the few lines of macro in their SAS program to perform the regression correction).
```
option nofmterr;
%include"H:\BRINDA2\brc_macros\BRC_nomalaria_2apps_source_code_psc_may2017.sas";run;
%BrindaRC_noM(LABEL ="BRINDA Inflammation Correction, BRC",
RES_DATALIB  =H:\BRINDA2\brc_macros,
DATA_IN      = researchdataName,
id             =,
crp                   =,
agp                   =,
biomarker      =,
outdata        =);
run;
```
4. Do quality checks to confirm macro is working as desired.
   a. Example: Biomarker values the sub-population of uninflamed individuals, i.e. those with log natural AGP and CRP values, below the BRINDA reference decile (lnAGP of -0.52, and lnCRP of -2.26) would not be inflammation corrected. Thus, biomarker original value will be equal to biomarker brinda corrected
5. Merging resultant dataset with primary data
   a. Note: after deriving the BRINDA corrected nutritional biomarker merge data with the primary research data. The same cut-offs for nutritional deficiency will then applied as one would to the uncorrected biomarker.
6. Done: Now have dataset with both unadjusted and inflammation adjusted biomarkers
   a. Note the current approach does not adjust for malaria or any additional covariates.