**HOW TO APPLY THE BRINDA APPROACH TO YOUR DATA**

**Objective:** To apply BRINDA regression inflammation correction (BRC) for both 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)*.

**Information needed to start:**
1. Research dataset should include: ID, nutrition biomarker, inflammation (AGP/CRP) variables
2. Nutritional biomarker indicator cut-offs for deficiency (from literature)
   
   *All sample code for the steps below are provided in the macro code.*

**How to apply macro to your data:**

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).

```sas
option nofmtterr;
%include "H:\BRINDA2\brc_macros\BRC_nomalaria_apps_source_code_psc_may2017.sas";run;
%BrindaRC_nM(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.

*DISCLAIMER: THIS OPEN SOURCE (‘AS IS’) MACRO IS MEANT TO FOSTER SCIENTIFIC/ACADEMIC SCHOLARSHIP INQUIRY AND COMES WITH ABSOLUTELY NO WARRANTY.
*NO CHANGES REQUIRED UNLESS USERS/ANALYSTS HAVE A VERY GOOD REASON TO CHANGE THIS SOURCE CODE
*USER FEEDBACK/SUGGESTIONS ARE ENCOURAGED AND WELCOMED:(LYU6@CDC.GOV)