%macro BRC_agponly_nomal(LABEL=,RES_DATALIB =,DATA_IN =,id=, agp=, biomarker=,outdata=);
/*set up library with your research data*/;
libname _datalib "&res_datalib";
data _data_in_agpo;
set _datalib.&data_in;
if &agp=0 then &agp=&agp+ 0.001;
else &agp=&agp;
   if &agp ne . then lnagp = log(&agp) ;
   if &biomarker ne . then ln&biomarker = log(&biomarker);
keep &id &agp &biomarker lnagp ln&biomarker;
run;

*** Set brinda reference deciles for children;
  %let lnagp_refdecile = -0.52;  * ln AGP brinda reference decile for children ;

/*NATURAL LOG (LN) CRP brinda reference deciles FOR CHILDREN (BRINDA EXTERNAL REF VALUES MUST REMAIN UNCHANGED ACROSS ANALYSES); */
/*USERS DESIRING TO USE NON-BRINDA REF brinda reference deciles CAN CHANGE THE REF VALUE ABOVE*/

*** Running linear regressions to derive pop biomarker_AGP beta coefficient;
ods output ParameterEstimates = beta_agp_psc;
proc reg data=_data_in_agpo;
   model ln&biomarker = lnagp ;   run; quit;

**declaring a macro for population APP regression coefficient;
data _null_;  
set beta_agp_psc;
if Variable = "lnagp" then call symput ('lnagpbeta', estimate);
run;

/*Applying regression adjustment equation to raw biomarker values than meet
inflammation criteria(subpopulation)*/
/*Inflammation adjusted biomarker variable will carry a suffix of "adjpsc".
*/
/*For example, "sfadjpsc", or rbpadjpsc or tfradjpsc etc ;*/

data &outdata;
  set _data_in_agpo;
  if &agp ne . then
    ln&biomarker.adj = ln&biomarker - &lnagpbeta*max(lnagp-&lnagp_refdecile, 0);
    &biomarker.adj = exp(ln&biomarker.adj);
  popbeta_&biomarker.&agp=&lnagpbeta;
  brcref_&agp=&lnagp_refdecile;
  label &biomarker.adj = 'brinda reg_corrected(BRC) biomaker'
  ln&biomarker.adj = 'brinda reg_corrected biomaker-nat_log units'
  popbeta &biomarker.&agp='Pop reg coeff app-biomarker'
  brcref_&agp='Brinda inflamm ref brinda reference decile agp-psc';
run;
%mend BRC_agponly_nomal;

/*Output data with biomarker in its name*/;
Objective: To apply BRINDA regression inflammation correction (BRC) for AGP & CRP

for a given nutritional biomarker - for preschool children ages 6-59 months;

Title: 'BRINDA REGRESSION INFLAMMATION CORRECTION (BRC) MACROS USAGE CODE IN BASE SAS';

options notmterr nocenter formchar="|----|+----|=|\<">

libname m "H:\BRINDA2\brc_macros";

Step 0: SPECIFY YOUR LIBNAME;

Step 1:

Note: The BRINDA REG correction equations - from papers:

if participant’s natural log CRP > brinda ref CRP &

natural log AGP > Brinda ref AGP

then the correction is applied using the expression:

Adjusted adjustedNB = exp(ln(biomarker) - f1(lnCRPobs - lnCRPref) -
fl2(logAGPobs - lnAGPref))

The entire computation is performed in base SAS by the source code macro("BRC_nomalaria_agponly_source_code_psc_may2017.sas");
Information needed:

1. Research dataset (should include: ID, Nutritional biomarker, inflammation markers (AGP/CRP) variables)*
2. Nutritional biomarker indicator cut-offs (FROM LITERATURE)*
3. SAS macro for performing BRINDA regression inflammation correction (BRC)*

STEP 2: Specify the SAS macro fields and supply working directory for your research data

1. REQUIRED: Specify brc sas macro location directory on your computer*
2. REQUIRED: Research data library dir i.e data you want to perform brc on is located*
3. REQUIRED: Name of the research datafile in #2 above*
4. OPTIONAL: Label for your output*
5. REQUIRED: ID - Identifier variable in your dataset*
6. REQUIRED: CRP - Exact name of CRP variable in your dataset*
7. REQUIRED: AGP - Exact name of AGP variable in your dataset*
8. REQUIRED: Biomarker - Exact name of nutritional biomaker variable in your dataset you wish to brinda correct*
9. REQUIRED: Outdata - Name of resultant dataset after brc*

NOTE: BRINDA EXTERNAL INFLAMMATION CORRECTION REFERENCE DECILE ARE IN BUILT INTO THE MACRO - NO USER EDITS NEEDED*

MINIMAL MACRO SKILLS REQUIRED OF USERS DESIRING TO USE NON-BRINDA INFLAMMATION REF DECILE***

STEP 3: Supply input code after each equal sign (=) in the macro call below***

```sas
%option nofmterr;
%include "H:\BRINDA2\brc_macros\BRC_nomalaria_agponly_source_code_psc_may2017.sas";
%BRC_agponly_nomal(LABEL ="BRINDA Inflammation Correction, BRC",
RES_DATALIB =H:\BRINDA2\brc_macros,
DATA_IN = researchdataName,
id =,
agp =,
biomarker =,
outdata =);
run;
```
/*STEP 4: DO QUALITY CHECKS TO CONFIRM MACRO IS WORKING AS DESIRED;*/

***outdataname is the dataset you gave in point # 9 above. it must be exact;***

proc print data=outdataname(obs=5);
var lnagp brcref_AGP popbeta_sfAGP lnsf lnsfadjpsc sfadjpsc;
run;

***STEP 5: MERGING RESULTANT DATASET WITH PRIMARY DATA***;

/*AFTER DERIVING THE BRINDA CORRECTED NUTRITIONAL BIOMARKER, WE MERGE DATA WITH THE PRIMARY RESEARCH DATA AND THEN APPLY*/
/*THE SAME CUT-OFFS ONE APPLIES TO THE UNCORRECTED BIOMAKER*/;

/*SAMPLE: A FERRITIN PROCESSED OUTPUT IS USED IN THIS EXAMPLE***;

***LET'S CALL THIS DATA=BRC_ADJFERRITINDATA_PSC" *******;

proc sort data=researchdata; by ID;
proc sort data=brc_adjferritindata_psc; by ID; run;

data RESEARDATA_W_BRC_INDICATORS;
merge researchdata brc_adjferritindata_psc(keep=Ori_id sfadjpsc);
/*SELECTING ONLY THE INFLAMMATION CORRECTED NUTRITIONAL BIOMAKER*/
/*AND ID AND MERGING WITH THE MAIN SET*/;
by ID;

/*NOW APPLYING THE NB CUT-OFF TO THE INFLAMMATION CORRECTED BIOMARKER;***/
/*USING FERRITIN CUT-OFF AS EXAMPLE***;
if sfadjpsc = . THEN SF_C1_brc = .;
    ELSE if sfadjpsc NE . & sfadjpsc <12 THEN SF_C1_brc = 1;
else if sfadjpsc GE 12 then SF_C1_brc = 0;
label SF_C1_brc = 'brinda inflamm reg_corrected Serum ferritin(SF) cut-off 1: Under 5y: <12 µg/L 0=Sufficient 1=Deficient';
run;

/*STEP 5: Performing Frequency tabulations to compare crude vs inflammation corrected prevalences*/;

proc freq data=RESEARDATA_W_BRC_INDICATORS;
tables SF_C1 SF_C1_brc;
run;

***WHERE SF_C1 = CRUDE INFLAMMATION UNCORRECTED DEFICIENCY INDICATOR AND SF_C1_BRC IS THE BRINDA INFLAMMATION CORRECTED DEFICIENCY INDICATOR***;
***NOTES: USERS ARE ADVISED TO APPLY/REPLICATE THE SHORT MACROS SEPARATELY TO EACH NUTRI BIOMARKER**; /*/*PRIOR TO MERGING THE DATASETS, MULTIPLE BRC CALCULATIONS CAN BE PERFORMED*/ /*MACRO IS CALLED WITH %INCLUDE, DOES NOT NEED TO BE CALLED MULTIPLE TIMES*/ /*ONLY ONE TIME INTIALIZING IS NEEDED FOR ALL BIOMAKERS INFLAMMATION CORRECTIONS*/

****AS SHOWN BELOW - FOR THE NEXT BIOMARKER IN YOUR DATABASE***;

%BRC_agponly_nomal(LABEL = "BRINDA Inflammation Correction, BRC",
RES_DATALIB = H:\BRINDA2\brc_macros,
DATA_IN = researchdataName,
 id =~,
crp =~,
agp =~,
biomarker =~,
outdata =~);
run;

*******************************************************************************
**************************;
***TO BE RELEASED AT FUTURE DATE. SAS MACROS FOR BRINDA INFLAMMATION CORRECTION FOR MULTIPLE NUTRITIONAL BIOMAKERS, INCORPORATING INDICATOR CUT-OFFS IN MACRO AND DEVELOPING A MACRO/BRC FUNCTIONS IN OTHER STATISTICAL PACKAGES************************;
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*******************************************************************************
*****************************************;
**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)*******************************************************************************;