%macro BRC_crponly_nomal(LABEL=,RES_DATALIB =,DATA_IN =,id=, crp=, biomarker=,outdata=);
/*set up library with your research data*/
libname _datalib "&res_datalib";
data _data_in_crpo;
set _datalib.&data_in;
/*contingency for zero APPS before log transformation*/
if &crp=0 then &crp=&crp+ 0.001;
else &crp=&crp;
**Log tranforming biomarkers;
if &crp ne . then lncrp = log(&crp) ;
if &biomarker ne . then ln&biomarker = log(&biomarker);
keep &id &crp &biomarker lncrp ln&biomarker;
run;

*** Set brinda reference decile for children;
%let lncrp_refdecile = -2.26; /*ln CRP decile for children*/
/*NATURAL LOG (LN) CRP brinda reference decile FOR CHILDREN (BRINDA EXTERNAL REF VALUES MUST REMAIN UNCHANGED ACROSS ANALYSES); */
/*USERS DESIRING TO USE NON-BRINDA REF brinda reference decile CAN CHANGE THE REF VALUE ABOVE*/

*** Running linear regressions to derive pop biomarker_crp beta coefficient;
ods output ParameterEstimates = beta_crp_psc;
proc reg data=_data_in_crpo;
   model ln&biomarker = lncrp ; run; quit;

**declaring a macro for population APP regression coefficient;
data _null_;
set beta_crp_psc;
if Variable = "lncrp" then call symput ("lncrpbeta", 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 ;*/
/*Output data with biomarker in its name*/
data &outdata;
set _data_in_crpo;
if &crp ne . then
    ln&biomarker.adj = ln&biomarker - &lncrpbeta*max(lncrp-
    &lncrp_refdecile, 0);
    &biomarker.adj = exp(ln&biomarker.adj);
popbeta_&biomarker.&crp=&lncrpbeta;
brcref_&crp=&lncrp_refdecile;
label &biomarker.adj = 'brinda reg_corrected(BRC) biomarker'
    ln&biomarker.adj = 'brinda reg_corrected biomarker-nat_log units'
    popbeta_&biomarker.&crp = 'Pop reg coeff app-biomarker'
    brcref_&crp = 'Brinda inflamm ref decile crp-psc';
run;
%mend BRC_crponly_nomal;

/*Output data with biomarker in its name*/;
Objective: To apply BRINDA regression inflammation correction (BRC) for AGP & CRP for a given nutritional biomaker – for preschool children ages 6-59 months.

---------------------------

**Step 0: SPECIFY YOUR LIBNAME**;

```
libname m "H:\BRINDA2\brc_macros";
```

**Step 1:**

```
/*recall: BRINDA REG Correction equation -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) - f2(logAGPobs - lnAGPref))*/;
```

****Objective: To apply BRINDA regression inflammation correction (BRC) for AGP & CRP for a given nutritional biomaker – for preschool children ages 6-59 months.****

---

**Notes:**

- BRC approach is effectively applied to the sub-population considered inflammed and above the external BRINDA reference decile max for both inflammation biomarkers.
- 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 = \(\exp(ln(biomarker) - f1(lnCRPobs - lnCRPref) - f2(logAGPobs - lnAGPref))\).
/*Information needed:*/
*****************************************************;
/*1. Research dataset(should include: ID, Nutritional biomaker, 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**********************;
*****************************************************;

option nofmterr;
%include "H:\BRINDA2\brc_macros\BRC_nomalaria_crponly_source_code_psc_may2017.sas";run

%BRC_crponly_nomal(LABEL ="BRINDA Inflammation Correction, BRC",
RES_DATALIB =H:\BRINDA2\brc_macros,
DATA_IN = researchdataName,
id =,
crp =,
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 lncre_crpncref CRP lnagp brc_ref AGP popbeta_sfAGP
popbeta_sfCRP lnspf lnspfadjpsc 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 EQ . 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 correct 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_crponly_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*************;
*****************************************************************************
*****************************************************************************
*****************************************************************************
*************************************;
**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)*****************************************************************************
*****************************************************************************;