%macro BrindaRC_noM(LABEL=,RES_DATALIB =,DATA_IN =,id=,crp=, agp=, biomarker=,outdata=);

/*set up library with your research data*/
libname _datalib "&res_datalib";
data _data_inwra;
set _datalib.&data_in;
/*contingency for zero APPS before log transformation*/
if &crp=0 then &crp=&crp+ 0.001;
else &crp=&crp;
if &agp=0 then &agp=&agp+ 0.001;
else &agp=&agp;

**Log tranforming biomarkers;
if &crp ne . then lncrp = log(&crp) ;
if &agp ne . then lnagp = log(&agp) ;
if &biomarker ne . then ln&biomarker = log(&biomarker);
keep &id &crp &agp &biomarker lncrp lnagp ln&biomarker;
run;

*** Set brinda reference deciles for children;
%let lncrp_refdecile  = -1.83 ; *ln CRP decile for wra-(15-49y) ;
%let lnagp_refdecile  = -0.63 ; * ln AGP decile for wra-(15-49y) ;

/*Natural log (ln) CRP and AGP deciles for Women (BRINDA external ref values must remain unchanged across analyses); */
/*Users desiring to use non-brinda ref deciles can change the 2 refs above*/
*******************************************************************
*** Run regression and capture internal pop beta coefficients for CRP and
AGP; *******************************************************************
ods output ParameterEstimates = betas_crpagp_wra;
proc reg data=_data_inwra;
model ln&biomarker = lncrp lnagp ;
rung quit;

/*Applying regression adjustment equation to raw biomarker values         */
/*Inflammation adjusted biomarker variable will carry a suffix of "adjpsc". */
/*For example, "sfaadjpsc", or rbpadjwra or tfradjwra etc ;*/
data &outdata;
set _data_inwra;
if &crp ne . and &agp ne . then
  ln&biomarker.adjwra= ln&biomarker - &lncrpbeta*max(lncrp-
&lncrp_refdecile,0) - &lnagpbeta*max(lnagp-
&lnagp_refdecile,0);
&biomarker.adjwra  = exp(ln&biomarker.adjpsc);
popbeta_&biomarker.&agp=&lnagpbeta;
popbeta_&biomarker.&crp=&lncrpbeta;
brcref_&crp=&lncrp_refdecile;
brcref_&agp=&lnagp_refdecile;
label &biomarker.adjpsc='brinda reg_corrected(BRC) biomaker'
   ln&biomarker.adjpsc='brinda reg_corrected biomaker-nat_log
   units'
popbeta_&biomarker.&crp='Pop reg coeff: crp(x1) against
   biomarker(Y)'
popbeta_&biomarker.&agp='Pop reg coeff: agp(x2) against
   biomarker(Y)'
brcref_&crp='Brinda inflamm
   ref decile crp-wra'
brcref_&agp='Brinda inflamm
   ref decile agp-wra';
rung;
%mend BrindaRC_noM;
/*Output data with biomarker in its name*/;
Objective: To apply BRINDA regression inflammation correction (BRC) for AGP & CRP

for a given nutritional biomaker - for Women of Reproductive ages 15-49y

TITLE 'BRINDA REGRESSION INFLAMMATION CORRECTION(BRC) MACROS USAGE CODE IN BASE SAS';
options nofmtterr nocenter formchar="|---|+|-----|-=|--/<>|";

libname m "H:\BRINDA2\brc_macros";

/*Step 0: ***SPECIFY YOUR LIBNAME***;*/

/*CHEATSHEET: PLEASE USE SEARCH/REPLACE TO SWAP THE LIBNAME IN THIS EXAMPLE WITH YOUR WORKING DIRECTORY AND YOU ARE ALL SET TO SUCCESSFULLY APPLY THIS MACRO*/

/**NOTES: BRC approach is effectively applied to the sub-population considered inflammed and above the*/
/*external BRINDA reference decile max for both inflammation biomarkers.*/
/*recall: 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) - fl1(lnCRPobs - lnCRPref) -
fl2(logAGPobs - lnAGPref))*/;
/*The entire computation is performed in base SAS by the source code macro("BRC_nomalaria_2apps_source_code_wra_may2017.sas");*/

*/

/*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***********************************;
*****************************************************************************

*****************************************************************************
***STEP 3 : SUPPLY INPUT CODE AFTER EACH EQUAL SIGN(=) IN THE MACRO CALL BELOW;*
*****************************************************************************

option nocmterr;
%include "H:\BRINDA2\brc_macros\BRC_nomalaria_2apps_source_code_wra_may2017.sas";
run;
%BrindaRC_noM(LABEL ="BRINDA Inflammation Correction, BRC", RES_DATA LIB =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 lncrp brcref_CRP lnagp brcref_AGP popbeta_sfAGP popbeta_sfCRP lnsf lnsfadjwra sfadjwra;
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_wra" *****;
***************************************************************************************;

proc sort data=researchdata; by ID;
proc sort data=brc_adjferritindata_wra; by id; run;

data RESEARDATA_W_BRC_INDICATORS;
merge researchdata brc_adjferritindata wra(keep=Ori_id sfadjwra);
/*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 sfadjwraEQ . THEN SF_C1_brc= ;
ELSE if sfadjwraNE . & sfadjwra<15 THEN SF_C1_brc=1;
else If sfadjwraGE 15 then SF_C1_brc=0;

label SF_C1_brc = 'brinda inflamm reg_corrected Serum ferritin(SF) cut-off 1: WOMEN 15-49y: <15 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***;

%BrindaRC_noM(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)******************************************************************************;
******************************************************************************;