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*****
*****;
*****Title: BRINDA Inflammation Correction for nutritional biomarkers for
Preschool children Ages 6-59months*****;
**Objective: To inflammation correct Using 2 acute phase proteins (AGP, alpha-
1-acid glycoprotein CRP, C-Reactive Protein)*
Version 0: brc_SAS_marco(O.Yaw Addo,CDC/DNPAO - May 2017), created/last
modified May 31,2017 *****;
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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)*****;
*****
*****;

%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_in;
  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 estimates;
  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 = -2.26 ; *ln CRP decile for children
;
  %let lnagp_refdecile = -0.52 ; * ln AGP decile for children
;

/*Natural log (ln) CRP and AGP deciles for children (BRINDA external ref
values must remain unchanged across analyses); */
/*Users desiring to use non-brinda ref deciles can change the 2 refs above*/

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*****;
*** Run regression and capture internal pop beta coefficients for CRP and
AGP;
*****/;
ods output ParameterEstimates = betas_crpagp_psc;
proc reg data=_data_in;
model ln&biomarker = lnocrp lnagp ;
run; quit;

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

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

data &outdata;
set _data_in;
if &crp ne . and &agp ne . then
ln&biomarker.adjpsc = ln&biomarker - &lnocrpbeta*max(lnocrp-
&lnocrp_refdecile,0)
- &lnagpbeta*max(lnagp-
&lnagp_refdecile,0);
&biomarker.adjpsc = exp(ln&biomarker.adjpsc);
popbeta_&biomarker.&agp=&lnagpbeta;
popbeta_&biomarker.&crp=&lnocrpbeta;

brcref_&crp=&lnocrp_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-psc'
brcref_&agp='Brinda inflamm
ref decile agp-psc';
run;
%mend BrindaRC_noM;

/*Output data with biomarker in its name*/;

```

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

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

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options nofmterr nocenter formchar="|----|+|---+=|-\<>";

```

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libname m "H:\BRINDA2\brc_macros";

```

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

```

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*****;
*****;
*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*****;
*****;

```

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/**NOTES: BRC approach is effectively applied to the sub-population
considered inflamed 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 adustedNB = exp(ln(biomarker) - fl1(lnCRPobs - lnCRPref) -
fl2(logAGPobs - lnAGPref) )*/;*/

```

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/*The entire computation is performed in base SAS by the source code
macro("BRC_nomalaria_2apps_source_code_may2017.sas");*/

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*****;
/*****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 adustedNB = exp(ln(biomarker) - fl1(lnCRPobs - lnCRPref) -
fl2(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*****;
*****
*****;

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

```

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*****;
/*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 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 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_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 prevalances*/;
*****
*****;

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 INITIALIZING 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_DATA LIB =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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