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*****
*****;
****Title: BRINDA Inflammation Correction for nutritional biomarkers for
Preschool children Ages 6-59months*****;
**Objective: To inflammation correct Using One acute phase proteins (AGP,
alpha-1-acid glycoprotein)*
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 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;

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    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 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*****;
*****;
```

```
/*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) )*/;*/
```

```
/*The entire computation is performed in base SAS by the source code
macro("BRC_nomalaria_agponly_source_code_psc_may2017.sas");*/
```

```
*****;
/*****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_agponly_source_code_psc_may2017.sas";run
;
%BRC_agponly_nomal(LABEL ="BRINDA Inflammation Correction, BRC",
RES_DATA LIB =H:\BRINDA2\brc_macros,
DATA_IN = researchdataName,
id =,
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 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 BIOMARKER*/
/*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***;

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