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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(C-
Reactive Protein, CRP)*
Version 0: brc_SAS_marco(O.Yaw Addo,CDC/DNPAO - May 2017), created/last
modified May 31,2017 *****;
*****
*****;

*****
*****;
**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_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_;

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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 ;*/
data &outdata;
set _data_in_crp;
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) biomaker'
ln&biomarker.adj='brinda reg_corrected biomaker-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*/;

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

TITLE 'BRINDA REGRESSION INFLAMMATION CORRECTION(BRC) MACROS USAGE CODE IN
BASE SAS';
options nofmterr 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 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_crponly_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) )*/;

*****;

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/*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_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;

*****
*****;

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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 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**;
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/*/*PRIOR TO MERGING THE DATASETS, MULTIPLE BRC CALCULATIONS CAN BE
PERFORMED*/*/
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/*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_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*****;
*****;
*****;
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