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*****;
* Project      : ZRHM-REXA-07-JP
*
* Program name  : T150204250201_ZRHM-REXA-07_V1.sas
*
* Author       : L. Yan
*
* Date created  : 05/20/2015
*
* Purpose      : Table T150204250201.
*
* Revision History :
*
* Date      Author      Ref      Revision (Date in YYYYMMDD format)
*
*****;

%let prgname=T150204250201_ZRHM_REXA_07_JP_V1;
options mprint;

options sasautos=("W:\pmp07\macros" sasautos) notes;
%init(delivery=9);

%titlecsv(prgname=&prgname., version=5);
%put &title1;
%put &title2;
%put &APPENDIX;
%put &endpoint;
%put &outname.;
%put &repversion.;

options missing="";

%macro cal_sumary_pvalue(wher=, outnum=, method=, used=, var=, in=, pflg=, paramcd=, avisit=);
title2 h=10pt j=1 "&used";

proc sort data=&in. out=anadt_&outnum.;
by usubjid;
where &wher. ;
run;

proc sort data=anadt_&outnum.;
by trtcd;
run;

%if &method = 1 %then %do;
title3 h=10pt j=1 "Paramcd: &paramcd, &avisit. Model: GLM, Method: Log";

proc means data = anadt_&outnum. noprint;
by trtcd;
var &var.;
output out=xlab_&outnum. n=n mean=mean median=med std=sd min=min max=max q1=q1 q3=q3 lclm=lclm uclm=uclm;
run;
%end;

%if &method = 2 %then %do;
title3 h=10pt j=1 "Paramcd: &paramcd, &avisit. Model: GLM, Method: Normal";

proc means data = anadt_&outnum. noprint;
by trtcd;
var aval;
output out=xlab_&outnum. n=n mean=mean median=med std=sd min=min max=max q1=q1 q3=q3 lclm=lclm uclm=uclm;
run;
%end;

data xlab_&outnum.;
set xlab_&outnum.;
n1 = trim(left(compress(put(n, 8.))));
if sd > . then mean1 = (trim(left(compress(put(mean, 8.1))))||' ( '||trim(left(compress(put(ceil(sd*100)/100, 8.2))))||')');
else mean1 = (trim(left(compress(put(mean, 8.1))))||' (NA)');
ci1=trim(left(compress(put(floor(lclm*100)/100, 8.2))))||' , '||trim(left(compress(put(ceil(uclm*100)/100, 8.2))));
median1 = trim(left(compress(put(med, 8.1))));
q1q3 = trim(left(compress(put(q1, 8.2))))||' , '||trim(left(compress(put(q3, 8.2))));
min1 = trim(left(compress(put(min, 8.))))||' , '||trim(left(compress(put(max, 8.0))));

run;

/*
proc mixed data=anadt_&outnum.;

Class trtcd sex UCPDGR1;

Model logaval = logbase sex UCPDGR1 trtcd / outp=pred;

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lsmeans trtcd / pdiff =control('mCC') alpha=0.05 cl;

ods output lsmeans=lsmeans_&outnum. (keep=trtcd lower upper estimate); *each arm;

ods output diffs=LSMeanDiffCL&outnum. (keep=trtcd lower upper probt estimate); * lsmean and C.I. for ratios;

ods output covparms=ROOTMSE&outnum.(rename=(estimate=mse)); *MSE;

run;
*/

proc glm data=anadt_&outnum.;
class trtp sex UCPDGR1;
%if &method = 1 %then %do;
model logaval = logbase sex UCPDGR1 trtp;
%end;
%if &method = 2 %then %do;
model aval = base sex UCPDGR1 trtp;
%end;
lsmeans trtp / pdiff =control('mCC') alpha=0.05 cl adjust=t;
lsmeans trtp / pdiff =control('SA') alpha=0.05 cl adjust=t;
ods output LSMeans=pval&outnum. (keep=ProbtDiff trtp where=(TRTP in ("THSm2.2"))); *p-value;
ods output LSMeanCL=lsmeans_&outnum. (keep=trtp lowercl uppercl lsmean); *lsmean, C.I. for each arm;
ods output LSMeanDiffCL=LSMeanDiffCL&outnum. (keep=trtp _trtp lowercl uppercl difference where=(TRTP in ("THSm2.2"))); *
lsmean and C.I. for ratios;
ods output FitStatistics=ROOTMSE&outnum. (keep=rootmse); *RootMSE;
run;quit;

ods output close;

data lsmeans_&outnum.;
set lsmeans_&outnum.;
if TRTP="THSm2.2" then trtcd=1;
else if TRTP="mCC" then trtcd=2;
else if TRTP="SA" then trtcd=3;

%if &method = 1 %then %do;
Estimate1 = exp(lsmean); /* Ratio of geometric mean */
LowerCL = exp(lowercl); /* 95% CI lower bound */
UpperCL = exp(uppercl); /* 95% CI upper bound */
%end;
%if &method = 2 %then %do;
Estimate1 = lsmean; /* Ratio of geometric mean */
LowerCL = lowercl; /* 95% CI lower bound */
UpperCL = uppercl; /* 95% CI upper bound */
%end;
run;

data ROOTMSE&outnum.;
set ROOTMSE&outnum.;
CVperc=100*sqrt(exp(rootmse**2)-1);
run;

proc sort data=lsmeans_&outnum. nodupkey;
by trtcd;
run;

data lsmeans_&outnum.;
length geomean geoci $100;
set lsmeans_&outnum.;
geomean=strip(put(ESTIMATE1, 8.2));
geoci=strip(put(floor(LowerCL*100)/100, 8.2))||", "||strip(put(ceil(UpperCL*100)/100, 8.2));

keep trtcd geomean geoci;
run;

proc sort data=LSMeanDiffCL&outnum. nodup;
by TRTP _TRTP;
run;

data LSMeanDiffCL&outnum.;
set LSMeanDiffCL&outnum.;
myord=1;
run;

data ROOTMSE&outnum.;
set ROOTMSE&outnum.;
myord=1;
run;

data LSMeanDiffCL&outnum.;
merge LSMeanDiffCL&outnum. ROOTMSE&outnum.;
by myord;
run;

data LSMeanDiffCL&outnum.;

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length geomean geoci $100;
set LSMeanDiffCL&outnum.;
if _TRTP eq "mCC" then trtcd=4;
if _TRTP eq "SA" then trtcd=5;
%if &method = 1 %then %do;

    difference = 100*exp(difference); /* Ratio of geometric mean */
    lowercl = 100*exp(lowercl); /* 95% CI lower bound */
    uppercl = 100*exp(uppercl); /* 95% CI upper bound */
%end;

%if &method = 2 %then %do;

    difference =difference; /* Ratio of geometric mean */
    lowercl = lowercl; /* 95% CI lower bound */
    uppercl = uppercl; /* 95% CI upper bound */
%end;

%if &method = 1 %then %do;
geomean=strip(put(round(difference, 0.01), 8.2))||" ("||strip(put(ceil(CVperc*100)/100, 8.2)) ||)";
%end;
%if &method = 2 %then %do;
geomean=strip(put(round(difference, 0.01), 8.2))*||" ("||strip(put(CVperc, 8.1)) ||)"/;
%end;

geoci=strip(put(floor(lowercl*100)/100, 8.2))||", "||strip(put(ceil(uppercl*100)/100, 8.2));

keep trtcd geomean geoci difference;
run;

data pval&outnum.;
set pval&outnum.;
if _n_=1;
trtcd=4;
keep trtcd ProbtDiff;
format ProbtDiff PVALUE6.3;
run;

proc sort data=LSMeanDiffCL&outnum.;
by trtcd;
run;

data LSMeanDiffCL&outnum.;
merge LSMeanDiffCL&outnum. pval&outnum.;
by trtcd;
run;

data LSMeanDiffCL&outnum.;
set LSMeanDiffCL&outnum.;
%if &method = 1 %then %do;
    if (difference < 100) then ProbtDiff=ProbtDiff/2;
    else ProbtDiff=1-ProbtDiff/2;
%end;
%if &method = 2 %then %do;
    if (difference < 0) then ProbtDiff=ProbtDiff/2;
    else ProbtDiff=1-ProbtDiff/2;
%end;
run;

data mrep_&outnum.;
set lsmeans_&outnum. LSMeanDiffCL&outnum.;
run;

proc sort data=mrep_&outnum.;
by trtcd;
run;

proc sort data=xlab_&outnum.;
by trtcd;
run;

data xlab_&outnum.;
merge xlab_&outnum.(in=a) mrep_&outnum.;
by trtcd;
run;

data xlab_&outnum.;
set xlab_&outnum.;
if geoci ne "";
run;

proc transpose data = xlab_&outnum. out=xlab_1_&outnum.;
id trtcd;
var n1 geomean geoci ProbtDiff;
run;

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data rep_&outnum.;
length _name_ _1 _2 _3 ord1 $100;
set xlab_1 &outnum.;
ord1="&outnum";
ordnum=input(ord1, best.);
if upcase(_name_)="N1" then do; _name_="n"; sord=0; end;
%if &method = 1 %then %do;
if upcase(_name_)="GEOMEAN" then do; _name_="Geometric LS Mean (CV%)"; sord=1; end;
if upcase(_name_)="GEOCI" then do; _name_="95% CI of Geometric Mean"; sord=2; end;
if upcase(_name_)="CI1" then do; _name_="95% CI of Mean"; sord=4; end;
%end;
%if &method = 2 %then %do;
if upcase(_name_)="GEOMEAN" then do; _name_="LS Mean"; sord=1; end;
if upcase(_name_)="GEOCI" then do; _name_="95% CI"; sord=2; end;
if upcase(_name_)="CI1" then do; _name_="95% CI"; sord=4; end;
%end;

if upcase(_name_)="MEAN1" then do; _name_="Mean (SD)"; sord=3; end;
if upcase(_name_)="MEDIAN1" then do; _name_="Median"; sord=5; end;
if upcase(_name_)="Q1Q3" then do; _name_="Q25, Q75"; sord=6; end;
if upcase(_name_)="MIN1" then do; _name_="Min, Max"; sord=7; end;
if upcase(_name_)="PROBTDIFF" then do; _name_="p-value (one-sided)"; sord=9; end;
run;

data rep;
set rep rep_&outnum.;
run;

%mend;

%macro mainloop(where1=, outn=, where=);

proc sort data=adam.adsl out=trt;
by usubjid;
where FASFL="Y";
run;

data trt;
set trt;
if TRT01P="THSm2.2" then trtcd=1;
else if TRT01P="mCC" then trtcd=2;
else if TRT01P="SA" then trtcd=3;
run;

/*
"ADAM.ADBX; PARAMCD = UTXB2CRE (Day 5, Day 30, Day 60, Day 90).
Use PPROTxxFL with xx in 1,2,3,4 for data at APUPER=1,2,3,4 respectively." ANL02FL="Y" and ANL03FL="Y"

*/

data indata1;
length group $4;
set adam.adbx;
group="A";
paramn=paramn+100;
used="The where clause used on the dataset adam.adbx: FASFL=Y and ANL02FL=Y and ANL03FL = Y";

if PARAMCD in ("UTXB2CRE") and avisitn in (105, 130, 160, 190, 191) and ANL02FL="Y" and ANL03FL eq "Y";
drop DTYPE ATPT;
run;

/*
Blood pressure, HbA1c, LDL, HDL, TG, TC, WBC, BASO, EOS, MONO, NEUT, LYM, ,body weight and waist circumference will be a
nalyzed in the regular scale.
8-epi-PGF2a, 11 DTX-B2, sICAM will be analyzed in the logarithmic scale.
Other risk markers will be logarithmically transformed prior to analysis if there is evidence of non-normality by means
of Shapiro-Wilks test using baseline
data from FAS population - if p-val <= 0.05 then analyze in log scale; otherwise, use regular scale.
*/

data anldata1;
set indata1;
if paramcd in ("SYSBP", "DIABP", "HBA1C", "LDL", "HDL", "TRIG", "CHOL", "WBC", "NEUT", "EOS", "BASO", "LYM", "MONO", "WEI
GHT", "WSTCIR") then method=2;
else if paramcd in ("UTXB2CRE", "UPGF2CRE" "ICAM1") then method=1;
else method=3;

if aval>0 then logaval=log(aval);
if base>0 then logbase=log(base);
run;

proc sort data=anldata1 out=fmt(keep=paramn param) nodupkey;
by paramn param;
run;

proc sort data=anldata1 out=check(keep=method paramcd) nodupkey;

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by method paramcd;
run;

data anldata1;
set anldata1;
if &where.;
run;

proc sort data=anldata1 out=check(keep=paramn avisitn avisit method used param paramcd) nodupkey;
by paramn avisitn avisit method;
where &where1.;
run;

data trt_1;
set trt;
run;

data anldata1;
set anldata1;
if TRTP="THSm2.2" then trtcd=1;
else if TRTP="mCC" then trtcd=2;
else if TRTP="SA" then trtcd=3;
run;

data check;
set check;
ord=_n_;
run;

%*cal_summary_pvalue(where=1, outnum=1, var=aval, in=anldata1, pflg=1);

data rep;
run;

data _null_;
set check;
call execute ('%cal_summary_pvalue(where=%str(avisitn=||avisitn||' and paramn=||paramn||' ), outnum=||ord||', met
hod=||method||', used=||used||', var=logaval, in=anldata1, paramcd=||paramcd||', avisit=||avisit||');');
run;

data frep;
set rep;
ord=ORDNUM;
run;

data frep;
merge frep(in=a) check;
by ord;
if a;
if avisitn>.;
run;

proc sort data=trt_1 nodupkey;
by trtcd usubjid;
run;

proc freq data = trt_1 noprint;
tables trtcd/ out= denom;
run;

data _null_;
set denom end=eof;

retain total 0;

total = total+count;

if trtcd= 1 then do;
call symput('trt1', trim(left(put(count,8)))));
end;
if trtcd= 2 then do;
call symput('trt2', trim(left(put(count,8)))));
end;
if trtcd= 3 then do;
call symput('trt3', trim(left(put(count,8)))));
end;
run;

%put trt1=&trt1 trt2=&trt2 trt3=&trt3;

%macro cal_part_main();

data frep;
set frep;

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%do i = 1 %to 100;
  if (&i-1)*4<ordnum<=&i*4 then pagen=&i;
%end;

run;

%mend;

%cal_part_main();
data frep&outn.;
set frep;
space=" ";
if _name_="p-value (one-sided)" then delete;
run;

%mend;

%trtrtf(g(pgmname=&loutname., pgmid=1, new=0, style=, bookmark=%lowcase(&outname.)));

title1 bold j=1 "&title1 &title2";
*footnote1 j=1 h=9pt "Study ID:ZRHM-REXA-07-JP          Program: &fprgname..sas          Status: &repversion./&fdate.";

%mainloop(wherel=%str(method=1), outn=1, where=%str((avisitn<=105 and FASFL="Y") or
(avisitn=130 and FASFL="Y") or (avisitn=160 and FASFL="Y") or (avisitn in (190, 191) and FASFL="Y") ));

ods listing;
ods rtf close;

%*mainloop(flg=FASFL, outn=2, where=%str(avisitn=130 and APUPER=2));
%*mainloop(flg=FASFL, outn=3, where=%str(avisitn=160 and APUPER=3));
%*mainloop(flg=FASFL, outn=4, where=%str(avisitn in (190, 191) and APUPER=4));

data odata.&prgname.;
set frep1 (in=a)/*frep3 (in=c) frep4 (in=d)*/;
*if a then group="FASFL";
*if b then group="FASFL";
*if c then group="FASFL";
*if d then group="FASFL";
run;

/*
proc sort data=anldata1 out=fmt(keep=paramn param) nodupkey;
by paramn param;
run;
*/

data fmt;
set fmt;
fmtname="grp";
start=paramn;
label="Parameter: "||strip(param);
run;

proc format cntlin=fmt;
run;

%global totalpage1;

data _null_;
  set frep1 end=eof;

  if eof then do;
    call symput('totalpage1', trim(left(put(pagen,8)))));
  end;

run;

%put totalpage1=&totalpage1;

%*title(prgname1=&prgname.);

%trtrtf(g(pgmname=&outname., pgmid=1, new=0, style=, bookmark=%lowcase(&outname.)));

/*****
title1 j=1 h=9pt "Study ID: ZRHM-REXA-07-JP" j=r "Page ^{thispage} of ^{lastpage}";
title2 " ";
title3 bold j=1 "&title1 &title2";

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title5 ^R/RTF'\brdrb\brdrs ' ';

footnote1 ^R/RTF'\brdrb\brdrs ' ';
footnote2 j=1 h=9pt "Note: mCC = Menthol conventional cigarettes; SA = Smoking abstinence; THSm2.2 = Tobacco Heating Sys
tem 2.2 Menthol .";
footnote3 j=1 h=9pt "Note: Adjusted geometric least squares (LS) means and confidence intervals (CIs) from an ANCOVA mod
el conducted with baseline value, study arm, ";
footnote4 j=1 h=9pt "sex and mCC consumption reported at screening as fixed effect factors. ";
footnote5 j=1 h=9pt " ";
footnote6 j=1 h=9pt "Program: &fprgname." j=c "Status: Draft/&fdate." j=r "&APPENDIX.";
/*****/

%macro reppart;

  %do i = 1 %to &totalpage1;

proc report data=frep1 headskip headline spacing=4 nowd split='-' style=[outputwidth=100%] style(header column)=[protec
tspecialchars=off];
  column pagen paramn avisitn avisit sord _name _1 space _2 space _3 space _4 space _5;
  where pagen=&i.;
  define pagen /order order=internal noprint;
  define paramn /order order=internal noprint;
  define avisitn /order order=internal noprint;
  define avisit /order "Time point" flow style(column)=[cellwidth=10% just=l];
  define sord /order order=internal noprint;

  define _name_ /display "Statistic" flow style(column)=[cellwidth=15% just=l];
  define _1 /display "THSm2.2" flow style(column)=[cellwidth=10% just=c];
  define space /display " " flow style(column)=[cellwidth=0.5% just=c];

  define _2 /display "mCC" flow style(column)=[cellwidth=10% just=c];
  define space /display " " flow style(column)=[cellwidth=0.5% just=c];

  define _3 /display "SA" flow style(column)=[cellwidth=10% just=c];
  define space /display " " flow style(column)=[cellwidth=0.5% just=c];

  define _4 /display "THSm2.2 : mCC Ratio (%)" flow style(column)=[cellwidth=10% just=c];
  define space /display " " flow style(column)=[cellwidth=0.5% just=c];

  define _5 /display "THSm2.2 : SA Ratio (%)" flow style(column)=[cellwidth=10% just=c];

COMPUTE after avisitn ;
LINE @1 "";
ENDCOMP;

break after pagen/page;

compute before pagen;
line @1 "";
endcomp;

compute before _page_ /style=[fontweight=bold fontsize=3.75];
line @1 "&title1 &title2";
line @1 " ";
LINE @1 paramn grp.;
line @1 ^R/RTF'\brdrb\brdrs\brdrw30\brsp20\b ' ';
endcomp;

compute after _page_ /style=[fontsize=1.75];
line @1 "Note: mCC = Menthol conventional cigarettes; SA = Smoking abstinence; THSm2.2 = Tobacco Heating System 2.2 Ment
hol.";
line @1 "Note: Adjusted geometric least squares (LS) means and confidence intervals (CIs) from an ANCOVA model conducted
with baseline value,";
line @1 "study arm, sex and mCC consumption reported at screening as fixed effect factors. ";
line @1 "No concomitant medication impacting 11-DTX-B2 were recorded.";
line @1 " ";
line @1 "&APPENDIX.";
line @1 "Study ID:ZRHM-REXA-07-JP Program: &fprgname..sas Status: &repversion./&fdate. Page: &i.
of &totalpage1";
endcomp;

run;
%end;

%mend;
%reppart;

ods listing;
ods rtf close;

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