**Supplemental Digital Content 9: SAS Implementation of Error Rate Formulas for Clinical MBI**

/\*Kristin Sainani, March 18, 2018\*/

/\*Code for calculating Type I and Type II error for clinical MBI, following the equations given in the paper\*/

%LET n=50; \*sample size per group;

%LET ES=0; \*true effect size;

%LET var=.364; \*true variance—the specific value of 0.364 is from a pre-post design with r=.818. Std dev at baseline=1.0. Variance in change scores=1+1-2\*.818=.364;

%LET deltab=0.2; \*threshold for benefit;

%LET deltah=0.2; \*threshold for harm;

%LET maxrisk=.005; \*maximum risk of harm;

%LET minben=.25; \*minimum risk of benefit;

**data** \_null\_;

df=2\*&n-**2**;

err=sqrt(**2**)\*sqrt(&var)/sqrt(&n); \*standard error;

th=Tinv((**1**-&maxrisk),df); \*T for harm, e.g. 2.68 for 99% CI;

tb=Tinv(**1**-&minben,df); \*T for benefit, e.g. .68 for 50% CI;

hterm=-&deltah+th\*err;

bterm=&deltab-tb\*err;

maxterm=((df)\*&n\*(&deltab+&deltah)\*\***2**)/(**2**\*&var\*(th+tb)\*\***2**);

pharmmax=**1**-probchi(maxterm,(df)); \*probability that the harm constraint is bigger;

pbenmax=**1**-pharmmax; \*probability that the benefit constraint is bigger;

Tharm=(hterm-&ES)/err;

Tben=(bterm-&ES)/err;

if &ES<&deltab then do;

TypeI=pharmmax\*(**1**-probT(Tharm,df))+pbenmax\*(**1**-ProbT(Tben,df));

typeII=**.**;

end;

if &ES>=&deltab then do;

typeII=pharmmax\*probT(Tharm, df)+pbenmax\*ProbT(Tben,df);

typeI=**.**;

end;

putlog TypeI TypeII;

**run**;

/\*Type I and II error curves by sample size, for comparison with simulations\*/

%LET ES=0.2; \*true effect size;

%LET var=.364; \*true variance;

%LET deltab=0.2; \*threshold for benefit;

%LET deltah=0.2; \*threshold for harm;

%LET maxrisk=.005; \*maximum risk of harm;

%LET minben=.25; \*minimum risk of benefit;

**data** errors;

do n=**10** to **150** by **10**;

df=2\*n-**2**;

err=sqrt(**2**)\*sqrt(&var)/sqrt(n); \*standard error;

th=Tinv((**1**-&maxrisk),df); \*T for harm, e.g. 2.68 for 99% CI;

tb=Tinv(**1**-&minben,df); \*T for benefit, e.g. .68 for 50% CI;

hterm=-&deltah+th\*err;

bterm=&deltab-tb\*err;

maxterm=((df)\*n\*(&deltab+&deltah)\*\***2**)/(**2**\*&var\*(th+tb)\*\***2**);

pharmmax=**1**-probchi(maxterm,(df));

pbenmax=**1**-pharmmax;

Tharm=(hterm-&ES)/err;

Tben=(bterm-&ES)/err;

TypeI=pharmmax\*(**1**-probT(Tharm,df))+pbenmax\*(**1**-ProbT(Tben,df));

typeII=pharmmax\*probT(Tharm, df)+pbenmax\*ProbT(Tben,df);

output;

end;

**run**;

/\*Graph Type I or II error against sample size\*/

goptions reset = all;

goptions htext=**3**;

axis1 label=(angle=**90**);

axis2 order=**10** to **150** by **20**;

**proc** **gplot** data=errors;

plot typeI\*n/vaxis=axis1 haxis=axis2;

symbol1 v=dot c=red i=join h=**2** w=**2**;

label N="Sample size per group";

label typeI="Type I error (%)";

**run**;

**proc** **gplot** data=errors;

plot typeII\*n/vaxis=axis1 haxis=axis2;

symbol1 v=dot c=red i=join h=**2** w=**2**;

label N="Sample size per group";

label typeII="Type II error (%)";

**run**;