

```

00001 /*-----*/
00002 /* validate correlations for steve moore for categorical adjustments */
00003 /*-----*/
00004 /*PROC IMPORT OUT= WORK.Subjdata */
00005 /*          DATAFILE= "C:\Users\bsc-default\Documents\Comets\Testing fil*/
00006 /*es\cometsInput_March_2018.xlsx" */
00007 /*          DBMS=EXCEL REPLACE;*/
00008 /*          RANGE="SubjectData$"; */
00009 /*          GETNAMES=YES;*/
00010 /*          MIXED=NO;*/
00011 /*          SCANTEXT=YES;*/
00012 /*          USEDATE=YES;*/
00013 /*          SCANTIME=YES;*/
00014 /*RUN;*/
00015 /*PROC IMPORT OUT= WORK.Subjmet */
00016 /*          DATAFILE= "C:\Users\bsc-default\Documents\Comets\Testing fil*/
00017 /*es\cometsInput_March_2018.xlsx" */
00018 /*          DBMS=EXCEL REPLACE;*/
00019 /*          RANGE="SubjectMetabolites$"; */
00020 /*          GETNAMES=YES;*/
00021 /*          MIXED=NO;*/
00022 /*          SCANTEXT=YES;*/
00023 /*          USEDATE=YES;*/
00024 /*          SCANTIME=YES;*/
00025 /*RUN;*/
00026
00027
00028 /*data marchtest;*/
00029 /* merge subjdata subjmet;*/
00030 /* by sample_id;*/
00031 /* run;*/
00032 /**/

```

```

00033 /**/
00034 libname comettst "...\\CometsTests";
00035 /**/
00036 /*data comettst.marchtest;*/
00037 /* set marchtest;*/
00038 /* run;*/
00039
00040 ods pdf file="sasdummytest.pdf";
00041
00042 data marchtest;
00043 set comettst.marchtest;
00044 keep age bmi_grp race_grp race: _1_2_3_BENZENETRIOL_SULFATE_2 _1_2_DIPALMITOYLGLYCEROL
00045 if race_grp ne . then racegrp1=race_grp=1;
00046 if race_grp ne . then racegrp2=race_grp=2;
00047 if race_grp ne . then racegrp0=race_grp=0;
00048 run;
00049
00050 title "March 2018 cell sizes";
00051 proc freq data=marchtest;
00052 table bmi_grp*race_grp / nocol norow nopercnt;
00053 run;
00054
00055 proc sort; by bmi_grp;
00056
00057 * with _1_2_3_BENZENETRIOL_SULFATE_2 _1_2_DIPALMITOYLGLYCEROL _1_2_PROPANEDIOL ;
00058
00059
00060
00061 title"march 2018 unadjusted";
00062 proc corr data=marchtest spearman nosimple;
00063 by bmi_grp;
00064 where bmi_grp=3;

```

```
00065     var age;
00066     with _1_2_PROPANEDIOL    ;
00067 run;
00068
00069 title" march2018 race adjusted with dummy group 1 and 2";
00070 proc corr data=marchtest spearman nosimple vardef=n;
00071 by bmi_grp;
00072 where bmi_grp=3;
00073     var age;
00074     partial racegrp1 racegrp2;
00075     with _1_2_PROPANEDIOL    ;
00076 run;
00077
00078 ods trace off;
00079 title" march2018 race adjusted dummy group 0 and 1";
00080 proc corr data=marchtest spearman nosimple;
00081 by bmi_grp;
00082 where bmi_grp=3;
00083     var age;
00084     partial racegrp0 racegrp1;
00085     with _1_2_PROPANEDIOL    ;
00086     ods output PartialSpearmanCorr=outsp;
00087 run;
00088 proc print data=outsp;
00089 format age page 12.8;
00090 run;
00091
00092
00093
00094 title"GLM method for residual correlation";
00095 proc glm data=marchtest;
00096 where bmi_grp=3;
```

```
00097 by bmi_grp;
00098 class race_grp;
00099 model _1_2_PROPANEDIOL = race_grp ;
00100 output out=metr1 r=resprop;
00101 run;
00102
00103 proc glm data=metr1;
00104 where bmi_grp=3;
00105 by bmi_grp;
00106 class race_grp;
00107 model age = race_grp ;
00108 output out=metr2 r=resage;
00109 run;
00110
00111 title"Reg method for residual correlation";
00112 proc reg data=metr2;
00113 where bmi_grp=3;
00114 by bmi_grp;
00115 model age = racegrp1 racegrp0 ;
00116 output out=metr3 r=resager;
00117 run;
00118
00119 proc reg data=metr3;
00120 where bmi_grp=3;
00121 by bmi_grp;
00122 model _1_2_PROPANEDIOL = racegrp1 racegrp2 ;
00123 output out=metr4 r=respropr;
00124 run;
00125
00126
00127 title"correlation via glm";
00128 proc corr data=metr4 spearman nosimple; 4
```

```
00129 var resage;  
00130 with resprop;  
00131 run;  
00132  
00133  
00134 title"correlation via reg";  
00135 proc corr data=metr4 spearman nosimple;  
00136 var resager;  
00137 with respropr;  
00138 run;  
00139 ods pdf close;
```