

Appendix:

Joint modeling of multivariate hearing thresholds measured longitudinally at multiple frequencies

Sample SAS code for implementing the joint modeling approaches discussed in the paper. After arranging the data as in WebTable 2 of the paper, then the following SAS codes can be used to implement the variations of mGLMM.

Note: fr_type2 is some grouped form of fr_type based on the variability profiles of HL outcomes in each frequency.

```
%macro mGLMM1(meth, distn, randm1, randm2);
proc glimmix data=fulldata;
class fr_type fr_type2;
model hl=fr_type fr_type*timec fr_type*entryage fr_type*male
fr_type*male*entryage/dist=&distn s noint DDFM=RESIDUAL CL ;
random &randm1 &randm2 / subject=subject type=chol g gcorr;
random lear/ subject=subject; *accounts for nesting by ear;
random _residual_ / subject=subject type=VC; *accounts for R-side;
%mend mGLMM1;
%macro mGLMM2(meth, distn, randm1, randm2);
proc glimmix data=fulldata ;
class fr_type fr_type2;
model hl=fr_type fr_type*timec fr_type*entryage fr_type*male
fr_type*male*entryage/dist=&distn s noint DDFM=RESIDUAL CL ;
random &randm1 &randm2/ subject=subject type=chol group=fr_type2 g gcorr;
random lear/ subject=subject group=fr_type2;
random _residual_ / subject=subject type=VC; *no group statement here;
%mend mGLMM2;
%macro mGLMM3(meth, distn, randm1, randm2);
proc glimmix data=fulldata ;
class fr_type fr_type2;
model hl=fr_type fr_type*timec fr_type*entryage fr_type*male
fr_type*male*entryage /dist=&distn s noint DDFM=RESIDUAL CL ;
random &randm1 &randm2/ subject=subject type=chol group=fr_type2 g gcorr;
random lear/ subject=subject group=fr_type2; run;
random _residual_ / subject=subject type=VC group=fr_type2;
%mend mGLMM3;
*****
*ANALYSIS
*****;
title "SHRI";
%mGLMM1(SHRI,normal, int, ); * SHRI;
title "SHRIS";
%mGLMM1(SHRIS, normal, int, timec); *SHRIS;
title "SPRI common R-side variance";
%mGLMM2(SPRI, normal, int, ); * SPRI;
title "SPRIS common R-side variance";
%mGLMM2(SPRIS, normal, int, timec); *SPRIS;
title "SPRI heterogeneous R-side variance- replacing fr_type2 by fr_type
leads to analysis equivalent to separate analysis";
%mGLMM3(HSPRI, normal, int, ); * HSPRI;
title "SPRIS heterogeneous R-side variance - replacing fr_type2 by fr_type
leads to analysis equivalent to separate analysis";
%mGLMM3(HSPRIS, normal, int, timec); *HSPRIS;
```