

Appendix R

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Appendix R-1

SAS Code for ANOVA and Contrasts

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```
options nodate nonumber;
libname lib "S:\NIEHS\EXP Studies\BasicResearch\Haseman\Cytotoxicity
Validation\Post Phase III Analysis and Data\data sets";

proc sort data=lib.anovadata; by chemical cell lab;

ods trace on;
ods listing close;
ods output OverallANOVA=temp;
ods output Contrasts=temp1;
proc glm data=lib.anovadata;
class lab;
by chemical cell;
model log_ic50=lab;
contrast 'Comparing IIVS to FRAME and ECBC'
lab -.5 -.5 1;
contrast 'Comparing ECBC to FRAME and IIVS'
lab 1 -.5 -.5;
contrast 'Comparing FRAME to ECBC and IIVS'
lab -.5 1 -.5;

run;ods listing;
*proc print data=temp1;run;

data lib.contrast_results; set temp1;
keep chemical cell Source ProbF;
run;

*proc print data=lib.contrast_results;run;

data lib.anova_results; set temp;
if Source="Error" then delete;
if Source="Corrected Total" then delete;
keep chemical cell ProbF;
run;

proc sort data=lib.anova_results; by chemical cell;

/*proc print data=lib.anova_results;
var chemical cell ProbF;
run;*/

data temp;
set lib.anova_results;
keep chemical cell ProbF;
run;
proc export data=temp
  outfile='S:\NIEHS\EXP Studies\BasicResearch\Haseman\Cytotoxicity
Validation\Post Phase III Analysis and Data\data sets\Anova Results.txt'
  dbms=TAB;

run;
```

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Appendix R-2

SAS Code for Regression Comparisons

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```
options nodate nonumber;
libname lib "S:\NIEHS\EXP Studies\BasicResearch\Haseman\Cytotoxicity
Validation\Post Phase III Analysis and Data\data sets";

/*DATA SORTED AND SUMMARIZED WITH ONE POINT PER CHEMICAL PER CELL TYPE*/
proc sort data=lib.regdata2;
  by cell;
proc reg data=lib.regdata2;
  by cell;
  model log_rc_ld50 = log_ic50 /clb;
  plot log_rc_ld50 * log_ic50 /conf pred;
  test_intercept: test intercept=0.625; /*RC Intercept*/

  test_slope: test log_ic50=0.435; /*RC Slope*/
  test_joint: test intercept=0.625, log_ic50=0.435;
  title "RC LD50 Data: Regression by Cell Type";
run;

proc reg data=lib.regdata2;
  by cell;
  model log_ref_ld50 = log_ic50 /clb;
  plot log_ref_ld50 * log_ic50 /conf pred;
  test_intercept: test intercept=0.625;
  test_slope: test log_ic50=0.435;
  test_joint: test intercept=0.625, log_ic50=0.435;
  title "New Ref. LD50 Data: Regression by Cell Type";
run;

proc sort data=lib.regdata3;
  by cell;
run;

proc reg data=lib.regdata3;
  by cell;
  model log_rc_ld50 = log_ic50 /clb;
  plot log_rc_ld50 * log_ic50 /conf pred;
  test_intercept: test intercept=2.02411; /*RC Rat Intercept wt
units*/
  test_slope: test log_ic50=0.37248; /*RC Rat Intercept wt units*/
  test_joint: test intercept=2.02411, log_ic50=0.37248;
  title "RC LD50 Data: By Cell with Mg/Kg";
run;

proc reg data=lib.regdata3;
  by cell;
  model log_ref_ld50 = log_ic50 /clb;
  plot log_ref_ld50 * log_ic50 /conf pred;
  test_intercept: test intercept=2.02411;
  test_slope: test log_ic50=0.37248;
  test_joint: test intercept=2.02411, log_ic50=0.37248;
  title "New Ref. LD50 Data: By Cell with Mg/Kg";
run;
```

```
/*DATA SORTED AND SUMMARIZED WITH ONE POINT PER CHEMICAL PER CELL TYPE PER LAB*/
```

```
proc sort data=lib.regdata;
  by lab cell;
proc reg data=lib.regdata;
  by lab cell;
  model log_rc_ld50 = log_ic50 /clb;
  plot log_rc_ld50 * log_ic50 /conf pred;
  test_intercept: test intercept=0.625;
  test_slope: test log_ic50=0.435;
  test_joint: test intercept=0.625, log_ic50=0.435;
  title "RC LD50 Data: Regression by Lab and Cell Type";
run;

proc reg data=lib.regdata;
  by lab cell;
  model log_ref_ld50 = log_ic50 /clb;
  plot log_ref_ld50 * log_ic50 /conf pred;
  test_intercept: test intercept=0.625;
  test_slope: test log_ic50=0.435;
  test_joint: test intercept=0.625, log_ic50=0.435;
  title "New Ref. LD50 Data: Regression by Lab and Cell Type";

run;

proc sort data=lib.regdata4;
  by cell lab;
run;

proc reg data=lib.regdata4;
  by cell lab;
  model log_rc_ld50 = log_ic50 /clb;
  plot log_rc_ld50 * log_ic50 /conf pred;
  test_intercept: test intercept=2.02411;
  test_slope: test log_ic50=0.37248;
  test_joint: test intercept=2.02411, log_ic50=0.37248;
  title "RC LD50 Data: By Cell and Lab with Mg/Kg";
run;

proc reg data=lib.regdata4;
  by cell lab;
  model log_ref_ld50 = log_ic50 /clb;
  plot log_ref_ld50 * log_ic50 /conf pred;
  test_intercept: test intercept=2.02411;
  test_slope: test log_ic50=0.37248;
  test_joint: test intercept=2.02411, log_ic50=0.37248;
  title "New Ref. LD50 Data: By Cell and Lab with Mg/Kg";
run;
```