Appendix D

D1 SAS Code for ANOVA and Contrasts D-3

D2 SAS Code for Regression Comparisons D-7

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Appendix D1

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 D2

SAS Code for Regression Comparisons

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```
dm 'output; clear';
dm 'log; clear';
*************************************************************************
*
*filename: task3.sas
*creation date: 08/02/06
*study:niceatm
*investigator:
*purpose: perform the individual lab regressions (tasks 1-4)
* note: 3 models are fit:
* (a) full model
* (b) reduced model with separate intercepts + common slope
* (c) separate intercepts + separate slopes model
*authors:mike riggs
*input data medium: sas data sets
*
**********************************************************************;
*
*
*compare rc to niceatm regressions, by cell type
*note: the input data set anal3 was created by taking the 47 3t3
*chemicals and the 51 nhk chemicals and computing their
*means by cell line
*
*
*
**********************************************************************;
proc mixed data=anal3 maxiter=200;
 by celline;
 class est_type;
 model log_ld50=est_type logic50_lab est_type*logic50_lab/outpredm=predat;
 title1 'ancova model (estimation type = trt) log-scale lab regressions, by
cell line';
 title2 '(test for slope differences)';
run;
quit;

****compute the full-model rsquare from the model residuals and predictions
***;
****note: proc mixed does not compute rsq, so you need to do it
yourself***;

data pred3t3 prednhk;
 set predat;
 if celline='3t3' then output pred3t3;
else output prednhk;
run;

proc summary data=pred3t3 nway;
 var log_ld50;
 output out=sumdat
mean=_mean_;
run;

data pred3t3;
 if _n_=1 then set sumdat;
 set pred3t3;
```

```
run;

data comp;
 set pred3t3 end=eof;
 sst+((log_ld50-_mean_)**2);
 sse+(resid**2);
 n=_n_ ;
 if eof then output;
run;

data comp;
 set comp;
 rsq=(sst-sse)/sst;
 label _mean_='response*mean'
sst='total sum*of squares'
sse='error sum*of squares'
rsq='r-squared';
run;

proc print data=comp split='*';
 var n _mean_ sst sse rsq;
 format rsq 5.3;
title1 'full ancova model r-square for 3t3 cell line (task 3)';
run;


proc summary data=prednhk nway;
 var log_ld50;
 output out=sumdat
mean=_mean_;
run;

data prednhk;
 if _n_=1 then set sumdat;
 set prednhk;
run;

data comp;
 set prednhk end=eof;
 sst+((log_ld50-_mean_)**2);
 sse+(resid**2);
 n=_n_ ;
 if eof then output;
run;

data comp;
 set comp;
 rsq=(sst-sse)/sst;
 label _mean_='response*mean'
sst='total sum*of squares'
sse='error sum*of squares'
rsq='r-squared';
run;

proc print data=comp split='*';
 var n _mean_ sst sse rsq;
 format rsq 5.3;
```

```
title1 'full ancova model r-square for nhk cell line (task 3)';
run;


proc mixed data=anal3 maxiter=200;
 by celline;
 class est_type;
 model log_ld50=est_type est_type*logic50_lab/noint solution cl alpha=0.05;
 * the following contrast is the simultaneous test of equal intercepts and
slopes ***;
 contrast 'lab vs. rc' est_type -1 1,
 est_type*logic50_lab -1 1;
 title1 'ancova model (trt=estimation type) log-scale lab regressions, by
cell line';
 title2 '(separate slope estimates)';
run;
quit;

proc mixed data=anal3 maxiter=200;
 by celline;
 model log_ld50=logic50_lab/solution cl alpha=0.05;
 title1 'ancova model (estimation type = trt) log-scale lab regressions, by
cell line';
 title2 '(estimate homogeneous slope with single intercept)';
run;
quit;
```

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