SAS codes used in FLIM manuscript

Figure 5B (TNF/macrophage area with metformin treatment)

**data** a;

input

**exptday treat$ tnfarea;**

datalines;

{input data}

**proc** **print**;

title 'TNF area as a proportion of total Macrophage area in 2DG treatment no transformation';

**run**;

**proc** **univariate** data=a;

histogram tnfarea / normal (mu=est sigma=est);

inset mean std skewness kurtosis / position=ne;

title 'TNF Area';

**run**;

**proc** **sgpanel** data=a;

panelby treat;

histogram tnfarea;

**proc** **sgpanel** data=a;

panelby treat;

vbox tnfarea;

title 'TNF area by treatment';

**run**;

**proc** **glimmix** plots=ResidualPanel;

class exptday treat;

model tnfarea = treat;

random exptday exptday\*treat;

lsmeans treat / pdiff cl;

output out=out1 pred=p resid=r;

title 'Analysis of tnf area by treatment';

**run**;

**proc** **univariate** data=out1 plot normal;

var r;

title 'residual analysis';

**run**;

Figure 6B (TNF/macrophage area in Stat6 mutant)

**data** a;

input

repeat genotype $ time perTNF;

datalines;

{input data}

**proc** **print**;

title 'Analysis of Percentage of TNF positive macrophages following burn in Stat6 mutants';

**run**;

**proc** **univariate** noprint;

histogram perTNF;

title 'Histogram of all data';

**run**;

**proc** **sgpanel** data=a;

panelby genotype;

histogram perTNF;

title 'Histogram of Percent TNF by genotype';

**run**;

**proc** **sgpanel** data=a;

panelby genotype;

vbox perTNF;

title 'Box plot of Percent TNF by genotype';

**run**;

**proc** **boxplot** data=a;

plot perTNF\*genotype;

title 'Box plots of Percent TNF positive macrophages by genotype, time and repeat';

**run**;

**proc** **mixed**;

title 'Mixed model of percent TNF positive macrophages';

class repeat genotype time;

model perTNF = genotype time time\*genotype/outp=newfile;

random repeat repeat\*genotype;

lsmeans genotype time genotype\*time / diff cl;

lsmeans time\*genotype / slice=time cl;

lsmeans time\*genotype / slice=genotype cl;

**run**;

ods graphics on;

**proc** **univariate** data=newfile plot normal;

title 'Analysis of Residuals';

var resid;

**run**;

Figure 6H (regen area burn metformin)

**data** a;

input

exptday treat$ regenarea;

datalines;

{input data}

**proc** **print**;

title 'regen area in metformin treatment';

**run**;

**proc** **univariate** data=a;

histogram regenarea / normal (mu=est sigma=est);

inset mean std skewness kurtosis / position=ne;

title 'Regen Area';

**run**;

**proc** **sgpanel** data=a;

panelby treat;

histogram regenarea;

**proc** **sgpanel** data=a;

panelby treat;

vbox regenarea;

title 'regen area by treatment';

**run**;

**proc** **mixed**; class exptday treat;

model regenarea = treat /outp=newfile;

random exptday exptday\*treat;

lsmeans treat / diff cl;

**run**;

**proc** **univariate** data=newfile plot normal;

var resid;

title 'residual analysis';

**run**;

Figure 6H (regen area burn Stat6 4dpb)

**data** a;

input

rep genotype $ regenarea;

datalines;

{insert data}

**proc** **print** data=a (obs=**15**);

title 'Stat6 4dpb wound area';

**run**;

**proc** **univariate** noprint;

histogram regenarea;

title 'histogram of entire experiment - regen area';

**run**;

**proc** **mixed**; class rep genotype;

model regenarea = genotype / outp=newfile;

random rep;

lsmeans genotype / adj = tukey diff cl;

title 'analysis of wound healing with tukey adjustment';

**run**;

**proc** **univariate** data=newfile plot normal;

title 'Residuals';

var resid;

**run**;

Figure 5 – figure supplement 1A (macrophage area burn metformin)

**data** a;

input

repday treatment$ macarea;

datalines;

{insert data}

**proc** **print** obs **10**;

**run**;

**proc** **sgpanel** data=a;

panelby treatment;

vbox macarea;

title 'boxplot macrophage area in burn by treatment';

**run**;

**proc** **mixed**; class repday treatment;

model macarea = treatment / outp=newfile;

random repday;

lsmeans treatment / diff cl;

title 'analysis of macrophage area in burn with metformin treatment';

**run**;

**proc** **univariate** data=newfile plot normal;

title 'Residuals for analysis of macrophage area in burn with metformin treatment';

var resid;

**run**;

Figure 6 – figure supplement 1A (total # macrophages in larvae)

**data** a;

input

repday genotype $ totmacnum;

datalines;

{insert data}

**proc** **print**;

**run**;

**proc** **univariate** noprint;

histogram totmacnum;

title 'histogram of entire experiment - total macrophage number';

**run**;

**proc** **mixed**; class repday genotype;

model totmacnum = genotype / outp=newfile;

random repday;

lsmeans genotype / adj = tukey diff cl;

title 'analysis of total macrophage number in Stat6 mutants, with tukey adjustment for multiple comparisons';

**run**;

**proc** **univariate** data=newfile plot normal;

title 'Residuals for analysis of total macrophage number in Stat6 mutants';

var resid;

**run**;

Figure 6 – figure supplement 1B (total # macrophages at burn 72hpb and 96hpb)

**data** a;

input

repday genotype $ hpb macnum;

datalines;

{insert data}

**proc** **print**;

title 'Analysis of number of macrophages in burn area in Stat6 mutants';

**run**;

**proc** **sgpanel** data=a;

panelby hpb;

vbox macnum/category=genotype boxwidth=**0.5**;

title 'macrophage number in burn by genotype and hpb';

**run**;

**proc** **mixed**;

title 'Analysis using Mixed model for number of macrophages in burn region in Stat6 mutants';

class repday genotype hpb;

model macnum = genotype hpb hpb\*genotype/outp=newfile;

random repday repday\*genotype;

lsmeans genotype hpb genotype\*hpb / diff cl;

lsmeans genotype\*hpb / slice=hpb cl;

lsmeans genotype\*hpb / slice=genotype cl;

**run**;

ods graphics on;

**proc** **univariate** data=newfile plot normal;

title 'Analysis of Residuals';

var resid;

**run**;