**PROC** **IMPORT** OUT= WORK.Env

DATAFILE= "\\Client\F$\Darger April\Sage.Env.April~v2.csv"

DBMS=CSV REPLACE;

GETNAMES=YES;

DATAROW=**2**;

guessingrows=**99**;

**RUN**;

**PROC** **IMPORT** OUT= WORK.Soil

DATAFILE= "\\Client\F$\Darger April\SoilEnvironmentaldataApril~v2.csv"

DBMS=CSV REPLACE;

GETNAMES=YES;

DATAROW=**2**;

guessingrows=**99**;

**RUN**;

/\* Merge datasets \*/

**proc** **sort** data=env; by id;

**proc** **sort** data=soil; by id;

**data** sage;

merge env soil;

by id;

**run**;

/\* Transform Relative Cover and Clay% \*/

**data** sage;

set sage;

if l\_relcov=**0** then l\_relcov\_trf = log( (l\_relcov+**0.3**) / (**100**-(l\_relcov+**0.3**)) );

else l\_relcov\_trf = log( (l\_relcov) / (**100**-(l\_relcov)) );

H1\_claypercent\_trf = log(h1\_claypercent);

**run**;

/\* fit a model to nonzero l\_relcov \*/

**proc** **reg** data=sage(where= (l\_relcov ne **0**));

model l\_relcov\_trf = h1\_dryhue h1\_dryvalue h1\_drychroma h1\_moistvalue h1\_moistchroma h1\_sandpercent h1\_claypercent\_trf h1\_ph h1\_effervescence h1\_depth

totaldepth awc100 depth200 elevation slope carbonatestage bioticcrustclass

/ selection=stepwise sle=**0.1** sls=**0.1**;

output out=m1 pred=pred;

**run**;

**proc** **sgplot** data=sage(where= (l\_relcov ne **0**));

title "Logit Relative Cover and Biotic Crust Class";

vbox l\_relcov\_trf / category=bioticcrustclass;

**run**;

**data** m1plus;

merge sage(where= (l\_relcov ne **0**)) m1;

**run**;

**proc** **sgpanel** data=m1plus;

panelby bioticcrustclass / columns=**7**;

reg x=h1\_claypercent\_trf y=pred / nomarkers;

scatter x=h1\_claypercent\_trf y=l\_relcov\_trf;

**run**;

/\* fit a model to binary form \*/

**data** sage;

set sage;

if l\_relcov =**0** then l\_relcov\_bin = **0**;

else if l\_relcov > **0** then l\_relcov\_bin = **1**;

**run**;

**proc** **logistic** data=sage desc;

model l\_relcov\_bin = h1\_dryhue h1\_dryvalue h1\_drychroma h1\_moistvalue h1\_moistchroma h1\_sandpercent h1\_claypercent\_trf h1\_ph h1\_effervescence h1\_depth

totaldepth awc100 depth200 elevation /\*aspect\*/ slope carbonatestage bioticcrustclass

/ selection=stepwise sle=**0.1** sls=**0.1**;

**run**;

**proc** **sgplot** data=sage;

vbox totaldepth / category=l\_relcov\_bin;

**proc** **sgplot** data=sage;

vbox h1\_ph / category=l\_relcov\_bin;

**proc** **sgplot** data=sage;

vbox bioticcrustclass / category=l\_relcov\_bin;

/\* Now Look at Sage Dead \*/

**data** sage;

set sage;

d\_relcov = l\_d\_relcov - l\_relcov;

**run**;

**data** sage;

set sage;

d\_denm2 = l\_d\_denm2 - l\_denm2;

**run**;

/\* Transform Relative Cover and Clay% \*/

**data** sage;

set sage;

if d\_relcov=**0** then d\_relcov\_trf = log( (d\_relcov+**0.3**) / (**100**-(d\_relcov+**0.3**)) );

else d\_relcov\_trf = log( (d\_relcov) / (**100**-(d\_relcov)) );

H1\_claypercent\_trf = log(h1\_claypercent);

**run**;

/\* fit a model to nonzero d\_relcov \*/

**proc** **reg** data=sage(where= (d\_relcov ne **0**));

model d\_relcov\_trf = h1\_dryhue h1\_dryvalue h1\_drychroma h1\_moistvalue h1\_moistchroma h1\_sandpercent h1\_claypercent\_trf h1\_ph h1\_effervescence h1\_depth

totaldepth awc100 depth200 elevation slope carbonatestage bioticcrustclass

/ selection=stepwise sle=**0.1** sls=**0.1**;

output out=m2 pred=pred;

**run**;

**proc** **sgplot** data=sage(where= (d\_relcov ne **0**));

vbox d\_relcov\_trf / category=h1\_dryhue;

**run**;

/\* fit a model to binary form \*/

**data** sage;

set sage;

if d\_relcov =**0** then d\_relcov\_bin = **0**;

else if d\_relcov > **0** then d\_relcov\_bin = **1**;

**run**;

**proc** **logistic** data=sage desc;

model d\_relcov\_bin = h1\_dryhue h1\_dryvalue h1\_drychroma h1\_moistvalue h1\_moistchroma h1\_sandpercent h1\_claypercent\_trf h1\_ph h1\_effervescence h1\_depth

totaldepth awc100 depth200 elevation /\*aspect\*/ slope carbonatestage bioticcrustclass

/ selection=stepwise sle=**0.1** sls=**0.1**;

**run**;

**proc** **sgplot** data=sage;

vbox totaldepth / category=d\_relcov\_bin;

**proc** **sgplot** data=sage;

vbox bioticcrustclass / category=d\_relcov\_bin;

**run**;

ods rtf file="\\Client\F$\Darger April\AprilTry\file.html" gpath="\\Client\F$\Darger April\AprilTry";

ods rtf close;

**Change Graph Color**

**proc** **sgplot** data=sage(where= (l\_relcov ne **0**));

title "Logit Live Relative Cover and Biotic Crust Class";

vbox l\_relcov\_trf / category=bioticcrustclass fillattrs= (color=H0F030FF);

xaxis label="Biotic Crust Class" ;

yaxis label="Logit Live Relative Cover";

**run**;

**Sgpanel code**

**PROC** **IMPORT** OUT= WORK.Env

DATAFILE= "E:\Darger April\Sage.Env.April~v2.csv"

DBMS=CSV REPLACE;

GETNAMES=YES;

DATAROW=**2**;

guessingrows=**99**;

**RUN**;

**PROC** **IMPORT** OUT= WORK.Soil

DATAFILE= "E:\Darger April\SoilEnvironmentaldataApril~v2.csv"

DBMS=CSV REPLACE;

GETNAMES=YES;

DATAROW=**2**;

guessingrows=**99**;

**RUN**;

/\* Merge datasets \*/

**proc** **sort** data=env; by id;

**proc** **sort** data=soil; by id;

**data** sage;

merge env soil;

by id;

**run**;

/\* Transform Relative Cover and Clay% \*/

**data** sage;

set sage;

if l\_relcov=**0** then l\_relcov\_trf = log( (l\_relcov+**0.3**) / (**100**-(l\_relcov+**0.3**)) );

else l\_relcov\_trf = log( (l\_relcov) / (**100**-(l\_relcov)) );

H1\_claypercent\_trf = log(h1\_claypercent);

**run**;

/\* fit a model to nonzero l\_relcov \*/

**proc** **reg** data=sage(where= (l\_relcov ne **0**));

model l\_relcov\_trf = h1\_dryhue h1\_dryvalue h1\_drychroma h1\_moistvalue h1\_moistchroma h1\_sandpercent h1\_claypercent\_trf h1\_ph h1\_effervescence h1\_depth

totaldepth awc100 depth200 elevation slope carbonatestage bioticcrustclass

/ selection=stepwise sle=**0.1** sls=**0.1**;

output out=m1 pred=pred;

**run**;

**data** m1plus;

merge sage(where= (l\_relcov ne **0**)) m1;

**run**;

ods graphics on /

width=**7**in

imagename="RelBiotic"

border=off;

ods html file="Sgplot.html" gpath="E:\Darger April\" DPI=**300**;

**proc** **sgpanel** data=m1plus;

title height=**20**pt "Logit Live Relative Cover and Clay Percent by Biotic Crust Class";

panelby bioticcrustclass / novarname columns=**7**;

reg x=h1\_claypercent\_trf y=pred /nomarkers legendlabel="Regression" lineattrs=(color=blue pattern=solid);

scatter x=h1\_claypercent\_trf y=l\_relcov\_trf / legendlabel="Logit Live Relative Cover" markerattrs=(color=black symbol=circlefilled);

colaxis LABELATTRS=(Family=Arial size=**17**) VALUEATTRS=(Family=Arial size=**10**)label="Surface Clay Percent Log Transformed";

rowaxis LABELATTRS=(Family=Arial size=**17**) VALUEATTRS=(Family=Arial size=**10**)label= "Logit Live Relative Cover";

**run**;

ods html close;

**Boxplots Code**

**proc** **template**;

define style styles.mystyle;

parent=styles.listing;

style GraphDataText from GraphDataText /

'GraphDataFont'=("Arial Symbol", **36**pt)

'GraphLabelFont'=("Arial Symbol", **36**pt)

'GraphValueFont'=("Arial Symbol", **36**pt);

end;

**run**;

ods graphics on /

imagename="RelBiotic"

width=**7**in

border=off;

ods html file="Plots.html" gpath="E:\Darger April\" DPI=**300** style=mystyle;

**PROC** **IMPORT** OUT= WORK.Env

DATAFILE= "E:\Darger April\Sage.Env.April~v2.csv"

DBMS=CSV REPLACE;

GETNAMES=YES;

DATAROW=**2**;

guessingrows=**99**;

**RUN**;

**PROC** **IMPORT** OUT= WORK.Soil

DATAFILE= "E:\Darger April\SoilEnvironmentaldataApril~v2.csv"

DBMS=CSV REPLACE;

GETNAMES=YES;

DATAROW=**2**;

guessingrows=**99**;

**RUN**;

/\* Merge datasets \*/

**proc** **sort** data=env; by id;

**proc** **sort** data=soil; by id;

**data** sage;

merge env soil;

by id;

**run**;

/\* Transform Relative Cover and Clay% \*/

**data** sage;

set sage;

if l\_relcov=**0** then l\_relcov\_trf = log( (l\_relcov+**0.3**) / (**100**-(l\_relcov+**0.3**)) );

else l\_relcov\_trf = log( (l\_relcov) / (**100**-(l\_relcov)) );

H1\_claypercent\_trf = log(h1\_claypercent);

**run**;

/\* fit a model to nonzero l\_relcov \*/

**proc** **reg** data=sage(where= (l\_relcov ne **0**));

model l\_relcov\_trf = h1\_dryhue h1\_dryvalue h1\_drychroma h1\_moistvalue h1\_moistchroma h1\_sandpercent h1\_claypercent\_trf h1\_ph h1\_effervescence h1\_depth

totaldepth awc100 depth200 elevation slope carbonatestage bioticcrustclass

/ selection=stepwise sle=**0.1** sls=**0.1**;

output out=m1 pred=pred;

**run**;

**proc** **sgplot** data=sage(where= (l\_relcov ne **0**));

title height=**20**pt justify=right "Logit Live Relative Cover and Biotic Crust Class";

vbox l\_relcov\_trf / category=bioticcrustclass DATALABELATTRS=(size=**17**);

xaxis label="Biotic Crust Class" LABELATTRS=(Family=Arial size=**17**) VALUEATTRS=(Family=Arial size=**17**);

yaxis label="Logit Live Relative Cover" LABELATTRS=(Family=Arial size=**17**) VALUEATTRS=(Family=Arial size=**17**);

**run**;

/\* fit a model to binary form \*/

**data** sage;

set sage;

if l\_relcov =**0** then l\_relcov\_bin = **0**;

else if l\_relcov > **0** then l\_relcov\_bin = **1**;

**run**;

**proc** **logistic** data=sage desc;

model l\_relcov\_bin = h1\_dryhue h1\_dryvalue h1\_drychroma h1\_moistvalue h1\_moistchroma h1\_sandpercent h1\_claypercent\_trf h1\_ph h1\_effervescence h1\_depth

totaldepth awc100 depth200 elevation /\*aspect\*/ slope carbonatestage bioticcrustclass

/ selection=stepwise sle=**0.1** sls=**0.1**;

**run**;

**proc** **sgplot** data=sage;

title height=**20**pt justify=right "Live Sagebrush P/A and Pedon Depth";

vbox totaldepth / category=l\_relcov\_bin;

yaxis label="Pedon Depth in cm" LABELATTRS=(Family=Arial size=**17**)VALUEATTRS=(Family=Arial size=**17**);

xaxis label="Live Sagebrush Presence/Absence" discreteorder=data LABELATTRS=(Family=Arial size=**17**)VALUEATTRS=(Family=Arial size=**17**);

**proc** **sgplot** data=sage;

title height=**20**pt justify=right "Live Sagebrush P/A and Surface Horizon pH";

vbox h1\_ph / category=l\_relcov\_bin;

yaxis label="Surface Horizon pH" LABELATTRS=(Family=Arial size=**17**)VALUEATTRS=(Family=Arial size=**17**);

xaxis label="Live Sagebrush Presence/Absence" discreteorder=data LABELATTRS=(Family=Arial size=**17**)VALUEATTRS=(Family=Arial size=**17**);

**proc** **sgplot** data=sage;

title height=**20**pt justify=right "Live Sagebrush P/A and Biotic Crust Class";

vbox bioticcrustclass / category=l\_relcov\_bin;

yaxis label="Biotic Crust Class" LABELATTRS=(Family=Arial size=**17**)VALUEATTRS=(Family=Arial size=**17**);

xaxis label="Live Sagebrush Presence/Absence" discreteorder=data LABELATTRS=(Family=Arial size=**17**)VALUEATTRS=(Family=Arial size=**17**);

**run**;

/\* Now Look at Sage Dead \*/

**data** sage;

set sage;

d\_relcov = l\_d\_relcov - l\_relcov;

**run**;

**data** sage;

set sage;

d\_denm2 = l\_d\_denm2 - l\_denm2;

**run**;

/\* Transform Relative Cover and Clay% \*/

**data** sage;

set sage;

if d\_relcov=**0** then d\_relcov\_trf = log( (d\_relcov+**0.3**) / (**100**-(d\_relcov+**0.3**)) );

else d\_relcov\_trf = log( (d\_relcov) / (**100**-(d\_relcov)) );

H1\_claypercent\_trf = log(h1\_claypercent);

**run**;

/\* fit a model to nonzero d\_relcov \*/

**proc** **reg** data=sage(where= (d\_relcov ne **0**));

model d\_relcov\_trf = h1\_dryhue h1\_dryvalue h1\_drychroma h1\_moistvalue h1\_moistchroma h1\_sandpercent h1\_claypercent\_trf h1\_ph h1\_effervescence h1\_depth

totaldepth awc100 depth200 elevation slope carbonatestage bioticcrustclass

/ selection=stepwise sle=**0.1** sls=**0.1**;

output out=m2 pred=pred;

**run**;

/\* fit a model to binary form \*/

**data** sage;

set sage;

if d\_relcov =**0** then d\_relcov\_bin = **0**;

else if d\_relcov > **0** then d\_relcov\_bin = **1**;

**run**;

**proc** **logistic** data=sage desc;

model d\_relcov\_bin = h1\_dryhue h1\_dryvalue h1\_drychroma h1\_moistvalue h1\_moistchroma h1\_sandpercent h1\_claypercent\_trf h1\_ph h1\_effervescence h1\_depth

totaldepth awc100 depth200 elevation /\*aspect\*/ slope carbonatestage bioticcrustclass

/ selection=stepwise sle=**0.1** sls=**0.1**;

**run**;

**proc** **sgplot** data=sage;

title height=**20**pt justify=right "Dead Sagebrush P/A and Pedon Depth";

vbox totaldepth / category=d\_relcov\_bin;

yaxis label="Pedon Depth in cm" LABELATTRS=(Family=Arial size=**17**)VALUEATTRS=(Family=Arial size=**17**);

xaxis label="Dead Sagebrush Presence/Absence" discreteorder=data LABELATTRS=(Family=Arial size=**17**)VALUEATTRS=(Family=Arial size=**17**);

**proc** **sgplot** data=sage;

title height=**20**pt justify=right "Dead Sagebrush P/A and Biotic Crust Class";

vbox bioticcrustclass / category=d\_relcov\_bin;

yaxis label="Biotic Crust Class" LABELATTRS=(Family=Arial size=**17**)VALUEATTRS=(Family=Arial size=**17**);

xaxis label="Dead Sagebrush Presence/Absence" discreteorder=data LABELATTRS=(Family=Arial size=**17**)VALUEATTRS=(Family=Arial size=**17**);

**run**;

ods html close;

**Code I might use**

/\* vbox \*/ OUTLIERATTRS=(symbol=circlefilled)