**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**;

/\* First look at soil variables: collinearity issues, etc...?\*/

**proc** **sgscatter** data=soil;

matrix h1\_dryhue -- h1\_depth;

**run**;

**proc** **freq** data=soil;

table (h1\_dryhue h1\_dryvalue h1\_drychroma h1\_moisthue)\*(h1\_dryvalue h1\_drychroma h1\_moisthue h1\_moistvalue) / measures;

**run**;

**proc** **sgscatter** data=soil;

matrix awc25 -- slope;

**run**;

**proc** **freq** data=soil;

table (depth50 depth100 depth150 )\*(depth100 depth150 depth200);

**run**;

**proc** **sgplot** data=soil;

vbox totaldepth / category=depth50;

**proc** **sgplot** data=soil;

vbox totaldepth / category=depth100;

**proc** **sgplot** data=soil;

vbox totaldepth / category=depth150;

**proc** **sgplot** data=soil;

vbox totaldepth / category=depth200;

**run**;

/\* Now start Looking at Sage too \*/

/\* Merge datasets \*/

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

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

**data** sage;

merge env soil;

by id;

**run**;

**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**;

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

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

**run**;

**proc** **reg** data=sage;

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

/ collinoint;

**run**;

**proc** **reg** data=sage;

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**;

**run**;

**proc** **sgscatter** data=sage;

matrix l\_relcov\_trf h1\_ph totaldepth bioticcrustclass;

**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**;

**%macro** ***skip***;

proc hpgenselect 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 /\*aspect\*/ slope carbonatestage bioticcrustclass / distribution=normal;

\* selection method=lasso(choose=aicc) details=all;

selection method=stepwise(sle=**0.1** sls=**0.1**) details=all;

output out=m1 pred=pred;

run;

**%mend**;

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

matrix l\_relcov\_trf h1\_claypercent\_trf h1\_ph bioticcrustclass;

**run**;

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

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

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

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

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

scatter x=bioticcrustclass y=l\_relcov\_trf;

**run**;

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

vbox l\_relcov\_trf / category=h1\_dryvalue;

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

vbox l\_relcov\_trf / category=carbonatestage;

**run**;

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

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**;

**%macro** ***skip***;

proc hpgenselect data=sage;

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 / distribution=binary;

\* selection method=lasso(choose=aicc) details=all;

selection method=stepwise(sle=**0.1** sls=**0.1**) details=all;

run;

**%mend**;

**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;

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

vbox elevation / category=l\_relcov\_bin;

**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**;

**proc** **sgscatter** data=sage;

matrix l\_d\_denm2 -- l\_relcov d\_relcov d\_denm2;

**run**;

**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**;

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

scatter x=d\_relcov y=d\_relcov\_trf;

**run**;

**proc** **reg** data=sage;

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

/ collinoint;

**run**;

**proc** **reg** data=sage;

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**;

**run**;

**proc** **sgscatter** data=sage;

matrix d\_relcov\_trf h1\_ph totaldepth;

**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**;

**%macro** ***skip***;

proc hpgenselect 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 /\*aspect\*/ slope carbonatestage bioticcrustclass / distribution=normal;

\* selection method=lasso(choose=aicc) details=all;

selection method=stepwise(sle=**0.1** sls=**0.1**) details=all;

output out=m1 pred=pred;

run;

**%mend**;

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

matrix d\_relcov\_trf h1\_dryhue ;

**run**;

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

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

**run**;

**data** m2plus;

merge sage(where= (d\_relcov ne **0**)) m2;

**run**;

**proc** **sgpanel** data=m2plus;

panelby bioticcrustclass / columns=**7**;

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

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

**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**;

**%macro** ***skip***;

proc hpgenselect data=sage;

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 / distribution=binary;

\* selection method=lasso(choose=aicc) details=all;

selection method=stepwise(sle=**0.1** sls=**0.1**) details=all;

run;

**%mend**;

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

vbox totaldepth / category=d\_relcov\_bin;

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

vbox h1\_effervescence / category=d\_relcov\_bin;

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

vbox bioticcrustclass / category=d\_relcov\_bin;

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

vbox h1\_dryvalue / category=d\_relcov\_bin;

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

vbox slope / category=d\_relcov\_bin;

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

vbox h1\_depth / category=d\_relcov\_bin;

**run**;

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

DATAFILE= "C:\Users\A00017434\Client work\Darger April\Sage.Env.April~v2.csv"

DBMS=CSV REPLACE;

GETNAMES=YES;

DATAROW=**2**;

guessingrows=**99**;

**RUN**;

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

DATAFILE= "C:\Users\A00017434\Client work\Darger April\SoilEnvironmentaldataApril~v2.csv"

DBMS=CSV REPLACE;

GETNAMES=YES;

DATAROW=**2**;

guessingrows=**99**;

**RUN**;

**proc** **sgscatter** data=soil;

matrix h1\_dryhue -- slope carbonatestage bioticcrustclass;

**run**;

**proc** **sgscatter** data=soil;

matrix h1\_dryhue -- h1\_depth;

**run**;

**proc** **freq** data=soil;

table (h1\_dryhue h1\_dryvalue h1\_drychroma h1\_moisthue)\*(h1\_dryvalue h1\_drychroma h1\_moisthue h1\_moistvalue) / measures;

**run**;

**proc** **sgscatter** data=soil;

matrix awc25 -- slope;

**run**;

**proc** **freq** data=soil;

table (depth50 depth100 depth150 )\*(depth100 depth150 depth200);

**run**;

**proc** **sgplot** data=soil;

vbox totaldepth / category=depth50;

**proc** **sgplot** data=soil;

vbox totaldepth / category=depth100;

**proc** **sgplot** data=soil;

vbox totaldepth / category=depth150;

**proc** **sgplot** data=soil;

vbox totaldepth / category=depth200;

**run**;

/\* Merge datasets \*/

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

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

**data** sage;

merge env soil;

by id;

**run**;

**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**;

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

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

**run**;

**proc** **reg** data=sage;

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

totaldepth awc100 depth200 elevation aspect slope carbonatestage bioticcrustclass

/ collinoint;

**run**;

**proc** **reg** data=sage;

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

totaldepth awc100 depth200 elevation aspect slope carbonatestage bioticcrustclass

/ selection=stepwise;

**run**;

**proc** **sgscatter** data=sage;

matrix l\_relcov\_trf h1\_claypercent h1\_ph totaldepth elevation bioticcrustclass;

**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 aspect slope carbonatestage bioticcrustclass

/ selection=stepwise;

output out=m1 pred=pred;

**run**;

**%macro** ***skip***;

proc hpgenselect 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 /\*aspect\*/ slope carbonatestage bioticcrustclass / distribution=normal;

\* selection method=lasso(choose=aicc) details=all;

selection method=stepwise(sle=**0.1** sls=**0.1**) details=all;

output out=m1 pred=pred;

run;

**%mend**;

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

matrix l\_relcov\_trf h1\_claypercent\_trf h1\_ph bioticcrustclass ;

**run**;

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

vbox l\_relcov\_trf / category=carbonatestage;

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

vbox l\_relcov\_trf / category=h1\_dryvalue;

**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**;

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

panelby h1\_claypercent\_trf / columns=**7**;

reg x=bioticcrustclass y=pred / nomarkers;

scatter x=bioticcrustclass 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;

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**;

**%macro** ***skip***;

proc hpgenselect data=sage;

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 / distribution=binary;

\* selection method=lasso(choose=aicc) details=all;

selection method=stepwise(sle=**0.1** sls=**0.1**) details=all;

run;

**%mend**;

**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;

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

vbox elevation / category=l\_relcov\_bin;

**run**;

**data** sage;

set sage;

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

**run**;

**proc** **sgscatter** data=sage;

matrix l\_d\_denm2 -- l\_relcov d\_relcov;

**run**;

**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**;

/\* First look at soil variables: collinearity issues, etc...?\*/

**proc** **sgscatter** data=soil;

matrix h1\_dryhue -- h1\_depth;

**run**;

**proc** **freq** data=soil;

table (h1\_dryhue h1\_dryvalue h1\_drychroma h1\_moisthue)\*(h1\_dryvalue h1\_drychroma h1\_moisthue h1\_moistvalue) / measures;

**run**;

**proc** **sgscatter** data=soil;

matrix awc25 -- slope;

**run**;

**proc** **freq** data=soil;

table (depth50 depth100 depth150 )\*(depth100 depth150 depth200);

**run**;

**proc** **sgplot** data=soil;

vbox totaldepth / category=depth50;

**proc** **sgplot** data=soil;

vbox totaldepth / category=depth100;

**proc** **sgplot** data=soil;

vbox totaldepth / category=depth150;

**proc** **sgplot** data=soil;

vbox totaldepth / category=depth200;

**run**;

/\* Now start Looking at Sage too \*/

/\* Merge datasets \*/

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

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

**data** sage;

merge env soil;

by id;

**run**;

**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**;

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

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

**run**;

**proc** **reg** data=sage;

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

/ collinoint;

**run**;

**proc** **reg** data=sage;

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**;

**run**;

**proc** **sgscatter** data=sage;

matrix l\_relcov\_trf h1\_ph totaldepth bioticcrustclass;

**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**;

**%macro** ***skip***;

proc hpgenselect 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 /\*aspect\*/ slope carbonatestage bioticcrustclass / distribution=normal;

\* selection method=lasso(choose=aicc) details=all;

selection method=stepwise(sle=**0.1** sls=**0.1**) details=all;

output out=m1 pred=pred;

run;

**%mend**;

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

matrix l\_relcov\_trf h1\_claypercent\_trf bioticcrustclass;

**run**;

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

vbox l\_relcov\_trf / category=bioticcrustclass;

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

vbox l\_relcov\_trf / category=h1\_claypercent\_trf;

**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**;

**%macro** ***skip***;

proc hpgenselect data=sage;

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 / distribution=binary;

\* selection method=lasso(choose=aicc) details=all;

selection method=stepwise(sle=**0.1** sls=**0.1**) details=all;

run;

**%mend**;

**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;

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

vbox elevation / category=l\_relcov\_bin;

**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**;

**proc** **sgscatter** data=sage;

matrix l\_d\_denm2 -- l\_relcov d\_relcov d\_denm2;

**run**;

**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**;

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

scatter x=d\_relcov y=d\_relcov\_trf;

**run**;

**proc** **reg** data=sage;

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

/ collinoint;

**run**;

**proc** **reg** data=sage;

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**;

**run**;

**proc** **sgscatter** data=sage;

matrix d\_relcov\_trf h1\_ph totaldepth;

**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**;

**%macro** ***skip***;

proc hpgenselect 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 /\*aspect\*/ slope carbonatestage bioticcrustclass / distribution=normal;

\* selection method=lasso(choose=aicc) details=all;

selection method=stepwise(sle=**0.1** sls=**0.1**) details=all;

output out=m1 pred=pred;

run;

**%mend**;

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

matrix d\_relcov\_trf h1\_dryhue ;

**run**;

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

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

**run**;

**data** m2plus;

merge sage(where= (d\_relcov ne **0**)) m2;

**run**;

**proc** **sgpanel** data=m2plus;

panelby bioticcrustclass / columns=**7**;

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

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

**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**;

**%macro** ***skip***;

proc hpgenselect data=sage;

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 / distribution=binary;

\* selection method=lasso(choose=aicc) details=all;

selection method=stepwise(sle=**0.1** sls=**0.1**) details=all;

run;

**%mend**;

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

vbox totaldepth / category=d\_relcov\_bin;

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

vbox h1\_effervescence / category=d\_relcov\_bin;

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

vbox bioticcrustclass / category=d\_relcov\_bin;

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

vbox h1\_dryvalue / category=d\_relcov\_bin;

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

vbox slope / category=d\_relcov\_bin;

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

vbox h1\_depth / category=d\_relcov\_bin;

**run**;