Data Reduction - Rocky Mountain & Artic Wolves

This project followed a study completed by Pierre Jolicouer, called the 'Multivariate Geographical Variation in the Wolf (Canis *lupus* L.) This study was specifically measuring morphometric data on Rocky Mountain and Artic wolves. Canis *lupus* or Gray Wolf has 40 sub species classified and is believed to be a species which shows a great deal of polymorphism geographically. Polymorphism qualities are potentially determined by three mechanisms; 1) Genetic Polymorphism, 2) Geographical conditioning, 3) Random order. While the Artic Wolf, Figure 1, is thought to be an ancestor of the Gray Wolf, native to the Canadian Artic, it is smaller in dimensions. Rocky Mountain wolves, Figure 2, are thought to be an ancestor to the wolves of Russia and Scandinavia which are traditionally a larger species of wolf. Figure 3 reveals comparisons between the European wolves vs. the North American characteristics found in the Canadian wolves.

Figure 1

Figure 2

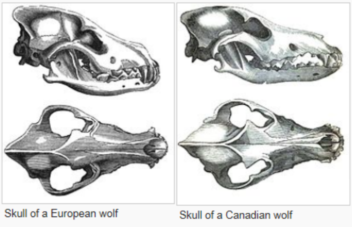


Figure 3

Problem Statement:

To develop a model based on Data Reduction techniques to find out what are the least set of morphometric variables needed to identify a particular species of wolves.

Constraints and Limitations:

The data collected was originally completed by Jolicoeur in 1958. The last since attempt to collect data on wolves was done in 1944. Limitations in the data come in the lack of use of multivariate processes to analyze geographic differentiation in the wolf. The data contained here is only pertained to morphological characteristics, the paper illustrate that "physiological, behavioral and ecological data could be done in similar manner", but is missing in our analysis. Beyond possibly lacking potential variables, it "failed to show clearly nature and extent of geographical variation". This is due to the data being purely observational and, as such, no casual inferences can be made about the relationship between the explanatory and response variable.

In addition, the data set contains only 25 observations of Artic and Rocky Mountain Wolves and which also is unbalanced in the two observations. The low sample might be due to various possible confounding factors, such as elusiveness of the animal or simply declining populations. As such we rely on Jolicoeur judgment to use morphological characteristics as significant variables of study.

A further limitation in this study, would be the lack of testing the sex variable fully in the project, I instead purely focus on statistical variability of wolf species.

Data Set Descriptions:

Our data's response variable is 'Location' and it is broken into two types, Artic (AR) and Rocky Mountain (RM). To use that variable in our SAS program, we have coded into SAS a 'Species', Explanatory Variable (EV), AR = 1 / RM =2. Listed below are our EVs employed in this study, refer to Figure 4 for identification of measurement points employed:

Variables:

- Location: rm=rocky mountain / ar=arctic
- Sex: m=male f=female
- X1 = palatal length
- X2 = postpalatal length
- X3 = zygomatic width
- X4 = palatal width outside the first upper molars
- X5 = palatal width inside the second upper molars
- X6 = width between the postglenoid foramina
- X7 = interorbital width
- X8 = least width of the braincase
- X9 = crown length of the first upper molar
- Species = 1 for AR / 2 for RM

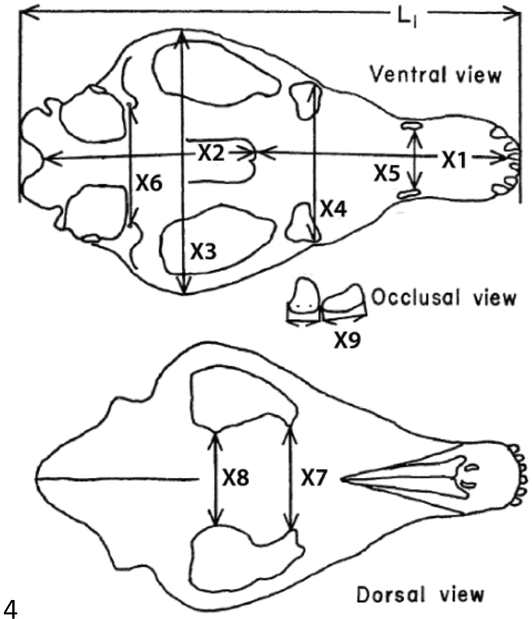


Figure 4

Each of these variables are common in either species morphological measurements and can impact certain possible trends in evolution of species, possibly being genetic, geographic, or random.

Variable Screening (Correlation Matrix):

We begin our analysis be examining the total structure of the data to see if an discrepancies exist which might need addressing before we begin data reduction steps.

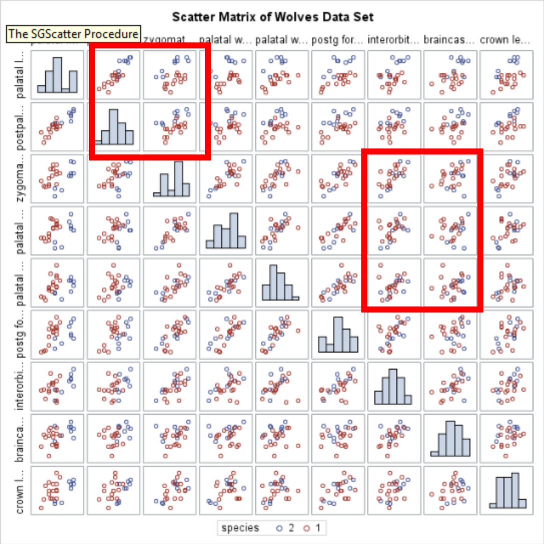
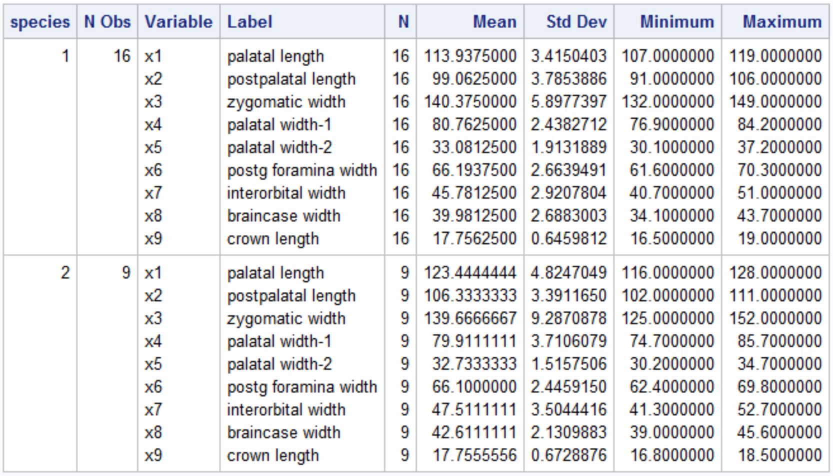


Figure 5

Scanning the results from the correlation matrix in Fig. 5, we see normal distribution with strong linear trends from several EVs, such as X1 & X2, very strong and neatly. While the others are also showing positive trends and will need further examining, but all is useable and not in need of a transformation. Also our analysis of means (Fig. 6) also seems to be loaded correctly and but seems to differ in mean weights, especially X1 & X3.

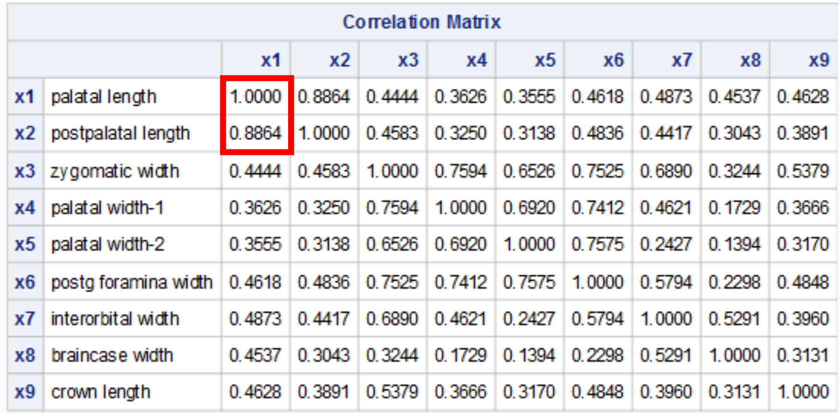


species	N Obs	Variable	Label	N	Mean	Std Dev	Minimum	Maximum
1	16	x1	palatal length	16	113.9375000	3.4150403	107.0000000	119.0000000
		x2	postpalatal length	16	99.0625000	3.7853886	91.0000000	106.0000000
		x3	zygomatic width	16	140.3750000	5.8977397	132.0000000	149.0000000
		x4	palatal width-1	16	80.7625000	2.4382712	76.9000000	84.2000000
		x5	palatal width-2	16	33.0812500	1.9131889	30.1000000	37.2000000
		x6	postg foramina width	16	66.1937500	2.6639491	61.6000000	70.3000000
		x7	interorbital width	16	45.7812500	2.9207804	40.7000000	51.0000000
		x8	braincase width	16	39.9812500	2.6883003	34.1000000	43.7000000
		x9	crown length	16	17.7562500	0.6459812	16.5000000	19.0000000
2	9	x1	palatal length	9	123.4444444	4.8247049	116.0000000	128.0000000
		x2	postpalatal length	9	106.3333333	3.3911650	102.0000000	111.0000000
		x3	zygomatic width	9	139.6666667	9.2870878	125.0000000	152.0000000
		x4	palatal width-1	9	79.9111111	3.7106079	74.7000000	85.7000000
		x5	palatal width-2	9	32.7333333	1.5157506	30.2000000	34.7000000
		x6	postg foramina width	9	66.1000000	2.4459150	62.4000000	69.8000000
		x7	interorbital width	9	47.5111111	3.5044416	41.3000000	52.7000000
		x8	braincase width	9	42.6111111	2.1309883	39.0000000	45.6000000
		x9	crown length	9	17.7555556	0.6728876	16.8000000	18.5000000

Figure 6

Exploratory Data Analysis:

For my process of selected an appropriate model I will attempt several selection methods. Principal Component Analysis (PCA), MANOVA, and the LASSO technique to see which model might best fit the data and also receive an appropriate Chi Square. So to start I will run PCA on the full model with all variables.



Correlation Matrix

		x1	x2	x3	x4	x5	x6	x7	x8	x9
x1	palatal length	1.0000	0.8864	0.4444	0.3626	0.3555	0.4618	0.4873	0.4537	0.4628
x2	postpalatal length	0.8864	1.0000	0.4583	0.3250	0.3138	0.4836	0.4417	0.3043	0.3891
x3	zygomatic width	0.4444	0.4583	1.0000	0.7594	0.6526	0.7525	0.6890	0.3244	0.5379
x4	palatal width-1	0.3626	0.3250	0.7594	1.0000	0.6920	0.7412	0.4621	0.1729	0.3666
x5	palatal width-2	0.3555	0.3138	0.6526	0.6920	1.0000	0.7575	0.2427	0.1394	0.3170
x6	postg foramina width	0.4618	0.4836	0.7525	0.7412	0.7575	1.0000	0.5794	0.2298	0.4848
x7	interorbital width	0.4873	0.4417	0.6890	0.4621	0.2427	0.5794	1.0000	0.5291	0.3960
x8	braincase width	0.4537	0.3043	0.3244	0.1729	0.1394	0.2298	0.5291	1.0000	0.3131
x9	crown length	0.4628	0.3891	0.5379	0.3666	0.3170	0.4848	0.3960	0.3131	1.0000

Figure 7

Running PCA, Fig 7, correlation Matrix show that the first load seems to be highly correlated with the first 2 EVs. And our Scree Plot in Fig. 8, also seems to demonstrate this assumption that the after the 2 component the line seems to level off, mirror what our Correlation Matrix states. This does however slight contradict the Eigenvector results, Fig.9, which seems to show that more than two EVs might be correlative. Studying PRIN1, we see X1, X2, X3, X4, X5, X6, X7 to all be quite close. Moving to PRIN2 it drops significantly, where X1 & X2 are all that seem to correlate.

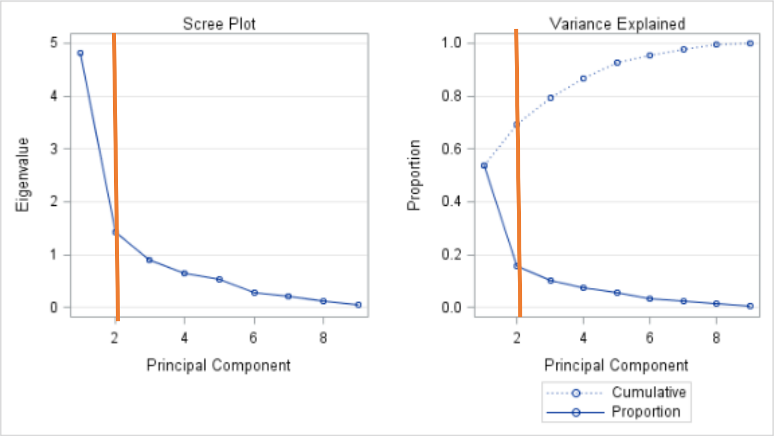
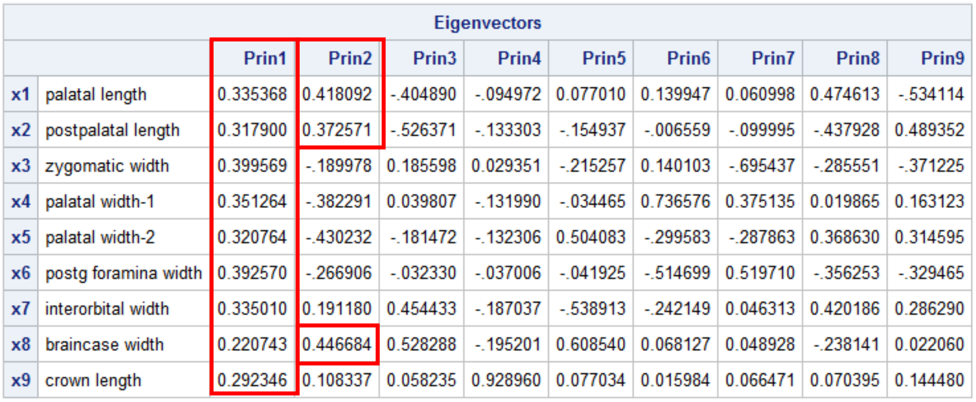


Figure 8



Eigenvectors

		Prin1	Prin2	Prin3	Prin4	Prin5	Prin6	Prin7	Prin8	Prin9
x1	palatal length	0.335368	0.418092	-.404890	-.094972	0.077010	0.139947	0.060998	0.474613	-.534114
x2	postpalatal length	0.317900	0.372571	-.526371	-.133303	-.154937	-.006559	-.099995	-.437928	0.489352
x3	zygomatic width	0.399569	-.189978	0.185598	0.029351	-.215257	0.140103	-.695437	-.285551	-.371225
x4	palatal width-1	0.351264	-.382291	0.039807	-.131990	-.034465	0.736576	0.375135	0.019865	0.163123
x5	palatal width-2	0.320764	-.430232	-.181472	-.132306	0.504083	-.299583	-.287863	0.368630	0.314595
x6	postg foramina width	0.392570	-.266906	-.032330	-.037006	-.041925	-.514699	0.519710	-.356253	-.329465
x7	interorbital width	0.335010	0.191180	0.454433	-.187037	-.538913	-.242149	0.046313	0.420186	0.286290
x8	braincase width	0.220743	0.446684	0.528288	-.195201	0.608540	0.068127	0.048928	-.238141	0.022060
x9	crown length	0.292346	0.108337	0.058235	0.928960	0.077034	0.015984	0.066471	0.070395	0.144480

Figure 9

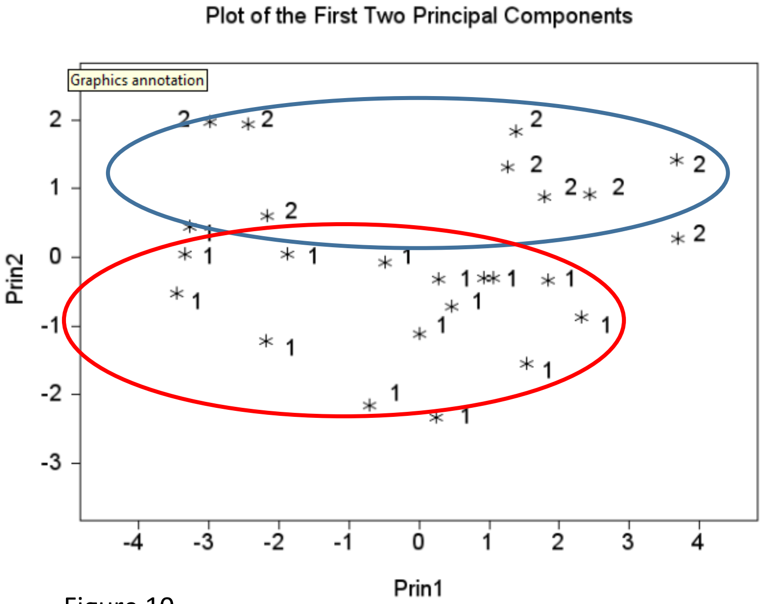
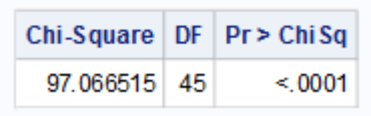
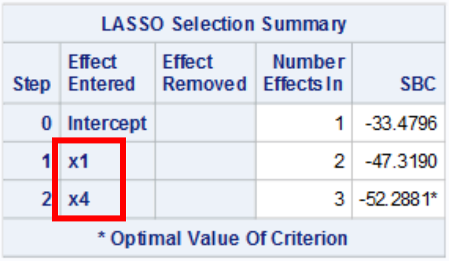


Figure 10



Chi-Square	DF	Pr > ChiSq
97.066515	45	<.0001

Figure 11



LASSO Selection Summary

Step	Effect Entered	Effect Removed	Number Effects In	SBC
0	Intercept		1	-33.4796
1	x1		2	-47.3190
2	x4		3	-52.2881*

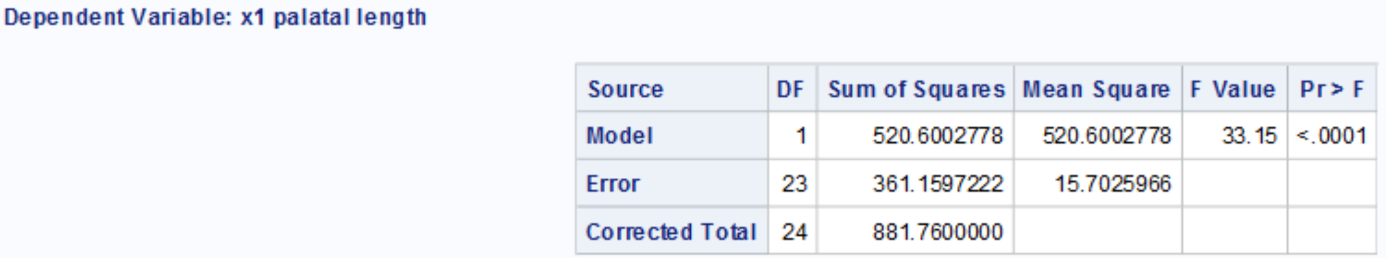
* Optimal Value Of Criterion

Figure 12

Studying the Plot of First two Principal Components, we can see that there are two distinct groups. Paired with a Full Model Chi Square test the full model does not fit within and we reject since we find a p-value of <.0001 significance. We will continue to push the model and find a Chi-Square which fails to reject.

Other METHODS

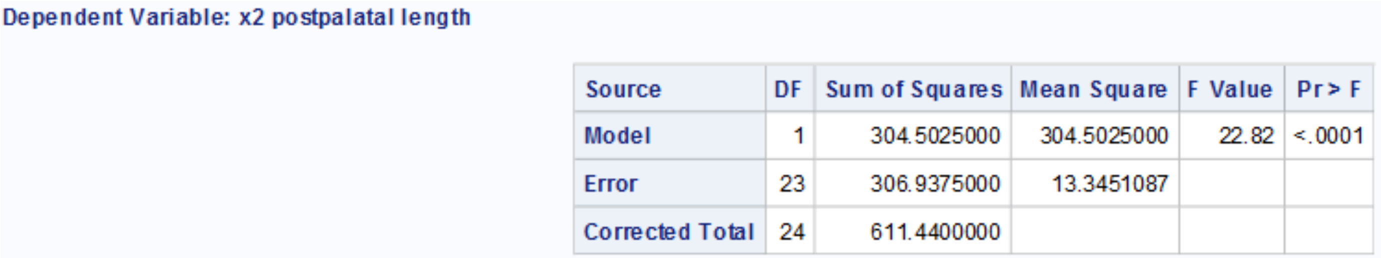
In determining further steps, I choose to run MANOVA on the full model to see what would return significant. Not too much of a surprise as we saw that X1, X2, X8 all return significant as can be seen in Fig. 13-15.



Dependent Variable: x1 palatal length

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	1	520.6002778	520.6002778	33.15	<.0001
Error	23	361.1597222	15.7025966		
Corrected Total	24	881.7600000			

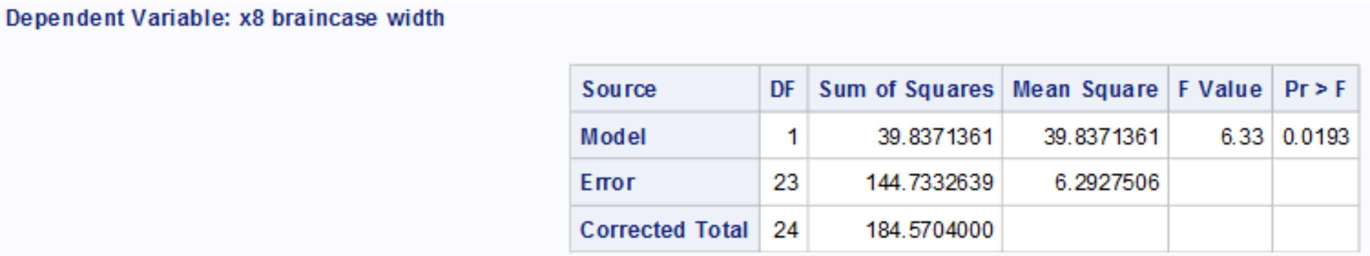
Fig.13



Dependent Variable: x2 postpalatal length

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	1	304.5025000	304.5025000	22.82	<.0001
Error	23	306.9375000	13.3451087		
Corrected Total	24	611.4400000			

Fig.14



Dependent Variable: x8 braincase width

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	1	39.8371361	39.8371361	6.33	0.0193
Error	23	144.7332639	6.2927506		
Corrected Total	24	184.5704000			

Fig.15

Model Selection:

Now we will compare the 3 models which I have received as significant to see which ones have the best overall factors of significance dealing with p-values and R^2 and Adjusted R, additionally we will reexamine what Chi-Square are received as well.

The three models are shown below:

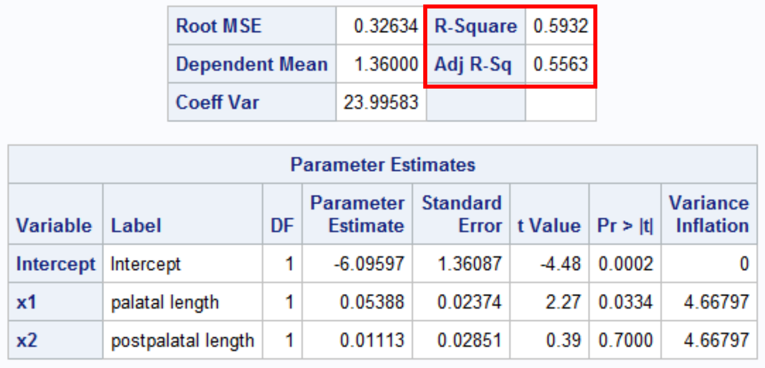
1) $\mathrm{Y}_{Species} = \beta_0 + \beta X1(\textit{palatal length}) + \beta X2(\textit{postpalatal length})$

2) $\mathrm{Y}_{Species} = \beta_0 + \beta X1(\textit{palatal length}) + \beta X4(\textit{postpalatal width})$

3) $\mathrm{Y}_{Species} = \beta_0 + \beta X1(\textit{palatal length}) + \beta X2(\textit{postpalatal length}) + \beta X8(\textit{least width of the braincase})$

4) $\mathrm{Y}_{Species} = \beta_0 + \beta X1(\textit{palatal length}) + \beta X2(\textit{postpalatal length}) + \beta X4(\textit{postpalatal width})$

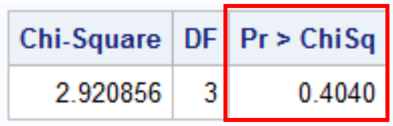
1) YSpecies = β_0 + βX1(palatal length) + βX2(postpalatal length)



Root MSE	0.32634	R-Square	0.5932
Dependent Mean	1.36000	Adj R-Sq	0.5563
Coeff Var	23.99583		

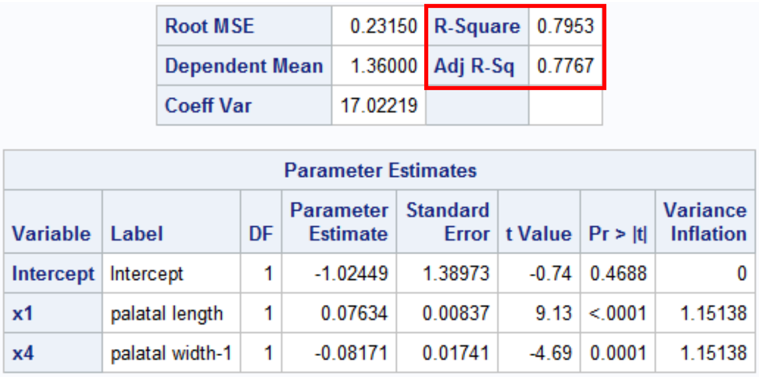
Parameter Estimates

Variable	Label	DF	Parameter Estimate	Standard Error	t Value	Pr > |t|	Variance Inflation
Intercept	Intercept	1	-6.09597	1.36087	-4.48	0.0002	0
x1	palatal length	1	0.05388	0.02374	2.27	0.0334	4.66797
x2	postpalatal length	1	0.01113	0.02851	0.39	0.7000	4.66797



Chi-Square	DF	Pr > ChiSq
2.920856	3	0.4040

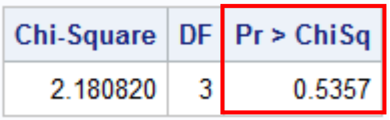
2) YSpecies = β_0 + βX1(palatal length) + βX4(postpalatal width)



Root MSE	0.23150	R-Square	0.7953
Dependent Mean	1.36000	Adj R-Sq	0.7767
Coeff Var	17.02219		

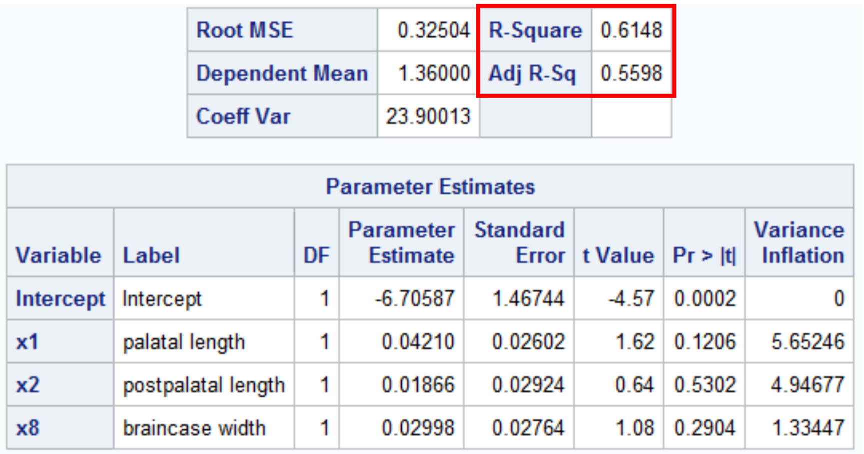
Parameter Estimates

Variable	Label	DF	Parameter Estimate	Standard Error	t Value	Pr > |t|	Variance Inflation
Intercept	Intercept	1	-1.02449	1.38973	-0.74	0.4688	0
x1	palatal length	1	0.07634	0.00837	9.13	<.0001	1.15138
x4	palatal width-1	1	-0.08171	0.01741	-4.69	0.0001	1.15138



Chi-Square	DF	Pr > ChiSq
2.180820	3	0.5357

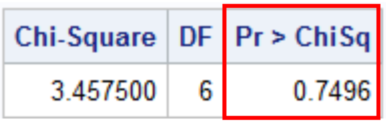
3) YSpecies = β_0 + βX1(palatal length) + βX2(postpalatal length) + βX8(least width of the braincase)



Root MSE	0.32504	R-Square	0.6148
Dependent Mean	1.36000	Adj R-Sq	0.5598
Coeff Var	23.90013		

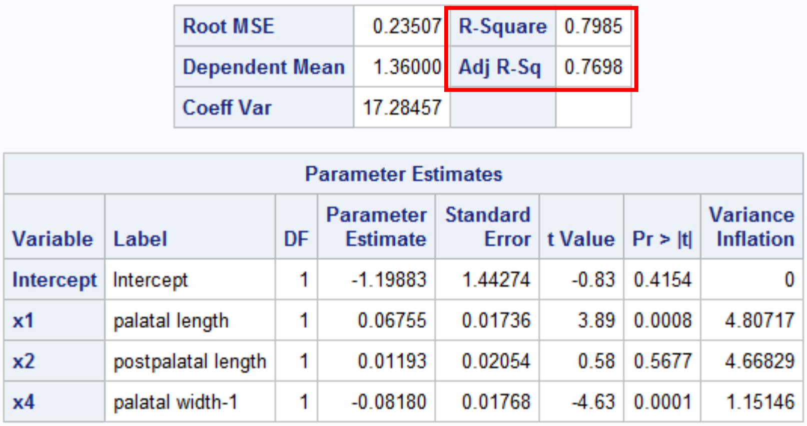
Parameter Estimates

Variable	Label	DF	Parameter Estimate	Standard Error	t Value	Pr > |t|	Variance Inflation
Intercept	Intercept	1	-6.70587	1.46744	-4.57	0.0002	0
x1	palatal length	1	0.04210	0.02602	1.62	0.1206	5.65246
x2	postpalatal length	1	0.01866	0.02924	0.64	0.5302	4.94677
x8	braincase width	1	0.02998	0.02764	1.08	0.2904	1.33447



Chi-Square	DF	Pr > ChiSq
3.457500	6	0.7496

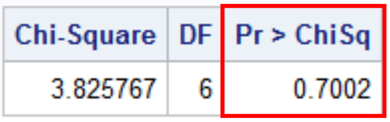
4) YSpecies = β_0 + βX1(palatal length) + βX2(postpalatal length) + βX4(postpalatal width)



Root MSE	0.23507	R-Square	0.7985
Dependent Mean	1.36000	Adj R-Sq	0.7698
Coeff Var	17.28457		

Parameter Estimates

Variable	Label	DF	Parameter Estimate	Standard Error	t Value	Pr > |t|	Variance Inflation
Intercept	Intercept	1	-1.19883	1.44274	-0.83	0.4154	0
x1	palatal length	1	0.06755	0.01736	3.89	0.0008	4.80717
x2	postpalatal length	1	0.01193	0.02054	0.58	0.5677	4.66829
x4	palatal width-1	1	-0.08180	0.01768	-4.63	0.0001	1.15146



Chi-Square	DF	Pr > ChiSq
3.825767	6	0.7002

After running the 4 different models, it seems that model #4 scores very well. In an effort to not to a “SAS Dump”, I will disclose that all model proved to be significant failing to prove the Null Hypothesis with a p-value <.0001. Model #4 was chosen because of the R^2 of 0.7985 and a significant 0.7002 provides strong evidence we can fail the Null Hypothesis of equal covariance matrices.

Going to the ‘Fit diagnostics’ (Figure 16) it is evident looking at our histogram and QQplot that the residual curve shows no signs against a normal distribution. The R-Student and Cook’s D only have one outlier, but we will keep since the group it is apart scores larger and is within the realm of possibilities.

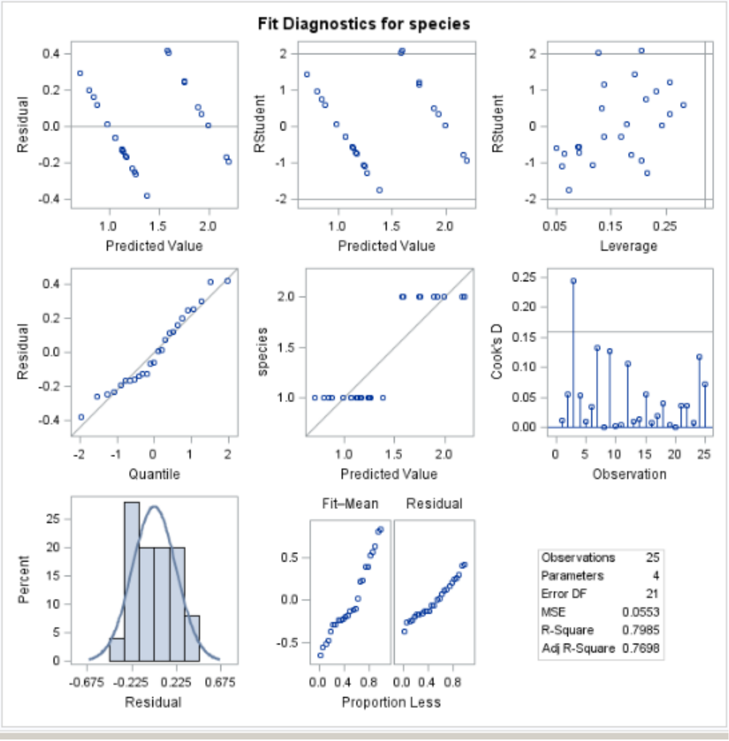
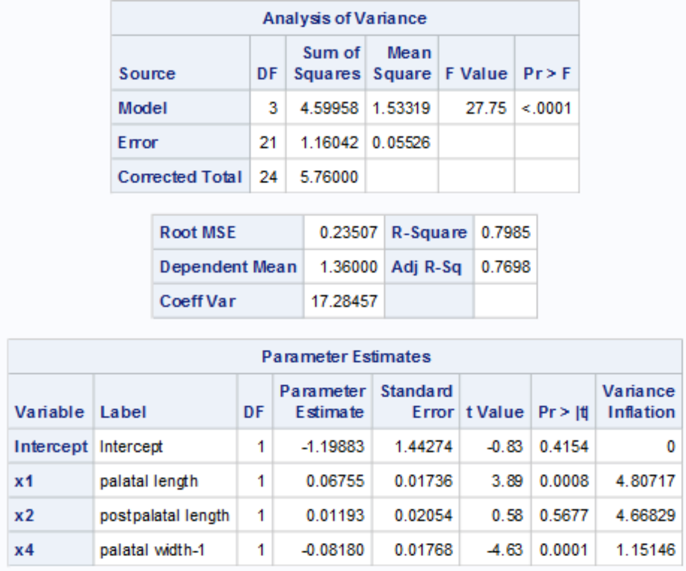


Figure 16

After examining for linearity, normality and constant variance our basic needs are reached. And find that this type of model which follows the width, length, depth of the skull, and width of brain cavity to be statistically significant variables with α= .05 level (n = 25, F = 29.06, p-Value = < .001).

YSpecies = β_0 + βX1(palatal length) + βX2(postpalatal length) + βX4(postpalatal width)



Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	3	4.59958	1.53319	27.75	<.0001
Error	21	1.16042	0.05526		
Corrected Total	24	5.76000			

Root MSE	0.23507	R-Square	0.7985
Dependent Mean	1.36000	Adj R-Sq	0.7698
Coeff Var	17.28457		

Parameter Estimates

Variable	Label	DF	Parameter Estimate	Standard Error	t Value	Pr > |t|	Variance Inflation
Intercept	Intercept	1	-1.19883	1.44274	-0.83	0.4154	0
x1	palatal length	1	0.06755	0.01736	3.89	0.0008	4.80717
x2	postpalatal length	1	0.01193	0.02054	0.58	0.5677	4.66829
x4	palatal width-1	1	-0.08180	0.01768	-4.63	0.0001	1.15146

Figure 17

Conclusion:

This data set is my second time around and I have a different answer. I did find in my previous attempt that only the EV X1 was a suffiecinet point in determining a species. But this time, I am adding two more variables to the model, X2 & X4. Before I conclude, this final model has been

```
DATA wolves;
LENGTH location $2 wolf $5 sex $1;
INPUT location $ wolf $ sex $ x1-x9;
subject=_n_;
if location = 'ar' then species = 1;
else if location = 'rm' then species = 2;
  LABEL
       X1 = 'palatal length'
       X2 = 'postpalatal length'
       X3 = 'zygomatic width'
       X4 = 'palatal width-1'
       X5 = 'palatal width-2'
       X6 = 'postg foramina width'
       X7 = 'interorbital width'
       X8 = 'braincase width'
       X9 = 'crown length';
datalines;
rm rmm1 m 126 104 141 81.0 31.8 65.7 50.9 44.0 18.2
rm rmm2 m 128 111 151 80.4 33.8 69.8 52.7 43.2 18.5
rm rmm3 m 126 108 152 85.7 34.7 69.1 49.3 45.6 17.9
rm rmm4 m 125 109 141 83.1 34.0 68.0 48.2 43.8 18.4
rm rmm5 m 126 107 143 81.9 34.0 66.1 49.0 42.4 17.9
rm rmm6 m 128 110 143 80.6 33.0 65.0 46.4 40.2 18.2
rm rmf1 f 116 102 131 76.7 31.5 65.0 45.4 39.0 16.8
rm rmf2 f 120 103 130 75.1 30.2 63.8 44.4 41.1 16.9
rm rmf3 f 116 103 125 74.7 31.6 62.4 41.3 44.2 17.0
ar arm1 m 117  99 134 83.4 34.8 68.0 40.7 37.1 17.2
ar arm2 m 115 100 149 81.0 33.1 66.7 47.2 40.5 17.7
ar arm3 m 117 106 142 82.0 32.6 66.0 44.9 38.2 18.2
ar arm4 m 117 101 144 82.4 32.8 67.5 45.3 41.5 19.0
ar arm5 m 117 103 149 82.8 35.1 70.3 48.3 43.7 17.8
ar arm6 m 119 101 143 81.5 34.1 69.1 50.1 41.1 18.7
ar arm7 m 115 102 146 81.4 33.7 66.4 47.7 42.0 18.2
ar arm8 m 117 100 144 81.3 37.2 66.8 41.4 37.6 17.7
ar arm9 m 114 102 141 84.1 31.8 67.8 47.8 37.8 17.2
ar arm10 m 110  94 132 76.9 30.1 62.1 42.0 40.4 18.1
ar arf1 f 112  94 134 79.5 32.1 63.3 44.9 42.7 17.7
ar arf2 f 109  91 133 77.9 30.6 61.9 45.2 41.2 17.1
ar arf3 f 112  99 139 77.2 32.7 67.4 46.9 40.9 18.3
ar arf4 f 112  99 133 78.5 32.5 65.5 44.2 34.1 17.5
ar arf5 f 113  97 146 84.2 35.4 68.7 51.0 43.6 17.2
ar arf6 f 107  97 137 78.1 30.7 61.6 44.9 37.3 16.5
;
RUN;

proc print data = wolves;
run;

proc means data = wolves;
class species;
var x1 x2 x3 x4 x5 x6 x7 x8 x9;
run;

proc univariate data=wolves;
histogram;
```

```
run;

*****Scatterplot Matrix Testing Variables*************************
;
title "Scatter Matrix of Wolves Data Set";
proc sgscatter data = wolves;
matrix x1 x2 x3 x4 x5 x6 x7 x8 x9  / diagonal=(histogram) group=species;
run;
ods listing style = rtf;
ods graphics on;

proc princomp data = wolves plots out=pcwolves;
var x1 x2 x3 x4 x5 x6 x7 x8 x9;
title 'Plot of the First Two Principal Components';
%plotit(data=pcwolves, labelvar=species,
plotvars=Prin2 Prin1, Color=black, color=blue);
run;

proc discrim data = wolves outstat=wolvestat
wcov pcov method=normal pool=test
manova listerr crosslisterr;
class species;
var x1 x2 x3 x4 x5 x6 x7 x8 x9;
run;

proc reg data=wolves;
title 'Reg Analysis / AIC VIF CLI';
model species = x1 x2 x3 x4 x5 x6 x7 x8 x9 / AIC VIF CLI;
run;
******
MANOVA;
proc glm data =wolves;
class species;
model x1 x2 x3 x4 x5 x6 x7 x8 x9 = species;
manova h = species;
run;

proc glmselect data = wolves;
model species = x1 x2 x3 x4 x5 x6 x7 x8 x9 / selection = LASSO;
run;


*******Other methods***;

proc discrim data = wolves pool=test crossvalidate;
class species;
var x1 x2 x3 x4 x5 x6 x7 x8 x9;
run;

proc reg data=wolves;
title 'Reg Analysis / AIC VIF CLI';
model species = x1 x2  / AIC VIF CLI;
run;

proc discrim data = wolves outstat=wolvestat
wcov pcov method=normal pool=test
manova listerr crosslisterr;
class species;
var x1 x2;
run;

proc reg data=wolves;
title 'Reg Analysis / AIC VIF CLI';
```

```
model species = x1 x4  / AIC VIF CLI;
run;

proc discrim data = wolves outstat=wolvestat
wcov pcov method=normal pool=test
manova listerr crosslisterr;
class species;
var x1 x4;
run;

proc reg data=wolves;
title 'Reg Analysis / AIC VIF CLI';
model species = x1 x2 x8 / AIC VIF CLI;
run;

proc discrim data = wolves outstat=wolvestat
wcov pcov method=normal pool=test
manova listerr crosslisterr;
class species;
var x1 x2 x8;
run;

proc reg data=wolves;
title 'Reg Analysis / AIC VIF CLI';
model species = x1 x2 x4 / AIC VIF CLI;
run;

proc discrim data = wolves outstat=wolvestat
wcov pcov method=normal pool=test
manova listerr crosslisterr;
class species;
var x1 x2 x4;
run;

*Leave out CV;
proc glmselect data = wolves;
model species = x1 x2 x4 / selection = forward(STOP=Press);
run;
*10 Fold CV;
proc glmselect data = wolves;
model species = x1 x2 x4 / selection = forward(Choose=CV)CVmethod=Random(10);
run;

*5 Fold CV;
proc glmselect data = wolves;
model species = x1 x2 x4 / selection = forward(STOP=Press);
run;
```

Bibliography:

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2. Jolicoeur, Pierre (1959). *Multivariate Geographical Variation in the Wolf Canis lupus L.* Vancouver: Society for the Study of Evolution.