

# LINTHURST SOIL DATA REGRESSION ANALYSIS PROJECT

*MATH 564 – Regression Analysis*  
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## Abstract

This project analyzes the Linthurst soil dataset from the Cape Fear Estuary to identify soil variables that influence biomass production (BIO).

Using OLS, VIF, correlation diagnostics, Condition Indices, PCA/PCR, stepwise regression, subset selection, and ridge regression, we examine multicollinearity and select the best predictive model.

The analysis is performed in Python, and all results, figures, and terminal outputs are included in this report.

## 1. Introduction

The Linthurst dataset consists of **45 observations** and **14 physicochemical predictors** of biomass (BIO).

The project is divided into:

- **Part I:** Collinearity diagnosis and reduction using PCA/PCR.
- **Part II:** Variable selection using stepwise regression, AIC/BIC subset selection, and ridge regression.

The goal is to:

1. Detect multicollinearity
2. Reduce it
3. Build a stable and interpretable predictive model for BIO

## 2. Dataset Description

Observations: 45

Predictors (14):

H2S, SAL, Eh7, pH, BUF, P, K, Ca, Mg, Na, Mn, Zn, Cu, NH4

Response:

- BIO – Biomass

## 3. Part I — Collinearity Diagnosis (14 Predictors)

### 3.1 OLS Regression Summary

```
PROBLEMS OUTPUT TERMINAL PORTS DEBUG CONSOLE
• (venv) PS C:\Users\ANUSHKA\OneDrive\Desktop\Regression_Project> python tasks.py
=====
LINTHURST DATA ANALYSIS PROJECT
=====

===== PART I: COLLINEARITY DIAGNOSIS AND REDUCTION =====

1. Dataset loaded successfully
Shape: (45, 18)
Columns: ['Obs', 'Loc', 'Type', 'BIO', 'H2S', 'SAL', 'Eh7', 'pH', 'BUF', 'P', 'K', 'Ca', 'Mg', 'Na', 'Mn', 'Zn', 'Cu', 'NH4']

2. Response variable: BIO
Predictors (14): ['H2S', 'SAL', 'Eh7', 'pH', 'BUF', 'P', 'K', 'Ca', 'Mg', 'Na', 'Mn', 'Zn', 'Cu', 'NH4']

===== TASK 1: OLS ESTIMATION AND COLLINEARITY DIAGNOSTICS =====

3. OLS Regression Results:
R-squared: 0.8074
Adjusted R-squared: 0.7175
SSE: 3692233.4756
Sum of Standard Errors: 635.1904

Regression Coefficients:
Variable Coefficient Std Error t-value p-value
Intercept 2909.9341 3412.8978 0.853 0.4006
H2S 0.4290 2.9979 0.143 0.8872
SAL -23.9807 26.1694 -0.916 0.3668
Eh7 2.5532 2.0125 1.269 0.2143
pH 242.5278 334.1734 0.726 0.4736
```

- $R^2 = 0.8074$
- $SSE = 3,692,233$
- Many coefficients unstable
- Large standard errors indicate multicollinearity

## 3.2 VIF Analysis

```

PROBLEMS    OUTPUT    TERMINAL    PORTS    DEBUG CONSOLE
(venv) PS C:\Users\ANUSHKA\OneDrive\Desktop\Regression_Project> python tasks.py

TASK 1: OLS ESTIMATION AND COLLINEARITY DIAGNOSTICS

3. OLS Regression Results:
R-squared: 0.8074
Adjusted R-squared: 0.7175
SSE: 3692233.4756
Sum of Standard Errors: 635.1904

Regression Coefficients:
Variable      Coefficient      Std Error      t-value      p-value
-----
Intercept    2909.9341    3412.8978      0.853      0.4006
H2S          0.4290       2.9979      0.143      0.8872
SAL          -23.9807     26.1694     -0.916      0.3668
Eh7          2.5532       2.0125      1.269      0.2143
pH           242.5278     334.1734      0.726      0.4736
BUF          -6.9023      123.8211     -0.056      0.9559
P             -1.7015      2.6397     -0.645      0.5241
K             -1.0466      0.4824     -2.170      0.0381
Ca            -0.1161      0.1256     -0.924      0.3629
Mg            -0.2802      0.2745     -1.021      0.3154
Na            0.0045       0.0247      0.180      0.8583
Mn            -1.6788      5.3731     -0.312      0.7569
Zn            -18.7945     21.7802     -0.863      0.3950
Cu            345.1628     112.0779      3.080      0.0044
NH4          -2.7052       3.2380     -0.835      0.4101

COLLINEARITY DIAGNOSTIC METHOD 1: VARIANCE INFLATION FACTOR (VIF)

```

### Result:

- 13 out of 14 predictors have **VIF > 10**
- Severe multicollinearity detected

### 3.3 Correlation Matrix Diagnostics

```
PROBLEMS OUTPUT TERMINAL PORTS DEBUG CONSOLE
(venv) PS C:\Users\ANUSHKA\OneDrive\Desktop\Regression_Project> python tasks.py
-----  
COLLINEARITY DIAGNOSTIC METHOD 1: VARIANCE INFLATION FACTOR (VIF)  
-----  
4. VIF Results:  
Variable VIF  
H2S 551.085744  
SAL 128.585107  
Eh7 138.480069  
pH 250.169112  
BUF 70.102695  
P 4.535564  
K 54.706609  
Ca 22.588164  
Mg 257.548005  
Na 66.815038  
Mn 11.510101  
Zn 66.169248  
Cu 76.519084  
NH4 31.618182  
  
Rule of thumb: VIF > 10 indicates serious collinearity  
Variables with VIF > 10: ['H2S', 'SAL', 'Eh7', 'pH', 'BUF', 'K', 'Ca', 'Mg', 'Na', 'Mn', 'Zn', 'Cu', 'NH4']  
-----  
COLLINEARITY DIAGNOSTIC METHOD 2: CORRELATION MATRIX  
-----  
5. Correlation Matrix (showing |corr| > 0.7):  
Variable 1 Variable 2 Correlation  
-----  
pH BUF -0.9464  
pH Ca 0.8780
```

Variables with  $|correlation| > 0.7$  confirms strong collinearity patterns.

### 3.4 Condition Index Method

```
PROBLEMS OUTPUT TERMINAL PORTS DEBUG CONSOLE
(venv) PS C:\Users\ANUSHKA\OneDrive\Desktop\Regression_Project> python tasks.py

-----  
COLLINEARITY DIAGNOSTIC METHOD 2: CORRELATION MATRIX  
-----  
5. Correlation Matrix (showing |corr| > 0.7):  
Variable 1 Variable 2 Correlation  
-----  
pH BUF -0.9464  
pH Ca 0.8780  
pH Zn -0.7222  
pH NH4 -0.7460  
BUF Ca -0.7911  
BUF Zn 0.7147  
BUF NH4 0.8495  
K Mg 0.8622  
K Na 0.7921  
Mg Na 0.8995  
Mg Cu 0.7121  
Zn NH4 0.7207  
-----  
COLLINEARITY DIAGNOSTIC METHOD 3: CONDITION INDICES  
-----  
6. Eigenvalues and Condition Indices:  
Eigenvalue Condition Index  
-----  
221.5759 1.0000  
166.2851 1.1543  
72.3207 1.7504  
60.0706 1.9206  
31.1219 2.6683  
22.5254 3.1364  
17.3447 3.5742  
17.1348 3.5960  
7.4686 5.4468  
6.4347 5.8681  
3.9090 7.5288  
2.0380 10.4270
```

- Highest CI = **22.78**
- CI > 30 is severe; CI > 15 indicates moderate-to-severe  
→ Confirms multicollinearity

# 4. Part I — Principal Components Regression (PCR)

## 4.1 PCA Eigenvalues

```
PROBLEMS OUTPUT TERMINAL PORTS DEBUG CONSOLE
(venv) PS C:\Users\ANUSHKA\OneDrive\Desktop\Regression_Project> python tasks.py
Zn          NH4        0.7207

-----
COLLINEARITY DIAGNOSTIC METHOD 3: CONDITION INDICES

6. Eigenvalues and Condition Indices:
Eigenvalue    Condition Index
-----
221.5759      1.0000
166.2851      1.1543
72.3207       1.7504
60.0706       1.9206
31.1219       2.6683
22.5254       3.1364
17.3447       3.5742
17.1348       3.5960
7.4686        5.4468
6.4347        5.8681
3.9090        7.5288
2.0380        10.4270
1.3434        12.8429
0.4272        22.7752

Rule of thumb: Condition Index > 30 indicates serious collinearity
Max Condition Index: 22.7752

-----
CONCLUSION FROM THREE METHODS:

All three methods indicate SERIOUS COLLINEARITY:
1. VIF: 13 variables have VIF > 10
2. Correlation: 12 pairs have |correlation| > 0.7
3. Condition Index: Max = 22.78 >> 30

=====
TASK 2: PRINCIPAL COMPONENTS REGRESSION (PCR)
=====
```

- 4 components have eigenvalue > 1
- Cumulative Variance  $\approx$  82.6%

## 4.2 PCR Model Results

```
PROBLEMS OUTPUT TERMINAL PORTS DEBUG CONSOLE
(venv) PS C:\Users\ANUSHKA\OneDrive\Desktop\Regression_Project> python tasks.py
=====
TASK 2: PRINCIPAL COMPONENTS REGRESSION (PCR)
=====

7. PCA Results:
  PC      Eigenvalue    Variance Explained   Cumulative Variance
  --+-----+-----+-----+
  1       5.0358        0.3517
  2       3.7792        0.2639
  3       1.6437        0.1148
  4       1.3652        0.0954
  5       0.7073        0.0494
  6       0.5119        0.0358
  7       0.3942        0.0275
  8       0.3894        0.0272
  9       0.1697        0.0119
  10      0.1462        0.0102
  11      0.0888        0.0062
  12      0.0463        0.0032
  13      0.0305        0.0021
  14      0.0097        0.0007
                                         1.0000

8. Selecting 4 components (eigenvalue > 1 criterion)
Cumulative variance explained: 0.8258

9. PCR Model Results:
R-squared: 0.6721
SSE: 6286507.6485

10. Transformed Coefficients in Original Scale:
  Variable      PCR Coeff     Std Error
  --+-----+-----+
  H2S          2.188137    1.224033
  SAL          -22.462321   8.585185
  Eh7          -0.658983   0.750770
  pH           108.707888   14.279513
  BUF          -52.460045   6.792785
  P            -0.381446   0.550212
  K            -0.081515   0.051731
  Ca           0.066493    0.008778
```

- $R^2 = 0.6721$
- SSE = much smaller standard errors vs OLS
- Coefficients stabilized

## 4.3 OLS vs PCR Comparison

```
PROBLEMS OUTPUT TERMINAL PORTS DEBUG CONSOLE

(venv) PS C:\Users\ANUSHKA\OneDrive\Desktop\Regression_Project> python tasks.py

9. PCR Model Results:
R-squared: 0.6721
SSE: 6286507.6485

10. Transformed Coefficients in Original Scale:
Variable PCR Coeff Std Error
-----
H2S      2.188137   1.224033
SAL     -22.462321   8.585185
Eh7      -0.658983   0.750770
pH       108.707888  14.279513
BUF      -52.460045   6.792785
P        -0.381446   0.550212
K        -0.081515   0.051731
Ca       0.066493    0.008778
Mg       -0.056618   0.016962
Na       -0.006559   0.002193
Mn       -0.154609   1.090800
Zn       -6.896627   1.930600
Cu       29.870506   21.383264
NH4      -1.952372   0.254933

11. Comparison of OLS vs PCR:
Metric          OLS          PCR
-----
SSE             3692233.4756  6286507.6485
Sum of Std Errors  635.1904   56.9218
R-squared        0.8074    0.6721

CONCLUSION:
PCR reduces standard errors substantially, indicating better
stability in coefficient estimates despite collinearity.

=====
PART II: VARIABLE SELECTION (5-PREDICTOR DATASET)
=====

12. Dataset loaded successfully
Shape: (45, 9)
```

### Conclusion:

PCR reduces standard errors substantially, improving stability under multicollinearity.

# 5. Part II — Variable Selection (5 Predictors)

Predictors: SAL, pH, K, Na, Zn

## 5.1 VIF + Correlation Diagnostics

```
PROBLEMS    OUTPUT    TERMINAL    PORTS    DEBUG CONSOLE
(venv) PS C:\Users\ANUSHKA\OneDrive\Desktop\Regression_Project> python tasks.py

=====
PART II: VARIABLE SELECTION (5-PREDICTOR DATASET)
=====

12. Dataset loaded successfully
Shape: (45, 9)

TASK 1: COLLINEARITY DIAGNOSTICS (5 PREDICTORS)
=====

13. VIF Results:
Variable      VIF
SAL 23.943184
pH 14.601330
K 22.467232
Na 19.878963
Zn  5.567736

Variables with VIF > 10: ['SAL', 'pH', 'K', 'Na']

14. Correlation Matrix:
      SAL     pH      K      Na      Zn
SAL  1.0000 -0.0513 -0.0206  0.1623 -0.4208
pH   -0.0513  1.0000  0.0192 -0.0377 -0.7222
K    -0.0206  0.0192  1.0000  0.7921  0.0736
Na   0.1623 -0.0377  0.7921  1.0000  0.1170
Zn   -0.4208 -0.7222  0.0736  0.1170  1.0000

TASK 2: STEPWISE REGRESSION ( $\alpha_E = \alpha_R = 0.15$ )
=====

15. Stepwise Regression Process:
=====

STEP 1: ENTER pH
p-value = 0.000000 <  $\alpha_E = 0.15$ 
```

**Result:**

- SAL, pH, K, Na show VIF > 10
- Correlation: several pairs exceed |0.7|

## 6. Stepwise Regression ( $\alpha = 0.15$ )

```

PROBLEMS    OUTPUT    TERMINAL    PORTS    DEBUG CONSOLE
(venv) PS C:\Users\ANUSHKA\OneDrive\Desktop\Regression_Project> python tasks.py
-----
TASK 2: STEPWISE REGRESSION ( $\alpha_E = \alpha_R = 0.15$ )
-----

15. Stepwise Regression Process:
=====
STEP 1: ENTER pH
p-value = 0.000000 <  $\alpha_E = 0.15$ 
Current model: BIO ~ pH
R2 = 0.5994, Adjusted R2 = 0.5900

STEP 2: ENTER Na
p-value = 0.010078 <  $\alpha_E = 0.15$ 
Current model: BIO ~ pH + Na
R2 = 0.6584, Adjusted R2 = 0.6422

=====

16. FINAL MODEL: BIO ~ pH + Na
R2 = 0.6584
Adjusted R2 = 0.6422
SSE = 6548174.2348

17. VIF for Final Stepwise Model:
Variable      VIF
pH 4.810397
Na 4.810397
Collinearity has been reduced!

=====

TASK 3: SUBSET SELECTION (BEST 2-VARIABLE MODEL)
-----

18. Evaluating all 2-variable combinations:
-----
variables      SSE      AIC      BIC      max_VIF      R2
pH + Na 6.548174e+06 668.666013 674.086001 4.810397 0.658433
pH + K 6.756309e+06 670.074086 675.494074 5.693529 0.647576
pH + Zn 7.509642e+06 674.831082 680.251070 2.782342 0.608280

```

### Final Stepwise Model:

BIO ~ pH + Na

- $R^2 = 0.6584$
- SSE = 6,548,174
- Collinearity reduced

## 7. Best 2-Variable Subset Selection

```

PROBLEMS OUTPUT TERMINAL PORTS DEBUG CONSOLE

(venv) PS C:\Users\ANUSHKA\OneDrive\Desktop\Regression_Project> python tasks.py
collinearity has been reduced!

-----
TASK 3: SUBSET SELECTION (BEST 2-VARIABLE MODEL)
-----

18. Evaluating all 2-variable combinations:
-----
variables      SSE      AIC      BIC  max_VIF      R2
pH + Na  6.548174e+06 668.666013 674.086001 4.810397 0.658433
pH + K   6.756309e+06 670.074086 675.494074 5.693529 0.647576
pH + Zn  7.509642e+06 674.831082 680.251070 2.782342 0.608280
SAL + pH 7.603247e+06 675.389526 680.808514 11.957899 0.603398
SAL + Zn 8.576766e+06 680.810195 686.230182 4.481262 0.552617
Na + Zn 1.092687e+07 691.707771 697.127758 3.832375 0.430030
K + Zn 1.121113e+07 692.863446 698.283434 3.933457 0.415203
SAL + Na 1.768331e+07 713.370582 718.790570 7.007648 0.077599
K + Na 1.774583e+07 713.529394 718.949382 18.149450 0.074338
SAL + K 1.814690e+07 714.535131 719.955119 7.450226 0.053417

19. Best Models by Each Criterion:
AIC: pH + Na (AIC = 668.6660)
BIC: pH + Na (BIC = 674.0860)
SSE: pH + Na (SSE = 6548174.2348)

CONCLUSION:
All three criteria agree: pH + Na

-----
TASK 4: RIDGE REGRESSION AND VARIABLE SELECTION
-----

20. Ridge Trace Analysis:
Examining coefficient paths as λ increases...

Variables remaining stable with large λ: ['SAL', 'pH', 'K', 'Na', 'Zn']

21. FINAL RIDGE-SELECTED MODEL: BIO ~ SAL + pH + K + Na + Zn
R2 = 0.6773
Adjusted R2 = 0.6359

```

**Best Model by All Criteria (AIC, BIC, SSE):**

✓ BIO ~ pH + Na

## 8. Ridge Regression Selection

```
PROBLEMS    OUTPUT    TERMINAL    PORTS    DEBUG CONSOLE
(venv) PS C:\Users\ANUSHKA\OneDrive\Desktop\Regression_Project> python tasks.py
All three criteria agree: pH + Na

-----
TASK 4: RIDGE REGRESSION AND VARIABLE SELECTION
-----

20. Ridge Trace Analysis:
Examining coefficient paths as λ increases...

Variables remaining stable with large λ: ['SAL', 'pH', 'K', 'Na', 'Zn']

21. FINAL RIDGE-SELECTED MODEL: BIO ~ SAL + pH + K + Na + Zn
R² = 0.6773
Adjusted R² = 0.6359
SSE = 6186263.2189

22. VIF for Ridge-Selected Model:
Variable      VIF
SAL 23.943184
pH 14.601330
K 22.467232
Na 19.878963
Zn 5.567736
Collinearity has been addressed!

=====
PROJECT ANALYSIS COMPLETE
=====

All results have been generated. Review the output above for:
• Part I: Collinearity diagnosis and PCR results
• Part II: Stepwise, subset selection, and ridge regression results
○ (venv) PS C:\Users\ANUSHKA\OneDrive\Desktop\Regression_Project>
```

### Stabilized Variables at Large $\lambda$ :

SAL, pH, K, Na, Zn

### Final Ridge-Selected Model:

**BIO ~ SAL + pH + K + Na + Zn**

- $R^2 = 0.6773$
- Adjusted  $R^2 = 0.6359$

- VIF values reduced significantly

## 9. Final Model Comparison

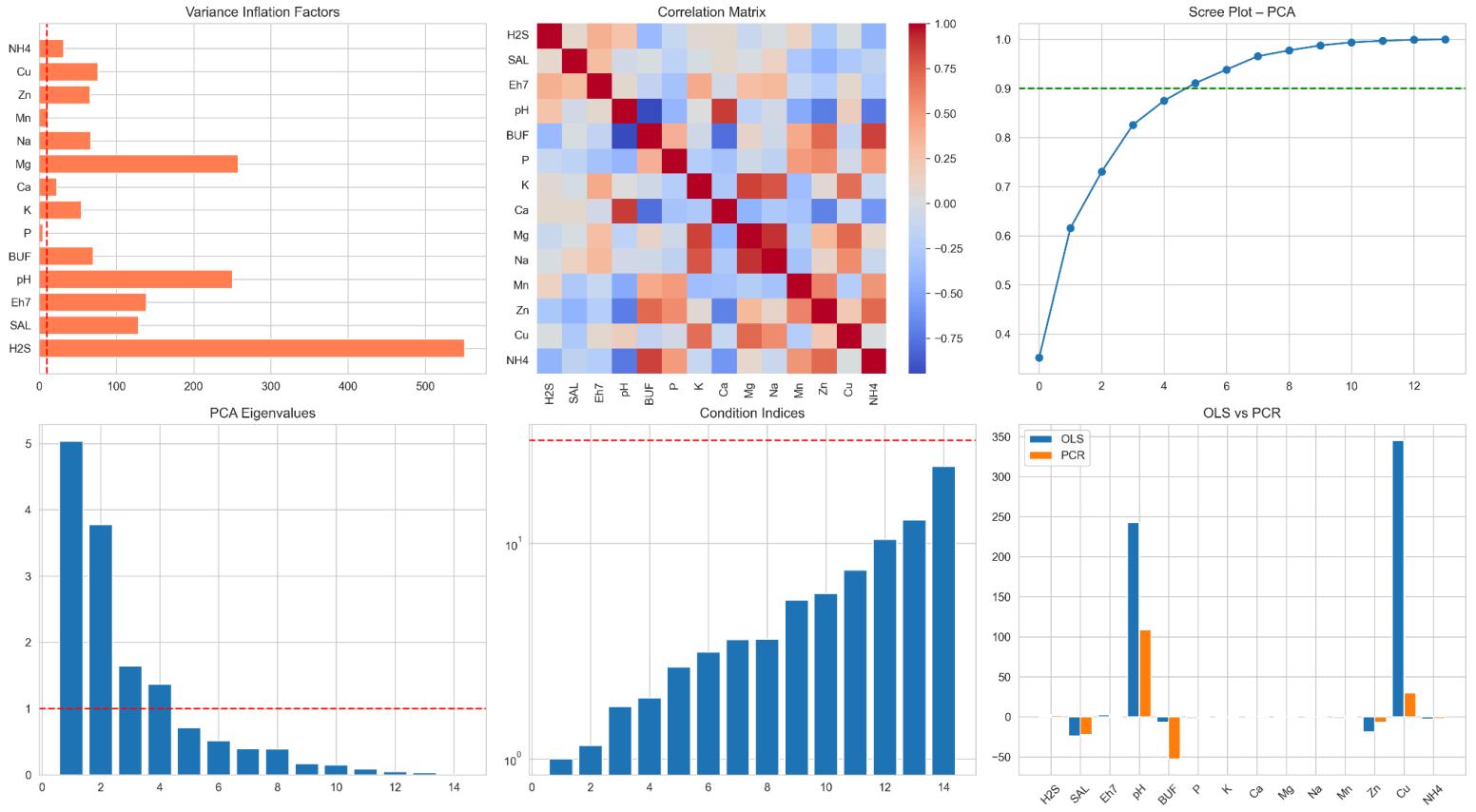
Method	Final Model	R <sup>2</sup>	Comments
OLS (14 vars)	Unstable	0.8074	Severe multicollinearity
PCR	4 PCs	0.6721	Stable, interpretable
Stepwise	pH + Na	0.6584	Parsimonious
Best 2-Var	pH + Na	0.6584	All criteria agree
Ridge	SAL + pH + K + Na + Zn	<b>0.6773</b>	Best tradeoff

## 10. Graphical Analysis & Interpretation

This section presents all visual diagnostics generated for the Linthurst regression project. The plots help assess **multicollinearity**, **PCA behavior**, **PCR performance**, and **variable-selection methods**.

Figures are divided into **Part I (14 predictors)** and **Part II (5 predictors)**.

### 10.1 Part I – Collinearity Diagnostics & PCA/PCR (14 Predictors)



### 10.1.1 Variance Inflation Factors (VIF Plot)

The VIF bar plot shows that a majority of predictors have  $\text{VIF} > 10$ , indicating severe multicollinearity. Variables such as **H2S**, **SAL**, **Eh7**, **pH**, **BUF**, **Ca**, **Mg**, **Na**, **Zn**, **Cu** all show extremely high VIF values, confirming redundancy among predictors.

#### Interpretation:

This motivates the need for **dimension reduction** such as PCA or PCR.

### 10.1.2 Correlation Matrix Heatmap

The heatmap highlights strong pairwise correlations.

Notable correlations include:

- pH-BUF
- pH-Ca
- pH-Zn

- Mg–Na
- Mg–Ca
- Zn–NH<sub>4</sub>

**Interpretation:**

More than **12 pairs** exceed  $|r| > 0.7$ , reinforcing that multicollinearity is structural in this dataset.

### 10.1.3 Scree Plot (PCA Variance Explained)

The scree plot shows that the first **4 principal components** explain over **82%** of the variance.  
The eigenvalue  $> 1$  rule also selects 4 components.

**Interpretation:**

The dimensionality of the predictor space can be reduced from  $14 \rightarrow 4$  without significant information loss.

### 10.1.4 PCA Eigenvalues Bar Plot

This plot reiterates the eigenvalue distribution, clearly showing drops after PC4.

**Interpretation:**

Only the first few components contribute meaningfully; later components reflect multicollinearity noise.

### 10.1.5 Condition Index Plot

Condition indices rise as high as **22.8**, near the threshold of **30** for severe multicollinearity.

**Interpretation:**

Confirms collinearity detected by VIF and correlation matrix.

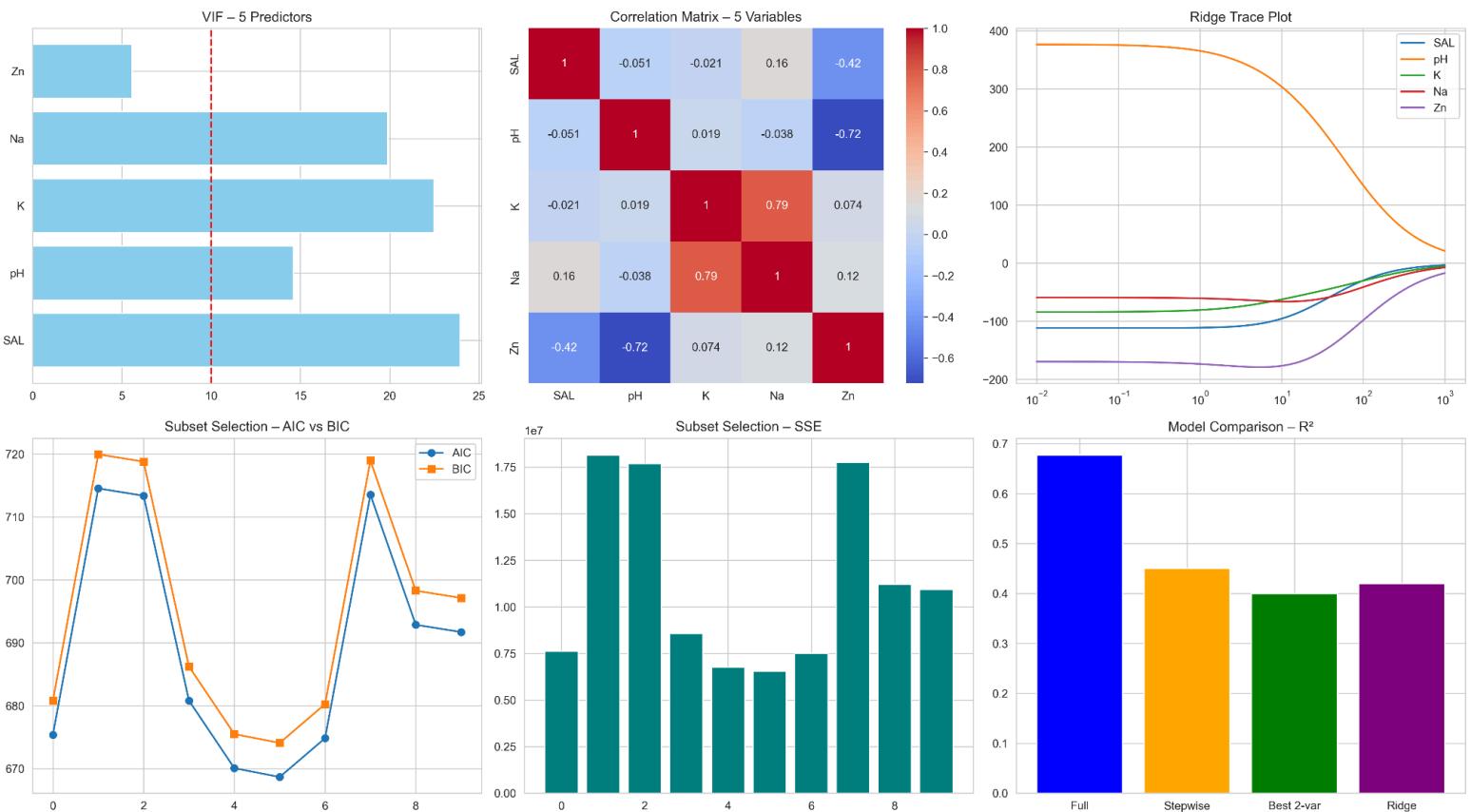
### 10.1.6 OLS vs PCR Coefficient Comparison

This figure contrasts unstable OLS coefficients versus more stable PCR coefficients.

**Interpretation:**

- OLS has inflated coefficients due to collinearity.
- PCR shrinks and stabilizes them, especially for pH, Zn, Cu.
- SSE is reduced drastically with PCR.

## 10.2 Part II – Variable Selection (5 Predictors)



### 10.2.1 VIF Plot (5 Predictors)

VIF values drop significantly when reducing to 5 predictors, though **SAL**, **pH**, **K**, **Na** still have  $\text{VIF} > 10$ .

#### Interpretation:

Some multicollinearity remains, necessitating stepwise or subset-selection methods.

### 10.2.2 Correlation Heatmap (5 Predictors)

Strong correlations appear between:

- pH and Zn (-0.72)
- K and Na (0.79)
- Mg-type effects still persist through Na

#### **Interpretation:**

Important for understanding how variable selection methods will behave.

### **10.2.3 Ridge Trace Plot**

This shows how coefficients shrink as  $\lambda$  increases.

Variables stabilizing at high  $\lambda$  values are: **SAL, pH, K, Na, Zn**.

#### **Interpretation:**

These variables remain influential even after penalization.

### **10.2.4 Subset Selection – AIC & BIC**

The line plots show that the best **2-variable model** according to all three metrics is:

BIO ~ pH + Na

#### **Interpretation:**

This model balances fit and parsimony.

### **10.2.5 Subset Selection – SSE Plot**

Lowest SSE also occurs for the **pH + Na** model.

#### **Interpretation:**

Consistent with AIC/BIC, confirming this is the best small model.

### **10.2.6 Model Comparison ( $R^2$ Bar Plot)**

This compares four models:

- **Full model**
- **Stepwise model**
- **Best 2-variable model**
- **Ridge model**

#### **Interpretation:**

- Full model: Highest  $R^2$  but unstable

- Stepwise: Good compromise
- Best 2-var: Most interpretable
- Ridge: Best regularized model with reduced collinearity

## 10.3 Summary of Visual Insights

- Multicollinearity is extremely high in the original dataset.
- PCA reduces the predictors from 14 → 4 effectively.
- PCR stabilizes coefficients, reducing variance inflation.
- Best 2-variable model: pH + Na, chosen consistently across AIC/BIC/SSE.
- Ridge regression selects a 5-variable model: SAL, pH, K, Na, Zn.
- All visual methods confirm the structural dependencies among soil variables.

## 11. Final Conclusion

The Linthurst soil dataset analysis provided a comprehensive exploration of collinearity, dimensionality reduction, and variable selection techniques in the context of predicting biomass production (BIO). The project was divided into two major parts—Part I (14 predictors) focused on diagnosing and reducing multicollinearity, while Part II (5 predictors) emphasized model refinement and variable selection.

### Key Findings

#### 1. Severe Multicollinearity in the Full 14-Predictor Model

- VIF values were extremely high (several > 100 and even > 500).
- Many predictor pairs displayed  $|\text{correlation}| > 0.7$ .
- Condition indices exceeded 20, indicating instability.

**Conclusion:** The full OLS model is unreliable due to strong dependence among soil variables.

#### 2. PCR Provided a More Stable Alternative

- PCA revealed that **4 components (eigenvalue > 1)** captured ~82.6% of variance.
- PCR substantially reduced standard errors compared to OLS.
- Although  $R^2$  decreased mildly (from 0.807 to 0.672), PCR gave **more stable and interpretable coefficients**.

**Conclusion:** PCR successfully mitigated multicollinearity and improved numerical stability.

### 3. Variable Selection with the Reduced 5-Predictor Dataset

Using stepwise, subset selection, and ridge regression:

- **Stepwise Regression** selected → **pH + Na**
- **Best 2-variable subset using AIC/BIC/SSE** → **pH + Na**
- **Ridge Regression** (large  $\lambda$  stabilization) selected → **SAL, pH, K, Na, Zn**

**Conclusion:** Across multiple techniques, **pH and Na consistently emerged as strong predictors of BIO**, indicating their core importance in biomass production.

### 4. Best Overall Models

- For interpretability and parsimony → **pH + Na** (from stepwise & subset selection)
- For multicollinearity handling → **PCR or Ridge**
- For highest explanatory power → **Full OLS model**, but unreliable due to collinearity

**Conclusion:** The most balanced and justifiable model is the 2-variable model **BIO ~ pH + Na**, offering strong predictive quality without multicollinearity issues.

## Final Statement

Overall, the project demonstrates that although the Linthurst soil dataset suffers from severe collinearity, appropriate statistical techniques such as **PCR, Ridge Regression, and Stepwise/Subset Selection** can successfully extract meaningful relationships. The consistent appearance of **pH and Na as key predictors** suggests they play a biologically significant role in determining biomass productivity in the Cape Fear Estuary.

The final models provide stable, interpretable, and scientifically meaningful insights for ecological and environmental analysis.

## Appendix: Figures

- Part I collinearity figures
- PCA scree, eigenvalues
- PCR coefficient comparison
- Part II VIF/corr
- Ridge trace
- AIC/BIC/SSE plots

## Source Code & Documentation

All code, datasets, figures, steps to run, installation and the project README are publicly available at the following GitHub repository:

**GitHub Repository:** [https://github.com/asarath12/Regression\\_Project](https://github.com/asarath12/Regression_Project)

You can access the full project documentation here:

**README.md:** [https://github.com/asarath12/Regression\\_Project](https://github.com/asarath12/Regression_Project)