

```

import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.cluster import MiniBatchKMeans, KMeans,
AgglomerativeClustering, AffinityPropagation, Birch, DBSCAN,
MeanShift, SpectralClustering
from sklearn.mixture import GaussianMixture
from sklearn.cluster import OPTICS
from scipy.cluster.hierarchy import linkage, dendrogram

from sklearn.metrics import silhouette_score, adjusted_rand_score,
homogeneity_completeness_v_measure

df=pd.read_csv("Crop_recommendation.csv")

df.head()

      Nitrogen  phosphorus  potassium  temperature  humidity
ph \
0         90          42          43     20.879744   82.002744  6.502985
1         85          58          41     21.770462   80.319644  7.038096
2         60          55          44     23.004459   82.320763  7.840207
3         74          35          40     26.491096   80.158363  6.980401
4         78          42          42     20.130175   81.604873  7.628473

      rainfall  label  Unnamed: 8  Unnamed: 9
0  202.935536  rice      NaN      NaN
1  226.655537  rice      NaN      NaN
2  263.964248  rice      NaN      NaN
3  242.864034  rice      NaN      NaN
4  262.717340  rice      NaN      NaN

df.isnull()

      Nitrogen  phosphorus  potassium  temperature  humidity  ph
rainfall \
0       False       False      False      False      False  False
1       False       False      False      False      False  False
2       False       False      False      False      False  False
3       False       False      False      False      False  False
4       False       False      False      False      False  False

```

```
4      False    False    False    False    False    False    False
False
...
...
2195  False    False    False    False    False    False    False
False
2196  False    False    False    False    False    False    False
False
2197  False    False    False    False    False    False    False
False
2198  False    False    False    False    False    False    False
False
2199  False    False    False    False    False    False    False
False
```

```
      label  Unnamed: 8  Unnamed: 9
0      False      True      True
1      False      True      True
2      False      True      True
3      False      True      True
4      False      True      True
...
...
2195  False      True      True
2196  False      True      True
2197  False      True      True
2198  False      True      True
2199  False      True      True
```

[2200 rows x 10 columns]

```
df.isnull().sum()
```

```
Nitrogen          0
phosphorus        0
potassium         0
temperature       0
humidity          0
ph                0
rainfall          0
label             0
Unnamed: 8        2200
Unnamed: 9        2200
dtype: int64
```

```
df=df.dropna(axis=1)
```

```
df
```

```
      Nitrogen  phosphorus  potassium  temperature  humidity
ph \
0           90          42          43     20.879744   82.002744
```

```

6.502985
1          85        58       41   21.770462  80.319644
7.038096
2          60        55       44   23.004459  82.320763
7.840207
3          74        35       40   26.491096  80.158363
6.980401
4          78        42       42   20.130175  81.604873
7.628473
...
.
2195      107        34       32   26.774637  66.413269
6.780064
2196      99         15       27   27.417112  56.636362
6.086922
2197      118        33       30   24.131797  67.225123
6.362608
2198      117        32       34   26.272418  52.127394
6.758793
2199      104        18       30   23.603016  60.396475
6.779833

      rainfall    label
0     202.935536  rice
1     226.655537  rice
2     263.964248  rice
3     242.864034  rice
4     262.717340  rice
...
2195  177.774507  coffee
2196  127.924610  coffee
2197  173.322839  coffee
2198  127.175293  coffee
2199  140.937041  coffee

```

[2200 rows x 8 columns]

`df.describe()`

	Nitrogen	phosphorus	potassium	temperature	humidity
\count	2200.000000	2200.000000	2200.000000	2200.000000	2200.000000
mean	50.551818	53.362727	48.149091	25.616244	71.481779
std	36.917334	32.985883	50.647931	5.063749	22.263812
min	0.000000	5.000000	5.000000	8.825675	14.258040
25%	21.000000	28.000000	20.000000	22.769375	60.261953

50%	37.000000	51.000000	32.000000	25.598693	80.473146
75%	84.250000	68.000000	49.000000	28.561654	89.948771
max	140.000000	145.000000	205.000000	43.675493	99.981876

	ph	rainfall
count	2200.000000	2200.000000
mean	6.469480	103.463655
std	0.773938	54.958389
min	3.504752	20.211267
25%	5.971693	64.551686
50%	6.425045	94.867624
75%	6.923643	124.267508
max	9.935091	298.560117

```

train, test = train_test_split(df, test_size=0.2, random_state=42)
X_train = train[['Nitrogen', 'phosphorus', 'potassium', 'temperature',
'humidity', 'ph', 'rainfall']].values
X_test = test[['Nitrogen', 'phosphorus', 'potassium', 'temperature',
'humidity', 'ph', 'rainfall']].values
target = train['label']

# MiniBatchKMeans
mini_batch_kmeans = MiniBatchKMeans(n_clusters=5, random_state=42)
mini_batch_kmeans.fit(X_train)

/usr/local/lib/python3.10/dist-packages/sklearn/cluster/
_kmeans.py:870: FutureWarning: The default value of `n_init` will
change from 3 to 'auto' in 1.4. Set the value of `n_init` explicitly
to suppress the warning
    warnings.warn(
    MiniBatchKMeans(n_clusters=5, random_state=42)

# KMeans
kmeans = KMeans(n_clusters=5, random_state=42)
kmeans.fit(X_train)

/usr/local/lib/python3.10/dist-packages/sklearn/cluster/
_kmeans.py:870: FutureWarning: The default value of `n_init` will
change from 10 to 'auto' in 1.4. Set the value of `n_init` explicitly
to suppress the warning
    warnings.warn(
    KMeans(n_clusters=5, random_state=42)

```

```

# AgglomerativeClustering
agglomerative = AgglomerativeClustering(n_clusters=5)
agglomerative.fit(X_train)

AgglomerativeClustering(n_clusters=5)

# AffinityPropagation
affinity_propagation = AffinityPropagation()
affinity_propagation.fit(X_train)

AffinityPropagation()

# Birch
birch = Birch(n_clusters=5)
birch.fit(X_train)

Birch(n_clusters=5)

# DBSCAN
dbscan = DBSCAN()
dbscan.fit(X_train)

DBSCAN()

# MeanShift
mean_shift = MeanShift()
mean_shift.fit(X_train)

MeanShift()

# SpectralClustering
spectral_clustering = SpectralClustering(n_clusters=5,
random_state=42)
spectral_clustering.fit(X_train)

/usr/local/lib/python3.10/dist-packages/sklearn/manifold/
_spectral_embedding.py:274: UserWarning: Graph is not fully connected,
spectral embedding may not work as expected.
    warnings.warn(
/usr/local/lib/python3.10/dist-packages/sklearn/manifold/_spectral_emb
eding.py:393: UserWarning: Exited at iteration 168 with accuracies
[3.66082342e-15 2.07760736e-05 1.42376730e-05 2.03805669e-05
 5.19939067e-05 2.40275609e-05]
not reaching the requested tolerance 2.6226043701171875e-05.
Use iteration 138 instead with accuracy
1.915155369337418e-05.

_, diffusion_map = lobpcg(
/usr/local/lib/python3.10/dist-packages/sklearn/manifold/_spectral_emb
eding.py:393: UserWarning: Exited postprocessing with accuracies
[1.18534300e-15 2.07303497e-05 1.56798612e-05 1.79976679e-05
 2.33353322e-05 3.71661112e-05]

```

```
not reaching the requested tolerance 2.6226043701171875e-05.  
    _, diffusion_map = lobpcg(  
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:420  
: ConvergenceWarning: Number of distinct clusters (3) found smaller  
than n_clusters (5). Possibly due to duplicate points in X.  
    est = KMeans()  
  
SpectralClustering(n_clusters=5, random_state=42)  
  
# GaussianMixture  
gmm = GaussianMixture(n_components=5, random_state=42)  
gmm.fit(X_train)  
  
GaussianMixture(n_components=5, random_state=42)  
  
# OPTICS  
optics = OPTICS()  
optics.fit(X_train)  
  
OPTICS()  
  
# Hierarchical clustering (linkage and dendrogram)  
linkage_matrix = linkage(X_train, method='ward')  
dendrogram(linkage_matrix)  
  
{'icoord': [[5.0, 5.0, 15.0, 15.0],  
[35.0, 35.0, 45.0, 45.0],  
[25.0, 25.0, 40.0, 40.0],  
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[75.0, 75.0, 85.0, 85.0],  
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```

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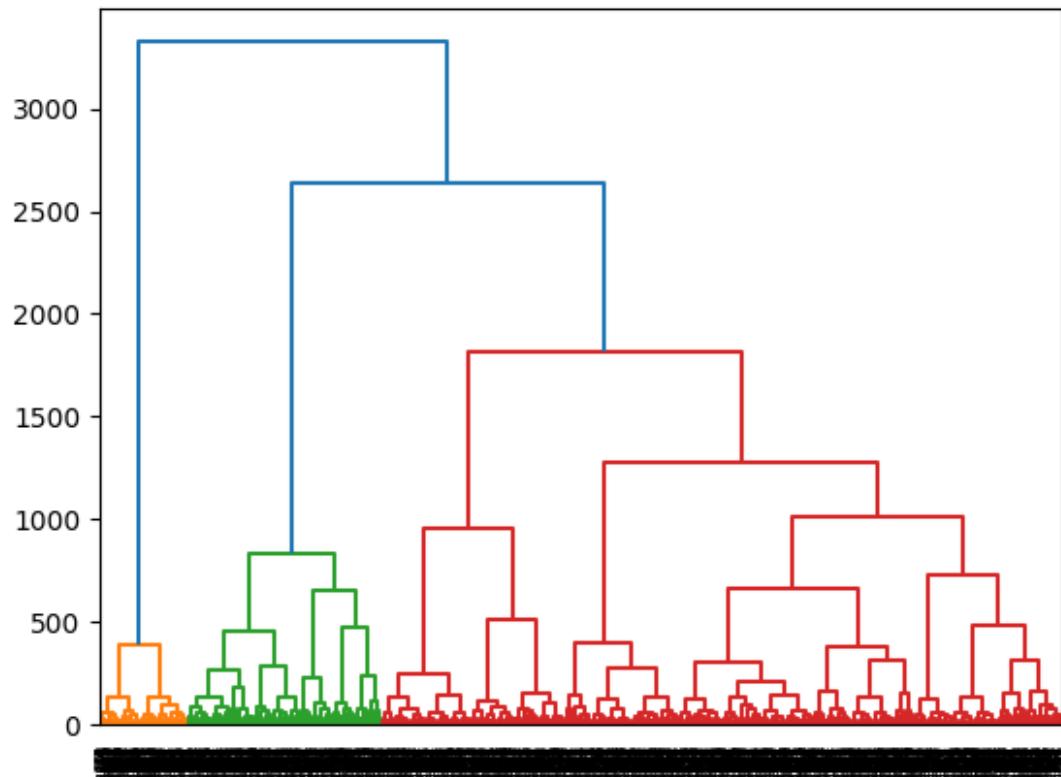












## #*MiniBatchKMeans*

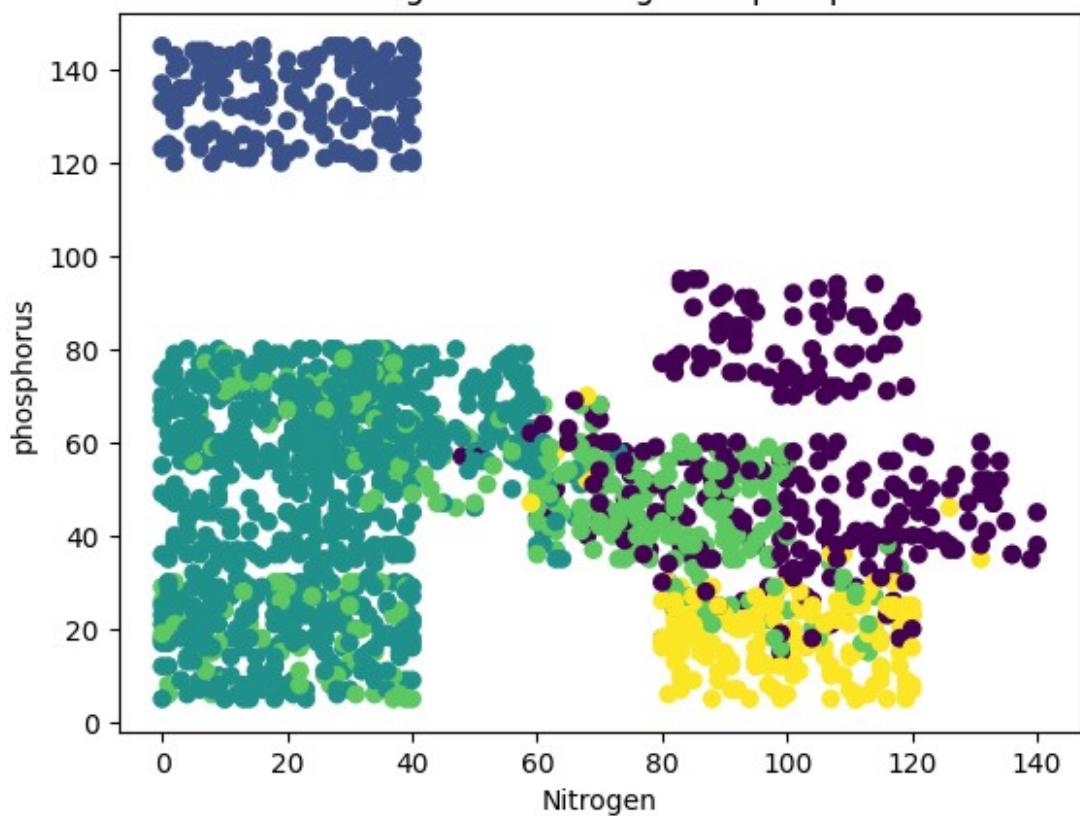
```
# Get the predicted cluster labels for the training data  
train_cluster_labels = mini_batch_kmeans.labels_
```

```
# Compute evaluation metrics
silhouette_avg = silhouette_score(X_train, train_cluster_labels)
ari = adjusted_rand_score(target, train_cluster_labels)
homogeneity, completeness, v_measure =
homogeneity_completeness_v_measure(target, train_cluster_labels)

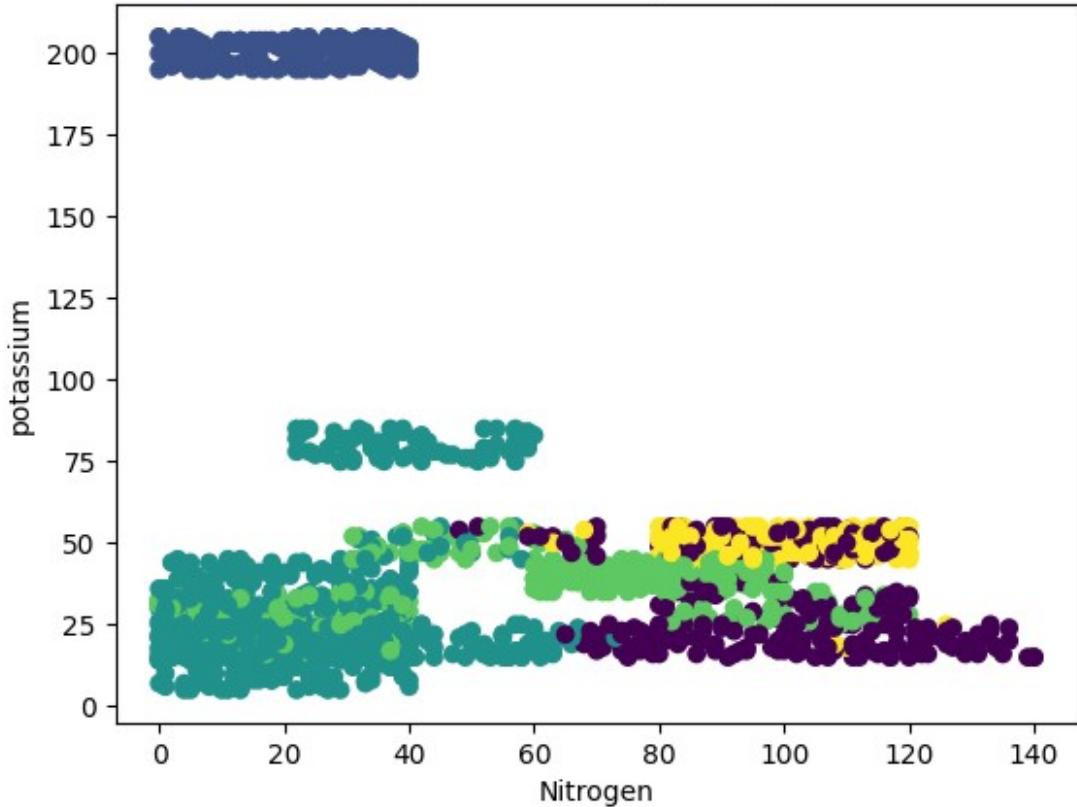
# Create scatter plots for different feature combinations
features = ['Nitrogen', 'phosphorus', 'potassium', 'temperature',
'humidity', 'ph', 'rainfall']
for i in range(len(features)):
    for j in range(i+1, len(features)):
        plt.scatter(X_train[:, i], X_train[:, j],
c=train_cluster_labels, cmap='viridis')
        plt.xlabel(features[i])
        plt.ylabel(features[j])
        plt.title(f'Clustering Result: {features[i]} vs
{features[j]}')
        plt.show()

# Print evaluation metrics
print("Silhouette Score:", silhouette_avg)
print("Adjusted Rand Index:", ari)
print("Homogeneity:", homogeneity)
print("Completeness:", completeness)
print("V-measure:", v_measure)
```

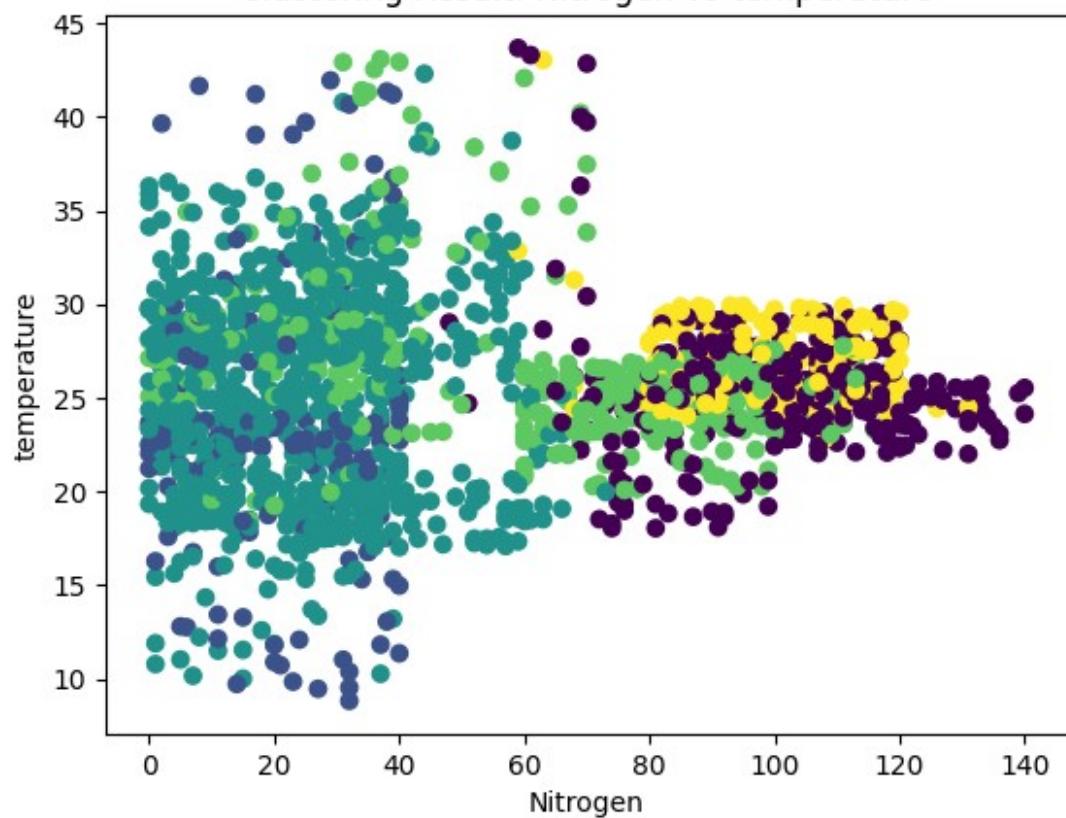
Clustering Result: Nitrogen vs phosphorus



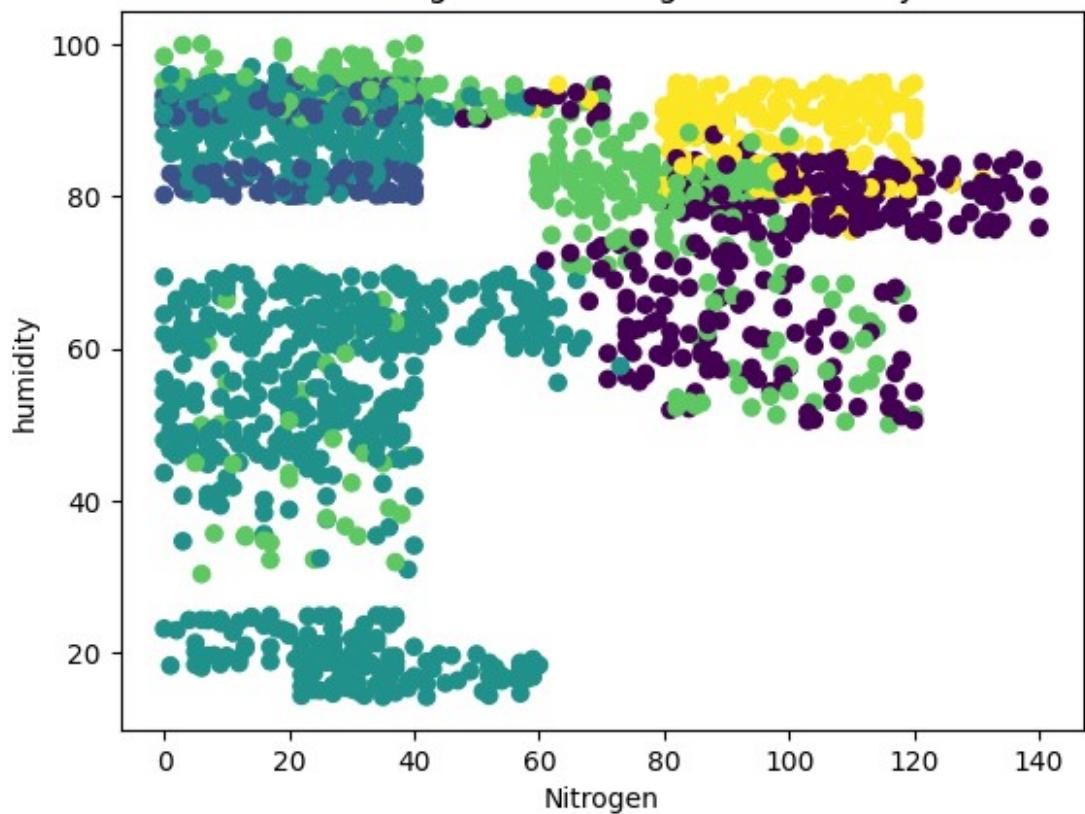
Clustering Result: Nitrogen vs potassium



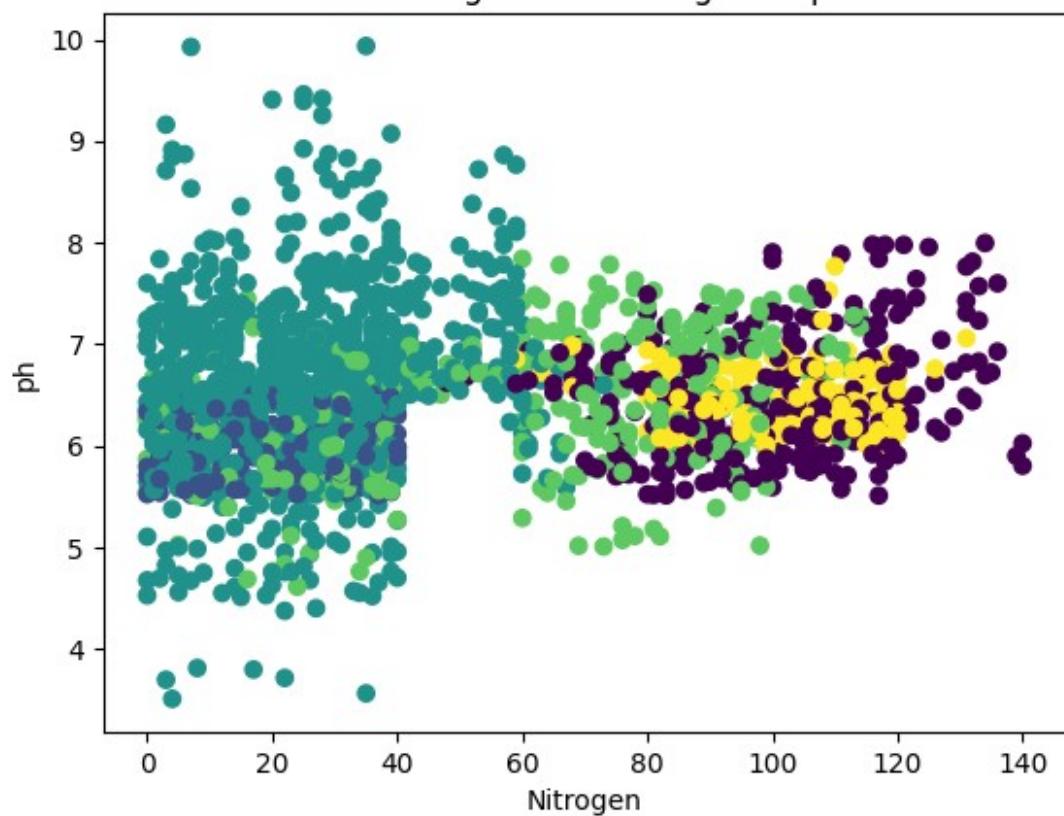
Clustering Result: Nitrogen vs temperature



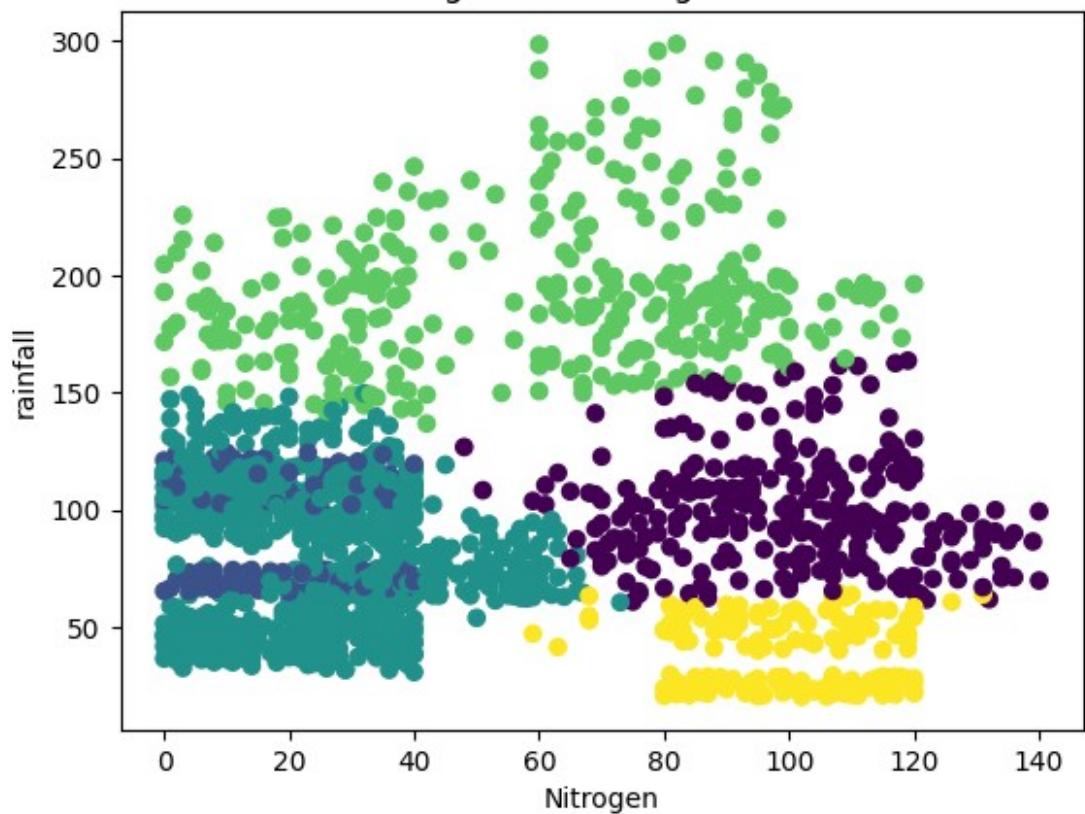
Clustering Result: Nitrogen vs humidity



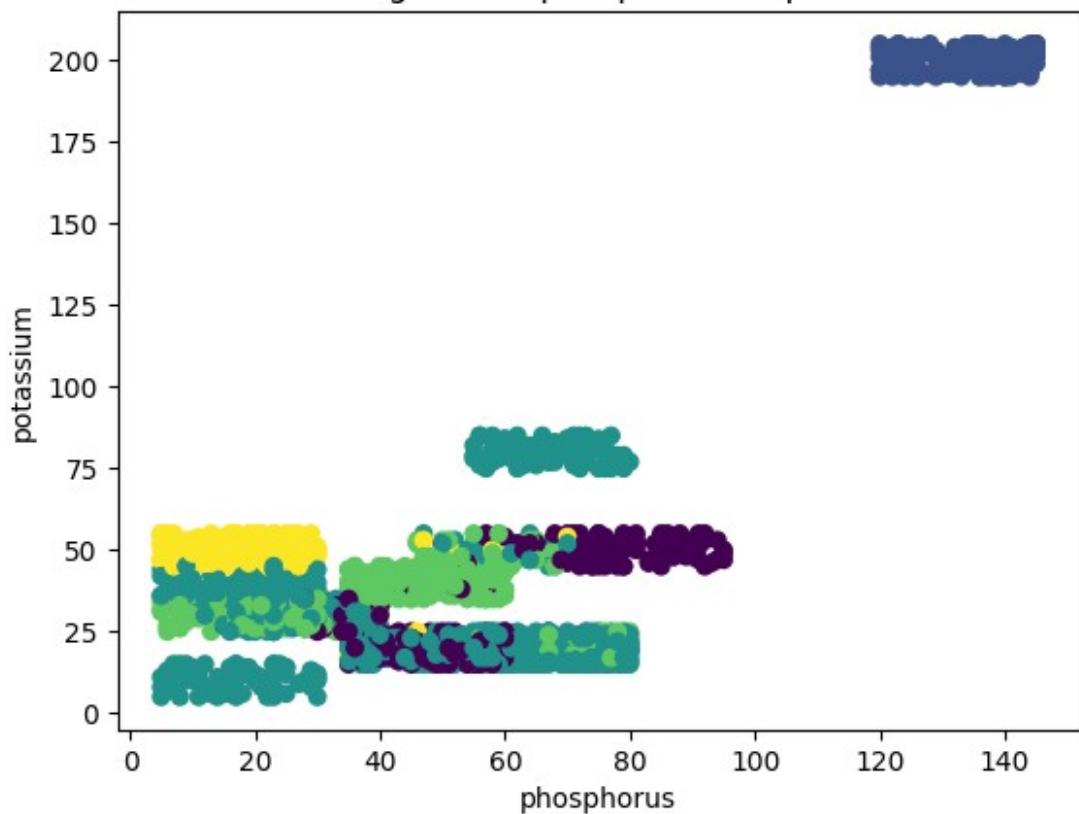
Clustering Result: Nitrogen vs ph



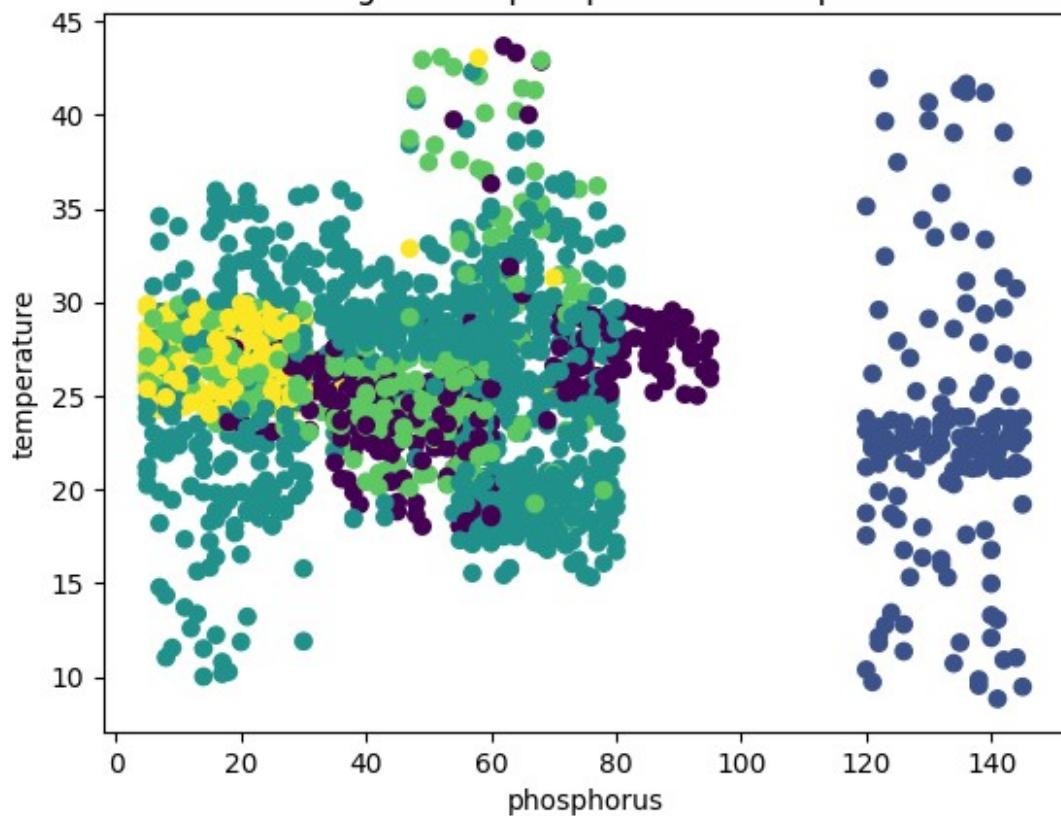
Clustering Result: Nitrogen vs rainfall



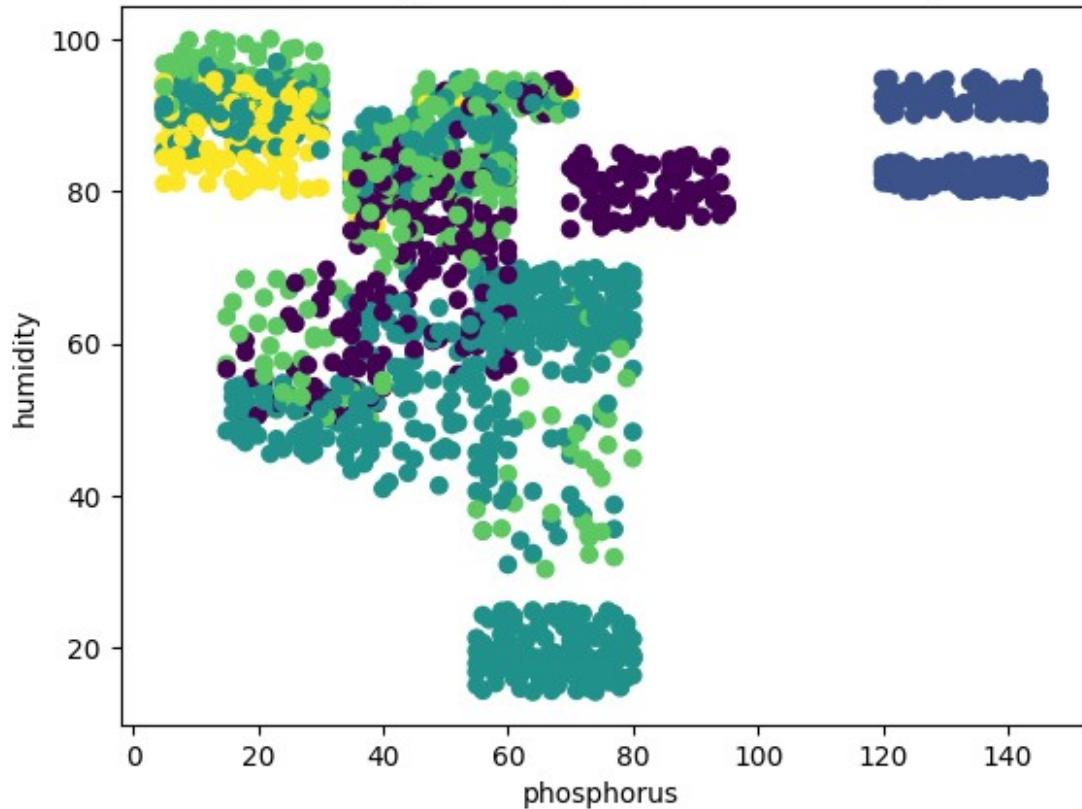
Clustering Result: phosphorus vs potassium



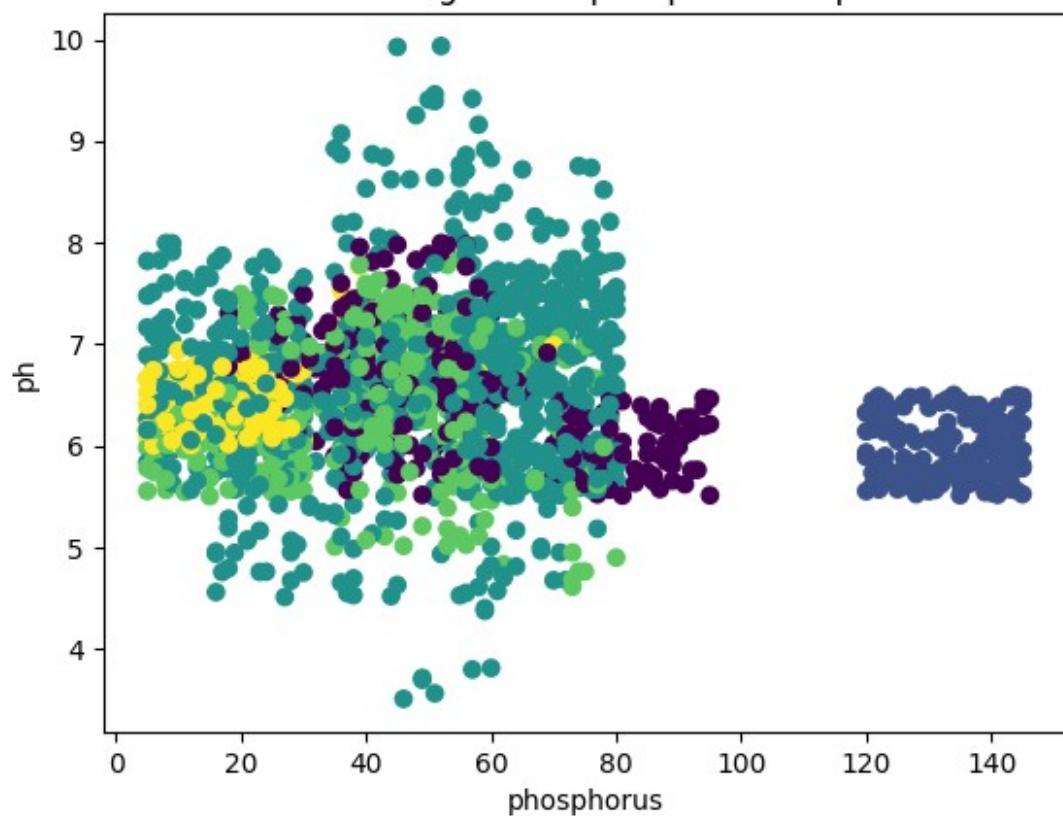
## Clustering Result: phosphorus vs temperature



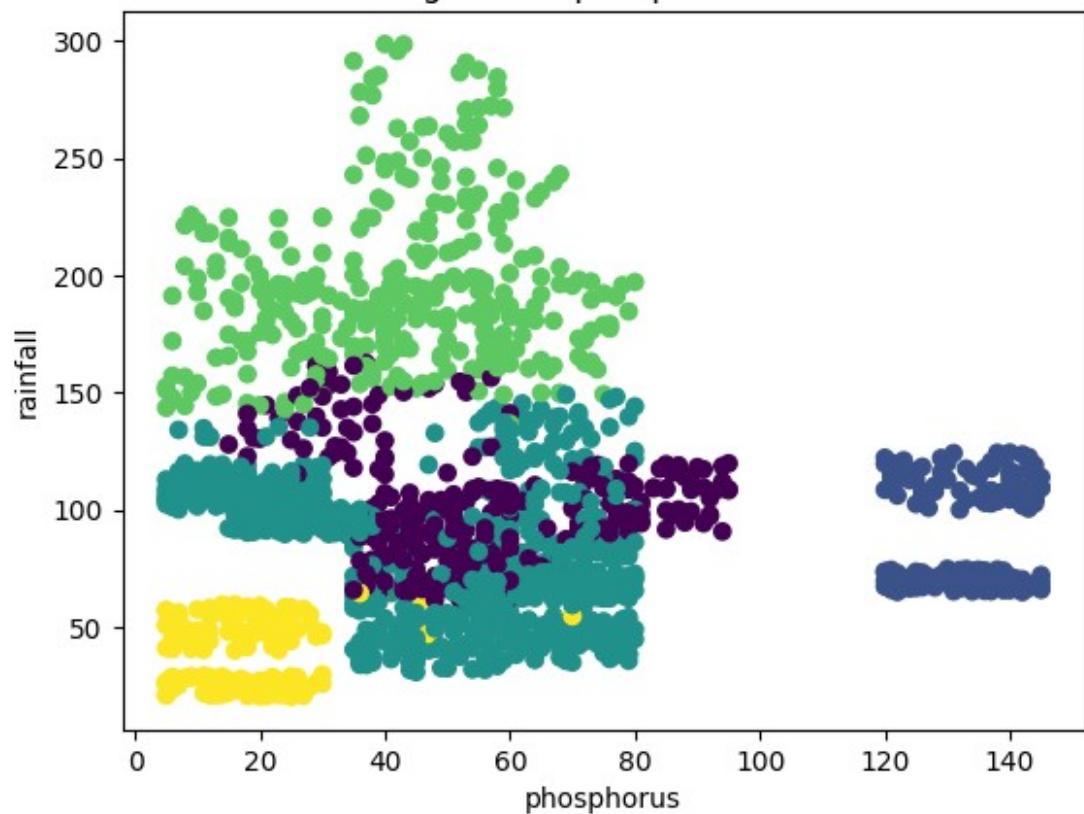
Clustering Result: phosphorus vs humidity



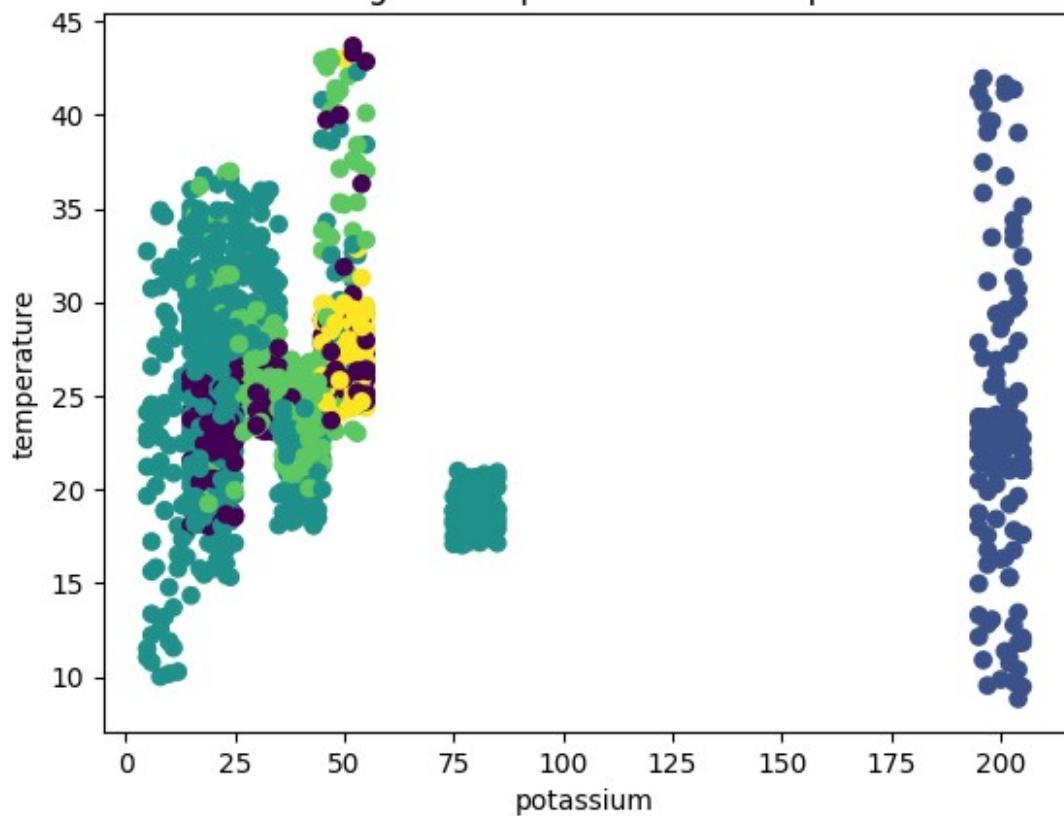
Clustering Result: phosphorus vs ph



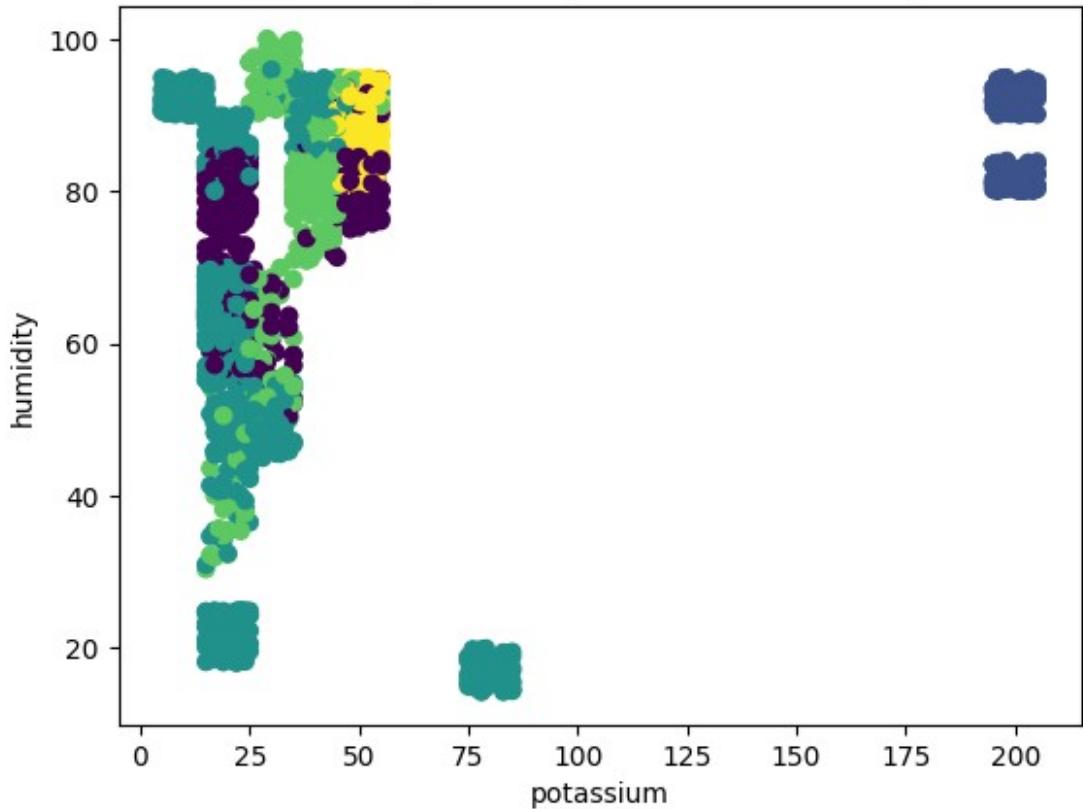
Clustering Result: phosphorus vs rainfall



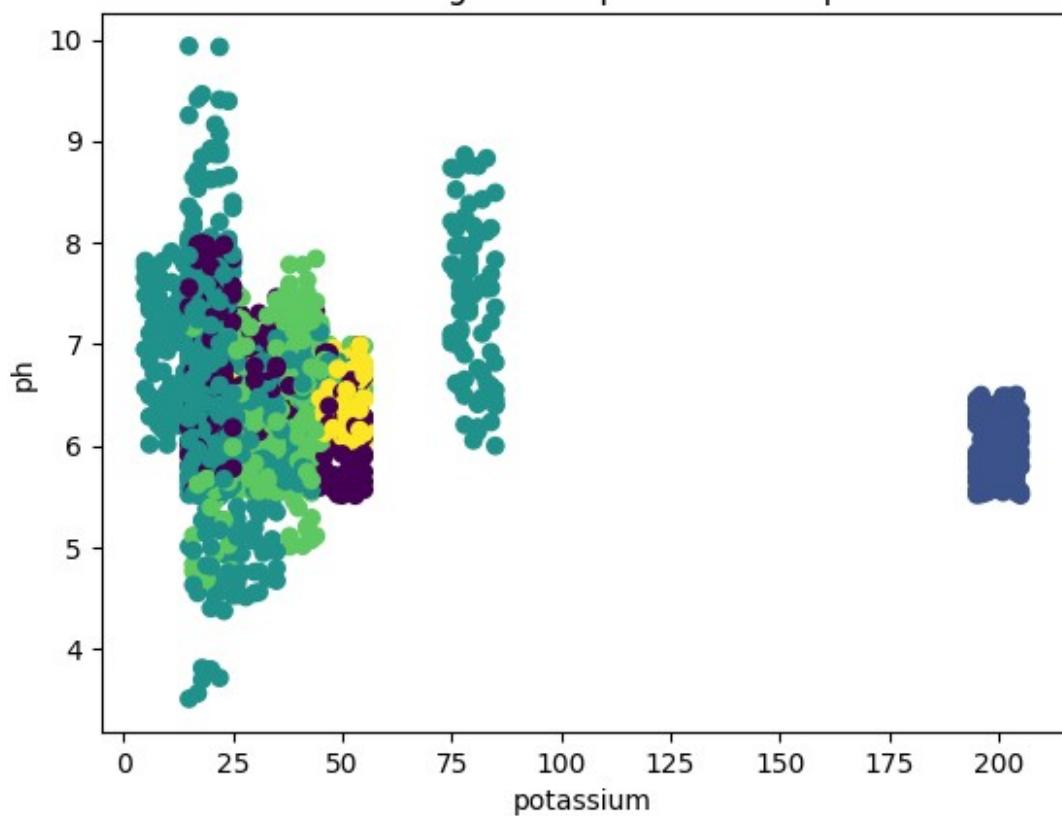
Clustering Result: potassium vs temperature



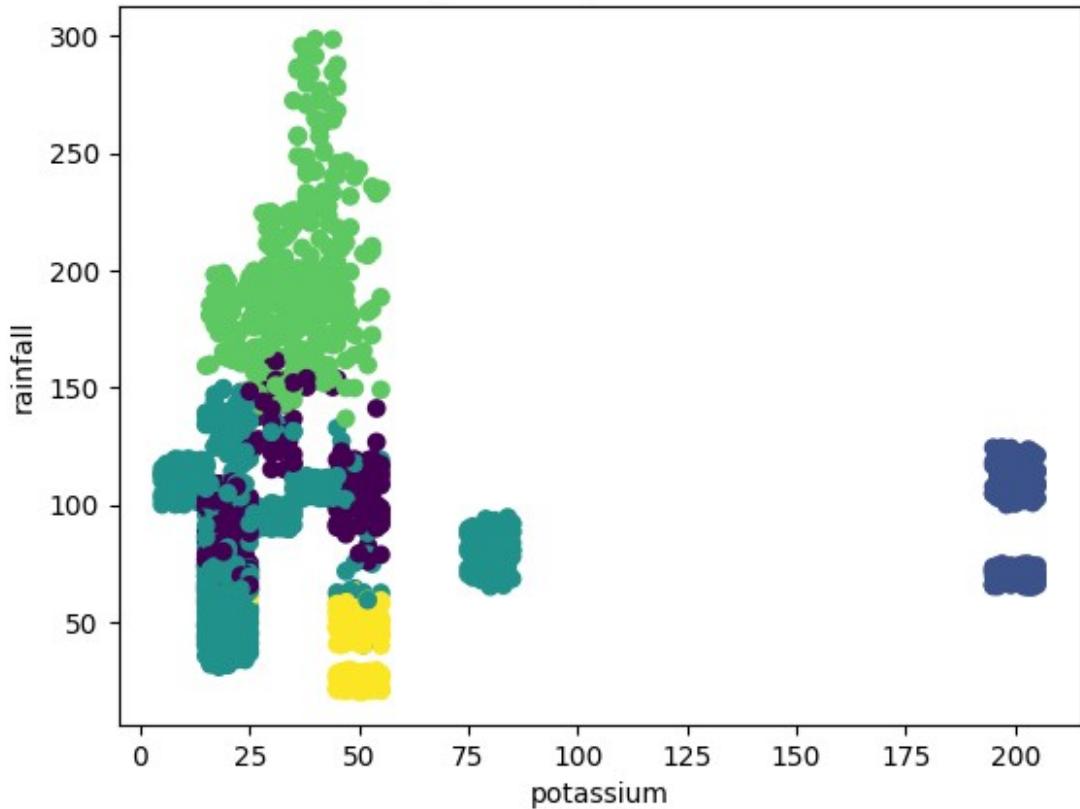
Clustering Result: potassium vs humidity



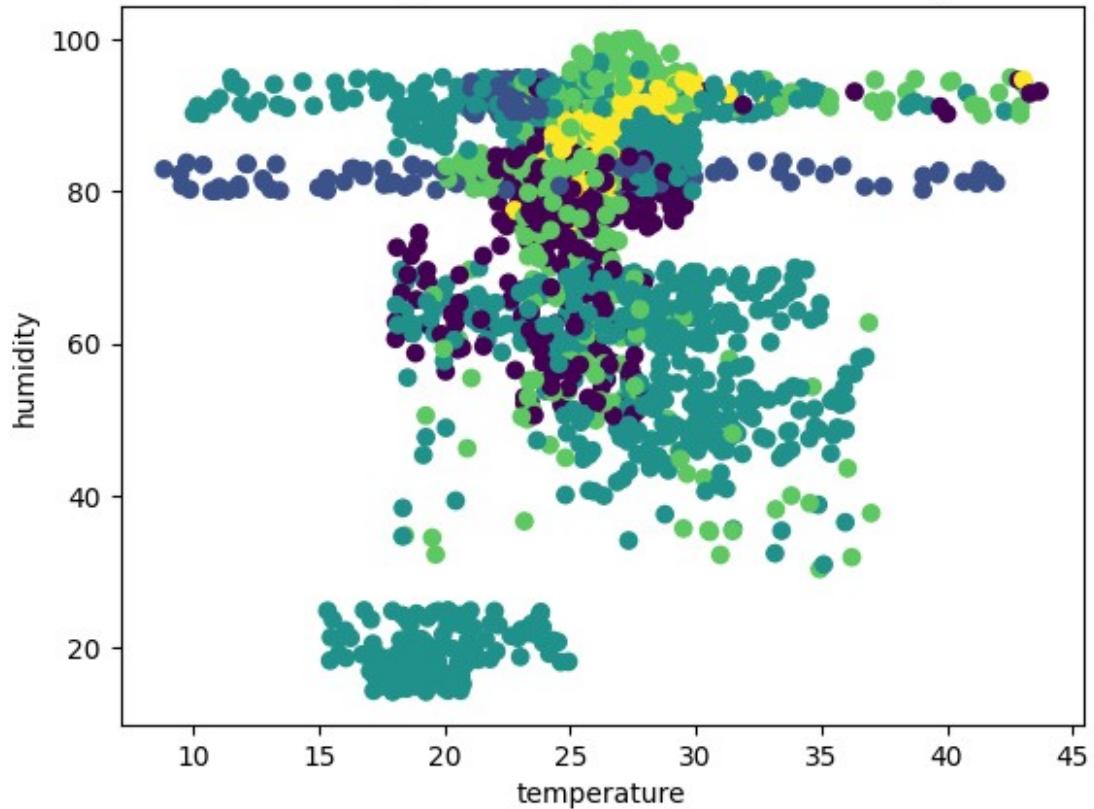
Clustering Result: potassium vs ph



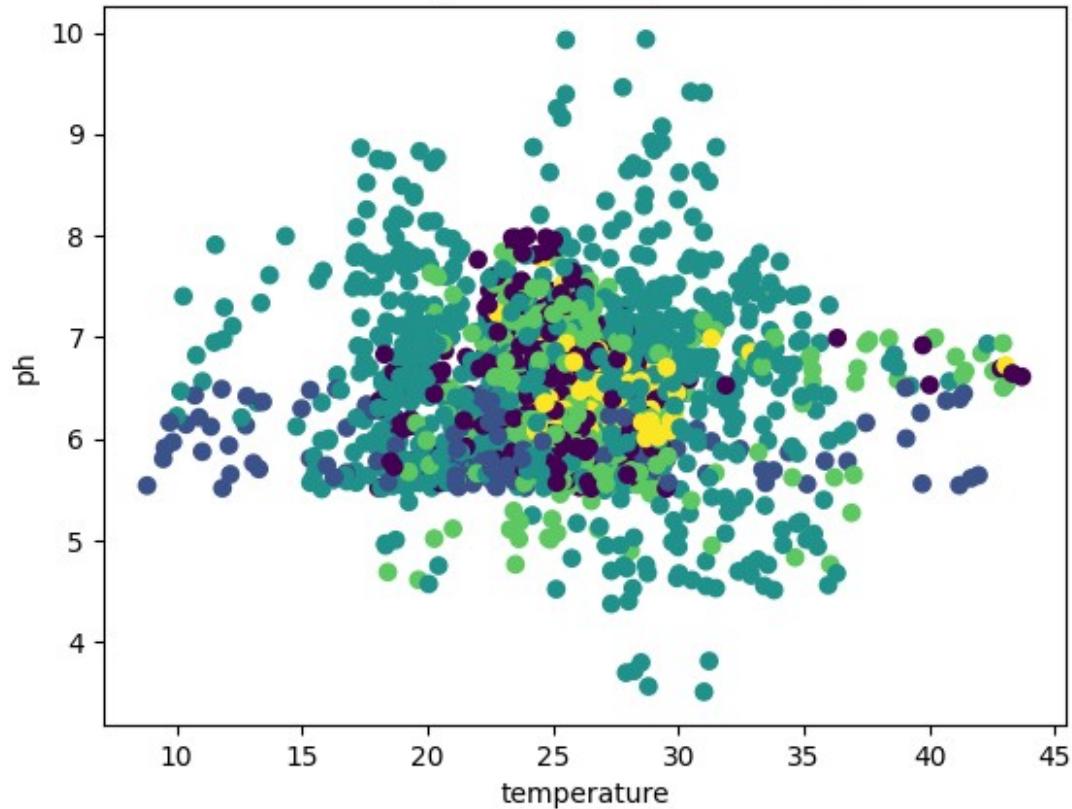
Clustering Result: potassium vs rainfall



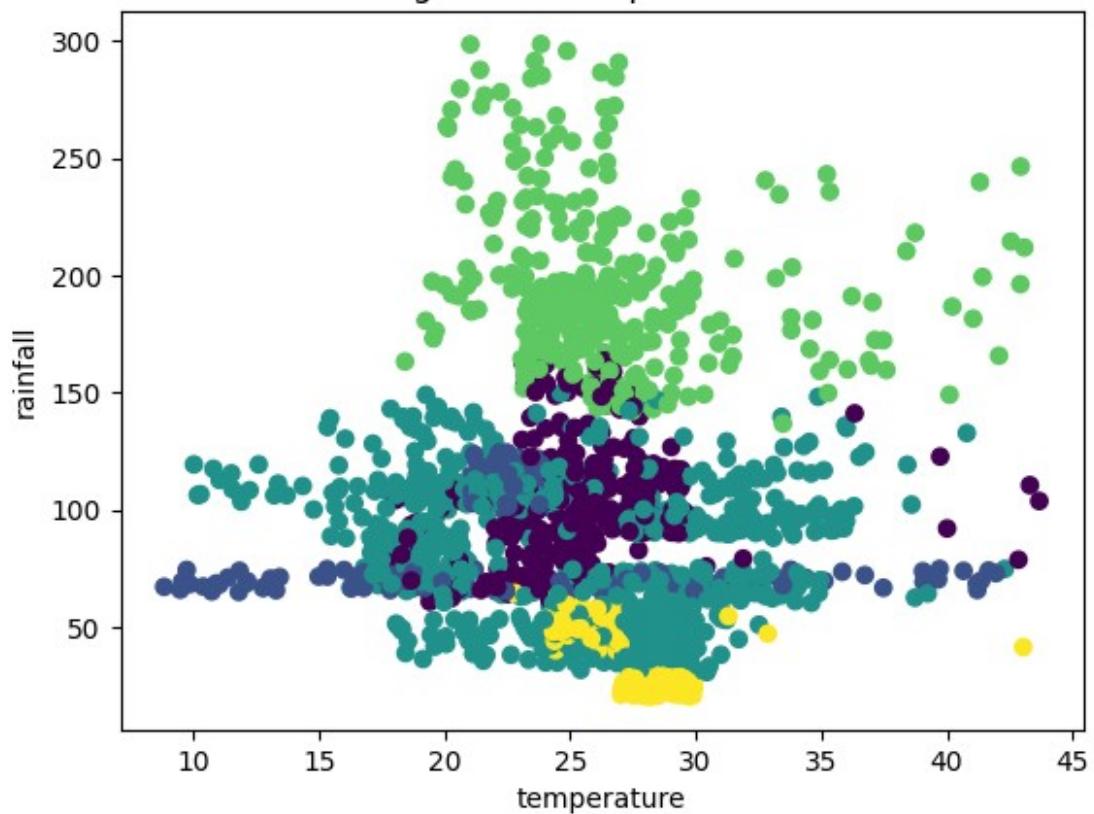
Clustering Result: temperature vs humidity



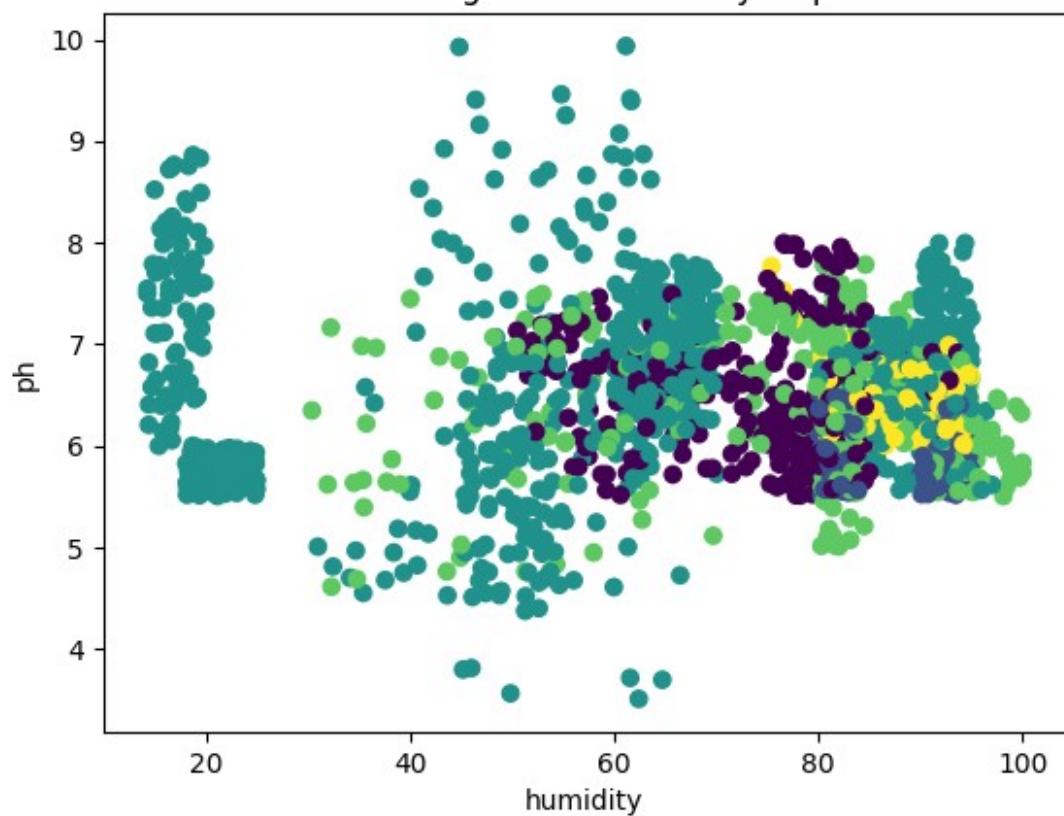
Clustering Result: temperature vs ph



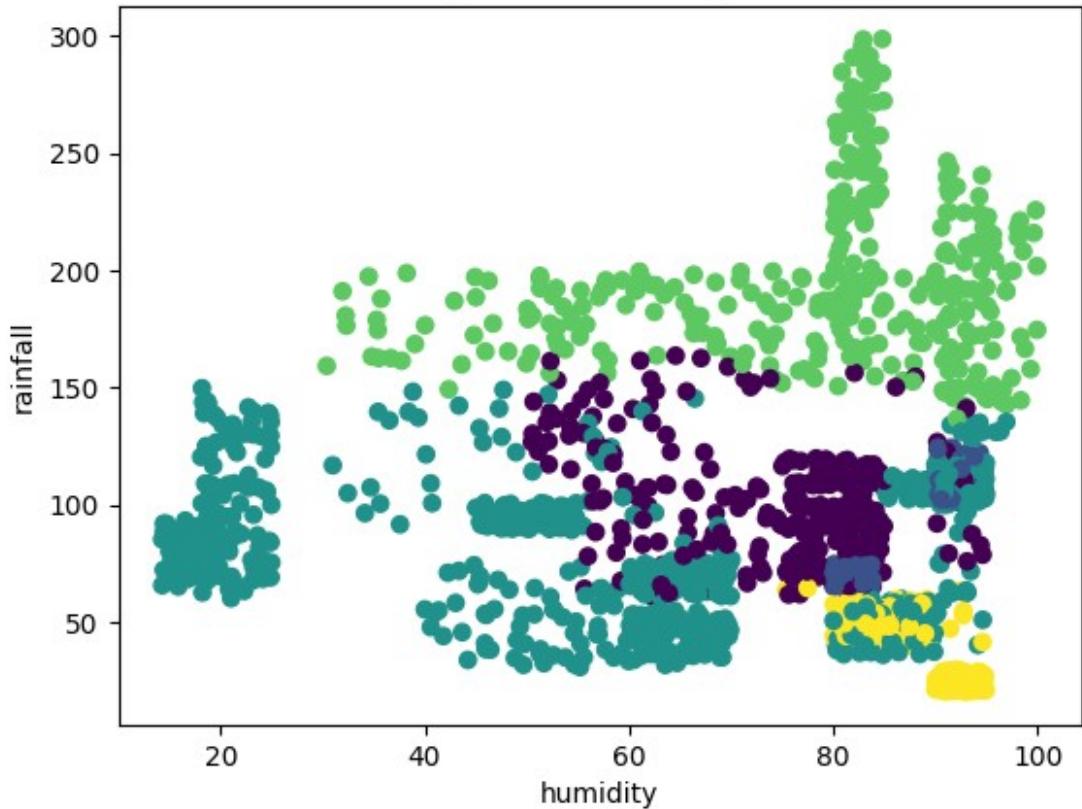
Clustering Result: temperature vs rainfall

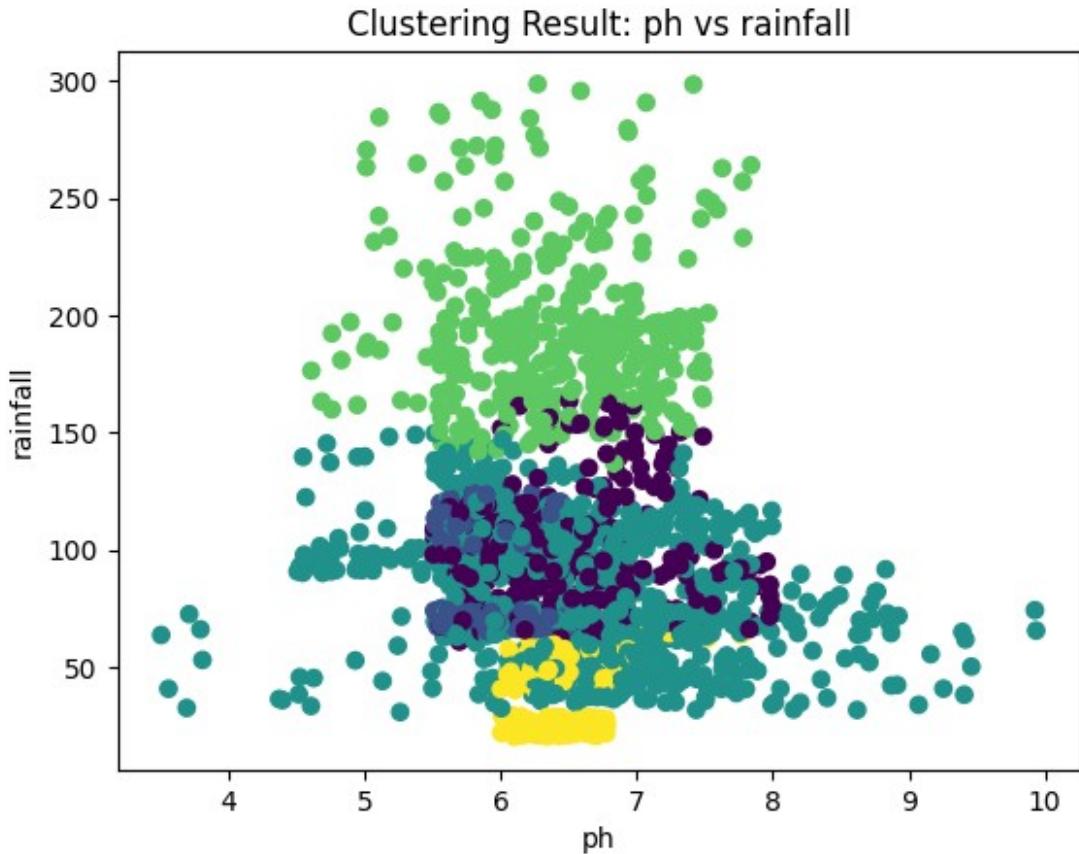


Clustering Result: humidity vs ph



Clustering Result: humidity vs rainfall





Silhouette Score: 0.39284654635569805

Adjusted Rand Index: 0.1748657408252106

Homogeneity: 0.40032462178571476

Completeness: 0.8738497770730168

V-measure: 0.5490984308233174

### #KMeans

```
# Get the predicted cluster labels for the training data
train_cluster_labels = kmeans.labels_

# Compute evaluation metrics
silhouette_avg = silhouette_score(X_train, train_cluster_labels)
ari = adjusted_rand_score(target, train_cluster_labels)
homogeneity, completeness, v_measure =
homogeneity_completeness_v_measure(target, train_cluster_labels)

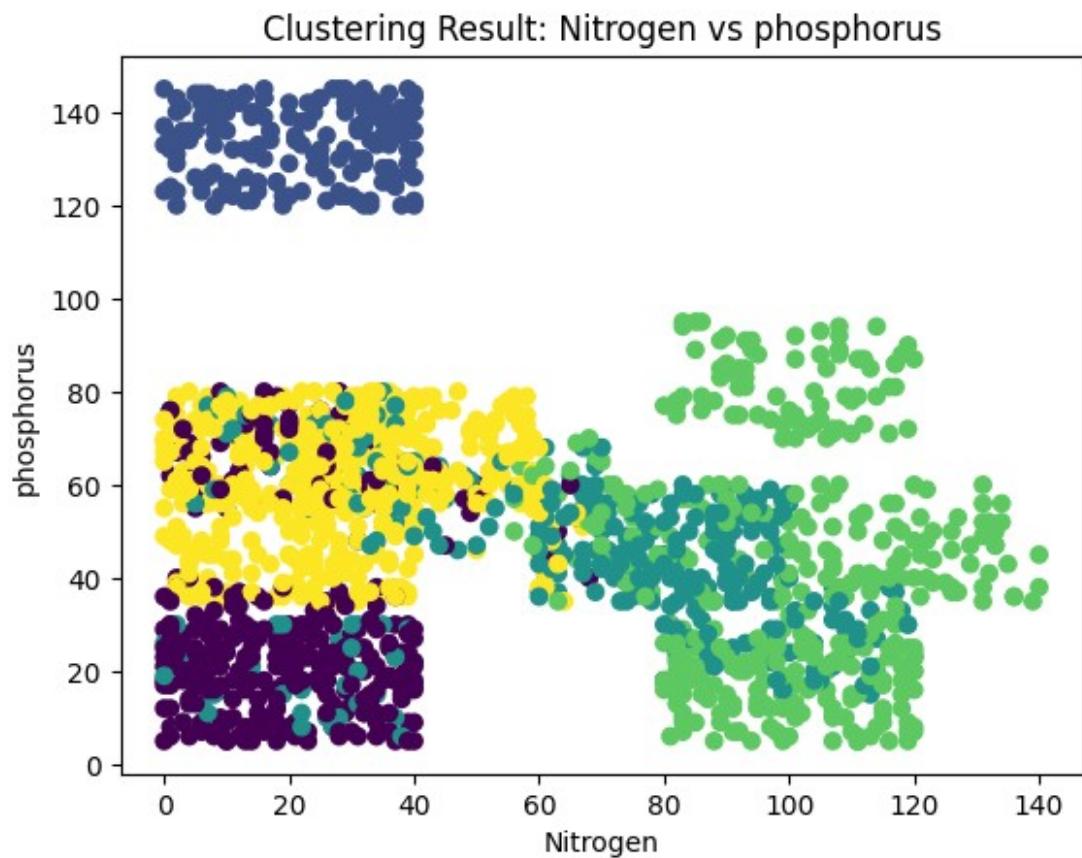
# Create scatter plots for different feature combinations
features = ['Nitrogen', 'phosphorus', 'potassium', 'temperature',
'humidity', 'ph', 'rainfall']
for i in range(len(features)):
    for j in range(i+1, len(features)):
        plt.scatter(X_train[:, 0], X_train[:, 1],
```

```

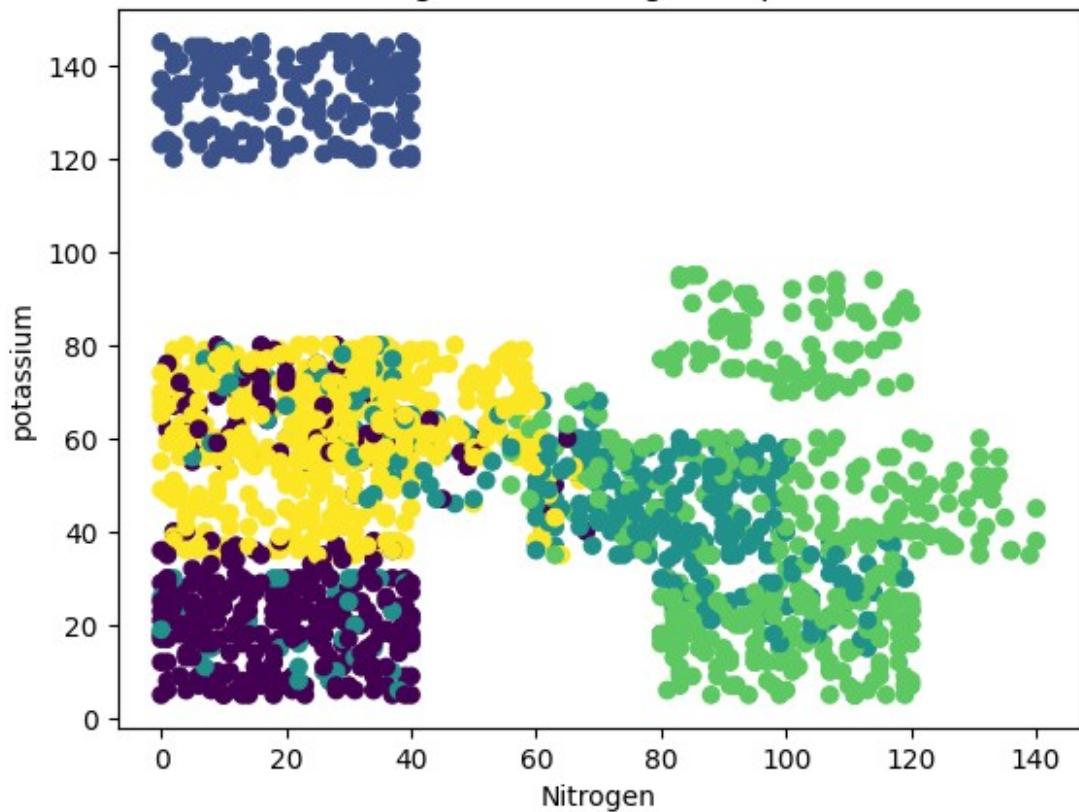
c=train_cluster_labels, cmap='viridis')
    plt.xlabel(features[i])
    plt.ylabel(features[j])
    plt.title(f'Clustering Result: {features[i]} vs
{features[j]}')
    plt.show()

# Print evaluation metrics
print("Silhouette Score:", silhouette_avg)
print("Adjusted Rand Index:", ari)
print("Homogeneity:", homogeneity)
print("Completeness:", completeness)
print("V-measure:", v_measure)

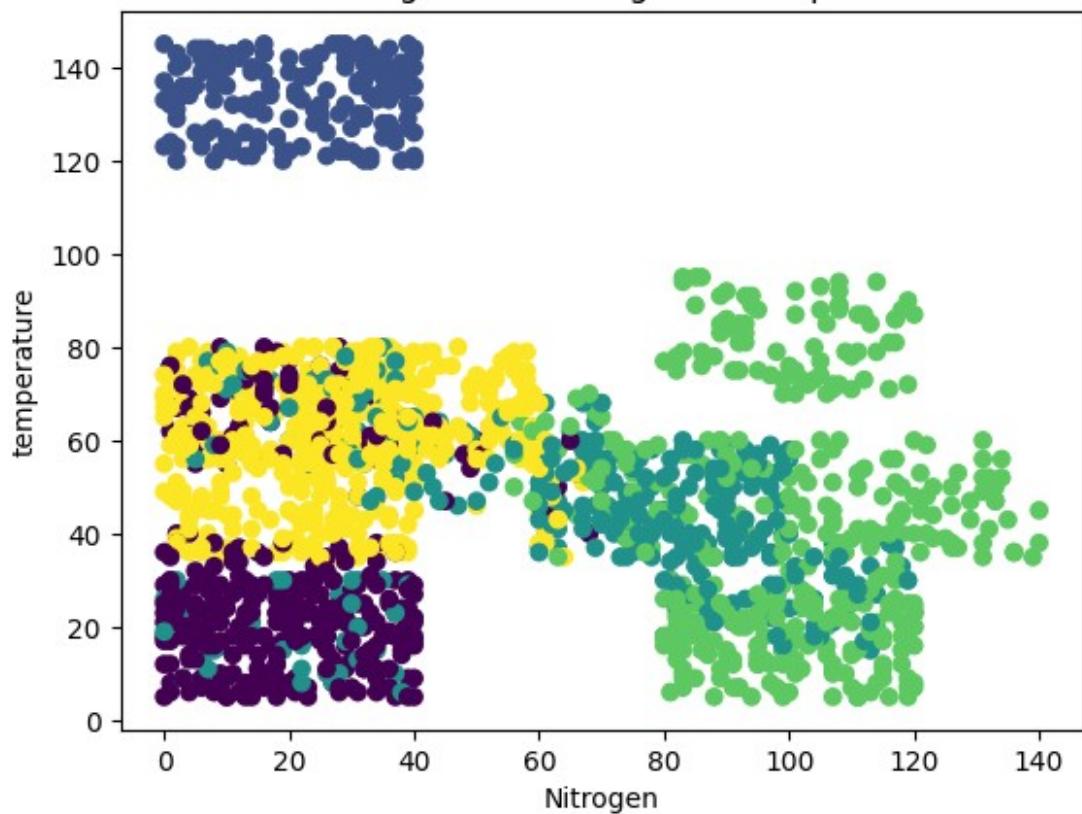
```



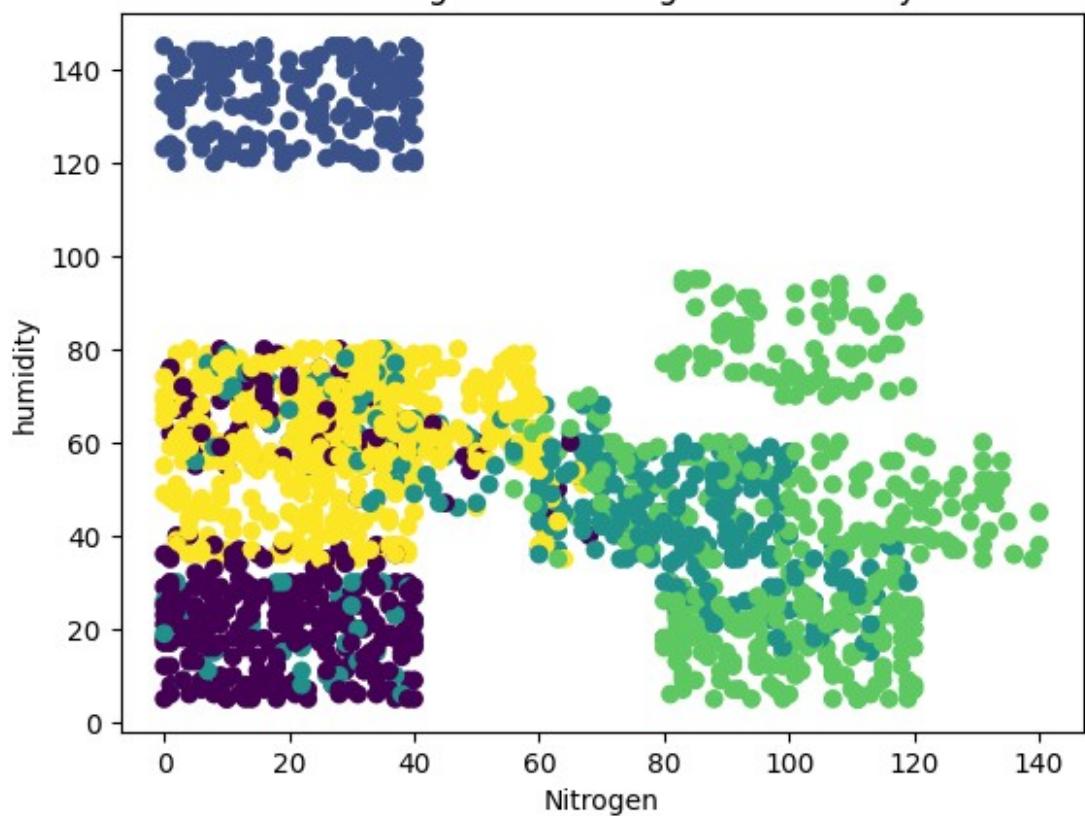
Clustering Result: Nitrogen vs potassium



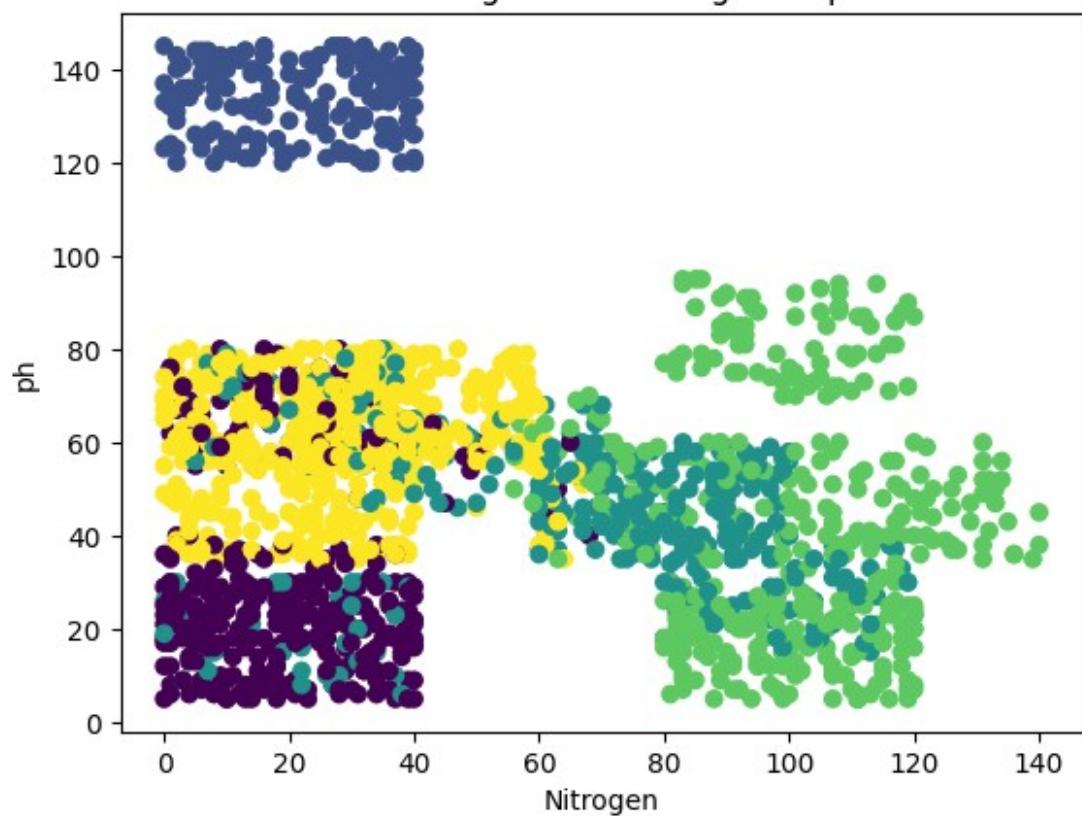
Clustering Result: Nitrogen vs temperature



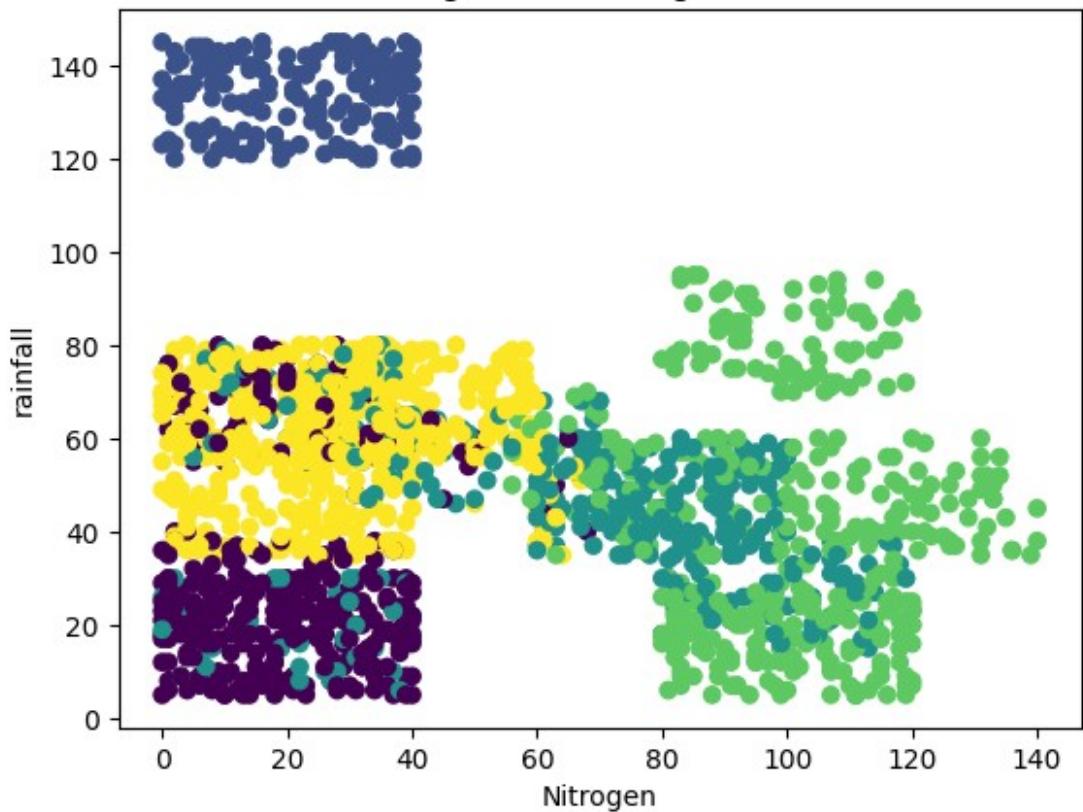
Clustering Result: Nitrogen vs humidity



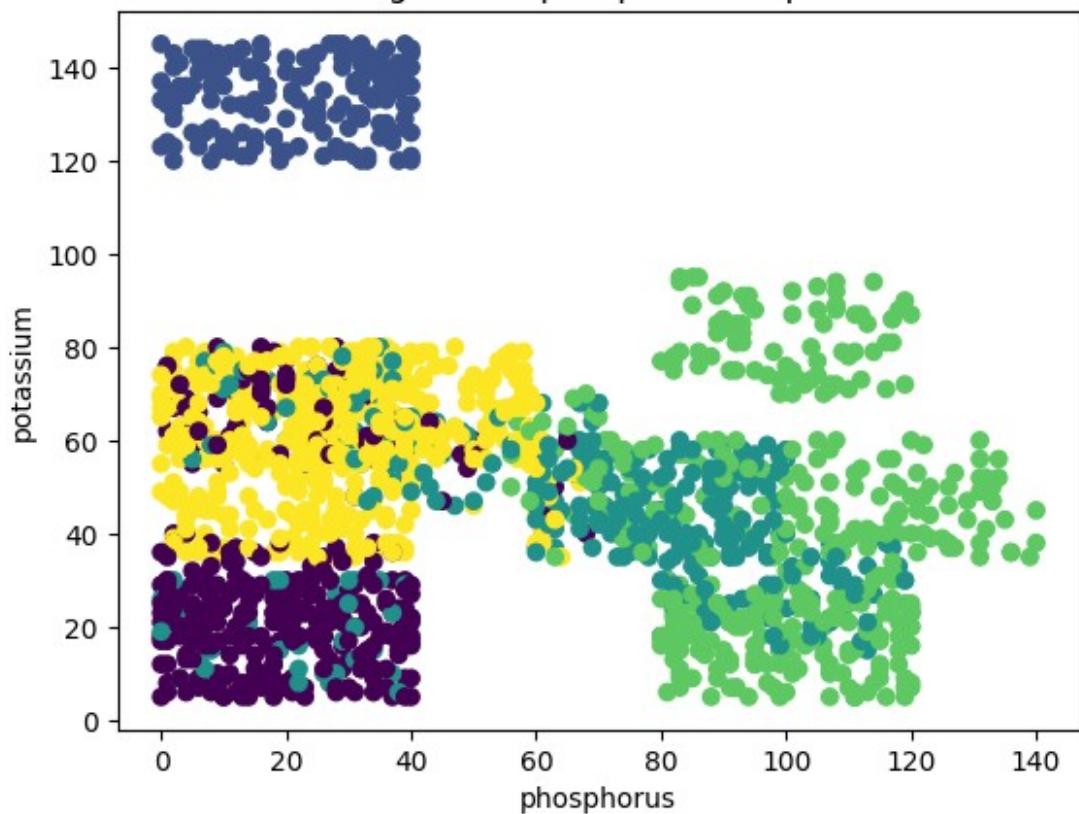
Clustering Result: Nitrogen vs ph



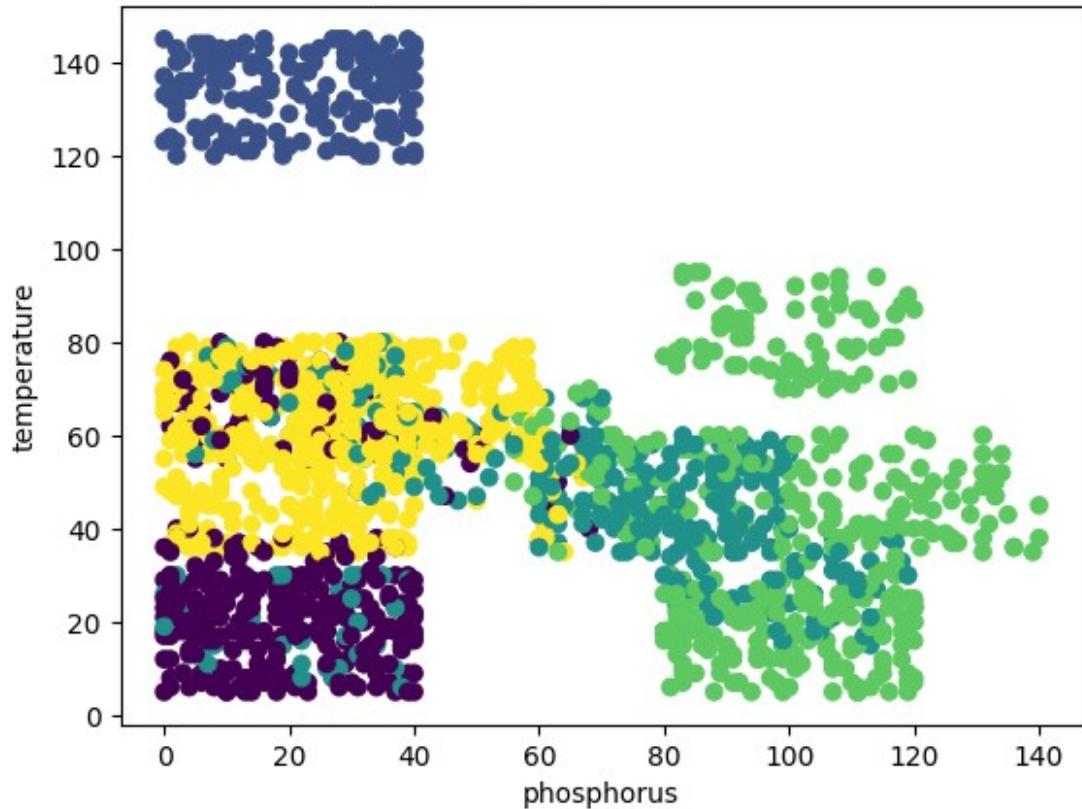
Clustering Result: Nitrogen vs rainfall



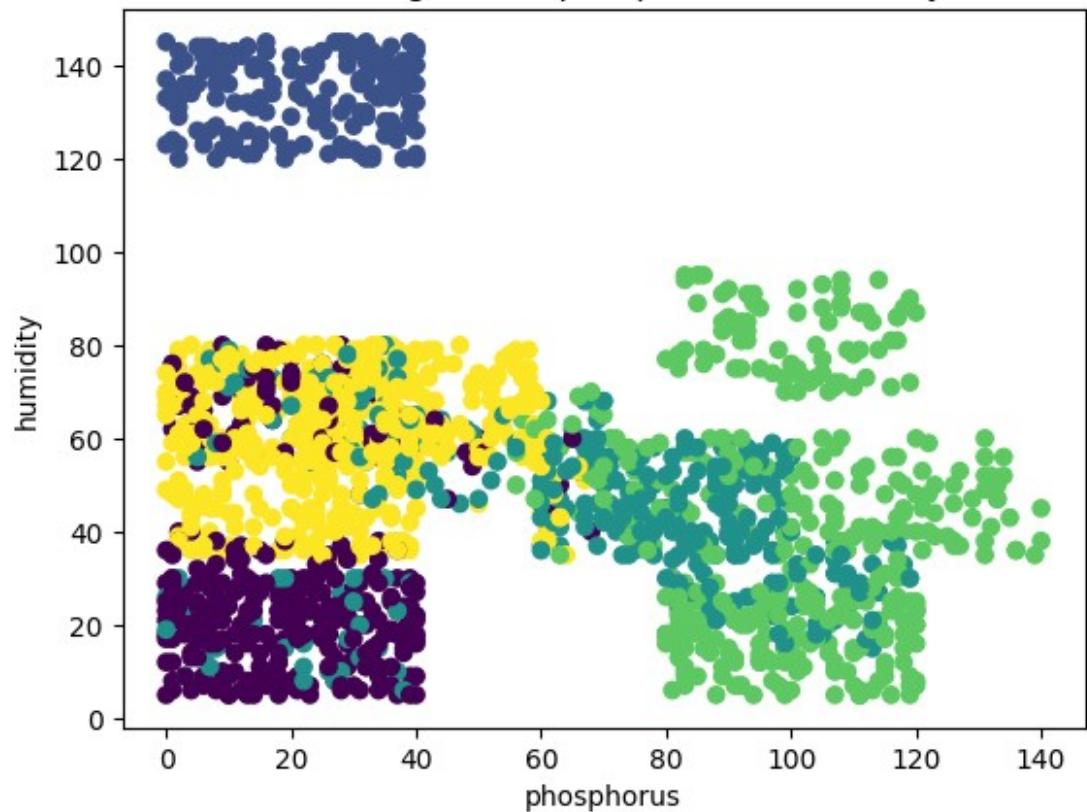
Clustering Result: phosphorus vs potassium



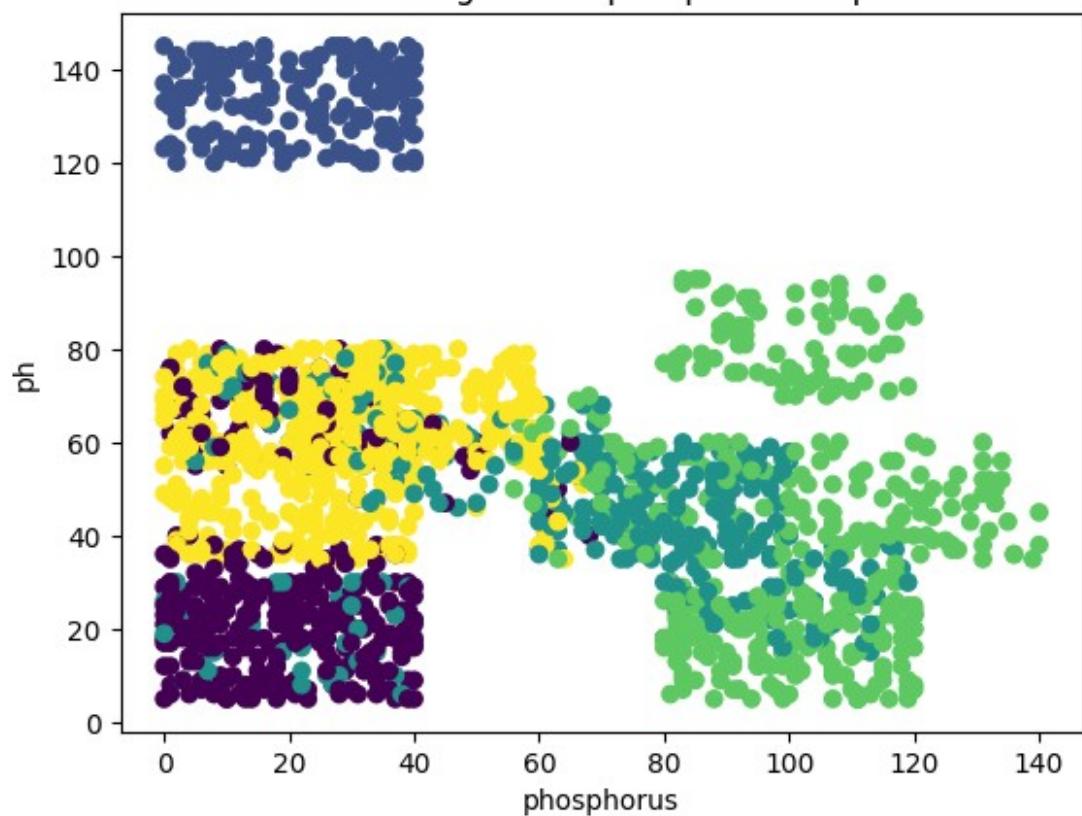
Clustering Result: phosphorus vs temperature



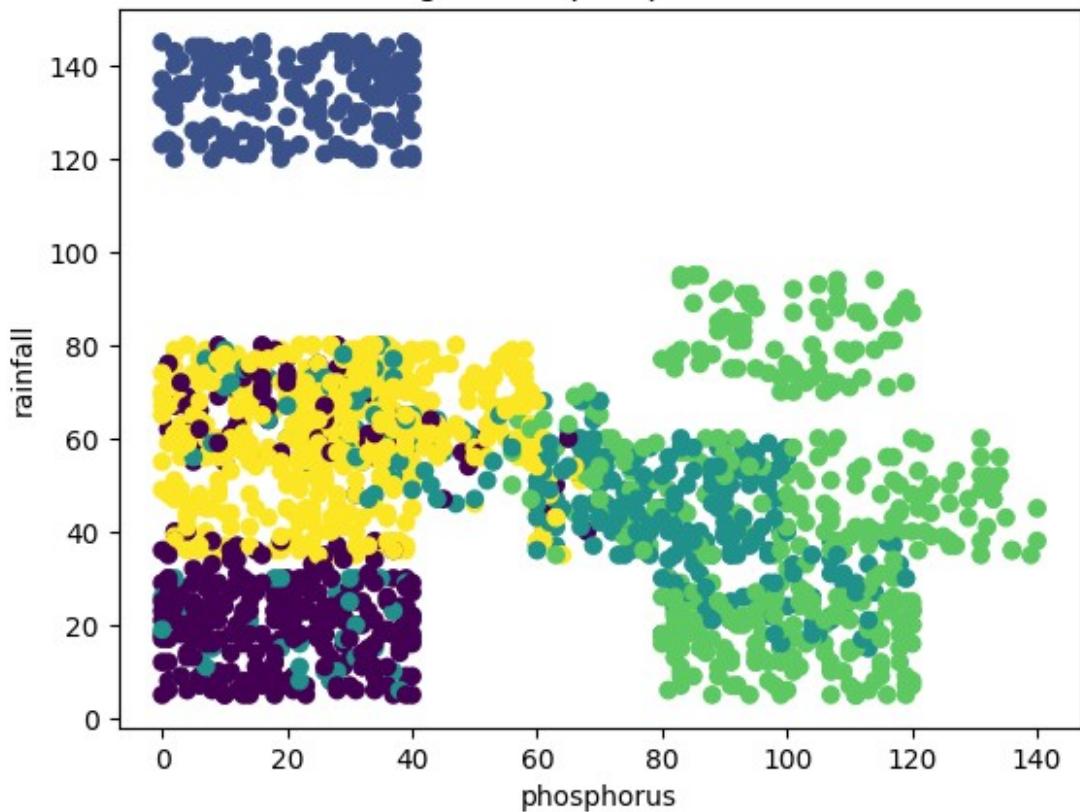
Clustering Result: phosphorus vs humidity



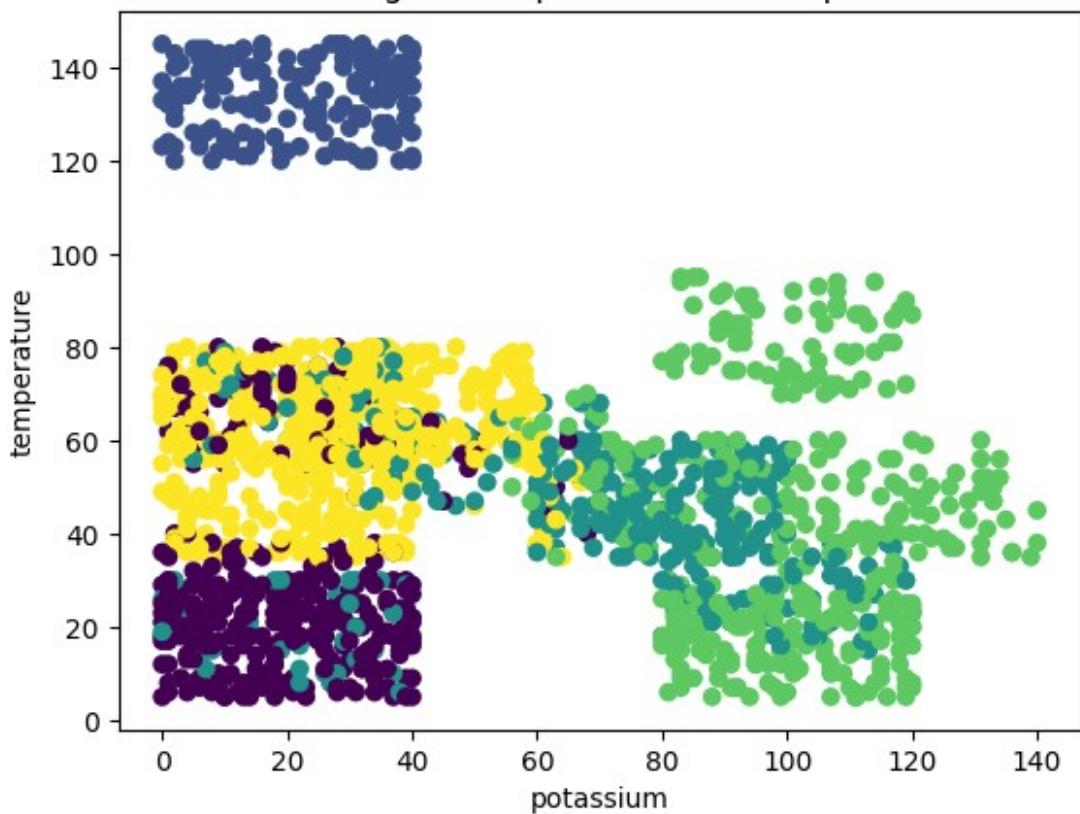
Clustering Result: phosphorus vs ph



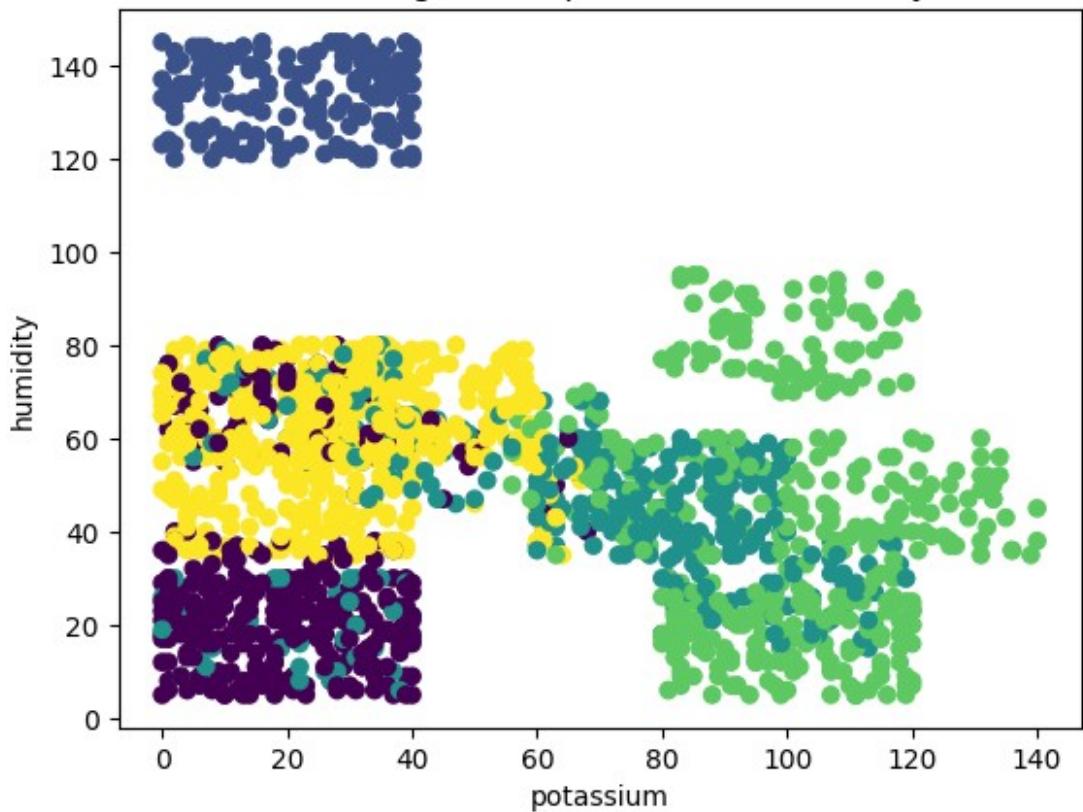
Clustering Result: phosphorus vs rainfall



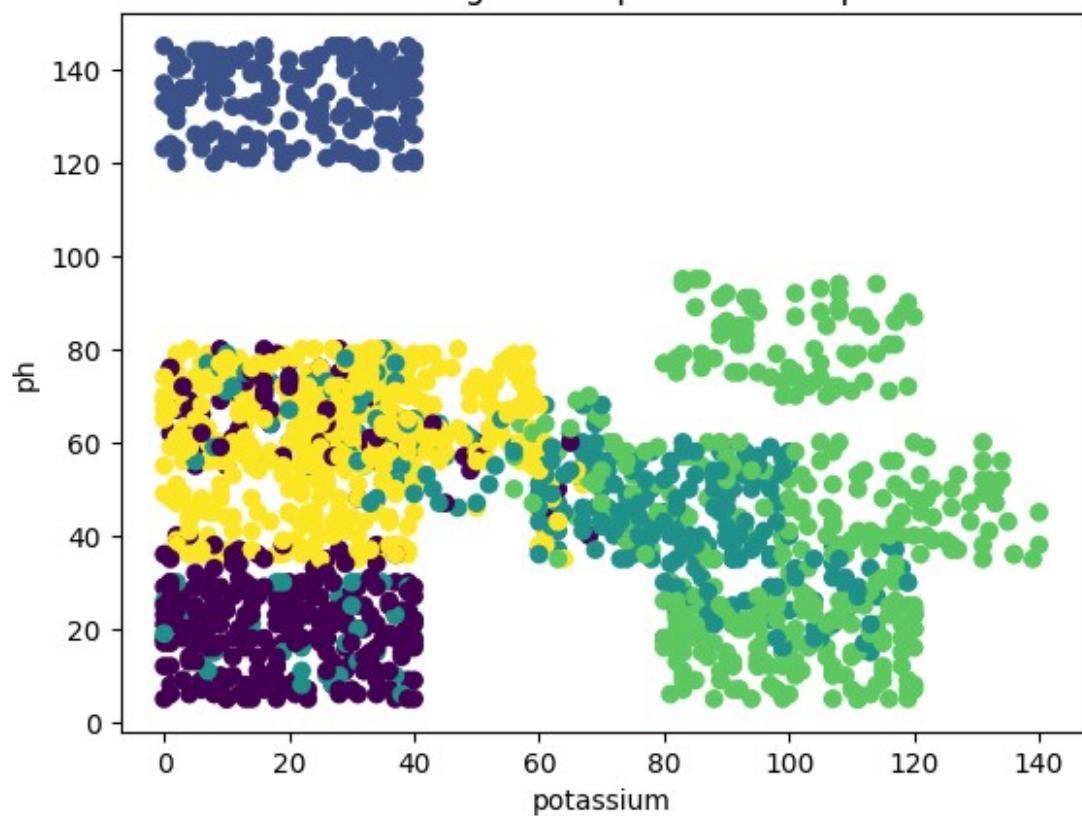
Clustering Result: potassium vs temperature



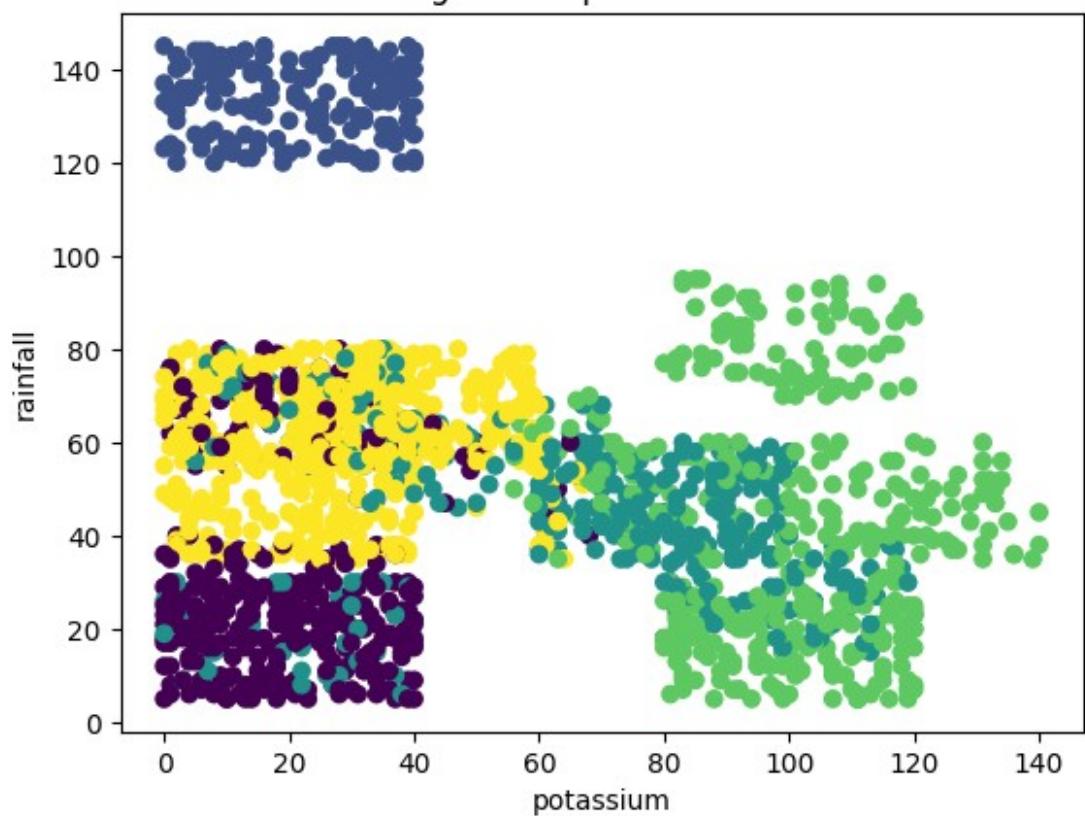
Clustering Result: potassium vs humidity



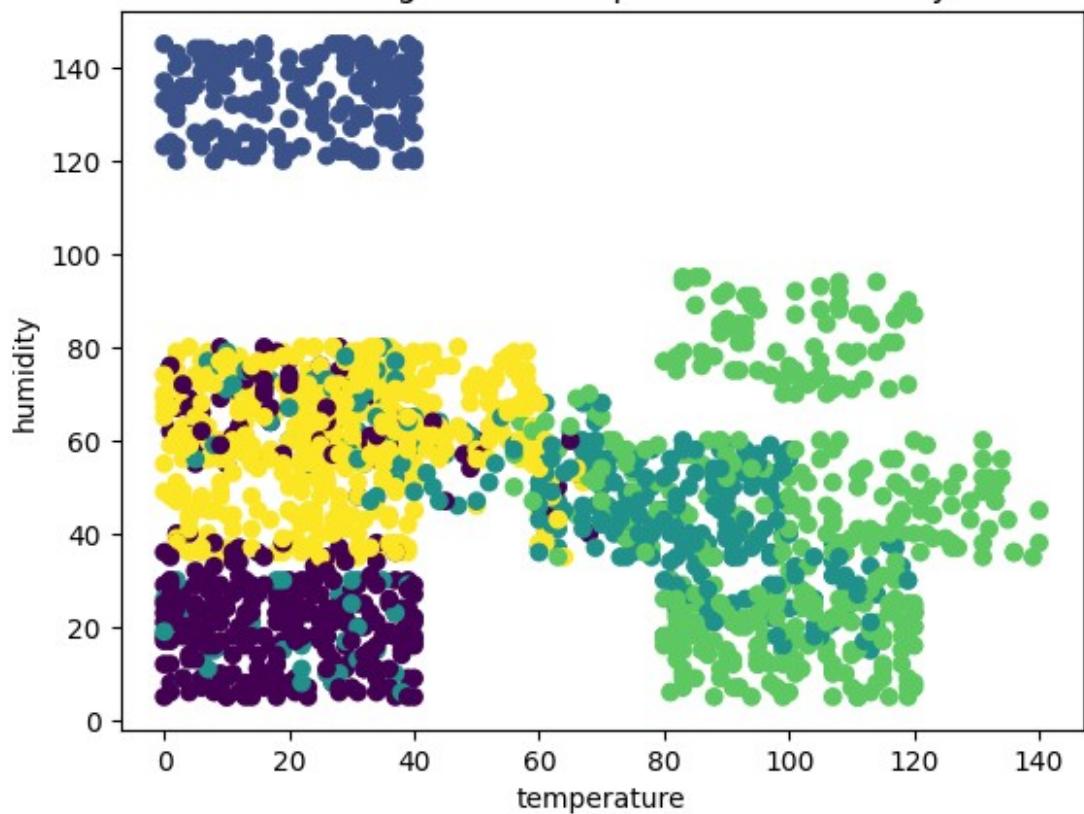
Clustering Result: potassium vs ph



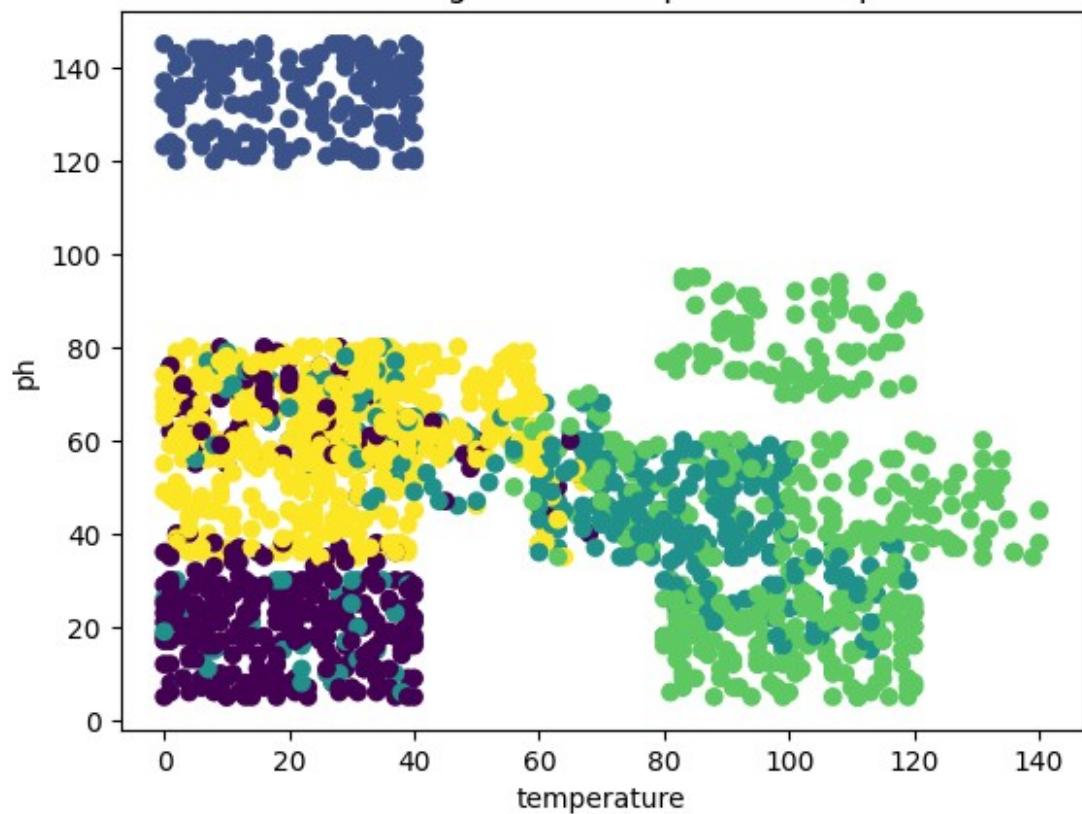
Clustering Result: potassium vs rainfall



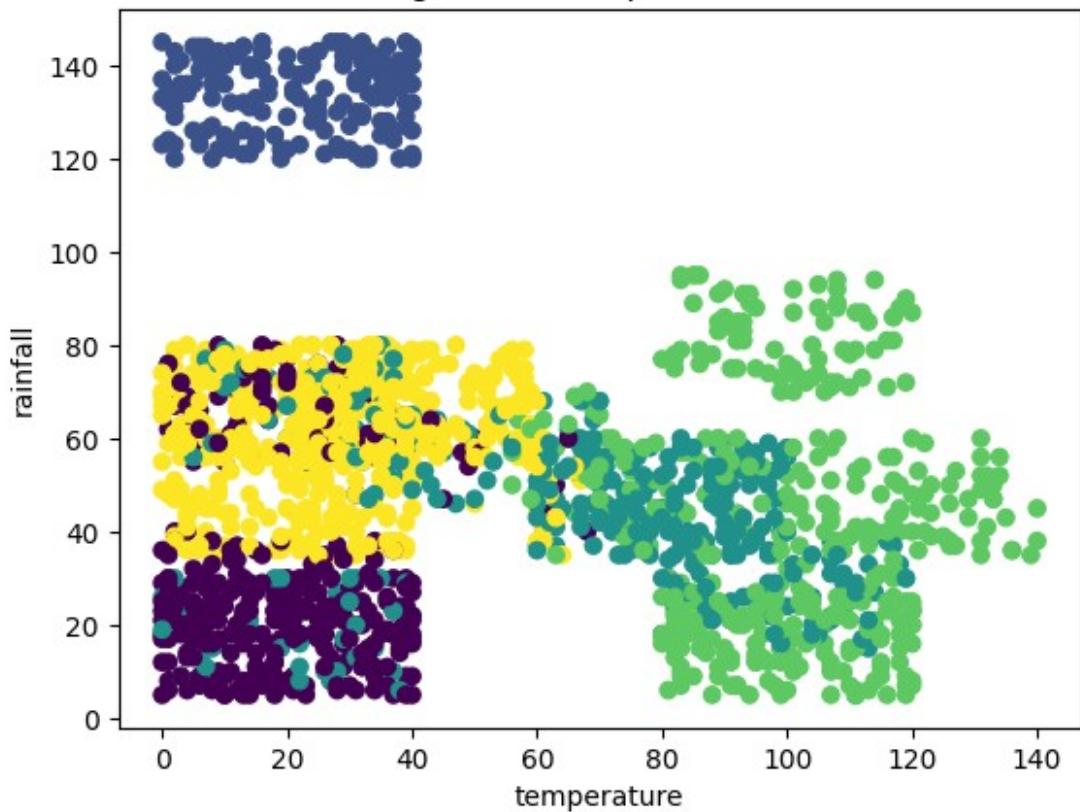
Clustering Result: temperature vs humidity



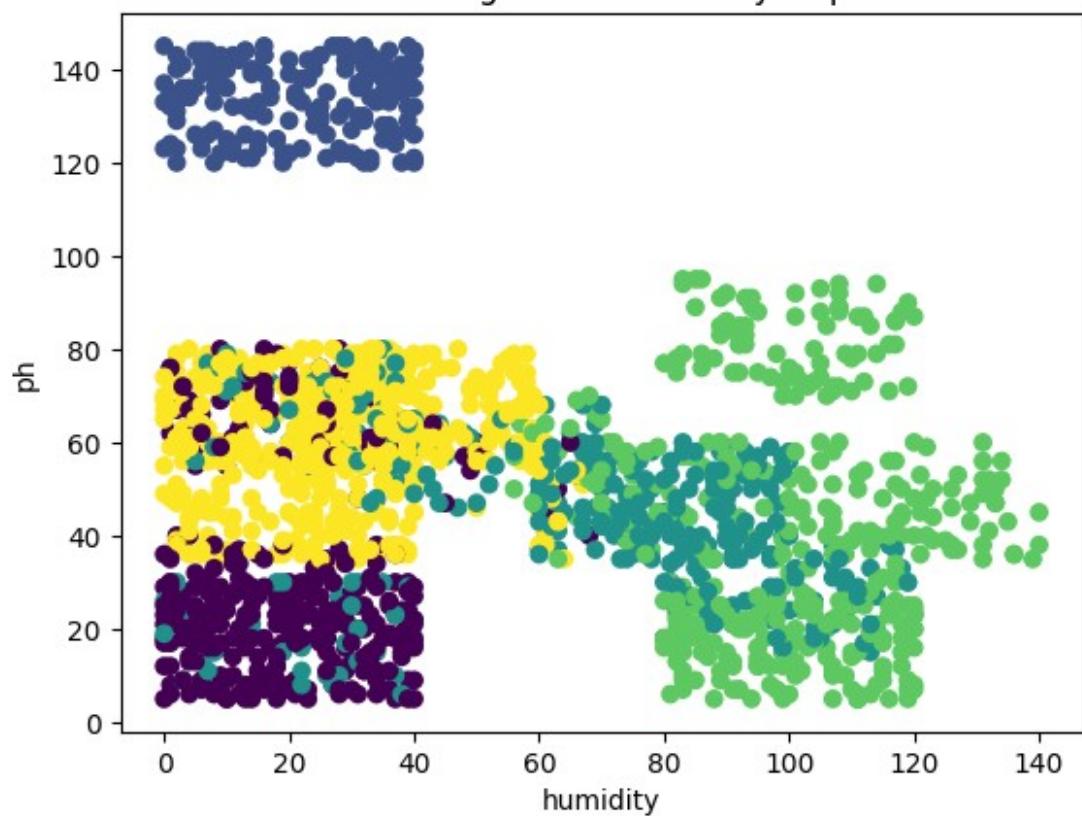
Clustering Result: temperature vs ph



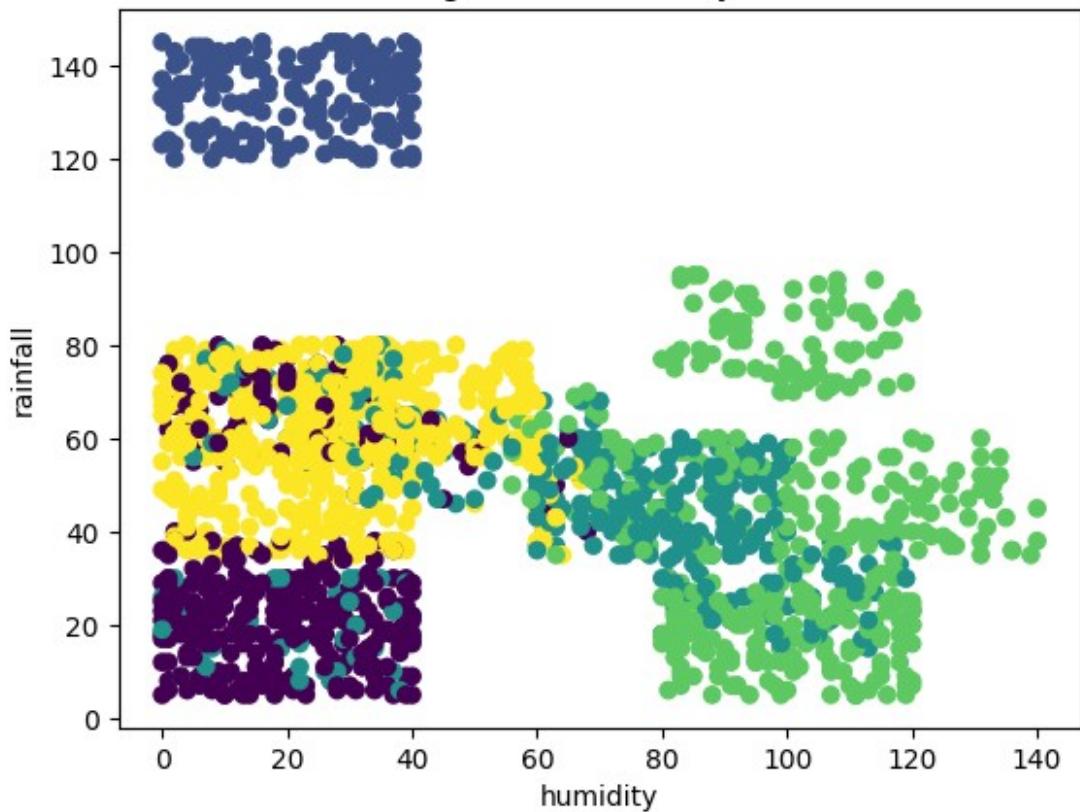
Clustering Result: temperature vs rainfall

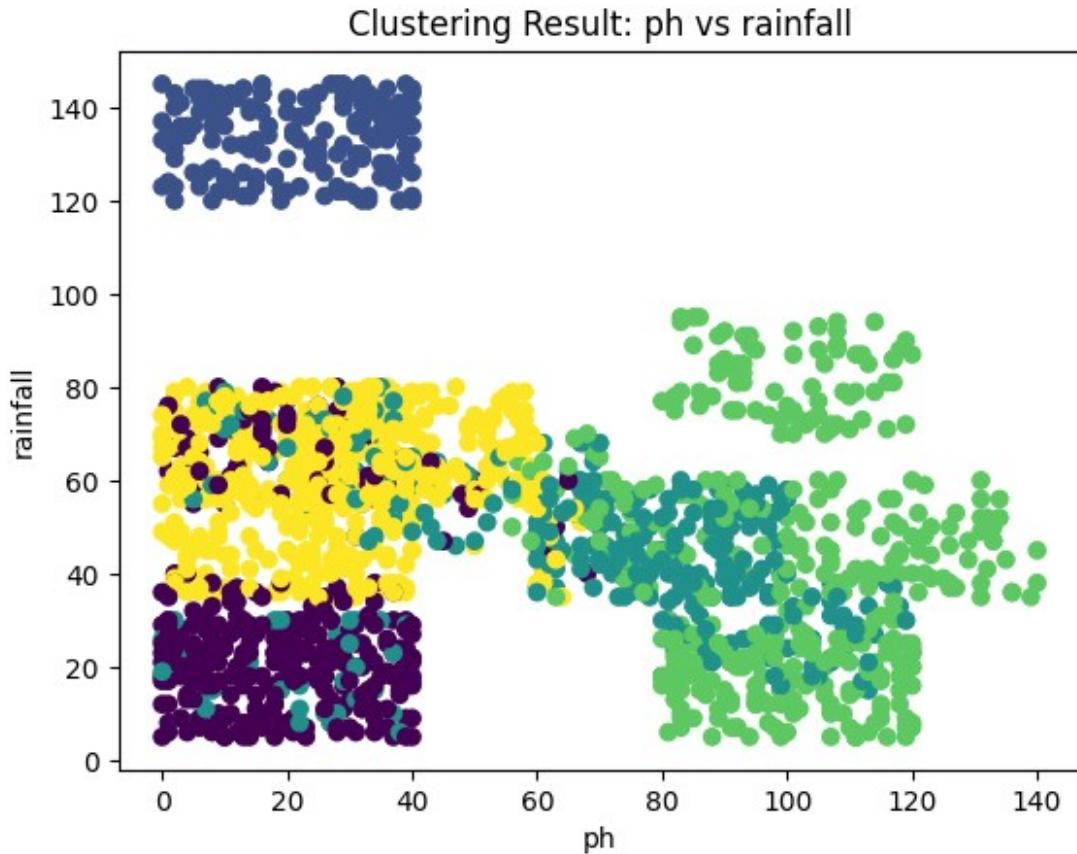


Clustering Result: humidity vs ph



Clustering Result: humidity vs rainfall





```

Silhouette Score: 0.3880142086658608
Adjusted Rand Index: 0.23887132731300023
Homogeneity: 0.4318346434455172
Completeness: 0.8579334632429804
V-measure: 0.5744992286260481

```

```

# AgglomerativeClustering

# Get the predicted cluster labels for the training data
train_cluster_labels = agglomerative.labels_

# Compute evaluation metrics
silhouette_avg = silhouette_score(X_train, train_cluster_labels)
ari = adjusted_rand_score(target, train_cluster_labels)
homogeneity, completeness, v_measure =
homogeneity_completeness_v_measure(target, train_cluster_labels)

# Create scatter plots for different feature combinations
features = ['Nitrogen', 'phosphorus', 'potassium', 'temperature',
'humidity', 'ph', 'rainfall']
for i in range(len(features)):
    for j in range(i+1, len(features)):
        plt.scatter(X_train[:, 0], X_train[:, 1],

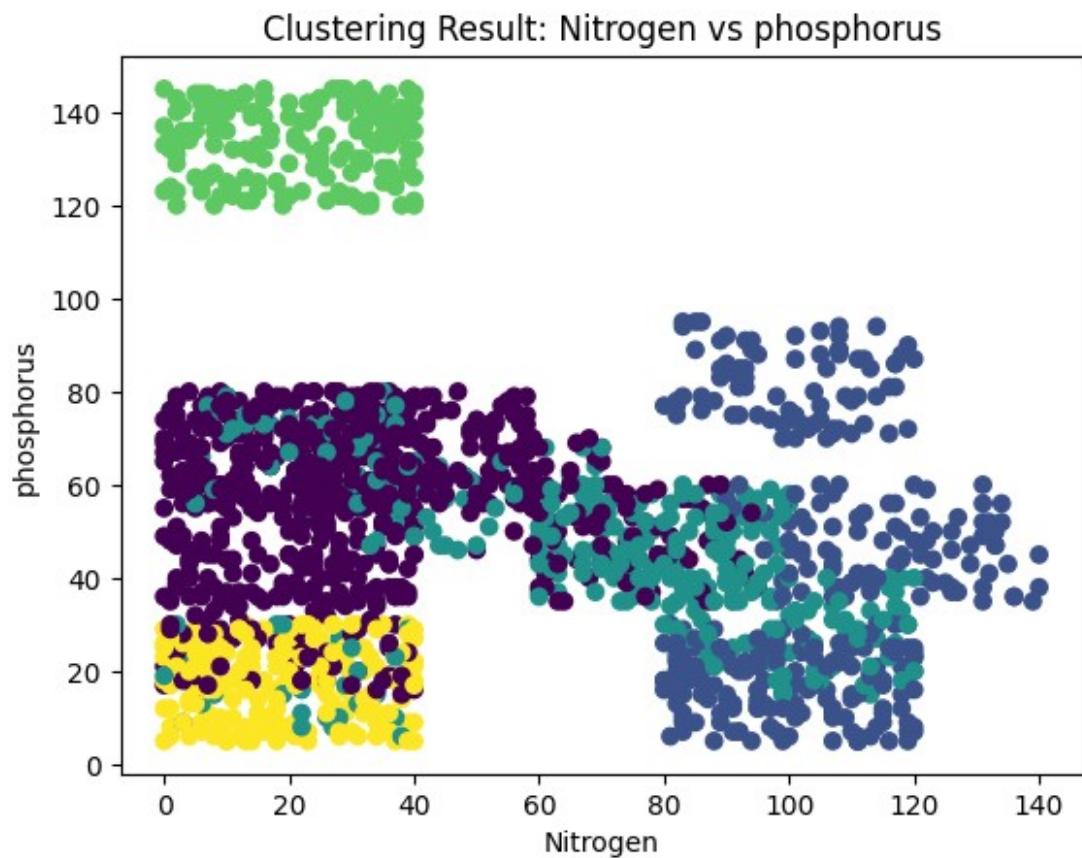
```

```

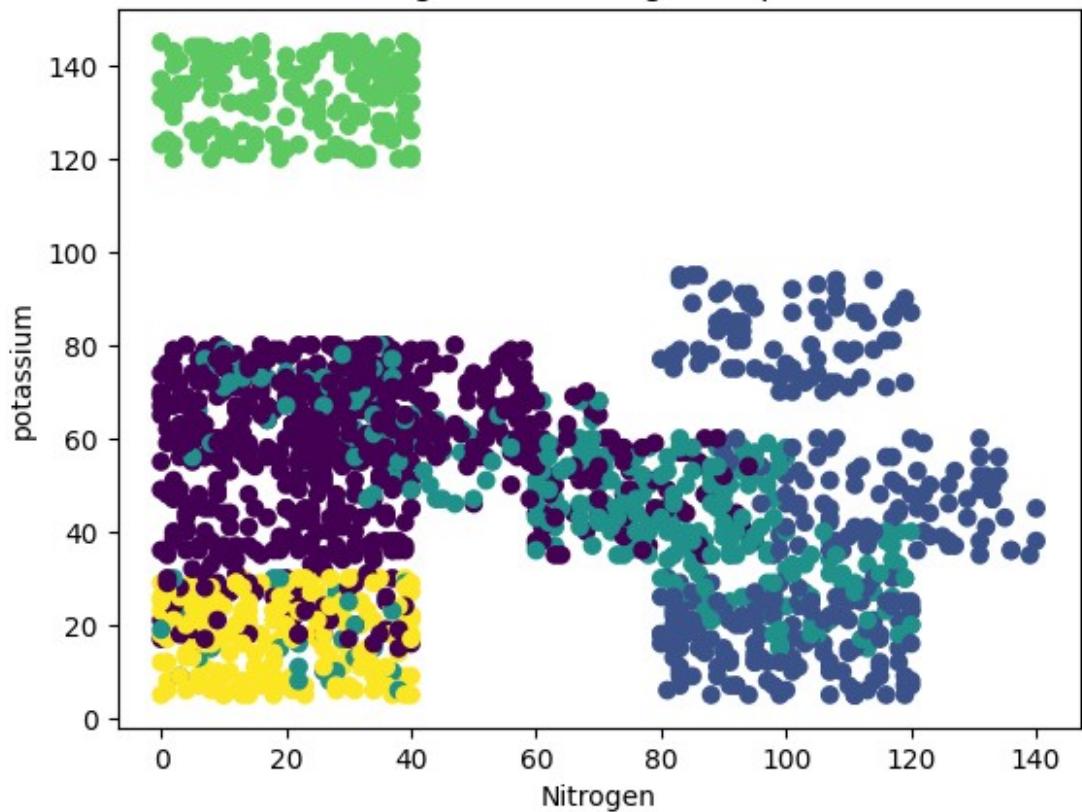
c=train_cluster_labels, cmap='viridis')
    plt.xlabel(features[i])
    plt.ylabel(features[j])
    plt.title(f'Clustering Result: {features[i]} vs
{features[j]}')
    plt.show()

# Print evaluation metrics
print("Silhouette Score:", silhouette_avg)
print("Adjusted Rand Index:", ari)
print("Homogeneity:", homogeneity)
print("Completeness:", completeness)
print("V-measure:", v_measure)

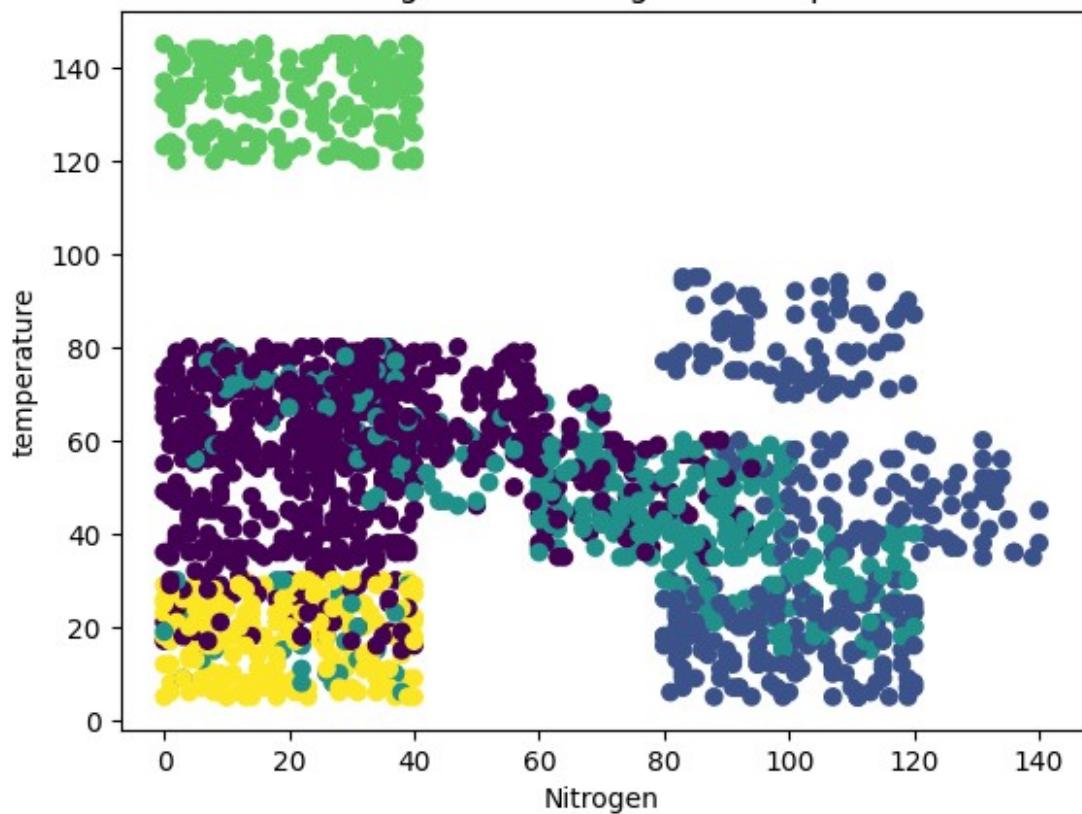
```



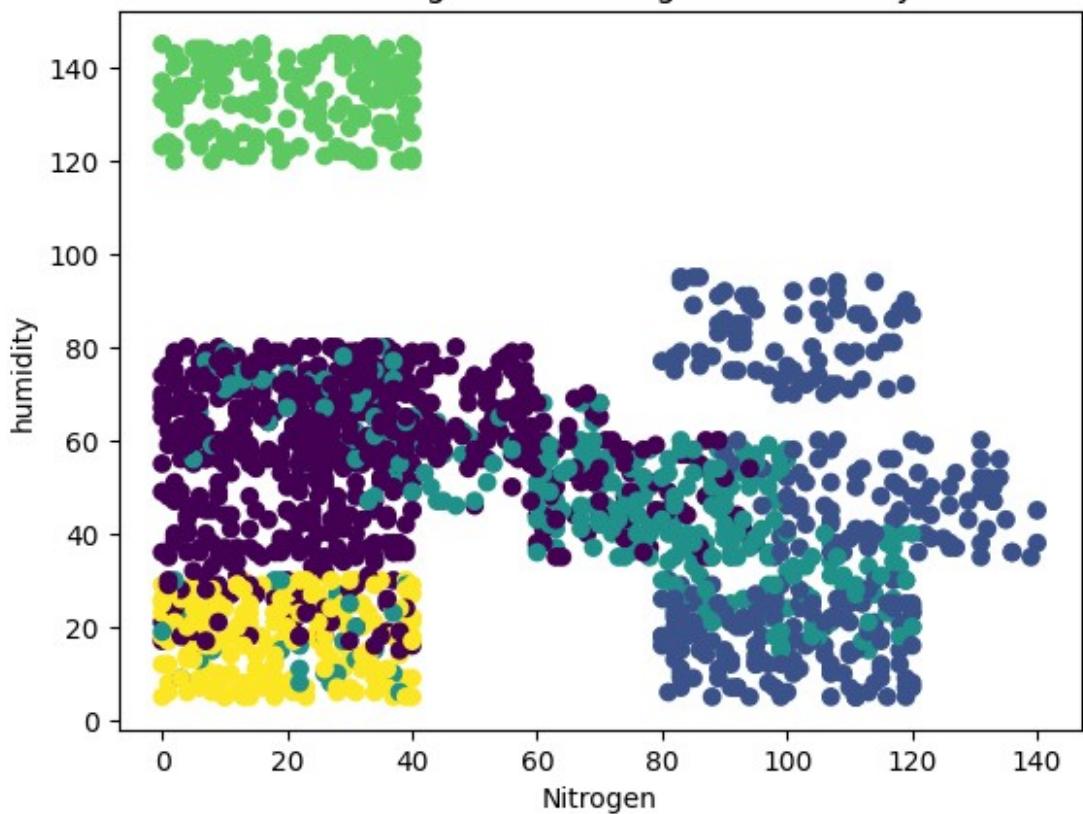
Clustering Result: Nitrogen vs potassium



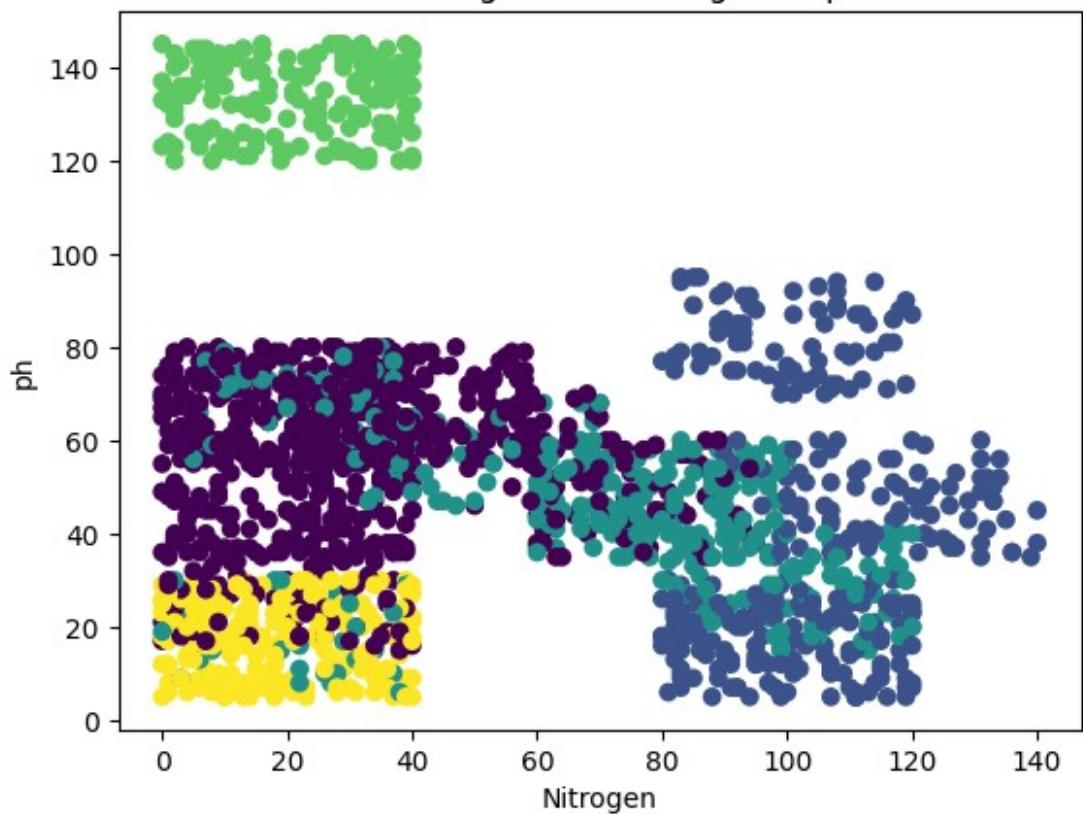
Clustering Result: Nitrogen vs temperature



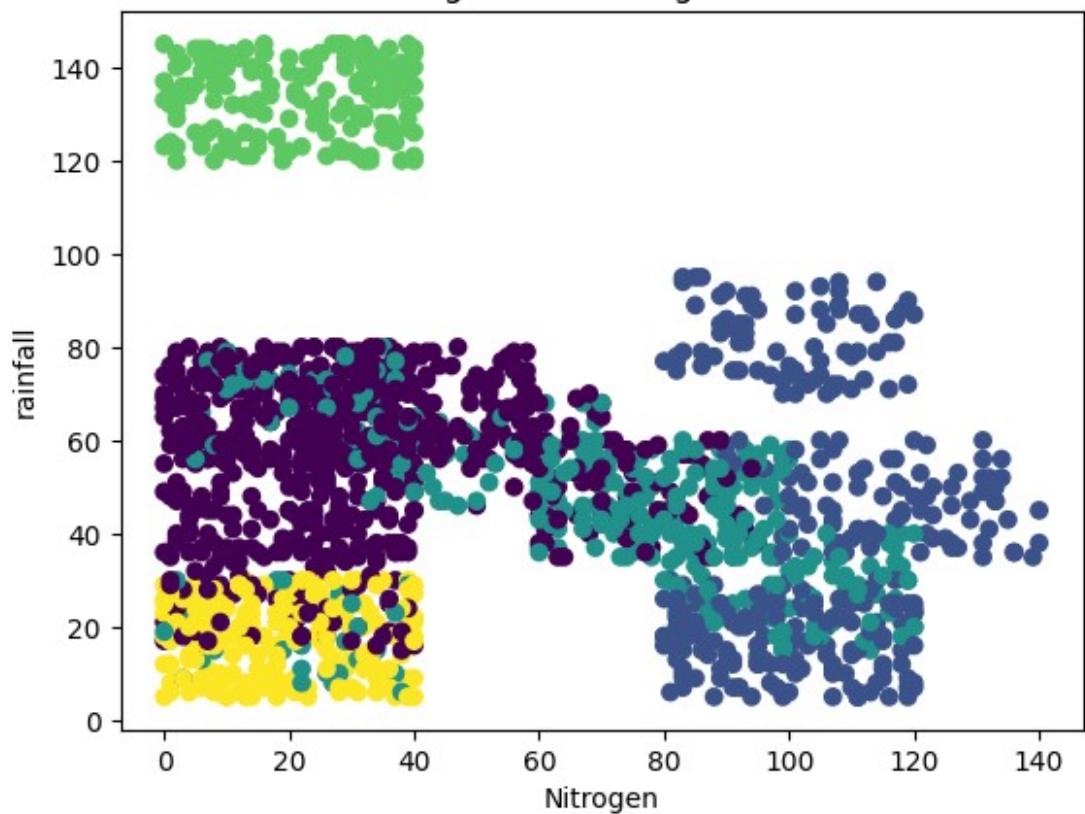
Clustering Result: Nitrogen vs humidity



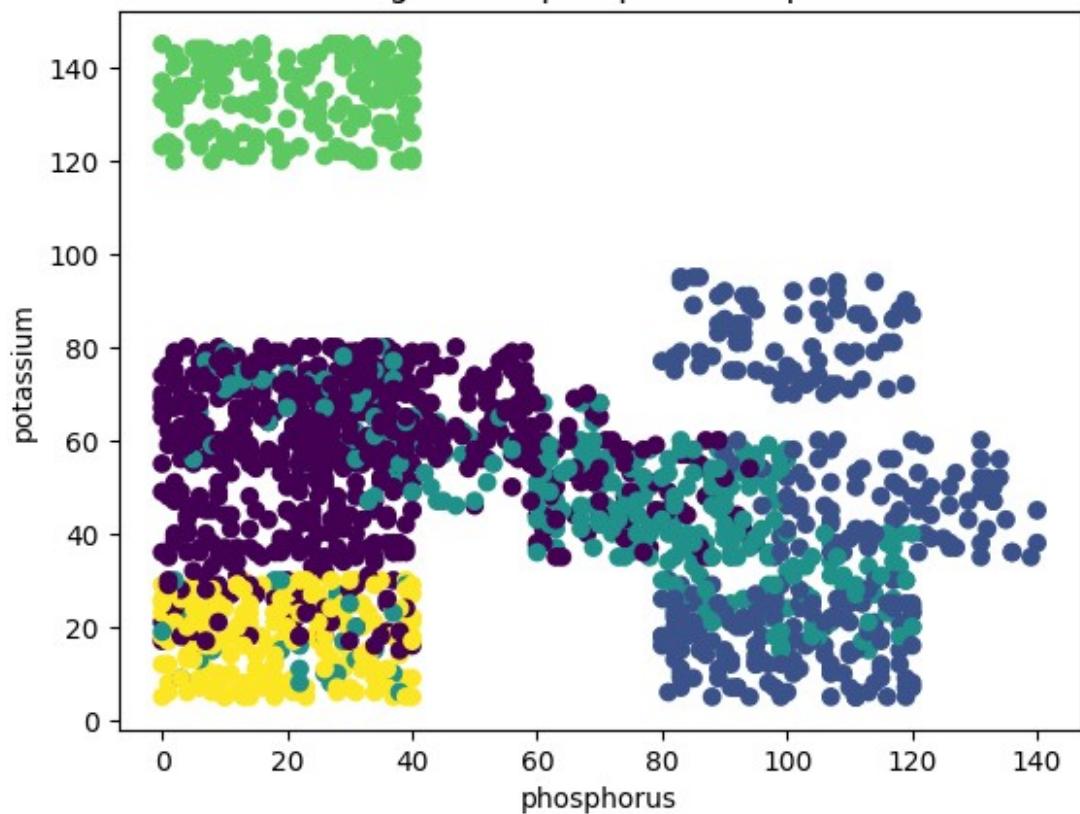
Clustering Result: Nitrogen vs ph



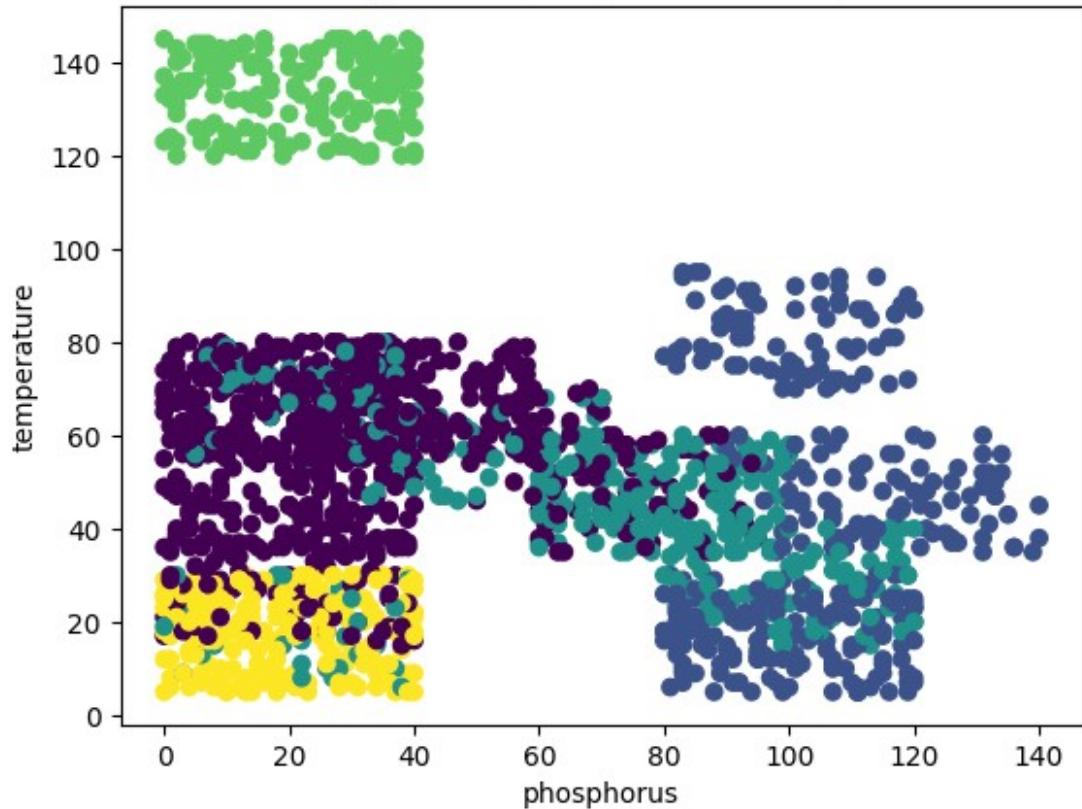
Clustering Result: Nitrogen vs rainfall



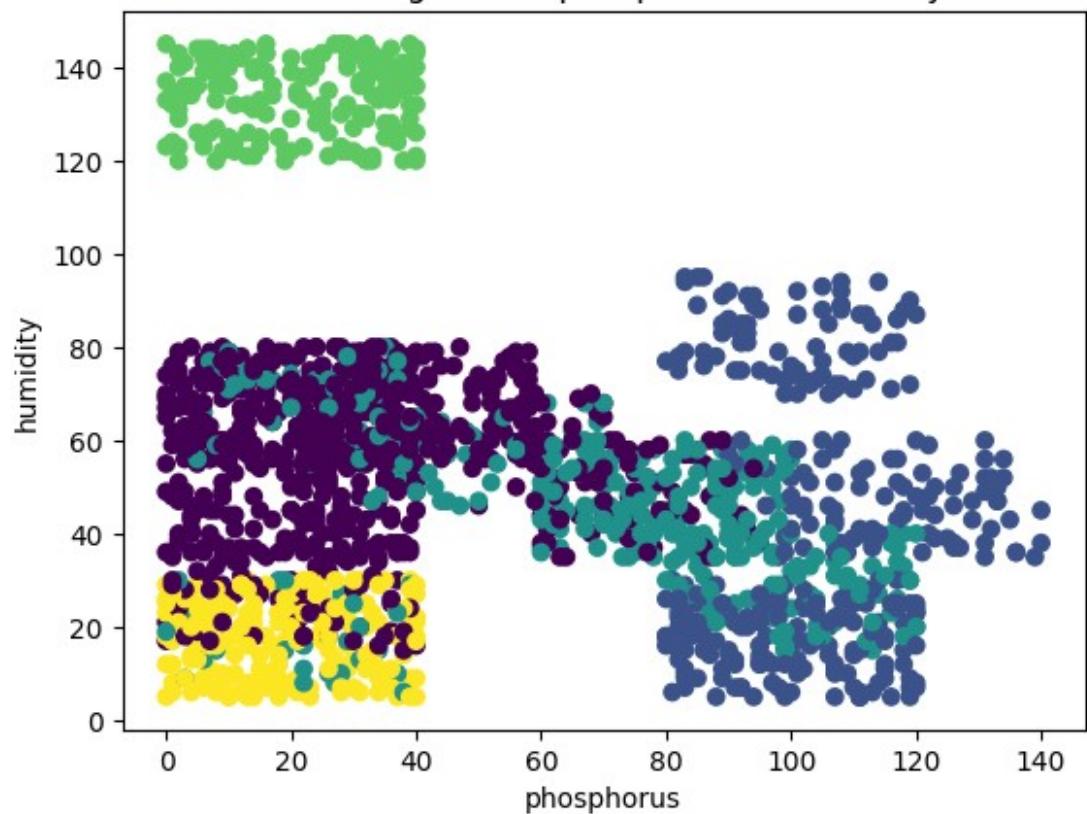
Clustering Result: phosphorus vs potassium



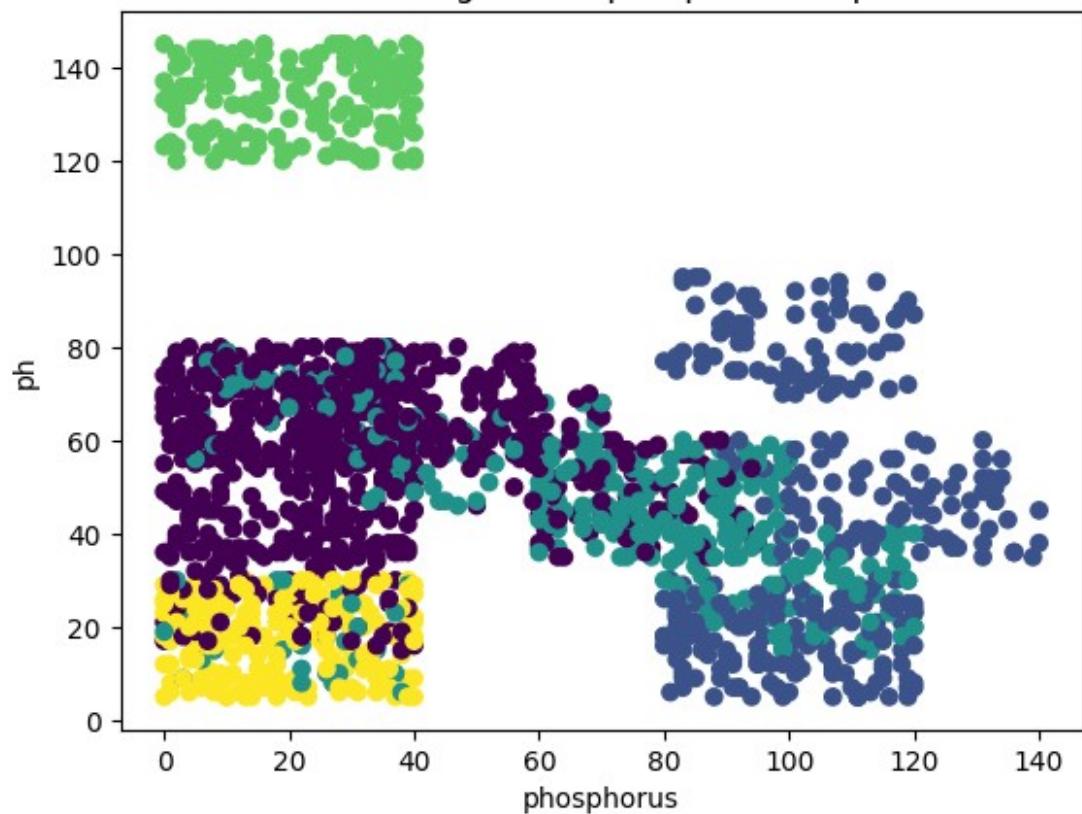
Clustering Result: phosphorus vs temperature



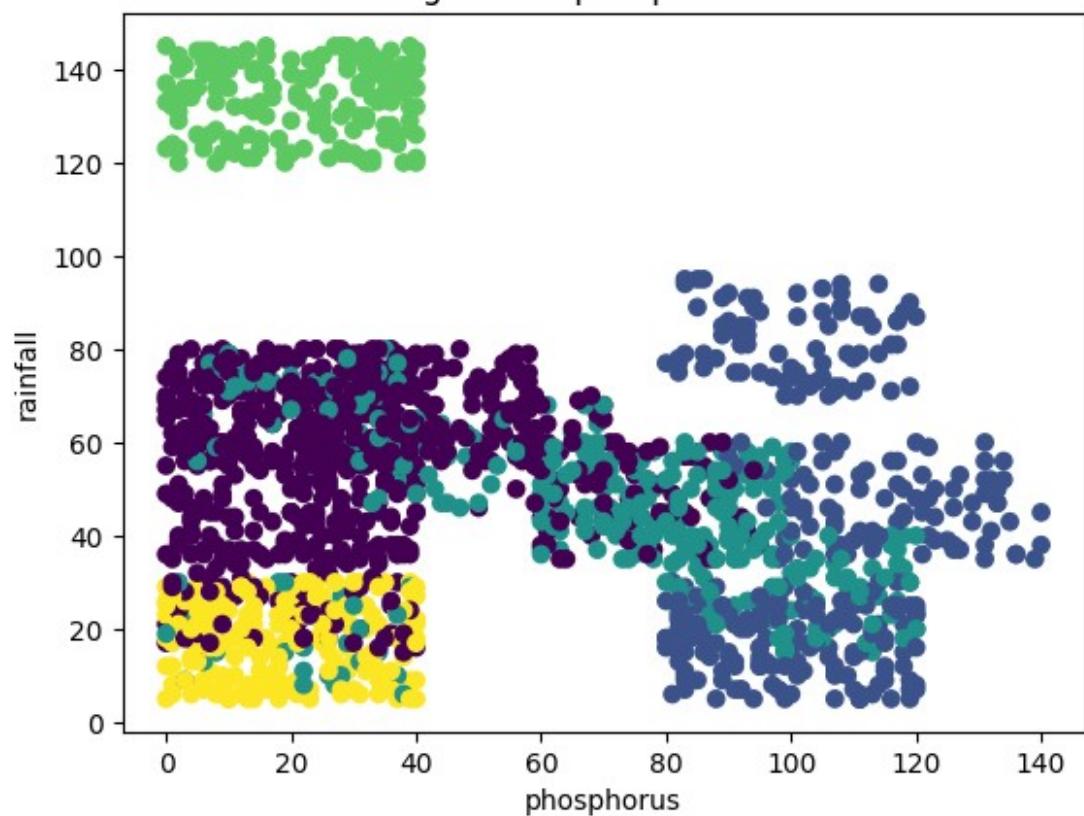
Clustering Result: phosphorus vs humidity



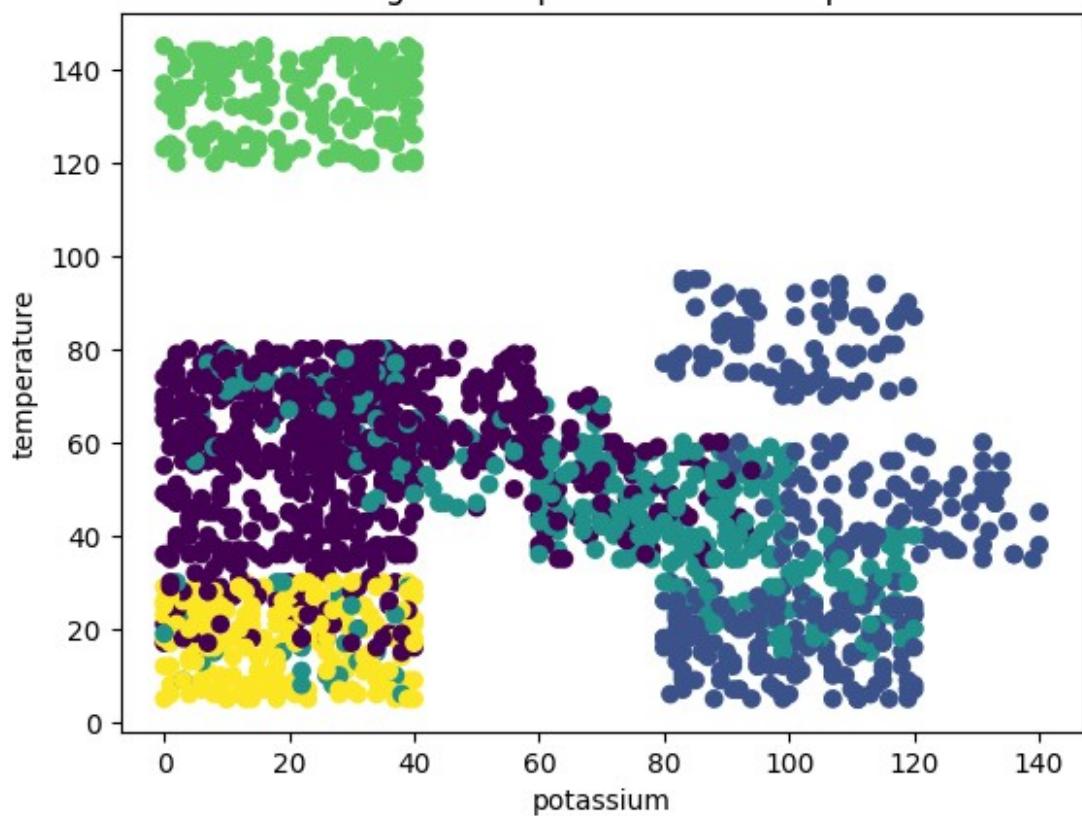
Clustering Result: phosphorus vs ph



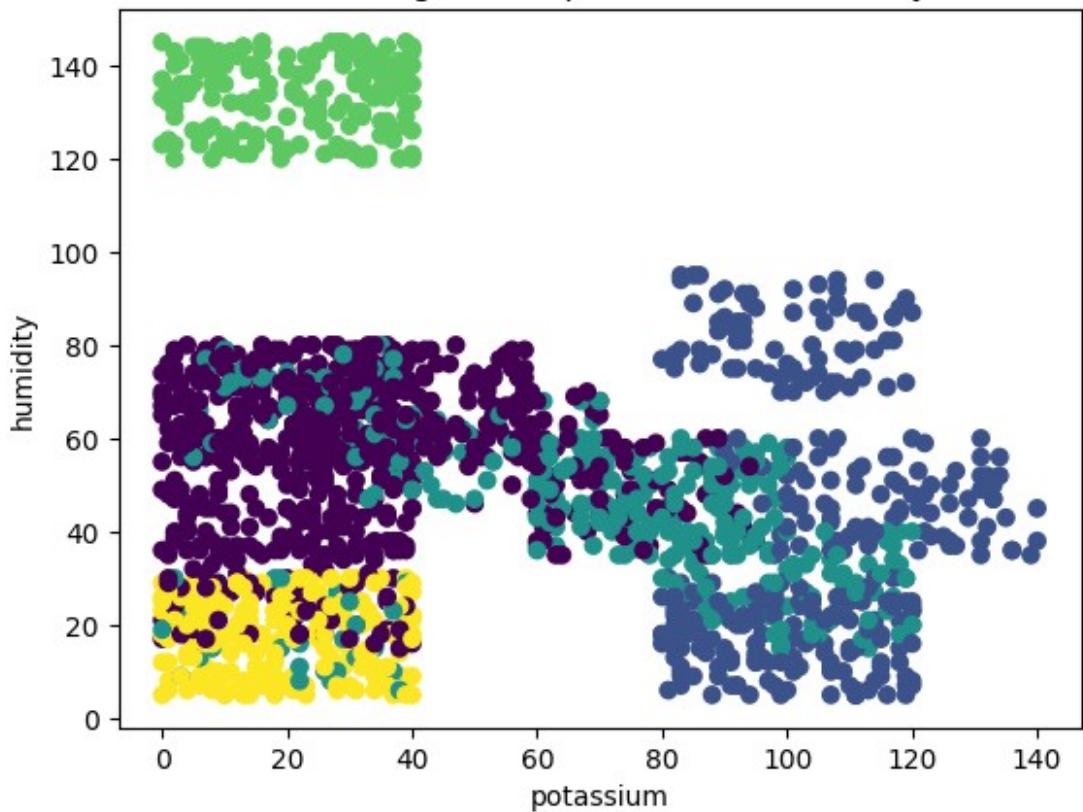
Clustering Result: phosphorus vs rainfall



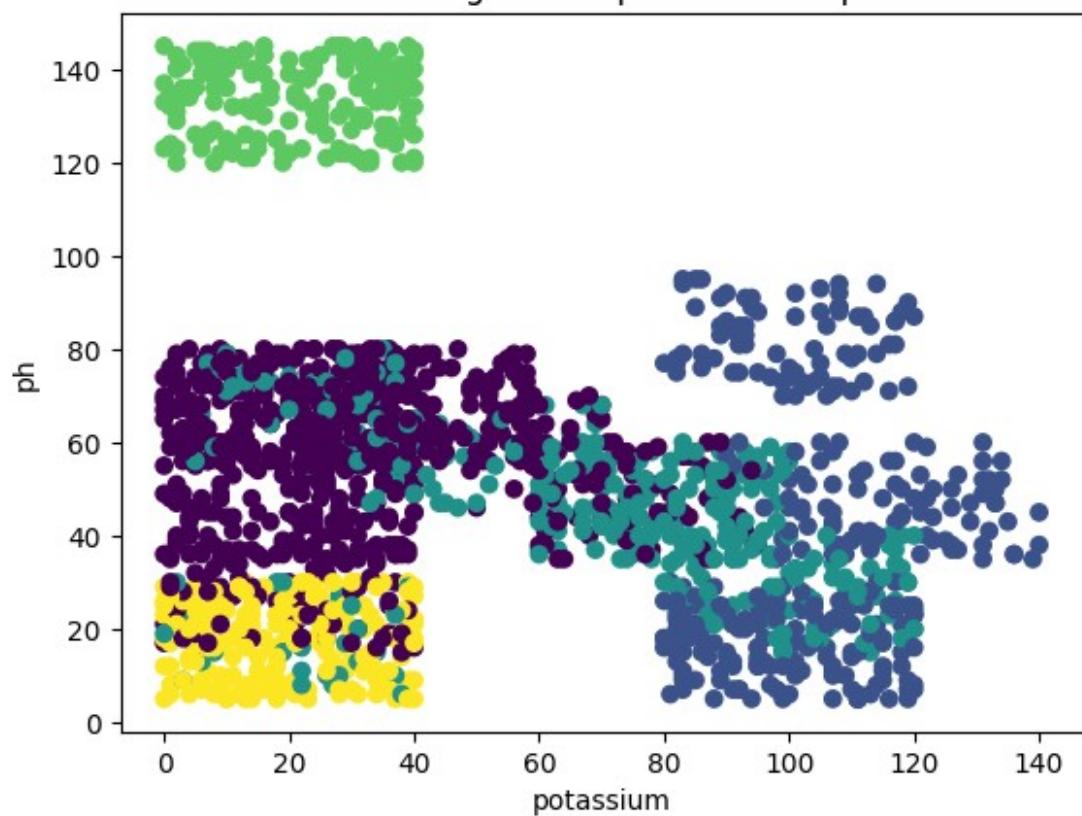
Clustering Result: potassium vs temperature



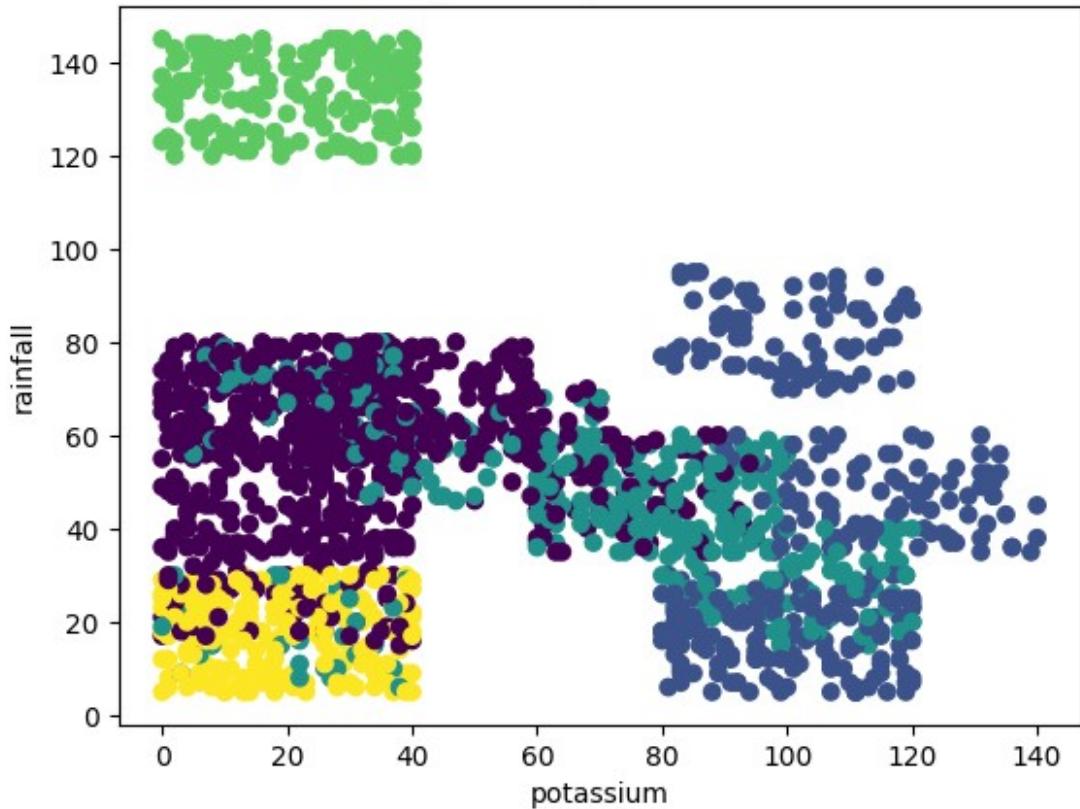
Clustering Result: potassium vs humidity



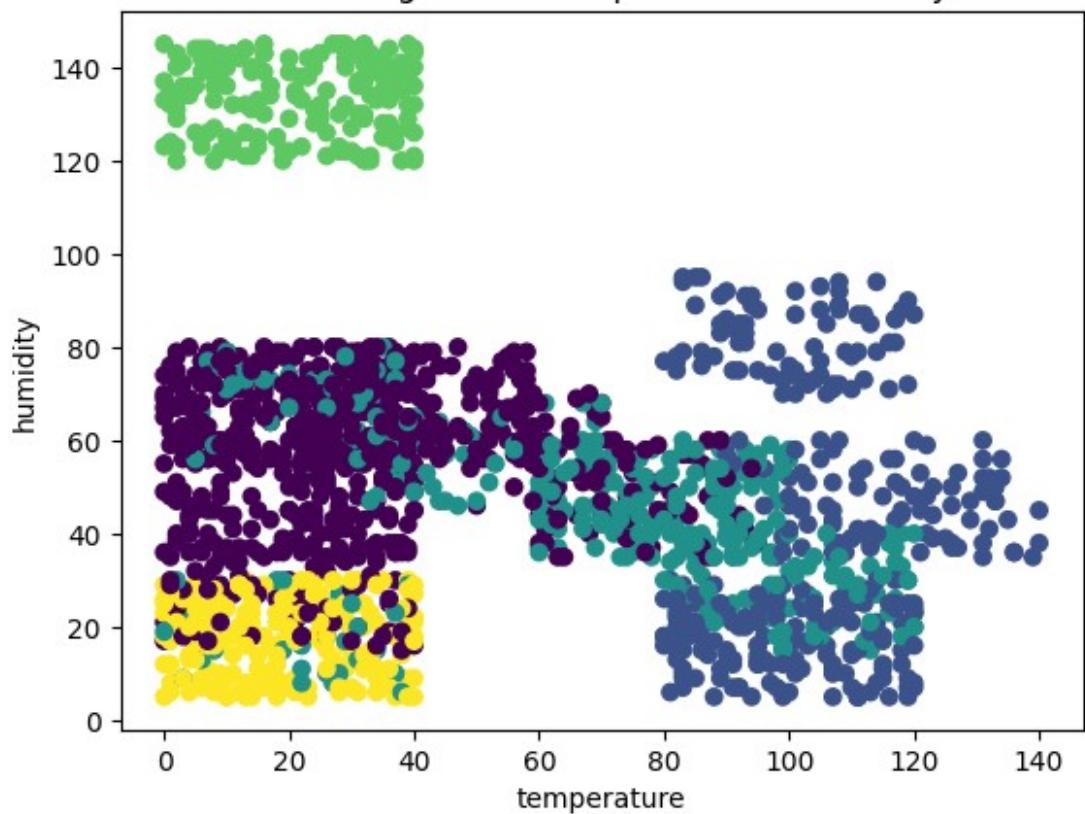
Clustering Result: potassium vs ph



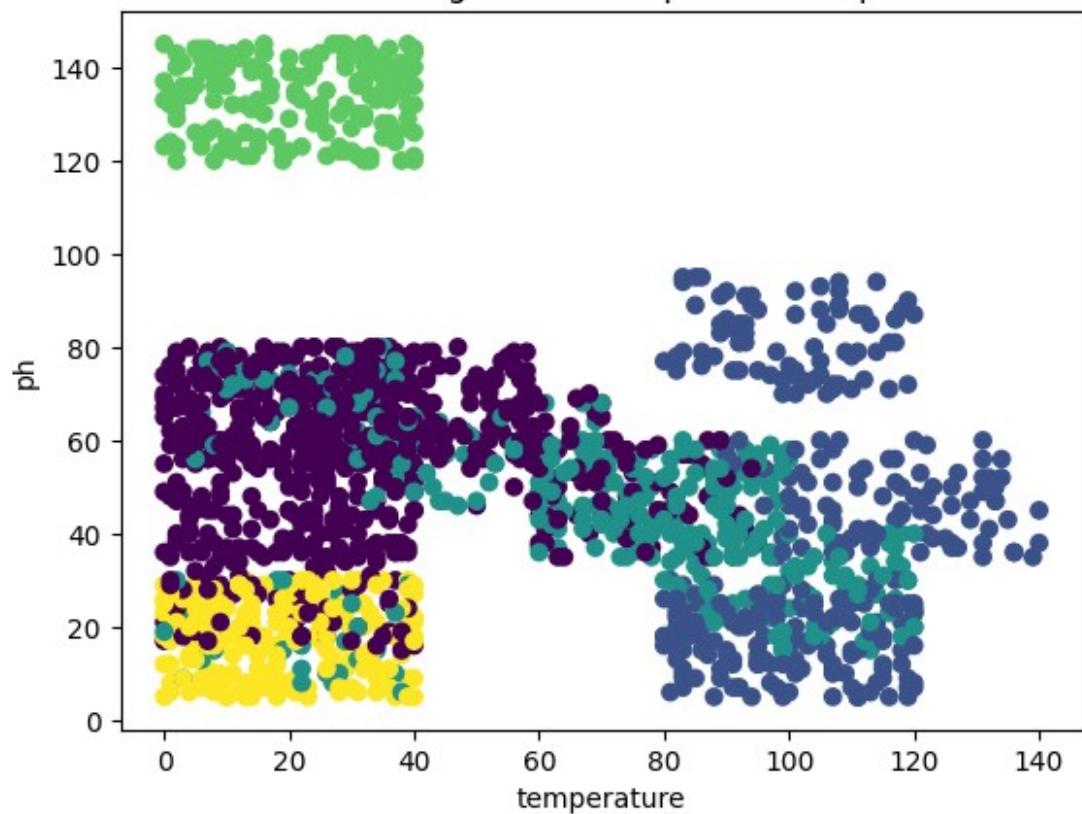
Clustering Result: potassium vs rainfall



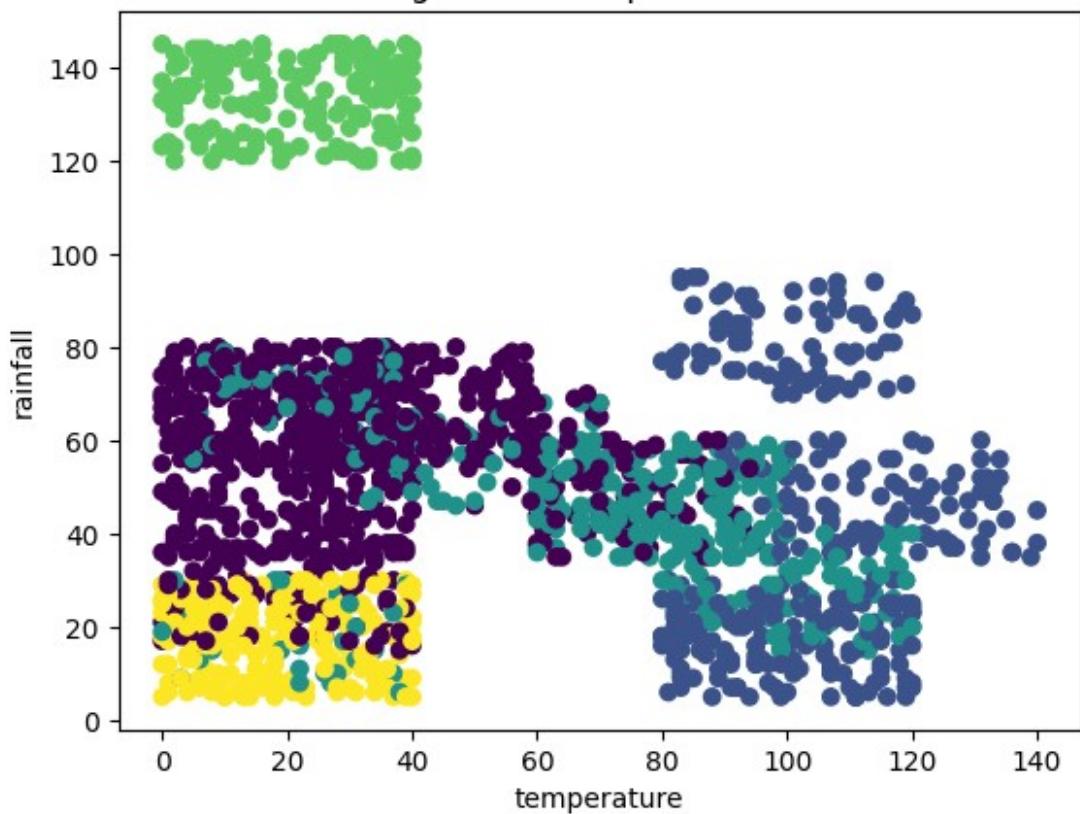
Clustering Result: temperature vs humidity



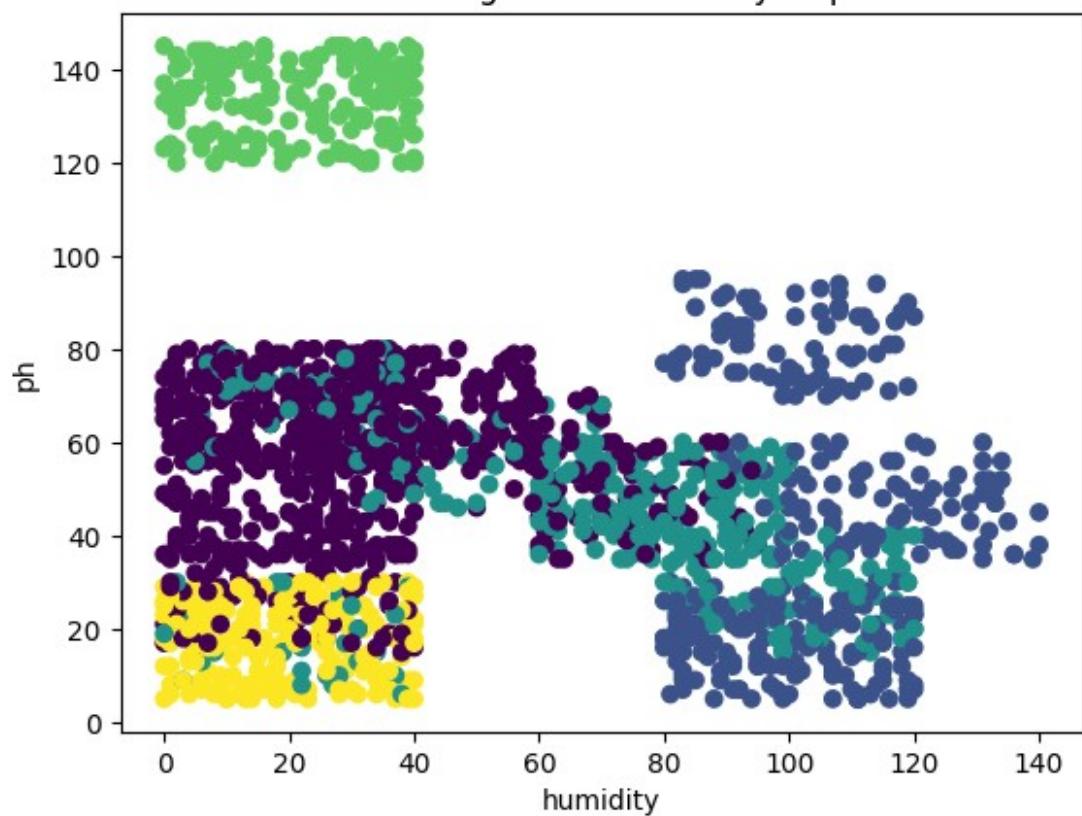
Clustering Result: temperature vs ph



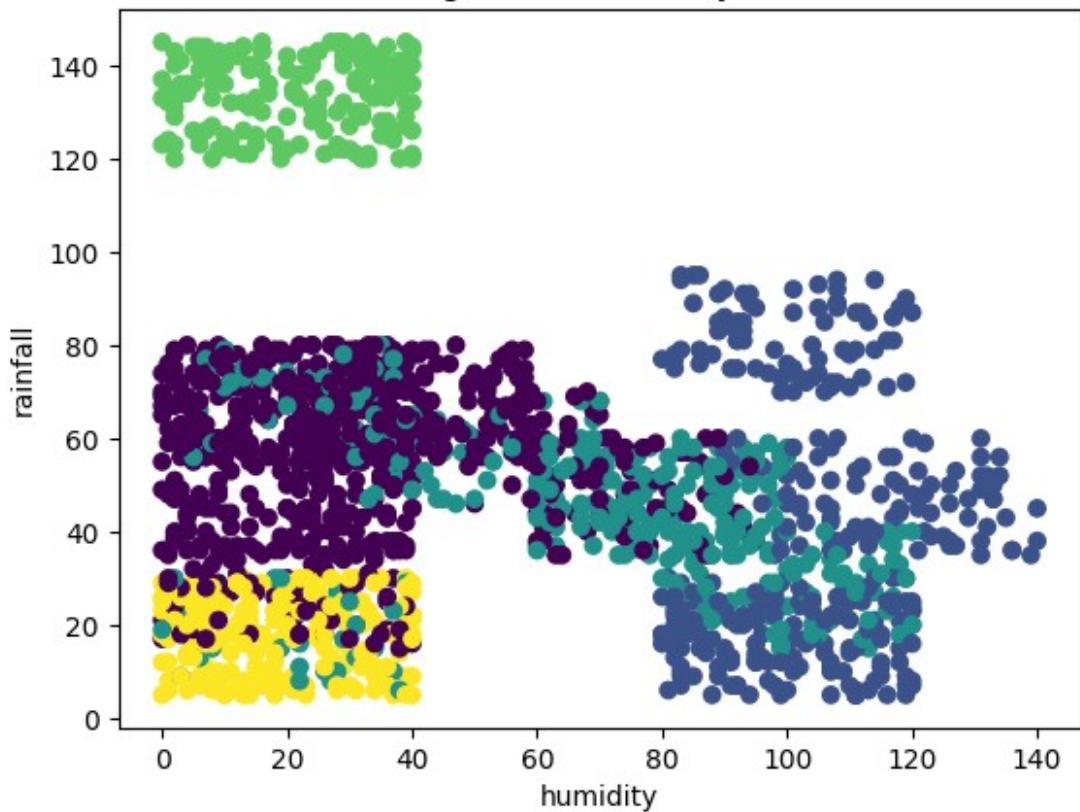
Clustering Result: temperature vs rainfall

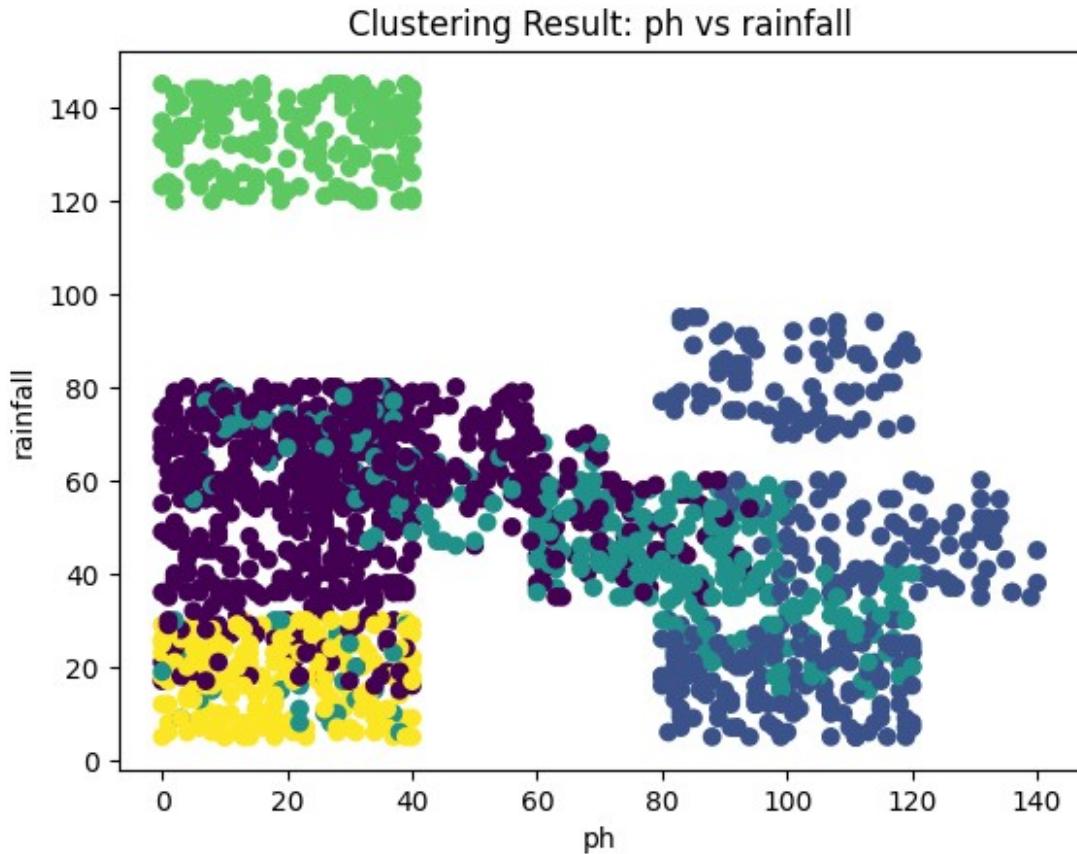


Clustering Result: humidity vs ph



Clustering Result: humidity vs rainfall





Silhouette Score: 0.36990069163203215  
 Adjusted Rand Index: 0.21771191100971643  
 Homogeneity: 0.4446816673547052  
 Completeness: 0.9293280011722735  
 V-measure: 0.6015316115260477

#### #AffinityPropagation

```
# Get the predicted cluster labels for the training data
train_cluster_labels = affinity_propagation.labels_

# Compute evaluation metrics
silhouette_avg = silhouette_score(X_train, train_cluster_labels)
ari = adjusted_rand_score(target, train_cluster_labels)
homogeneity, completeness, v_measure =
homogeneity_completeness_v_measure(target, train_cluster_labels)

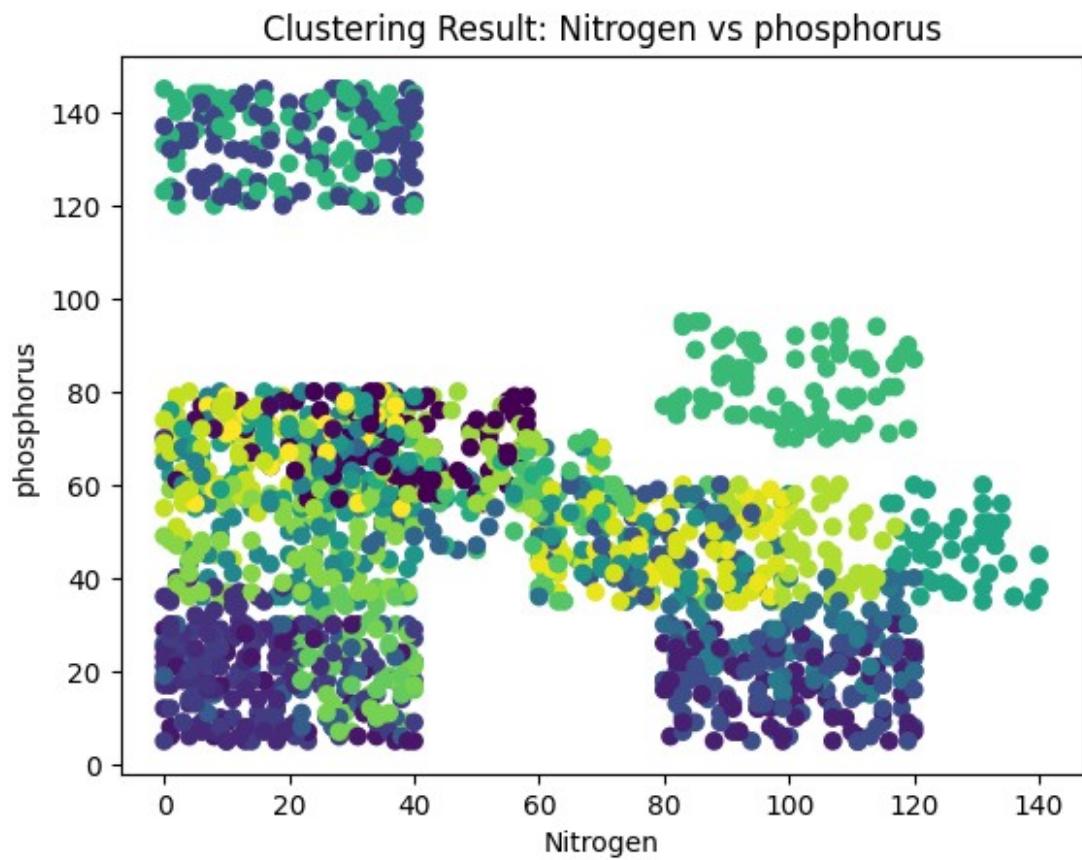
# Create scatter plots for different feature combinations
features = ['Nitrogen', 'phosphorus', 'potassium', 'temperature',
'humidity', 'ph', 'rainfall']
for i in range(len(features)):
    for j in range(i+1, len(features)):
        plt.scatter(X_train[:, 0], X_train[:, 1],
```

```

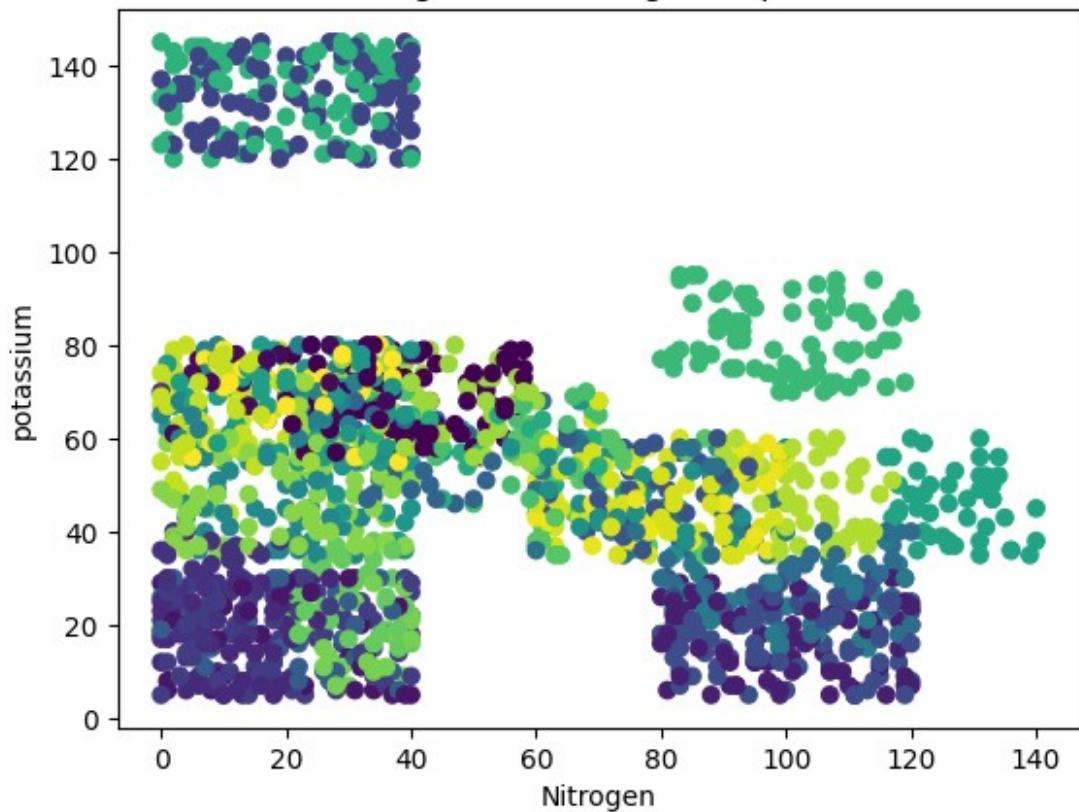
c=train_cluster_labels, cmap='viridis')
    plt.xlabel(features[i])
    plt.ylabel(features[j])
    plt.title(f'Clustering Result: {features[i]} vs
{features[j]}')
    plt.show()

# Print evaluation metrics
print("Silhouette Score:", silhouette_avg)
print("Adjusted Rand Index:", ari)
print("Homogeneity:", homogeneity)
print("Completeness:", completeness)
print("V-measure:", v_measure)

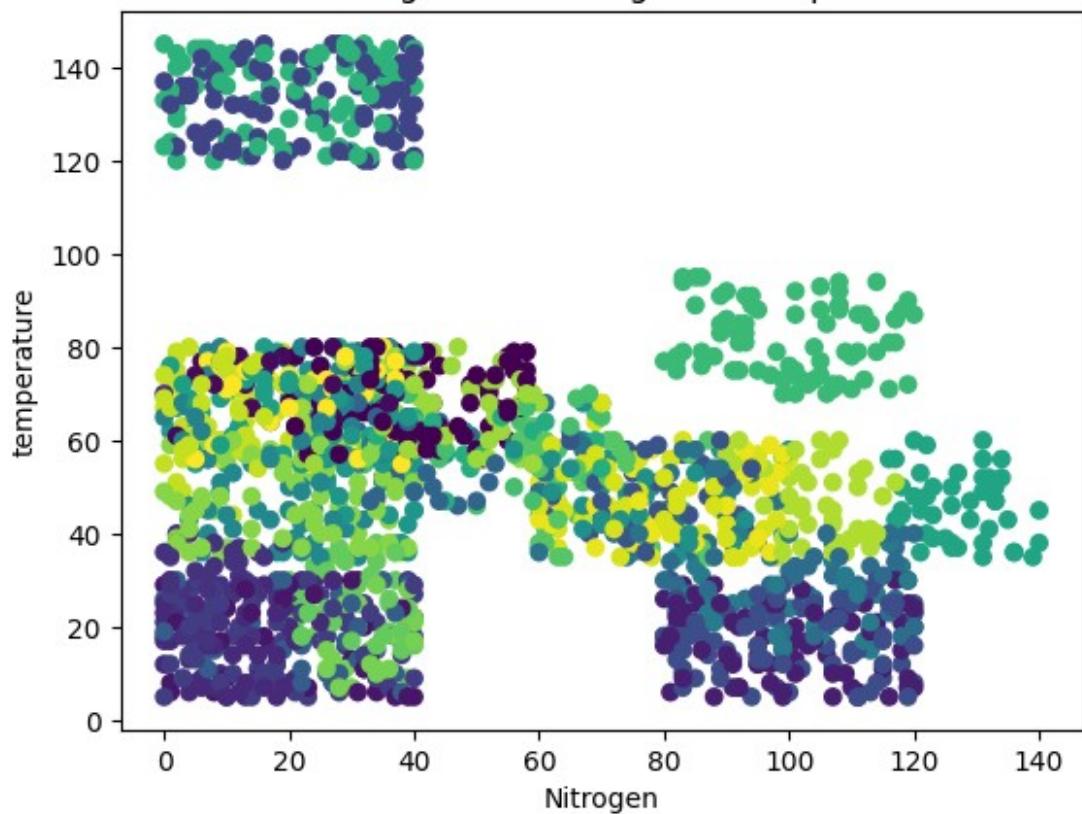
```



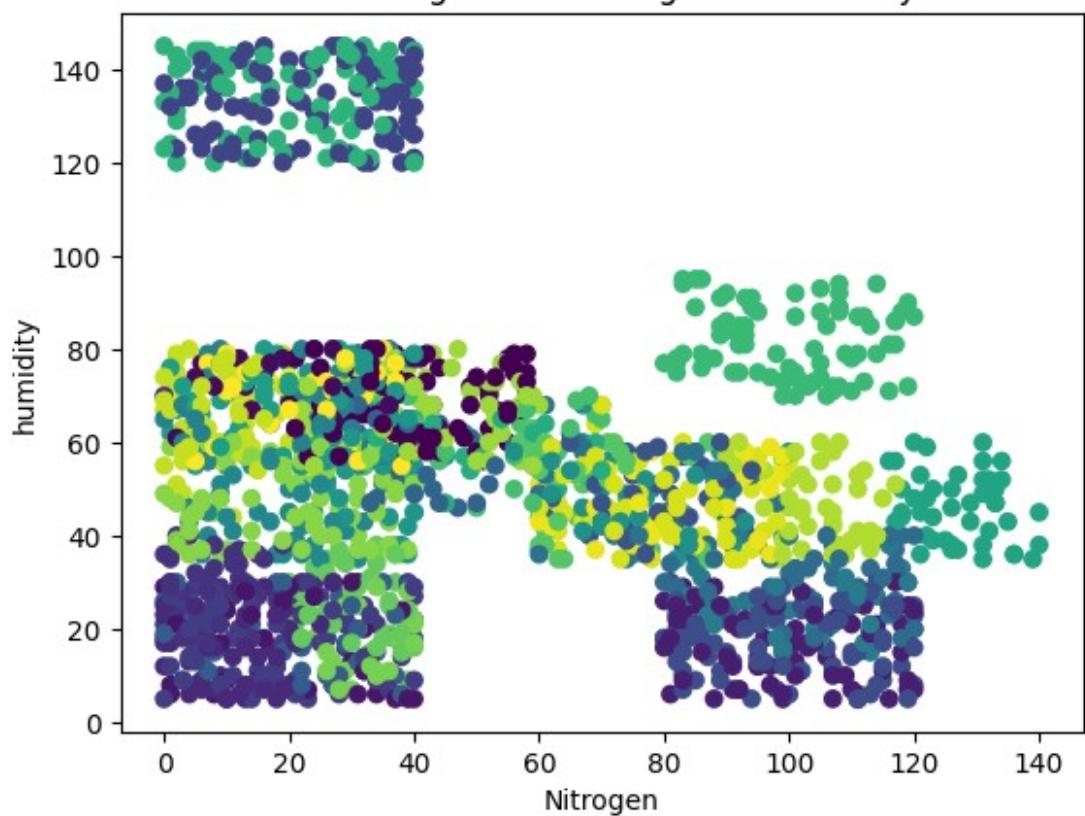
Clustering Result: Nitrogen vs potassium



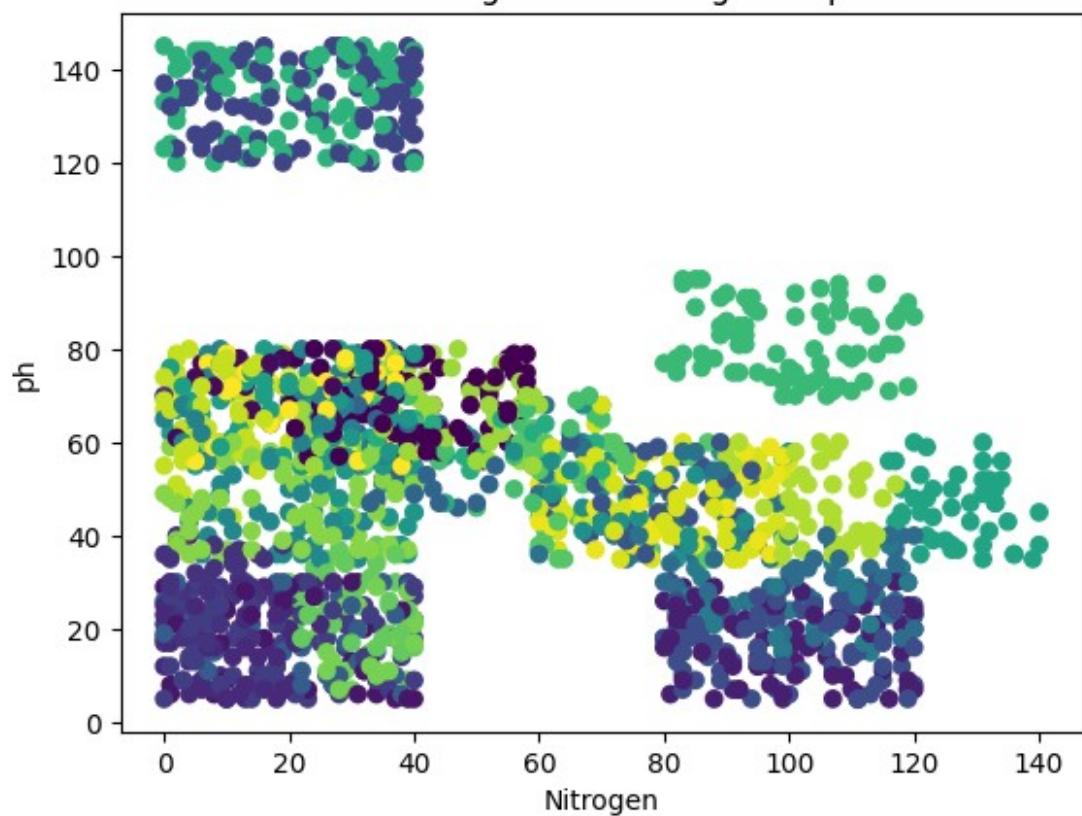
Clustering Result: Nitrogen vs temperature



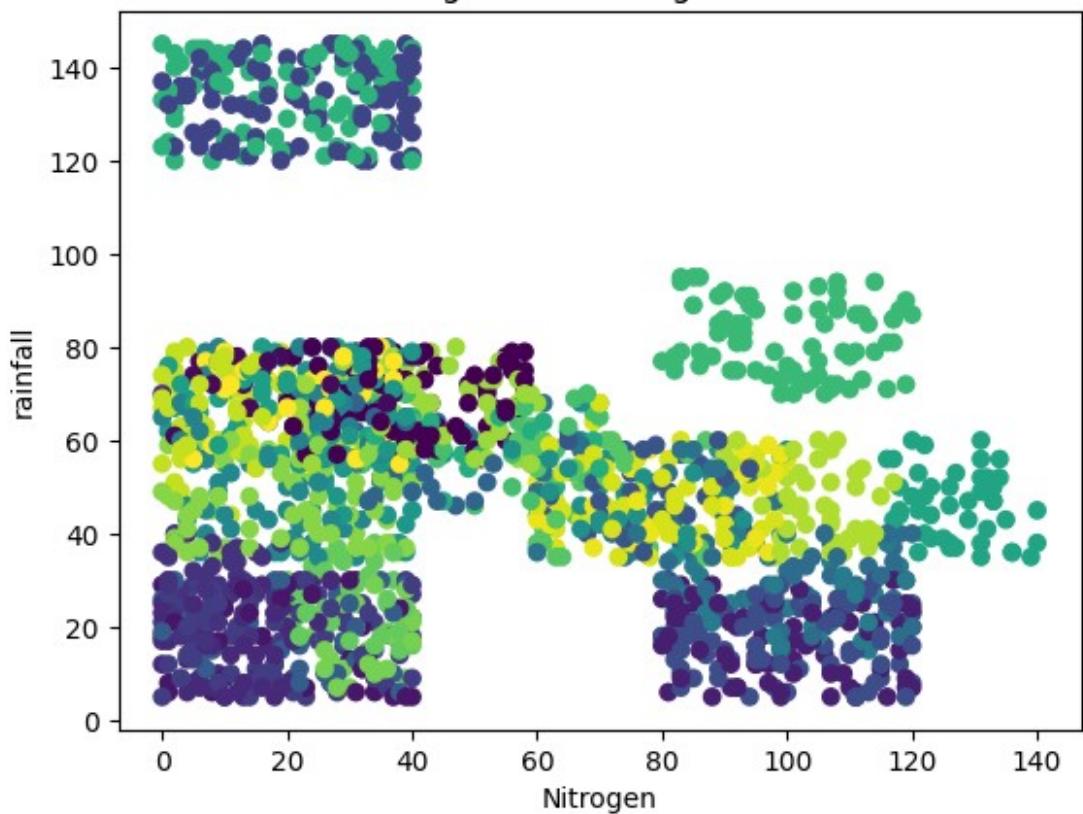
Clustering Result: Nitrogen vs humidity



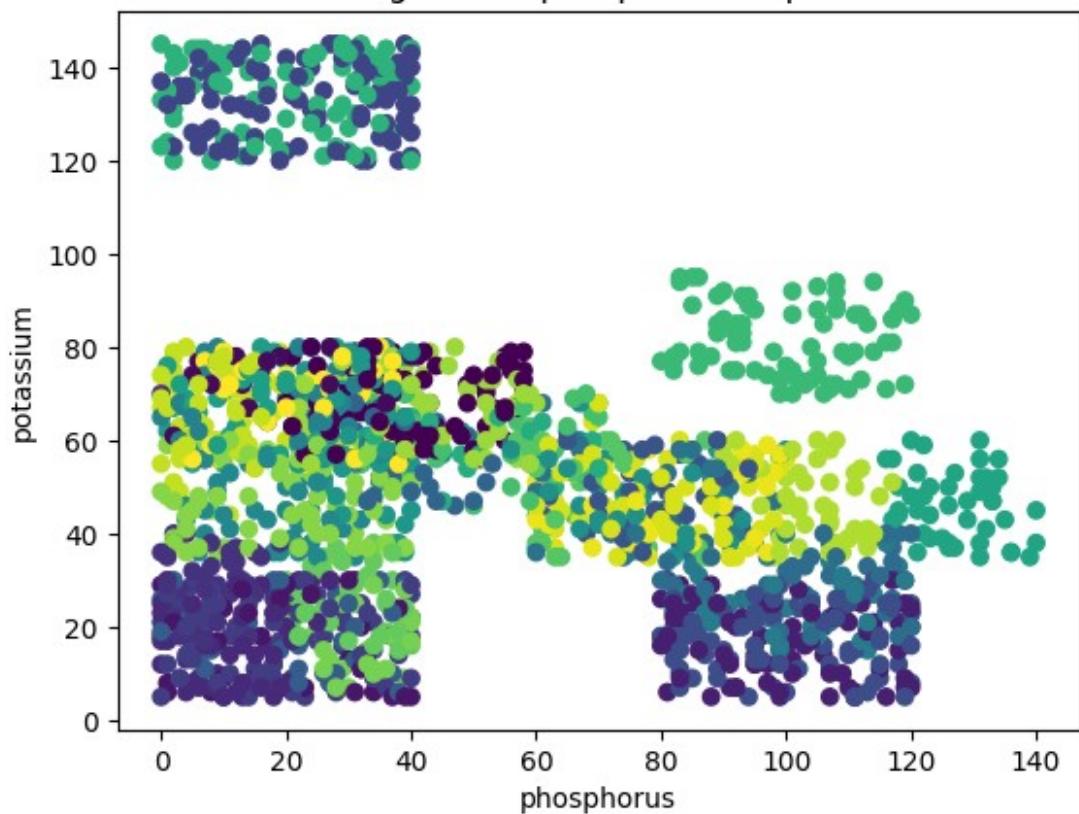
Clustering Result: Nitrogen vs ph



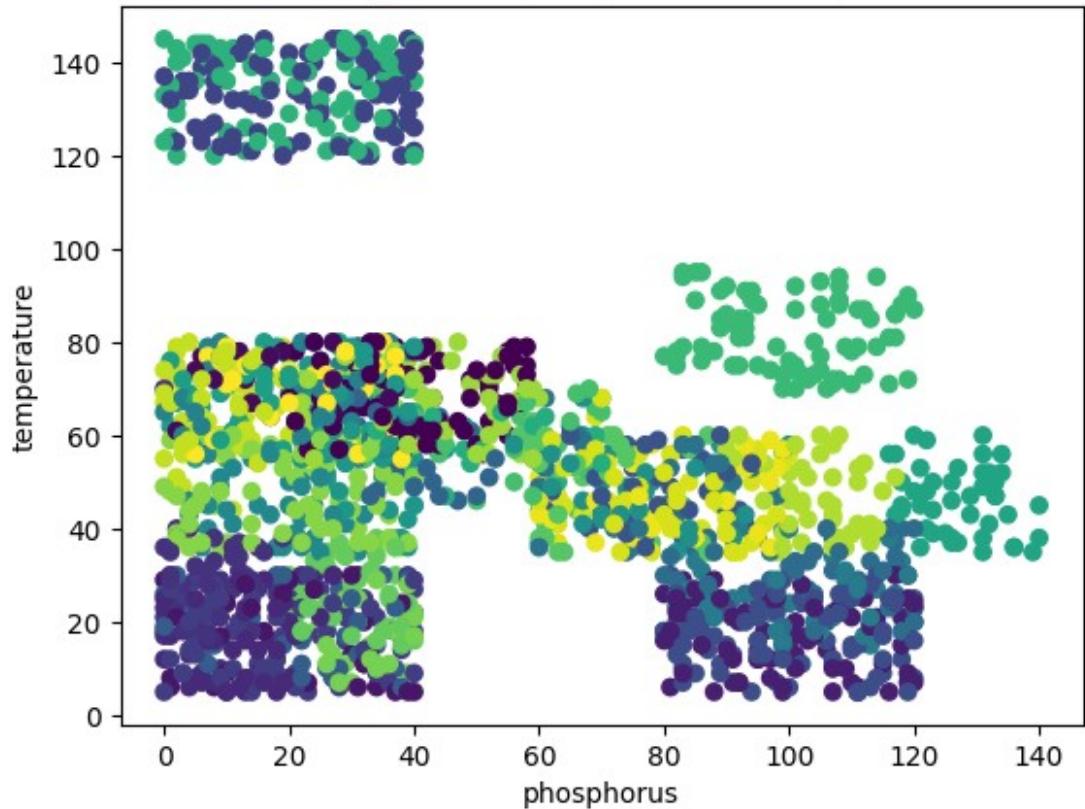
Clustering Result: Nitrogen vs rainfall



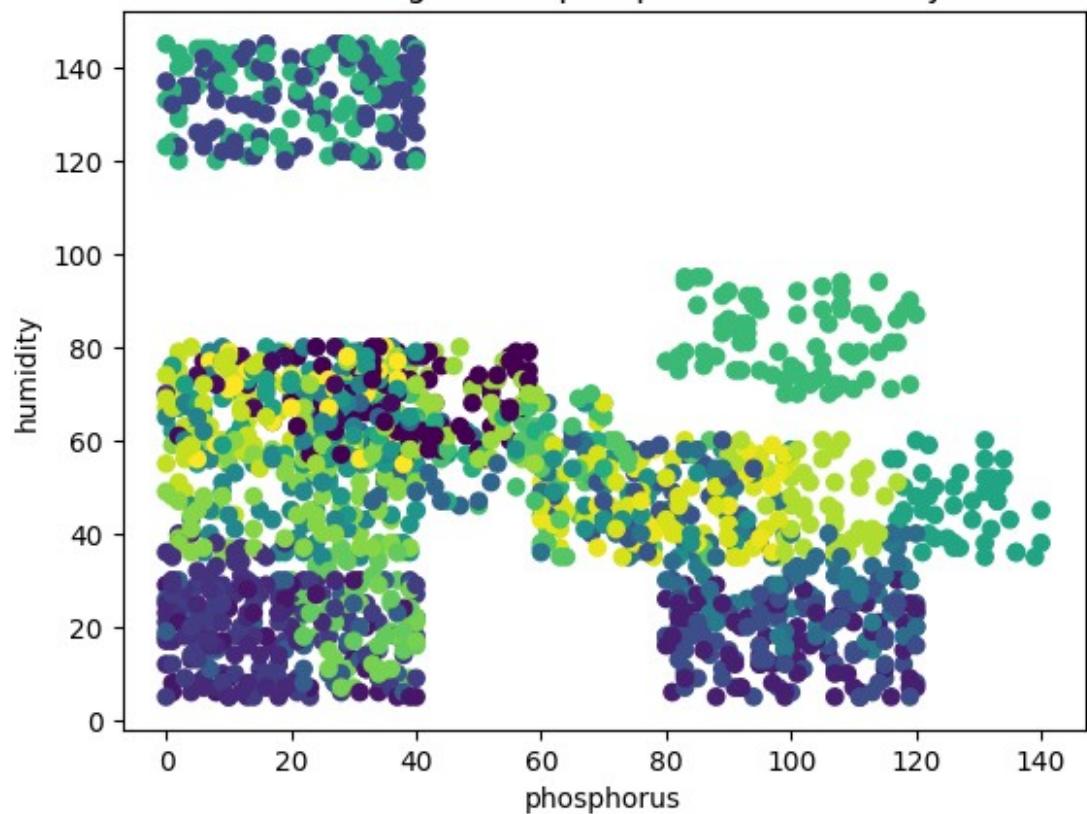
Clustering Result: phosphorus vs potassium



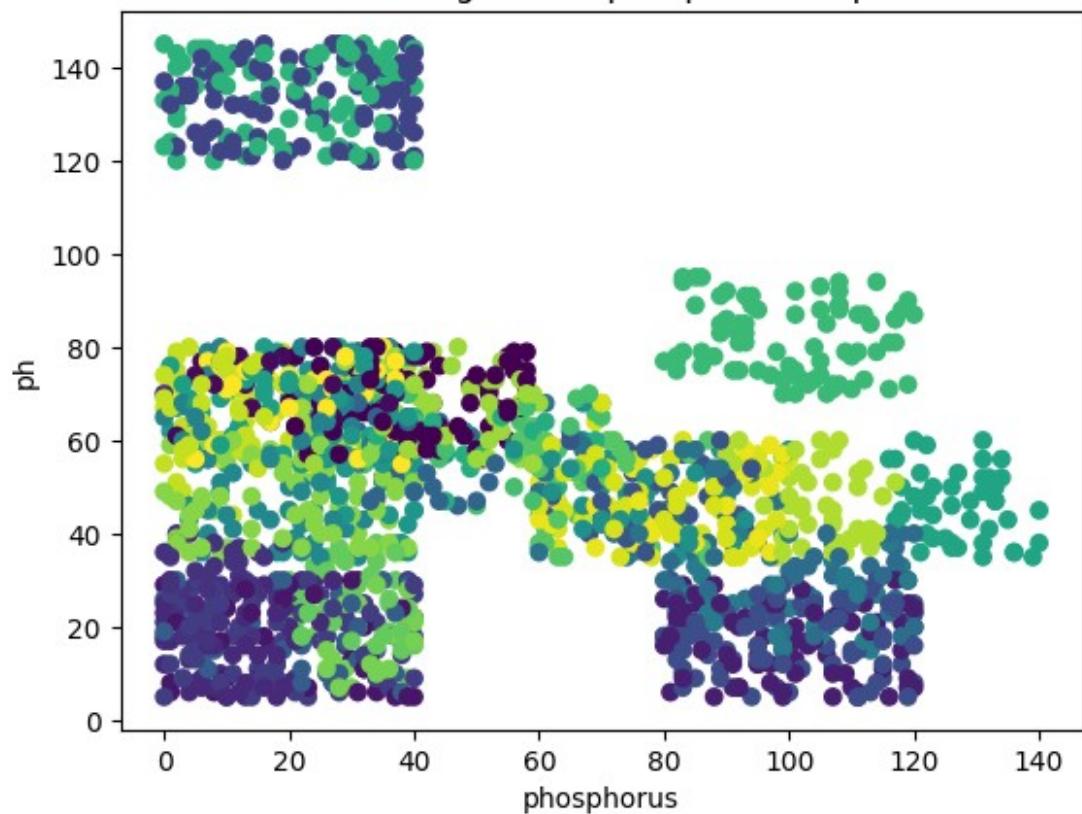
Clustering Result: phosphorus vs temperature



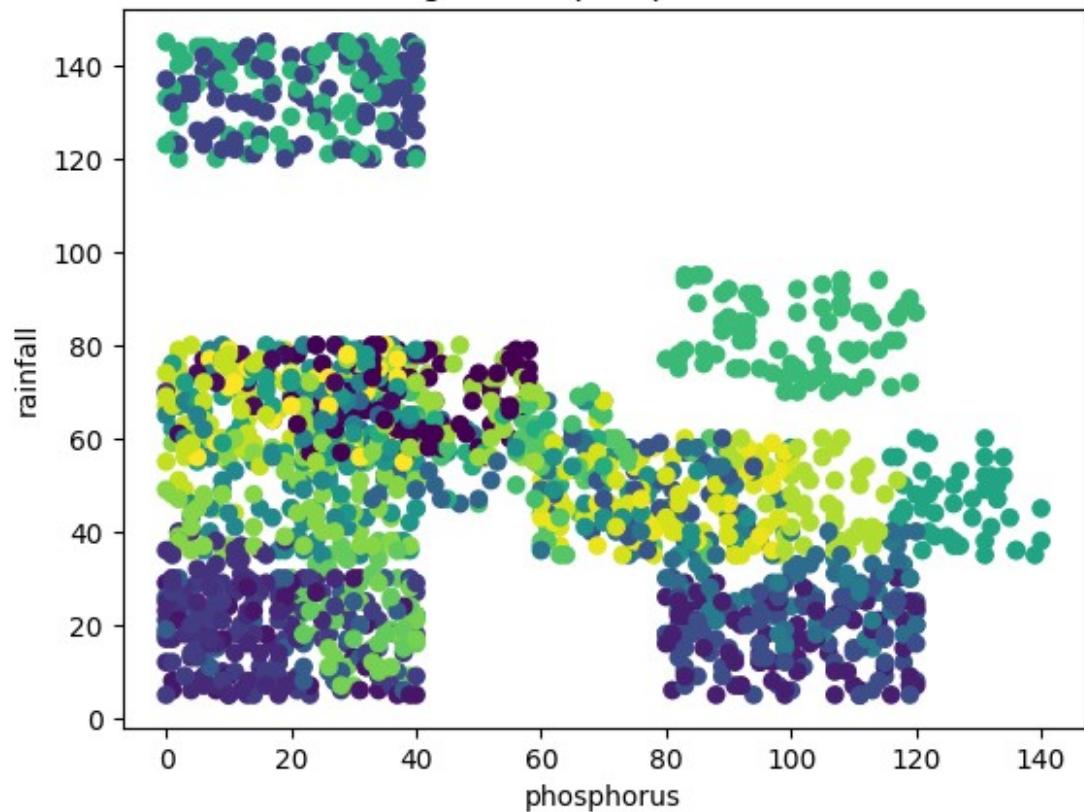
Clustering Result: phosphorus vs humidity



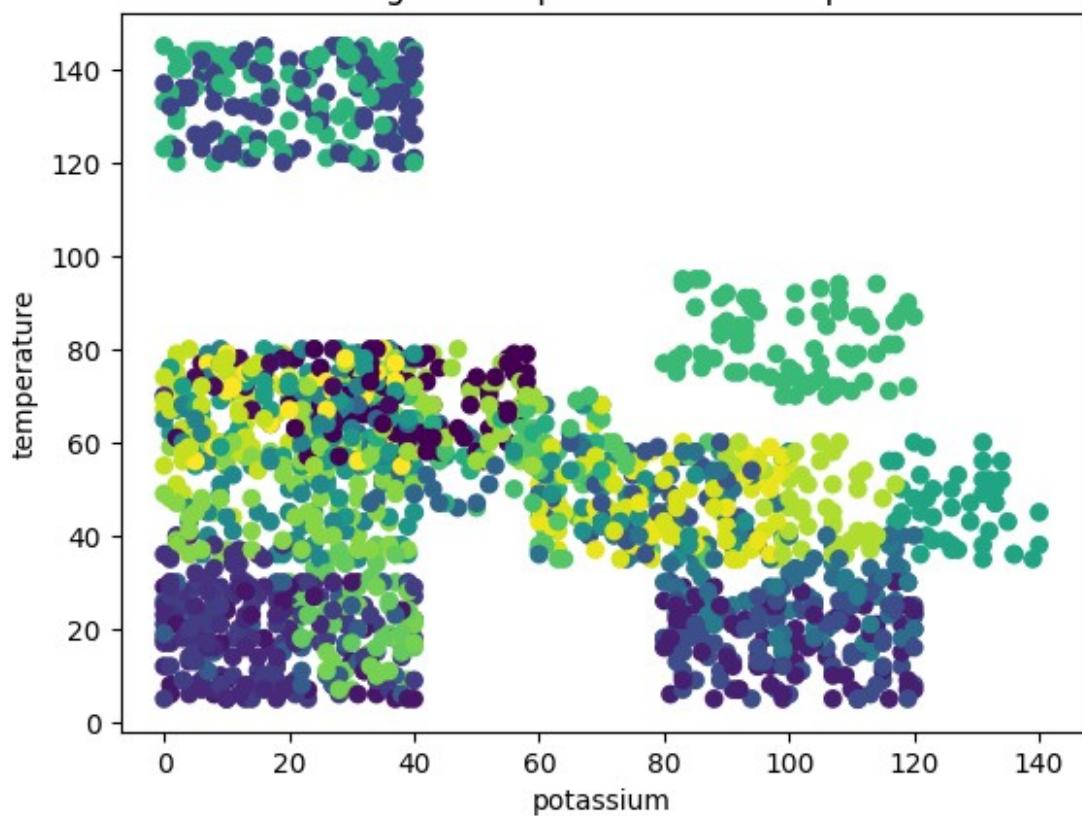
Clustering Result: phosphorus vs ph



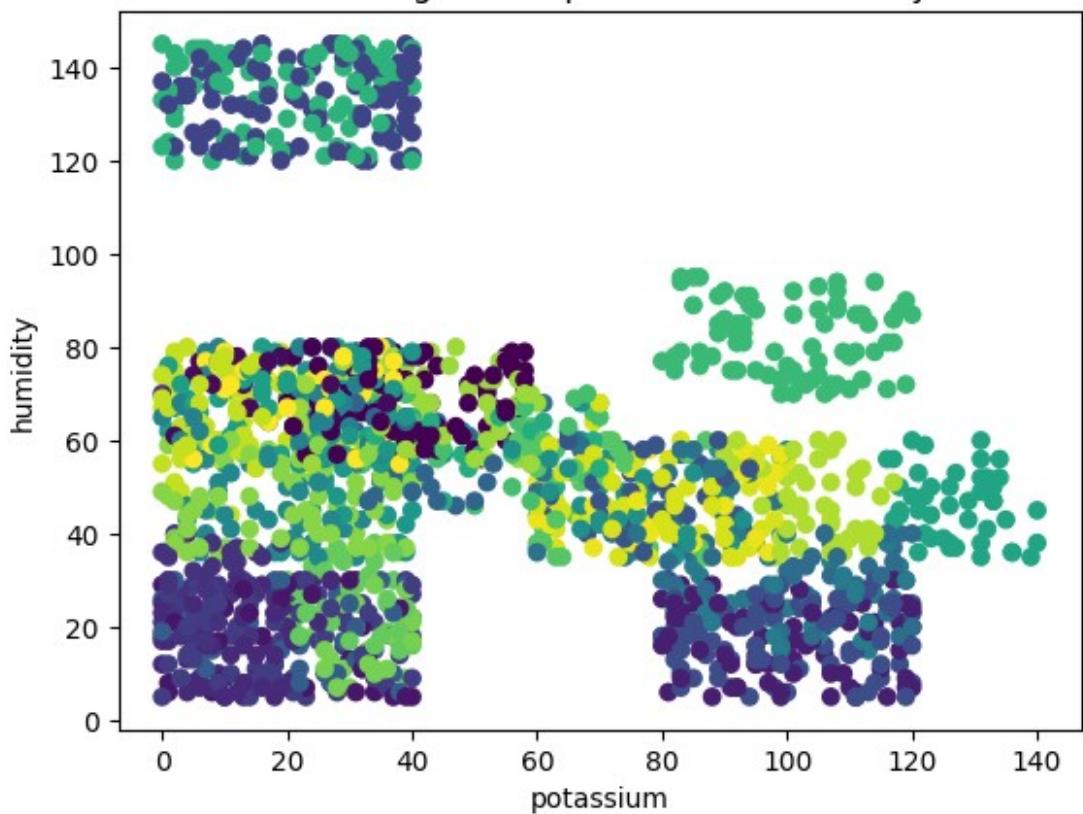
Clustering Result: phosphorus vs rainfall



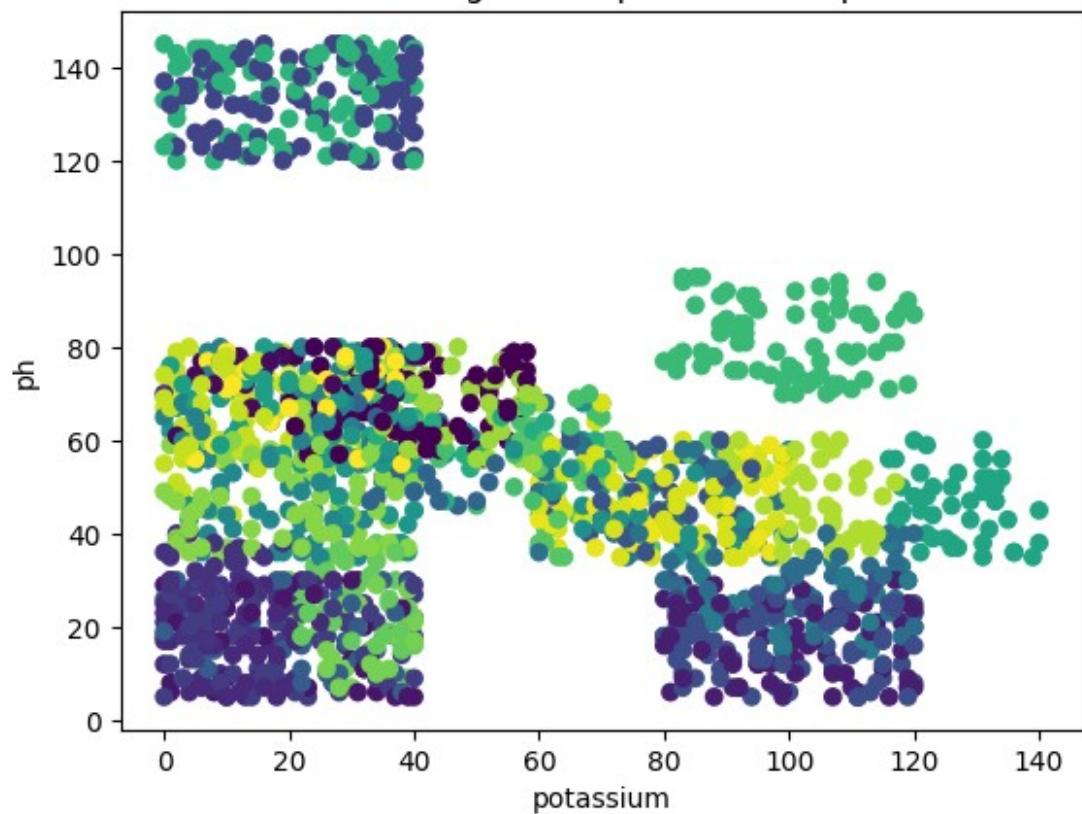
Clustering Result: potassium vs temperature



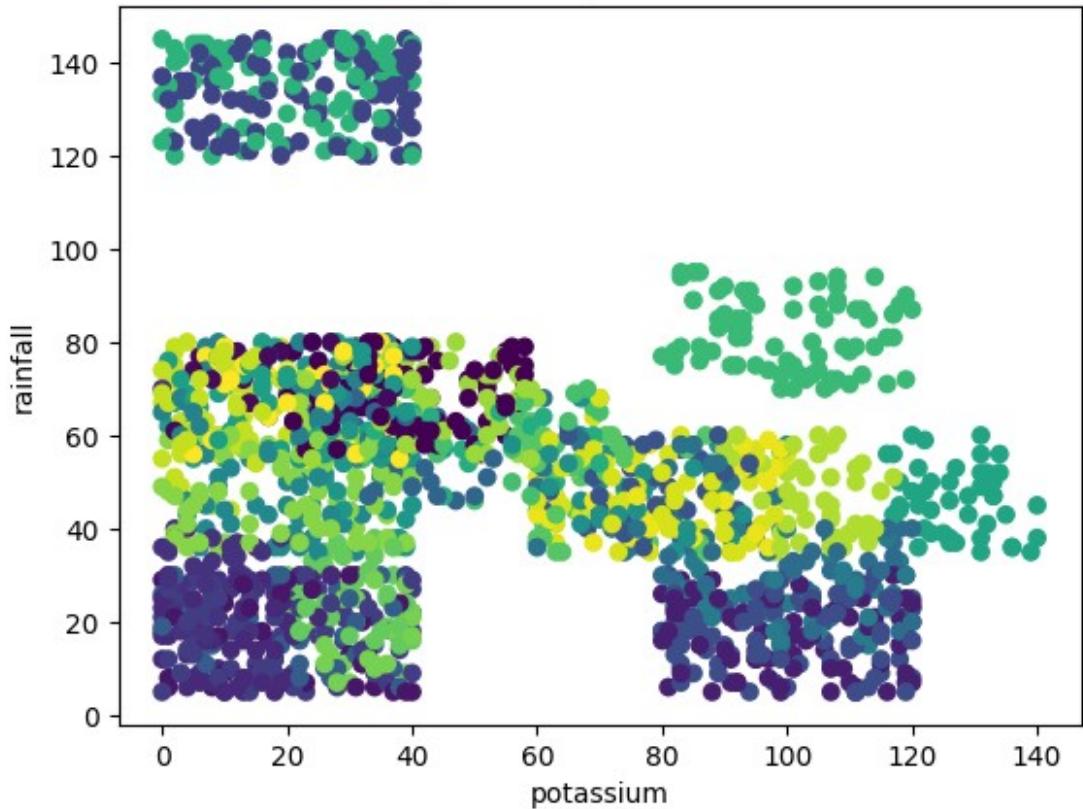
Clustering Result: potassium vs humidity



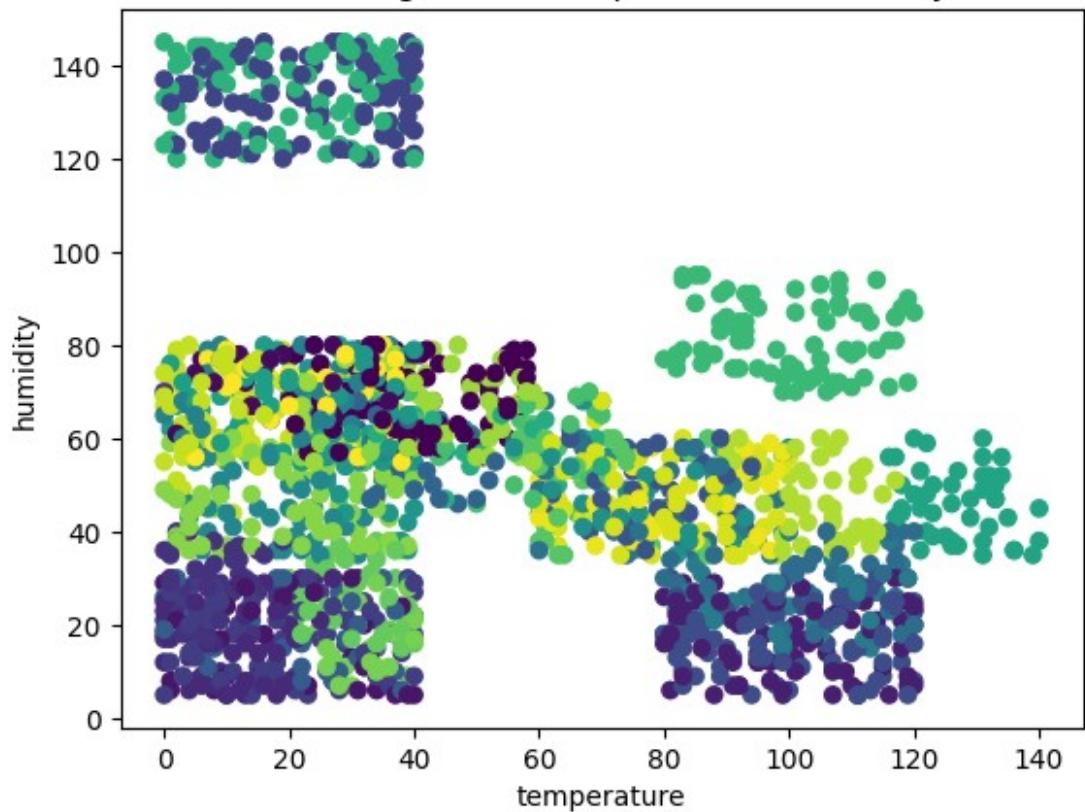
Clustering Result: potassium vs ph



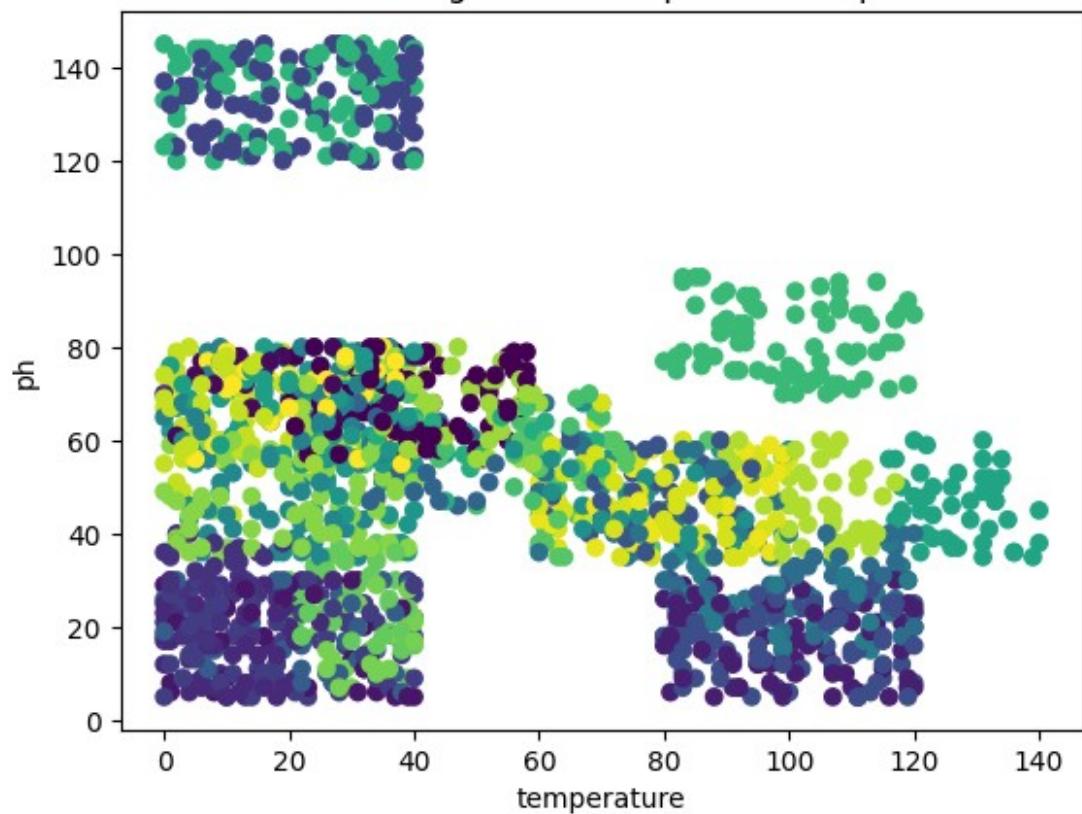
Clustering Result: potassium vs rainfall



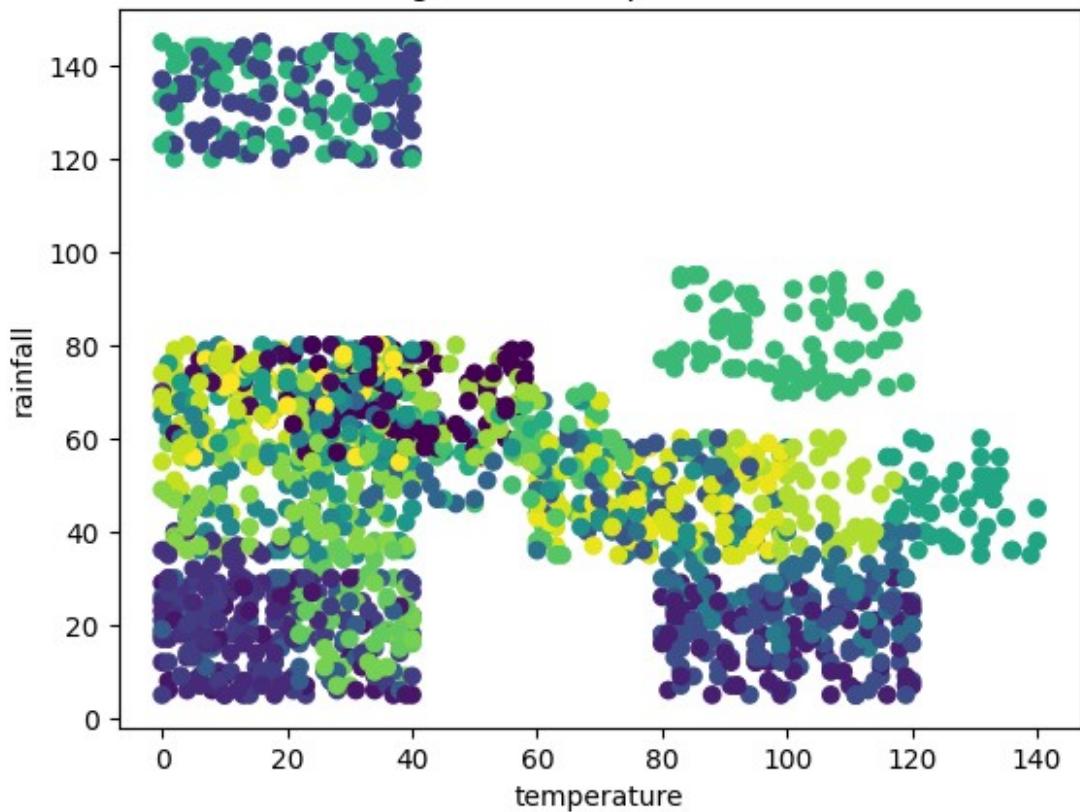
Clustering Result: temperature vs humidity



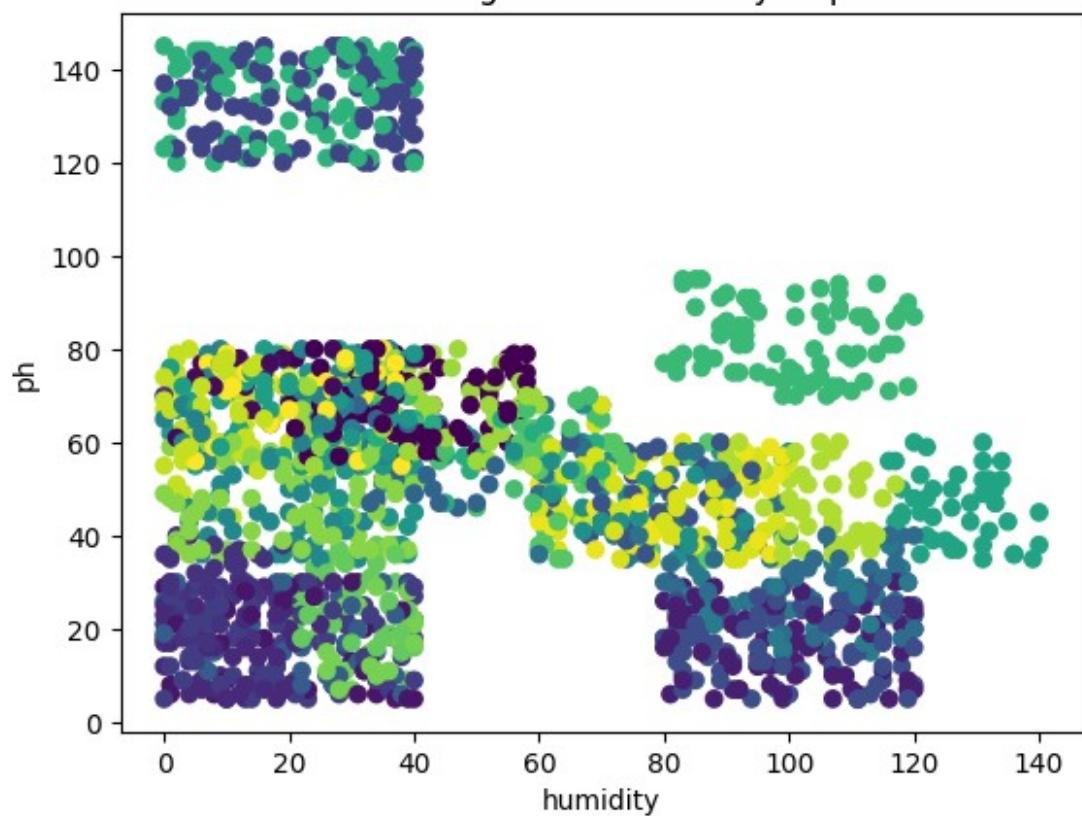
Clustering Result: temperature vs ph



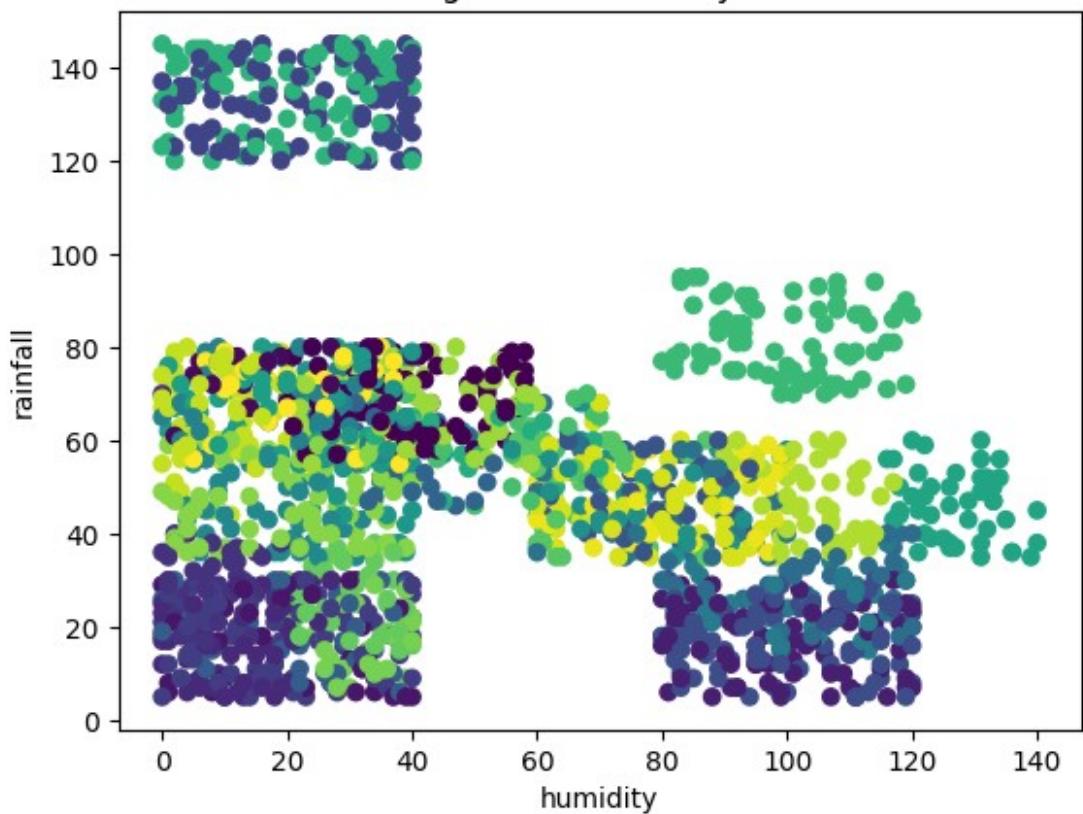
Clustering Result: temperature vs rainfall

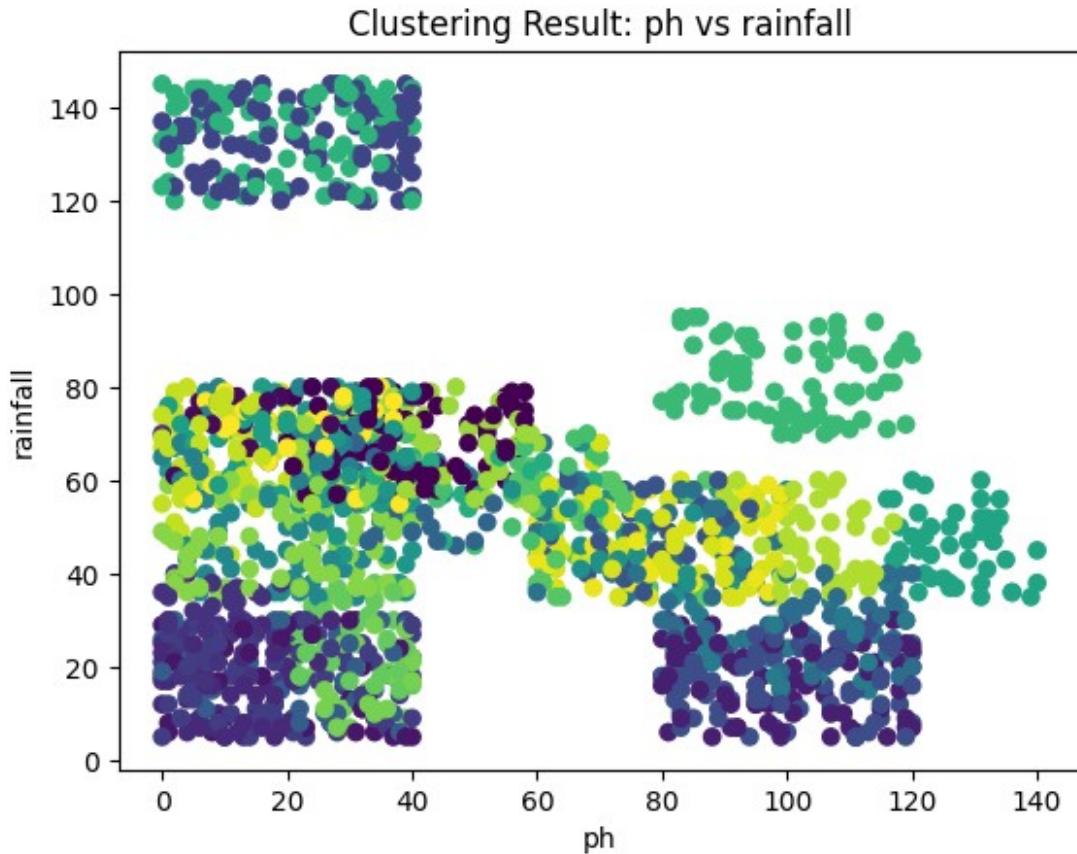


Clustering Result: humidity vs ph



Clustering Result: humidity vs rainfall





```

Silhouette Score: 0.368500876146879
Adjusted Rand Index: 0.7451747561934313
Homogeneity: 0.9429264229511191
Completeness: 0.8386322623658429
V-measure: 0.8877266023749769

```

*#Birch*

```

# Get the predicted cluster labels for the training data
train_cluster_labels = birch.labels_

# Compute evaluation metrics
silhouette_avg = silhouette_score(X_train, train_cluster_labels)
ari = adjusted_rand_score(target, train_cluster_labels)
homogeneity, completeness, v_measure =
homogeneity_completeness_v_measure(target, train_cluster_labels)

# Create scatter plots for different feature combinations
features = ['Nitrogen', 'phosphorus', 'potassium', 'temperature',
'humidity', 'ph', 'rainfall']
for i in range(len(features)):
    for j in range(i+1, len(features)):
        plt.scatter(X_train[:, 0], X_train[:, 1],

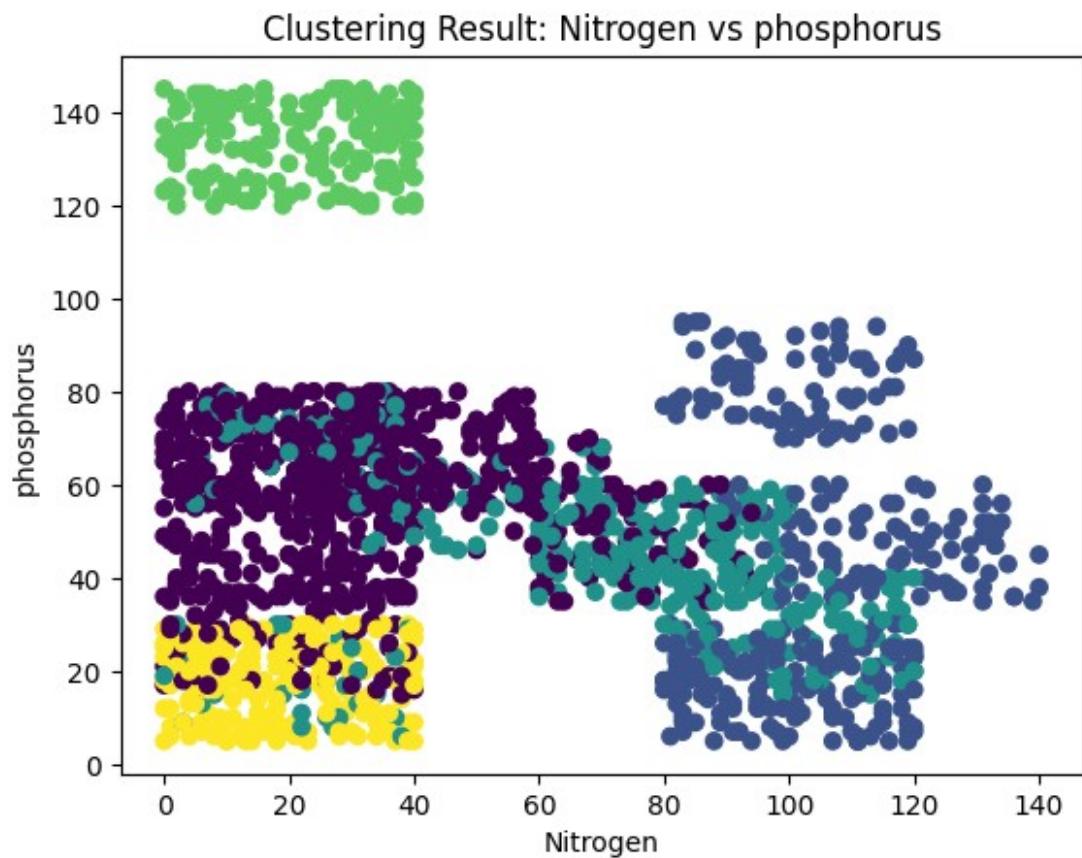
```

```

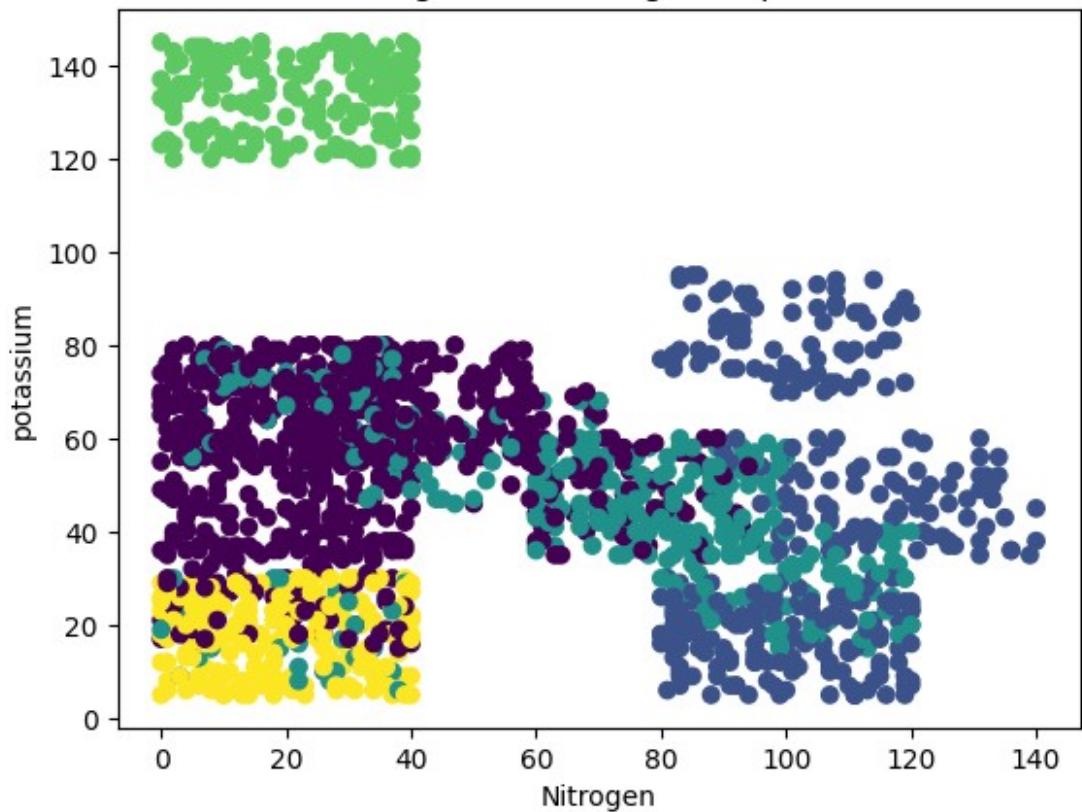
c=train_cluster_labels, cmap='viridis')
    plt.xlabel(features[i])
    plt.ylabel(features[j])
    plt.title(f'Clustering Result: {features[i]} vs
{features[j]}')
    plt.show()

# Print evaluation metrics
print("Silhouette Score:", silhouette_avg)
print("Adjusted Rand Index:", ari)
print("Homogeneity:", homogeneity)
print("Completeness:", completeness)
print("V-measure:", v_measure)

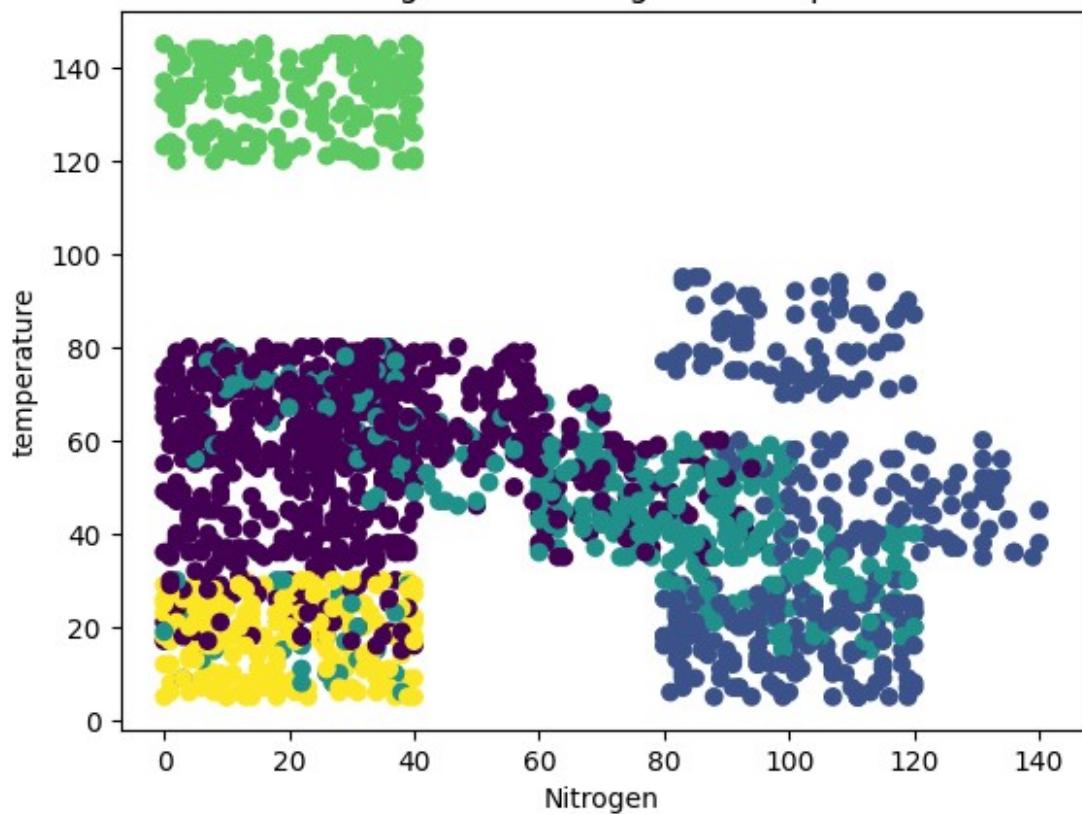
```



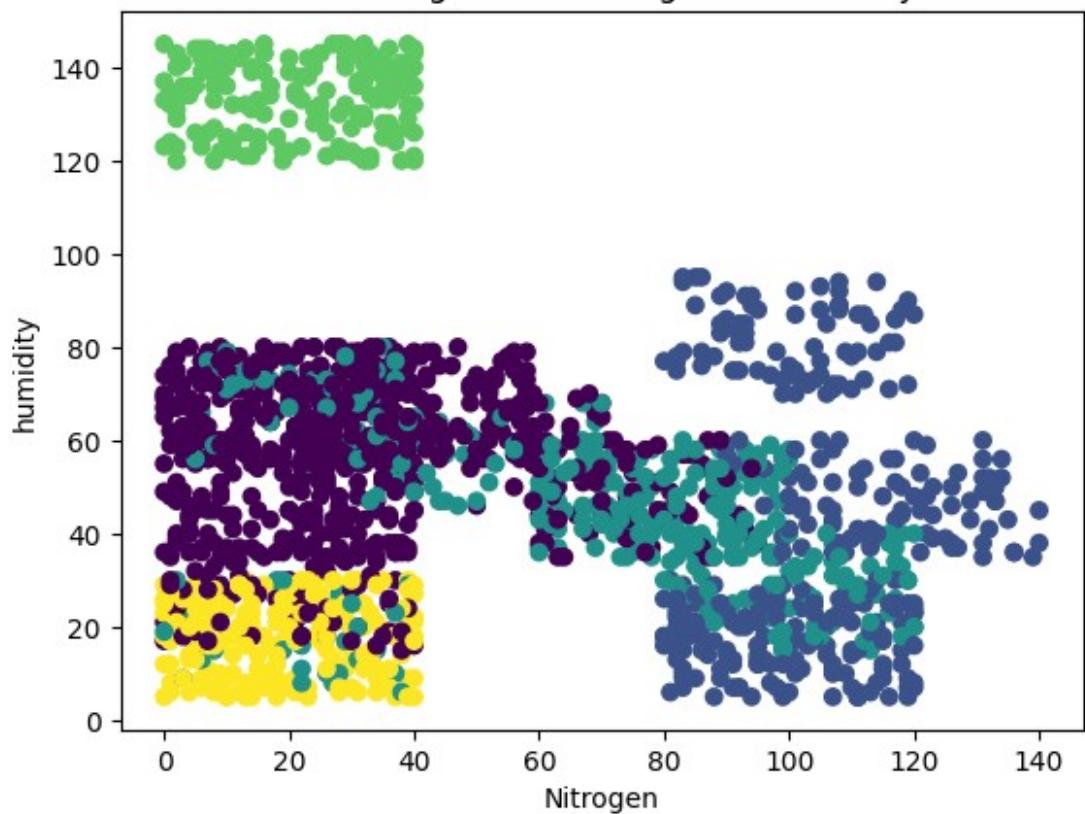
Clustering Result: Nitrogen vs potassium



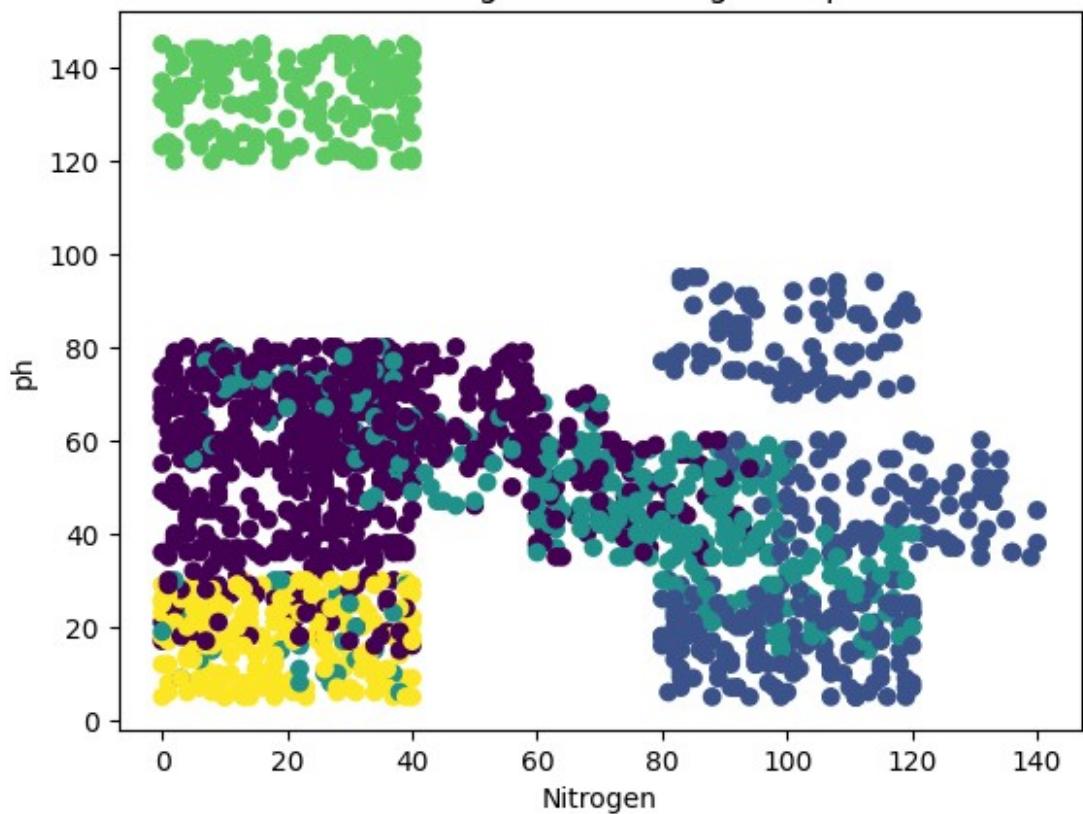
Clustering Result: Nitrogen vs temperature



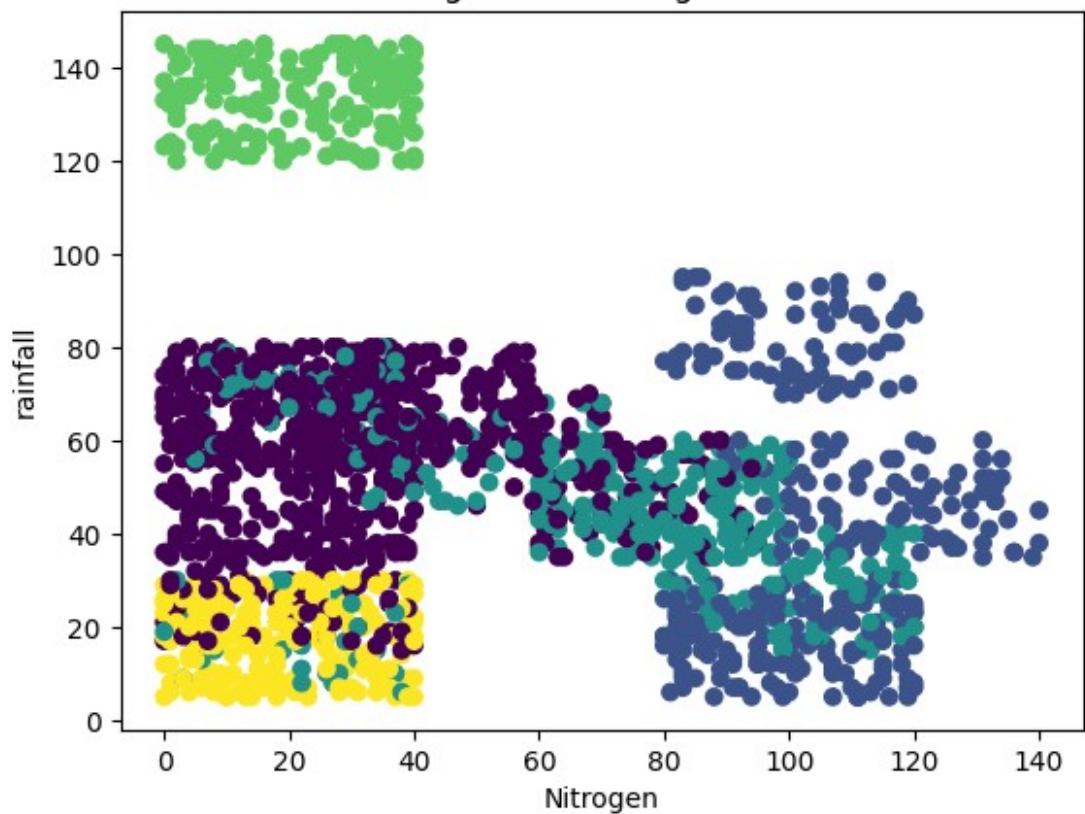
Clustering Result: Nitrogen vs humidity



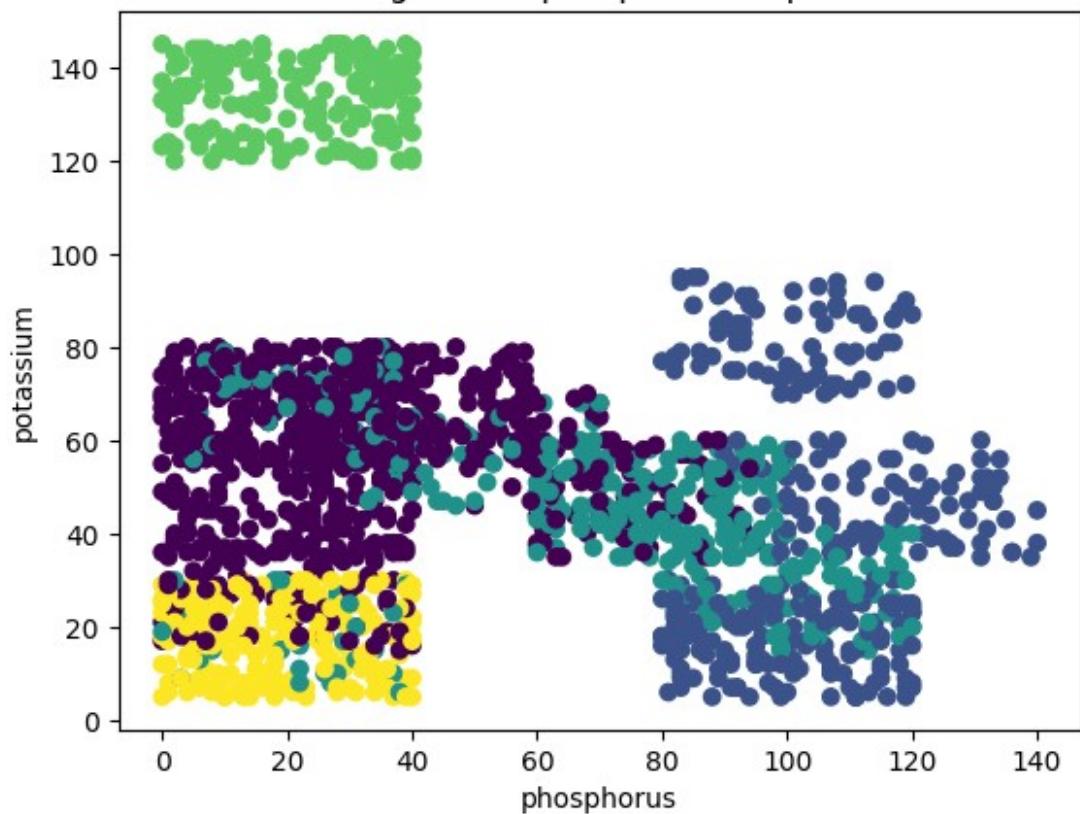
Clustering Result: Nitrogen vs ph



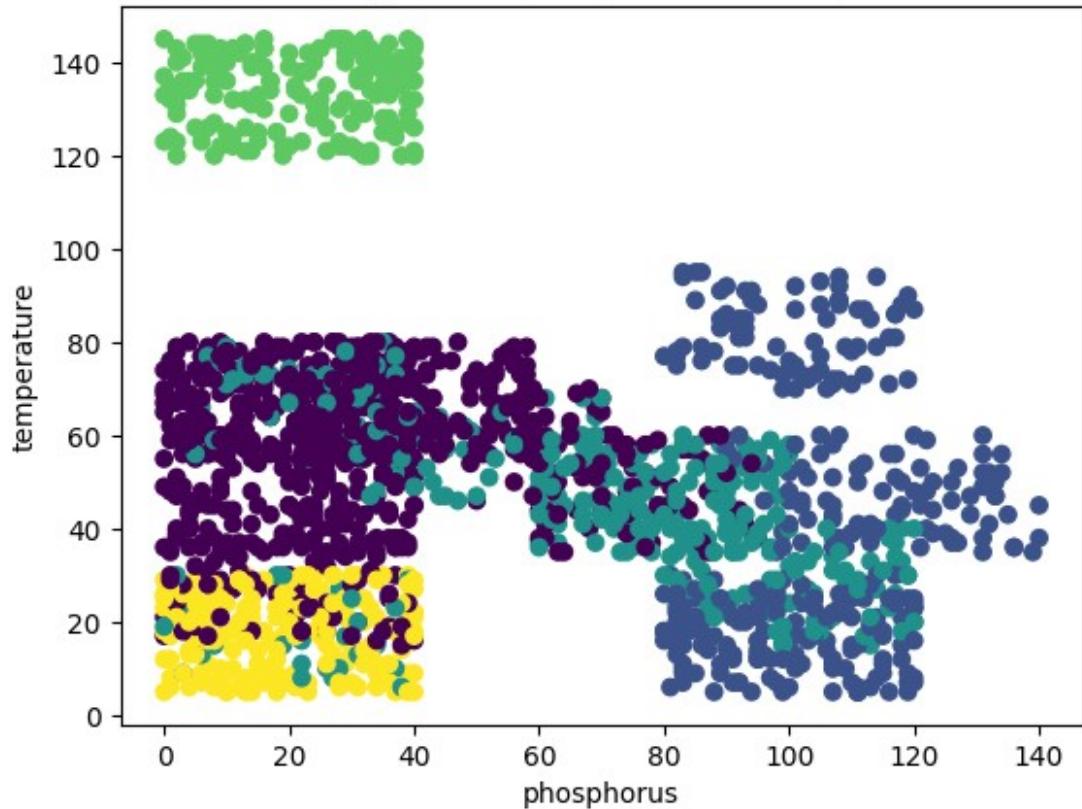
Clustering Result: Nitrogen vs rainfall



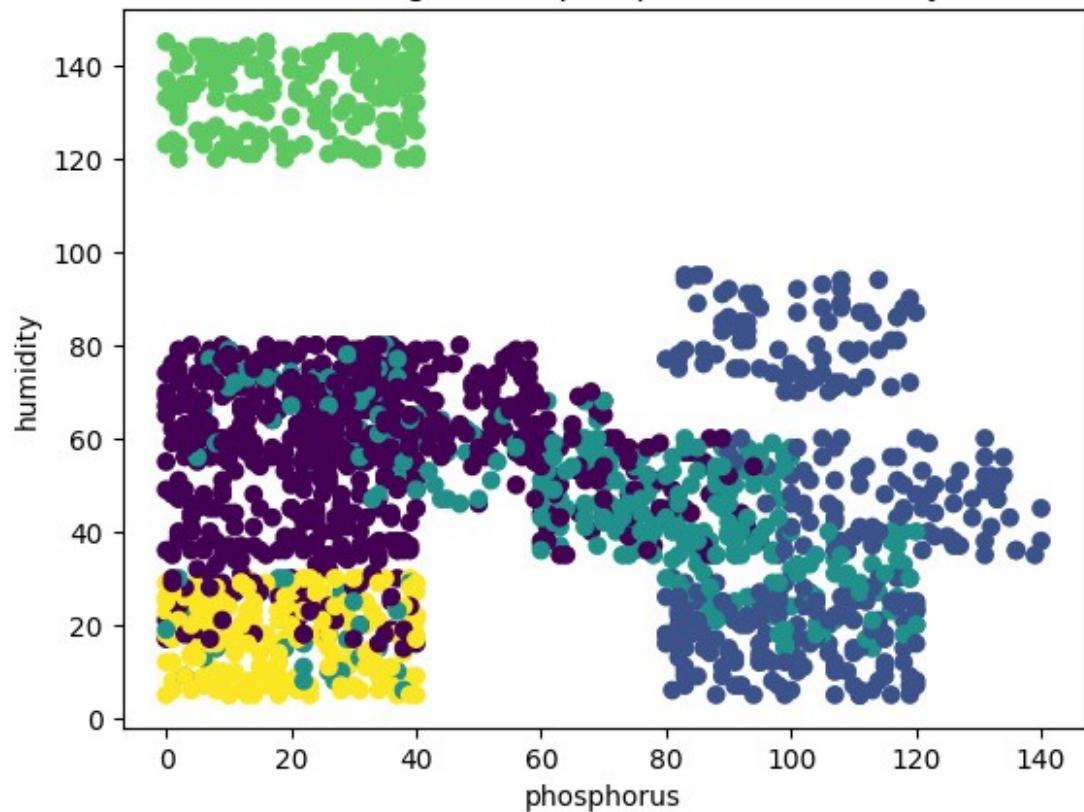
Clustering Result: phosphorus vs potassium



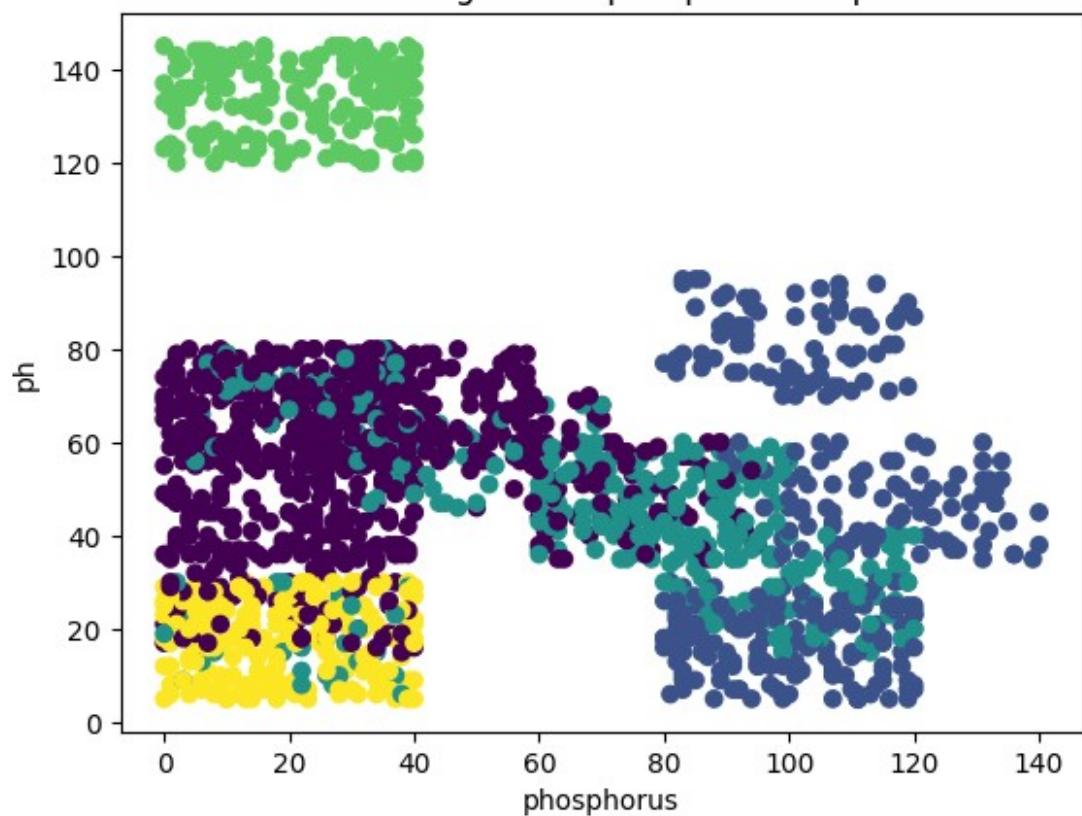
Clustering Result: phosphorus vs temperature



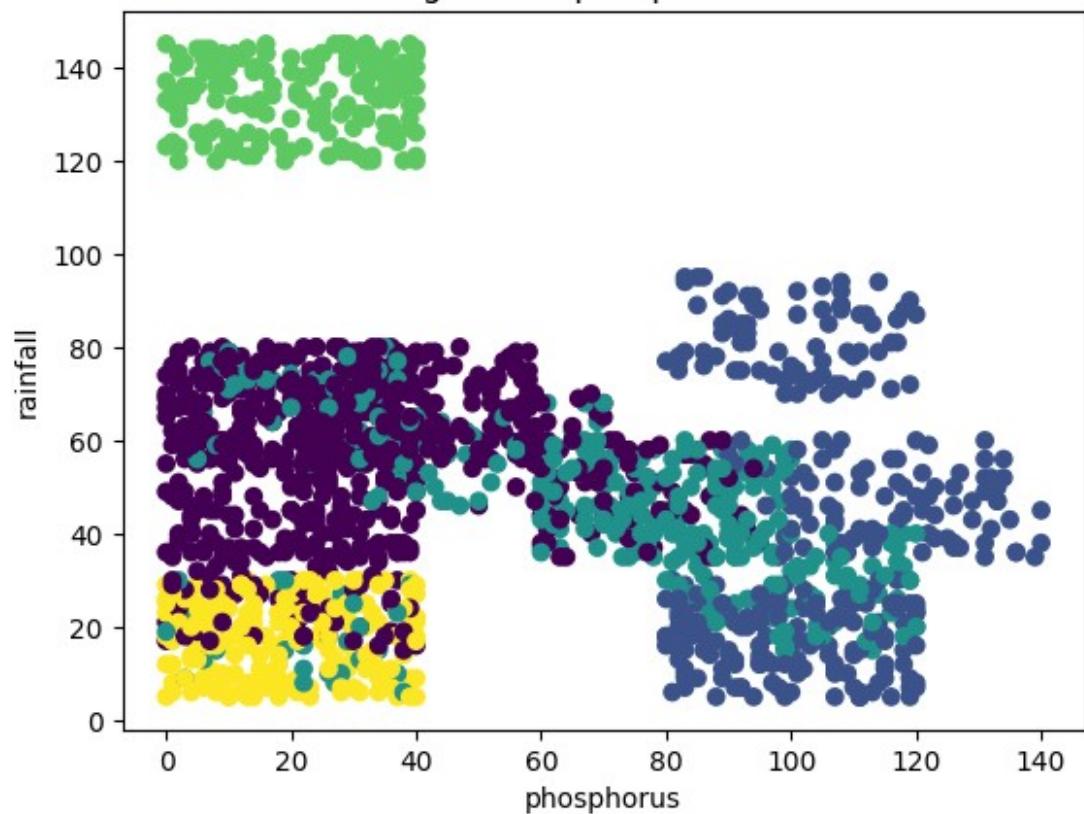
Clustering Result: phosphorus vs humidity



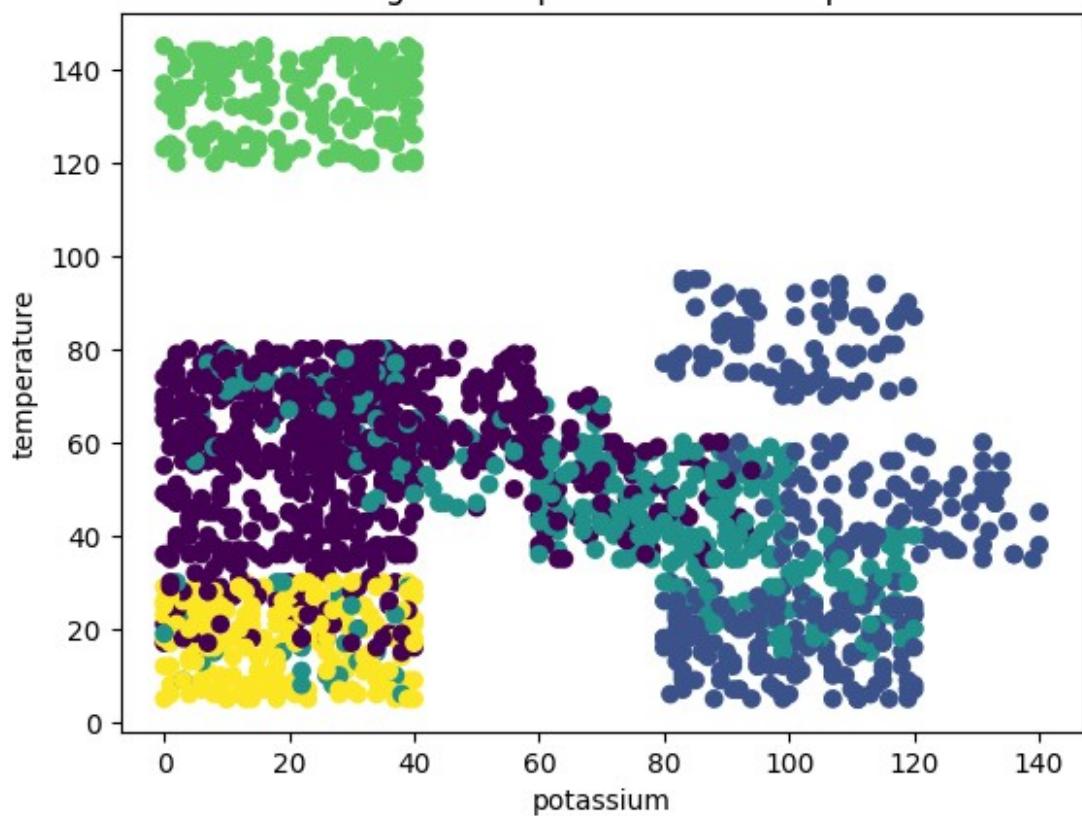
Clustering Result: phosphorus vs ph



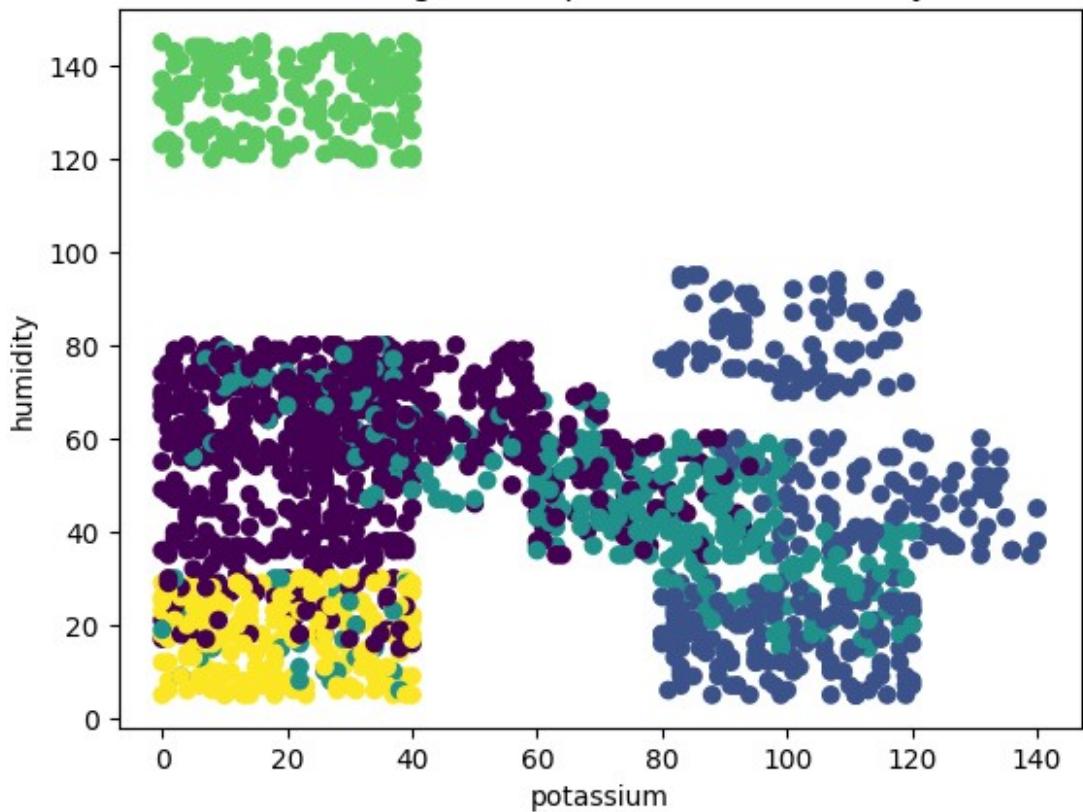
Clustering Result: phosphorus vs rainfall



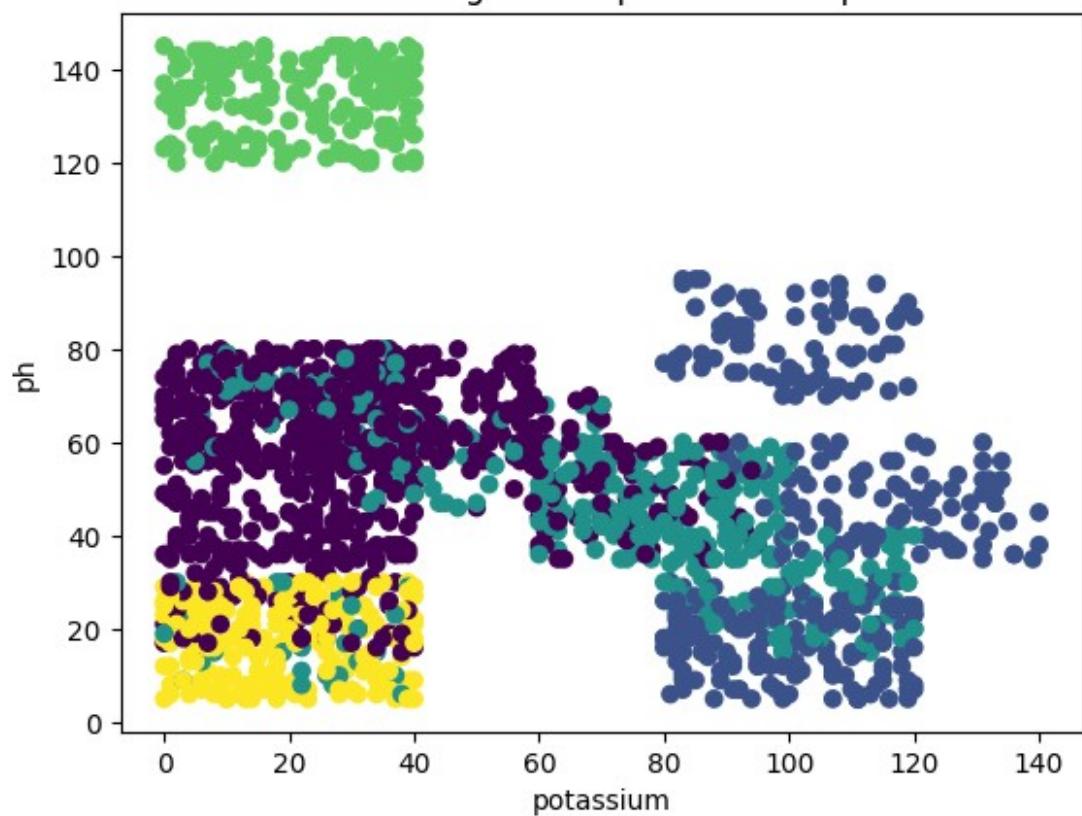
Clustering Result: potassium vs temperature



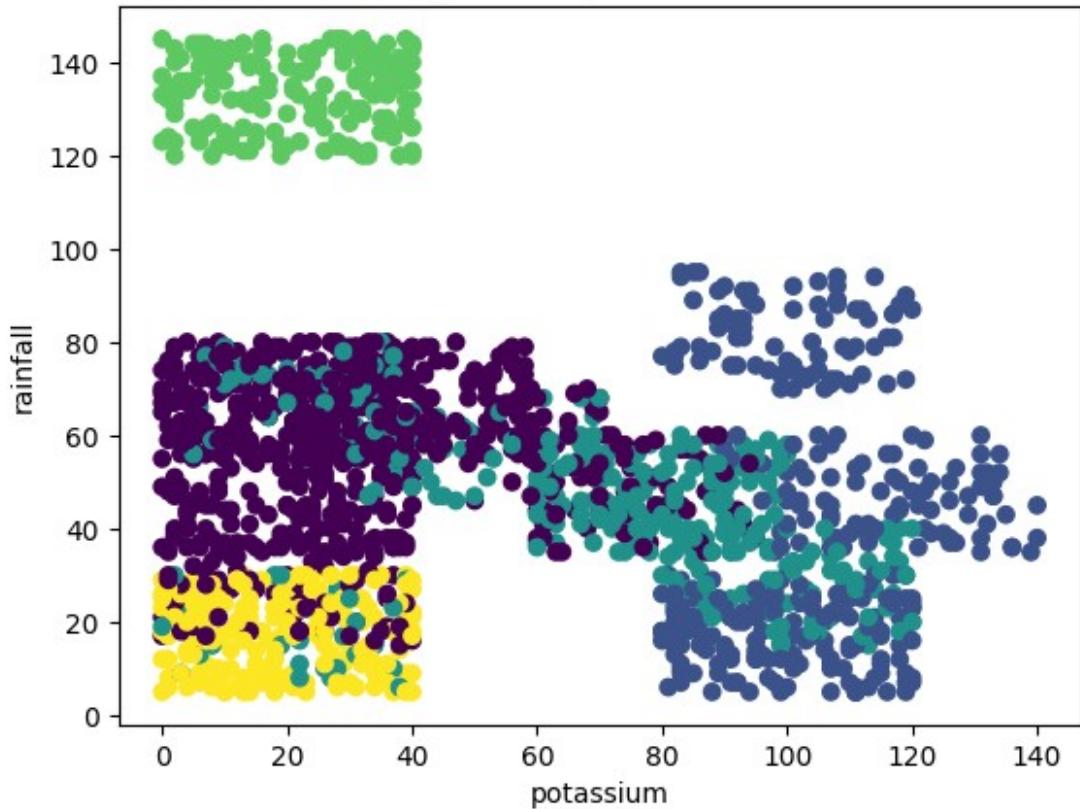
Clustering Result: potassium vs humidity



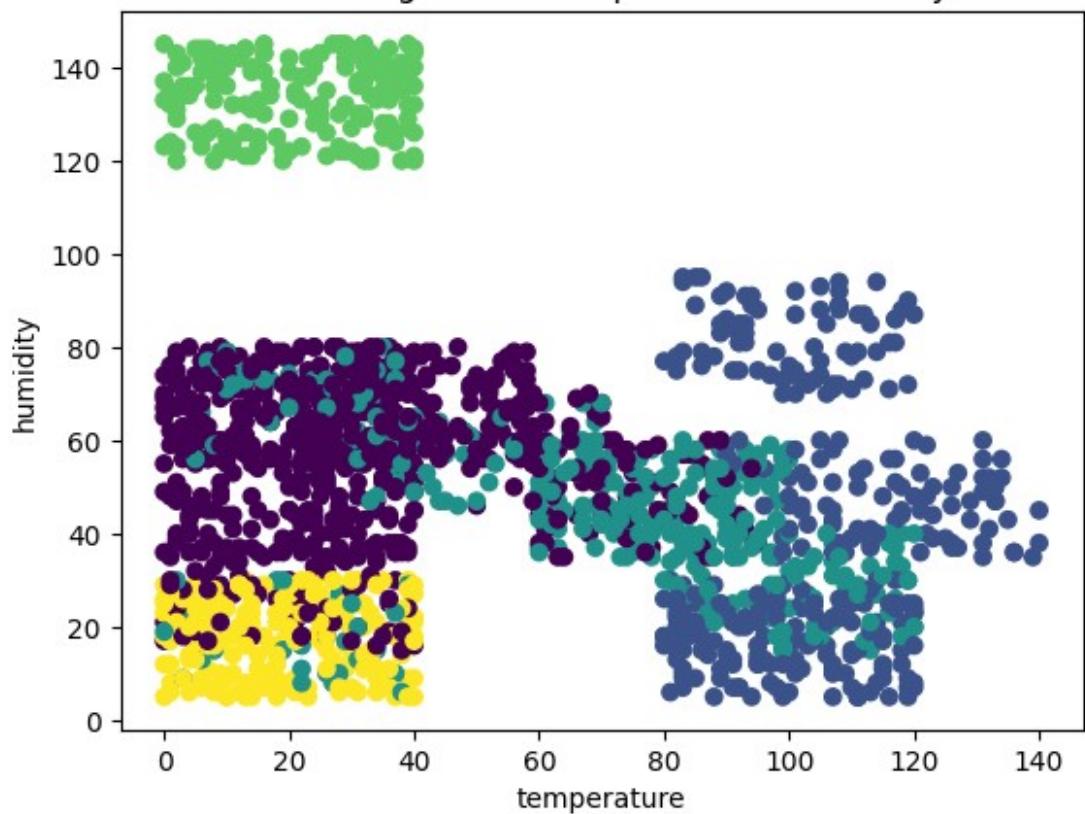
Clustering Result: potassium vs ph



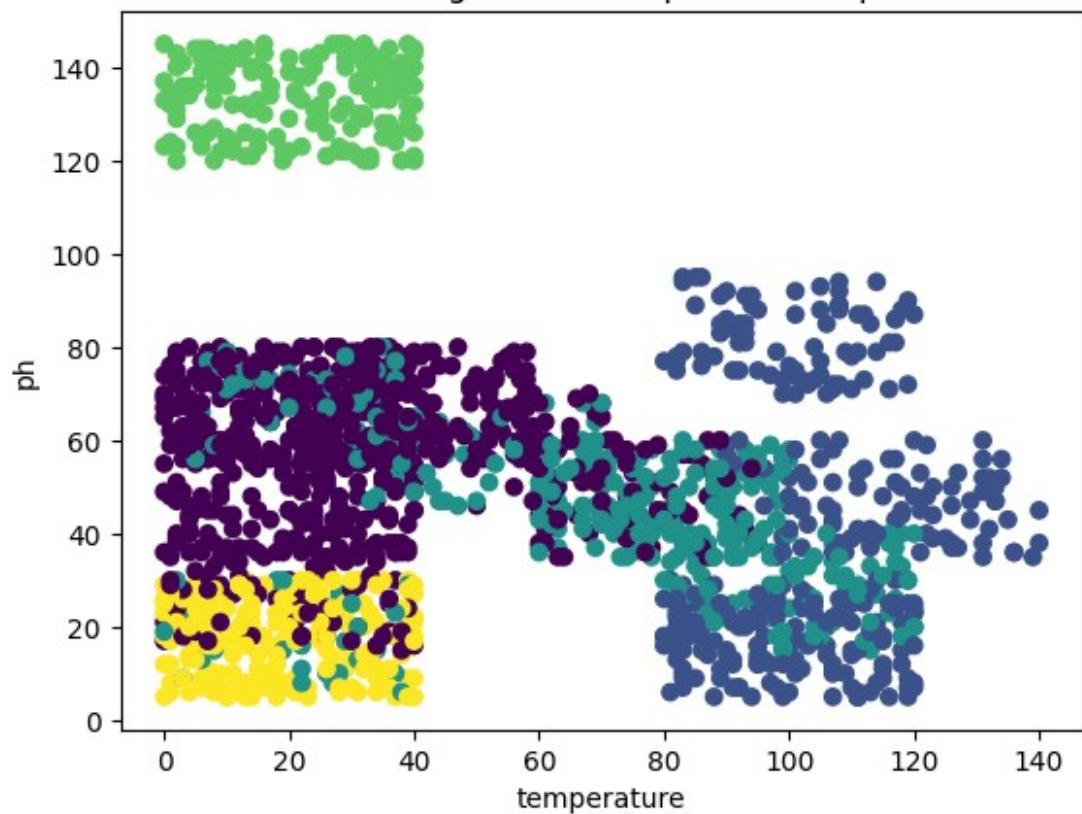
Clustering Result: potassium vs rainfall



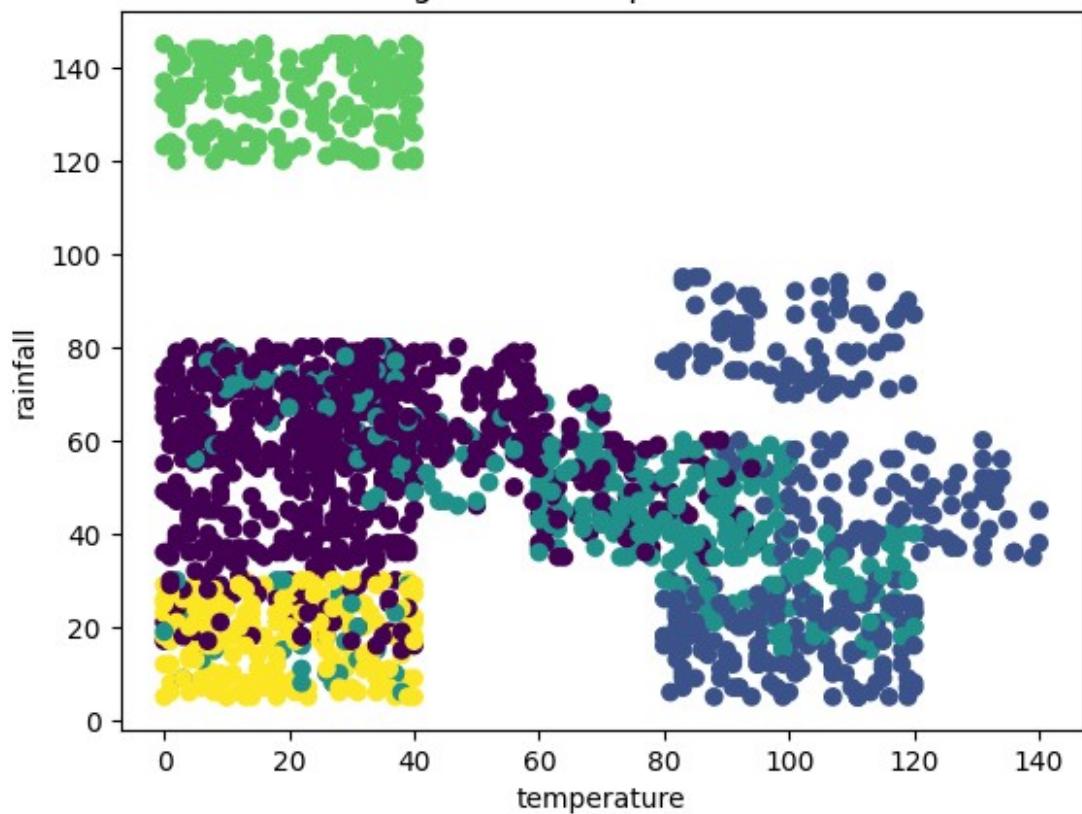
Clustering Result: temperature vs humidity



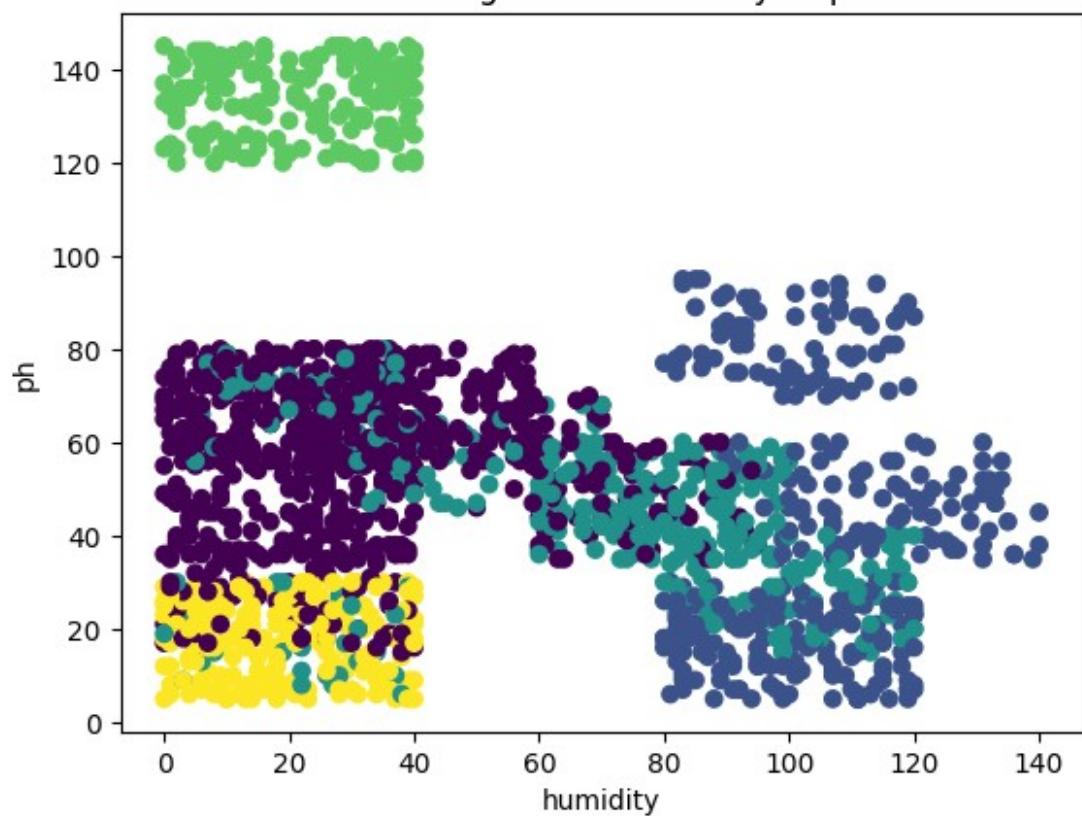
Clustering Result: temperature vs ph



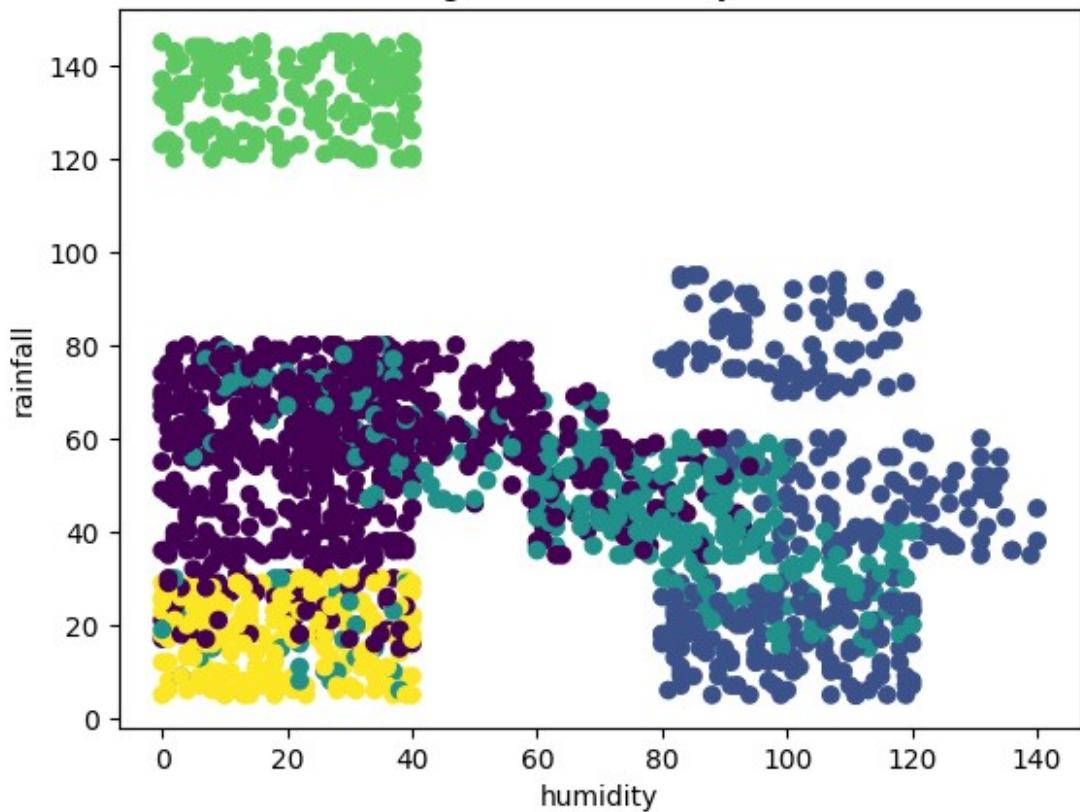
Clustering Result: temperature vs rainfall

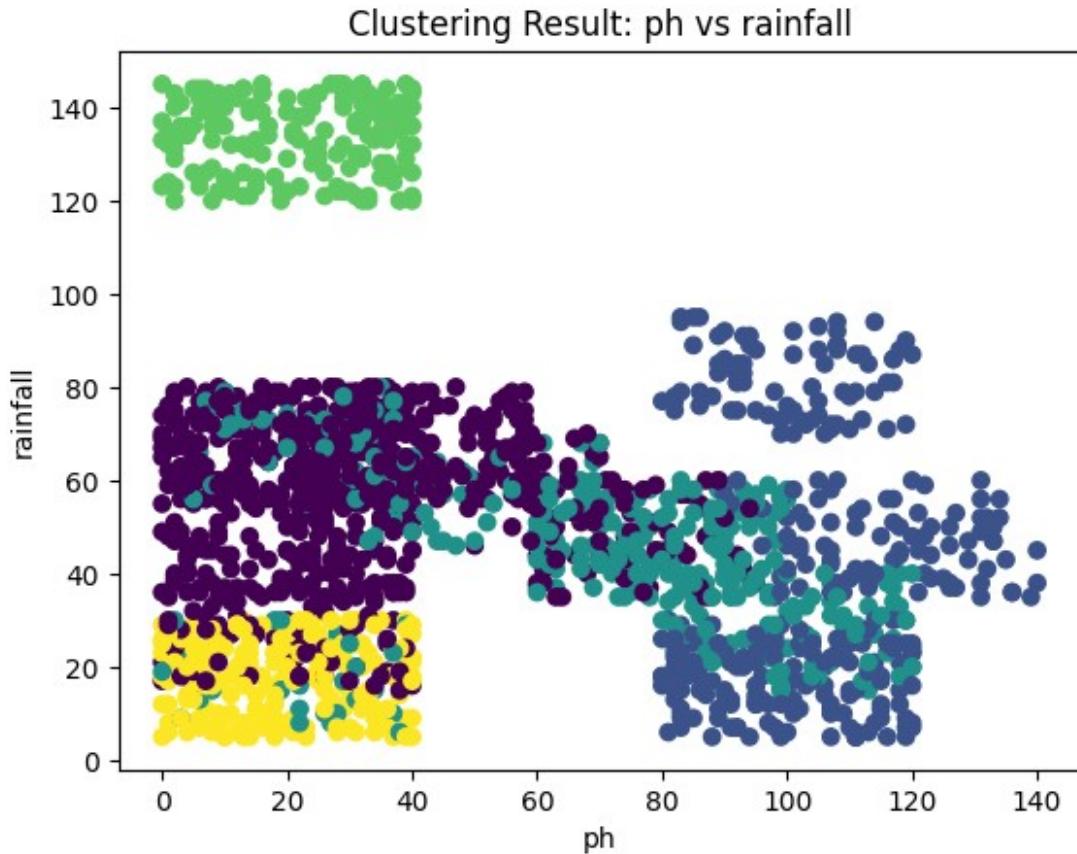


Clustering Result: humidity vs ph



Clustering Result: humidity vs rainfall





Silhouette Score: 0.36990069163203215  
 Adjusted Rand Index: 0.21771191100971643  
 Homogeneity: 0.4446816673547052  
 Completeness: 0.9293280011722735  
 V-measure: 0.6015316115260477

#### #DBSCAN

```

# Get the predicted cluster labels for the training data
train_cluster_labels = dbSCAN.labels_

# Compute evaluation metrics (silhouette score is not applicable to
# DBSCAN)
ari = adjusted_rand_score(target, train_cluster_labels)
homogeneity, completeness, v_measure =
homogeneity_completeness_v_measure(target, train_cluster_labels)

# Create scatter plots for different feature combinations
features = ['Nitrogen', 'phosphorus', 'potassium', 'temperature',
'humidity', 'ph', 'rainfall']
for i in range(len(features)):
  for j in range(i+1, len(features)):
    plt.scatter(X_train[:, 0], X_train[:, 1],

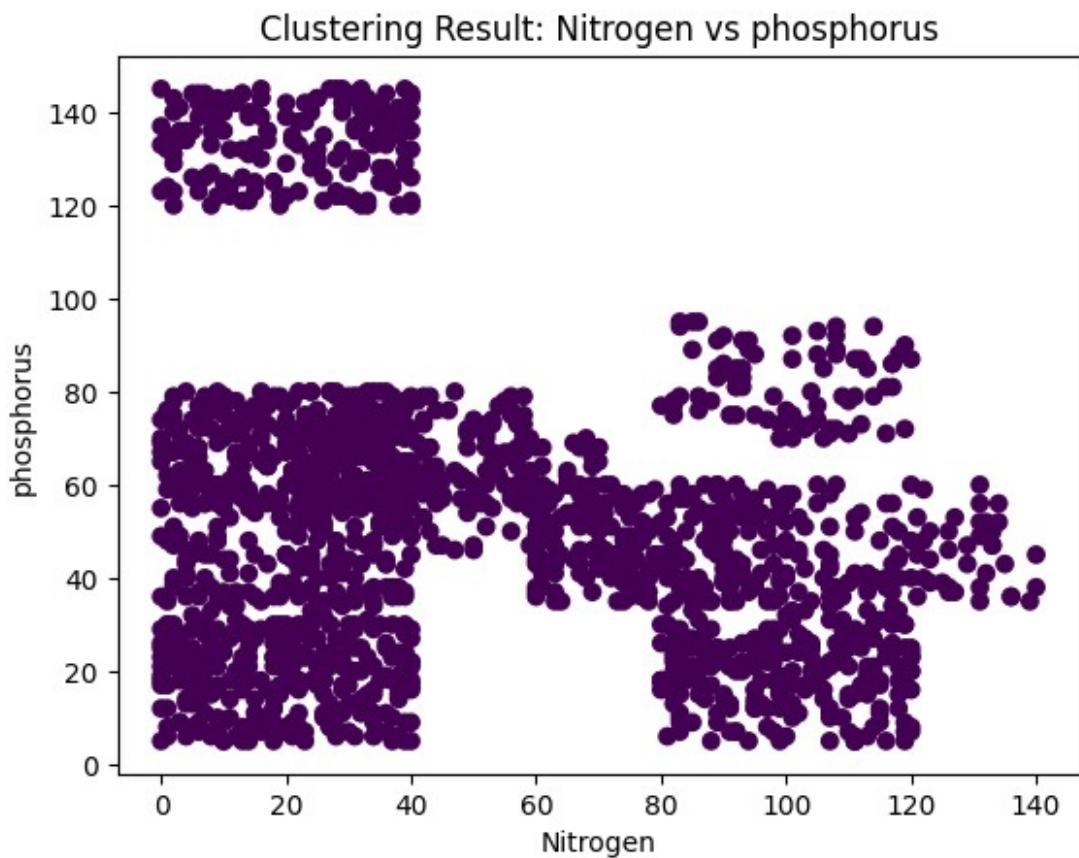
```

```

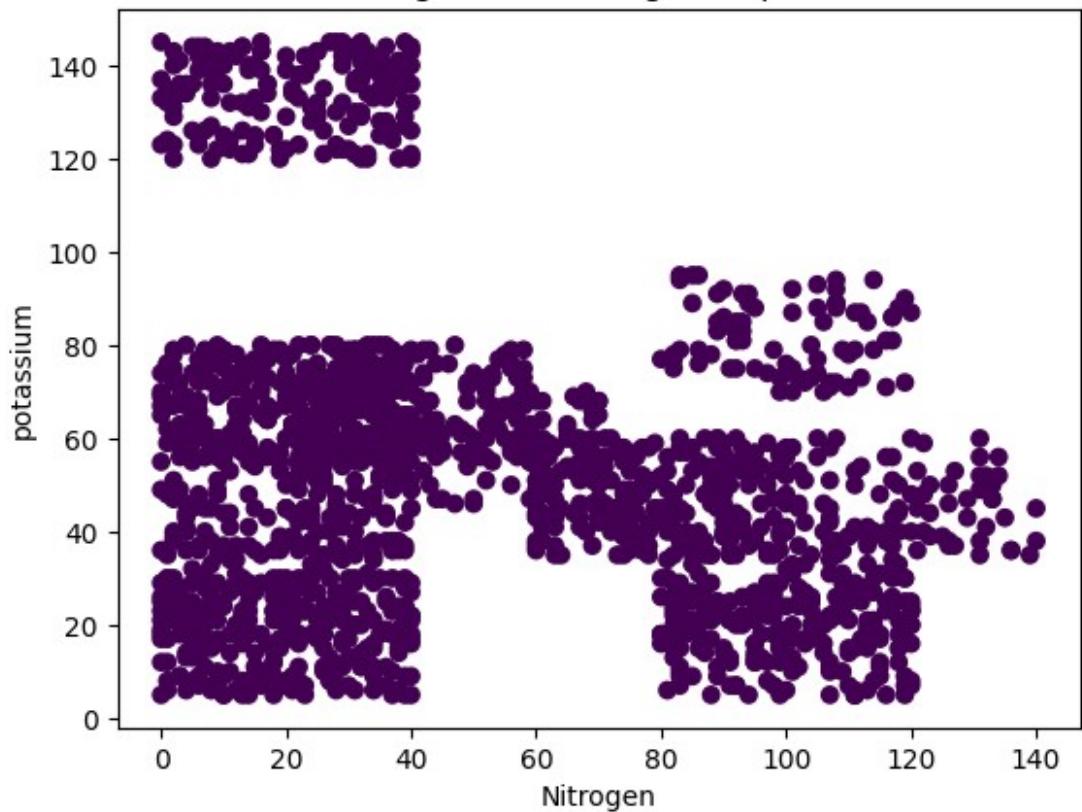
c=train_cluster_labels, cmap='viridis')
    plt.xlabel(features[i])
    plt.ylabel(features[j])
    plt.title(f'Clustering Result: {features[i]} vs
{features[j]}')
    plt.show()

# Print evaluation metrics
print("Adjusted Rand Index:", ari)
print("Homogeneity:", homogeneity)
print("Completeness:", completeness)
print("V-measure:", v_measure)

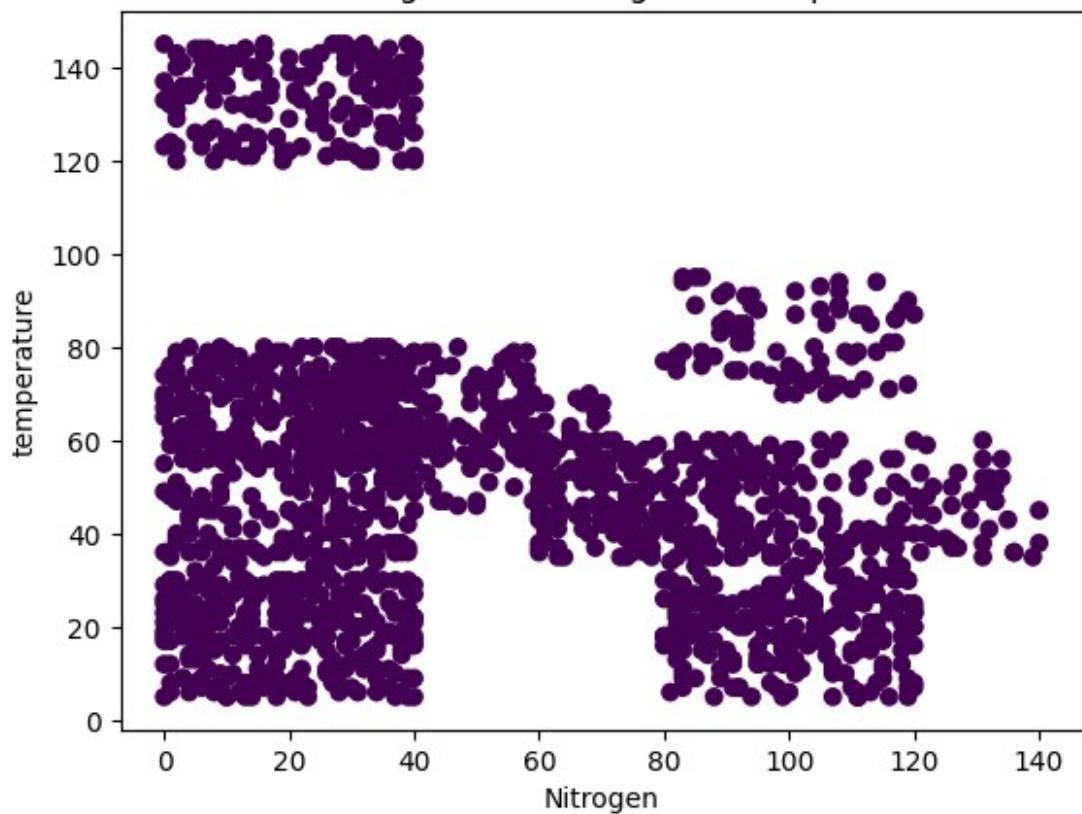
```



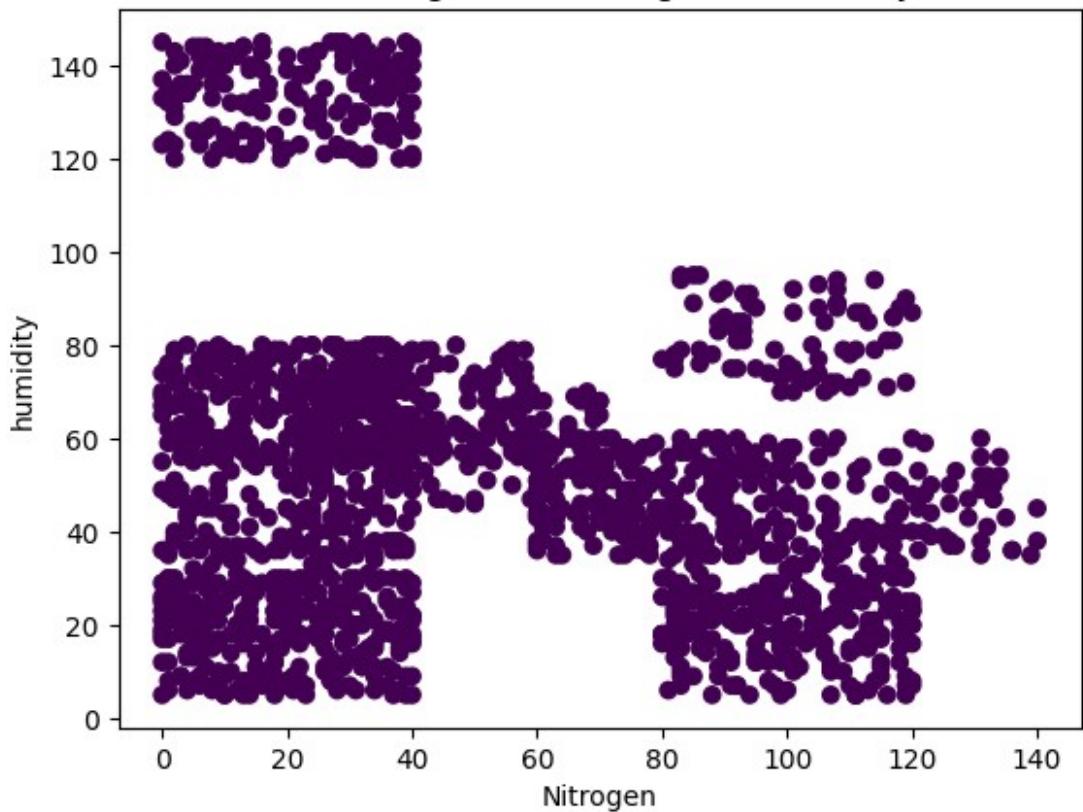
Clustering Result: Nitrogen vs potassium



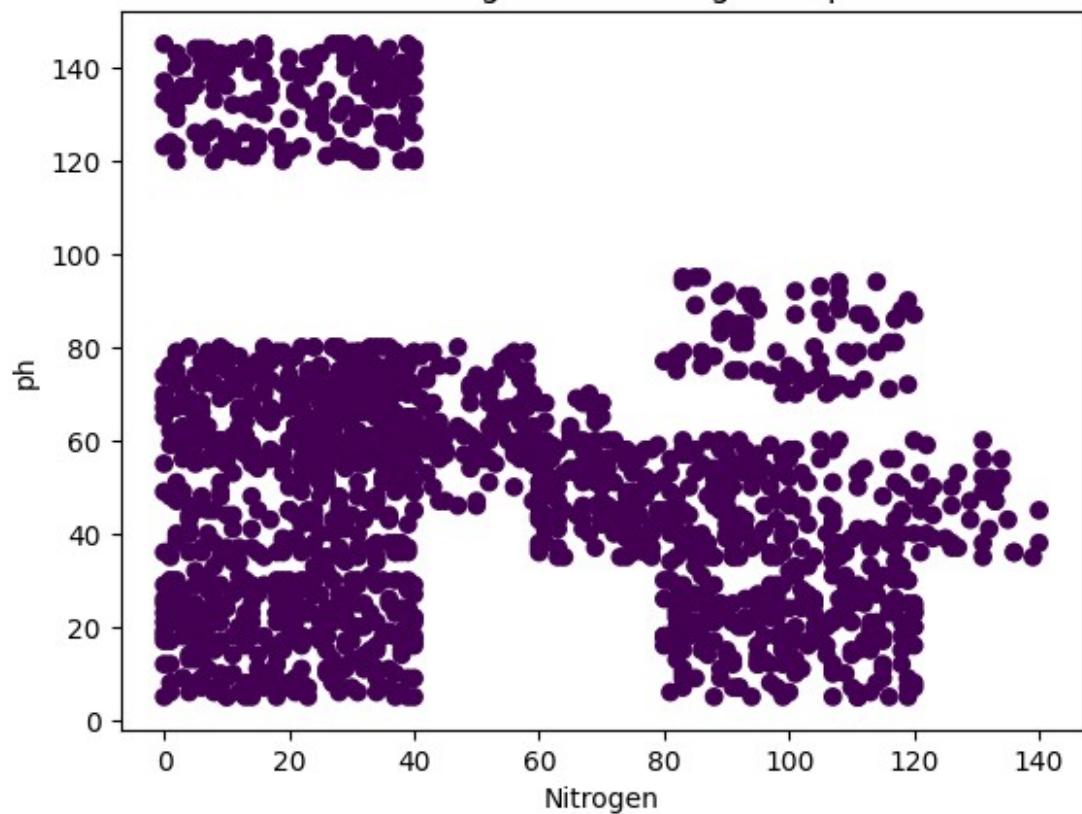
Clustering Result: Nitrogen vs temperature



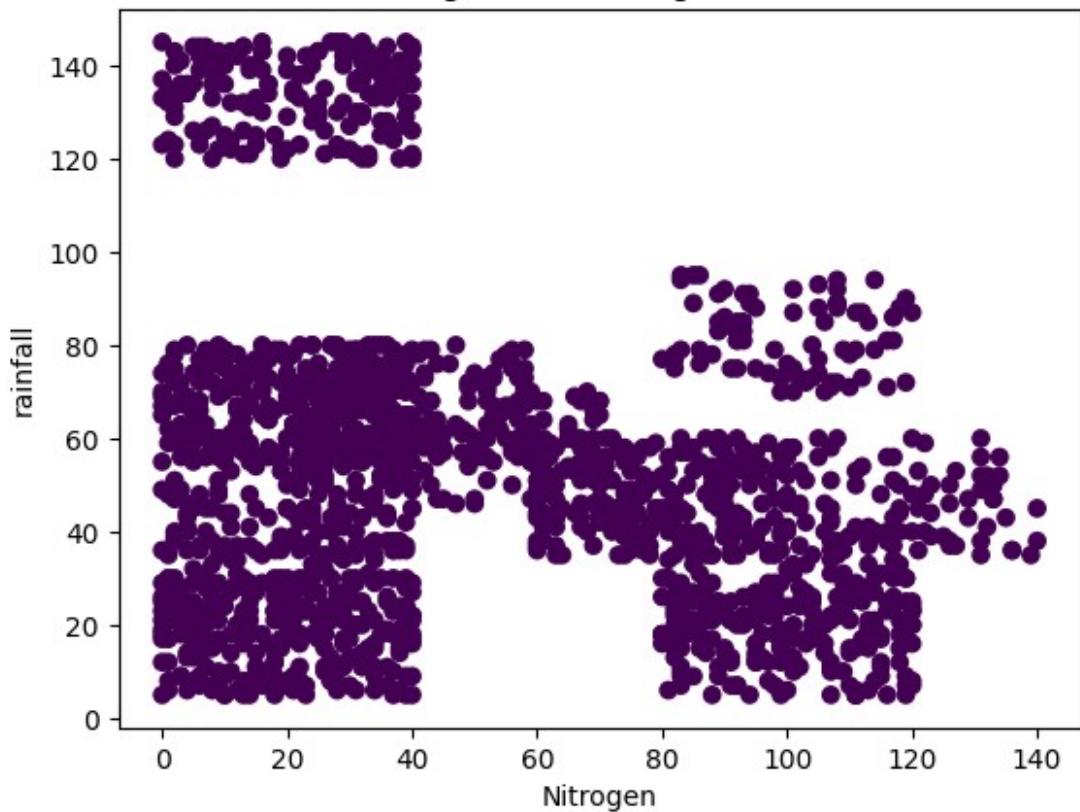
Clustering Result: Nitrogen vs humidity



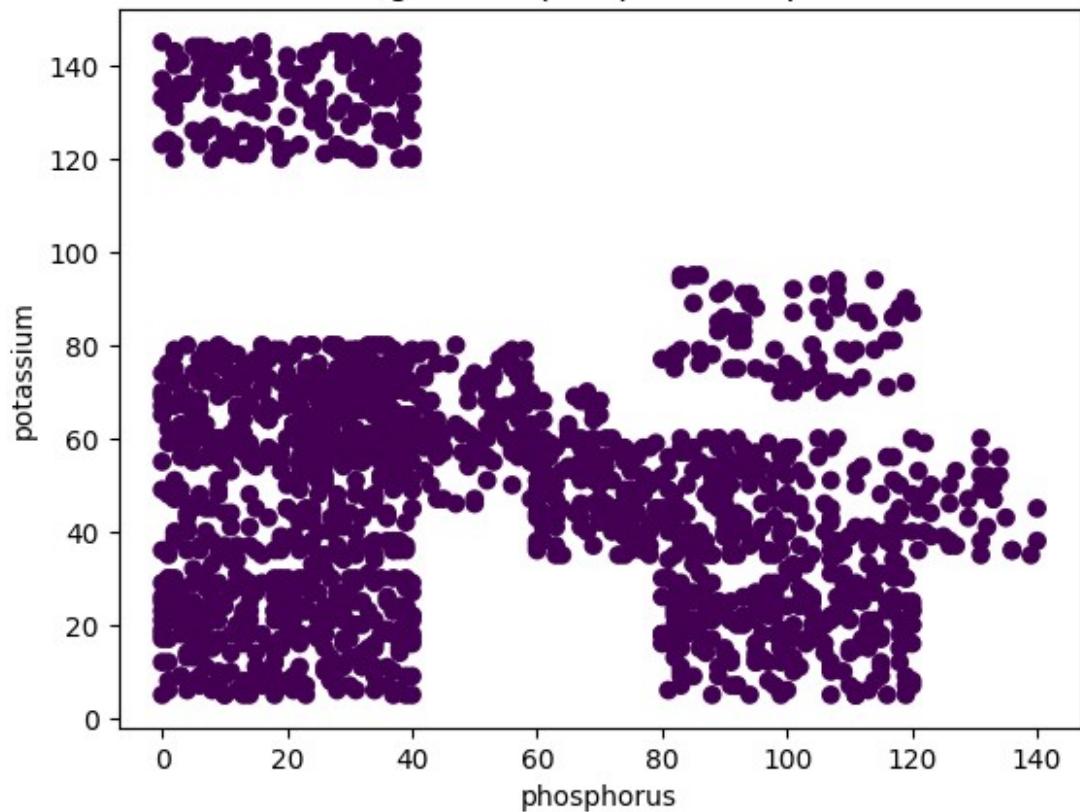
Clustering Result: Nitrogen vs ph



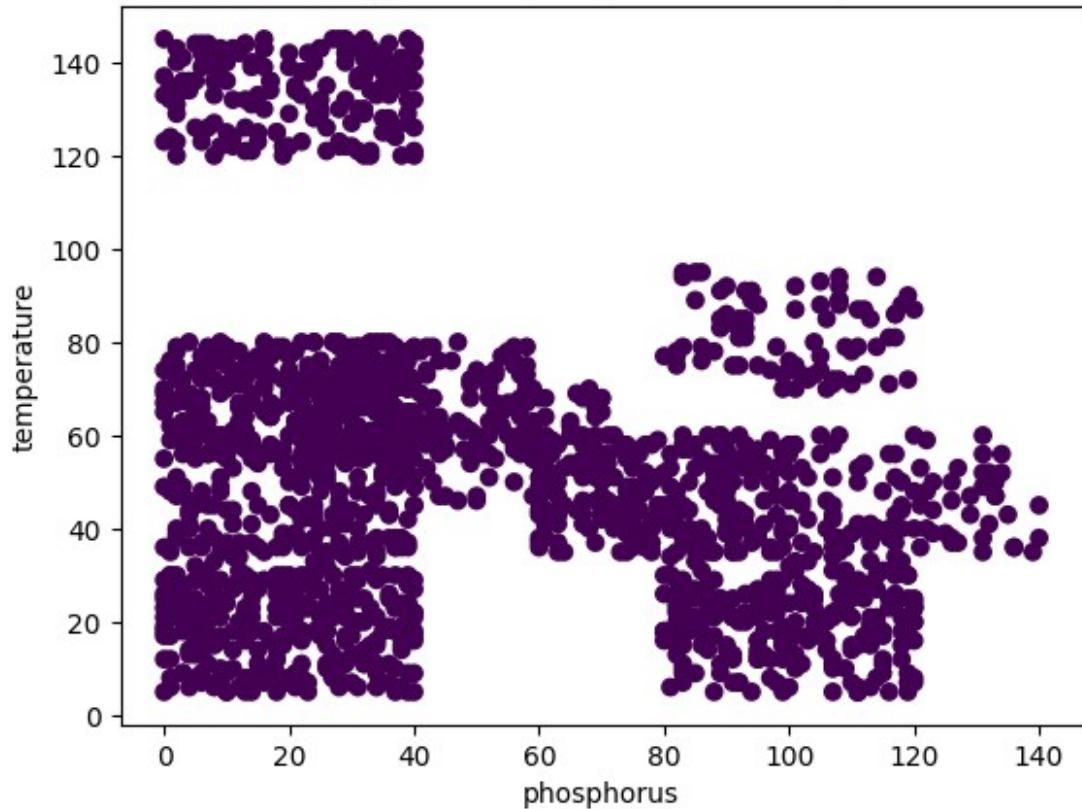
Clustering Result: Nitrogen vs rainfall



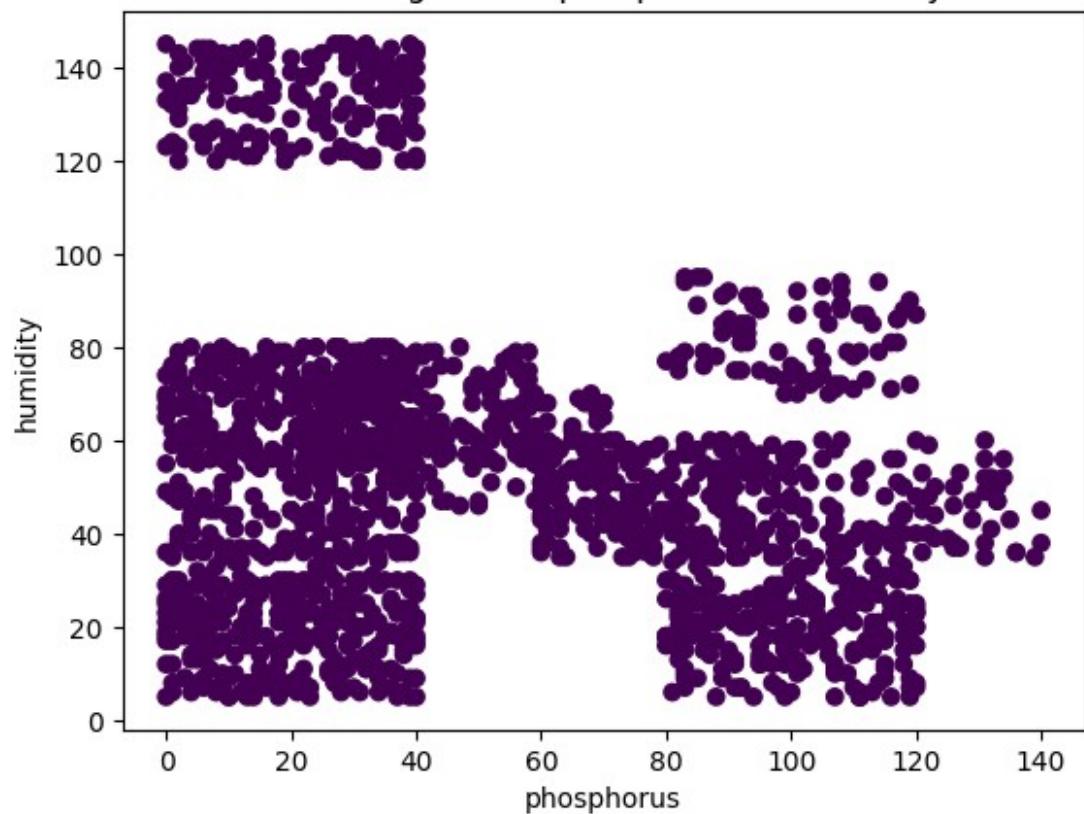
Clustering Result: phosphorus vs potassium



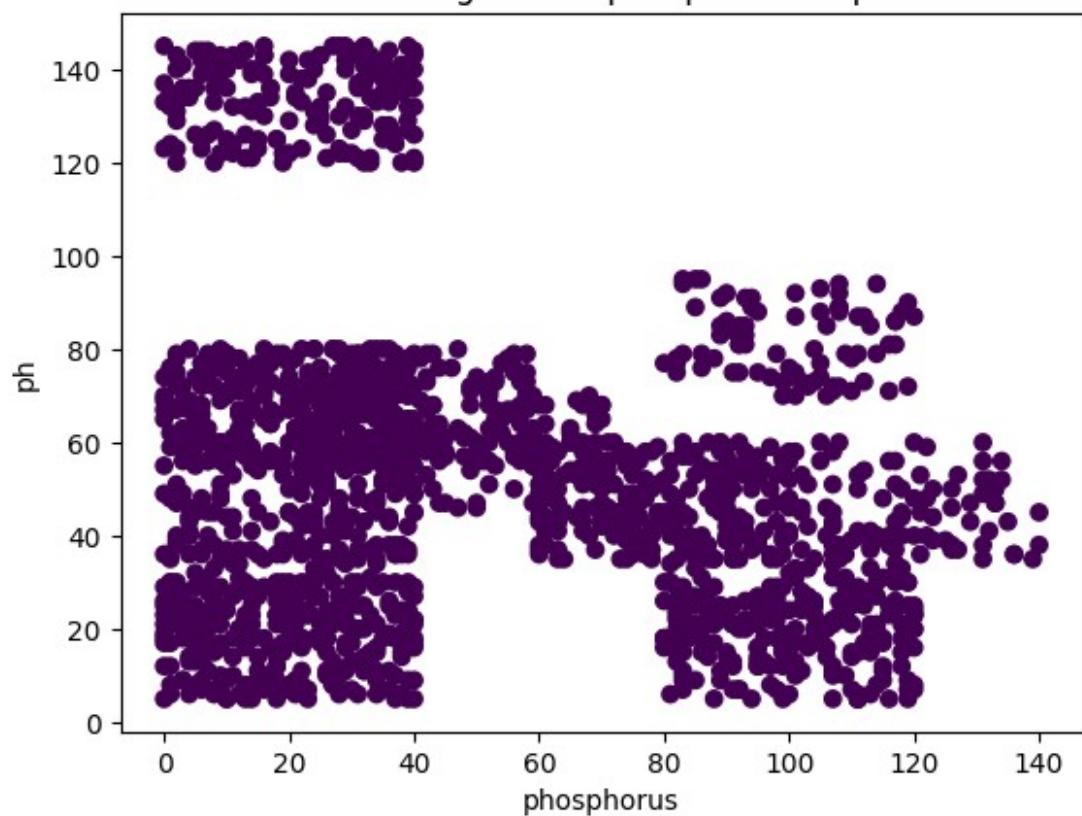
Clustering Result: phosphorus vs temperature



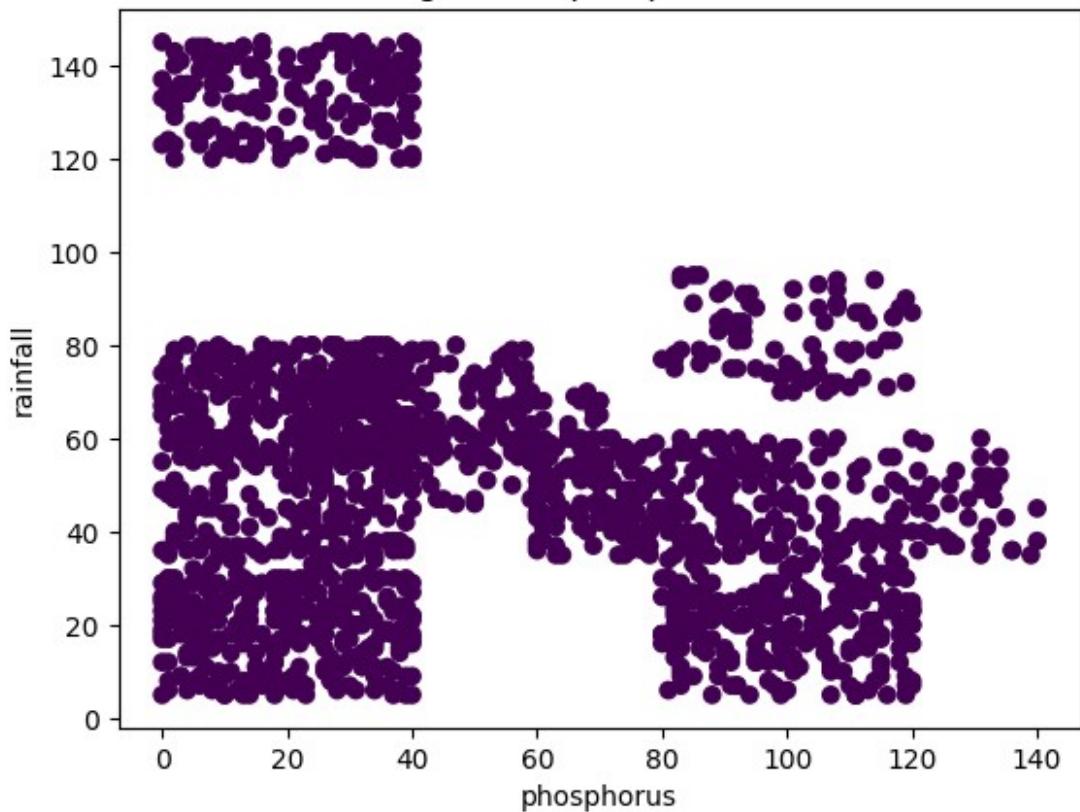
Clustering Result: phosphorus vs humidity



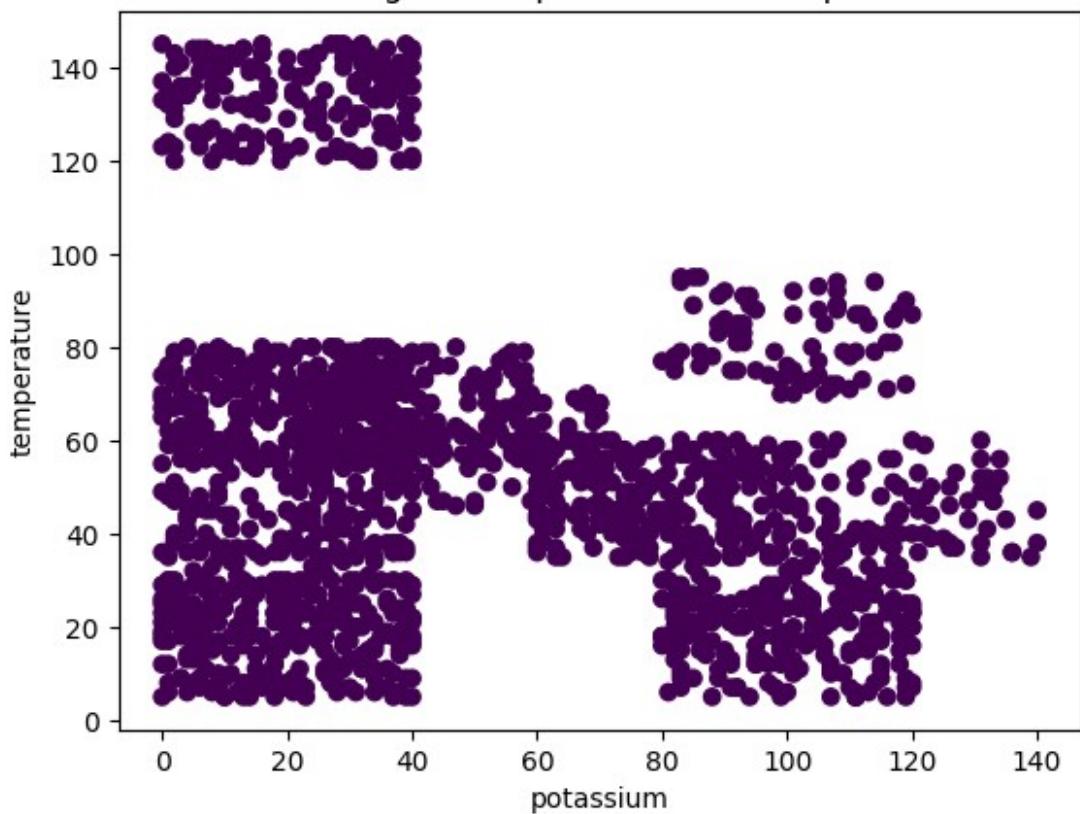
Clustering Result: phosphorus vs ph



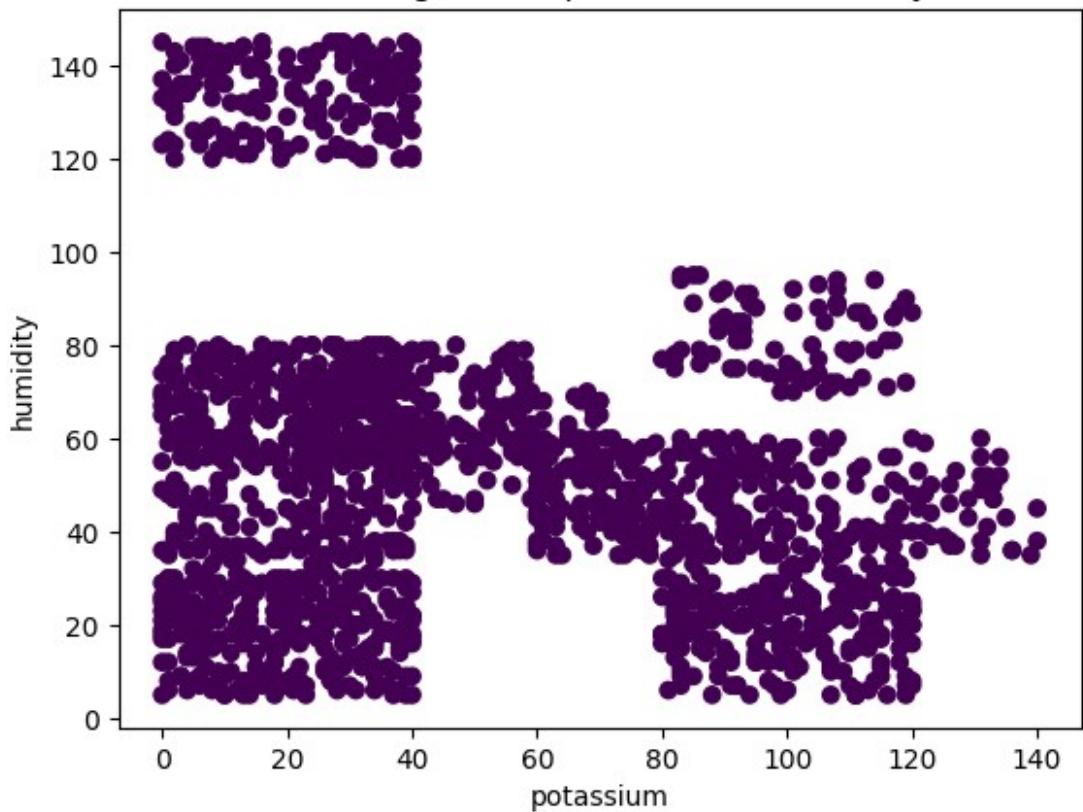
Clustering Result: phosphorus vs rainfall



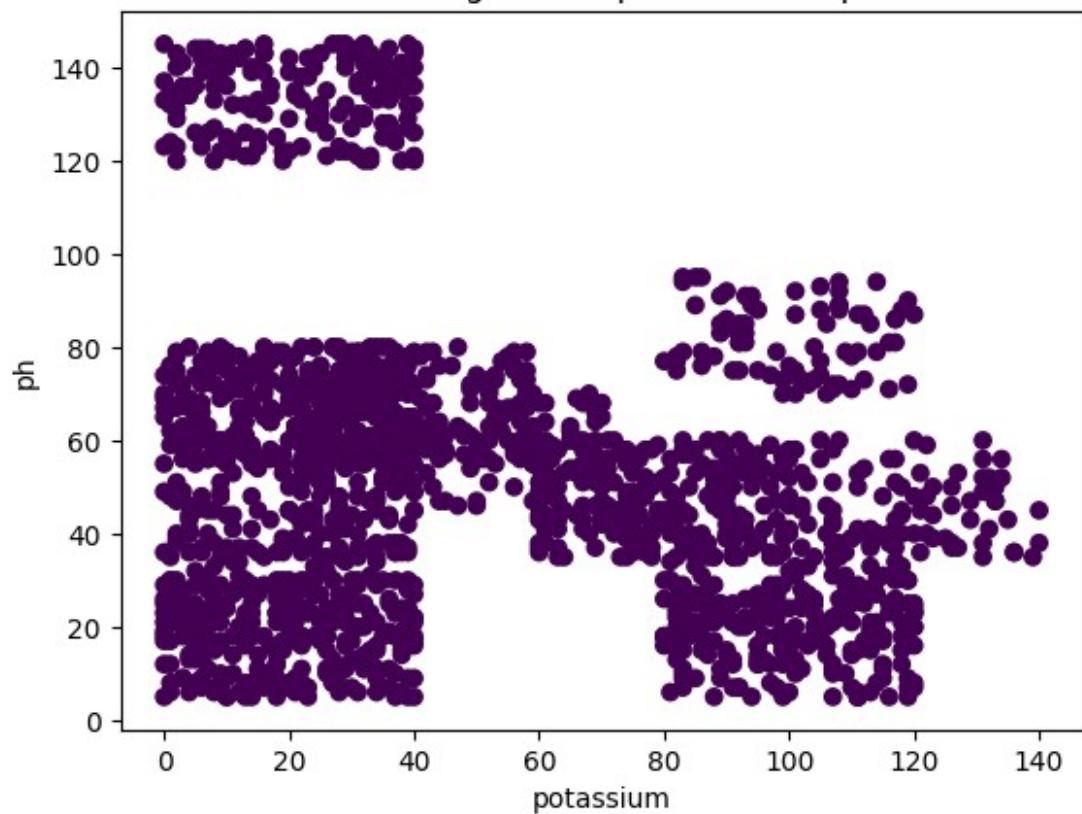
Clustering Result: potassium vs temperature



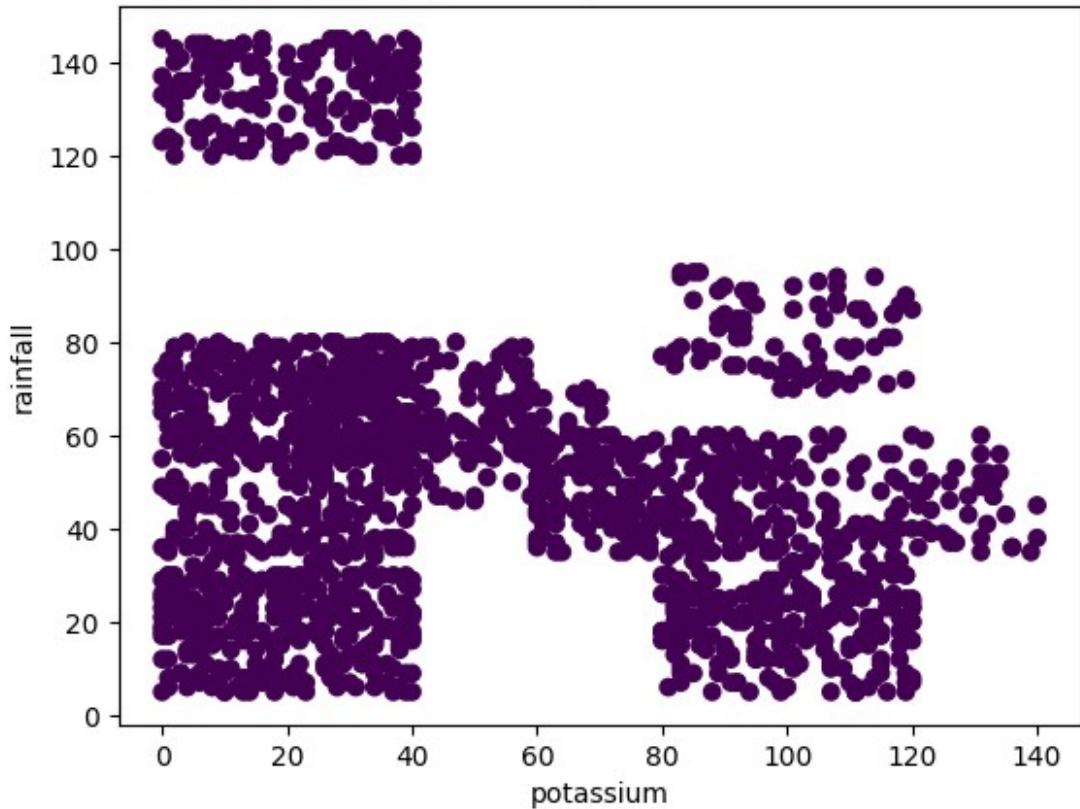
Clustering Result: potassium vs humidity



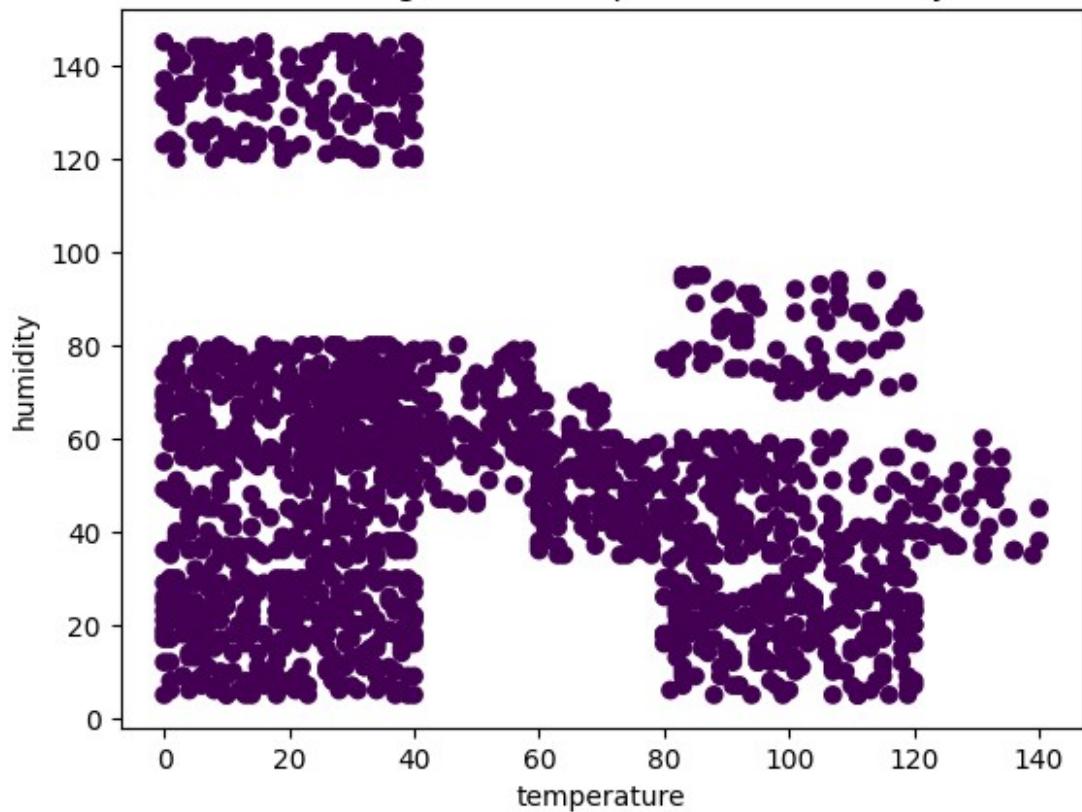
Clustering Result: potassium vs ph



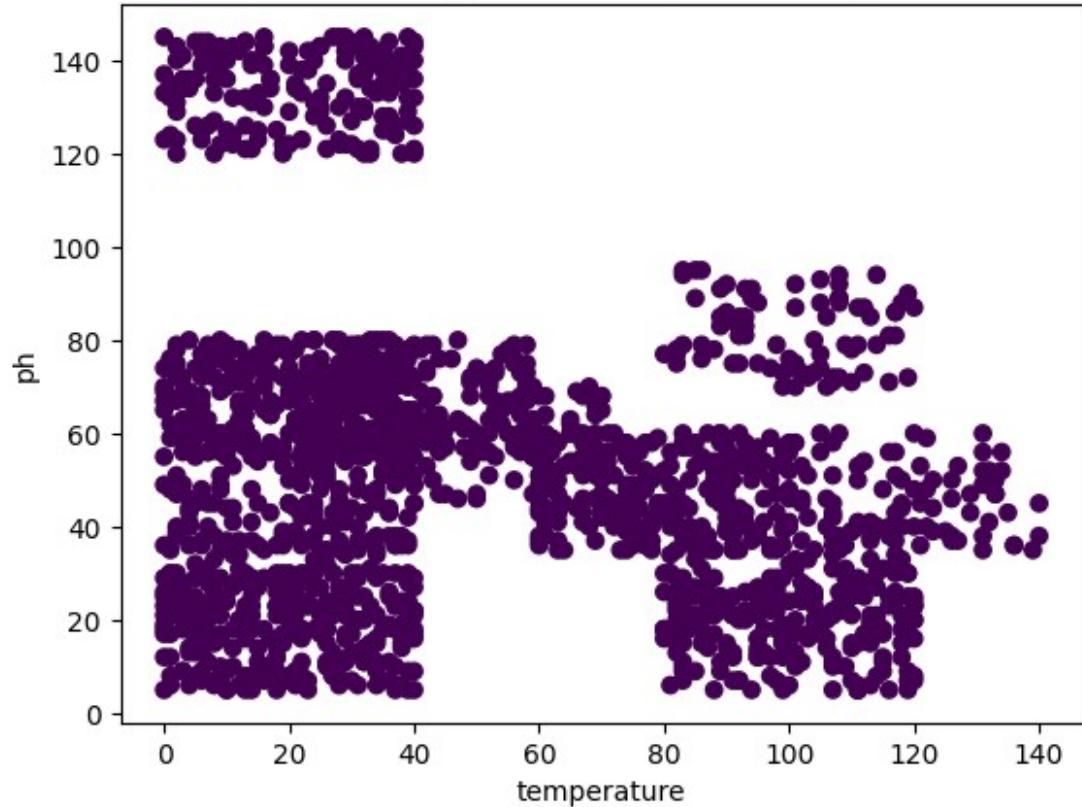
Clustering Result: potassium vs rainfall



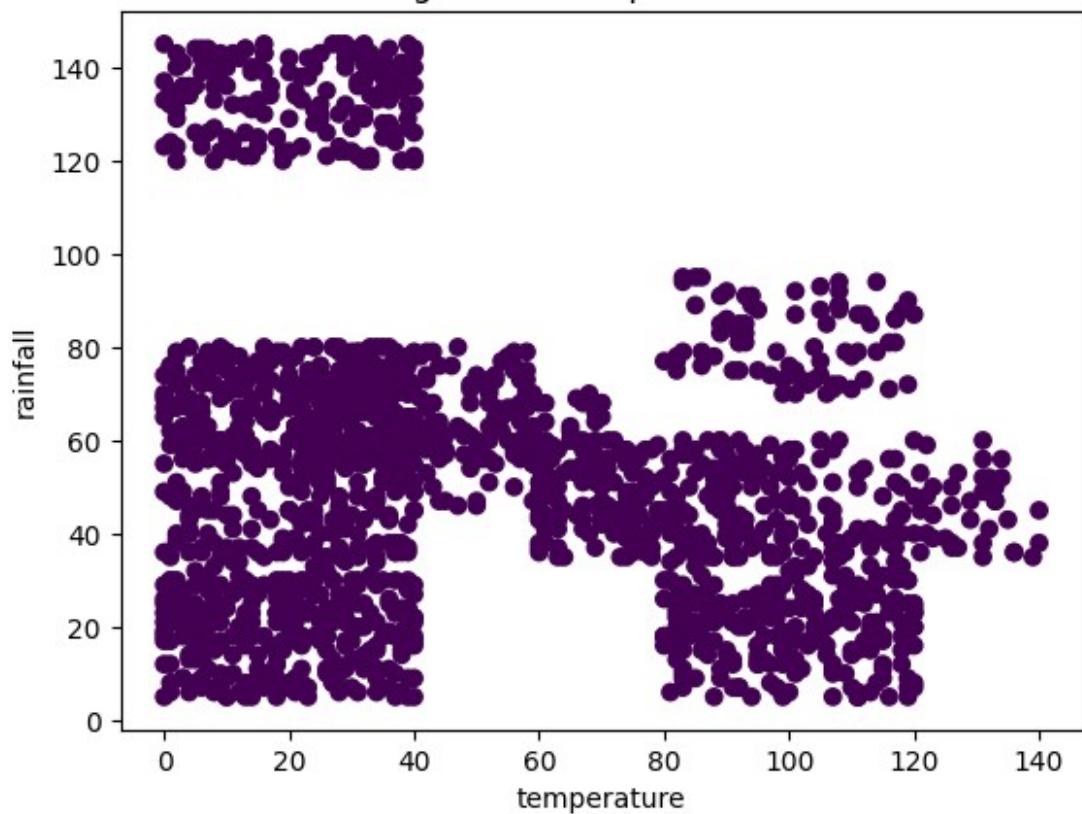
Clustering Result: temperature vs humidity



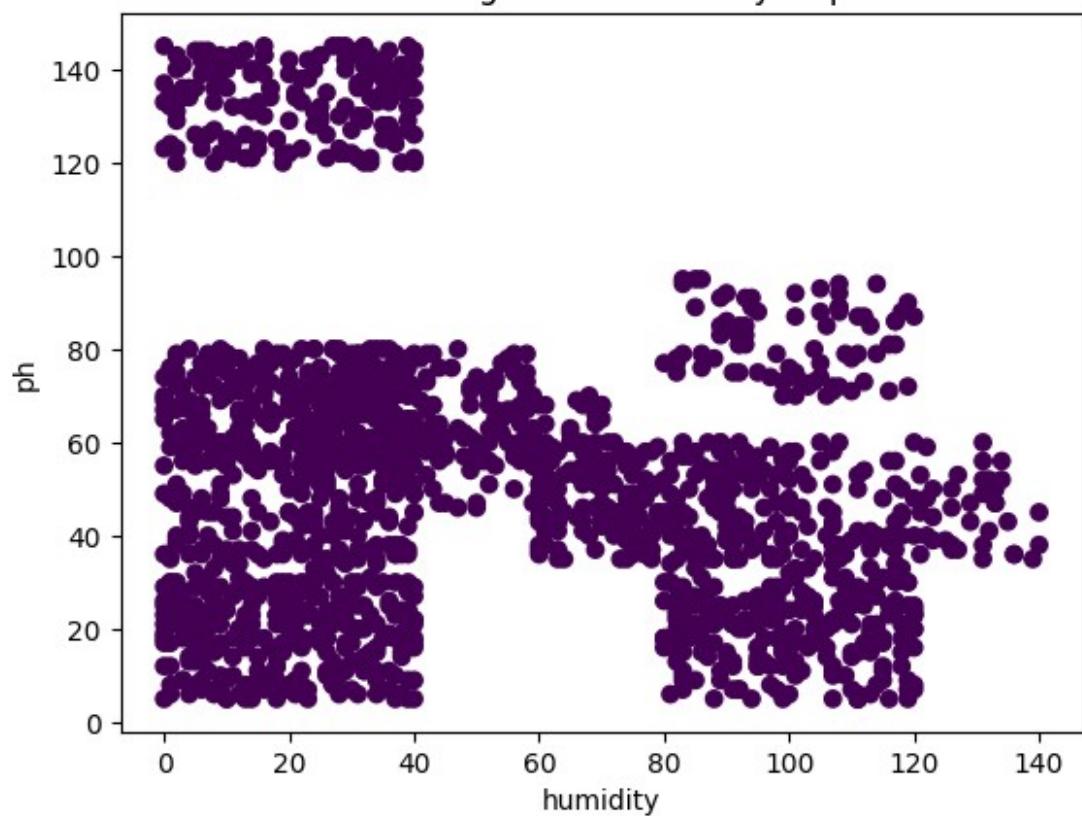
Clustering Result: temperature vs ph



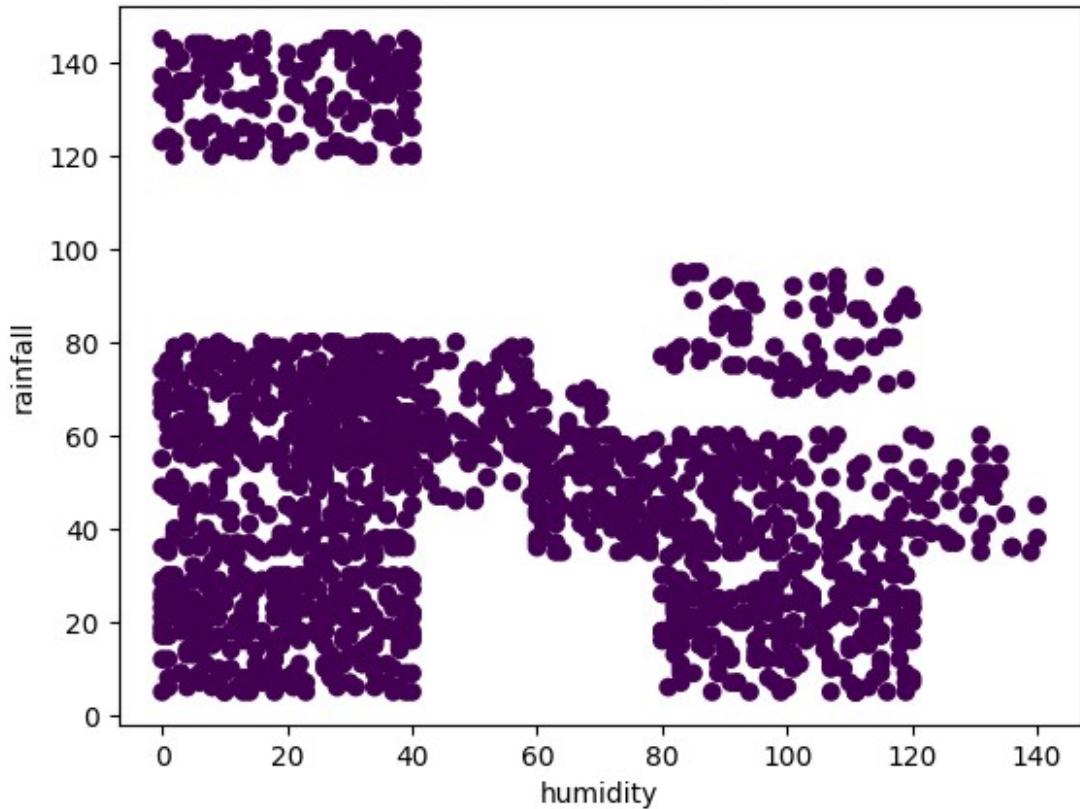
Clustering Result: temperature vs rainfall

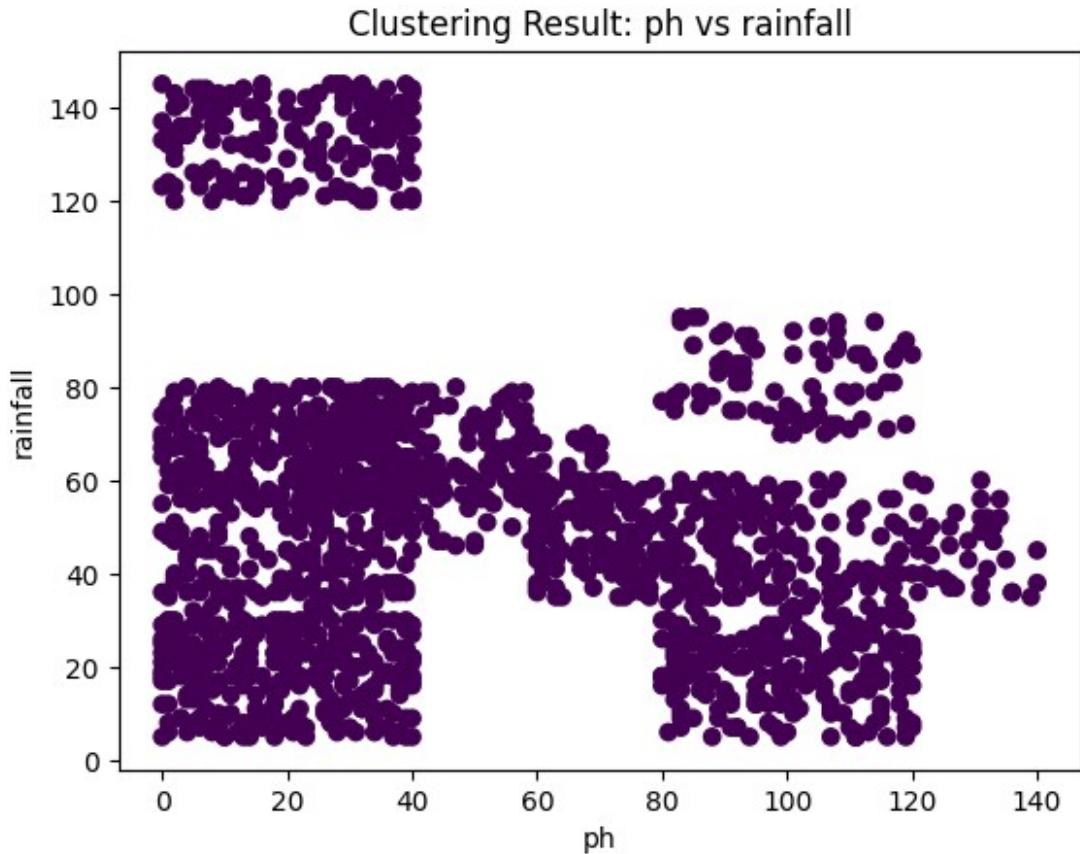


Clustering Result: humidity vs ph



Clustering Result: humidity vs rainfall





Adjusted Rand Index: 0.0

Homogeneity: 0.0

Completeness: 1.0

V-measure: 0.0

#MeanShift

```
# Get the predicted cluster labels for the training data
train_cluster_labels = mean_shift.labels_

# Compute evaluation metrics
silhouette_avg = silhouette_score(X_train, train_cluster_labels)
ari = adjusted_rand_score(target, train_cluster_labels)
homogeneity, completeness, v_measure =
homogeneity_completeness_v_measure(target, train_cluster_labels)

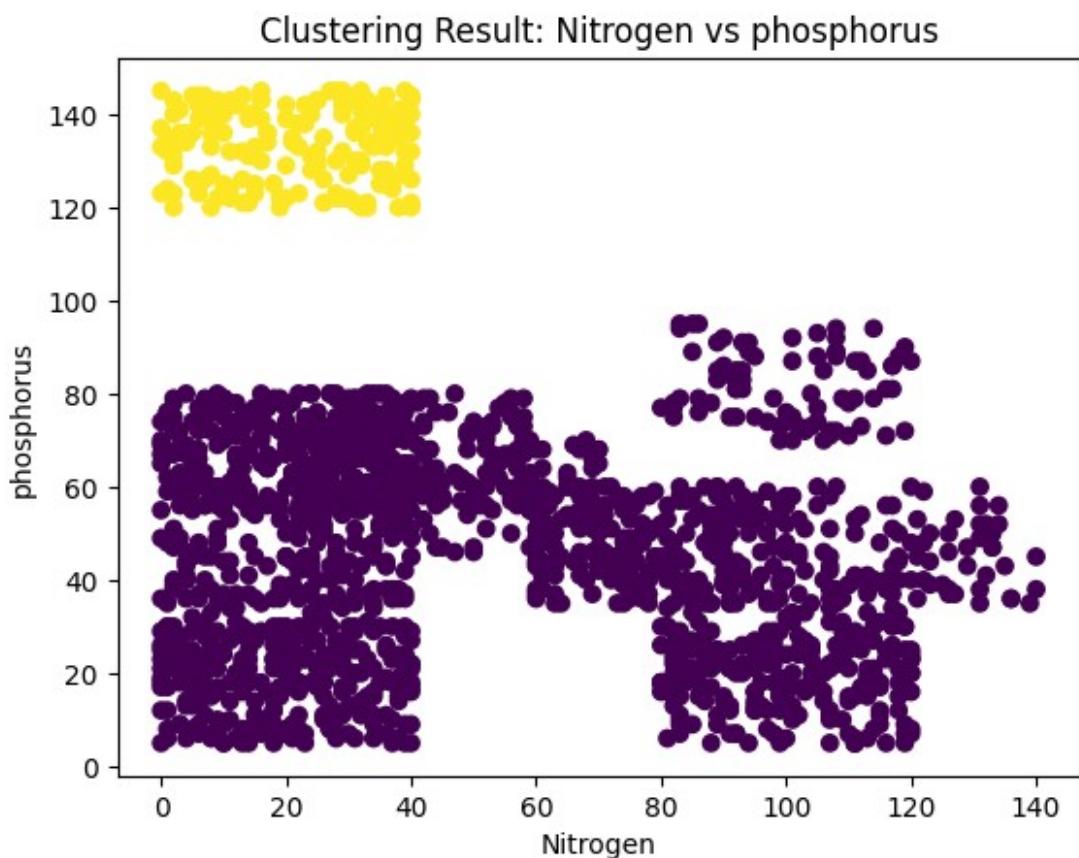
# Create scatter plots for different feature combinations
features = ['Nitrogen', 'phosphorus', 'potassium', 'temperature',
'humidity', 'ph', 'rainfall']
for i in range(len(features)):
    for j in range(i+1, len(features)):
        plt.scatter(X_train[:, 0], X_train[:, 1],
c=train_cluster_labels, cmap='viridis')
```

```

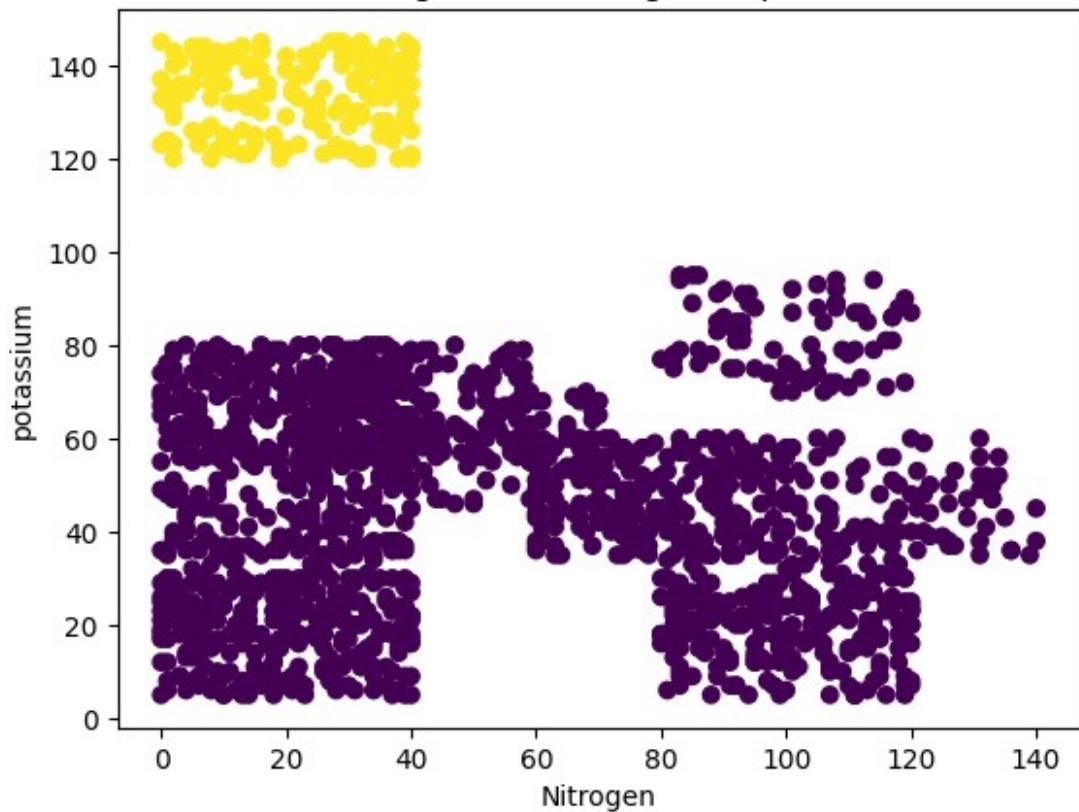
plt.xlabel(features[i])
plt.ylabel(features[j])
plt.title(f'Clustering Result: {features[i]} vs
{features[j]}')
plt.show()

# Print evaluation metrics
print("Silhouette Score:", silhouette_avg)
print("Adjusted Rand Index:", ari)
print("Homogeneity:", homogeneity)
print("Completeness:", completeness)
print("V-measure:", v_measure)

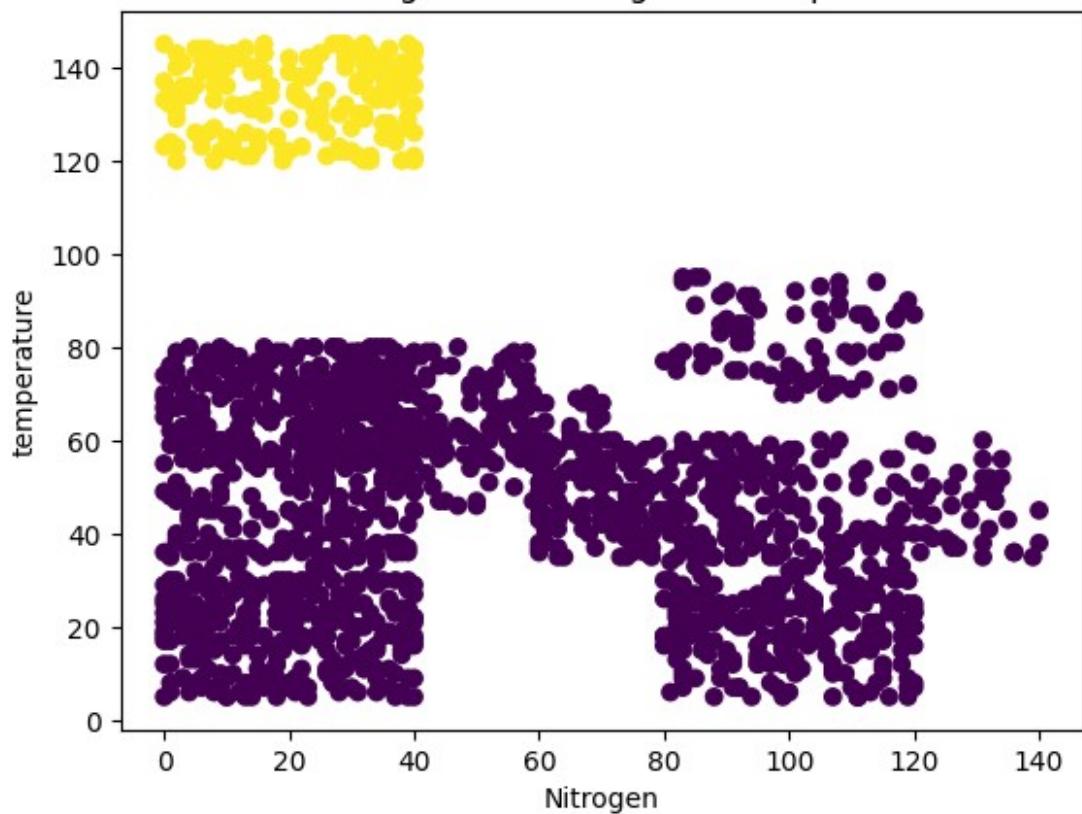
```



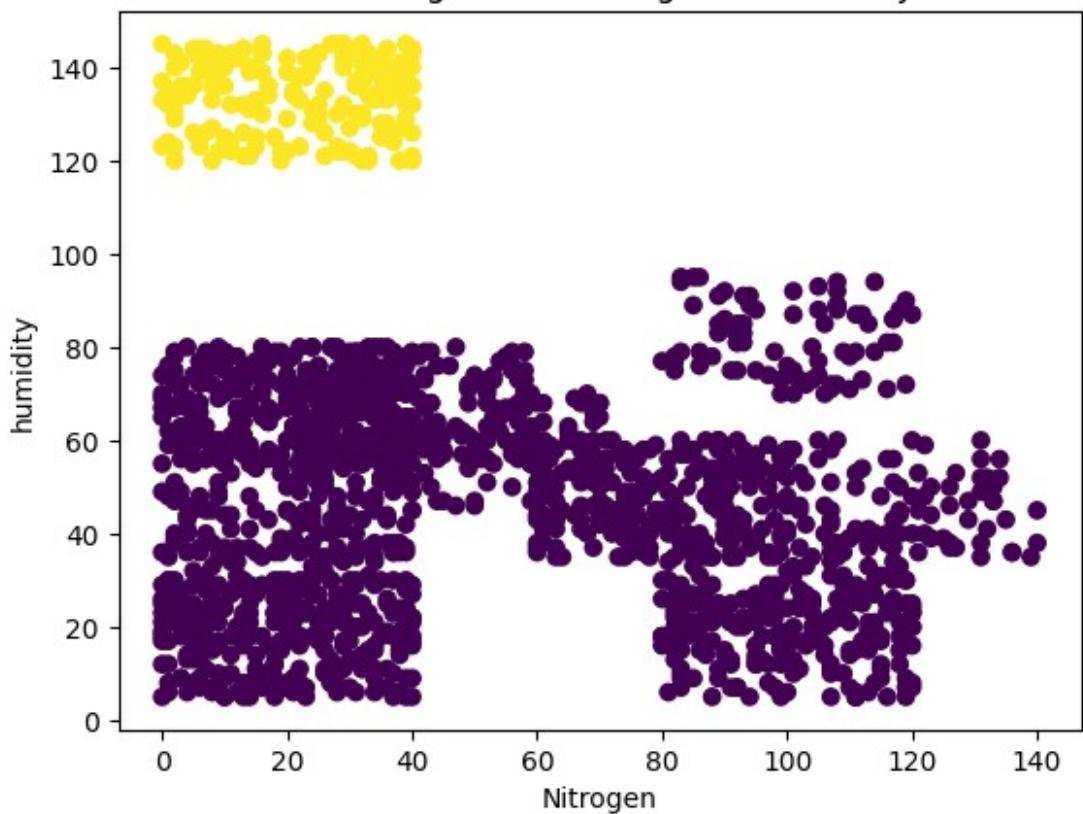
Clustering Result: Nitrogen vs potassium



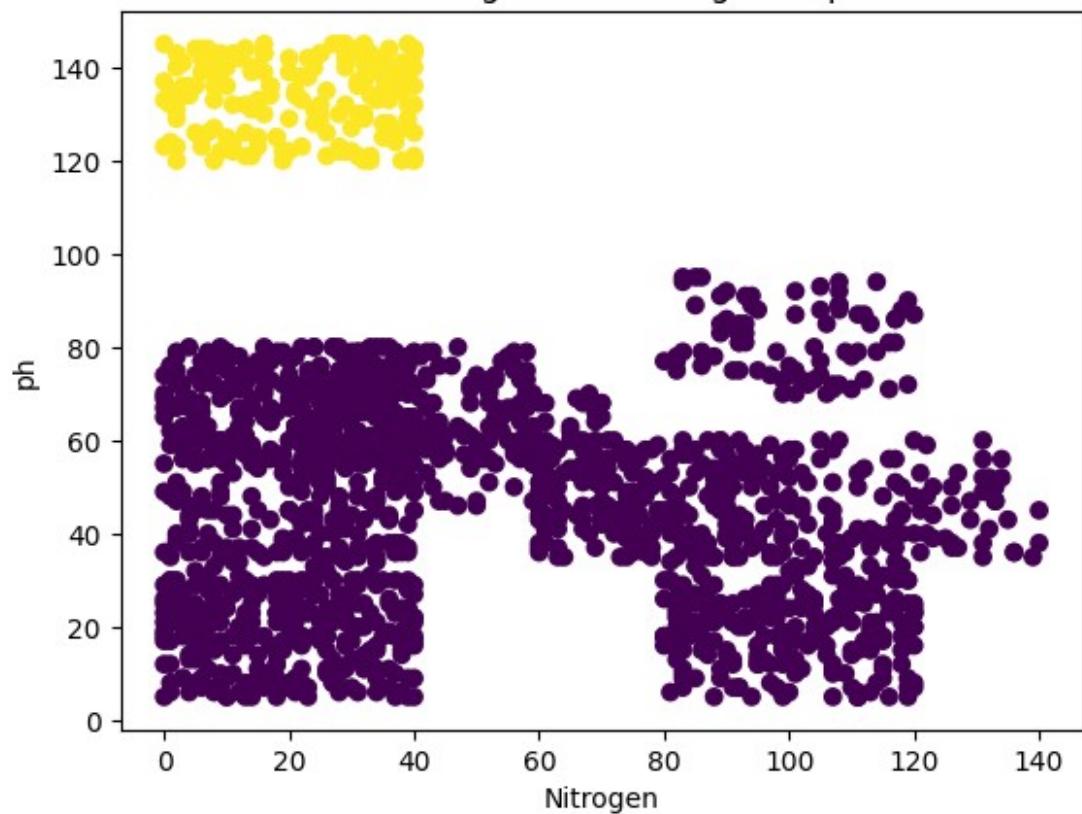
Clustering Result: Nitrogen vs temperature



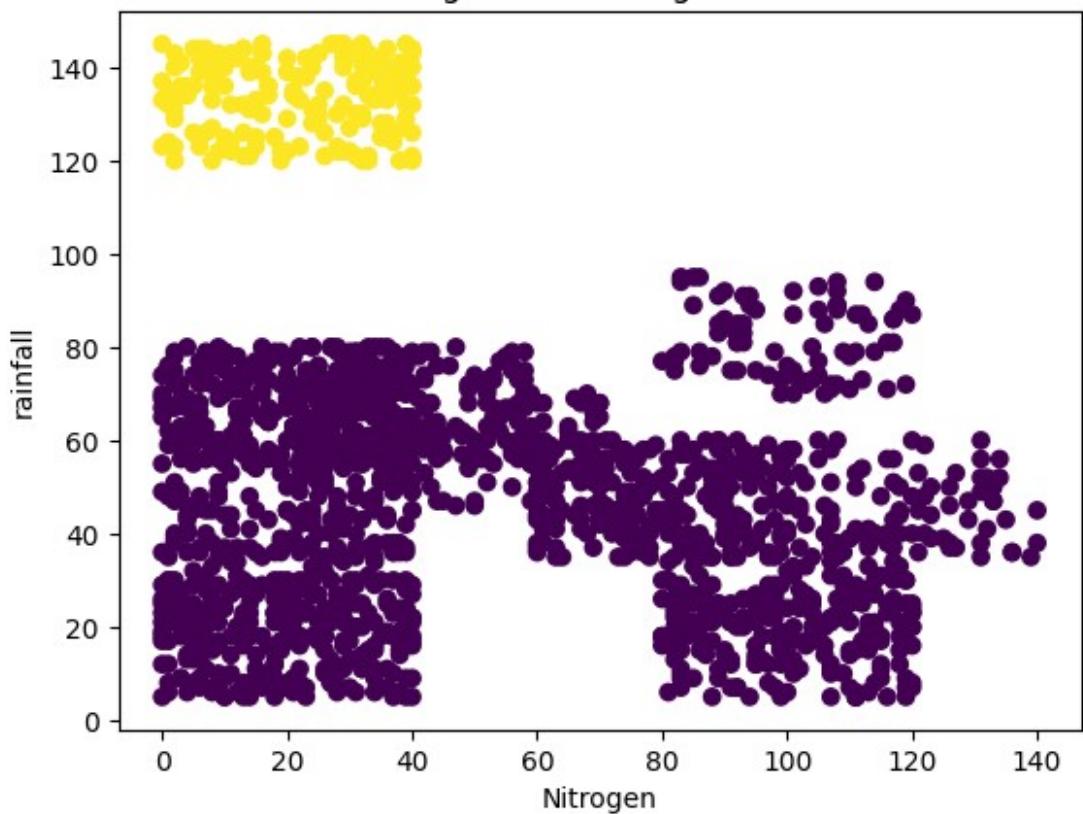
Clustering Result: Nitrogen vs humidity



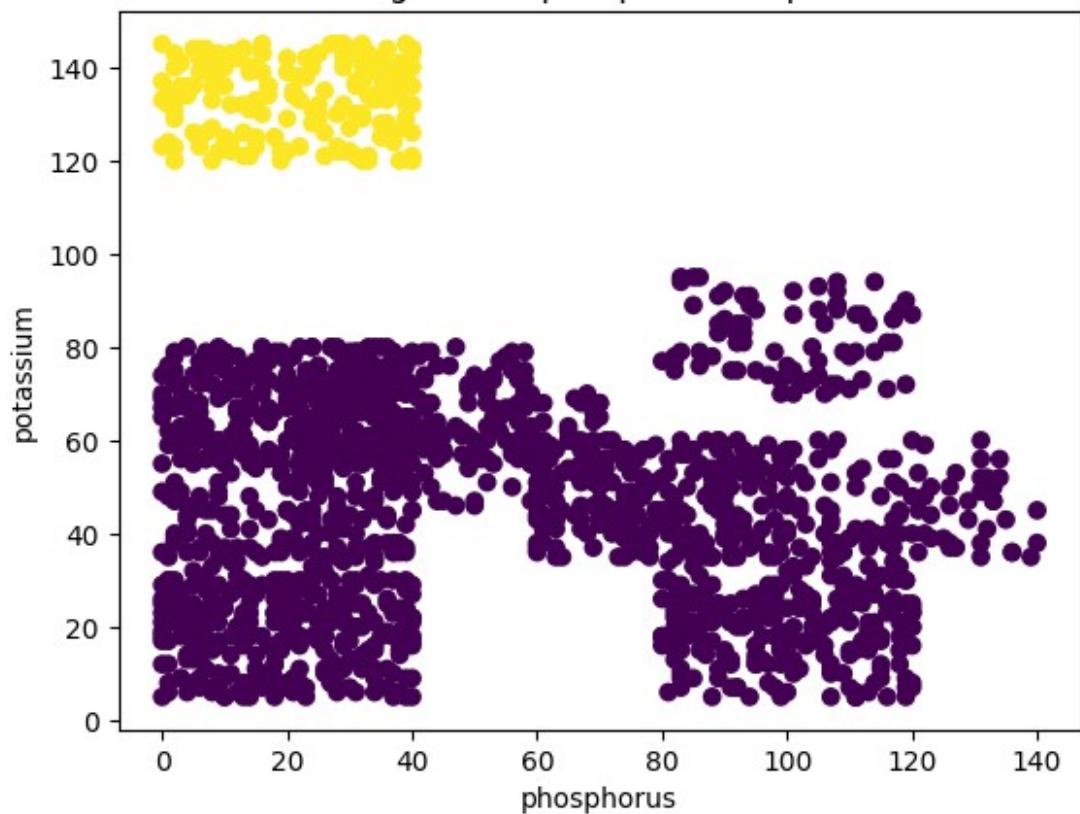
Clustering Result: Nitrogen vs ph



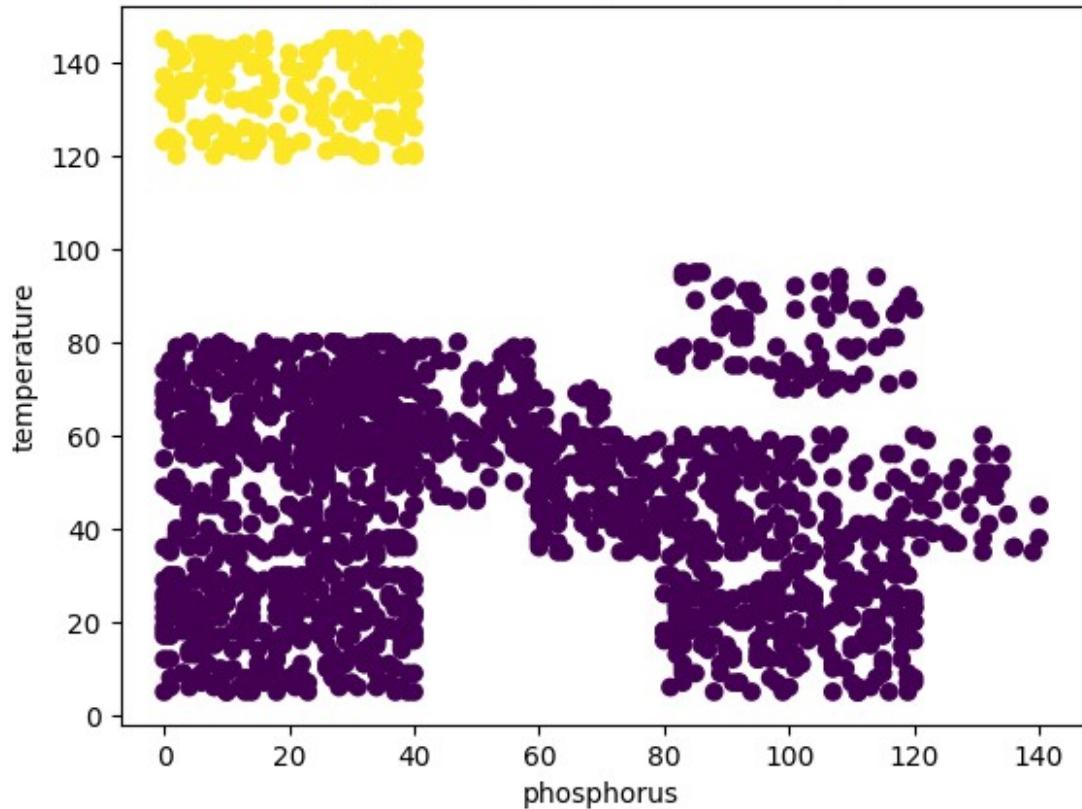
Clustering Result: Nitrogen vs rainfall



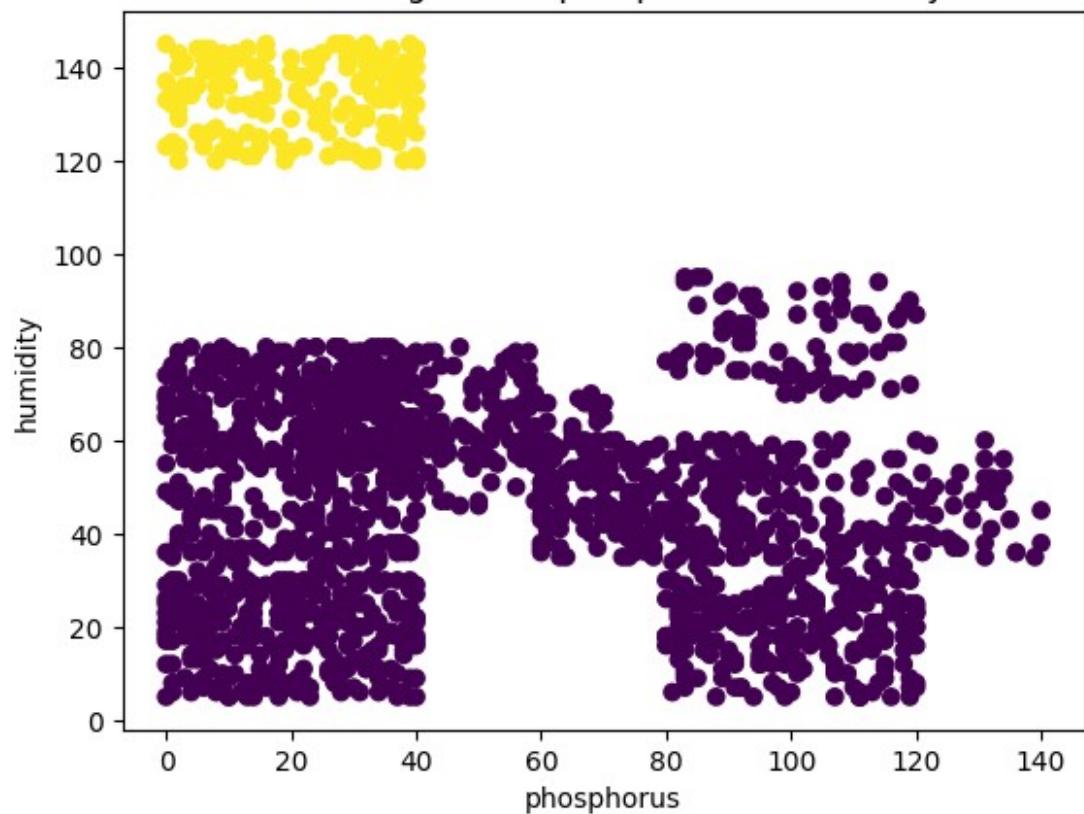
Clustering Result: phosphorus vs potassium



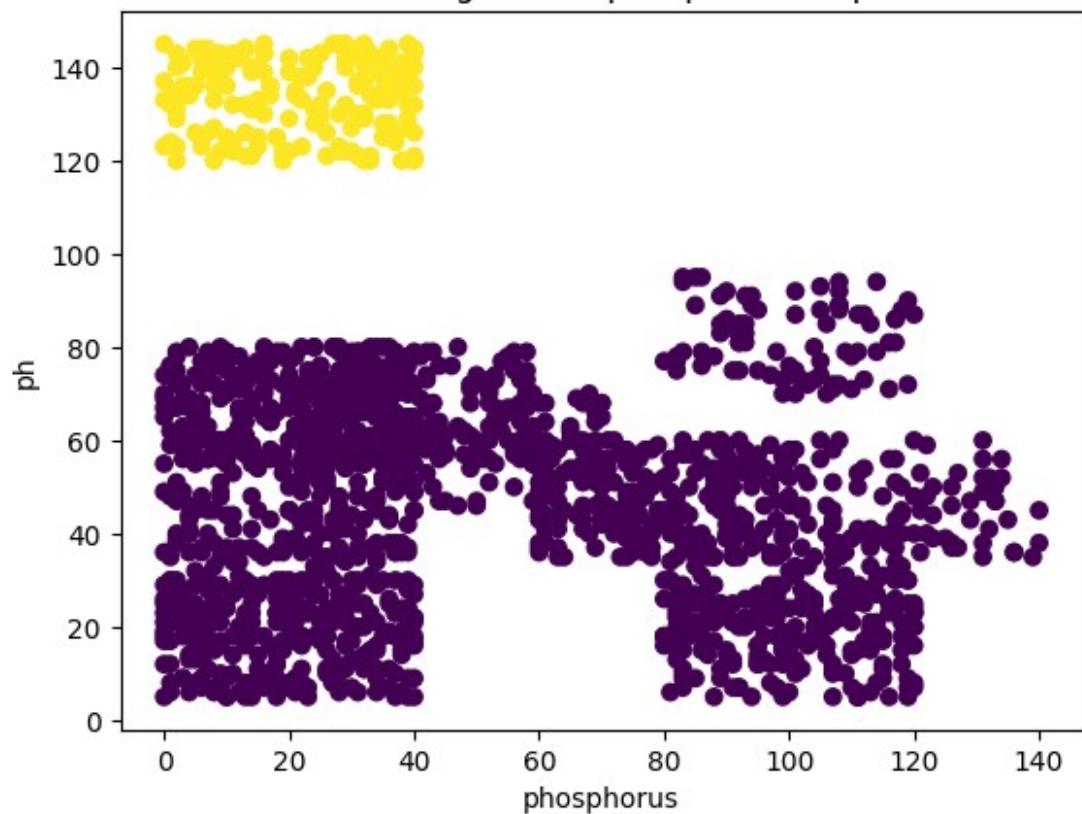
Clustering Result: phosphorus vs temperature



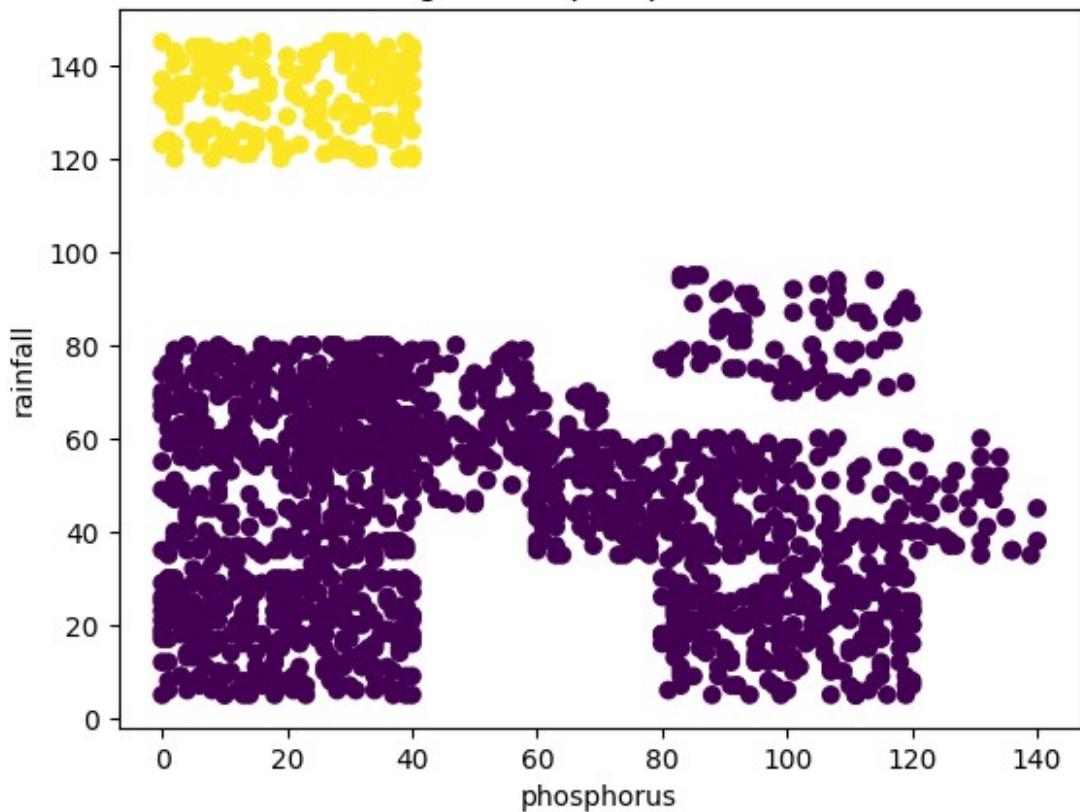
Clustering Result: phosphorus vs humidity



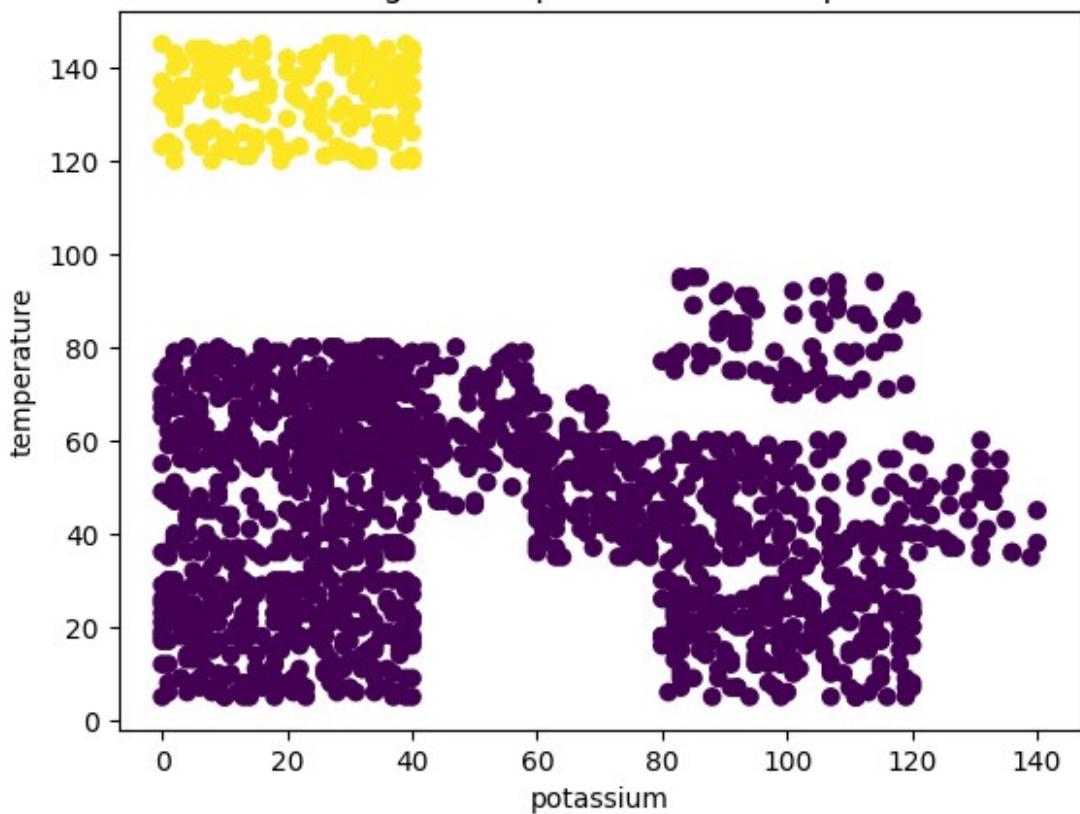
Clustering Result: phosphorus vs ph



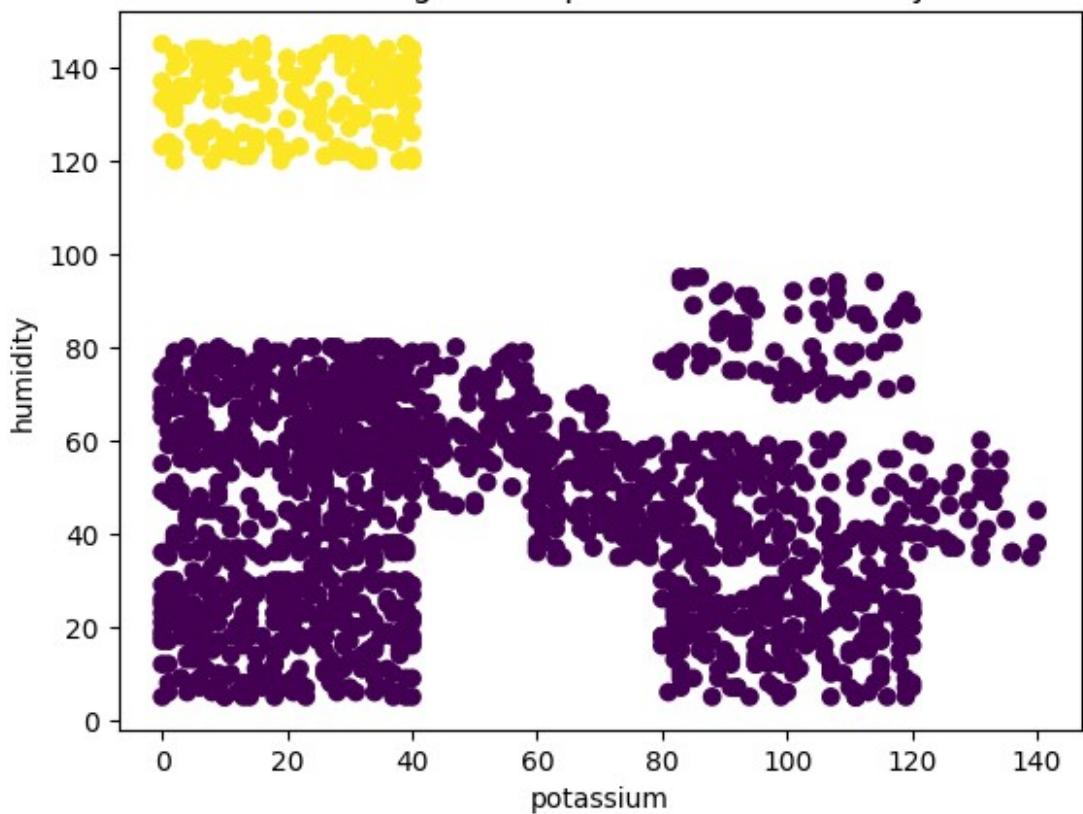
Clustering Result: phosphorus vs rainfall



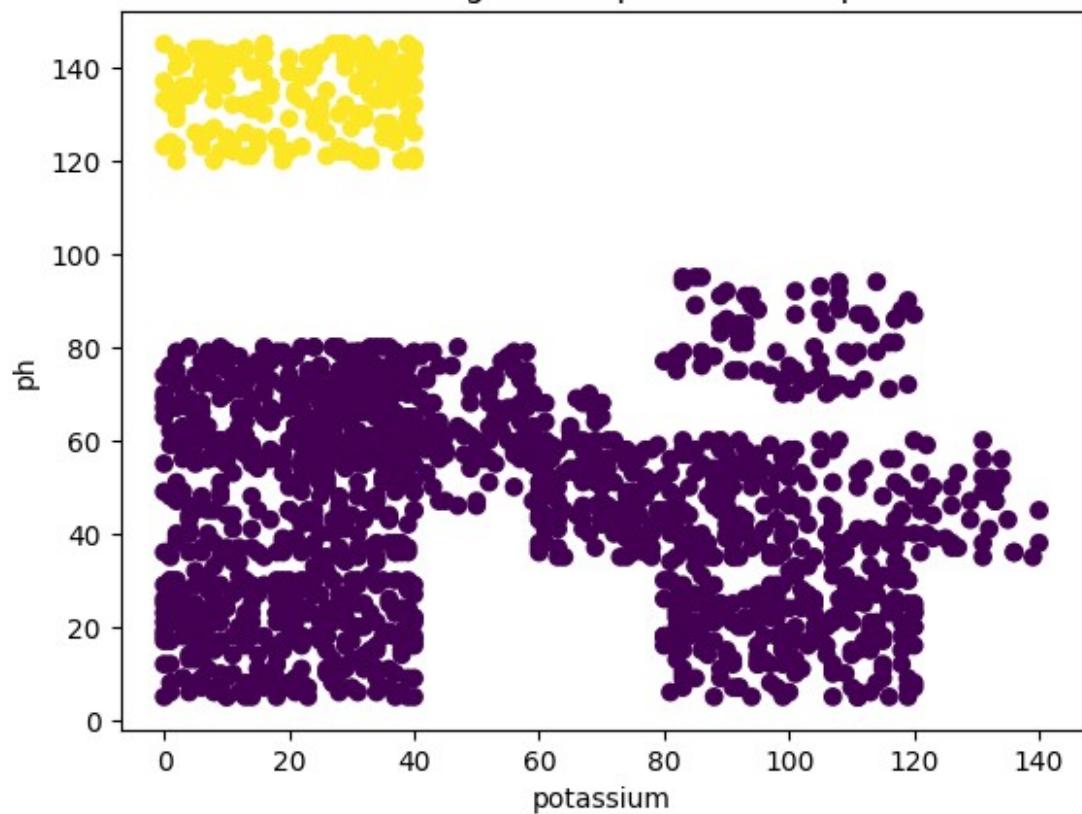
Clustering Result: potassium vs temperature



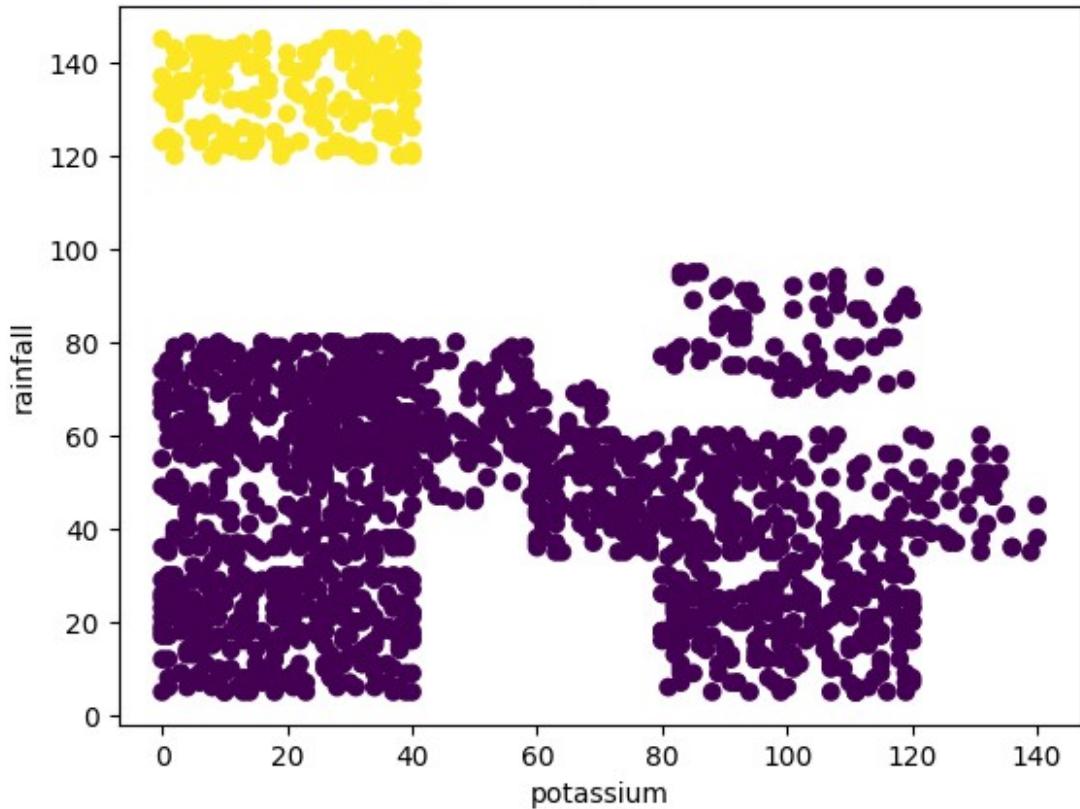
Clustering Result: potassium vs humidity



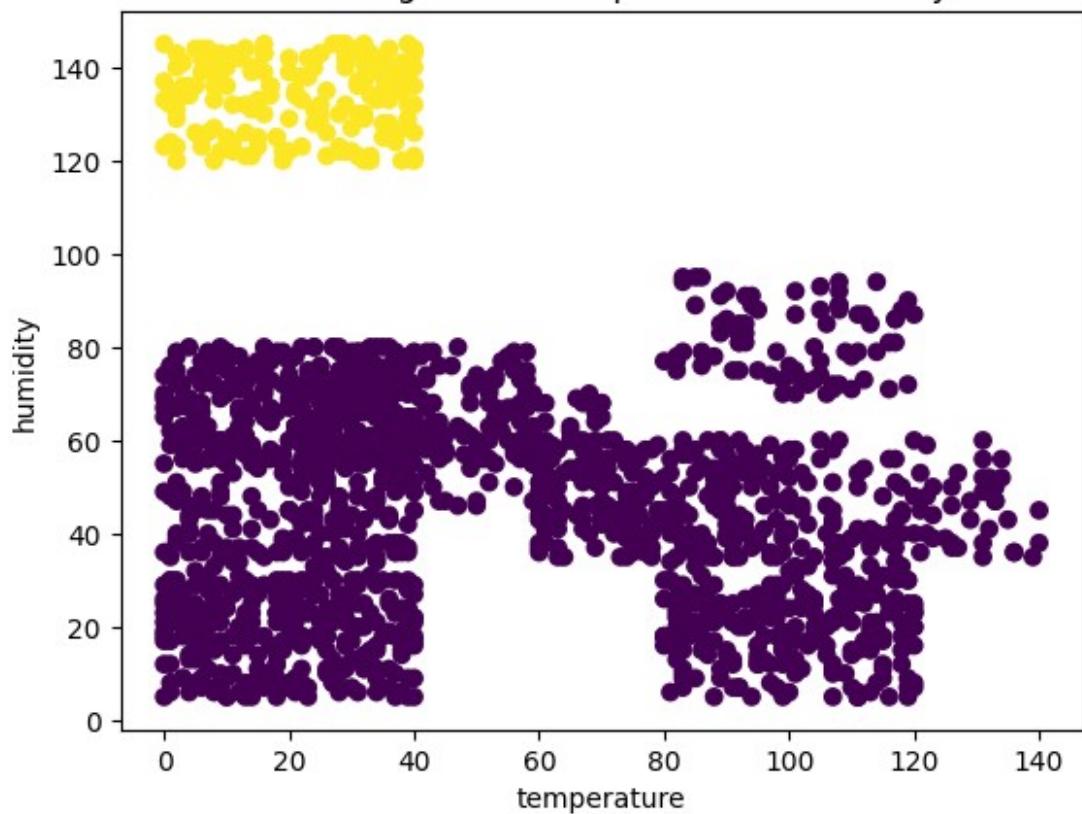
Clustering Result: potassium vs ph



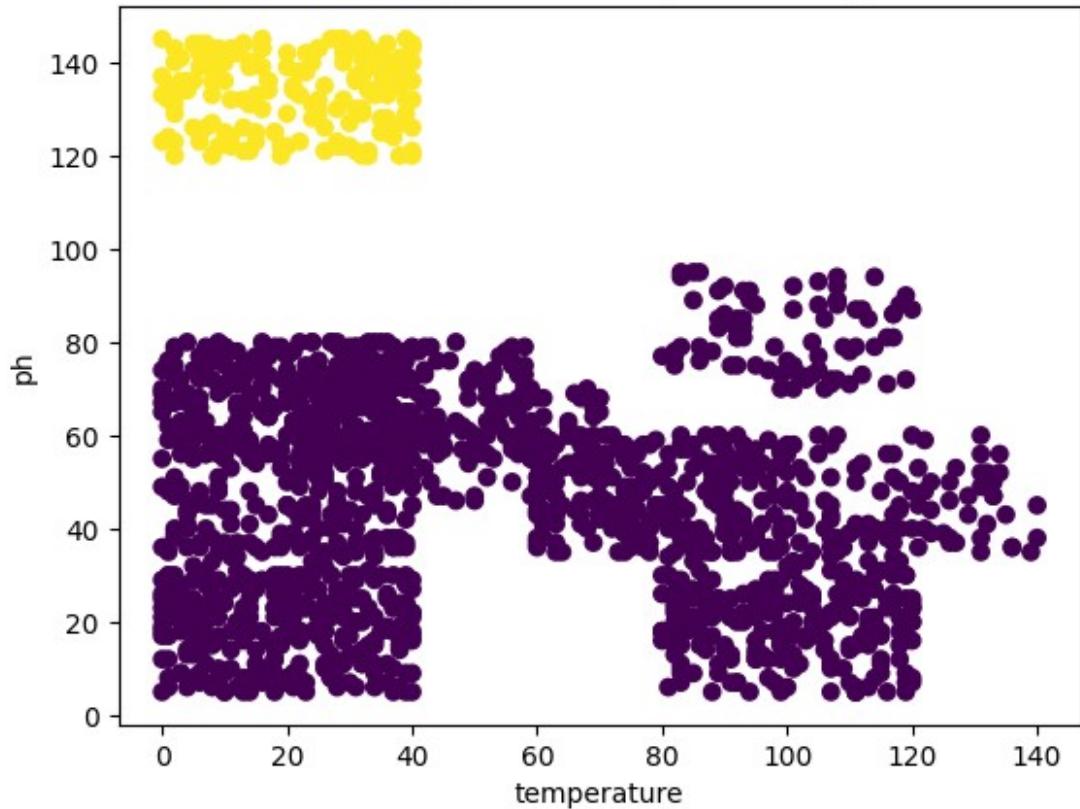
Clustering Result: potassium vs rainfall



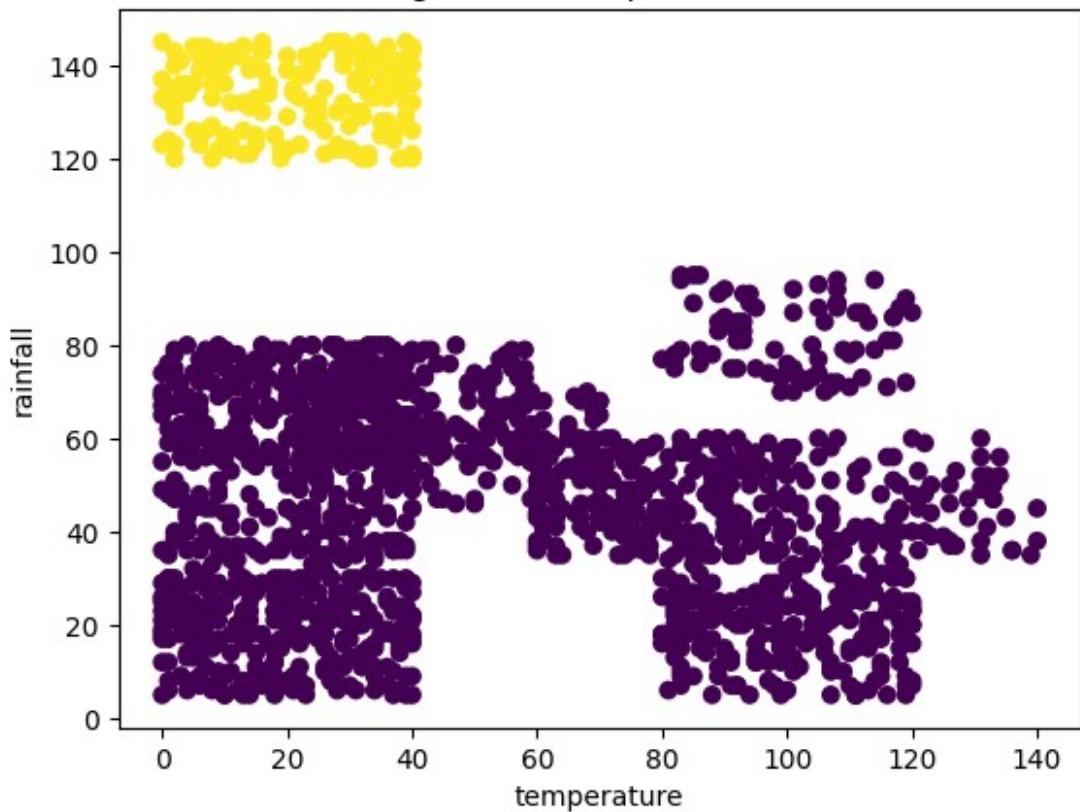
Clustering Result: temperature vs humidity



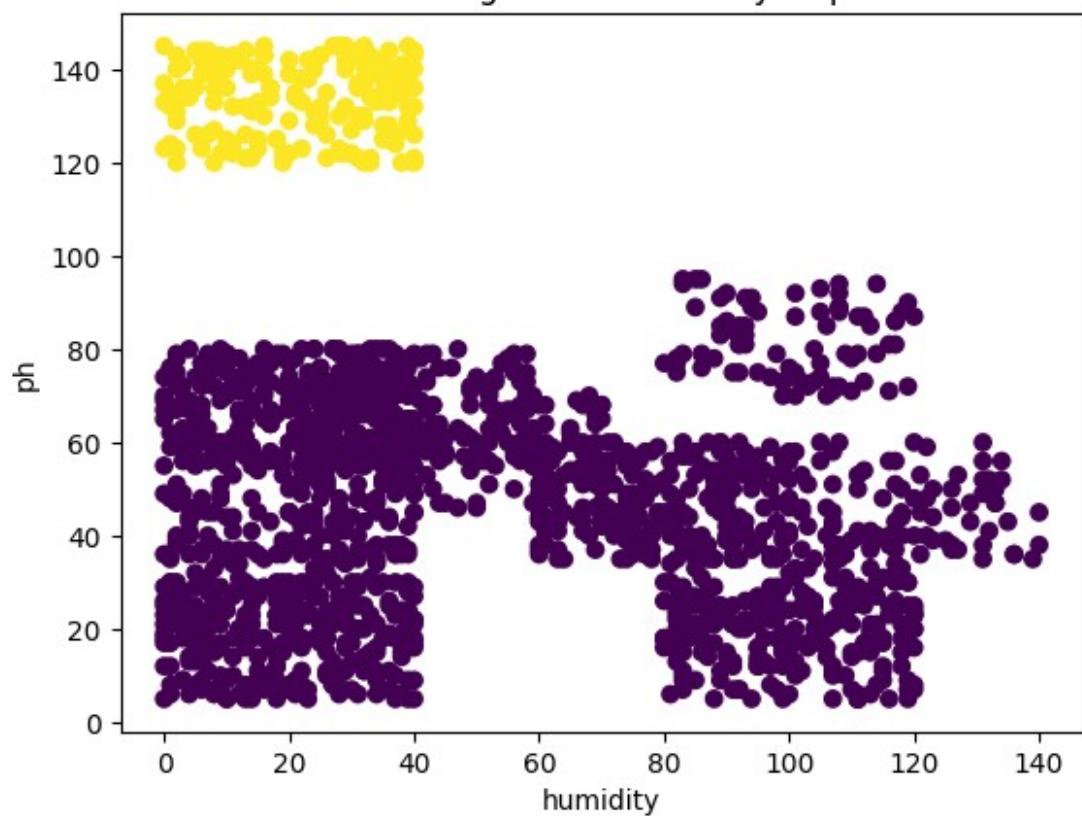
Clustering Result: temperature vs ph



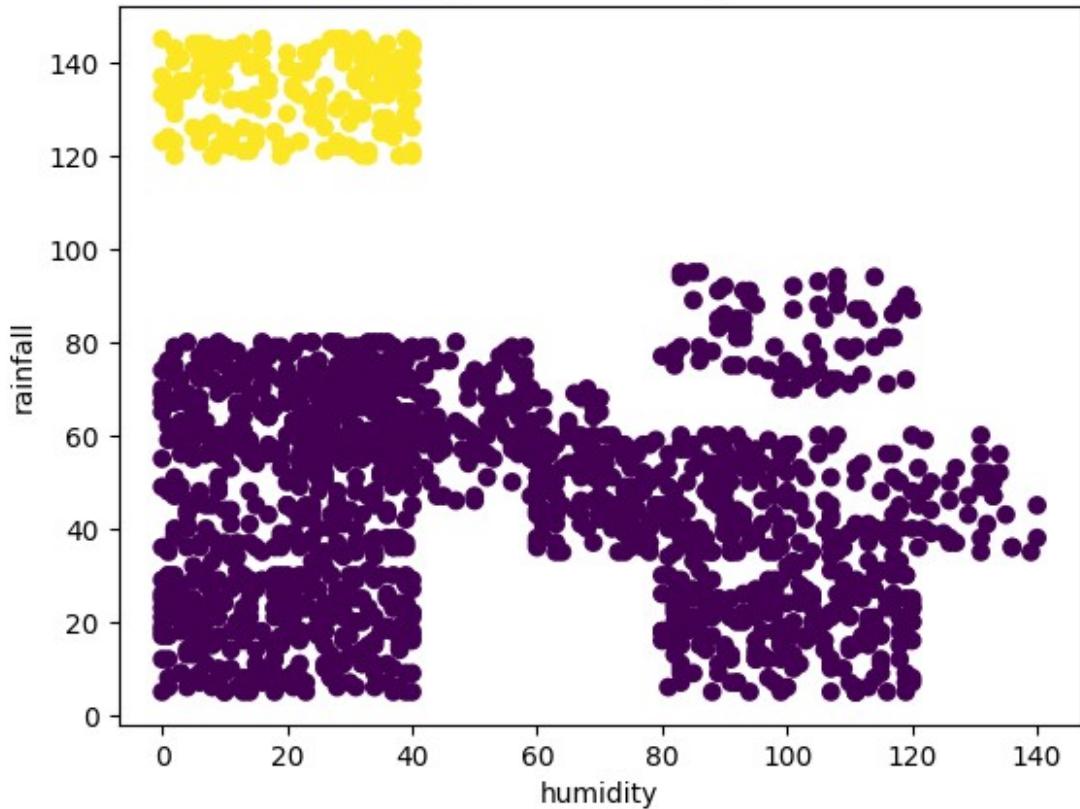
Clustering Result: temperature vs rainfall

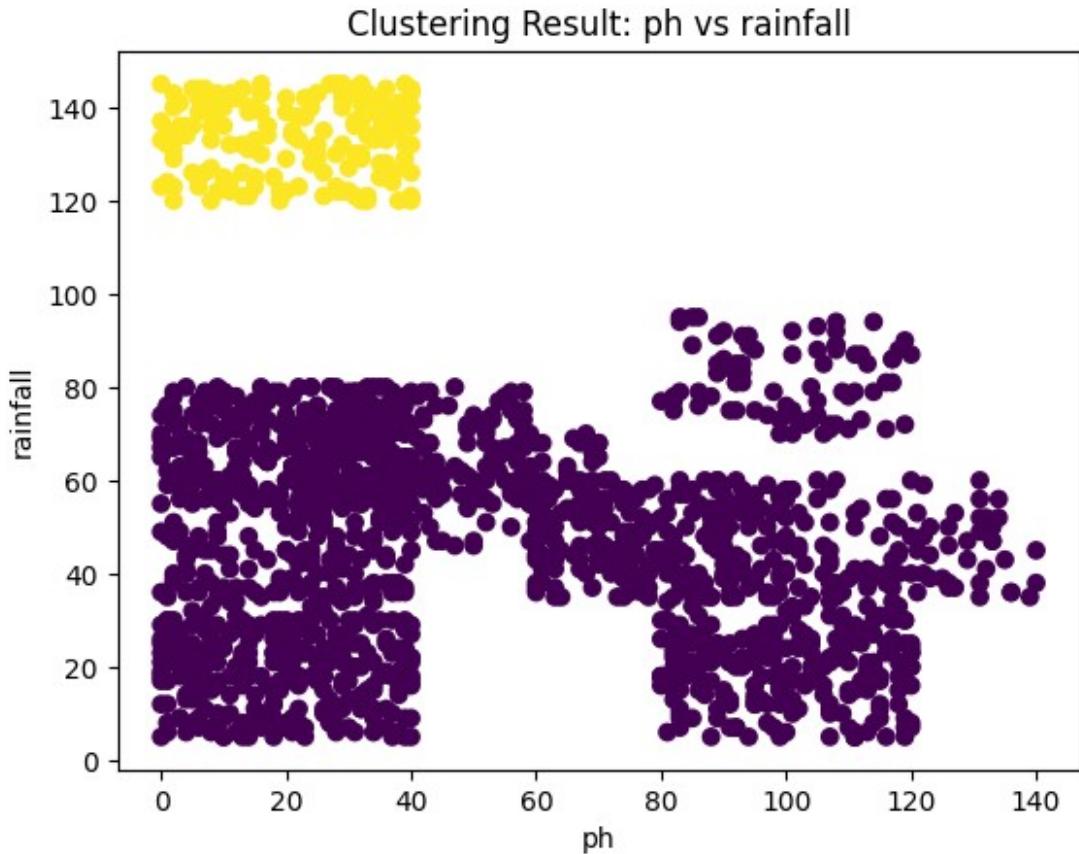


Clustering Result: humidity vs ph



Clustering Result: humidity vs rainfall





Silhouette Score: 0.5467470270493778  
 Adjusted Rand Index: 0.01888084657755322  
 Homogeneity: 0.09985647799386856  
 Completeness: 1.0000000000000004  
 V-measure: 0.18158092440571183

### #SpectralClustering

```

# Get the predicted cluster labels for the training data
train_cluster_labels = spectral_clustering.labels_

# Compute evaluation metrics
silhouette_avg = silhouette_score(X_train, train_cluster_labels)
ari = adjusted_rand_score(target, train_cluster_labels)
homogeneity, completeness, v_measure =
homogeneity_completeness_v_measure(target, train_cluster_labels)

# Create scatter plots for different feature combinations
features = ['Nitrogen', 'phosphorus', 'potassium', 'temperature',
'humidity', 'ph', 'rainfall']
for i in range(len(features)):
  for j in range(i+1, len(features)):
    plt.scatter(X_train[:, 0], X_train[:, 1],

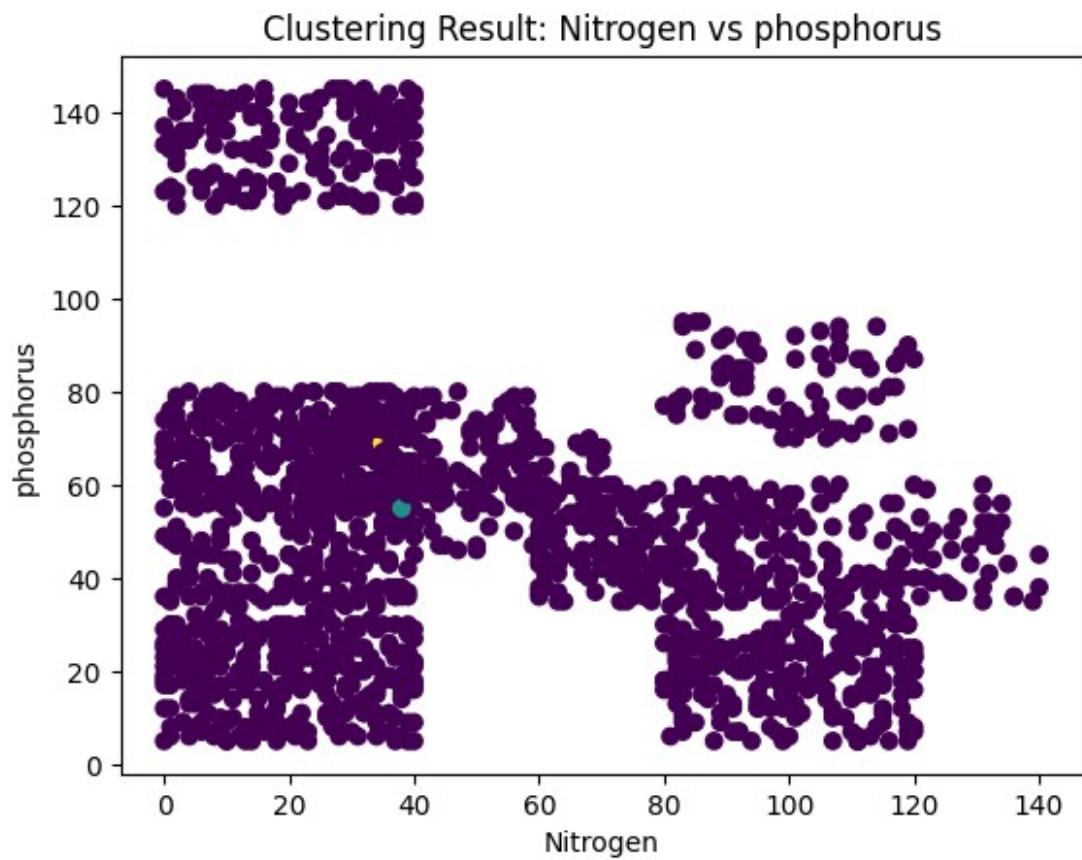
```

```

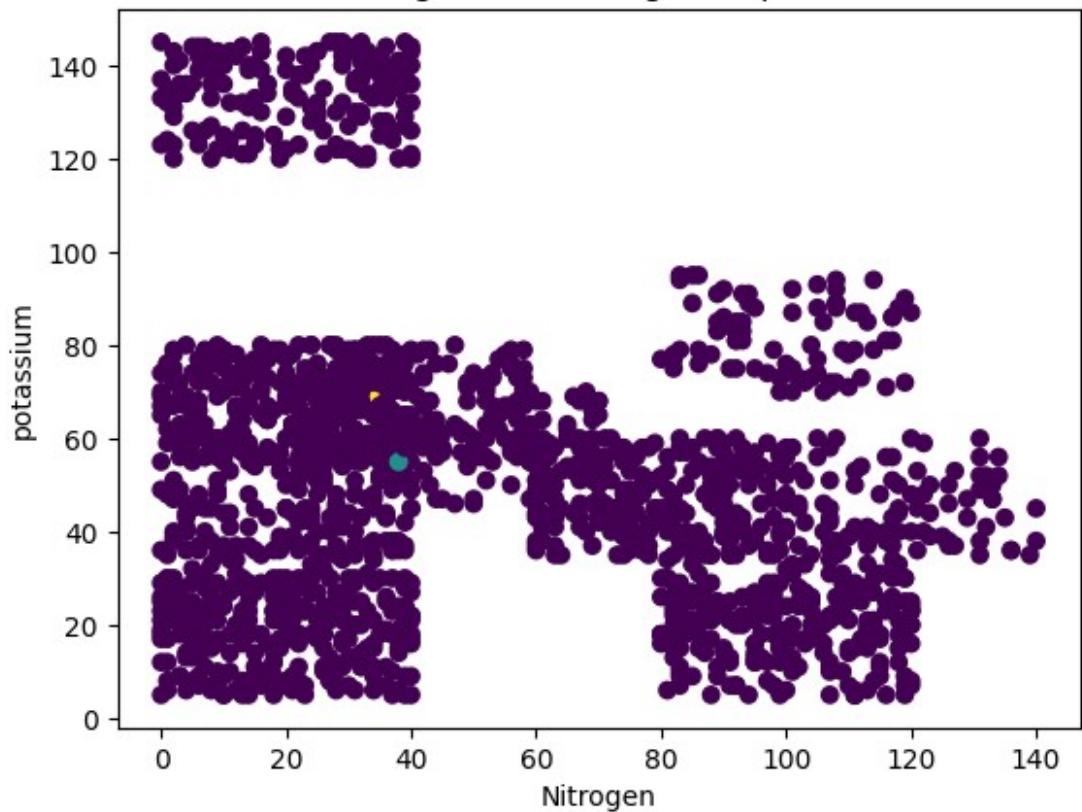
c=train_cluster_labels, cmap='viridis')
    plt.xlabel(features[i])
    plt.ylabel(features[j])
    plt.title(f'Clustering Result: {features[i]} vs
{features[j]}')
    plt.show()

# Print evaluation metrics
print("Silhouette Score:", silhouette_avg)
print("Adjusted Rand Index:", ari)
print("Homogeneity:", homogeneity)
print("Completeness:", completeness)
print("V-measure:", v_measure)

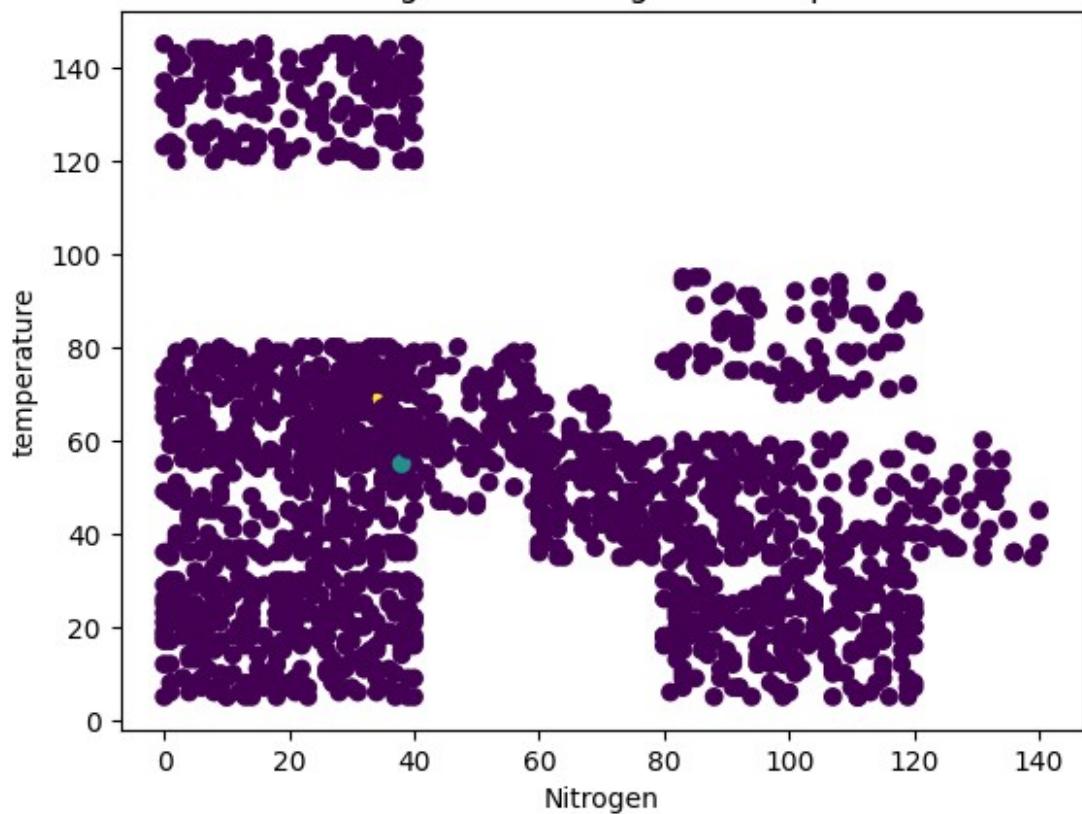
```



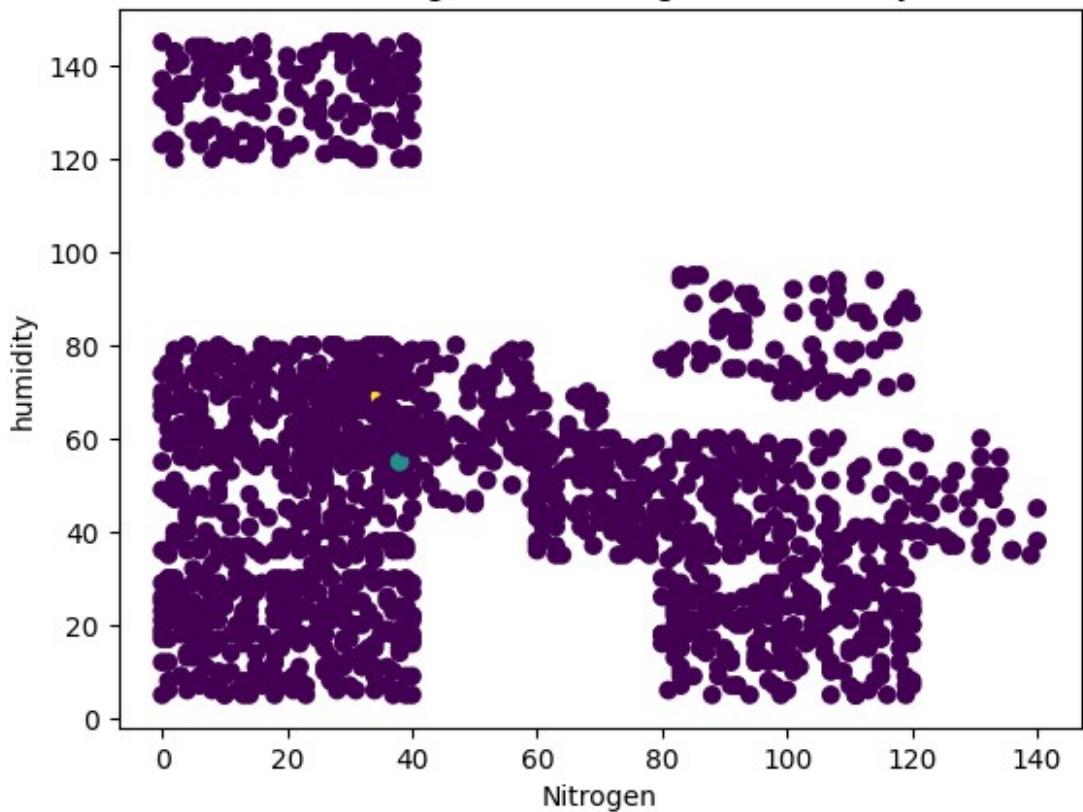
Clustering Result: Nitrogen vs potassium



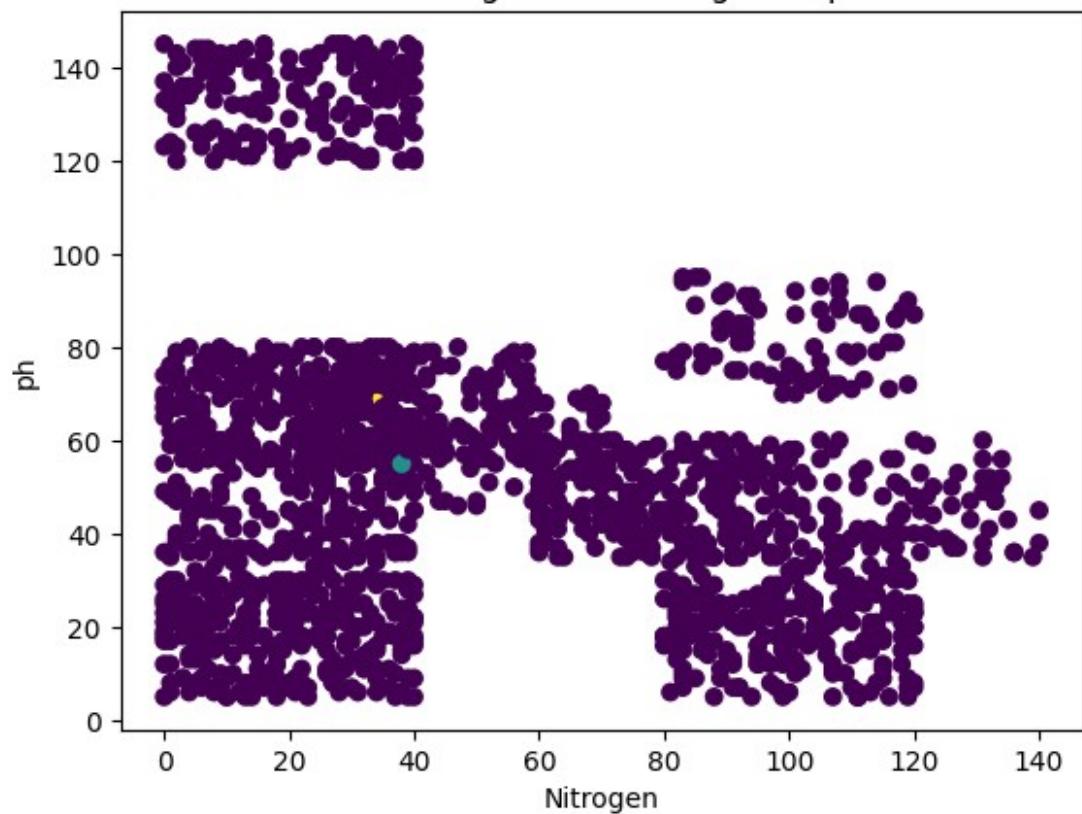
Clustering Result: Nitrogen vs temperature



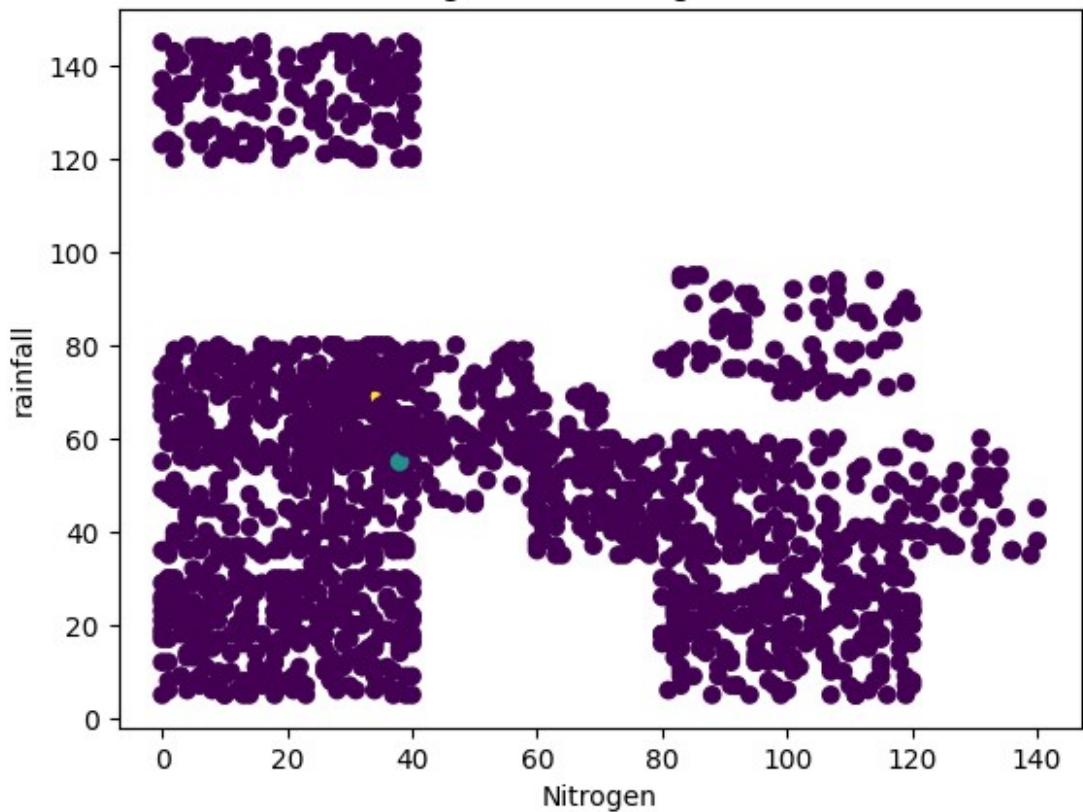
Clustering Result: Nitrogen vs humidity



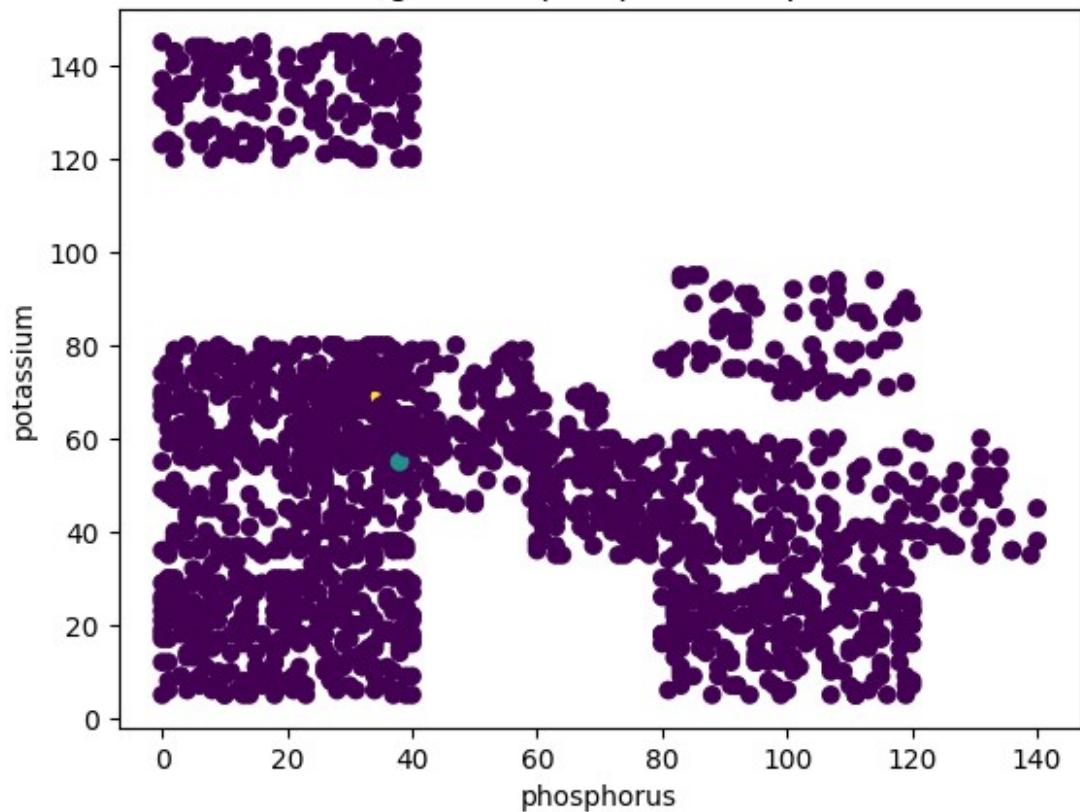
Clustering Result: Nitrogen vs ph



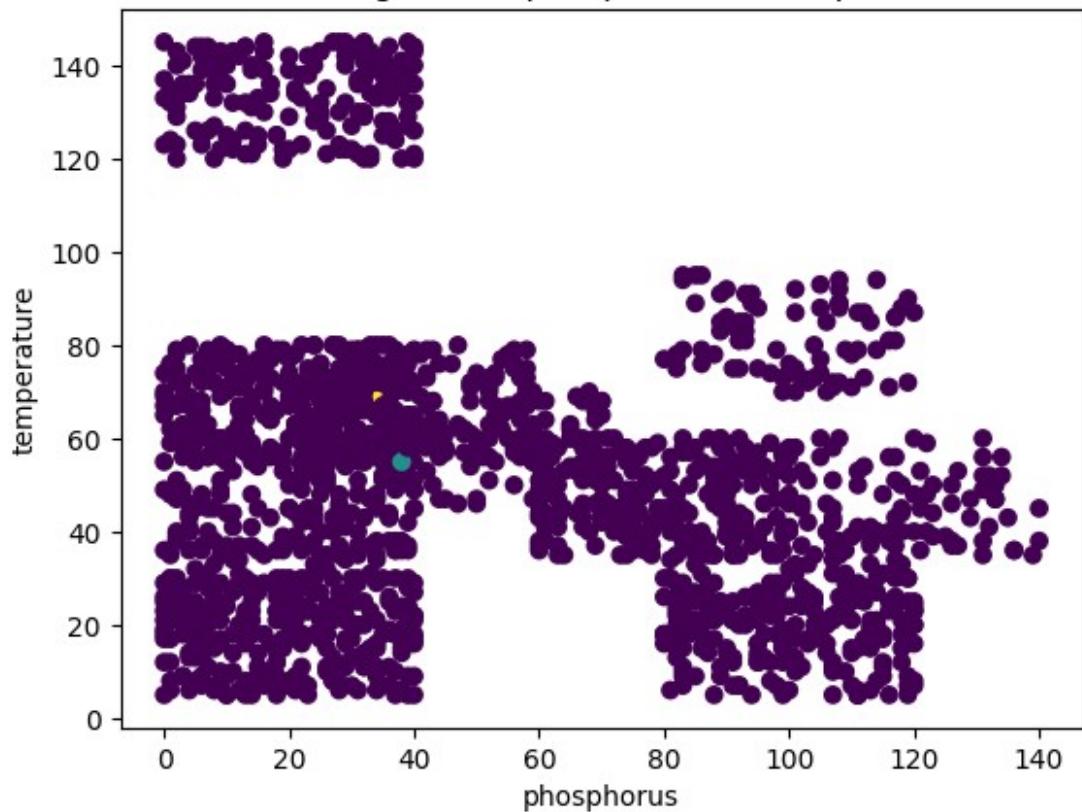
Clustering Result: Nitrogen vs rainfall



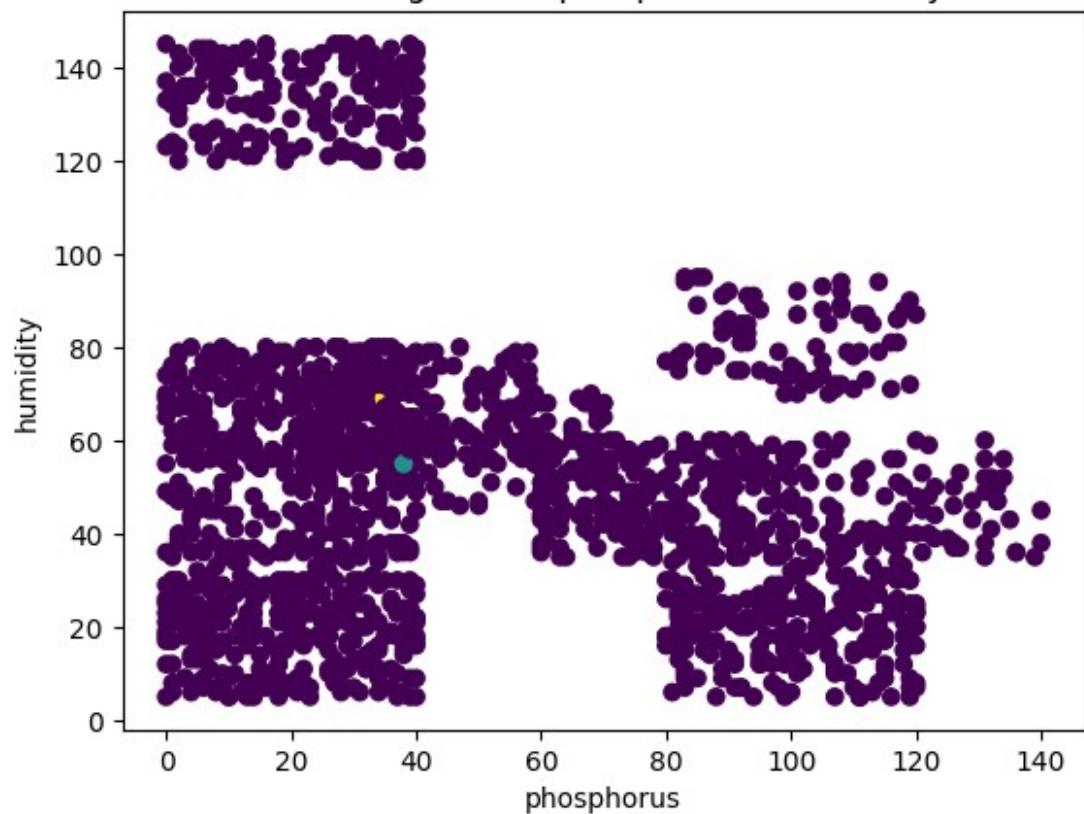
Clustering Result: phosphorus vs potassium



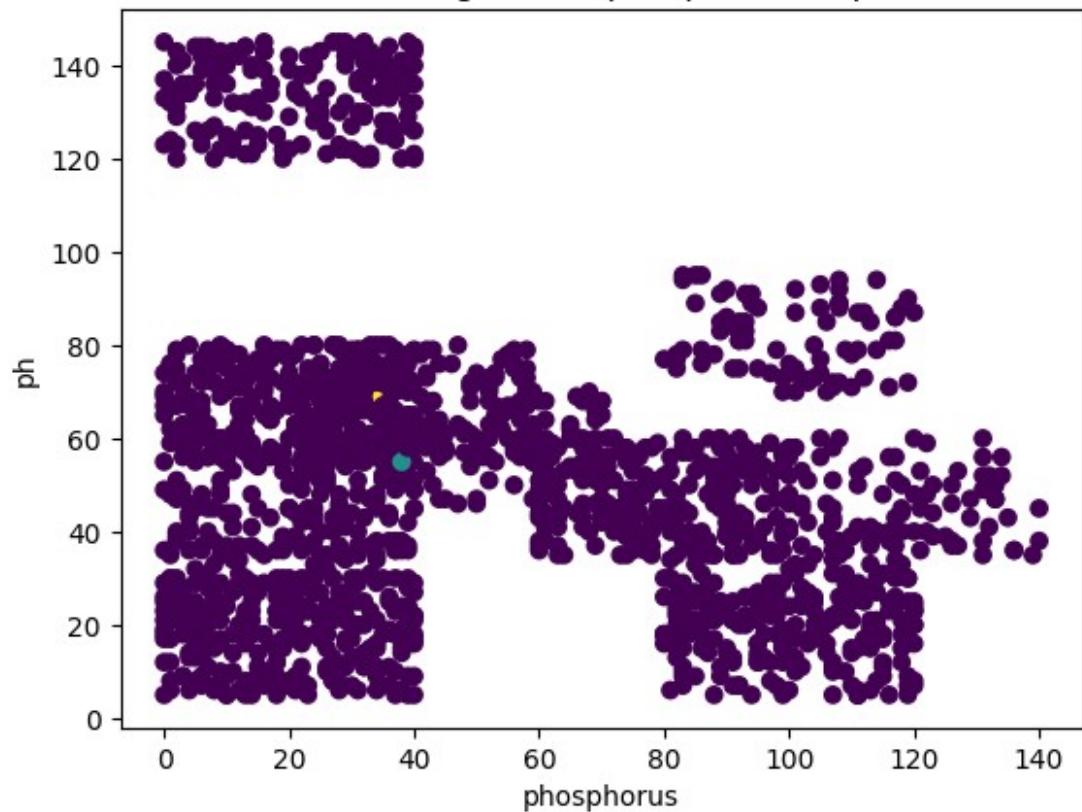
Clustering Result: phosphorus vs temperature



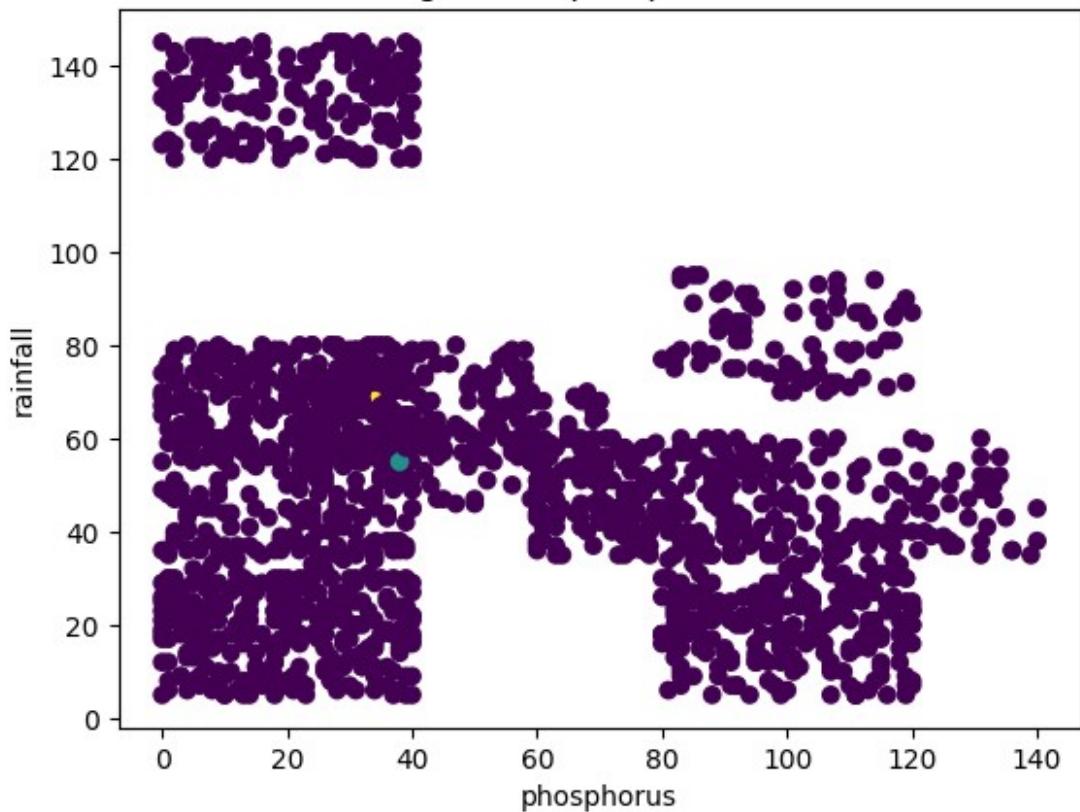
Clustering Result: phosphorus vs humidity



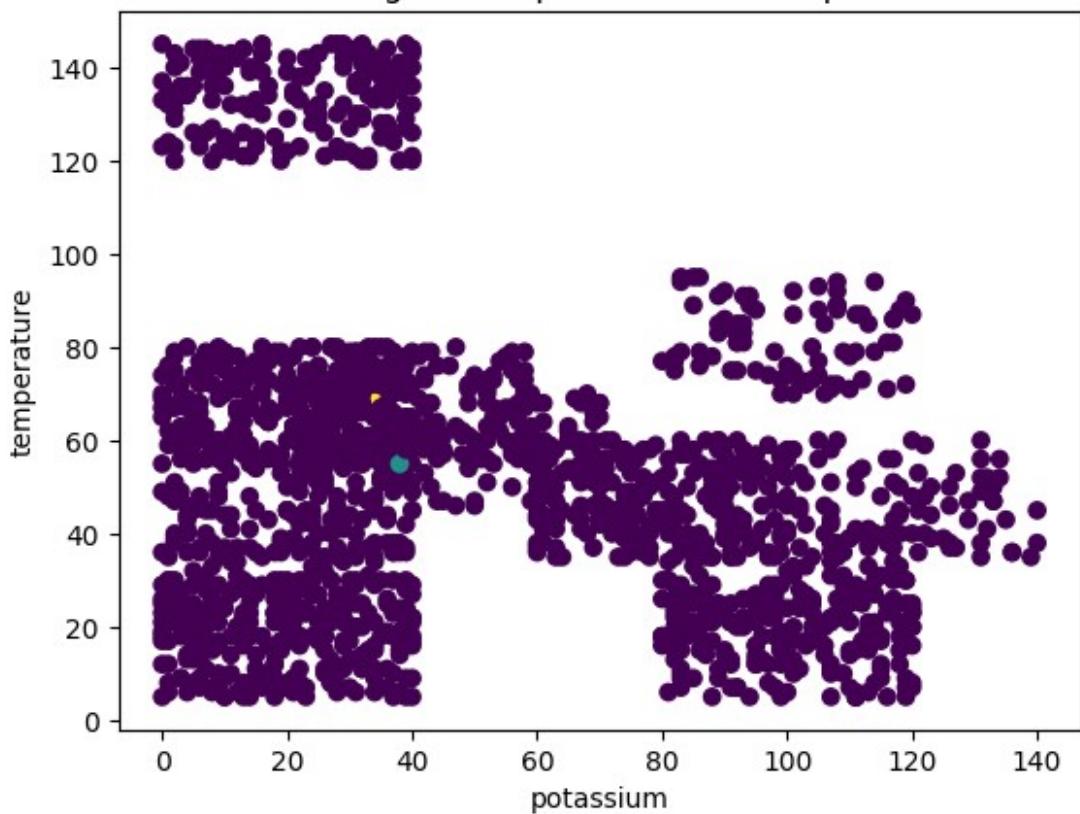
Clustering Result: phosphorus vs ph



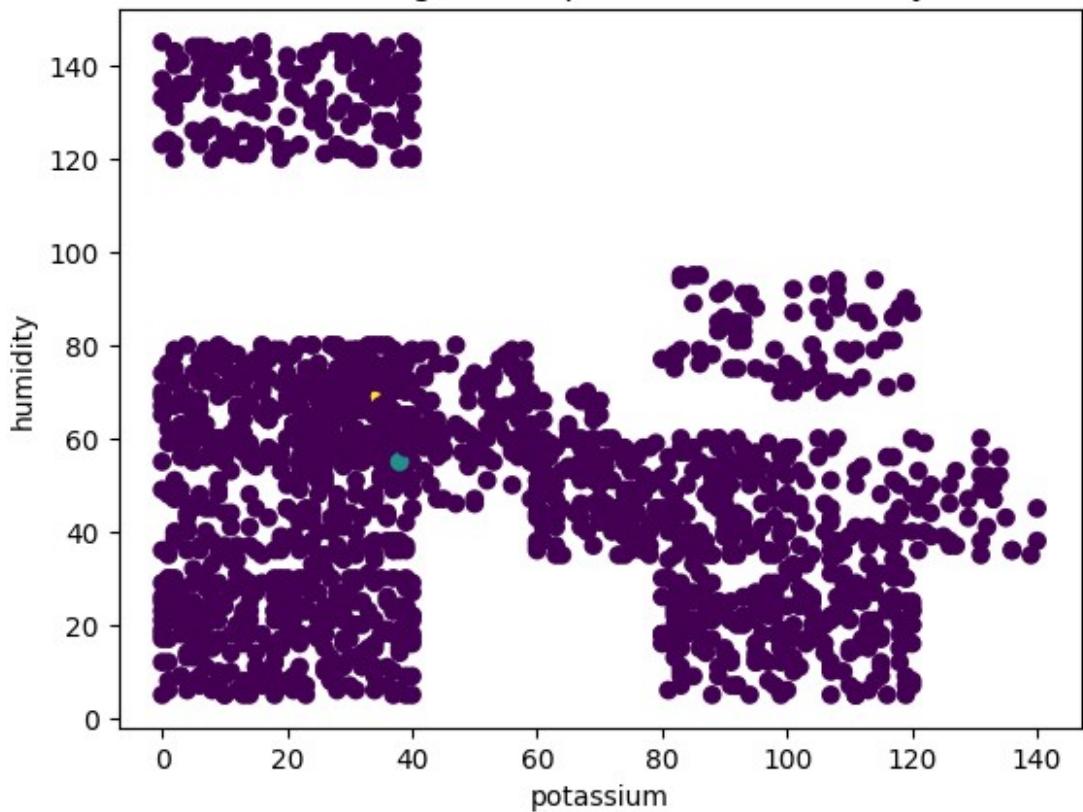
Clustering Result: phosphorus vs rainfall



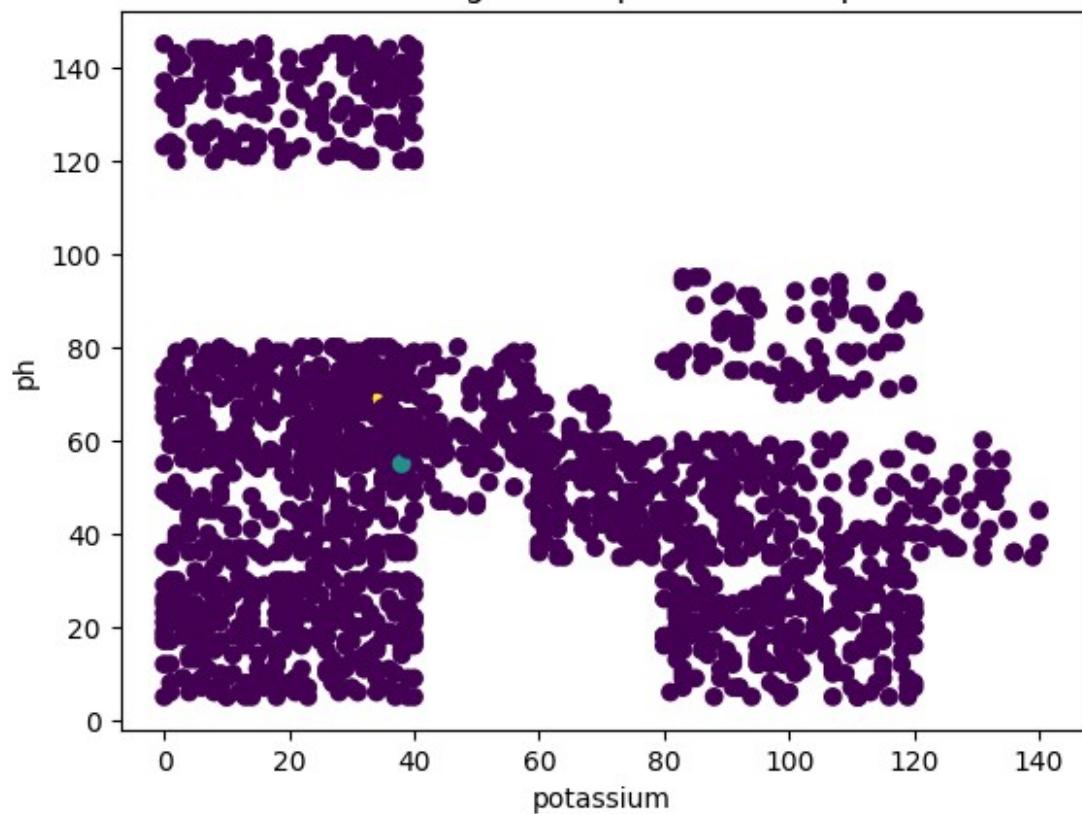
Clustering Result: potassium vs temperature



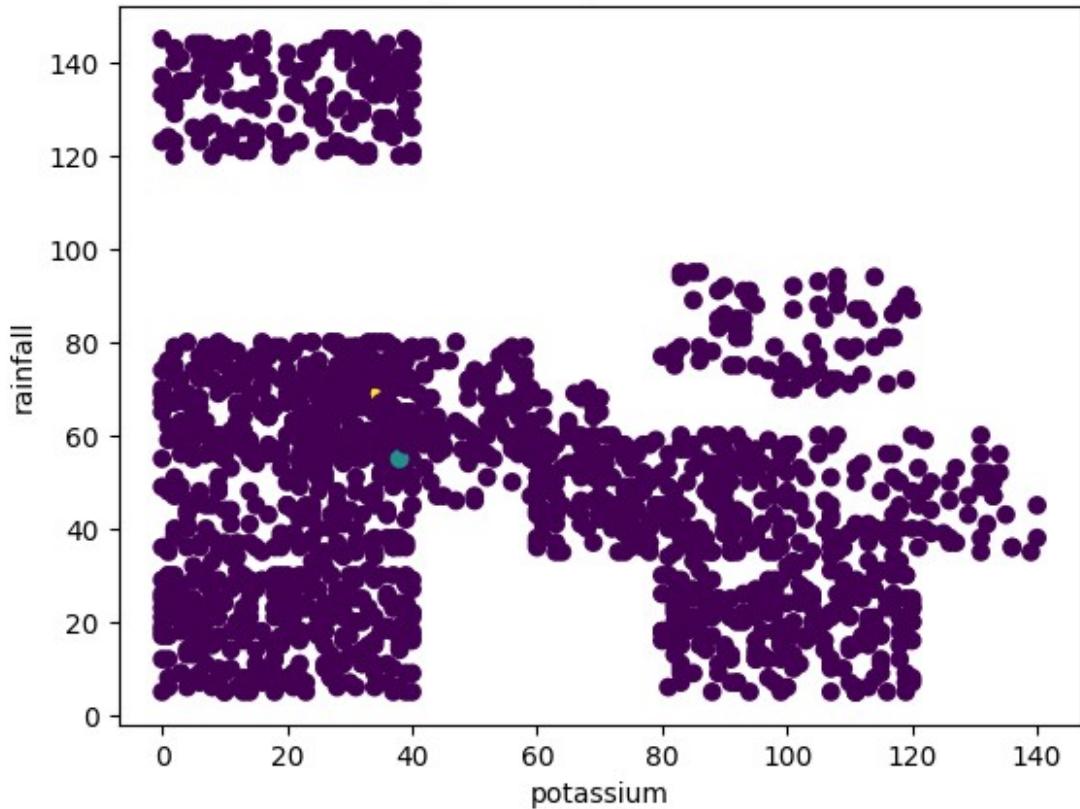
Clustering Result: potassium vs humidity



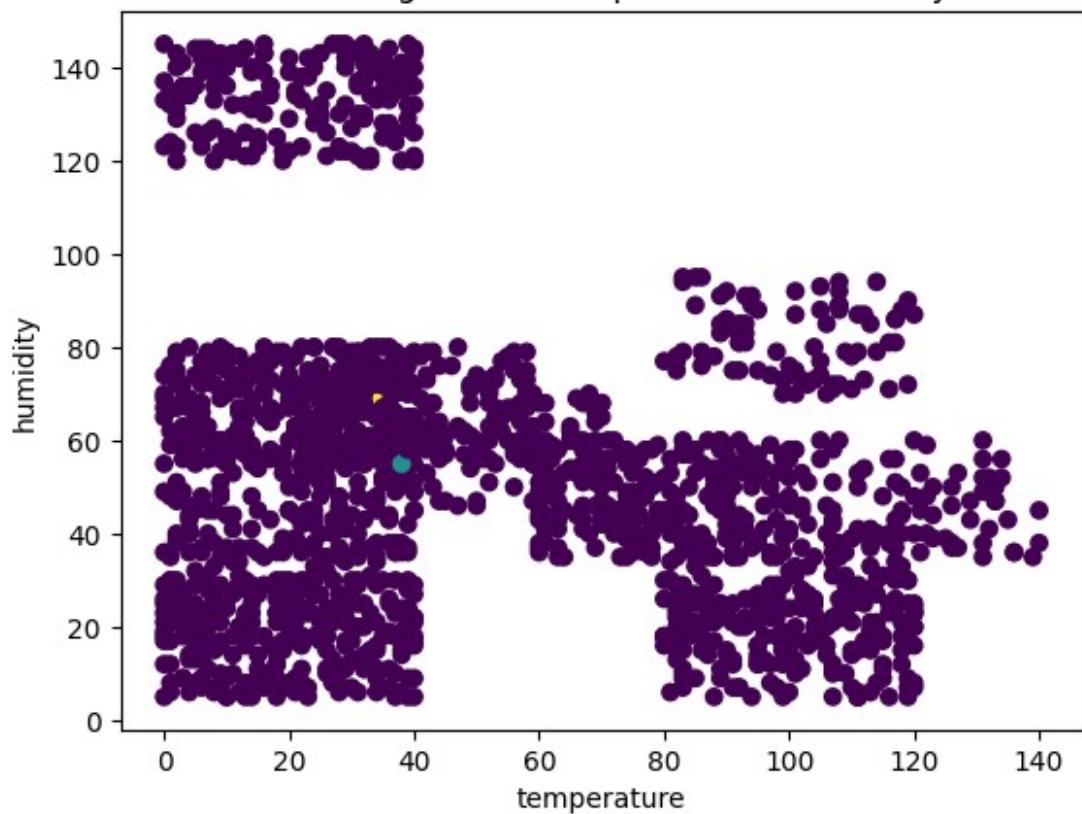
Clustering Result: potassium vs ph



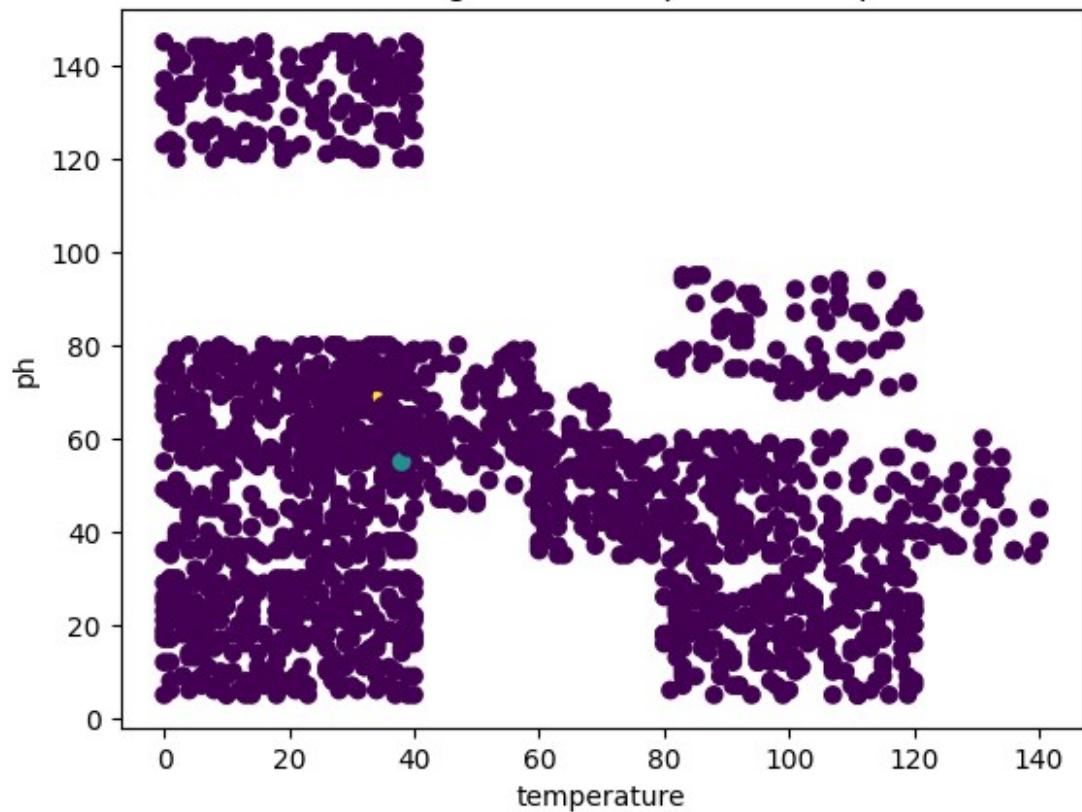
Clustering Result: potassium vs rainfall



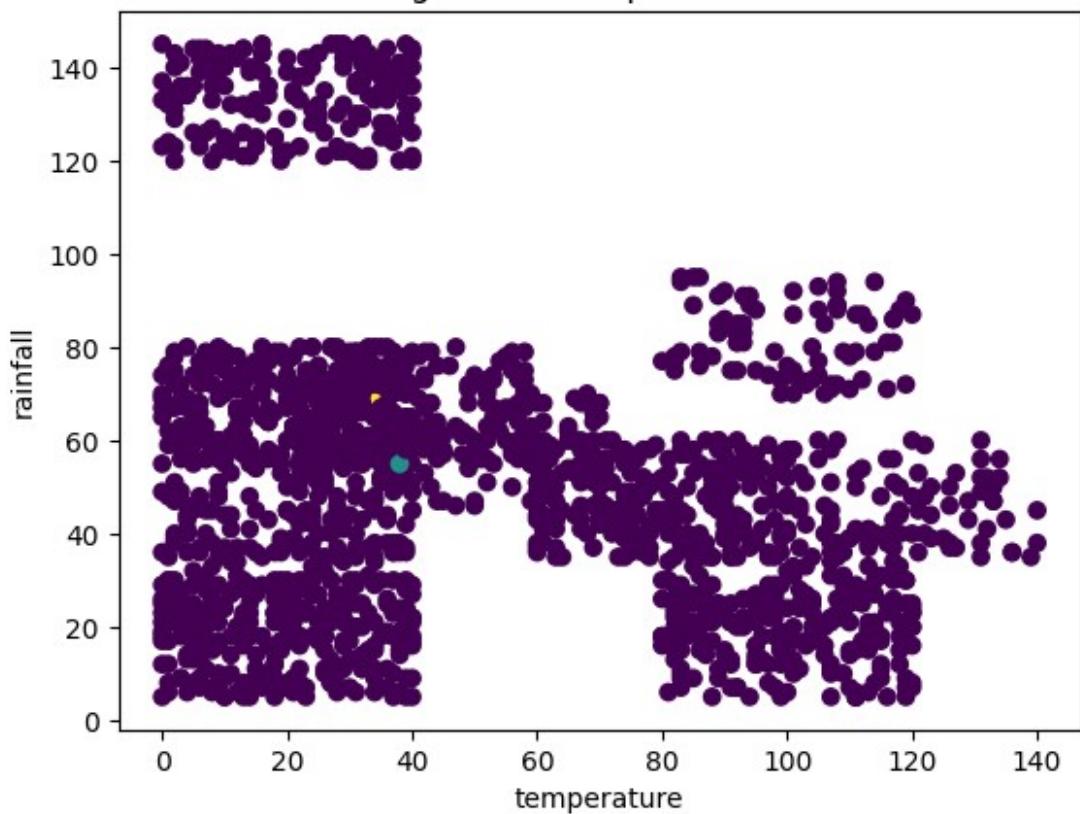
Clustering Result: temperature vs humidity



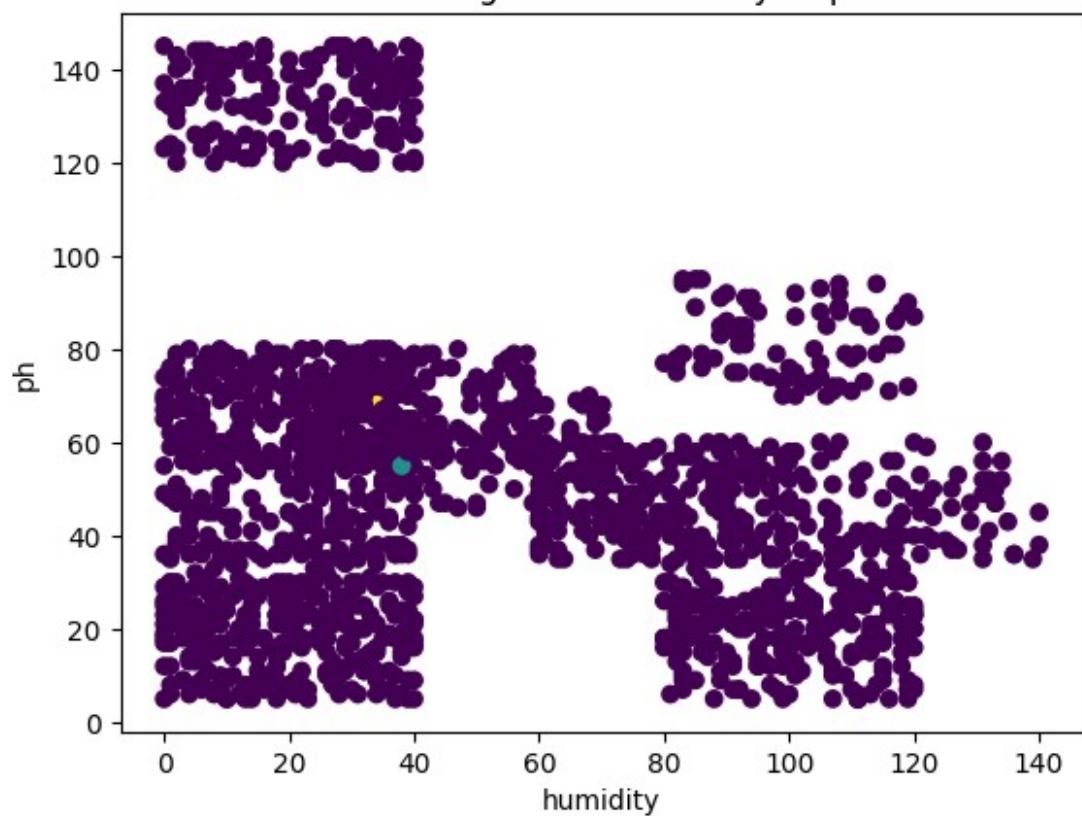
Clustering Result: temperature vs ph



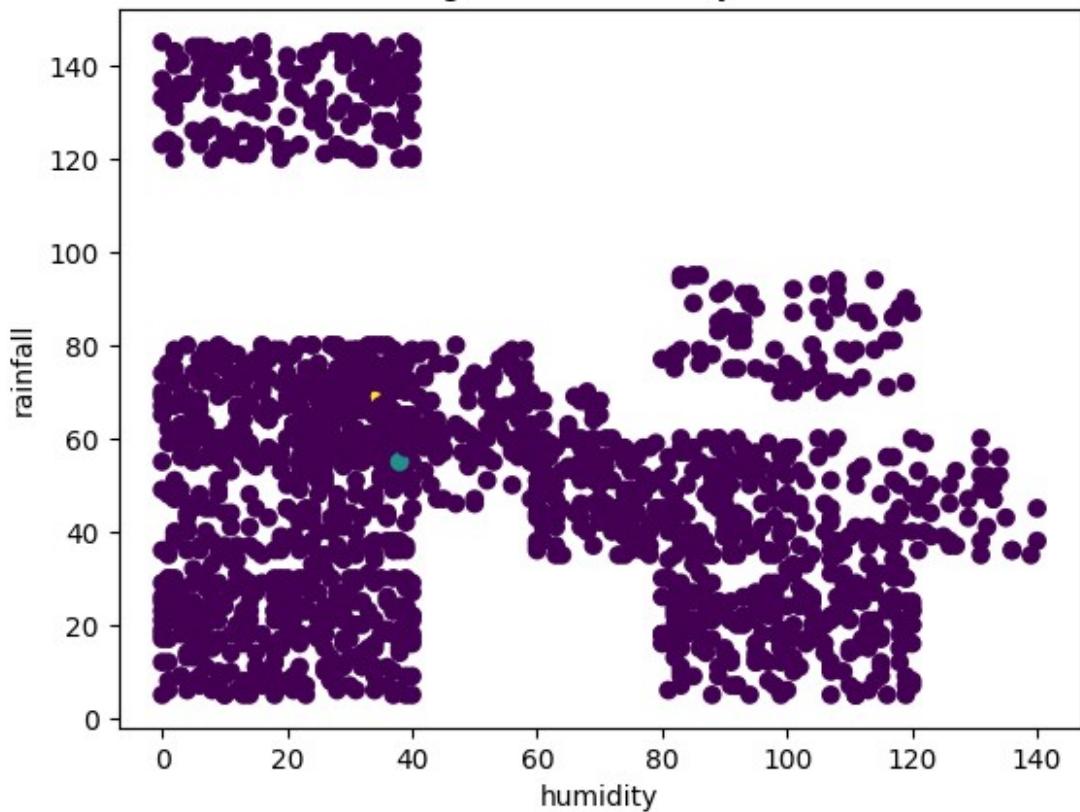
Clustering Result: temperature vs rainfall



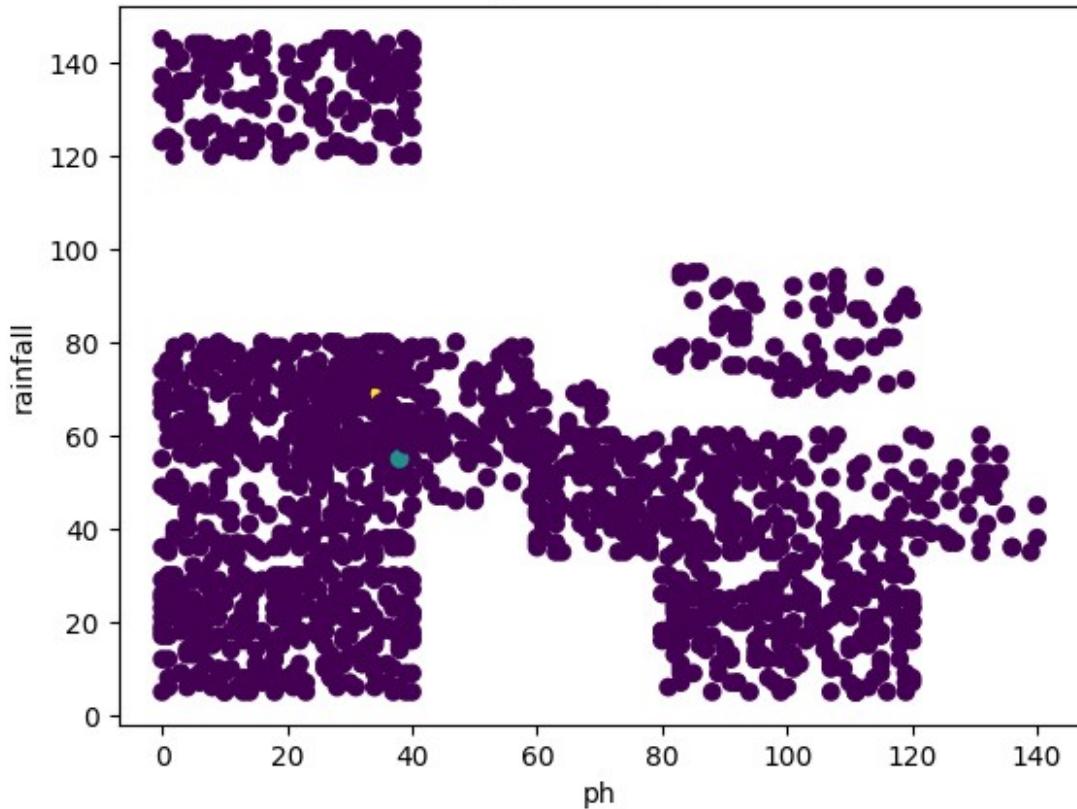
Clustering Result: humidity vs ph



Clustering Result: humidity vs rainfall



Clustering Result: ph vs rainfall



Silhouette Score: -0.270589272008577  
Adjusted Rand Index: 8.585910623203282e-06  
Homogeneity: 0.001153041174756407  
Completeness: 0.3700462454109585  
V-measure: 0.002298919060149236

#### #GaussianMixture

```
# Get the predicted cluster labels for the training data
train_cluster_labels = gmm.predict(X_train)

# Compute evaluation metrics
silhouette_avg = silhouette_score(X_train, train_cluster_labels)
ari = adjusted_rand_score(target, train_cluster_labels)
homogeneity, completeness, v_measure =
homogeneity_completeness_v_measure(target, train_cluster_labels)

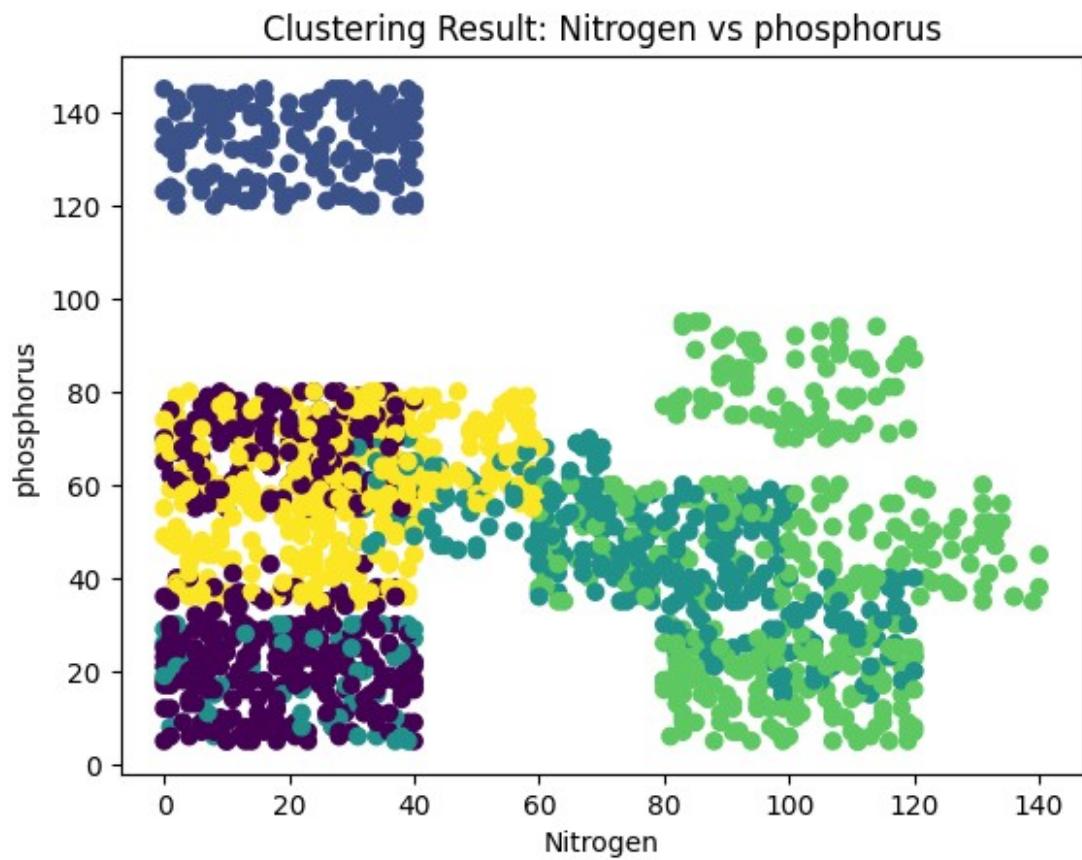
# Create scatter plots for different feature combinations
features = ['Nitrogen', 'phosphorus', 'potassium', 'temperature',
'humidity', 'ph', 'rainfall']
for i in range(len(features)):
    for j in range(i+1, len(features)):
        plt.scatter(X_train[:, 0], X_train[:, 1],
```

```

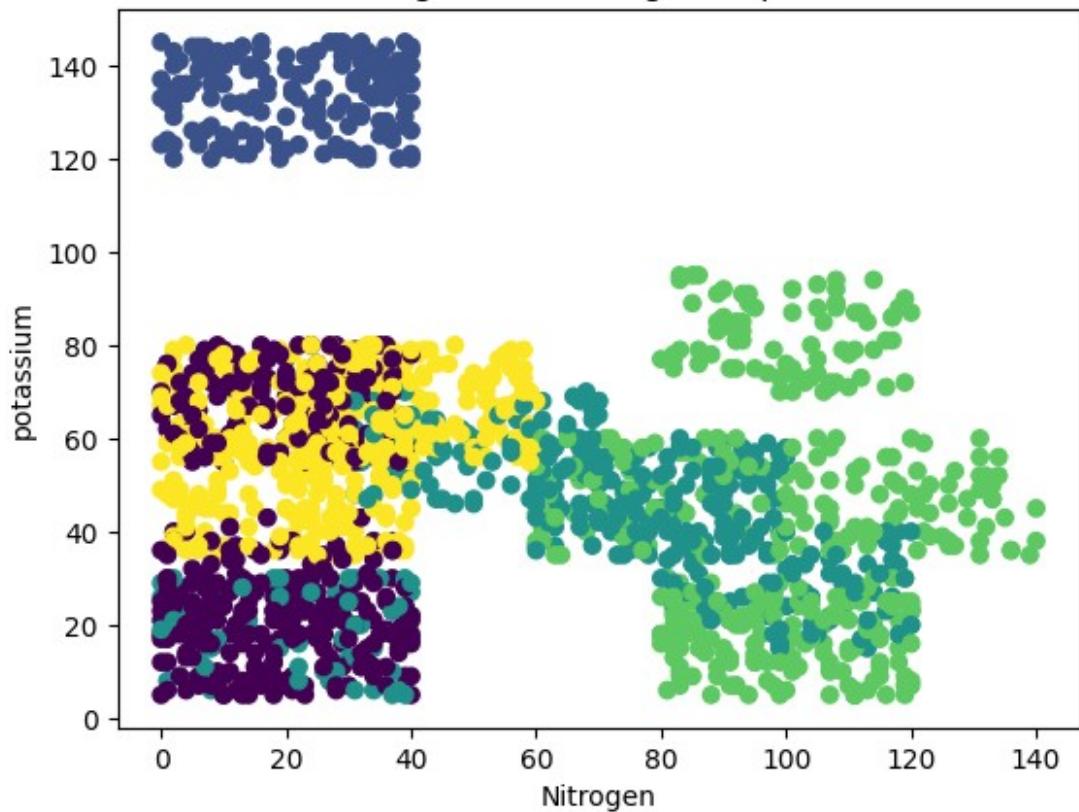
c=train_cluster_labels, cmap='viridis')
    plt.xlabel(features[i])
    plt.ylabel(features[j])
    plt.title(f'Clustering Result: {features[i]} vs
{features[j]}')
    plt.show()

# Print evaluation metrics
print("Silhouette Score:", silhouette_avg)
print("Adjusted Rand Index:", ari)
print("Homogeneity:", homogeneity)
print("Completeness:", completeness)
print("V-measure:", v_measure)

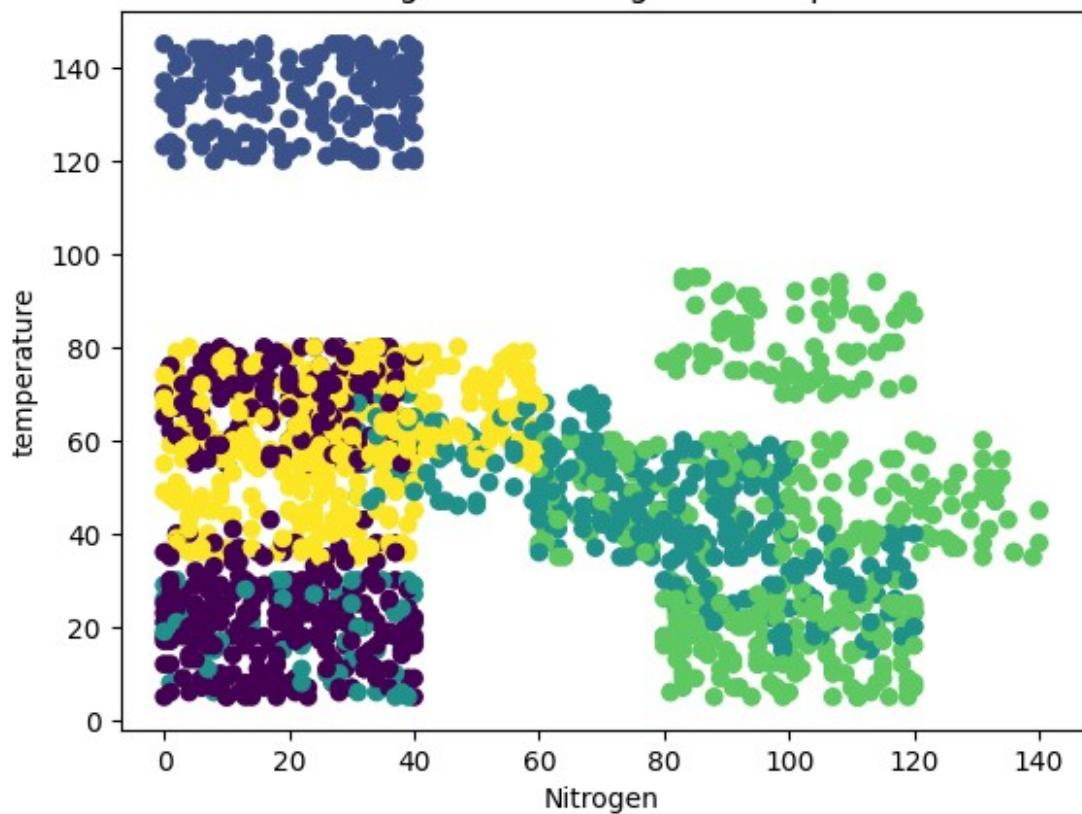
```



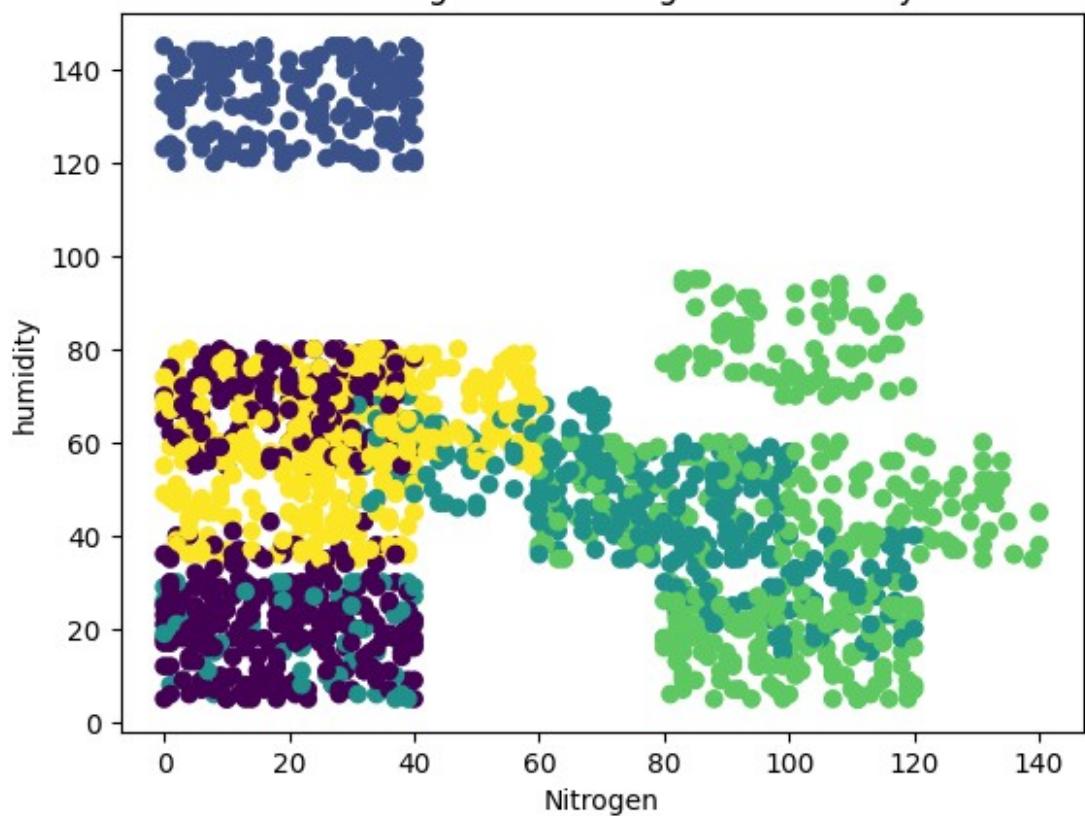
Clustering Result: Nitrogen vs potassium



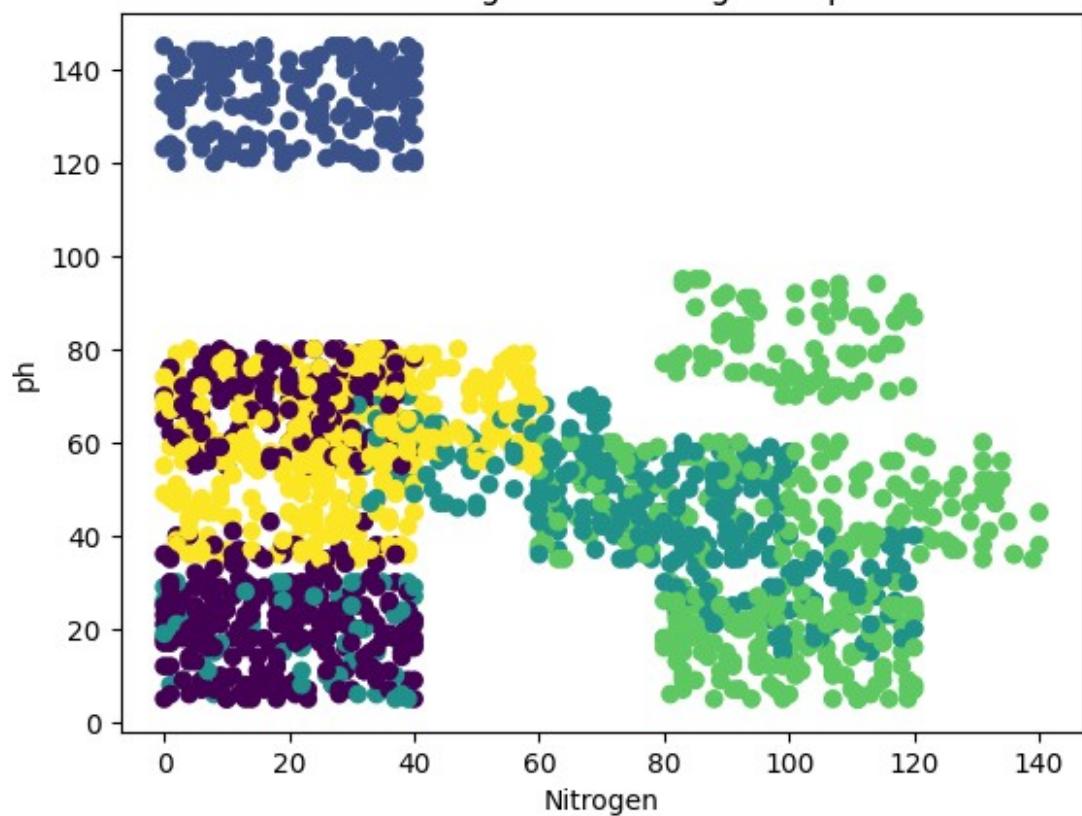
Clustering Result: Nitrogen vs temperature



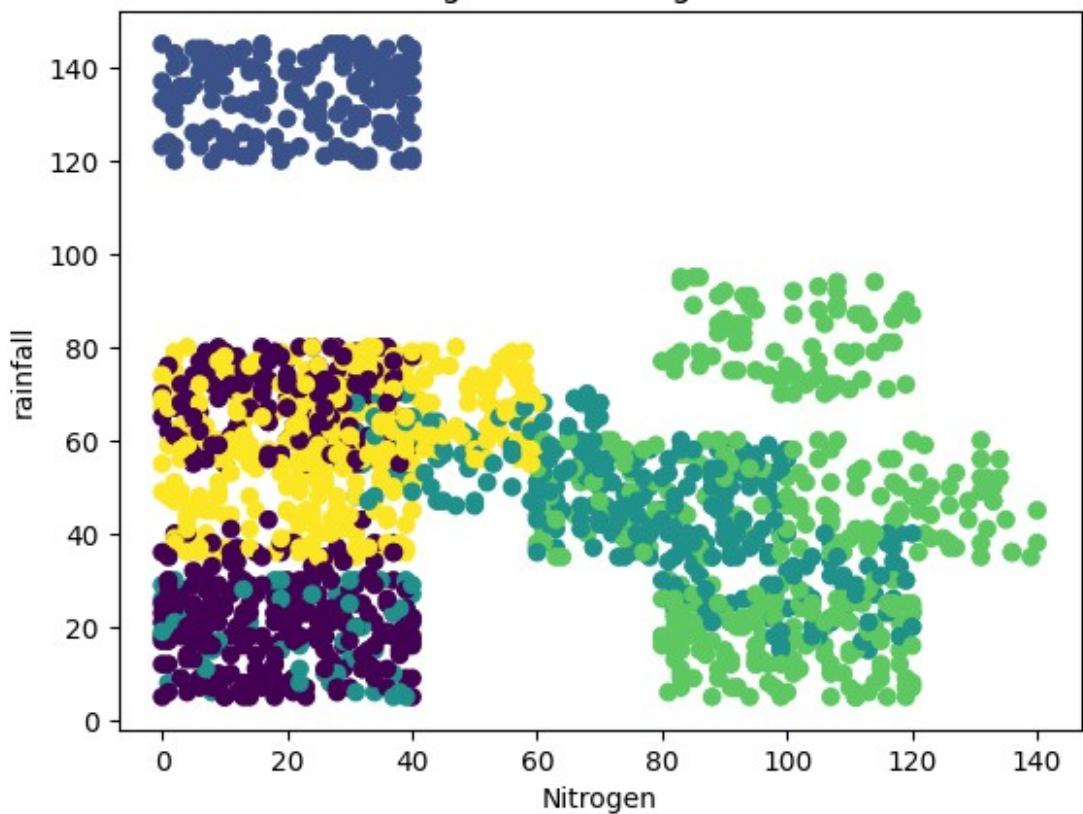
Clustering Result: Nitrogen vs humidity



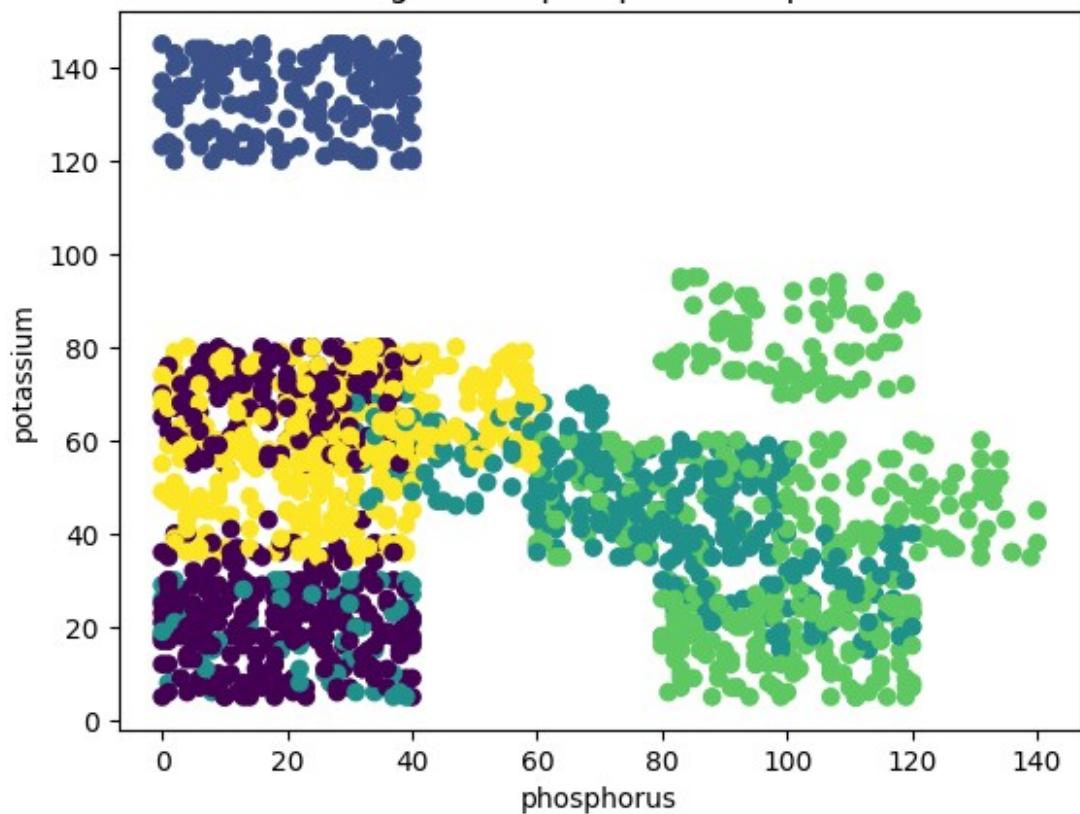
Clustering Result: Nitrogen vs ph



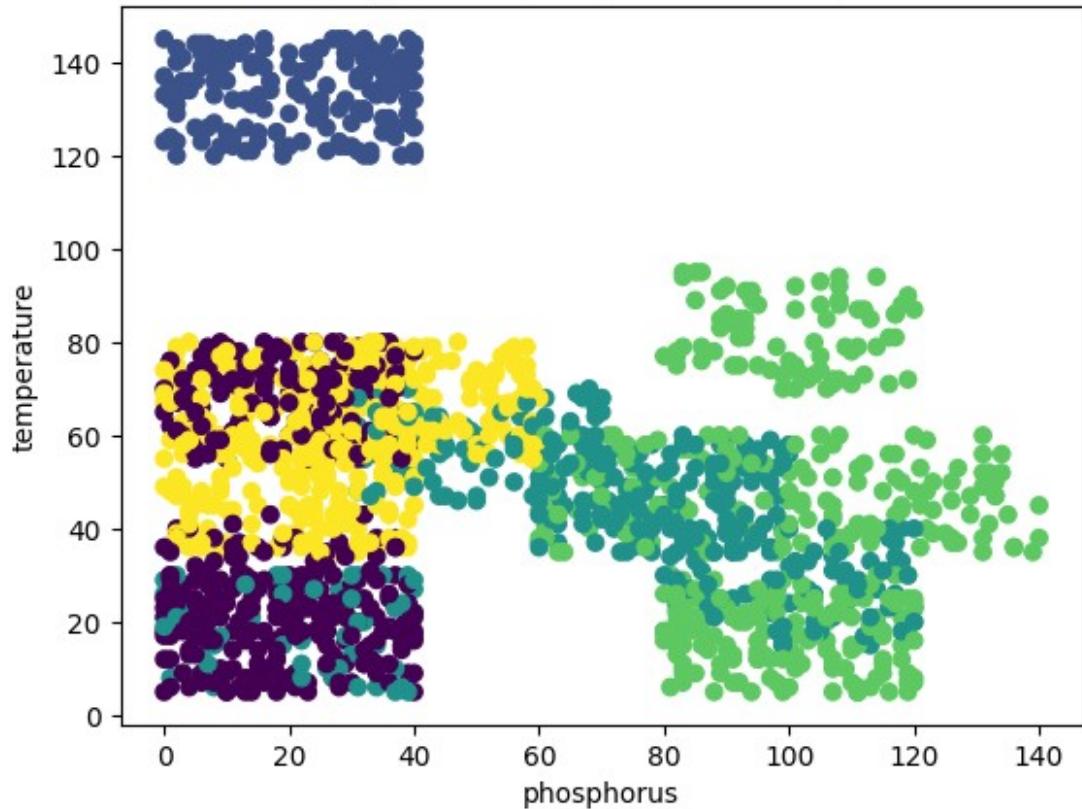
Clustering Result: Nitrogen vs rainfall



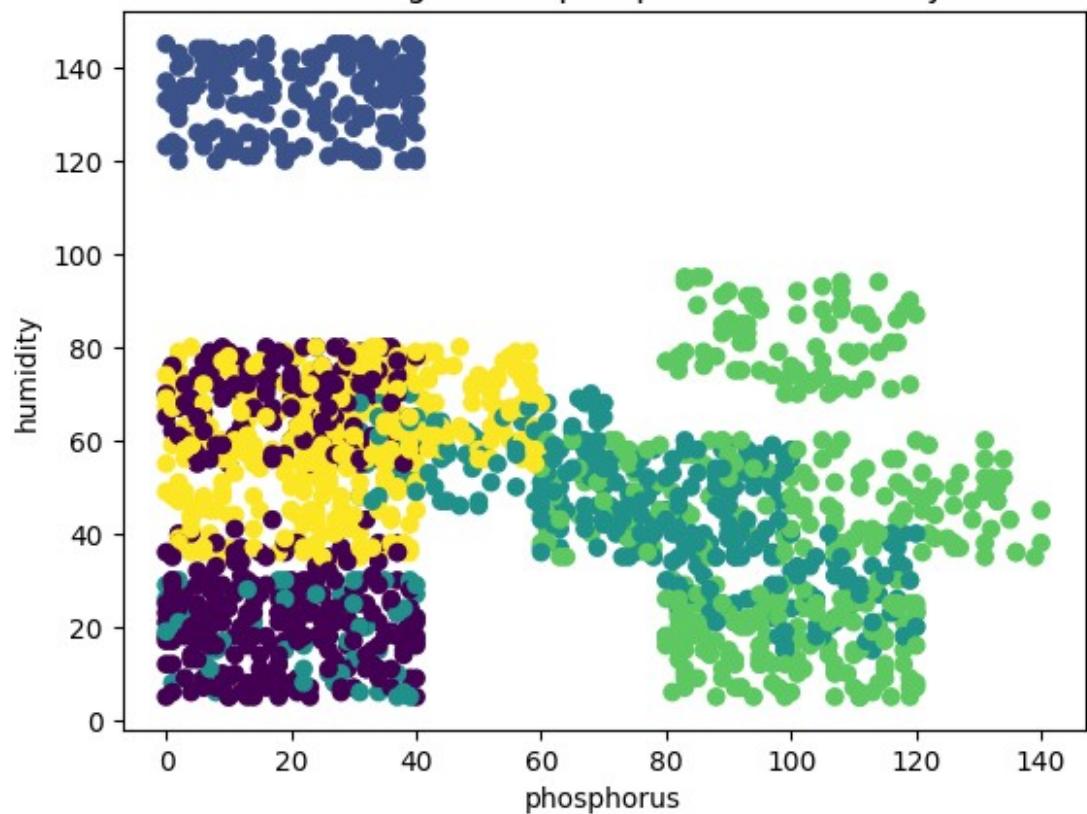
Clustering Result: phosphorus vs potassium



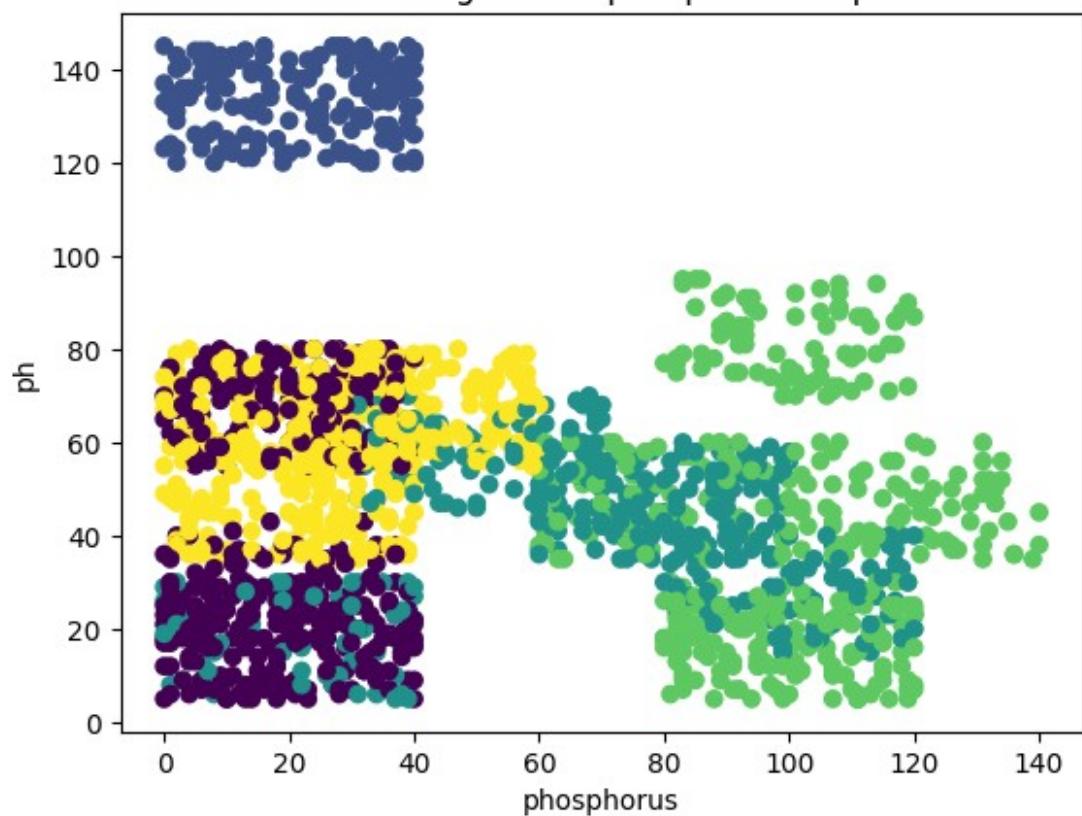
Clustering Result: phosphorus vs temperature



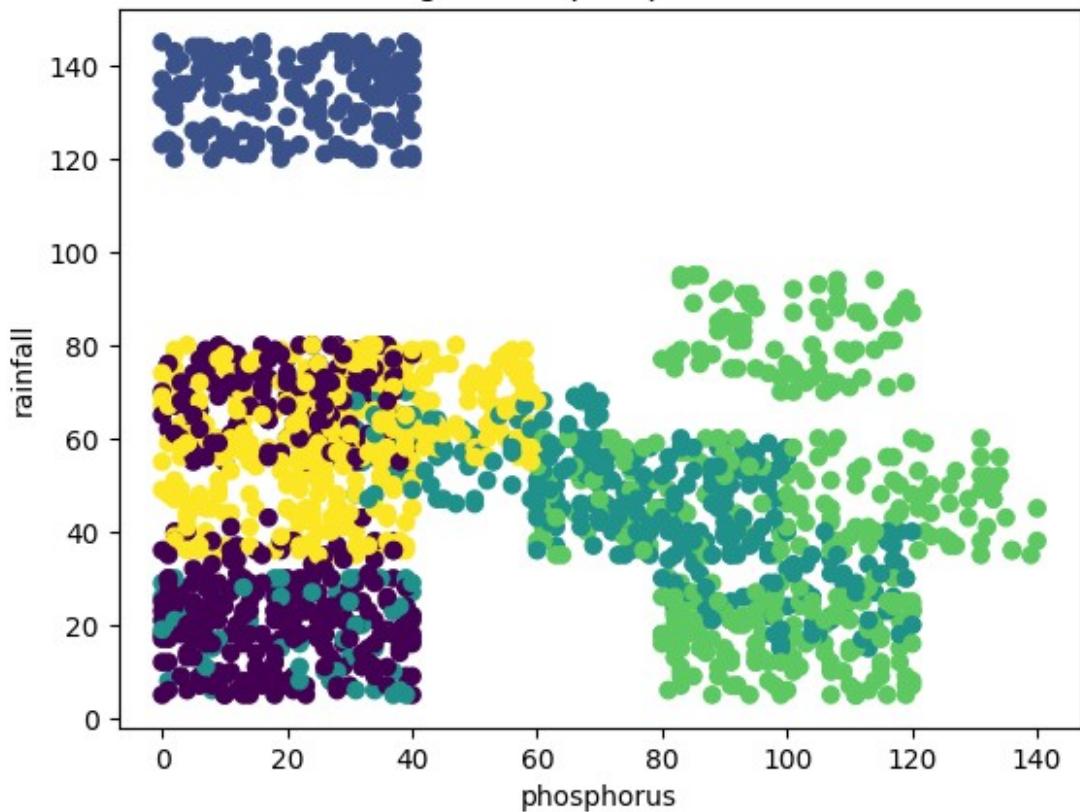
Clustering Result: phosphorus vs humidity



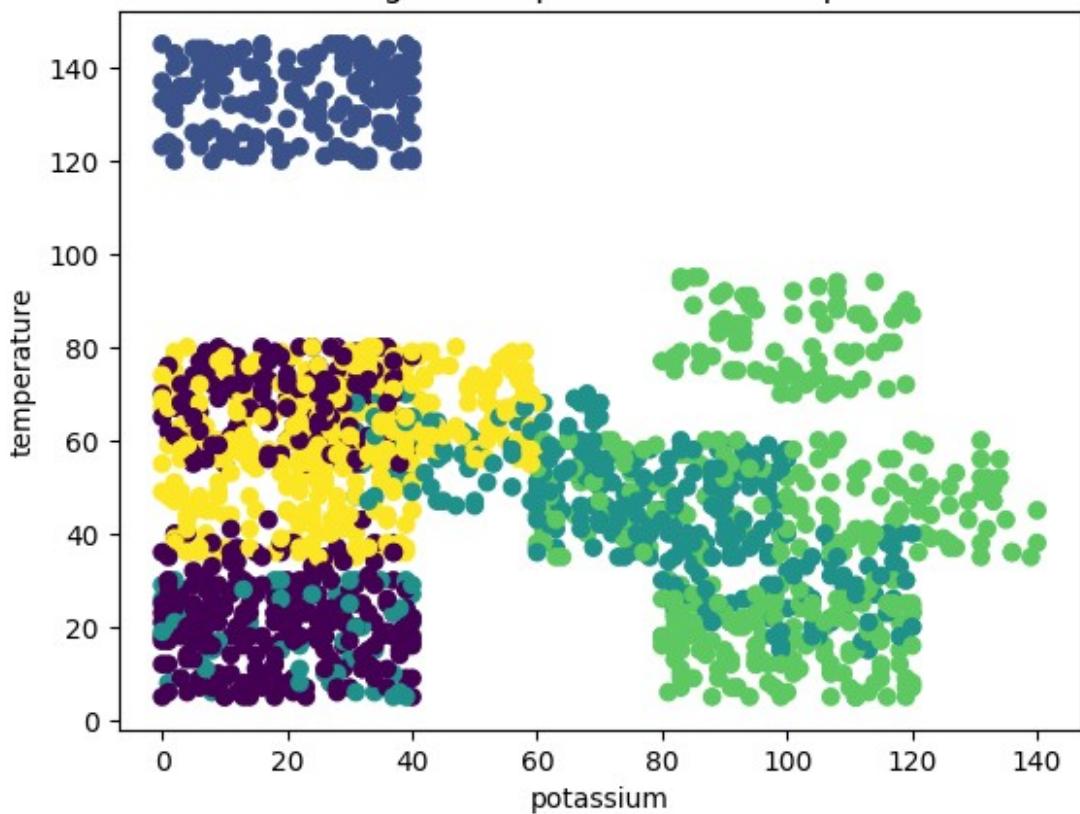
Clustering Result: phosphorus vs ph



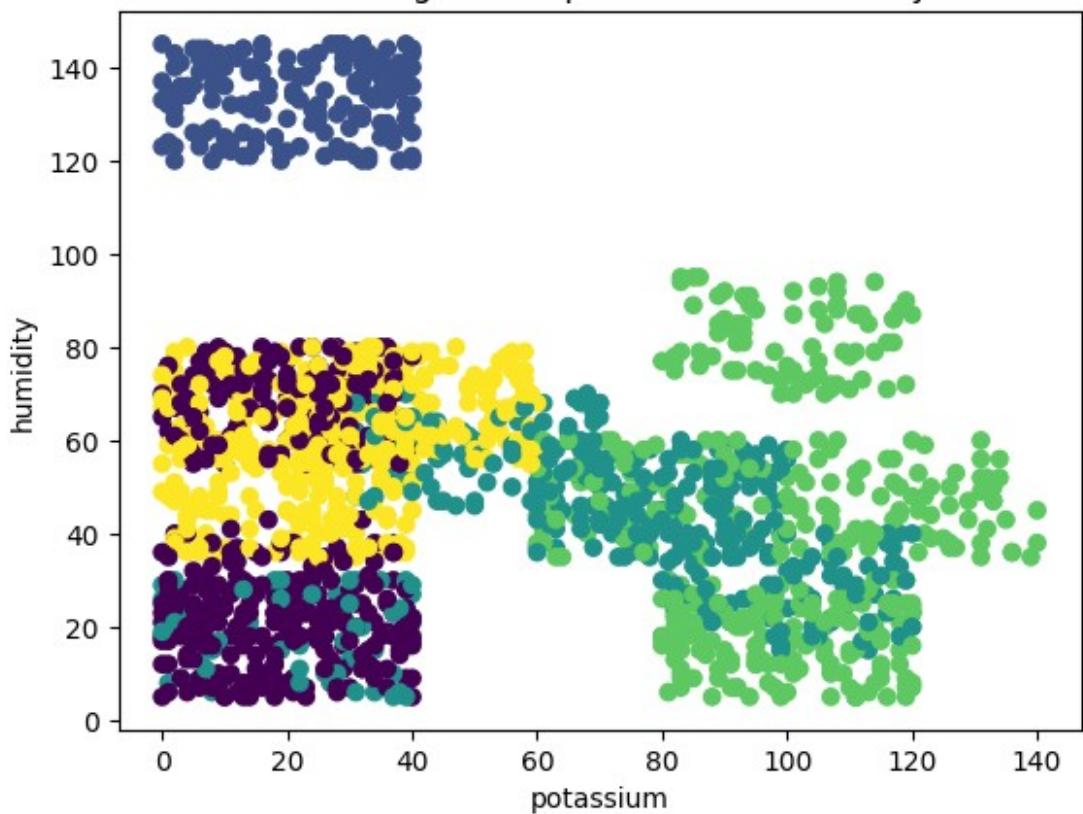
Clustering Result: phosphorus vs rainfall



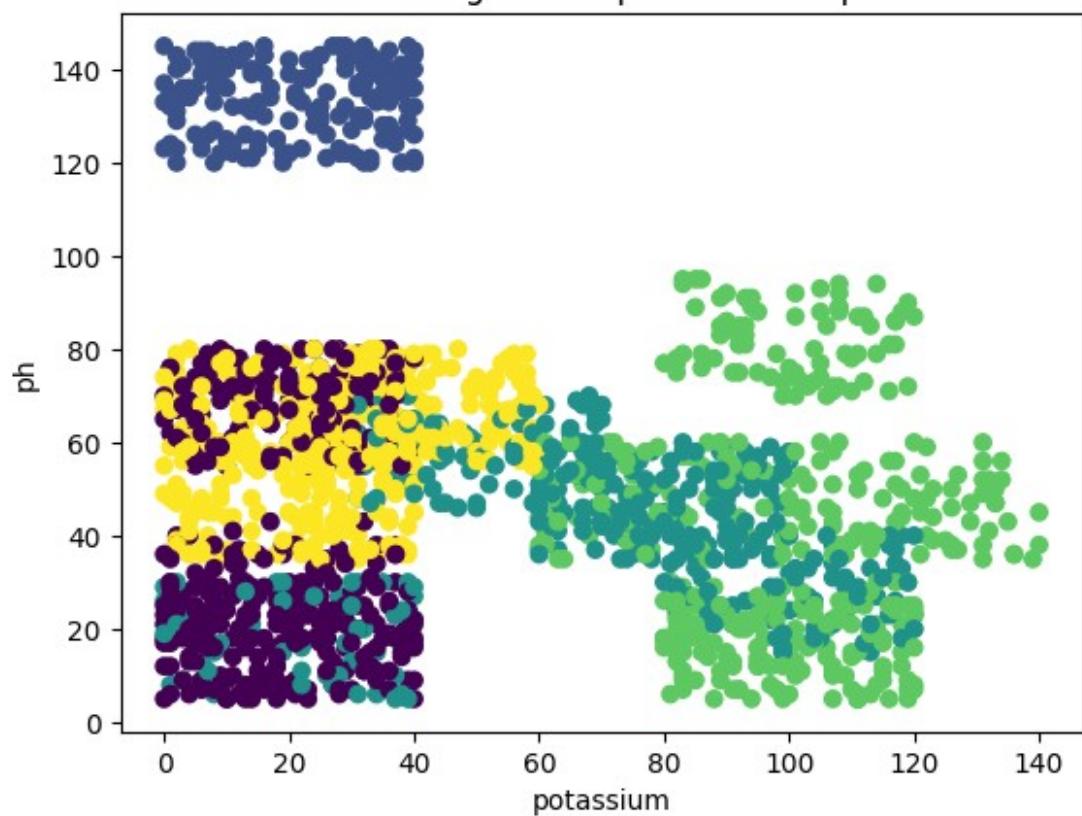
Clustering Result: potassium vs temperature



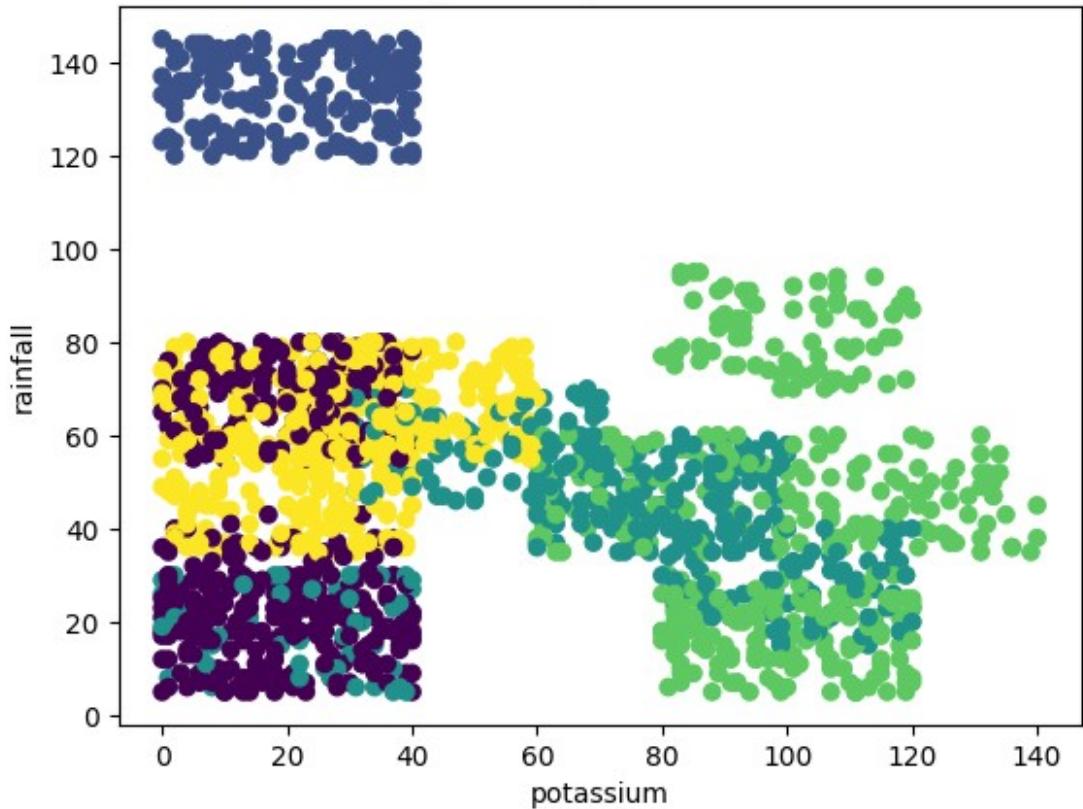
Clustering Result: potassium vs humidity



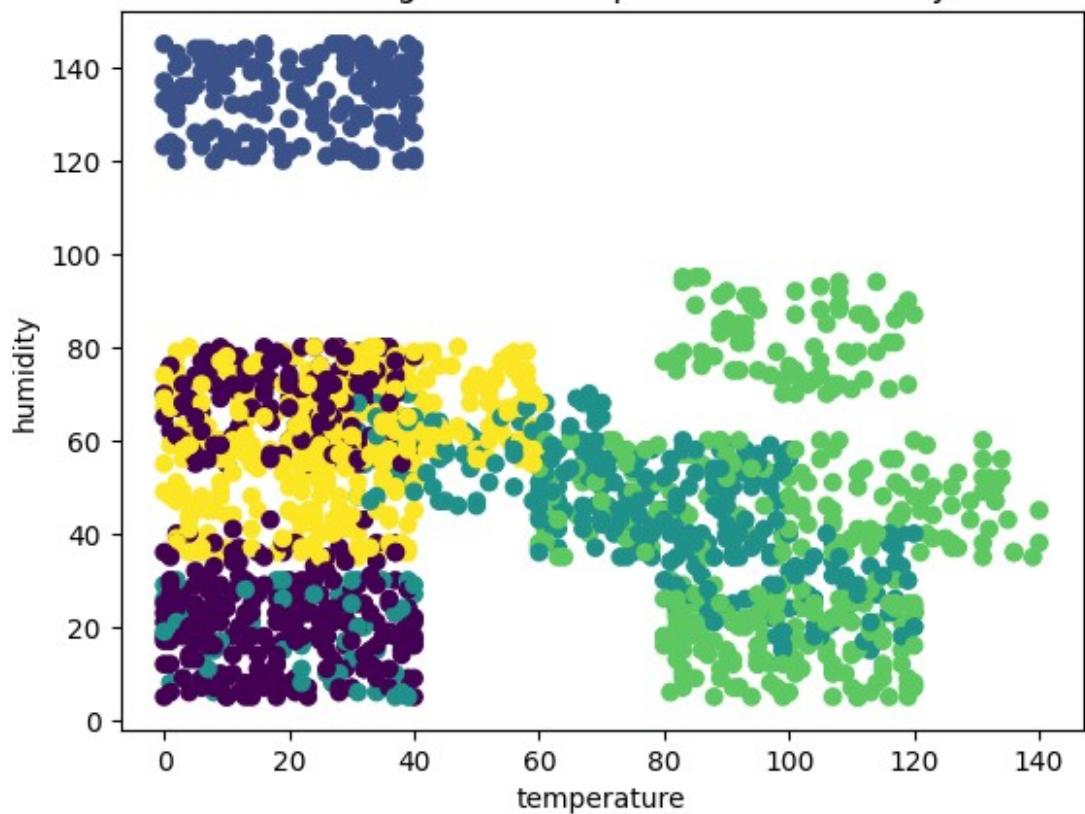
Clustering Result: potassium vs ph



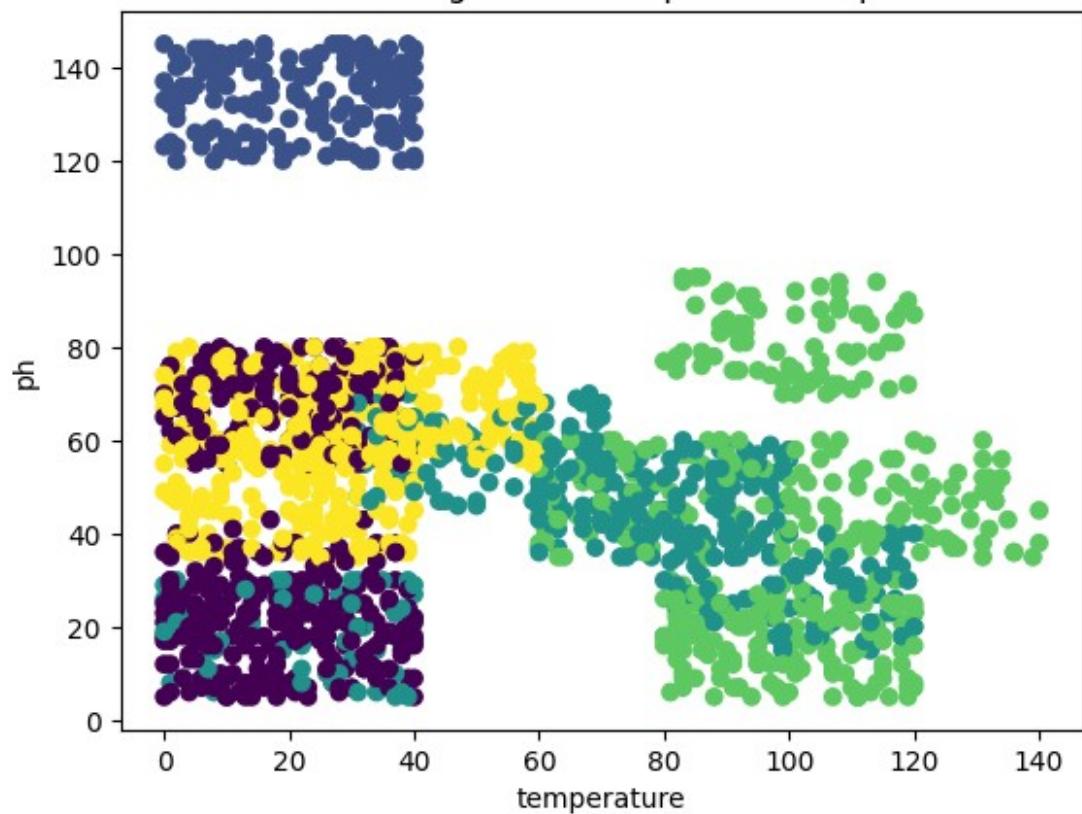
Clustering Result: potassium vs rainfall



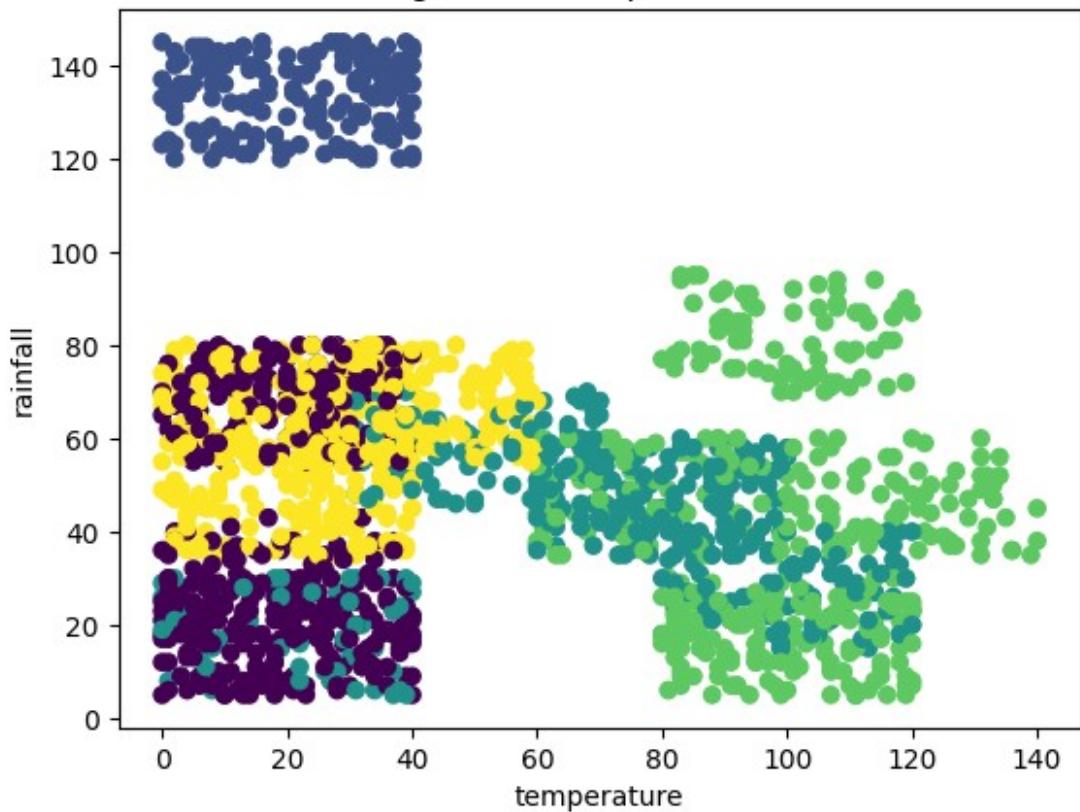
Clustering Result: temperature vs humidity



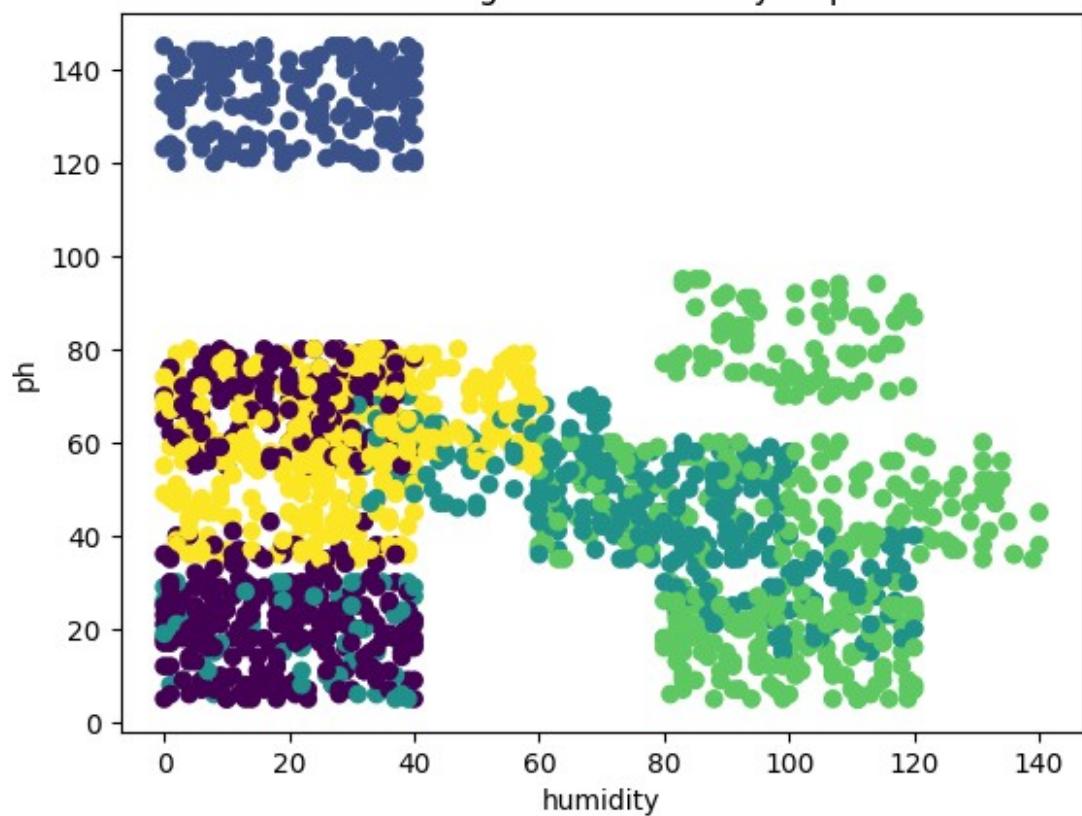
Clustering Result: temperature vs ph



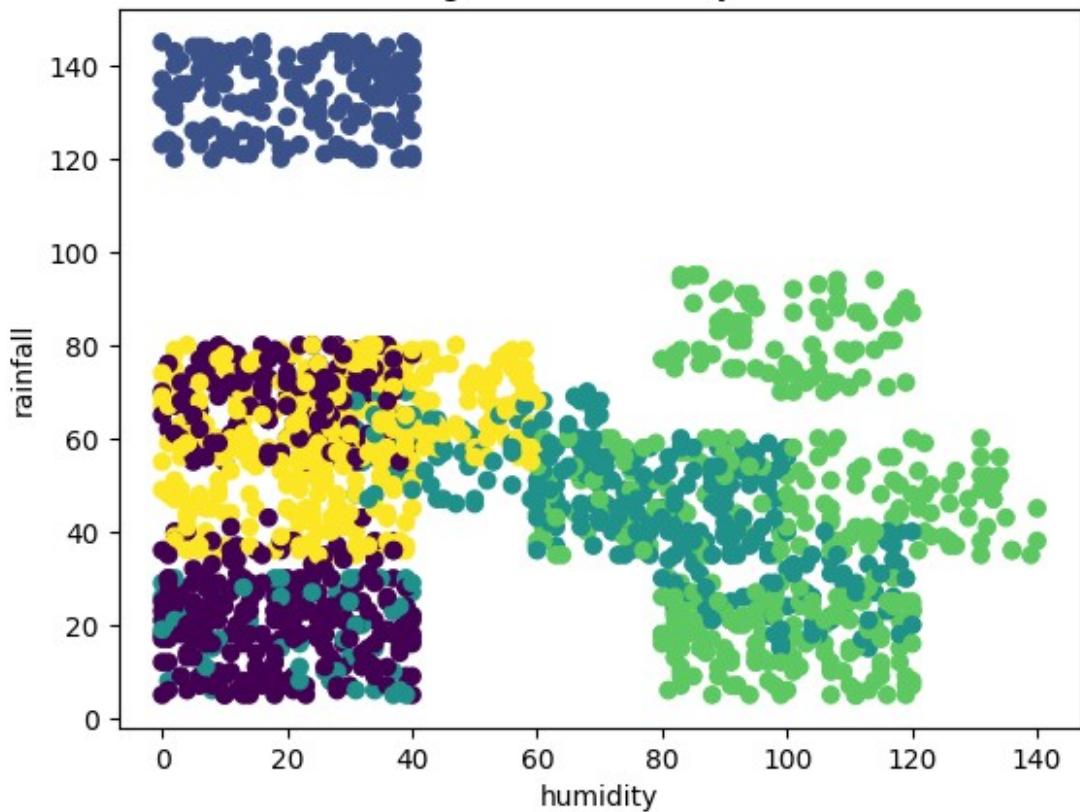
Clustering Result: temperature vs rainfall

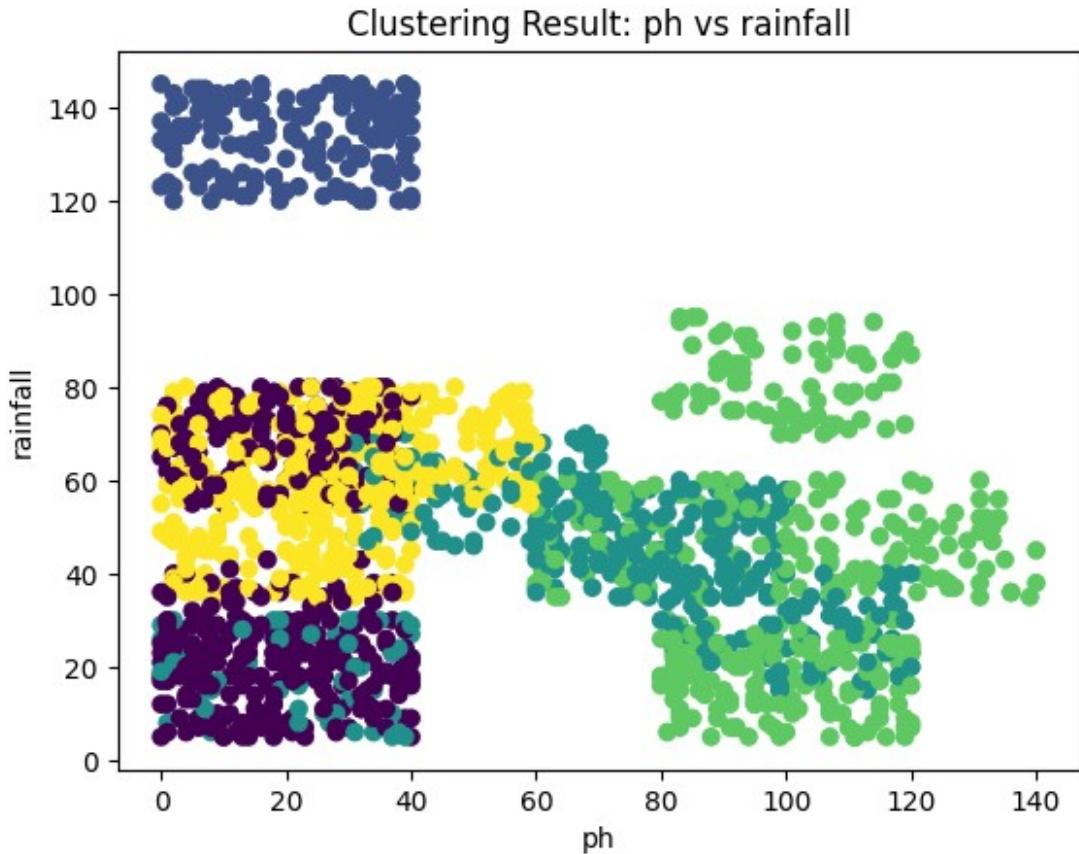


Clustering Result: humidity vs ph



Clustering Result: humidity vs rainfall





Silhouette Score: 0.34221671586215324  
 Adjusted Rand Index: 0.28478777409763506  
 Homogeneity: 0.4911732977694198  
 Completeness: 0.9693748667398314  
 V-measure: 0.6519895223467367

### #OPTICS

```

# Get the predicted cluster labels for the training data
train_cluster_labels = optics.labels_

# Compute evaluation metrics (silhouette score is not applicable to
# OPTICS)
ari = adjusted_rand_score(target, train_cluster_labels)
homogeneity, completeness, v_measure =
homogeneity_completeness_v_measure(target, train_cluster_labels)

# Create scatter plots for different feature combinations
features = ['Nitrogen', 'phosphorus', 'potassium', 'temperature',
'humidity', 'ph', 'rainfall']
for i in range(len(features)):
  for j in range(i+1, len(features)):
    plt.scatter(X_train[:, 0], X_train[:, 1],

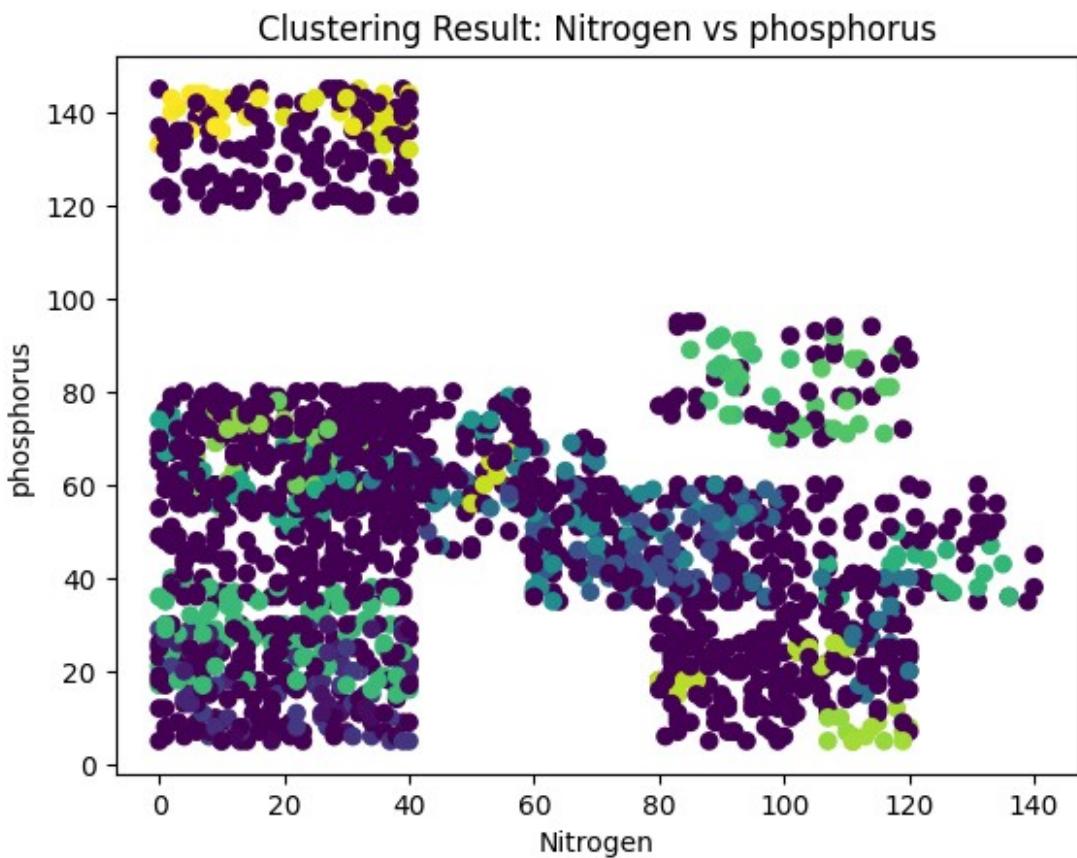
```

```

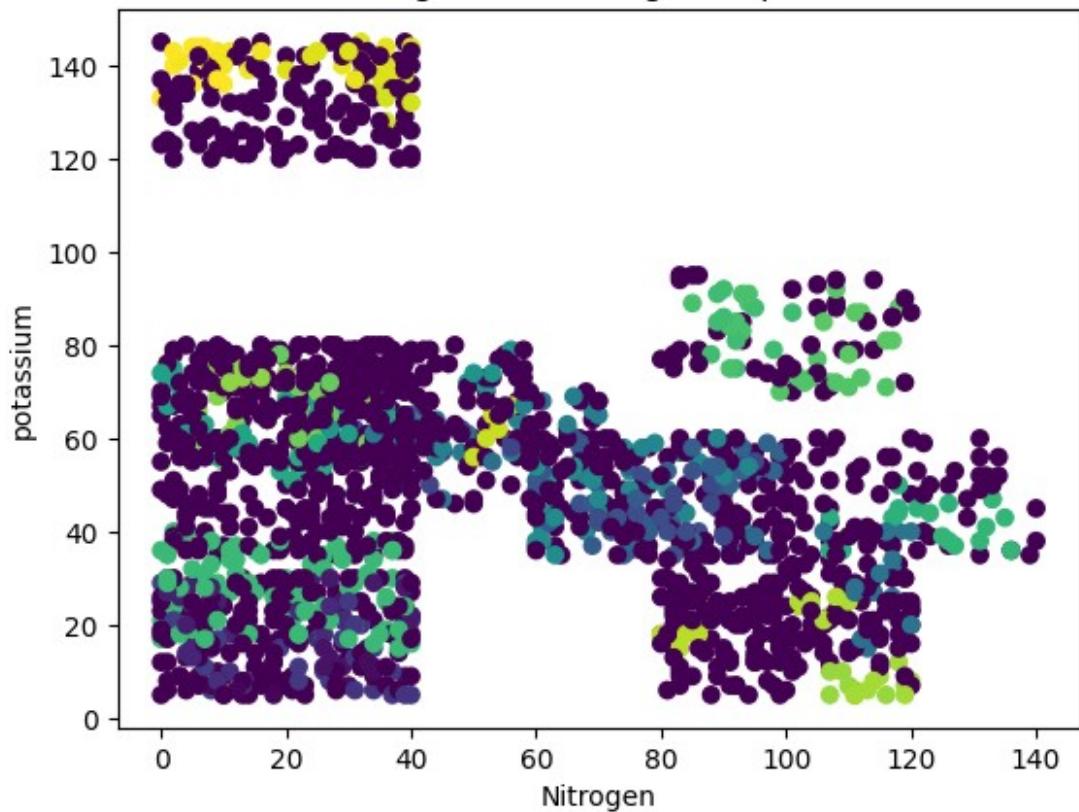
c=train_cluster_labels, cmap='viridis')
    plt.xlabel(features[i])
    plt.ylabel(features[j])
    plt.title(f'Clustering Result: {features[i]} vs
{features[j]}')
    plt.show()

# Print evaluation metrics
print("Adjusted Rand Index:", ari)
print("Homogeneity:", homogeneity)
print("Completeness:", completeness)
print("V-measure:", v_measure)

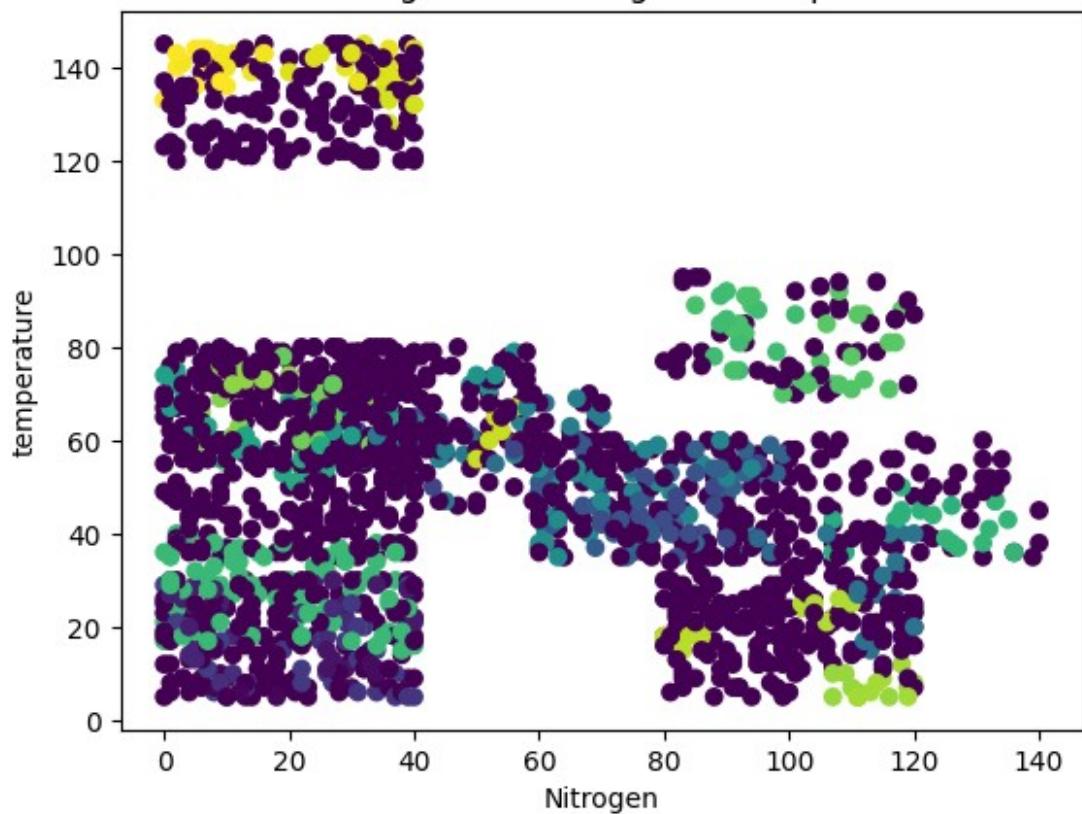
```



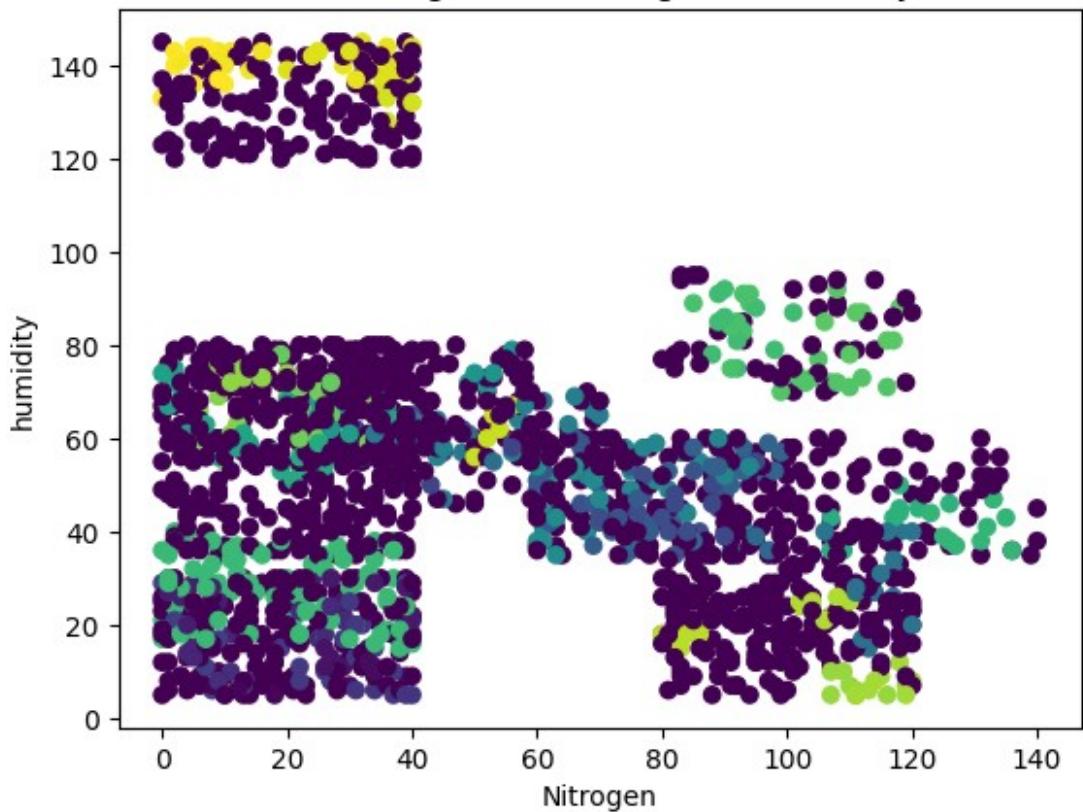
Clustering Result: Nitrogen vs potassium



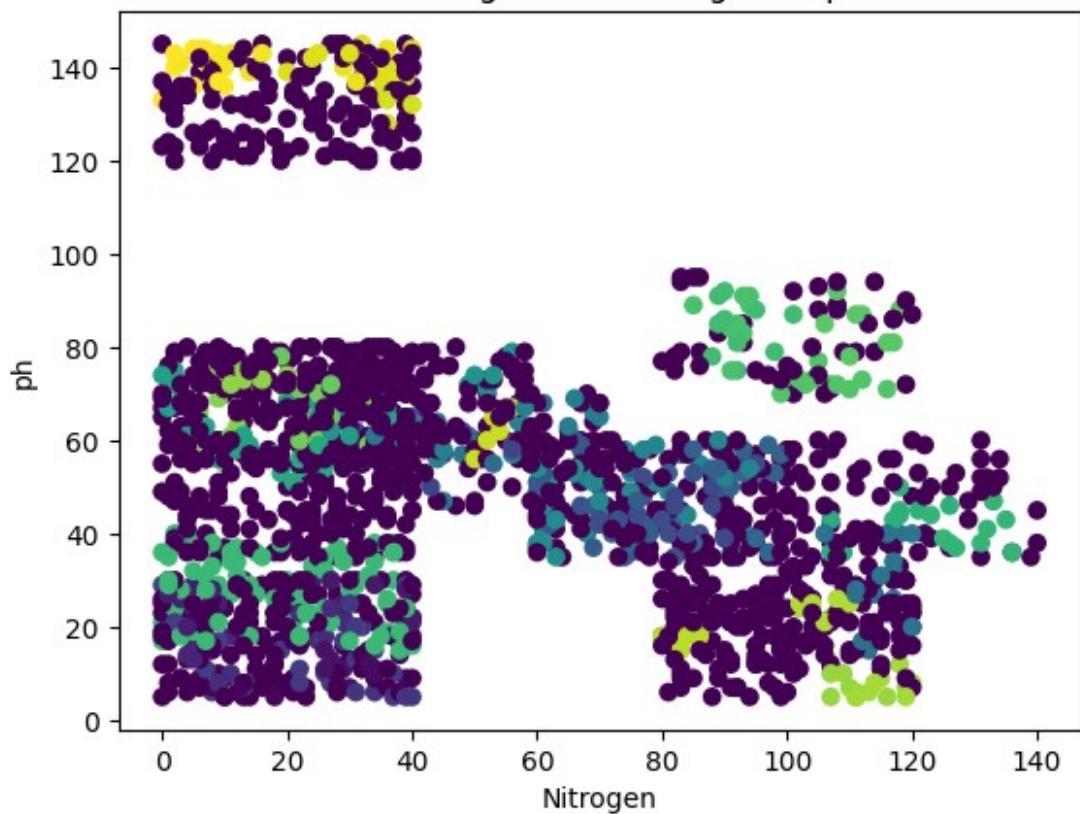
Clustering Result: Nitrogen vs temperature



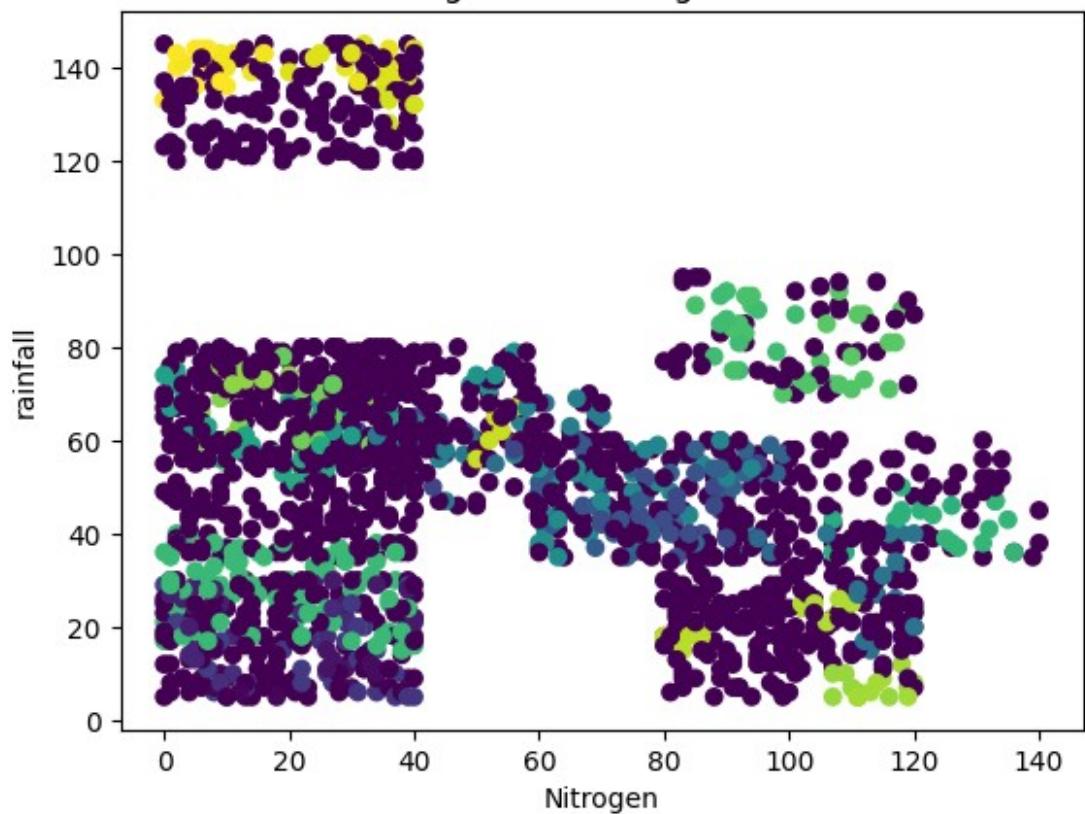
Clustering Result: Nitrogen vs humidity



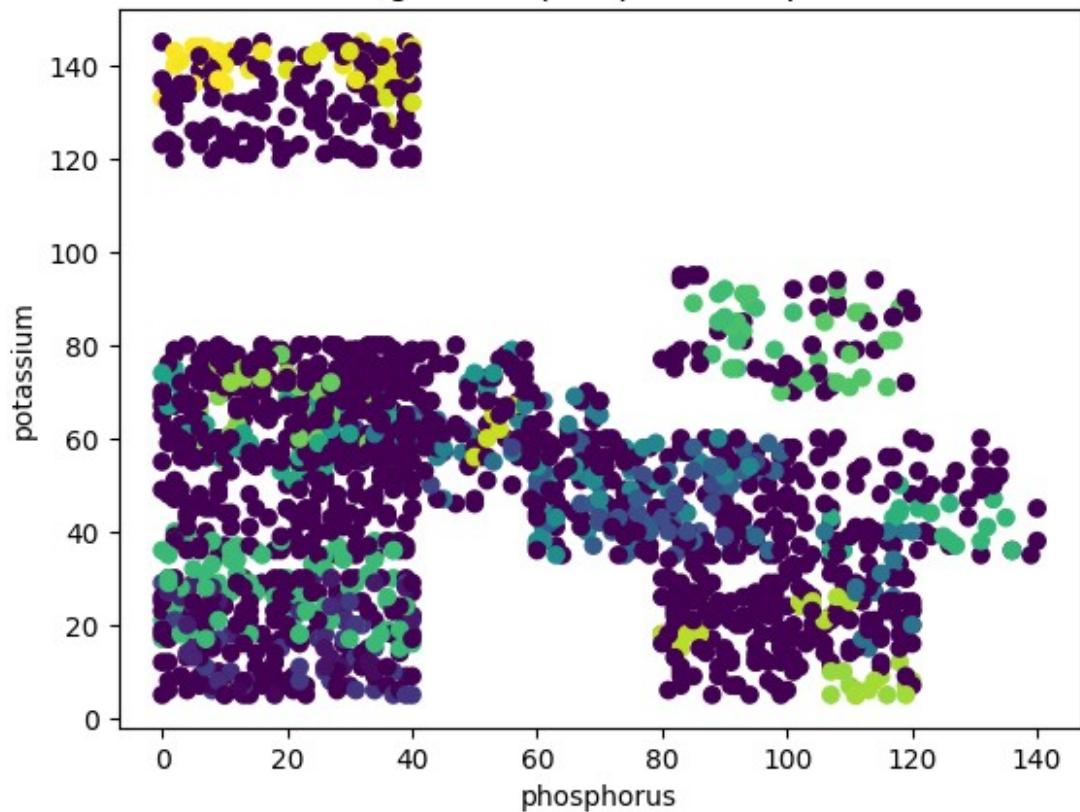
Clustering Result: Nitrogen vs ph



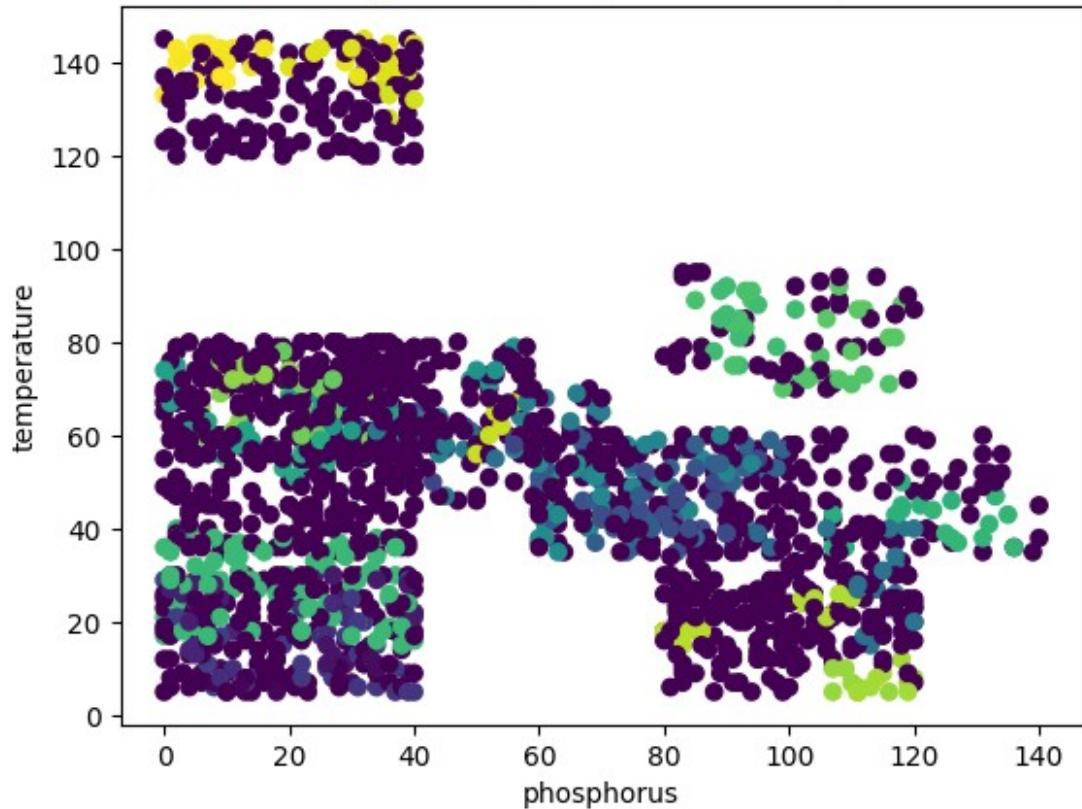
Clustering Result: Nitrogen vs rainfall



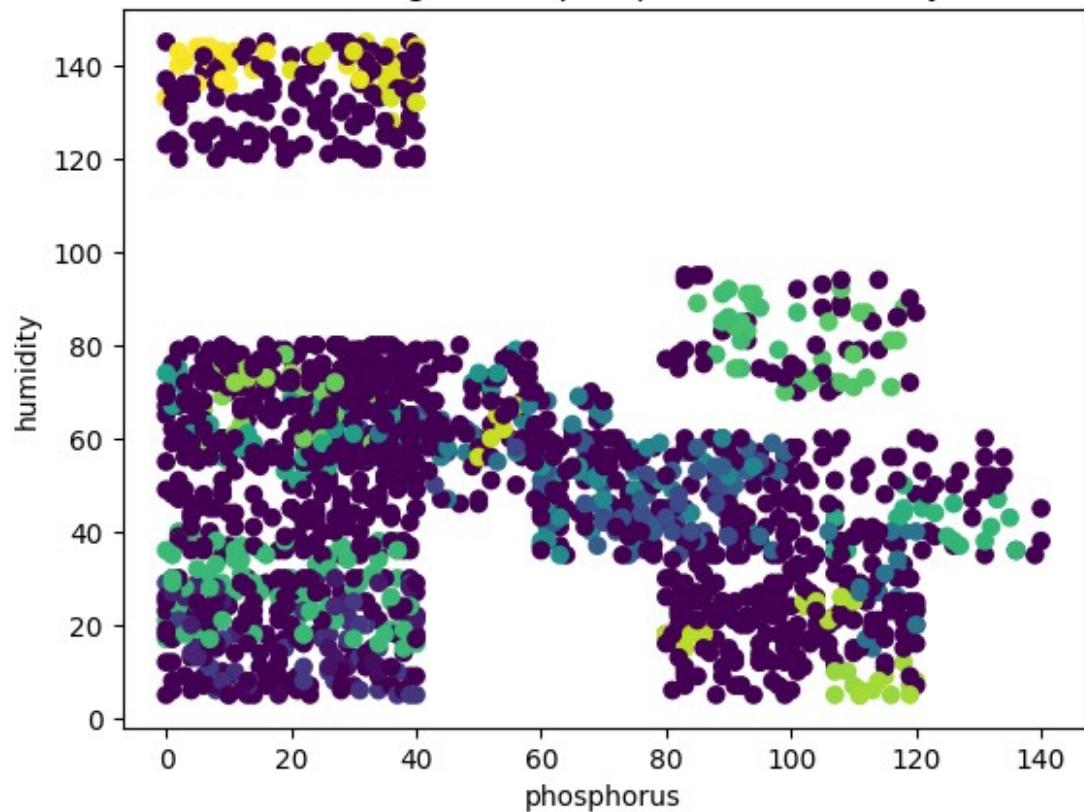
Clustering Result: phosphorus vs potassium



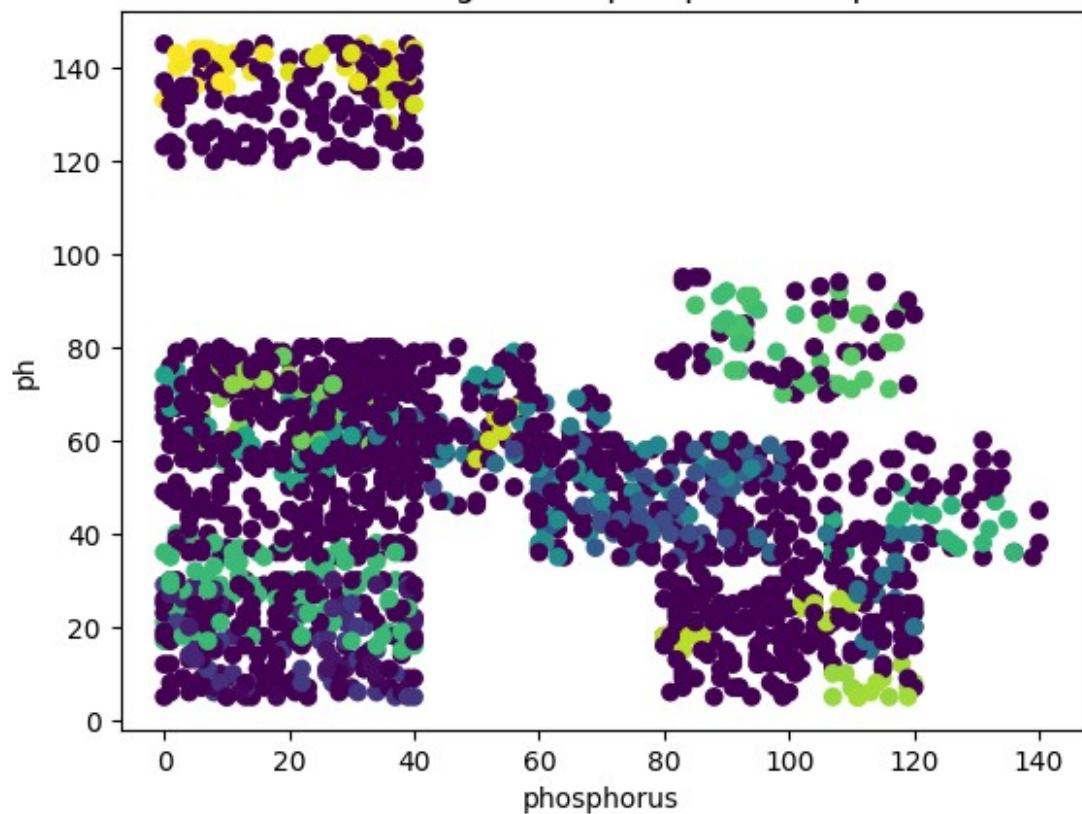
Clustering Result: phosphorus vs temperature



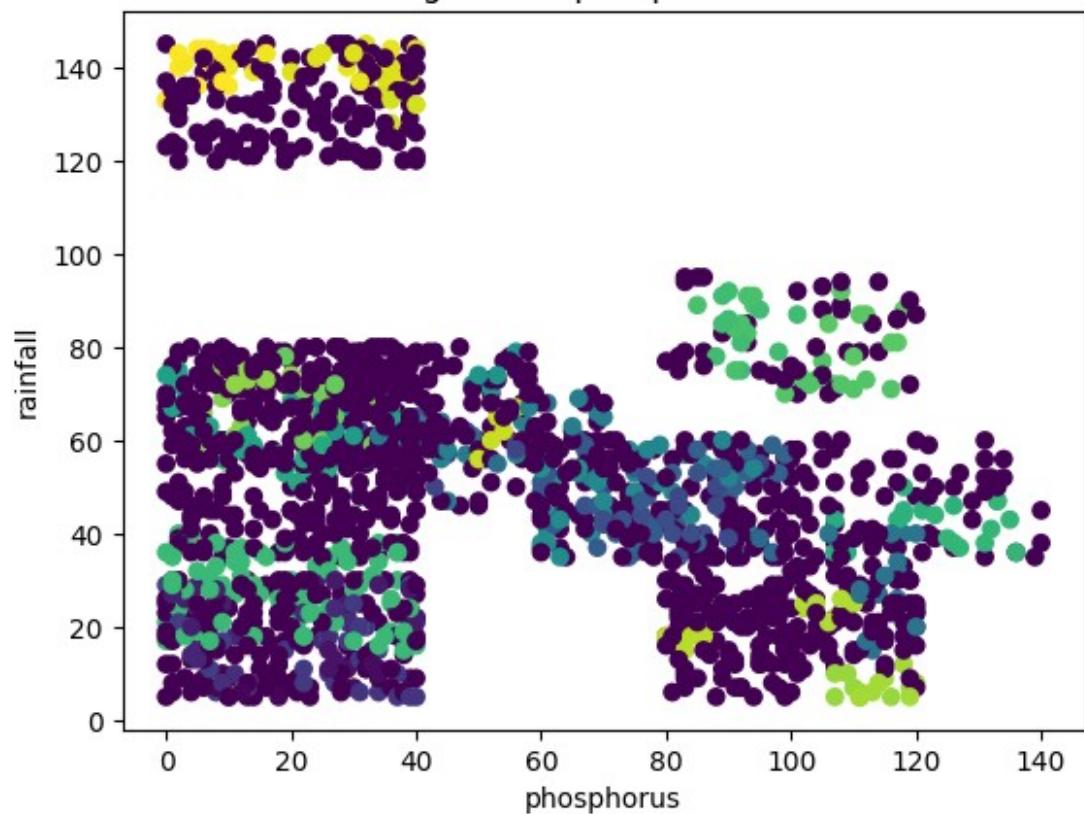
Clustering Result: phosphorus vs humidity



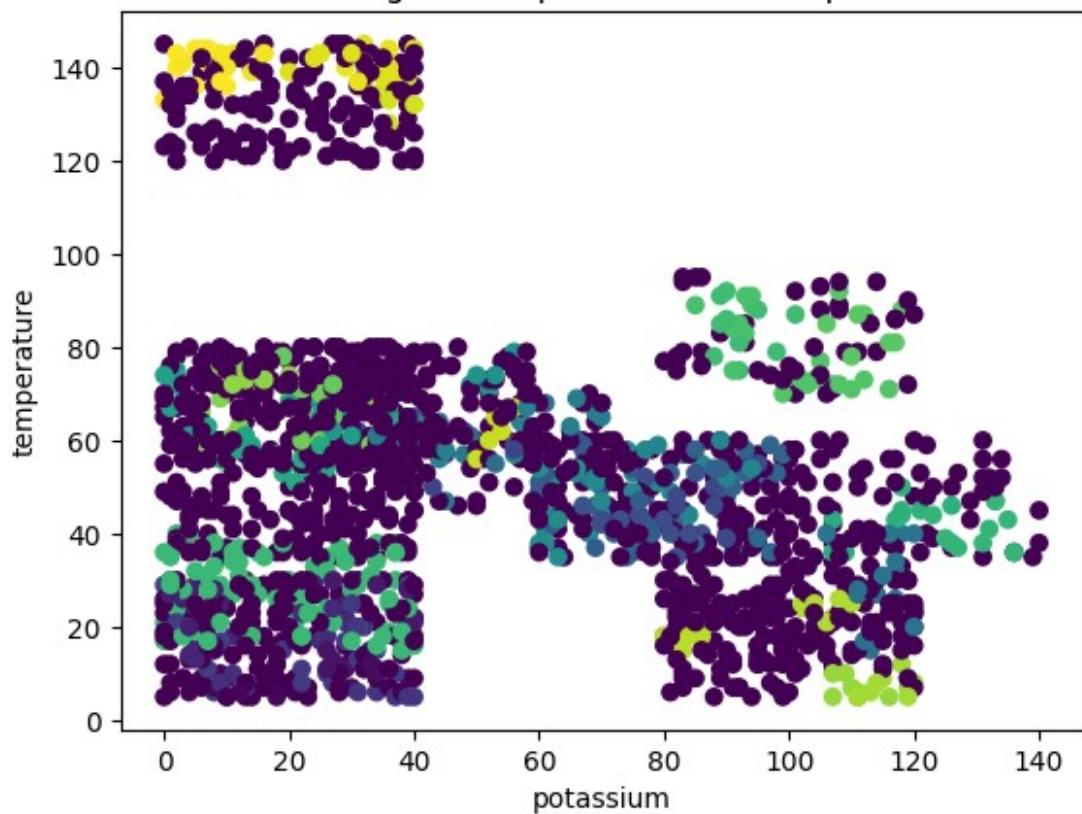
Clustering Result: phosphorus vs ph



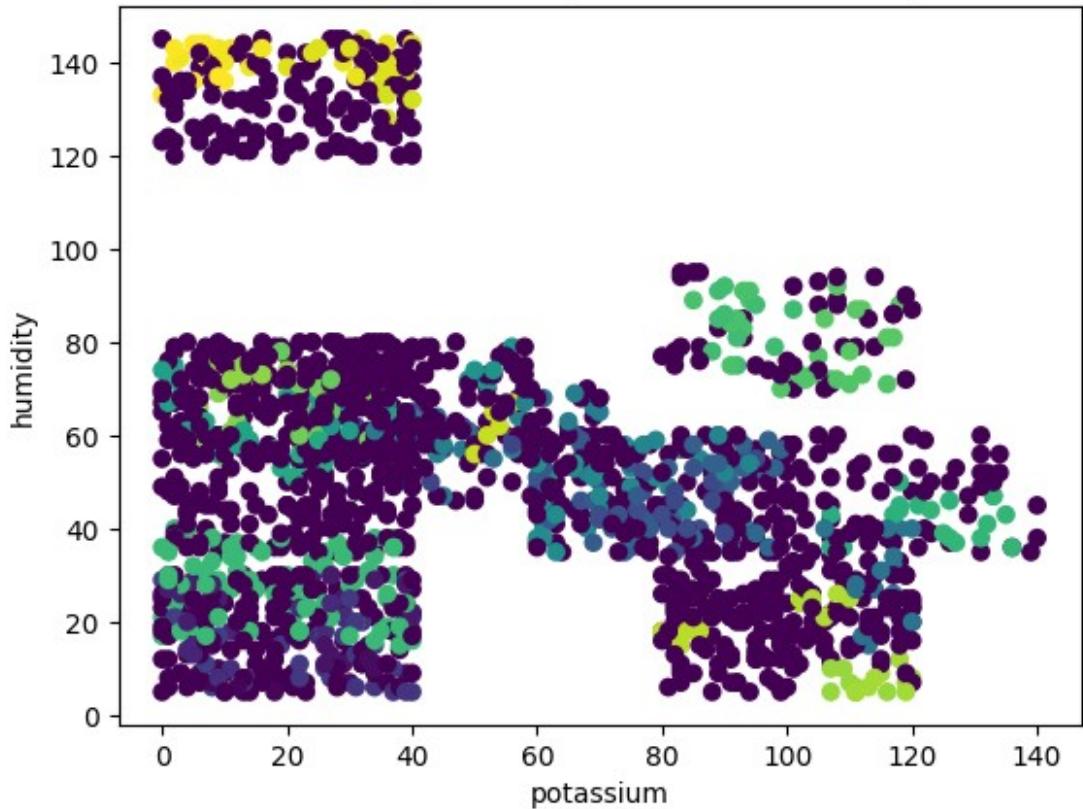
Clustering Result: phosphorus vs rainfall



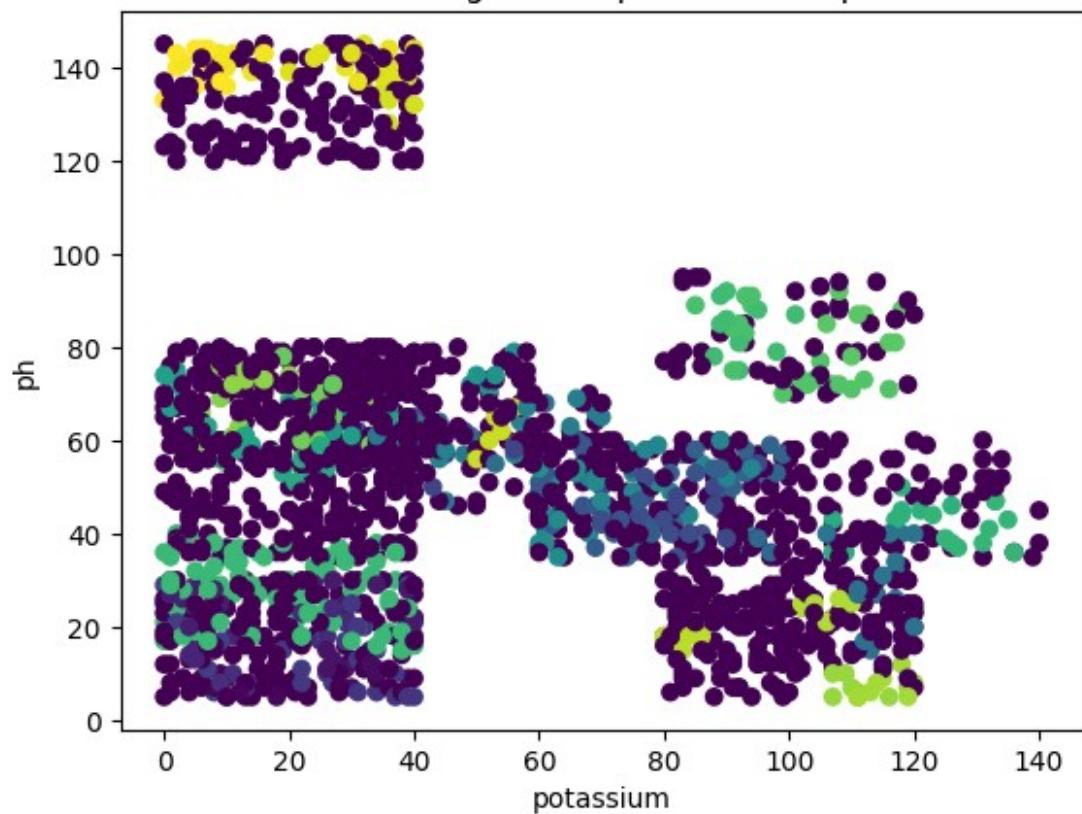
Clustering Result: potassium vs temperature



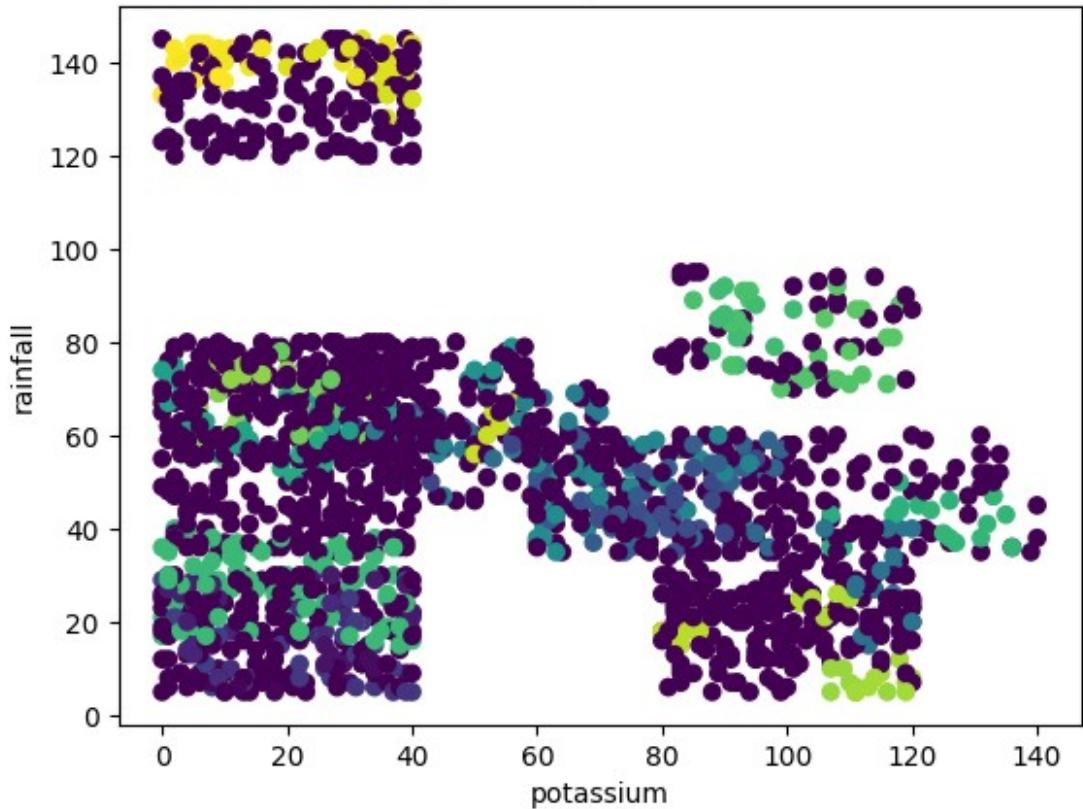
Clustering Result: potassium vs humidity



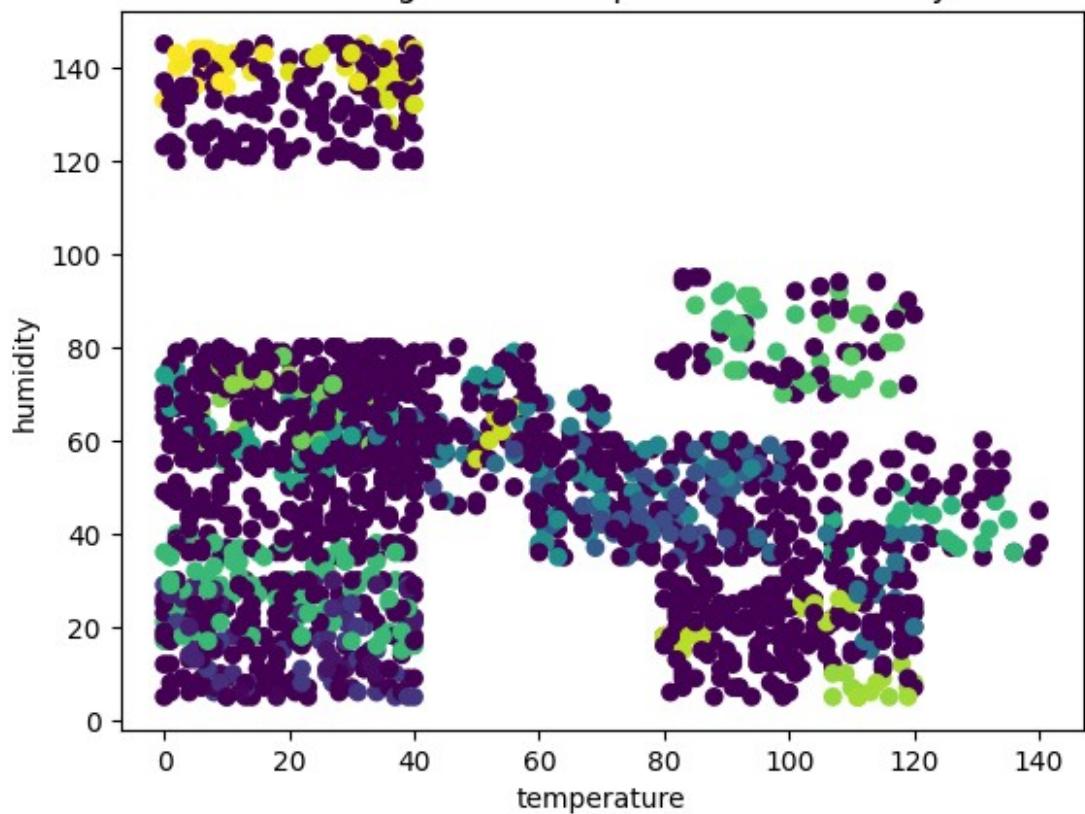
Clustering Result: potassium vs ph



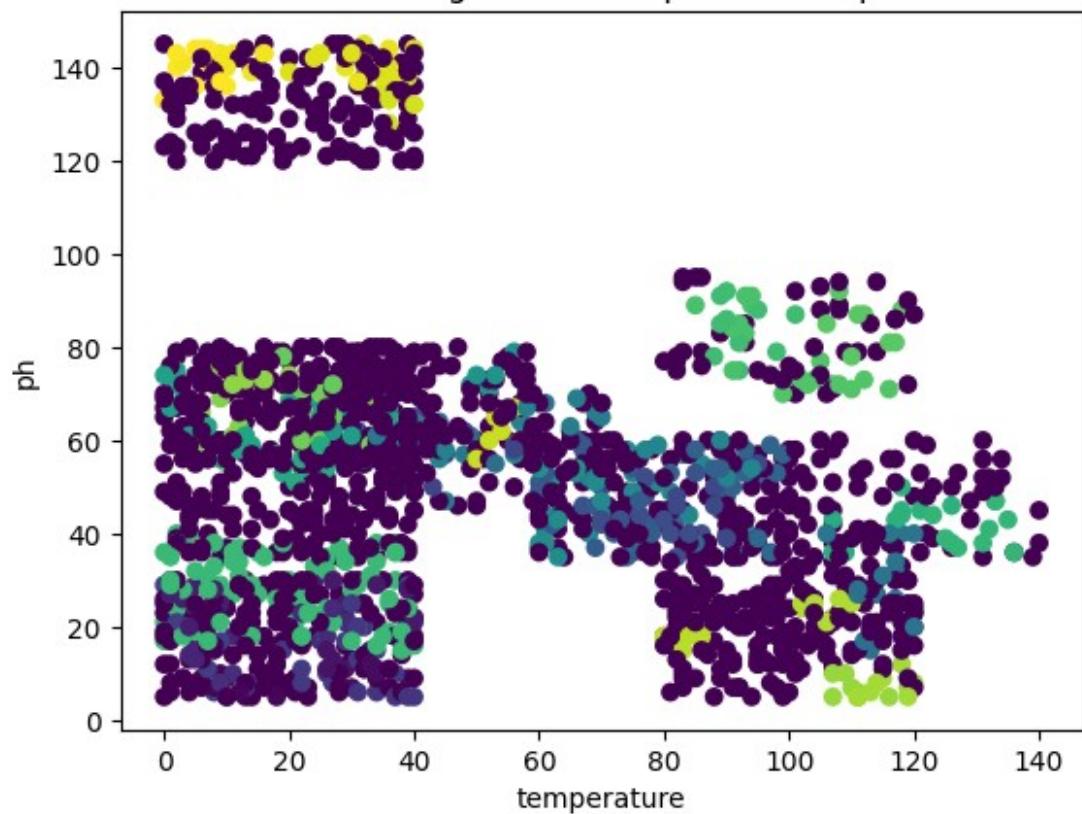
Clustering Result: potassium vs rainfall



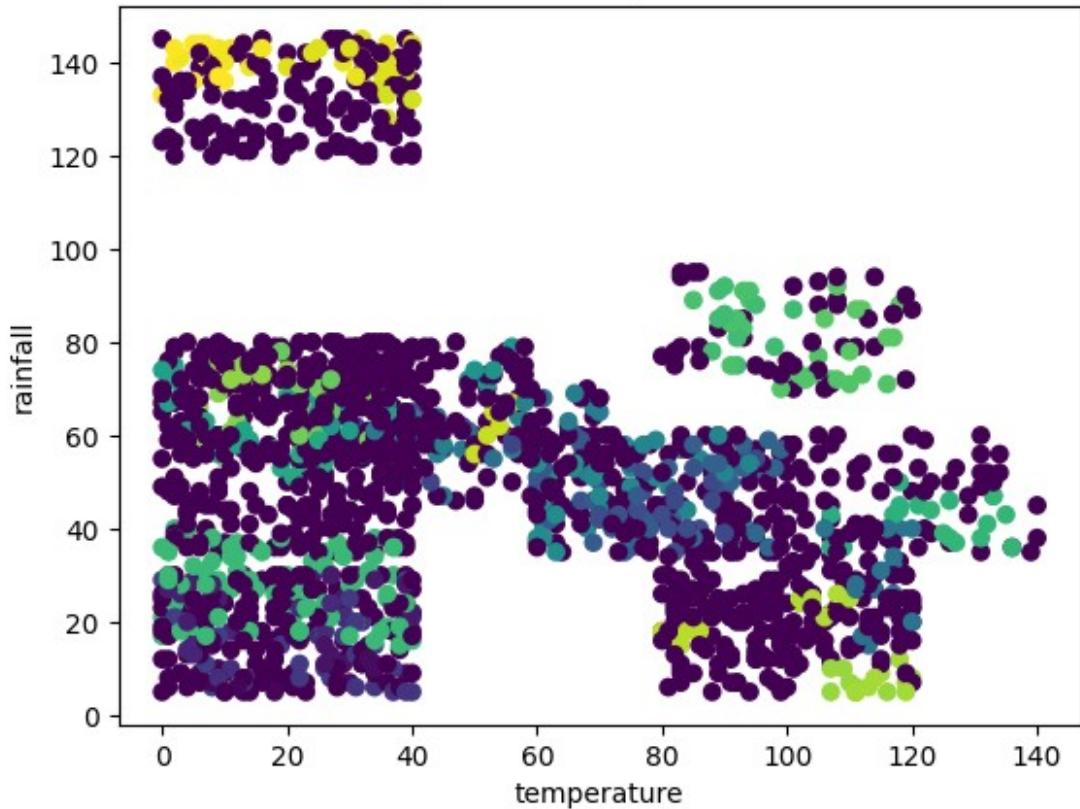
Clustering Result: temperature vs humidity



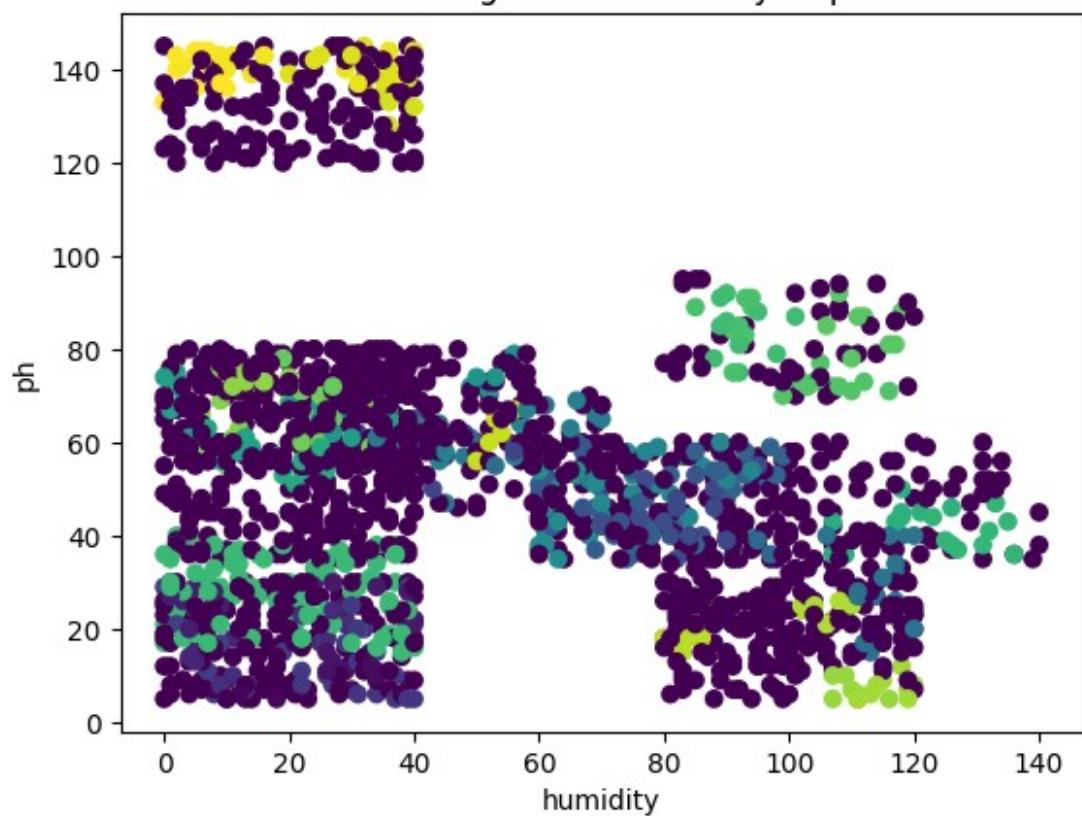
Clustering Result: temperature vs ph



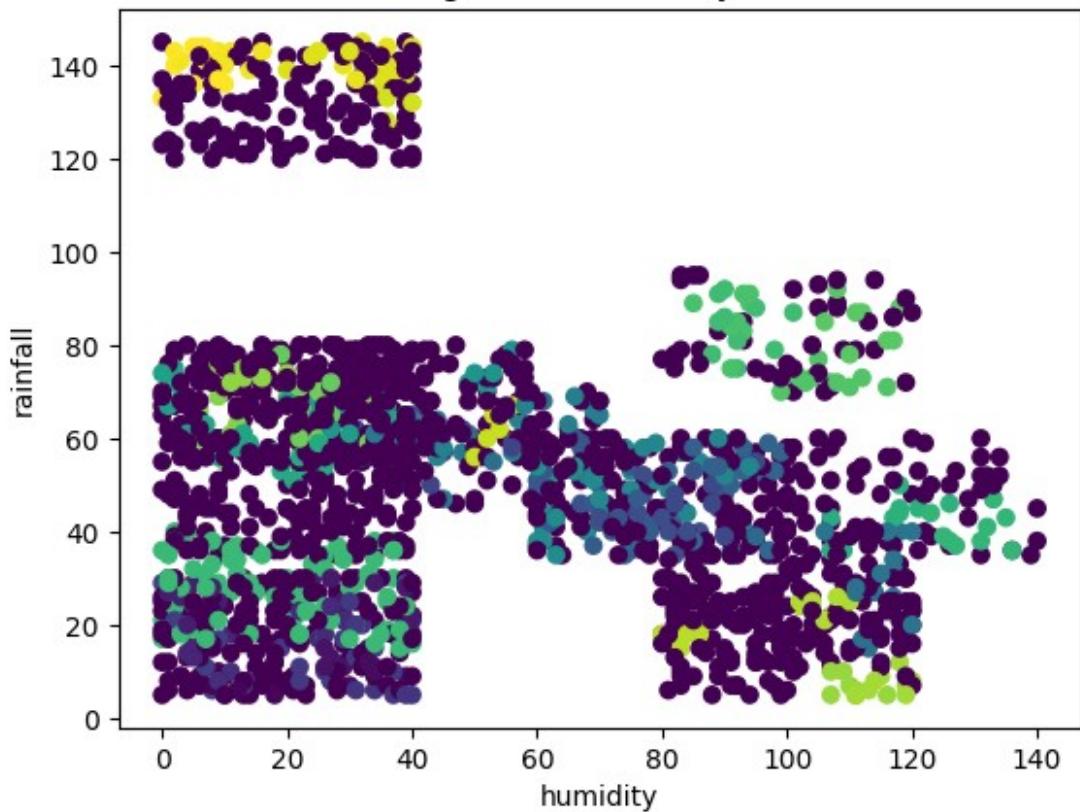
Clustering Result: temperature vs rainfall



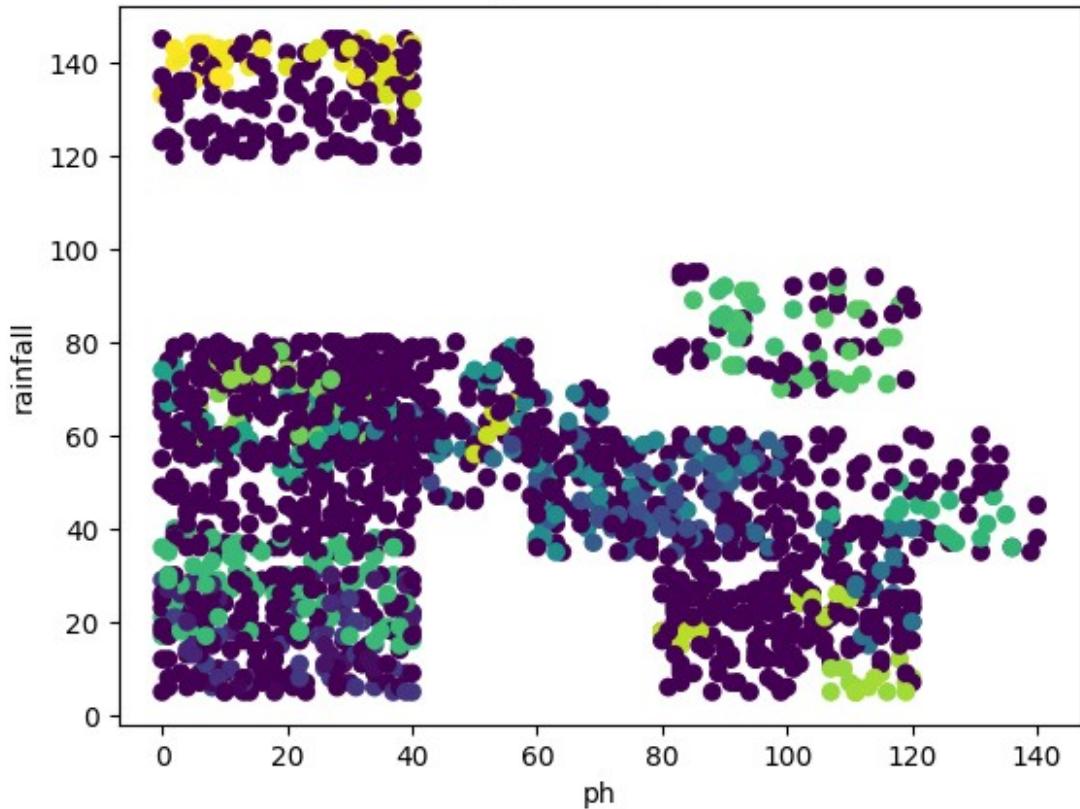
Clustering Result: humidity vs ph



Clustering Result: humidity vs rainfall



Clustering Result: ph vs rainfall



Adjusted Rand Index: 0.022125785779513074

Homogeneity: 0.332676057224183

Completeness: 0.5552951223151325

V-measure: 0.4160797020089311

```
from scipy.cluster.hierarchy import fcluster
# hierarchical clustering
# Create scatter plots for different feature combinations
features = ['Nitrogen', 'phosphorus', 'potassium', 'temperature',
'humidity', 'ph', 'rainfall']
for i in range(len(features)):
    for j in range(i+1, len(features)):
        # Scatter plot
        plt.scatter(X_train[:, i], X_train[:, j],
c=train_cluster_labels, cmap='viridis')
        plt.xlabel(features[i])
        plt.ylabel(features[j])
        plt.title(f'Scatter Plot: {features[i]} vs {features[j]}')
        plt.show()

# Plotting the dendrogram
```

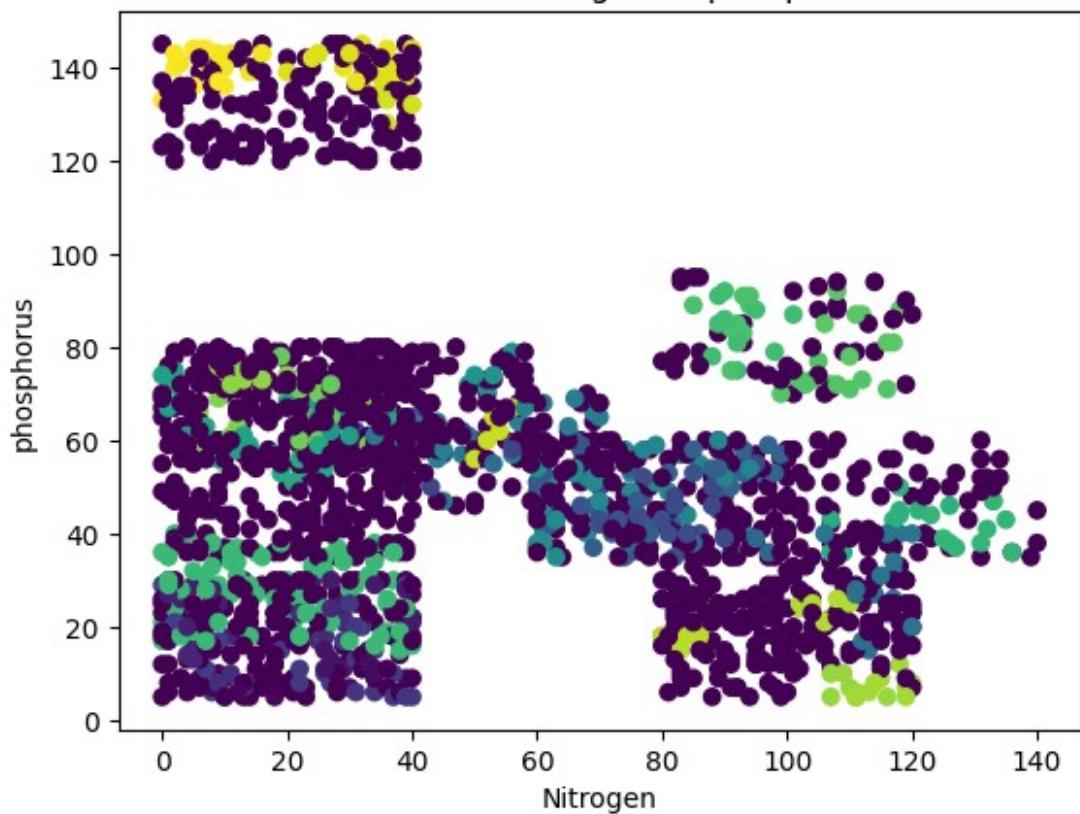
```
plt.figure(figsize=(10, 6))
dendrogram(linkage_matrix)
plt.xlabel('Samples')
plt.ylabel('Distance')
plt.title('Hierarchical Clustering Dendrogram')
plt.show()

# Set the desired number of clusters based on the dendrogram visualization
threshold = 50
train_cluster_labels = fcluster(linkage_matrix, threshold,
criterion='distance')

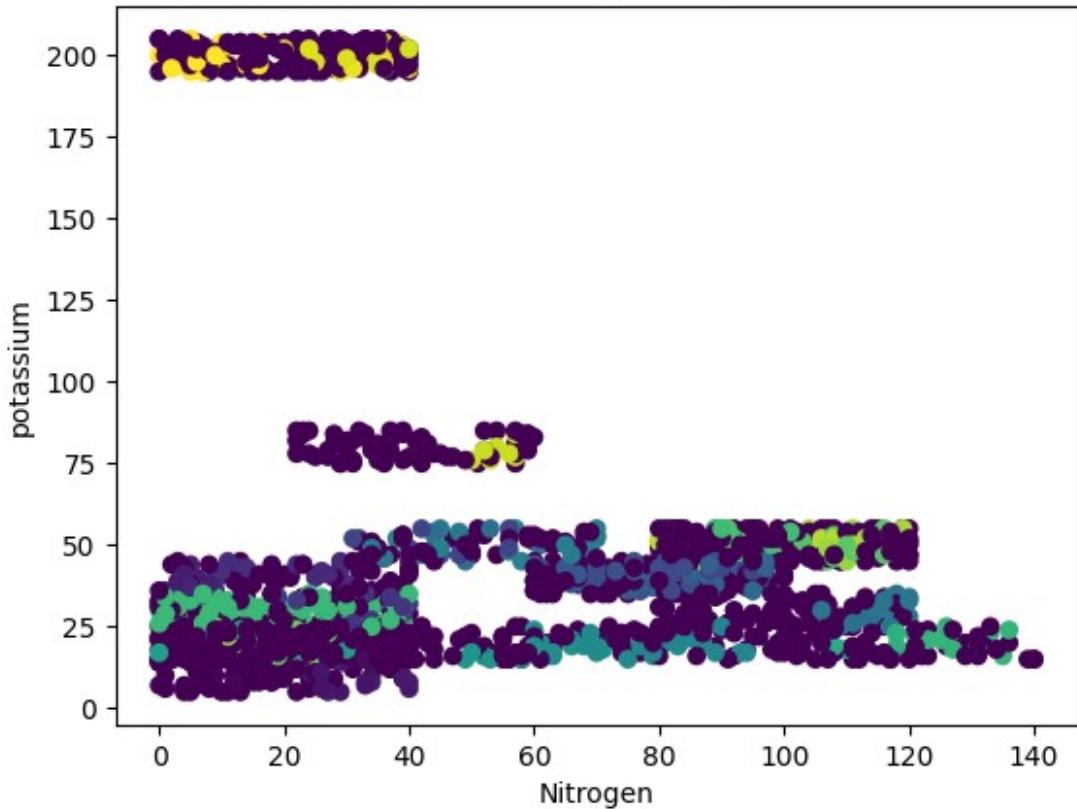
# Compute evaluation metrics
silhouette_avg = silhouette_score(X_train, train_cluster_labels)
ari = adjusted_rand_score(target, train_cluster_labels)
homogeneity, completeness, v_measure =
homogeneity_completeness_v_measure(target, train_cluster_labels)

# Print evaluation metrics
print("Silhouette Score:", silhouette_avg)
print("Adjusted Rand Index:", ari)
print("Homogeneity:", homogeneity)
print("Completeness:", completeness)
print("V-measure:", v_measure)
```

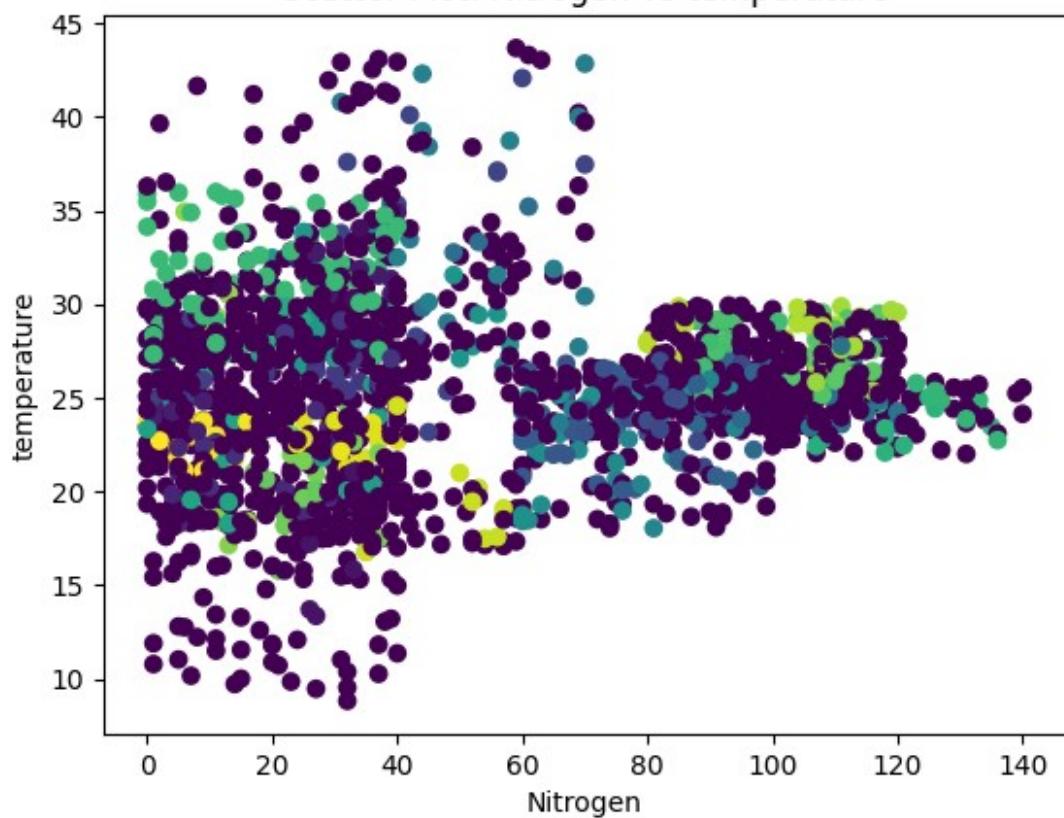
Scatter Plot: Nitrogen vs phosphorus



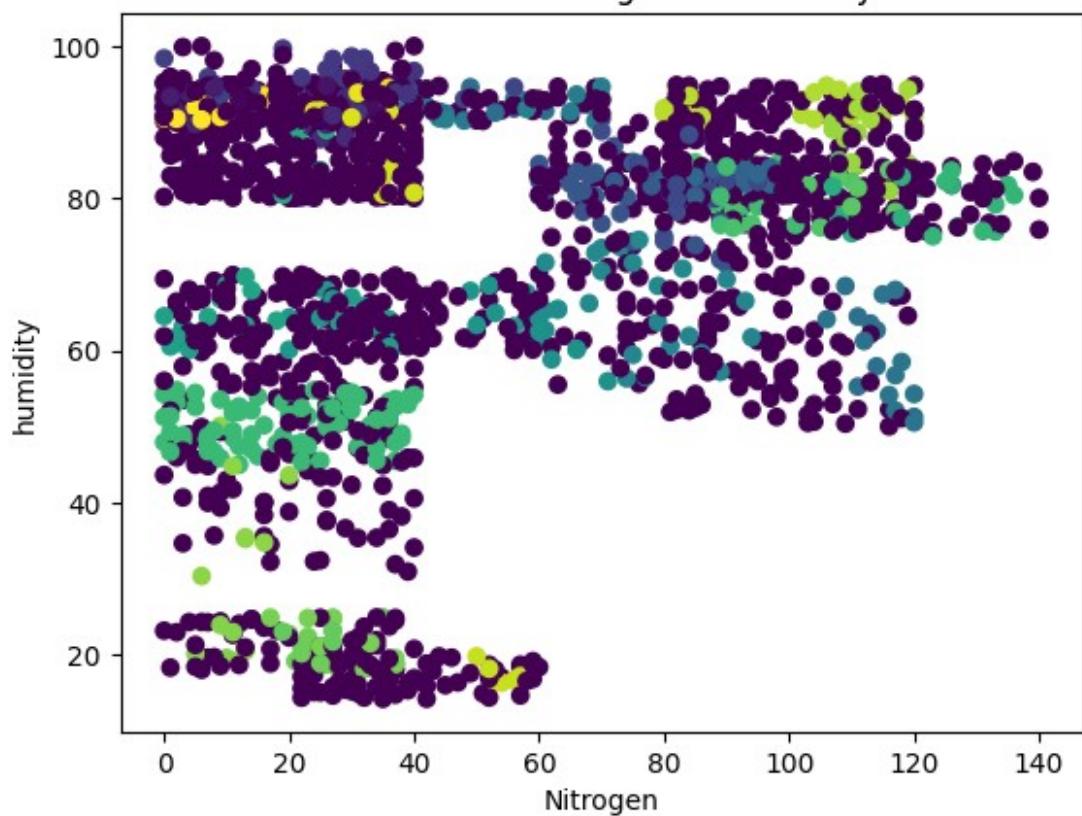
Scatter Plot: Nitrogen vs potassium



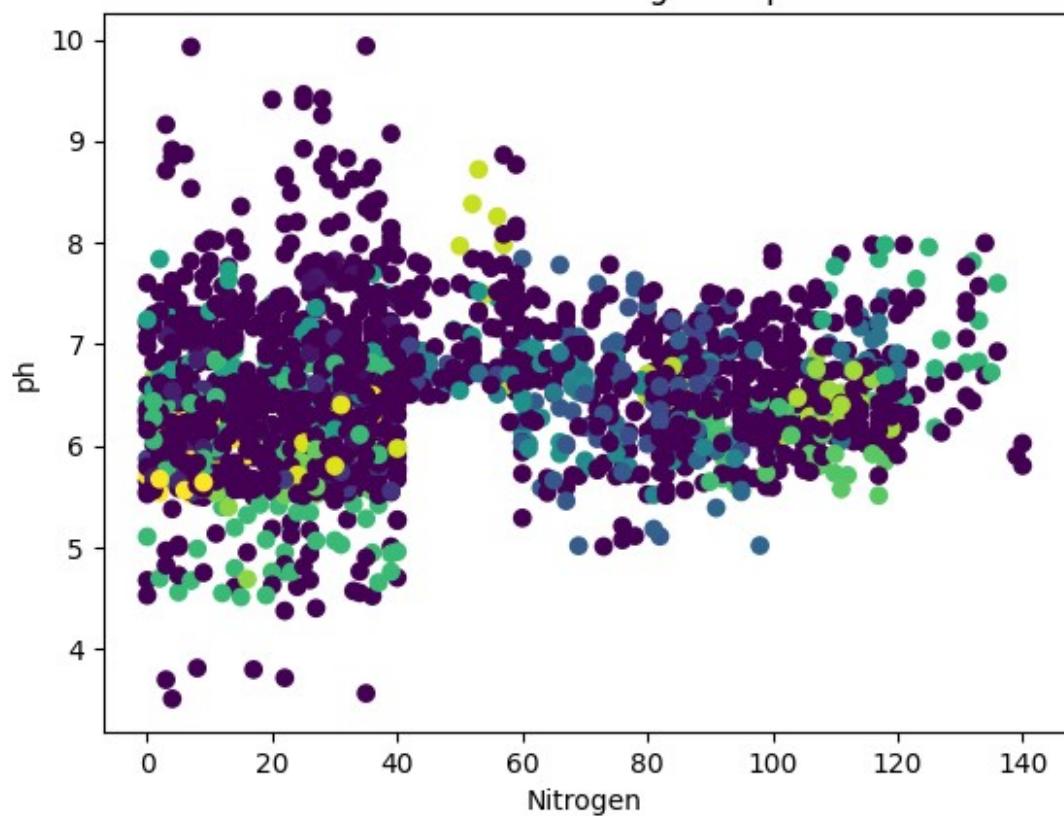
Scatter Plot: Nitrogen vs temperature



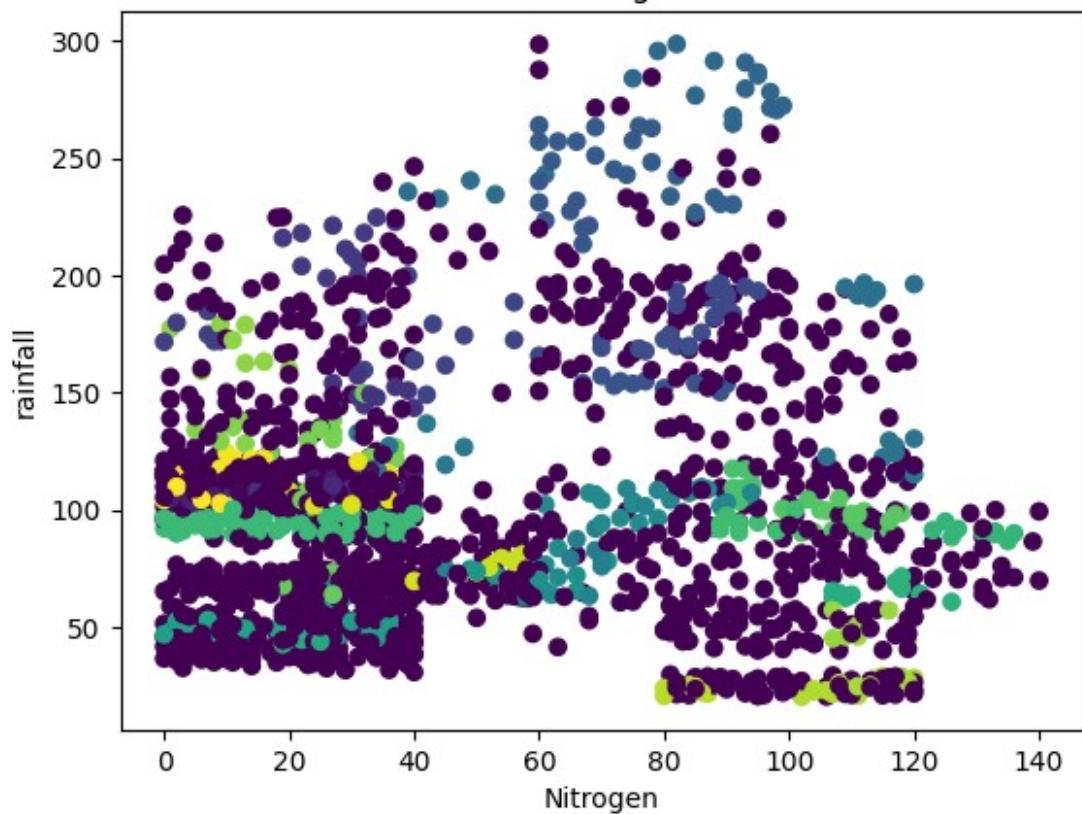
Scatter Plot: Nitrogen vs humidity



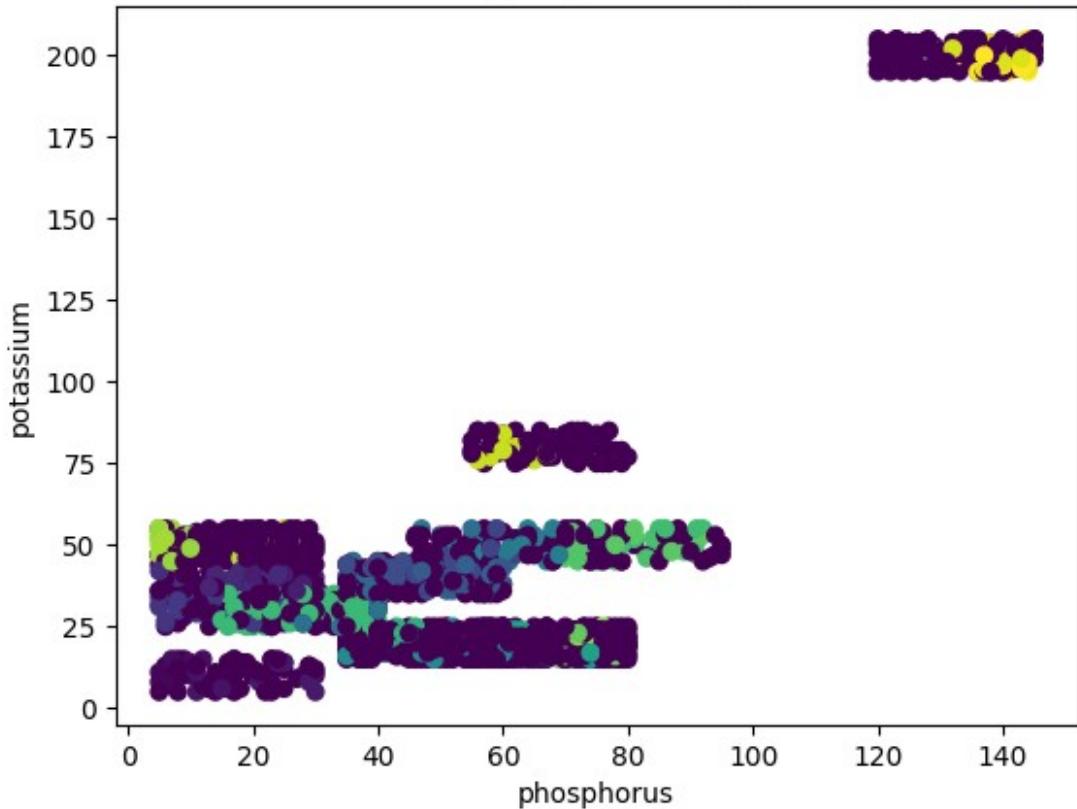
Scatter Plot: Nitrogen vs ph



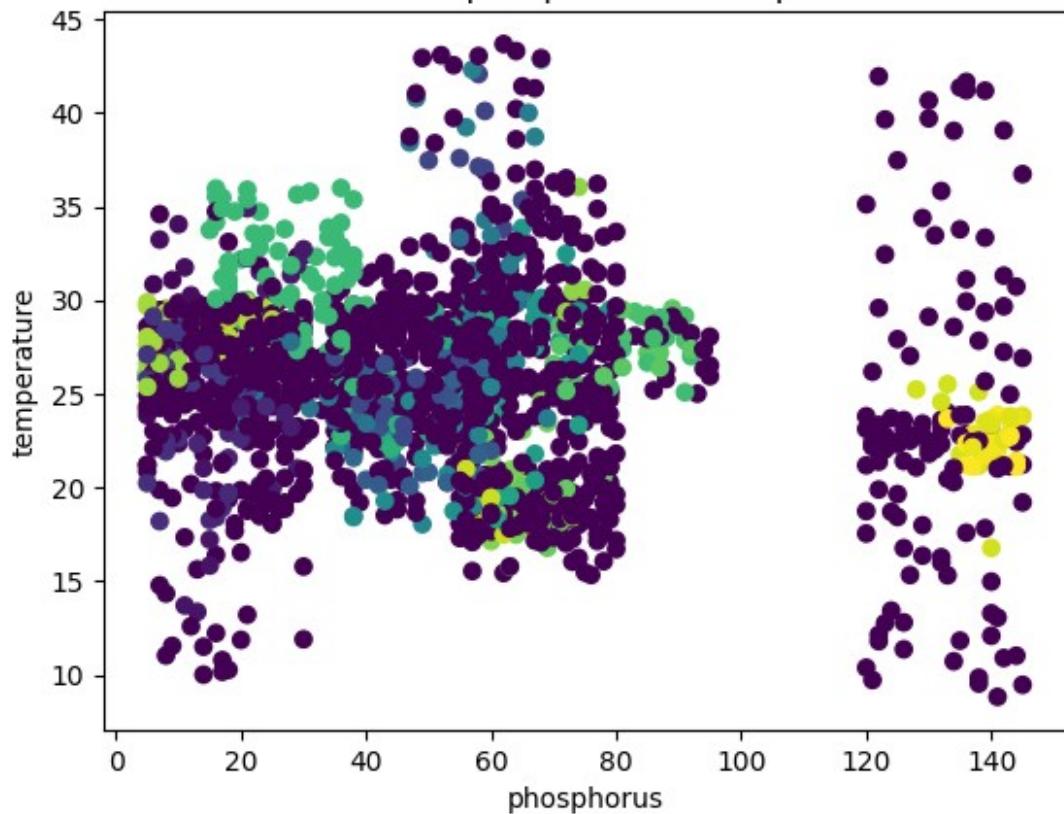
Scatter Plot: Nitrogen vs rainfall



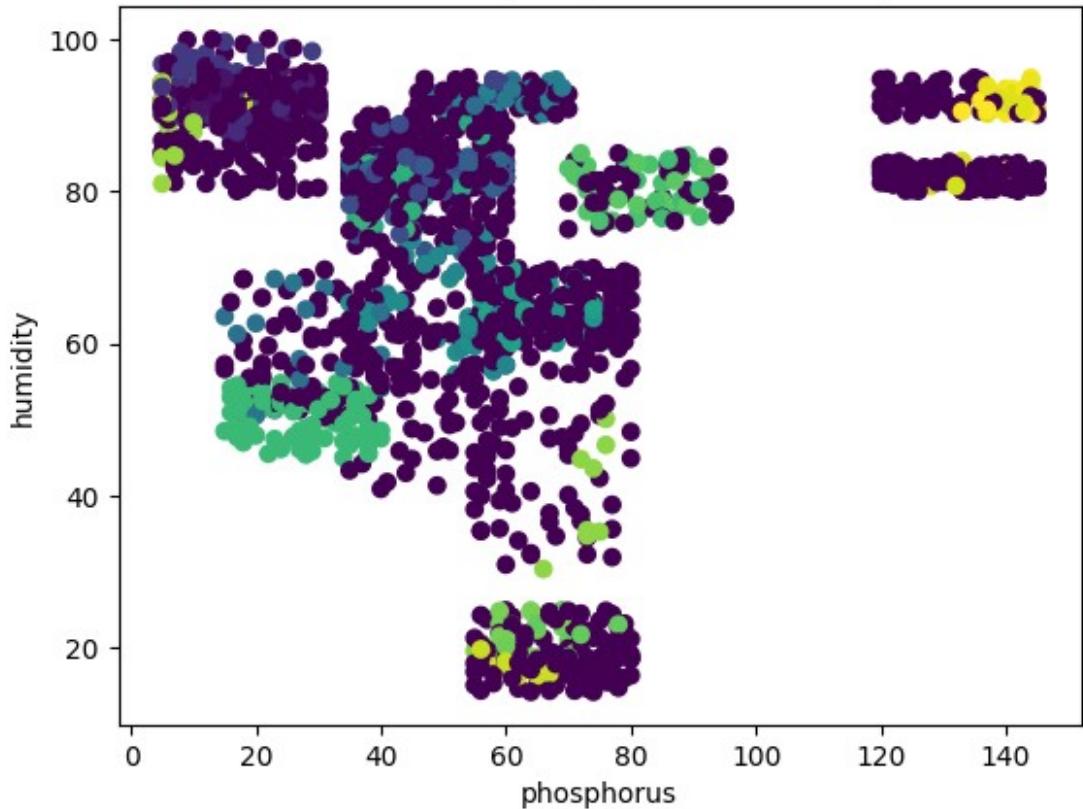
Scatter Plot: phosphorus vs potassium



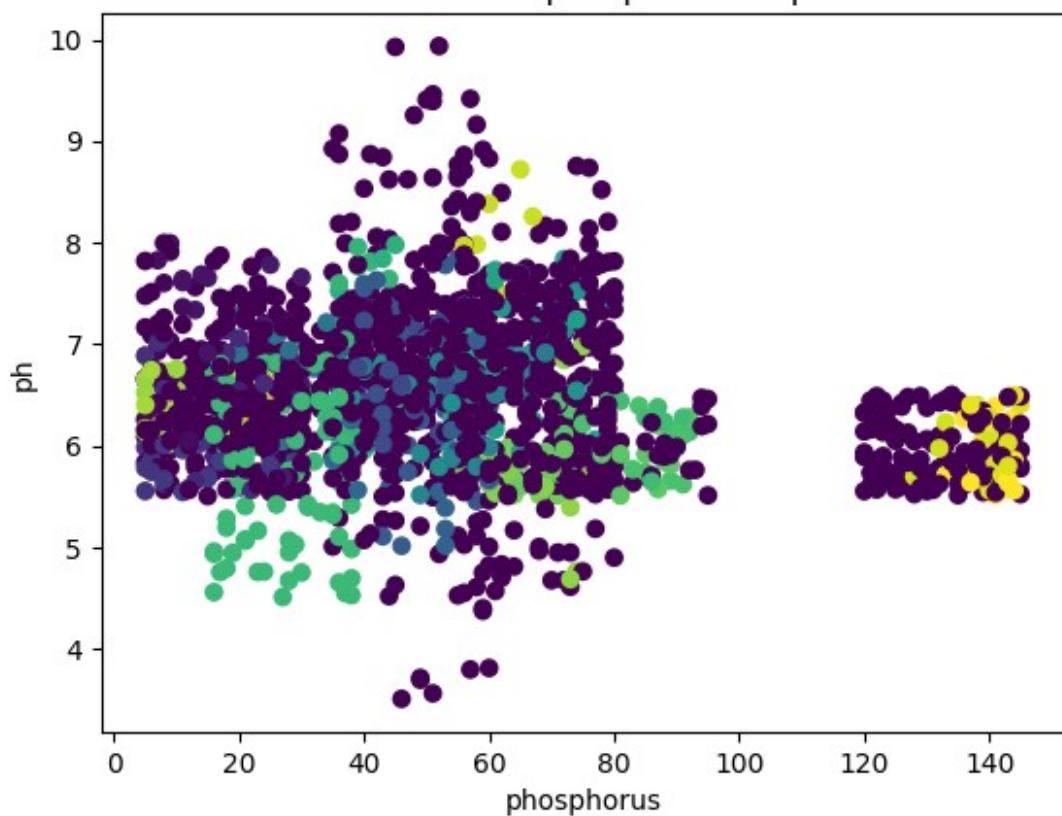
Scatter Plot: phosphorus vs temperature



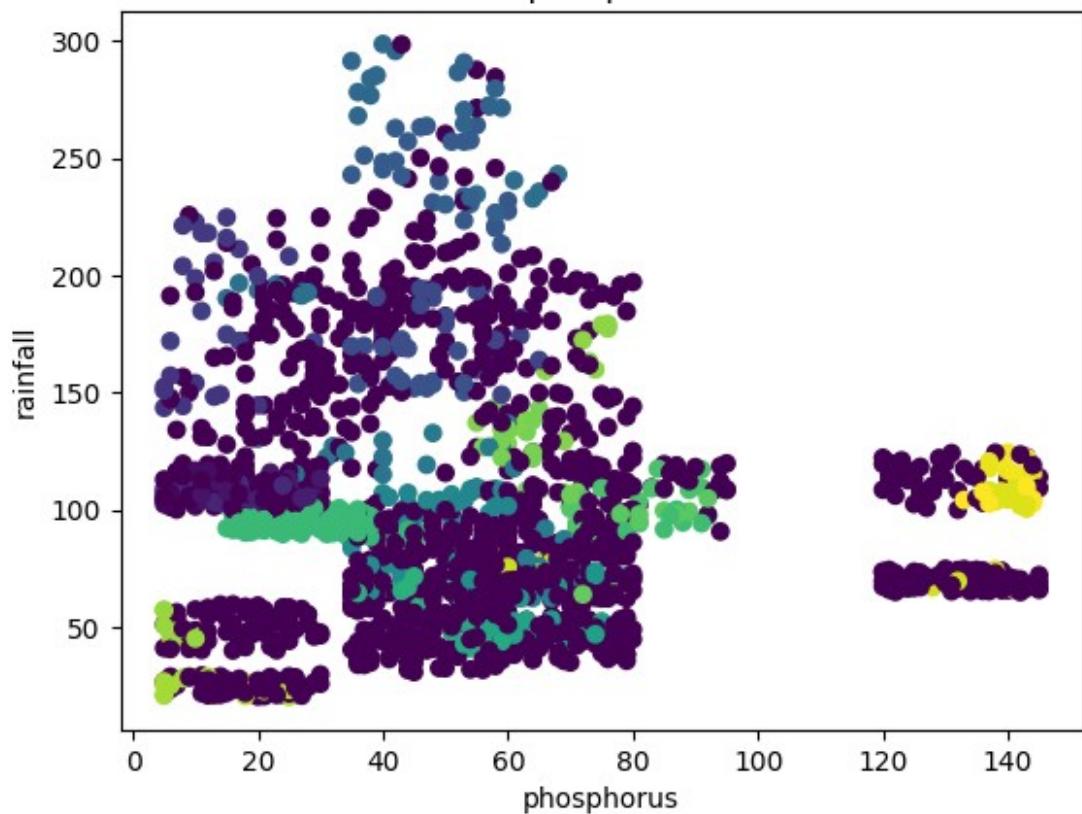
Scatter Plot: phosphorus vs humidity



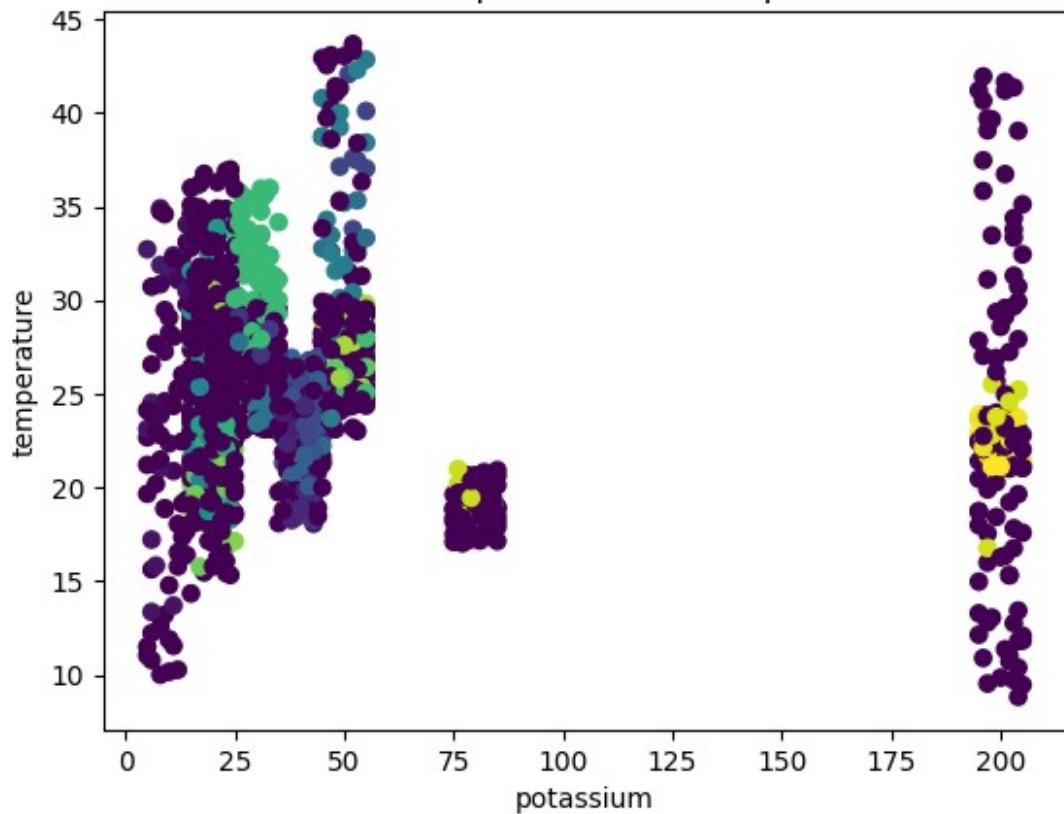
Scatter Plot: phosphorus vs ph



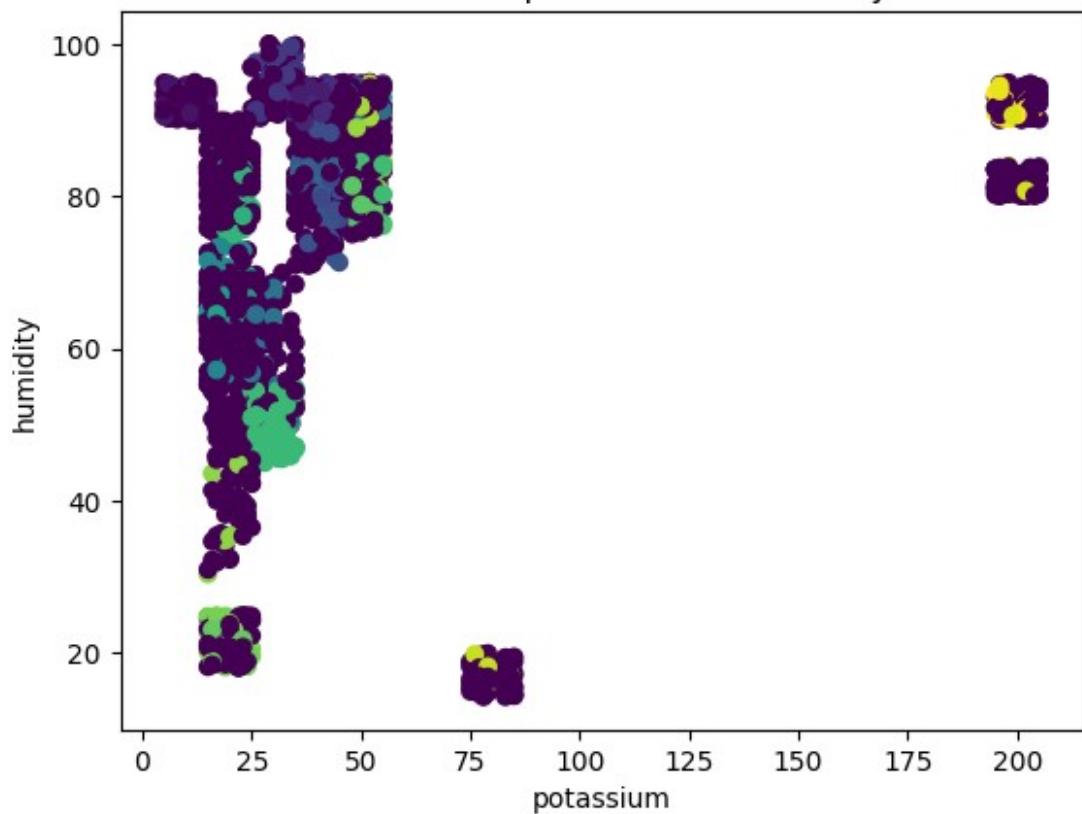
Scatter Plot: phosphorus vs rainfall



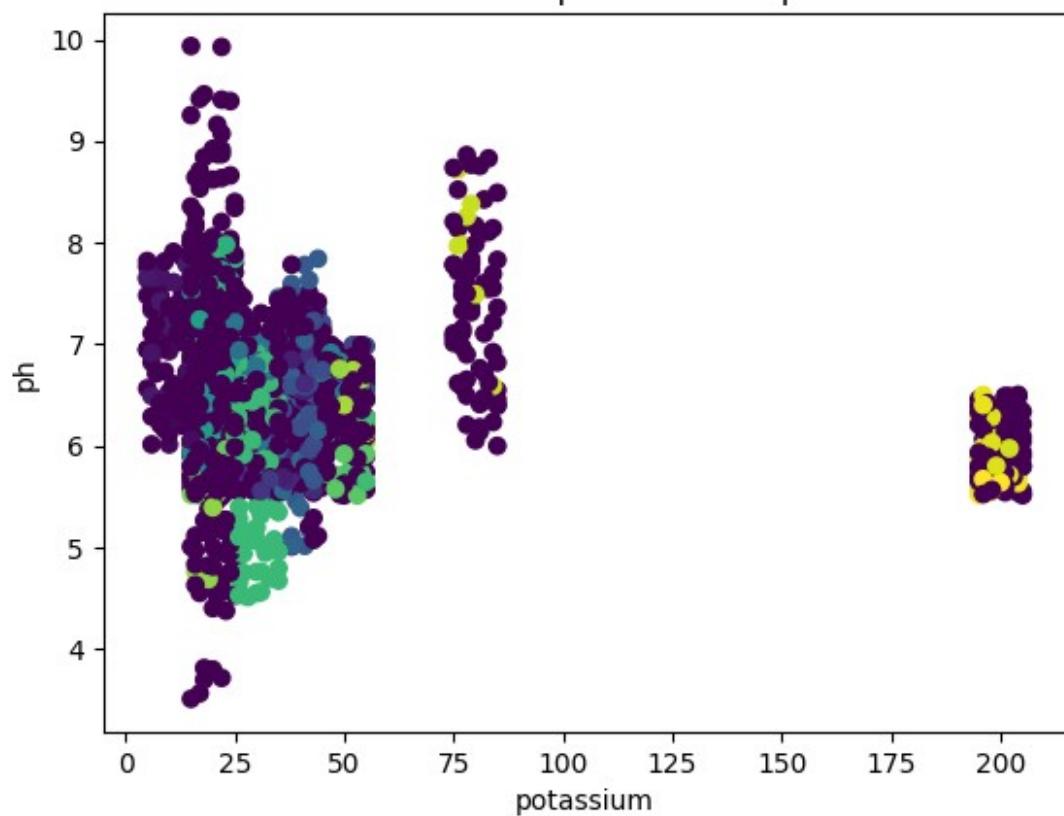
Scatter Plot: potassium vs temperature



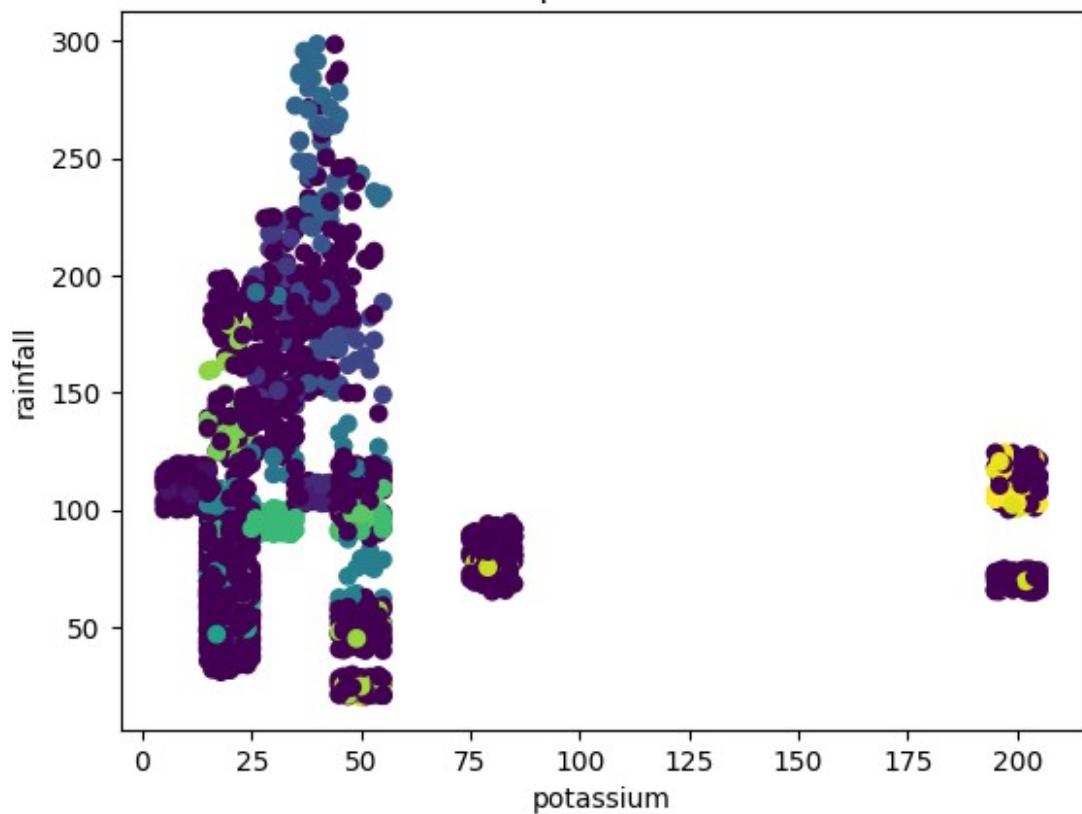
Scatter Plot: potassium vs humidity



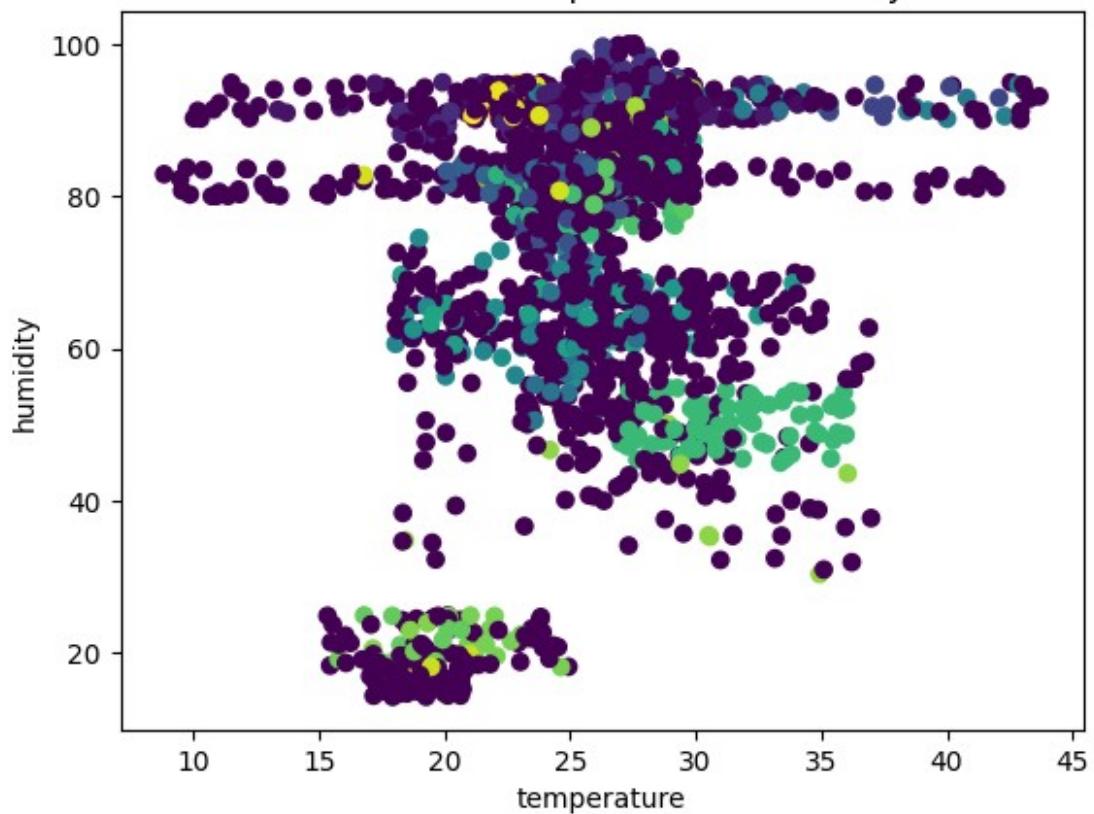
Scatter Plot: potassium vs ph



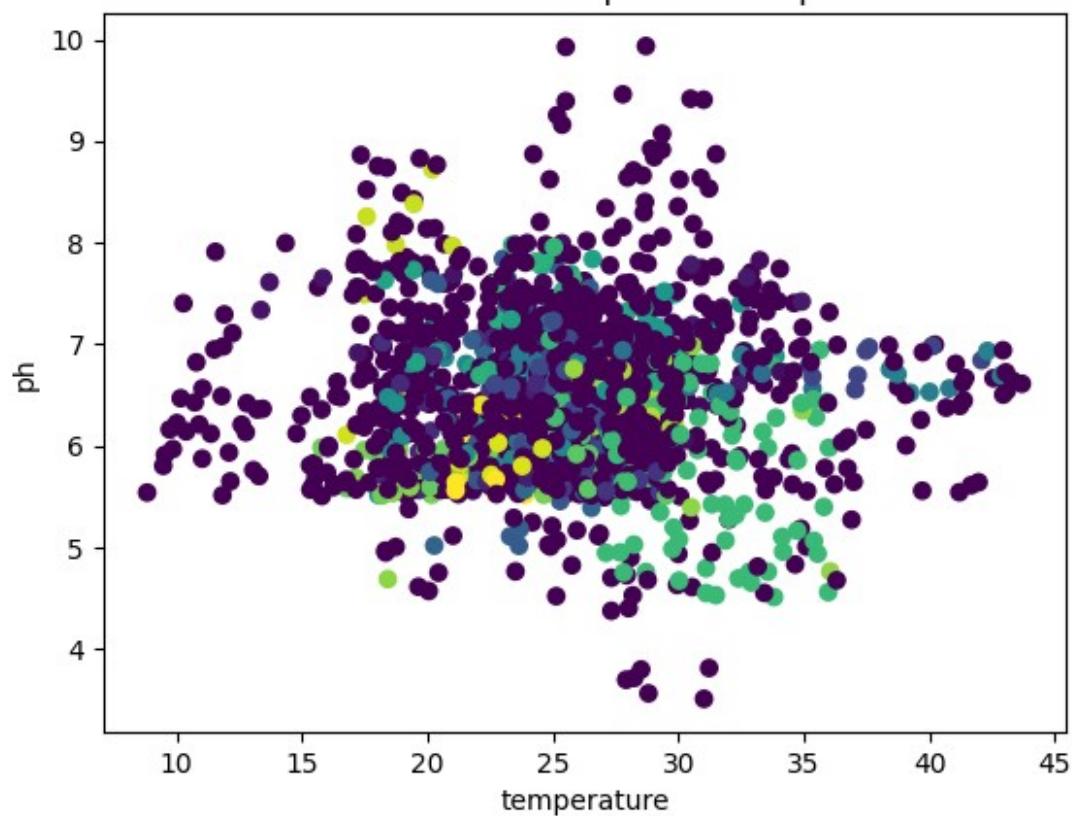
Scatter Plot: potassium vs rainfall



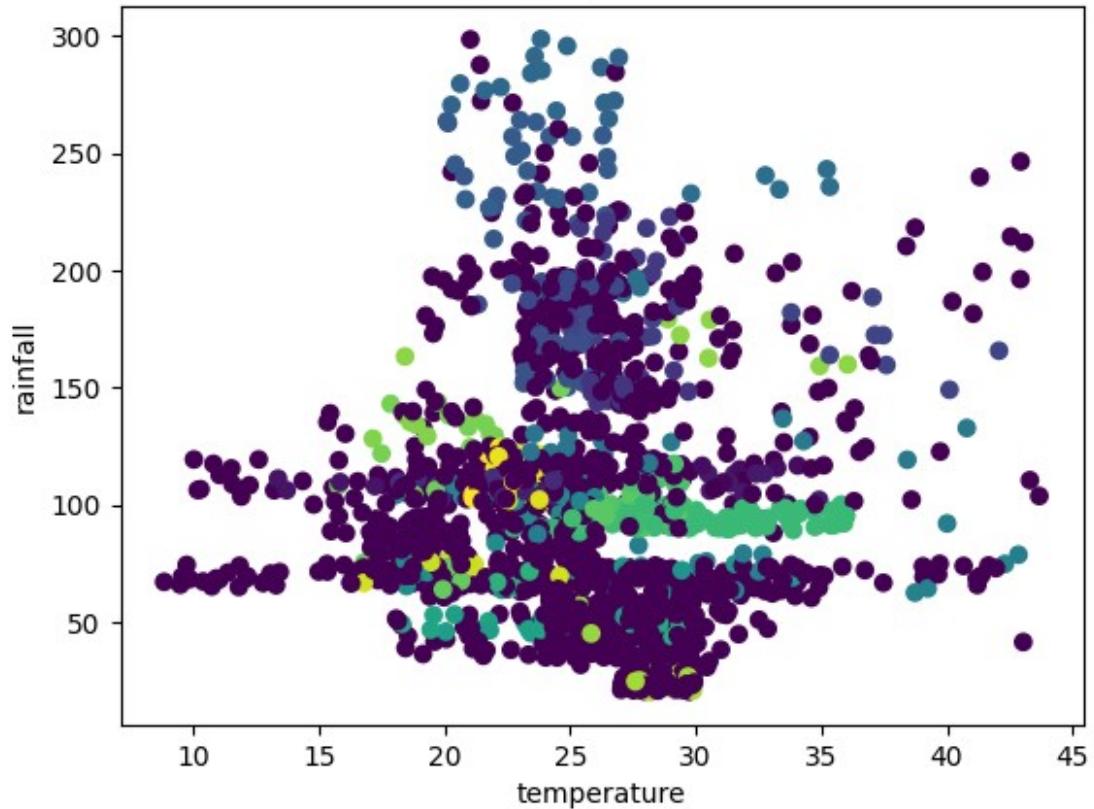
Scatter Plot: temperature vs humidity



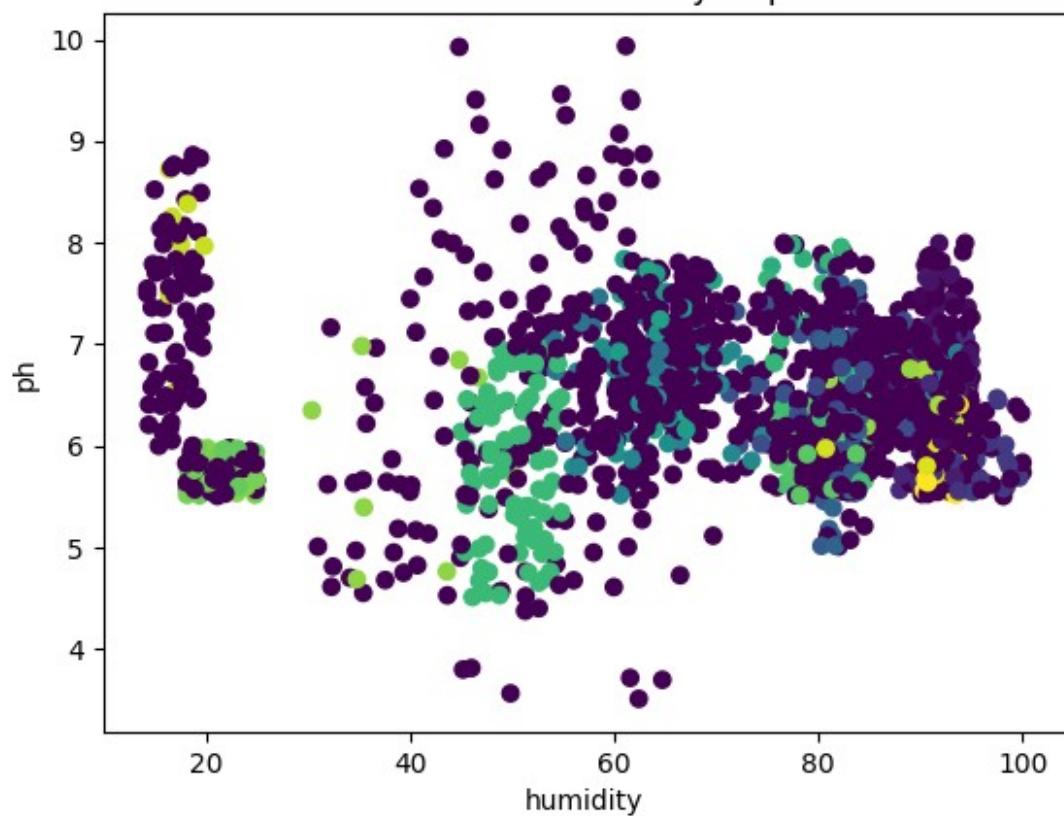
Scatter Plot: temperature vs ph



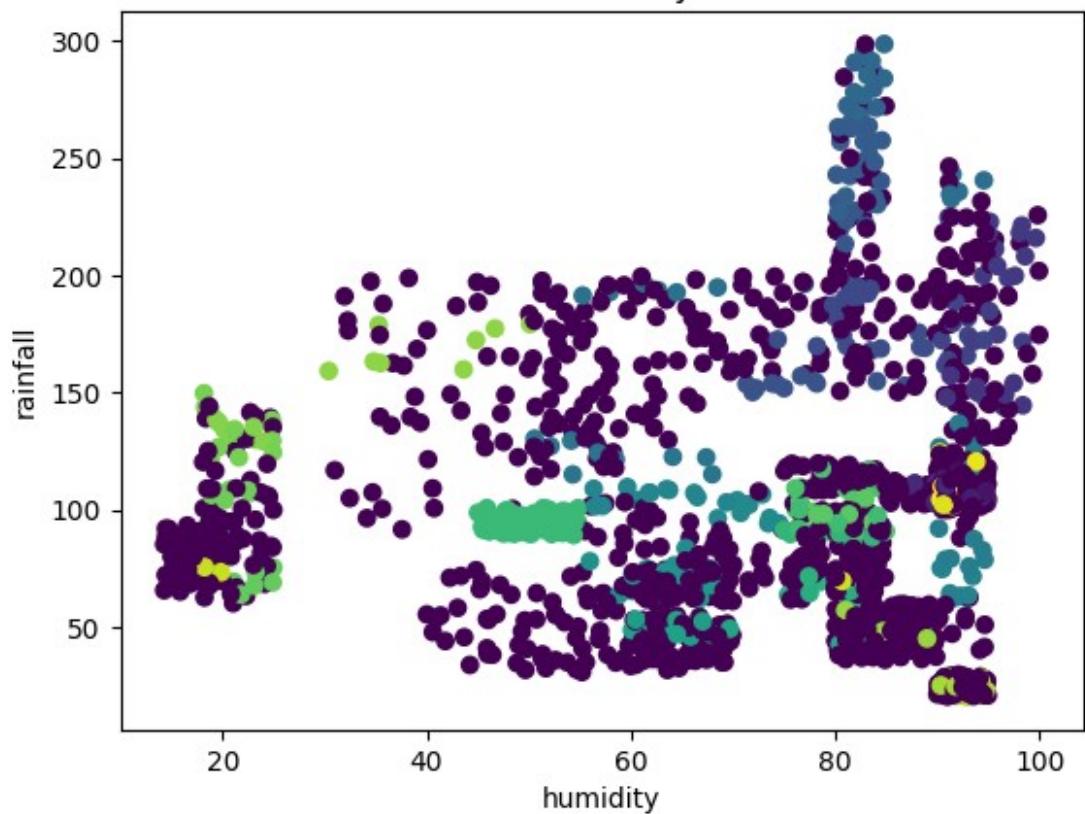
Scatter Plot: temperature vs rainfall



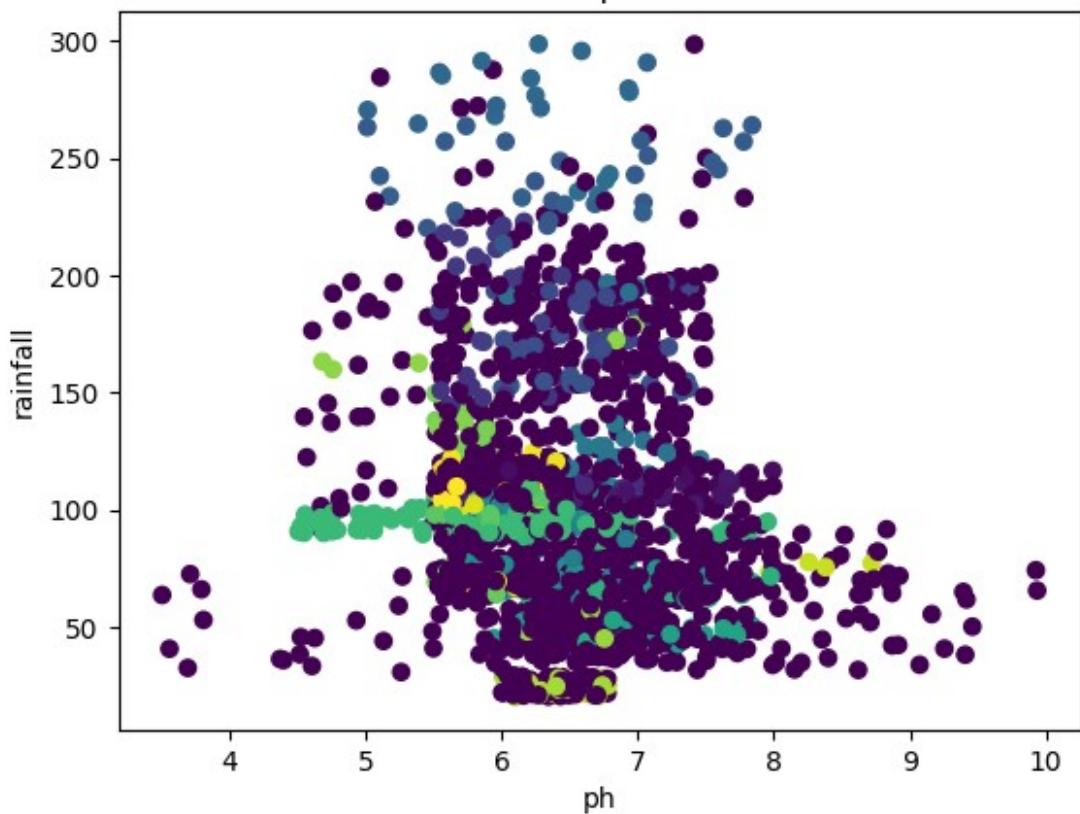
Scatter Plot: humidity vs ph



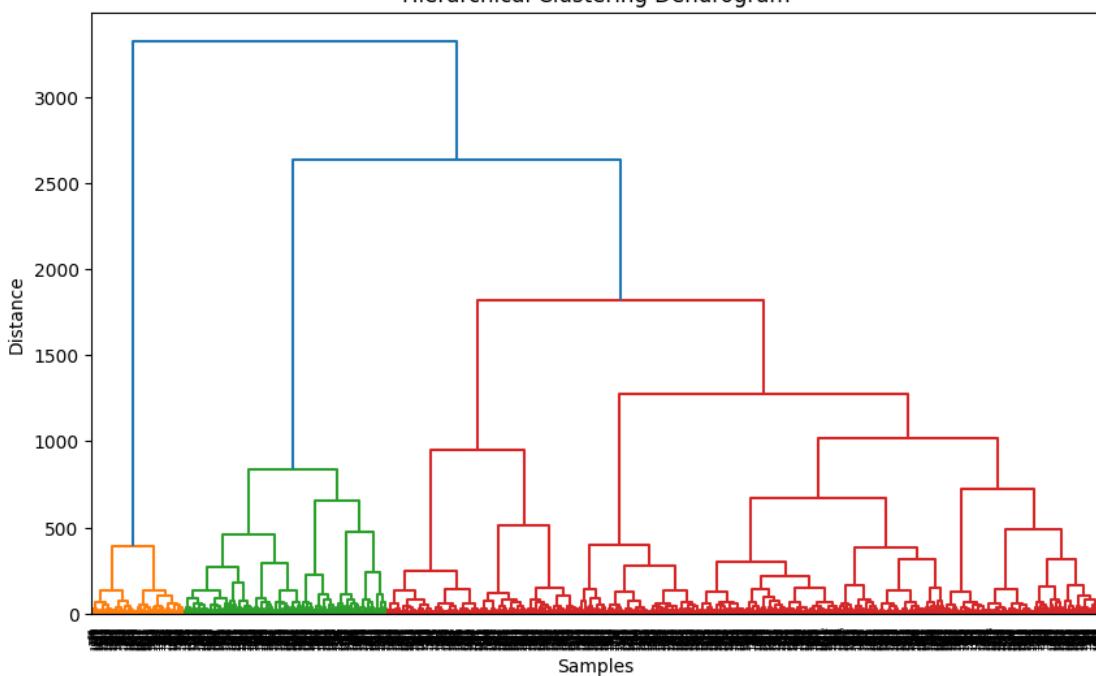
Scatter Plot: humidity vs rainfall



Scatter Plot: ph vs rainfall



Hierarchical Clustering Dendrogram



Silhouette Score: 0.24939705130709375  
Adjusted Rand Index: 0.30928048957013204

Homogeneity: 0.9864190436604117

Completeness: 0.6413153113568584

V-measure: 0.7772836325085729