

Report for 02935 Introduction to applied statistics and R for  
PhD students, Winter 2025

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# Summary

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# Introduction

# Description of data

The data process in the following report was collected in Kangerluasunnguaq (Kobbefjord, Nuuk) in Southeast Greenland in 2024. The data was collected in 100 plots placed in an area of interest of approximately 12 km<sup>2</sup> by randomised stratified sampling. Stratification was based on elevation (5 bins) and NDVI (4 bins).

Within each circular plot of 1 m<sup>2</sup> the abundance and maximum height of all vascular plant species was recorded. Abundance was assessed by means of the well known Braun-Blanquet scale (8 step version).

In all plots soil temperature, soil moisture, and general vegetation height, was measured as well. Soil temperature was measured with a generic thermometer (°C, 4 measurements, mean calculated). Soil moisture was measured with a ThetaProbe (% water content, 4 measurements, mean calculated). General vegetation height was measured with a generic ruler (cm, 4 measurements, mean calculated)

The final processed data contains data from 100 plots and 72 species of vascular plants.

```
stat_mappingplants <- readRDS("~/Library/CloudStorage/OneDrive-Aarhusuniversitet/MappingPlants/admin  
stat_mappingplants$taxon <- as.factor(stat_mappingplants$taxon)  
str(stat_mappingplants)
```

```
'data.frame':  631 obs. of  14 variables:  
 $ plot_name      : chr  "MP002" "MP003" "MP004" "MP005" ...  
 $ taxon          : Factor w/ 74 levels "Agrostis mertensii",...: 65 61 24 5 61 5 5 24 61  
 $ height         : int   15 14 7 6 23 37 23 9 35 2 ...  
 $ bb            : Factor w/ 8 levels "0.5","2.5","12.5",...: 3 4 3 4 3 5 3 4 6 3 ...  
 $ bb_num         : num   12.5 37.5 12.5 37.5 12.5 62.5 12.5 37.5 87.5 12.5 ...  
 $ mean_soil_moisture : num   95.42 3.22 25.23 35.2 28.3 ...  
 $ mean_soil_temp   : num    7.05 6.5 4 6.9 4.58 ...  
 $ mean_veg_height  : num    9.25 2.25 10.75 3 6.25 ...  
 $ rowid          : int    1 2 3 4 5 6 7 9 10 11 ...  
 $ position        : chr   "taxon_1" "taxon_1" "taxon_1" "taxon_1" ...  
 $ bryophyte_braun_blanquet_1: Factor w/ 8 levels "+ (<5 %; few individuals)",...: 7 4 7 7 5 4 6 8 3  
 $ lichen_braun_blanquet    : Factor w/ 9 levels "+ (<5 %; few individuals)",...: 2 6 4 7 4 3 2 4 2  
 $ bare_ground_braun_blanquet: Factor w/ 9 levels "+ (<5 %; few individuals)",...: 2 5 8 9 2 2 2 4 4  
 $ other_vegetation_type    : logi   NA NA NA NA NA NA ...
```

# Scientific question

- Does the most common species have different preferences (= abundance) for soil moisture and/or temperature?
  - \*
- What model can describe the relationship between the abundance of the most common species (> 10 observations in plots) and soil moisture?
- Can PCA reveal any kind of structure in the collected data based the abundance of different species?
  - If so, what do these structures indicate?

# Statistical analyses

The relationship between soil moisture and abundance of a given species cannot be assumed to be linear. Any given species of plants will have a preference for soil moisture (a wide or narrow interval) where frequency is highest. Abundance of said species will decrease with higher or lower soil moisture than this optimum. Hence, the relation could be considered to have somewhat a bell shape, but uncertain whether this would be symmetrical.

Thus, for the purpose of the analysis a generalised additive model (GAM) have been chosen. This choice was made with emphasis on the fact that this model does not make any assumptions about the relationship of the explanatory and response variable.

- Estimation: Which parameter values fit the observations best? How certain are we of our estimates?
- Model check : Are the assumptions on the underlying model fulfilled? Logically this should come first, but for practical reasons it comes after estimation.
- Simplifying the model (testing)

Model choice (expected relationship, data types)

## results

## discussion

Assumed model

assumption

evaluation

- Statistical analyses
- results
- discussion

## PCA

```
select_cols_list <- function(df) {  
  column_list <- colnames(df)  
  column_string <- paste(column_list, collapse = ",\n")  
  cat(column_string, "\n")  
  invisible(column_string)  
}
```

```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v dplyr      1.1.4      v readr      2.1.5
v forcats    1.0.0      v stringr    1.5.1
v ggplot2    3.5.1      v tibble     3.2.1
v lubridate  1.9.3      v tidyr      1.3.1
v purrr      1.0.2
-- Conflicts ----- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()     masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(janitor)
```

Attaching package: 'janitor'

The following objects are masked from 'package:stats':

chisq.test, fisher.test

```
stat_mappingplants <- readRDS("~/Library/CloudStorage/OneDrive-Aarhusuniversitet/MappingPlants/admin
wide_data <- stat_mappingplants[-c(590, 288), ] |>
  filter(rowid < 102) |>
  pivot_wider(id_cols = plot_name, names_from = taxon, values_from = bb_num) |>
  clean_names()
```

Warning: Values from `bb\_num` are not uniquely identified; output will contain list-cols.

```
* Use `values_fn = list` to suppress this warning.
* Use `values_fn = {summary_fun}` to summarise duplicates.
* Use the following dplyr code to identify duplicates.
{data} |>
  dplyr::summarise(n = dplyr::n(), .by = c(plot_name, taxon)) |>
  dplyr::filter(n > 1L)
```

```
wide_data2 <- wide_data |>
  mutate(across(-1, ~ as.numeric(as.character(.)))) |>
  mutate(across(-1, ~ replace_na(., 0)))
```

Warning: There were 74 warnings in `mutate()`.

The first warning was:

i In argument: `across(-1, ~as.numeric(as.character(.)))`.

Caused by warning:

! NAs introduced by coercion

i Run `dplyr::last\_dplyr\_warnings()` to see the 73 remaining warnings.

```
sum(is.na(wide_data2))
```

```
[1] 0
```



```
#pca_stat <- wide_data2[, -1 ]

pca_stat <- wide_data2[, !(names(wide_data2) %in% c("plot_name", "phleum_commutatum"))]

wide_data2
```

```
# A tibble: 100 x 75
  plot_name scirpus_caespitosus salix_glauca empetrum_nigrum betula_nana
  <chr>          <dbl>          <dbl>          <dbl>          <dbl>
1 MP002          12.5            0            0.5            0
2 MP003           0          37.5          37.5            0
3 MP004           0            0          12.5          37.5
4 MP005           0            0           0.5          37.5
5 MP006           0          12.5          62.5            0
6 MP007           0            0          87.5          62.5
7 MP001           0            0          87.5          12.5
8 MP008           0            0          37.5           0.1
9 MP009           0          87.5          62.5            0
10 MP010          0            0            0            0
# i 90 more rows
# i 70 more variables: salix_herbacea <dbl>, carex_bigelowii <dbl>,
# vaccinium_uliginosum <dbl>, oxyria_digyna <dbl>, huperzia_selago <dbl>,
# gnaphalium_supinum <dbl>, poa_alpina <dbl>, poa_glauca <dbl>,
# saxifraga_oppositifolia <dbl>, juncus_trifidus <dbl>,
# angelica_archangelica <dbl>, luzula_spicata <dbl>, carex_glareosa <dbl>,
# deschampsia_flexuosa <dbl>, polygonum_viviparum <dbl>, ...
```

```
select_cols_list(wide_data)
```

```
plot_name,
scirpus_caespitosus,
salix_glauca,
empetrum_nigrum,
betula_nana,
salix_herbacea,
carex_bigelowii,
vaccinium_uliginosum,
oxyria_digyna,
huperzia_selago,
gnaphalium_supinum,
poa_alpina,
poa_glauca,
saxifraga_oppositifolia,
juncus_trifidus,
angelica_archangelica,
luzula_spicata,
carex_glareosa,
deschampsia_flexuosa,
polygonum_viviparum,
phyllodoce_coerulea,
luzula_multiflora,
luzula_confusa,
silene_aucaulis,
carex_rariflora,
loiseleuria_procumbens,
salix_arctophila,
festuca_brachyphylla,
```

```

ledum_groenlandicum,
lycopodium_annotinum,
eriphorum_angustifolium,
chamaenerion_latifolium,
rhodiola_rosea,
calamagrostis_langsdorfii,
festuca_rubra,
juniperus_communis,
diphasiastrum_complanatum,
campanula_gieseckiana,
luzula_parviflora,
gymnocarpium_dryopteris,
taraxacum_croceum,
plantago_maritima,
linnaea_borealis_ssp_americana,
deschampsia_alpina,
cerastium_alpinum,
sibbaldia_procumbens,
listera_cordata,
potentilla_tridentata,
carex_brunnescens,
tofieldia_pusilla,
dryopteris_assimilis,
diphasiastrum_alpinum,
pyrola_grandiflora,
potentilla_crantzii,
poa_pratensis,
carex_scirpoidea,
bartsia_alpina,
coptis_trifolia,
veronica_wormskjoldii,
agrostis_mertensii,
veronica_alpina,
harrimanella_hypnoides,
diapensia_lapponica,
stellaria_calycantha,
scirpis_caespitosus,
chamaenerion_angustifolium,
alchemilla_alpina,
pedicularis_lapponica,
viscaria_alpina,
pedicularis_flammea,
equisetum_silvaticum,
hieracium_hyparcticum,
poa_nemoralis,
carex_canescens,
phleum_commutatum

```

```
str(wide_data2)
```

```

tibble [100 x 75] (S3: tbl_df/tbl/data.frame)
 $ plot_name           : chr [1:100] "MP002" "MP003" "MP004" "MP005" ...
 $ scirpus_caespitosus : num [1:100] 12.5 0 0 0 0 0 0 0 0 0 ...
 $ salix_glauca        : num [1:100] 0 37.5 0 0 12.5 0 0 0 87.5 0 ...
 $ empetrum_nigrum     : num [1:100] 0.5 37.5 12.5 0.5 62.5 87.5 87.5 37.5 62.5 0 ...
 $ betula_nana         : num [1:100] 0 0 37.5 37.5 0 62.5 12.5 0.1 0 0 ...
 $ salix_herbacea      : num [1:100] 0 0 0 0 0 0 0 0.5 0 12.5 ...
 $ carex_bigelowii     : num [1:100] 12.5 0 2.5 0.1 0 0.1 2.5 2.5 0.5 0.1 ...

```

\$ vaccinium_uliginosum	: num [1:100]	37.5 0 0 12.5 37.5 0 37.5 2.5 12.5 0 ...
\$ oxyria_digyna	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ huperzia_selago	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ gnaphalium_supinum	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ poa_alpina	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ poa_glauca	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ saxifraga_oppositifolia	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ juncus_trifidus	: num [1:100]	0 0.5 0 0 0 0 0 0 12.5 ...
\$ angelica_archangelica	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ luzula_spicata	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ carex_glareosa	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ deschampsia_flexuosa	: num [1:100]	0.1 2.5 0 0 0 0 0.5 0.1 0 12.5 ...
\$ polygonum_viviparum	: num [1:100]	0 0 0 0 0 0 0 0.01 0 ...
\$ phyllodoce_coerulea	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ luzula_multiflora	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ luzula_confusa	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ silene_aucaulis	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ carex_rariflora	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ loiseleuria_procumbens	: num [1:100]	0 0 0 0.1 0 0 0 0.5 0 0 ...
\$ salix_arctophila	: num [1:100]	0 0 0 0 0 0 0 0.1 0 ...
\$ festuca_brachyphylla	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ ledum_groenlandicum	: num [1:100]	0 0 0 0 0 0 2.5 0 0.1 0 ...
\$ lycopodium_annotinum	: num [1:100]	0 0 0 0 0 12.5 12.5 0 0 0 ...
\$ eriophorum_angustifolium	: num [1:100]	0.5 0 0 0 0 0 0 0 0 ...
\$ chamaenerion_latifolium	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ rhodiola_rosea	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ calamagrostis_langsdorfii	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ festuca_rubra	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ juniperus_communis	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ diphasiastrum_complanatum	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ campanula_gieseckiana	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ luzula_parviflora	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ gymnocarpium_dryopteris	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ taraxacum_croceum	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ plantago_maritima	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ linnaea_borealis_ssp_americana	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ deschampsia_alpina	: num [1:100]	0 0 0 0 0 2.5 0 0 0 ...
\$ cerastium_alpinum	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ sibbaldia_procumbens	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ listera_cordata	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ potentilla_tridentata	: num [1:100]	0 0 0 0 0 0 0 0.1 0 0 ...
\$ carex_brunnescens	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ tofieldia_pusilla	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ dryopteris_assimilis	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ diphasiastrum_alpinum	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ pyrola_grandiflora	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ potentilla_crantzii	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ poa_pratensis	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ carex_scirpoidea	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ bartsia_alpina	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ coptis_trifolia	: num [1:100]	0.1 0 0 0 0 0 0 0 0 ...
\$ veronica_wormskjoldii	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ agrostis_mertensii	: num [1:100]	0 0 0 0 0 0 0 0.1 0 0 ...
\$ veronica_alpina	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ harrimanella_hypnoides	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ diapensia_lapponica	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ stellaria_calycantha	: num [1:100]	0 0 0 0 0 0 0 0 0 ...
\$ scirpis_caespitosus	: num [1:100]	0 0 0 0 0 0 0 0 0 ...

```

$ chamaenerion_angustifolium : num [1:100] 0 0 0 0 0 0 0 0 0 0 ...
$ alchemilla_alpina          : num [1:100] 0 0 0 0 0 0 0 0 0 0 ...
$ pedicularis_lapponica      : num [1:100] 0 0 0 0 0 0 0 0 0 0 ...
$ viscaria_alpina            : num [1:100] 0 0 0 0 0 0 0 0 0 0 ...
$ pedicularis_flammea        : num [1:100] 0 0 0 0 0 0 0 0 0 0 ...
$ equisetum_silvaticum       : num [1:100] 0 0 0 0 0 0 0 0 0 0 ...
$ hieracium_hyparcticum      : num [1:100] 0 0 0 0 0 0 0 0 0 0 ...
$ poa_nemoralis              : num [1:100] 0 0 0 0 0 0 0 0 0 0 ...
$ carex_canescens            : num [1:100] 0 0 0 0 0 0 0 0 0 0 ...
$ phleum_commutatum          : num [1:100] 0 0 0 0 0 0 0 0 0 0 ...

```

```

library(remotes)
#install_github("rwehrens/ChemometricsWithR")
library(ChemometricsWithR)

```

Attaching package: 'ChemometricsWithR'

The following objects are masked from 'package:stats':

loadings, screeplot

```

mp.PC<- PCA(scale(pca_stat))
names(mp.PC)

```

```

[1] "scores"          "loadings"         "var"              "totalvar"
[5] "centered.data"

```

```
summary(mp.PC)
```

PCA model of a mean-centered matrix of 100 by 73  
Number of PCs to cover 90 percent of the variance: 36

	Var	Cumul. var.
PC 1	6.990096	6.990096
PC 2	6.189466	13.179562
PC 3	5.185294	18.364856
PC 4	4.912269	23.277125
PC 5	4.147000	27.424125
PC 10	2.844822	44.163875

```
head(mp.PC$loadings,n=3)
```

	PC 1	PC 2	PC 3	PC 4	PC 5
scirpus_caespitosus	0.02100433	-0.006161716	0.04485609	-0.02040953	0.022014862
salix_glauca	0.13173551	-0.012393257	-0.29491885	0.06706374	0.003074665
empetrum_nigrum	0.11195949	-0.059020372	0.09955936	-0.04524340	0.102951999

	PC 6	PC 7	PC 8	PC 9
scirpus_caespitosus	-0.01070334	0.001886381	-0.015790608	0.04184768
salix_glauca	0.04213159	-0.072217579	0.005581509	-0.05499974
empetrum_nigrum	-0.01152914	-0.005923966	-0.124505825	-0.12162005

	PC 10	PC 11	PC 12	PC 13
scirpus_caespitosus	-0.08350966	0.13572460	-0.19619460	0.1178451925
salix_glauca	0.08794629	-0.04977709	-0.03169407	0.0009000675

empetrum_nigrum	-0.04417072	0.09561448	0.14110835	0.2260979780	
	PC 14	PC 15	PC 16	PC 17	PC 18
scirpus_caespitosus	-0.29606471	0.32195472	-0.30584119	0.27844279	-0.1556819
salix_glauca	0.06779358	-0.02434254	-0.06957532	-0.09870617	-0.2161373
empetrum_nigrum	-0.04026837	-0.06911963	0.03481842	-0.26378600	-0.1418917
	PC 19	PC 20	PC 21	PC 22	
scirpus_caespitosus	-0.03688733	0.08219921	-0.02632309	-0.08107269	
salix_glauca	0.28763692	-0.11624040	0.01881937	-0.11304595	
empetrum_nigrum	-0.12053869	0.23190783	-0.23672678	0.11942825	
	PC 23	PC 24	PC 25	PC 26	
scirpus_caespitosus	0.005920323	0.02583533	-0.002706221	-0.0063841258	
salix_glauca	-0.020034131	0.21090617	0.020712473	0.0552562673	
empetrum_nigrum	-0.076376525	0.02149509	0.076337547	-0.0008759939	
	PC 27	PC 28	PC 29	PC 30	
scirpus_caespitosus	-0.01235032	-0.006351271	-0.0004508112	-0.001880637	
salix_glauca	-0.03007107	-0.053747183	0.0122150141	0.010486240	
empetrum_nigrum	-0.05943550	-0.092907882	-0.0021266281	-0.009089968	
	PC 31	PC 32	PC 33	PC 34	
scirpus_caespitosus	-0.0005294618	-4.330027e-03	-0.003942000	-0.01164820	
salix_glauca	-0.0028367987	3.883299e-05	0.005483626	-0.03200222	
empetrum_nigrum	0.0053178113	6.635357e-03	-0.046141632	-0.03728587	
	PC 35	PC 36	PC 37	PC 38	
scirpus_caespitosus	0.007279788	0.003247243	-0.07964226	0.05519231	
salix_glauca	-0.005448427	0.085712291	-0.08231795	0.12146807	
empetrum_nigrum	0.012422508	0.218943192	0.07421728	0.09526953	
	PC 39	PC 40	PC 41	PC 42	
scirpus_caespitosus	0.046732112	-0.087891029	-0.03257312	0.01665405	
salix_glauca	-0.007933976	0.001354495	0.03853936	0.34630640	
empetrum_nigrum	-0.020675514	0.236217477	0.37853238	-0.20433026	
	PC 43	PC 44	PC 45	PC 46	PC 47
scirpus_caespitosus	0.2340775	-0.03691249	-0.1473914	0.02242724	0.42219471
salix_glauca	0.1098232	0.04922985	0.3103832	0.20366095	-0.25615454
empetrum_nigrum	-0.1423107	0.18213910	0.0983950	-0.28829884	0.01112796
	PC 48	PC 49	PC 50	PC 51	PC 52
scirpus_caespitosus	-0.05972950	-0.4185310	0.07174345	0.02288217	0.195073547
salix_glauca	0.07482800	-0.3007001	0.25197182	-0.05194691	0.004794277
empetrum_nigrum	-0.03764784	-0.2017732	0.14733233	0.13252190	0.064539043
	PC 53	PC 54	PC 55	PC 56	PC 57
scirpus_caespitosus	-0.09526304	0.05258177	0.01273185	-0.01375436	-0.01620886
salix_glauca	-0.05734825	-0.12130225	-0.29276822	-0.05469051	-0.01009490
empetrum_nigrum	-0.14677339	-0.12737275	0.02905490	-0.05343519	-0.02251625
	PC 58	PC 59	PC 60	PC 61	
scirpus_caespitosus	-0.001681217	0.027565765	0.003203019	0.021551603	
salix_glauca	0.041905006	0.009803703	0.013197221	0.024706333	
empetrum_nigrum	-0.053199793	-0.022391653	0.030225234	-0.001334788	
	PC 62	PC 63	PC 64	PC 65	
scirpus_caespitosus	0.004406572	-0.00189968	-0.005781142	-0.001845269	
salix_glauca	0.011636786	0.01156668	0.002059197	-0.007948177	
empetrum_nigrum	-0.018924221	-0.02008754	-0.032947698	0.010248391	
	PC 66	PC 67	PC 68	PC 69	
scirpus_caespitosus	-0.007530096	-2.438259e-04	-5.888249e-05	-2.001200e-06	
salix_glauca	-0.009066001	-5.959708e-05	2.601688e-04	4.458434e-08	
empetrum_nigrum	0.030096197	-5.657010e-04	-1.963269e-04	2.791209e-05	
	PC 70	PC 71	PC 72	PC 73	
scirpus_caespitosus	-1.925745e-16	0.000000e+00	0.000000e+00	0.000000e+00	
salix_glauca	3.036567e-18	-2.053227e-16	-1.121419e-16	-9.066401e-17	
empetrum_nigrum	-1.504270e-17	1.651743e-16	1.780040e-16	-1.314775e-17	

```
X<-var(scale(pca_stat))
T<-eigen(X)$vectors
sum(is.na(X))
```

```
[1] 0
```

```
head(T,n=3)
```

```
      [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
[1,] -0.02100433 -0.006161716 -0.04485609 -0.02040953 0.022014862 -0.01070334
[2,] -0.13173551 -0.012393257 0.29491885 0.06706374 0.003074665 0.04213159
[3,] -0.11195949 -0.059020372 -0.09955936 -0.04524340 0.102951999 -0.01152914
      [,7]      [,8]      [,9]      [,10]     [,11]     [,12]
[1,] -0.001886381 0.015790608 -0.04184768 0.08350966 -0.13572460 0.19619460
[2,] 0.072217579 -0.005581509 0.05499974 -0.08794629 0.04977709 0.03169407
[3,] 0.005923966 0.124505825 0.12162005 0.04417072 -0.09561448 -0.14110835
      [,13]     [,14]     [,15]     [,16]     [,17]     [,18]
[1,] 0.1178451925 -0.29606471 0.32195472 0.30584119 -0.27844279 0.1556819
[2,] 0.0009000675 0.06779358 -0.02434254 0.06957532 0.09870617 0.2161373
[3,] 0.2260979780 -0.04026837 -0.06911963 -0.03481842 0.26378600 0.1418917
      [,19]     [,20]     [,21]     [,22]     [,23]     [,24]
[1,] -0.03688733 0.08219921 -0.02632309 -0.08107269 -0.005920323 -0.02583533
[2,] 0.28763692 -0.11624040 0.01881937 -0.11304595 0.020034131 -0.21090617
[3,] -0.12053869 0.23190783 -0.23672678 0.11942825 0.076376525 -0.02149509
      [,25]     [,26]     [,27]     [,28]     [,29]
[1,] -0.002706221 -0.0063841258 0.01235032 0.006351271 0.0004508112
[2,] 0.020712473 0.0552562673 0.03007107 0.053747183 -0.0122150141
[3,] 0.076337547 -0.0008759939 0.05943550 0.092907882 0.0021266281
      [,30]     [,31]     [,32]     [,33]     [,34]
[1,] -0.001880637 -0.0005294618 4.330027e-03 0.003942000 0.01164820
[2,] 0.010486240 -0.0028367987 -3.883299e-05 -0.005483626 0.03200222
[3,] -0.009089968 0.0053178113 -6.635357e-03 0.046141632 0.03728587
      [,35]     [,36]     [,37]     [,38]     [,39]     [,40]
[1,] -0.007279788 0.003247243 -0.07964226 0.05519231 0.046732112 0.087891029
[2,] 0.005448427 0.085712291 -0.08231795 0.12146807 -0.007933976 -0.001354495
[3,] -0.012422508 0.218943192 0.07421728 0.09526953 -0.020675514 -0.236217477
      [,41]     [,42]     [,43]     [,44]     [,45]     [,46]
[1,] 0.03257312 0.01665405 -0.2340775 -0.03691249 -0.1473914 -0.02242724
[2,] -0.03853936 0.34630640 -0.1098232 0.04922985 0.3103832 -0.20366095
[3,] -0.37853238 -0.20433026 0.1423107 0.18213910 0.0983950 0.28829884
      [,47]     [,48]     [,49]     [,50]     [,51]     [,52]
[1,] -0.42219471 0.05972950 0.4185310 -0.07174345 -0.02288217 0.195073547
[2,] 0.25615454 -0.07482800 0.3007001 -0.25197182 0.05194691 0.004794277
[3,] -0.01112796 0.03764784 0.2017732 -0.14733233 -0.13252190 0.064539043
      [,53]     [,54]     [,55]     [,56]     [,57]     [,58]
[1,] 0.09526304 -0.05258177 0.01273185 0.01375436 -0.01620886 0.001681217
[2,] 0.05734825 0.12130225 -0.29276822 0.05469051 -0.01009490 -0.041905006
[3,] 0.14677339 0.12737275 0.02905490 0.05343519 -0.02251625 0.053199793
      [,59]     [,60]     [,61]     [,62]     [,63]
[1,] 0.027565765 0.003203019 0.021551603 0.004406572 0.00189968
[2,] 0.009803703 0.013197221 0.024706333 0.011636786 -0.01156668
[3,] -0.022391653 0.030225234 -0.001334788 -0.018924221 0.02008754
      [,64]     [,65]     [,66]     [,67]     [,68]
[1,] -0.005781142 -0.001845269 -0.007530096 2.438259e-04 -5.888249e-05
[2,] 0.002059197 -0.007948177 -0.009066001 5.959708e-05 2.601688e-04
[3,] -0.032947698 0.010248391 0.030096197 5.657010e-04 -1.963269e-04
      [,69]     [,70]     [,71]     [,72]     [,73]
```

```
[1,] 2.001200e-06 0.000000e+00 0.000000e+00 0.000000e+00 0.000000e+00
[2,] -4.458386e-08 1.771736e-13 1.386098e-14 9.456768e-15 6.592533e-15
[3,] -2.791209e-05 -8.039151e-13 -7.233469e-14 -4.887652e-14 -8.010915e-14
```

```
Lambda<-t(T)%*%X%*%T
round(Lambda, digits=3)
```

```
      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
[1,] 5.103 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[2,] 0.000 4.518 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[3,] 0.000 0.000 3.785 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[4,] 0.000 0.000 0.000 3.586 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[5,] 0.000 0.000 0.000 0.000 3.027 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[6,] 0.000 0.000 0.000 0.000 0.000 2.755 0.000 0.000 0.00 0.000 0.000 0.000
[7,] 0.000 0.000 0.000 0.000 0.000 0.000 2.689 0.000 0.00 0.000 0.000 0.000
[8,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 2.519 0.00 0.000 0.000 0.000
[9,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 2.18 0.000 0.000 0.000
[10,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 2.077 0.000 0.000
[11,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 2.024 0.000
[12,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 1.922
[13,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[14,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[15,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[16,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[17,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[18,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[19,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[20,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[21,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[22,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[23,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[24,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[25,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[26,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[27,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[28,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[29,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[30,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[31,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[32,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[33,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[34,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[35,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[36,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[37,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[38,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[39,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[40,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[41,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[42,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[43,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[44,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[45,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[46,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[47,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[48,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[49,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
[50,] 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.00 0.000 0.000 0.000
```

[illegible]



[illegible]

[illegible]

[illegible]

[illegible]

[45,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[46,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[47,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[48,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[49,]	0.25	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[50,]	0.00	0.222	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[51,]	0.00	0.000	0.202	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[52,]	0.00	0.000	0.000	0.154	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[53,]	0.00	0.000	0.000	0.000	0.144	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[54,]	0.00	0.000	0.000	0.000	0.000	0.117	0.000	0.000	0.000	0.000	0.000	0.000
[55,]	0.00	0.000	0.000	0.000	0.000	0.000	0.077	0.000	0.000	0.000	0.000	0.000
[56,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.049	0.000	0.000	0.000	0.000
[57,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.000	0.000	0.000
[58,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.028	0.000	0.000
[59,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.023	0.000
[60,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.018
[61,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[62,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[63,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[64,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[65,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[66,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[67,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[68,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[69,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[70,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[71,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[72,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
[73,]	0.00	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	[,61]	[,62]	[,63]	[,64]	[,65]	[,66]	[,67]	[,68]	[,69]	[,70]	[,71]	[,72]
[1,]	0.000	0.000	0.00	0.000	0.000	0.000	0	0	0	0	0	0
[2,]	0.000	0.000	0.00	0.000	0.000	0.000	0	0	0			

[illegible]

[13,]	0
[14,]	0
[15,]	0
[16,]	0
[17,]	0
[18,]	0
[19,]	0
[20,]	0
[21,]	0
[22,]	0
[23,]	0
[24,]	0
[25,]	0
[26,]	0
[27,]	0
[28,]	0
[29,]	0
[30,]	0
[31,]	0
[32,]	0
[33,]	0
[34,]	0
[35,]	0
[36,]	0
[37,]	0
[38,]	0
[39,]	0
[40,]	0
[41,]	0
[42,]	0
[43,]	0
[44,]	0
[45,]	0
[46,]	0
[47,]	0
[48,]	0
[49,]	0
[50,]	0
[51,]	0
[52,]	0
[53,]	0
[54,]	0
[55,]	0
[56,]	0
[57,]	0
[58,]	0
[59,]	0
[60,]	0
[61,]	0
[62,]	0
[63,]	0
[64,]	0
[65,]	0
[66,]	0
[67,]	0
[68,]	0
[69,]	0
[70,]	0

```
[71,] 0
[72,] 0
[73,] 0
```

```
T[,1]
```

```
[1] -0.021004331 -0.131735509 -0.111959486 -0.056976378 0.202676292
[6] -0.014694670 -0.072386727 0.247161852 0.229421437 0.199171478
[11] 0.251819925 0.313284131 0.034696574 0.007998462 0.115880504
[16] 0.272836747 -0.014638639 -0.081614239 0.073492611 -0.023138239
[21] 0.071193730 0.041788077 -0.007653613 0.004738740 -0.012700157
[26] 0.034850882 0.041174192 -0.040355572 -0.078673066 -0.024676040
[31] 0.042544727 0.246088636 -0.019151504 -0.014638639 -0.023047611
[36] -0.012884193 -0.069283461 0.049700002 -0.061304499 0.065189181
[41] -0.014638639 -0.083631731 -0.020692599 0.231255290 0.218233569
[46] 0.041995799 -0.026089629 -0.015797880 -0.011340840 -0.019545671
[51] -0.078849620 0.195632930 -0.019967238 0.196259069 -0.017824012
[56] 0.031106645 0.039854521 -0.039438934 0.004444741 0.304621489
[61] 0.063992000 -0.017528284 -0.052436775 -0.010596302 -0.081960925
[66] -0.019114722 -0.018871994 0.026575657 -0.009541663 0.035583343
[71] -0.095992771 -0.057609636 0.289437587
```

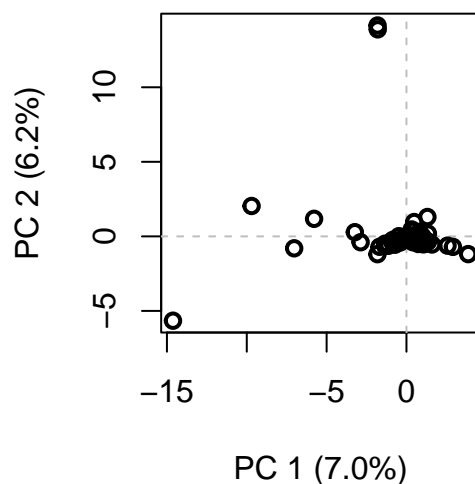
```
round(T[,1],digits=2)
```

```
[1] -0.02 -0.13 -0.11 -0.06 0.20 -0.01 -0.07 0.25 0.23 0.20 0.25 0.31
[13] 0.03 0.01 0.12 0.27 -0.01 -0.08 0.07 -0.02 0.07 0.04 -0.01 0.00
[25] -0.01 0.03 0.04 -0.04 -0.08 -0.02 0.04 0.25 -0.02 -0.01 -0.02 -0.01
[37] -0.07 0.05 -0.06 0.07 -0.01 -0.08 -0.02 0.23 0.22 0.04 -0.03 -0.02
[49] -0.01 -0.02 -0.08 0.20 -0.02 0.20 -0.02 0.03 0.04 -0.04 0.00 0.30
[61] 0.06 -0.02 -0.05 -0.01 -0.08 -0.02 -0.02 0.03 -0.01 0.04 -0.10 -0.06
[73] 0.29
```

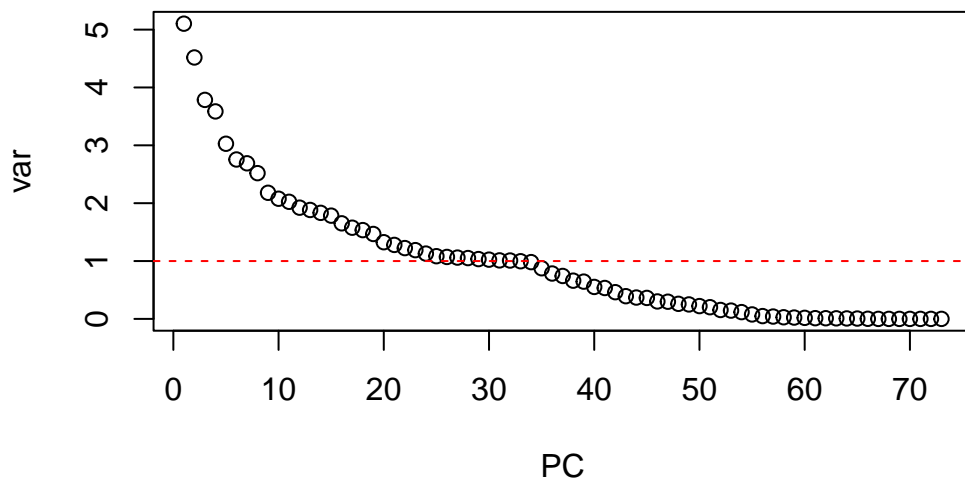
```
sum(diag(Lambda))
```

```
[1] 73
```

```
scoreplot(mp.PC, lwd=2)
```

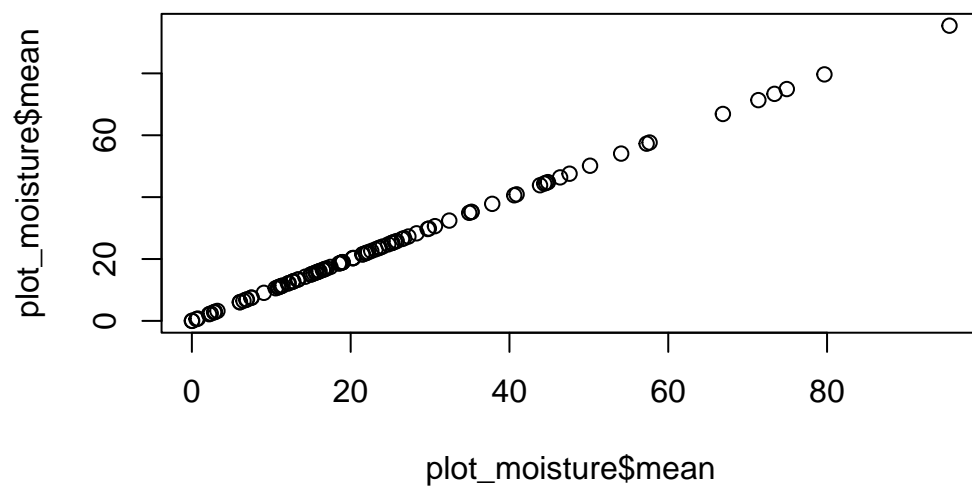






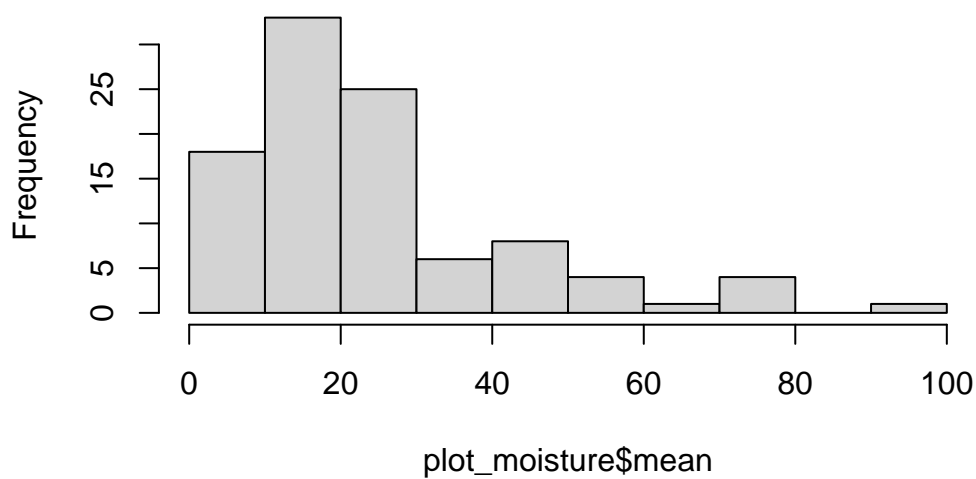
```
plot_moisture <- stat_mappingplants |>
  group_by(plot_name) |>
  summarize(mean = mean(mean_soil_moisture))

plot(x = plot_moisture$mean, y = plot_moisture$mean)
```



```
hist(plot_moisture$mean)
```

**Histogram of plot\_moisture\$mean**



```

# # Install and load vegan package
# install.packages("vegan")
# library(vegan)
#
# # Compute the Bray-Curtis dissimilarity matrix
# bray_curtis <- vegdist(pca_stat, method = "bray")
#
# # Convert to a matrix (since vegdist returns a dist object)
# bray_curtis_matrix <- as.matrix(bray_curtis)
#
# # Perform classical MDS (similar to PCA, but using dissimilarity matrix)
# mds <- cmdscale(bray_curtis_matrix, k = 2) # k is the number of dimensions you want to keep (e.g.
#
# # Plot the MDS result
# plot(mds, main = "PCA-like plot using Bray-Curtis Dissimilarity")

```

```

# #| label: chunk-6
# # Perform k-means clustering (example: 3 clusters)
# set.seed(42)
# kmeans_result <- kmeans(wide_data2[, -1], centers = 32) # Exclude first column (plot_name)
#
# # Add the cluster labels to the dataset
# wide_data2$cluster <- as.factor(kmeans_result$cluster)
#
# # Fit the tree model with k-means cluster labels as the response
# tree_model <- tree(cluster ~ ., data = wide_data2[, -1]) # Exclude non-numeric columns (plot_name)
#
# plot(tree_model)
# text(tree_model, pretty = 0)
#
# # Print the tree model
# summary(tree_model)

```

# Conclusion

# Appendix

When you click the **Render** button a document will be generated that includes both content and the output of embedded code. You can embed code like this:

You can add options to executable code like this

```
# stat_mappingplants <- readRDS("~/Library/CloudStorage/OneDrive-Aarhusuniversitet/MappingPlants/adm
#
# taxa <- pivot |>
#   group_by(taxon) |>
#   count()
#
# soil_moi <- stat_mappingplants
#
# plot(x = stat_mappingplants$mean_soil_moisture, y = stat_mappingplants$mean_veg_height)
#
# hist(stat_mappingplants$mean_soil_moisture)
#
# empnig <- stat_mappingplants[stat_mappingplants$taxon=="Empetrum nigrum",]
#
# plot(x = empnig$mean_soil_moisture, y = empnig$bb_num)
#
#
# par(mfrow = c(2,2), mgp = c(2,0.7,0), mar = c(3,3,1,1))
# model <- gam(bb_num ~ s(mean_soil_moisture), data = stat_mappingplants[stat_mappingplants$taxon ==
# plot(model)
# par(mfrow = c(1,1))
#
# summary(model)
#
# library(tree)
# model<-tree(bb_num ~ ., data = empnig)
# plot(model)
# text(model)
```

```
taxon_counts <- table(stat_mappingplants$taxon)

# Convert to a data frame for easier manipulation
taxon_summary <- data.frame(
  Taxon = names(taxon_counts),
  Count = as.vector(taxon_counts)
)

taxon_summary <- taxon_summary[order(-taxon_summary$Count), ]
```

```
# Count the occurrences of each taxon
taxon_counts <- table(stat_mappingplants$taxon)
```

```
# Get the names of taxons with more than 10 observations
frequent_taxons <- names(taxon_counts[taxon_counts > 10])

# Filter the dataset
filtered_df <- stat_mappingplants[stat_mappingplants$taxon %in% frequent_taxons, ]
```

```
veg_height <- stat_mappingplants |>
  group_by(plot_name) |>
  summarize(mean_tax = mean(height),
            mean_plot = mean(mean_veg_height))

plot(y = veg_height$mean_tax, x = veg_height$mean_plot)
```

