

solutions_exercise_multivariate

AUTHOR

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2. Multivariate analysis exercise

Libraries

Remember that you have to load the packages each time you start a new R session

```
library(vegan)
```

Loading required package: permute

Loading required package: lattice

This is vegan 2.6-8

```
library(tidyverse)
```

— Attaching core tidyverse packages — tidyverse 2.0.0 —

✓ dplyr	1.1.4	✓ readr	2.1.5
✓ forcats	1.0.0	✓ stringr	1.5.1
✓ ggplot2	3.5.1	✓ tibble	3.2.1
✓ lubridate	1.9.3	✓ tidyr	1.3.0
✓ purrr	1.0.2		

— Conflicts — tidyverse_conflicts() —

✗ dplyr::filter() masks stats::filter()

✗ dplyr::lag() masks stats::lag()

ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors

Load the data

```
itex.long <- read_csv("Data/itex.long.csv")
```

Lets look at the data to make sure it looks okay

```
head(itex.long)
```

A tibble: 6 × 6

...	1	SITE	SUBSITE	PLOT	SPECIES_NAME	SumAbund
-----	---	------	---------	------	--------------	----------

	<dbl>	<chr>	<chr>	<chr>	<chr>	<dbl>
1	1	ATQASUK	AD	ADC01	Alectoria nigricans	5
2	2	ATQASUK	AD	ADC01	Cassiope tetragona	5
3	3	ATQASUK	AD	ADC01	Cetraria cucullata	6
4	4	ATQASUK	AD	ADC01	Diapensia lapponica	6
5	5	ATQASUK	AD	ADC01	Dicranum acutifolium	1
6	6	ATQASUK	AD	ADC01	Ledum palustre	6

```
view(itex.long)
```

Here we have another ITEX dataset where we have information on species composition and species abundance within two different ITEX sites

```
unique(itex.long$SITE) # two sites
```

```
[1] "ATQASUK" "BARROW"
```

```
unique(itex.long$SUBSITE) # four subsites, two within each site
```

```
[1] "AD" "AW" "BD" "BW"
```

This is what the different habitats name represent: AD = ATQASUK dry AW = ATQASUK wet BD = Barrow dry BW = Barrow wet

Exercise

Using the ITEX dataset (itex.long.csv), plot the species composition from two sites and four sub-sites in an NMDS ordination space and group them based on their location.

Lets first think about how we should restructure our data to be able to fit an ordination. We need to convert our data from a long format to a wide format.

```
itex.wide <- itex.long %>%
  group_by(SITE, SUBSITE, PLOT) |>
  pivot_wider(names_from = SPECIES_NAME, values_from = SumAbund, id_cols = c(SITE, SUBSITE, PLOT))
  ungroup()
```

Take a look at the dataset to see how this turned out

```
view(itex.wide)
```

It looks good, our species are now columns and the species abundance within each plot is now rows

Now remember how ordinations only take in numerical values (!), so we need to remove all columns that are not numerical.

Lets take a look at the structure of our dataset.

```
str(itex.wide)
```

```
tibble [96 × 101] (S3: tbl_df/tbl/data.frame)
```

```
$ SITE : chr [1:96] "ATQASUK" "ATQASUK" "ATQASUK"
"ATQASUK" ...
$ SUBSITE : chr [1:96] "AD" "AD" "AD" "AD" ...
$ PLOT : chr [1:96] "ADC01" "ADC02" "ADC03" "ADC04" ...
$ Alectoria nigricans : num [1:96] 5 4 7 1 6 3 7 5 7 1 ...
$ Cassiope tetragona : num [1:96] 5 4 2 1 4 1 3 8 5 1 ...
$ Cetraria cucullata : num [1:96] 6 4 4 3 10 4 8 7 5 3 ...
$ Diapensia lapponica : num [1:96] 6 5 2 0 3 0 3 1 7 1 ...
$ Dicranum acutifolium : num [1:96] 1 2 6 3 3 0 0 0 0 0 ...
$ Ledum palustre : num [1:96] 6 11 1 5 8 4 13 21 9 16 ...
$ Luzula confusa : num [1:96] 4 2 6 3 13 6 21 12 2 2 ...
$ Salix phlebophylla : num [1:96] 5 6 3 0 0 1 0 2 0 7 ...
$ Vaccinium vitis-idaea : num [1:96] 17 19 28 8 12 9 9 11 3 4 ...
$ Alectoria ochroleuca : num [1:96] 0 1 0 0 0 0 1 0 0 0 ...
$ Carex bigelowii : num [1:96] 0 6 29 0 9 0 9 10 0 1 ...
$ Persicaria bistorta : num [1:96] 0 1 1 0 0 0 0 0 0 2 ...
$ Sphaerophorus globosus : num [1:96] 0 2 1 1 4 5 10 1 5 9 ...
$ Cetraria laevigata : num [1:96] 0 0 3 1 3 2 0 1 1 1 ...
$ Dactylina arctica : num [1:96] 0 0 1 0 3 0 0 1 0 0 ...
$ Trisetum spicatum : num [1:96] 0 0 5 8 3 3 4 8 0 0 ...
$ Hierochloa alpina : num [1:96] 0 0 0 9 0 4 0 1 11 4 ...
$ Cetraria nivalis : num [1:96] 0 0 0 0 2 2 1 0 3 1 ...
$ Dicranum elongatum : num [1:96] 0 0 0 0 2 0 0 0 0 0 ...
$ Dicranum spadiceum : num [1:96] 0 0 0 0 0 0 0 2 1 1 ...
$ Cladonia crustose : num [1:96] 0 0 0 0 0 0 0 0 1 2 ...
$ Cladonia uncialis : num [1:96] 0 0 0 0 0 0 0 0 0 1 ...
$ Cladonia gracilis : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cornicularia divergens : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Antennaria friesiana : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cladina mitis : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Minuartia obtusiloba : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cetraria delisei : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cladina rangiferina : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cladonia pyxidata : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Aulacomnium turgidum : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Racomitrium lanuginosum : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cetraria islandica : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cladonia coccifera : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cladonia squamosa : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Luzula nivalis : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Betula nana : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Carex aquatilis : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Carex rariflora : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Eriophorum angustifolium : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Eriophorum scheuchzeri/chamissonis : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Oncophorus wahlenbergii : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Pedicularis sudetica : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
```

\$ <i>Salix polaris</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Salix pulchra</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Aulacomnium palustre</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Persicaria vivipara</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Dupontia fisheri</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Gymnocolea inflata</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Ptychostomum capillare</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Rhytidium rugosum</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Loeskypnum badium</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Luzula wahlenbergii</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Ptilidium ciliare</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Carex rotundata</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Salix rotundifolia</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Arctagrostis latifolia</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Hylocomium splendens</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Peltigera canina</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Poa arctica</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Potentilla hyparctica</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Alopecurus alpinus</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Carex aquatilis</i> var. <i>minor</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Peltigera aphthosa</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Saxifraga cernua</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Saxifraga punctata</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Stellaria longipes</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Tomentypnum nitens</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Peltigera rufescens</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Peltigera leucophlebia</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Tephroseris integrifolia</i> subsp. <i>atropurpurea</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Cetraria ericetorum</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Pedicularis lanata</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Papaver lapponicum</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Cetraria richardsonii</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Peltigera malacea</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Pohlia cruda</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Lobaria linita</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Campyllum stellatum</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Cochlearia officinalis</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Draba lactea</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Eriophorum angustifolium</i> subsp. <i>triste</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Hierochloe pauciflora</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Meesia triquetra</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Saxifraga foliolosa</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Saxifraga hieraciifolia</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Cardamine pratensis</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Petasites frigidus</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Saxifraga hirculus</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Calamagrostis holmii</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Cerastium beeringianum</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Chrysosplenium tetrandrum</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Ranunculus nivalis</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ <i>Aneura pinguis</i>	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...

```
$ Silene uralensis subsp. apetala      : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Brachythecium turgidum               : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
[list output truncated]
```

We have 101 columns (or variables) but the three first ones are characters. Lets remove them.

```
itex.nmds <- itex.wide %>%
  dplyr::select(-SITE, -SUBSITE, -PLOT)
```

Did that work?

```
view(itex.nmds)
str(itex.nmds)
```

tibble [96 × 98] (S3: tbl_df/tbl/data.frame)

```
$ Alectoria nigricans      : num [1:96] 5 4 7 1 6 3 7 5 7 1 ...
$ Cassiope tetragona      : num [1:96] 5 4 2 1 4 1 3 8 5 1 ...
$ Cetraria cucullata      : num [1:96] 6 4 4 3 10 4 8 7 5 3 ...
$ Diapensia lapponica     : num [1:96] 6 5 2 0 3 0 3 1 7 1 ...
$ Dicranum acutifolium    : num [1:96] 1 2 6 3 3 0 0 0 0 0 ...
$ Ledum palustre          : num [1:96] 6 11 1 5 8 4 13 21 9 16 ...
$ Luzula confusa          : num [1:96] 4 2 6 3 13 6 21 12 2 2 ...
$ Salix phlebophylla      : num [1:96] 5 6 3 0 0 1 0 2 0 7 ...
$ Vaccinium vitis-idaea   : num [1:96] 17 19 28 8 12 9 9 11 3 4 ...
$ Alectoria ochroleuca    : num [1:96] 0 1 0 0 0 0 1 0 0 0 ...
$ Carex bigelowii        : num [1:96] 0 6 29 0 9 0 9 10 0 1 ...
$ Persicaria bistorta     : num [1:96] 0 1 1 0 0 0 0 0 0 2 ...
$ Sphaerophorus globosus  : num [1:96] 0 2 1 1 4 5 10 1 5 9 ...
$ Cetraria laevigata      : num [1:96] 0 0 3 1 3 2 0 1 1 1 ...
$ Dactylina arctica       : num [1:96] 0 0 1 0 3 0 0 1 0 0 ...
$ Trisetum spicatum       : num [1:96] 0 0 5 8 3 3 4 8 0 0 ...
$ Hierochloa alpina       : num [1:96] 0 0 0 9 0 4 0 1 11 4 ...
$ Cetraria nivalis        : num [1:96] 0 0 0 0 2 2 1 0 3 1 ...
$ Dicranum elongatum      : num [1:96] 0 0 0 0 2 0 0 0 0 0 ...
$ Dicranum spadiceum      : num [1:96] 0 0 0 0 0 0 0 2 1 1 ...
$ Cladonia crustose       : num [1:96] 0 0 0 0 0 0 0 0 1 2 ...
$ Cladonia uncialis       : num [1:96] 0 0 0 0 0 0 0 0 0 1 ...
$ Cladonia gracilis       : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cornicularia divergens  : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Antennaria friesiana    : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cladina mitis           : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Minuartia obtusiloba    : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cetraria delisei        : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cladina rangiferina     : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cladonia pyxidata       : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Aulacomnium turgidum    : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Racomitrium lanuginosum : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cetraria islandica      : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cladonia coccifera      : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cladonia squamosa       : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
```

\$ Luzula nivalis	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Betula nana	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Carex aquatilis	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Carex rariflora	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Eriophorum angustifolium	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Eriophorum scheuchzeri/chamissonis	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Oncophorus wahlenbergii	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Pedicularis sudetica	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Salix polaris	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Salix pulchra	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Aulacomnium palustre	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Persicaria vivipara	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Dupontia fisheri	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Gymnocolea inflata	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Ptychostomum capillare	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Rhytidium rugosum	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Loeskypnum badium	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Luzula wahlenbergii	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Ptilidium ciliare	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Carex rotundata	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Salix rotundifolia	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Arctagrostis latifolia	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Hylocomium splendens	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Peltigera canina	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Poa arctica	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Potentilla hyparctica	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Alopecurus alpinus	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Carex aquatilis var. minor	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Peltigera aphthosa	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Saxifraga cernua	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Saxifraga punctata	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Stellaria longipes	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Tomentypnum nitens	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Peltigera rufescens	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Peltigera leucophlebia	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Tephroseris integrifolia subsp. atropurpurea	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Cetraria ericetorum	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Pedicularis lanata	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Papaver lapponicum	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Cetraria richardsonii	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Peltigera malacea	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Pohlia cruda	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Lobaria linita	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Campylium stellatum	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Cochlearia officinalis	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Draba lactea	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Eriophorum angustifolium subsp. triste	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Hierochloe pauciflora	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Meesia triquetra	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Saxifraga foliolosa	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...
\$ Saxifraga hieraciifolia	: num [1:96]	0 0 0 0 0 0 0 0 0 0 0 ...

```

$ Cardamine pratensis      : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Petasites frigidus      : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Saxifraga hirculus      : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Calamagrostis holmii    : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cerastium beeringianum  : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Chrysosplenium tetrandrum : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Ranunculus nivalis     : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Aneura pinguis         : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Silene uralensis subsp. apetala : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Brachythecium turgidum  : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Cladonia cornuta       : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...
$ Carex subspathacea     : num [1:96] 0 0 0 0 0 0 0 0 0 0 ...

```

Yes that seemed to work, make sure that you make a new dataframe (in our case itex.nmds) instead of overwiting the old one, because we need information on the sites and subsites later on.

Now we can start making our NMDS

Here we are assigning a distance matrix to "dist" using Bray-Curtis index (remember how that index was suitable for species abundance data).

```
dist <- vegdist(itex.nmds, method = "bray")
```

Notice – if you get an error saying "Error in vegdist: (itex.nmds, method = "bray") : could not find function "vegdist" – you need to load the vegan package !!

Here is a way to estimate how many dimensions we need for our analysis

Functions are used in R to perform a certain tasks. First you define the function (in our case NMDS.scree) and then later on you can call that function to perform a task

```

NMDS.scree <- function(x) { # where x is the name of the data frame variable
  plot(rep(1, 5), replicate(5, metaMDS(x, autotransform = F, k = 1)$stress), xlim = c(1,
  for (i in 1:10) {
    points(rep(i + 1,5),replicate(5, metaMDS(x, autotransform = F, k = i + 1)$stress))
  }
}

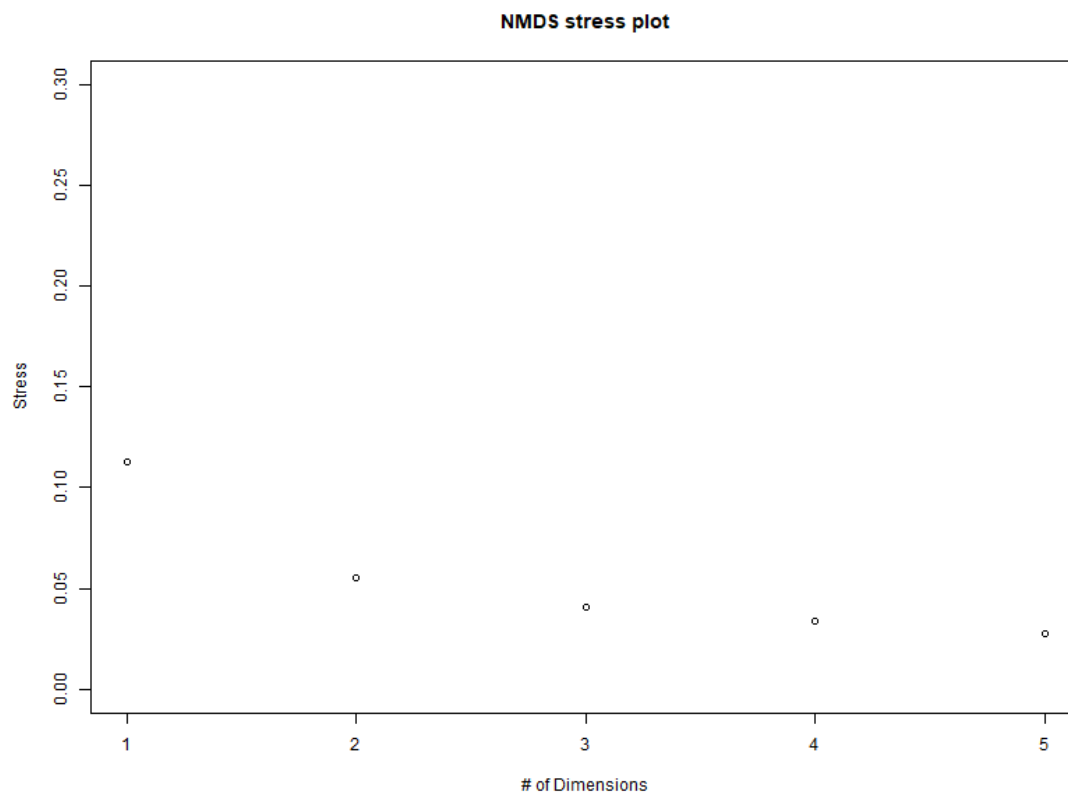
```

Here we are calling our function to perform a NMDS for 1-5 dimensions and then plotting the nr. of dimensions vs the stress.

We perform this to evaluate the optimal number of dimensions we will use in our analysis. Remember that we want our analysis to have as low stress as possible but also if we can get away with low number of dimentiontions that is good. So we will choose the number of dimention depedning on the difference in stress level between dimentiontions.

```
NMDS.scree(dist)
```

This could take a while...



Here we can see that between 2 and 3 dimensions, there isn't much difference - so we can go with 2 dimensions.

```
set.seed(2)
# set.seed() allows you to control the randomness in your code, making your results reproducible
```

Here, we perform the final analysis and check the result

```
NMDS1 <- metaMDS(dist, k = 2, trymax = 100, trace = F)
```

$k = 2$ defines the number of dimensions we want to use, in our case 2, $trymax$ determines the number of fits the ordination will perform to find the best fit, in our case 100 fits

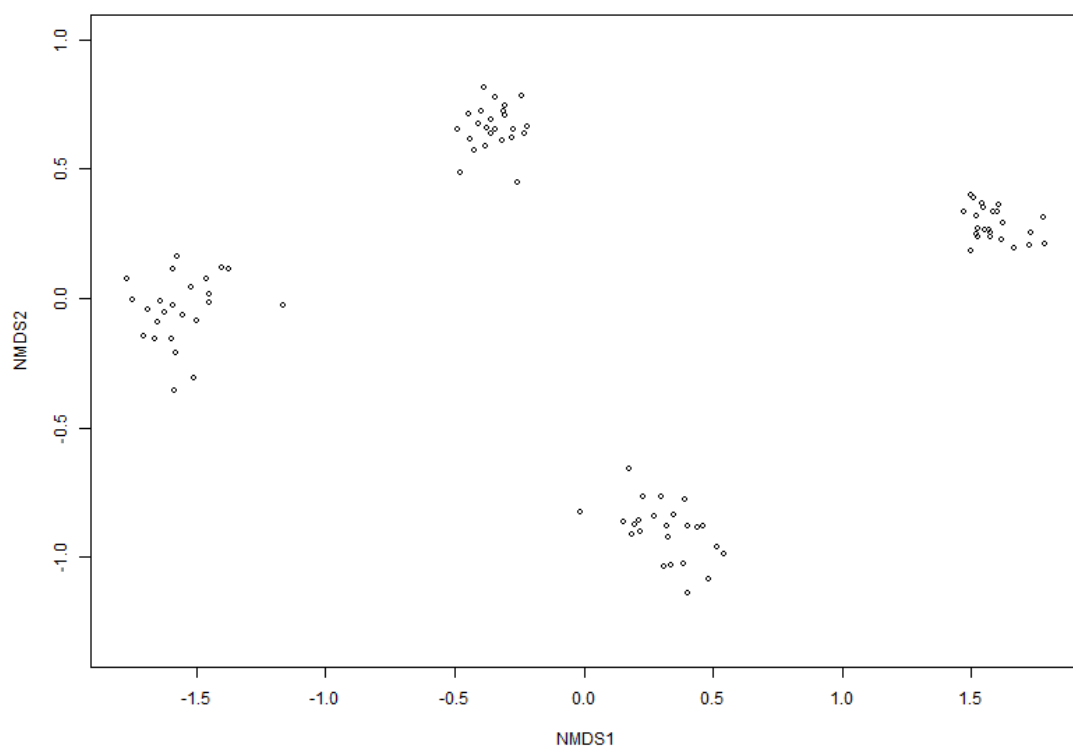
Lets check the results - check if the stress looks good.

```
NMDS1
stressplot(NMDS1)
```

From the summary of the ordination you can see that the stress is pretty good - around 0.06

Now we can plot our ordination

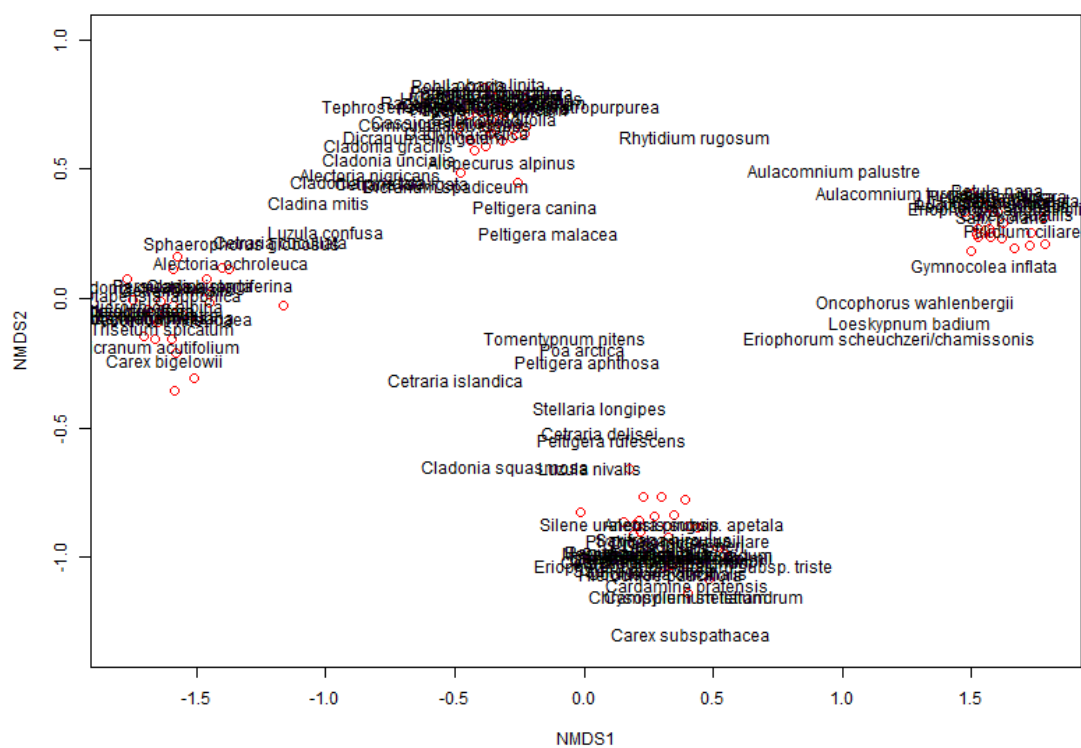
```
plot(NMDS1,)
```

This function only presents the plots in our analysis (so each row in our dataset). If we want to include species as well we can add the species scores by giving the metaMDS the original community matrix as input and specifying the distance measure.

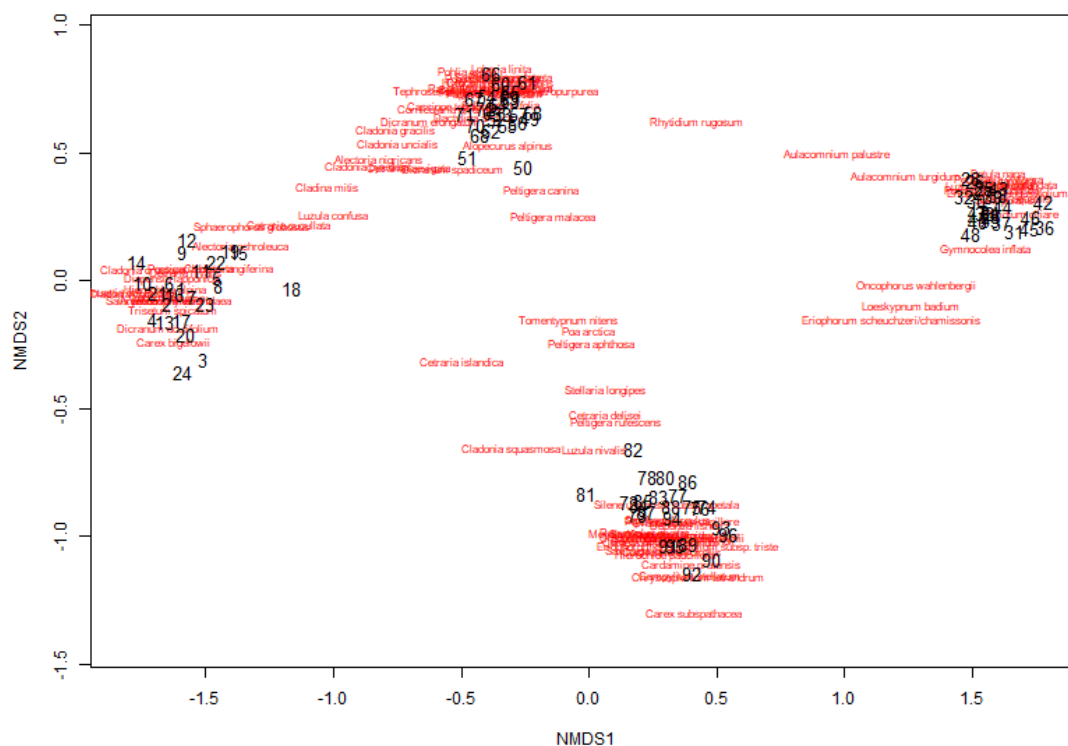
So essentially we are performing a new ordination analysis and instead of using vegsdist we define the distance within the ordination.

```
NMDS2 <- metaMDS(itex.nmds, k = 2, trymax = 100, trace = F, autotransform = FALSE, distan
plot(NMDS2)
plot(NMDS2, display = "sites", type = "n")
text(NMDS2, display = "species")
points(NMDS2, display = "sites", col = "red", cex = 1.25)
```



Alternatively, you can use the functions `ordiplot` and `orditorp`

```
ordiplot(NMDS2, type = "n")
orditorp(NMDS2, display = "species", col = "red", air = 0.01)
orditorp(NMDS2, display = "sites", cex = 1.1, air = 0.01)
```



Now this is a nice plot - we can see how the plots are really separated in space (represented as numbers) and each one of our four habitats (or subsites) associated with different plant species. But we don't know which group belongs to which subsite.

First we need to define our subsites in a vector.

```
subsites <- itex.wide$SUBSITE #remember how I told you not to overwrite this dataset, no
colors <- c(rep("#ff0000", 24), rep("#590004", 24), rep("#606c38", 24), rep("#283618", 24))
```

```
# Plot convex hulls with colors based on the group identity
ordiplot(NMDS2, type = "n")
#orditorp(NMDS2, display = "sites", type = "n", air = 0.01, cex = 1.25)
orditorp(NMDS2, display = "species", col = "#444444", air = 0.01)
for(i in unique(subsites)) {
  ordihull(NMDS2$points[subsites == i, ],
    draw = "polygon",
    groups = subsites[subsites == i],
    col = colors[subsites == i][1], # Use a single color per group
    label = TRUE)
}
```

