Vegetation data access and evaluation of taxon names
Version 0.2

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Abstract

An example session to show functionality and usage of R library *vegdata*.
After installation of package vegdata you can run this script with

```
> vignette("vegdata")
```

Most package functions expect an installation, or more precisely the directory structure, of the vegetation database program Turboveg for Windows (see `'http://www.synbiosys.alterra.nl/turboveg/'` and Hennekens & Schaminée (2001).

1 Preliminary notes

Turboveg uses dBase database format for storage. The package tries to deal with the many limitations of that format but it is essential, that you use "Database -> Reindex" in Turboveg every time you make an alteration in your Turboveg database and want to see these changed in R. Otherwise, when you delete a species occurrence in TV it will not be deleted immediately in the dBase file, instead it is only marked for deletion. That means it is still there when you access this file with R and will be deleted not until you reindex (*Database* -> *Reindex*) your Turboveg database.

2 Provided functionality

2.1 Taxonomic evaluation

One of the most important step in using vegetation data (from different sources) is to take care about the taxonomic content of the used taxon names. That is, to make sure, that exactly one (correct and valid) name defines one biological entity. Most researchers remember to convert synonyms to valid names but in many cases the care about e.g. monotypic subspecies or ambiguous taxonomic levels, is lacking. The package offers the function `tv.taxval()` with options for the adjustment of formas, synonyms, monotypic taxa, subspecies, members of aggregates and undetermined genera.

2.2 Cover standardization

Turboveg provides different abundance codes and all kinds of user defined cover codes can easily be added. For vegetation analysis an unique platform is needed which will mostly be the percentage cover of the observed area, so for every abundance code class the mean cover percentage is defined in Turboveg. Since different scales can occur in a database and the storage format of the code table in Turboveg is somewhat strange, the function `tv.coverperc()` provides automatic conversion for convenience.

2.3 Layer aggregation

The most frequently used sample unit in vegetation science is the so called relevé. A Braun-Blanquet relevé is a sample of names and coverage (abundance) of species in a specified area (usually between 1 an 1000 sqm) at a specific time. It contains (at least is intended to contain) a complete list of phytoautotrophic plants (or a defined subset) in that plot. This information can be stored in a three-column list of relevé ID, Taxon ID and performance measure (e.g. cover code).

Often additional information about the kind of occurrence of the specific plants is wanted. In Turboveg one additional column for the most widespread attribute is default: growth height classes. E.g. in a forest it is of interest, if a woody species reaches full height (tree layer) or occurs only as a small individual (herb layer). Other attributes like micro location (hummock or depression, rock or dead wood), development stage (juvenile or not, age, flowering status etc.) or the month of survey in a multi-seasonal survey could be of interest and can be added in Turboveg. For analysis you may want to differentiate species growing in different layers. Function `tv.veg()` provides options for species-plot attribute handling.

2.4 Vegetation matrix

Turboveg stores relevés as a list of occurrences (s. above) but almost all functions and programs for vegetation analyses are using plot / species crosstabulations with a 0 value for non-occurrence = observed absence. Function `tv.veg()` inflates the Turboveg list to matrix format with plots in rows and species in columns. Column names can be either species numbers, species lettercodes (default) or full names (with underscores instead of blanks).

3 Examples

Maybe the best way to introduce you into the functionalities of the package is a session with example code.

3.1 Preparations

We load the library as usual into our R environment.

```
> library(vegdata)
```

The package includes some example datasets and the taxonomic reference list Germansl 1.1, which can be loaded either with option sysPath=TRUE or after copying it to the "Data" and "Species" directories of your Turbowin installation.

If you want to learn more about the taxonomic reference list for Germany, please look at Jansen & Dengler (2008) or `'http://geobot.botanik.uni-greifswald.de/portal/reflist'`.

The package functions try to guess as many necessary things as possible. For that the path of your Turboveg installation is searched on MSWindows operation systems in the order 'O:/Turbowin', 'C:/Turbowin', 'C:/Programs/Turbowin' and 'C:/Programme/Turbowin'. Turboveg runs also on Linux systems with Wine. There it is searched in '~/.wine/drive_c/Turbowin'. In case of trouble, please specify option `tv_home` explicitly.

Using the default function settings you only have to specify the Turboveg database name. That is the name also occurring in Turbowin dialogues and can be found below the directory "Data". If you use subdirectories you have to include those (e.g. 'testdata/taxatest'). For general information about database structure see Turboveg Help).

```
> db1 <- "taxatest"
```

Main functions The package contains two main functions:

`tv.veg()` is a wrapper for a number of other functions to support the database load from Turboveg, taxonomic amendment, cover unification, layer combination and matrix generation.

`tv.site()` will load the site (header) data and does some basic corrections caused by Turbovegs dbase format.

Before you start to analyse a foreign dataset first check if there is a metainfo about the dataset available. Turboveg does not provide any metadata handling. So we recommend a simple text file named "metainfo.txt" and stored in the (Turboveg) database directory which can be loaded by:

```
> tv.metainfo(db1)
```

3.2 Site data

```
> site <- tv.site(db1)
```

```
 The following columns contain no data and are omitted
 [1] REFERENCE  TABLE_NR   NR_IN_TAB  PROJECT    AUTHOR     SYNTAXON   UTM
 [8] ALTITUDE   EXPOSITION MOSS_IDENT LICH_IDENT

 The following numeric columns contain only 0 values and are omitted
 [1] COV_TOTAL  COV_TREES  COV_SHRUBS COV_HERBS  COV_MOSSES COV_LICHEN COV_ALGAE
 [8] COV_LITTER COV_WATER  COV_ROCK   TREE_HIGH  TREE_LOW   SHRUB_HIGH SHRUB_LOW
[15] HERB_HIGH  HERB_LOW   HERB_MAX   CRYPT_HIGH

 The following numeric fields contain 0 values:
[1] INCLINATIO

 Please check if these are really measured as 0 values or if they are not measured
 and wrongly assigned because of Dbase restrictions.
 If so, use something like:
 site$Column_name[site$Column_name==0] <- NA
 summary(site[,c('INCLINATIO')])
```

The function `tv.site()` is quite straightforward. After loading the file tvhabita.dbf of the specified database, warnings are given for plots without specified relevé area or date and the fields are checked if they are empty (a lot of predefined header fields in Turboveg are often unused) or contain probably mistakable 0 values in numerical fields, due to DBase deficiencies (DBase can not handle NA = not available values reliably). It is stated in the output, if you have to check and possibly correct 0 values.

3.3 Vegetation data

Now we care about the species occurrence data.
Simple loading of species observation data from Turboveg is done by function `tv.obs()`

```
> obs <- tv.obs(db1)
```

```
reading observations ...
```

```
> head(obs)
```

```
  RELEVE_NR SPECIES_NR COVER_CODE LAYER DET_CERT SEASON MICROREL FLOWER
1         2         27         2b     0        0      0 Schlenke      0
2         2       4685          4     1        0      0 Schlenke      0
3         2       4685          1     2        1      0 Schlenke      0
4         2       4685          1     6        0      0     <NA>     10
5         1         31          3     6        0      0     <NA>      0
6         1      20096          +     6        0      0 Schlenke      1
```

Data is stored in Turboveg as a flat table of occurrence values, that is one species-plot occurrence per row. Field *RELEVE_NR* contains the plot number, *SPECIES_NR* the taxon codes, *COVER_CODE* the performance code and all other columns show species-plot attributes like growth height classes.

3.3.1 Names and entities

If you want to know the species name for a species number or letter code or vice versa you can use:

```
> tax("ACERNEG")
```

```
  SPECIES_NR LETTERCODE    ABBREVIAT   NATIVENAME SYNONYM VALID_NR
6          8    ACERNEG Acer negundo Eschen-Ahorn   FALSE        8
```

```
> tax(27, tax = TRUE)
```

```
     SPECIES_NR LETTERCODE                ABBREVIAT SYNONYM VALID_NR
3529         27       <NA> Achillea millefolium agg.   FALSE       27
                    VALID_NAME GRUPPE RANG   AGG       AGG_NAME
3529 Achillea millefolium agg.      S  AGG 60728 Achillea spec.
                              NACHWEIS                         SECUNDUM HYBRID
3529 BfN (Wisskirchen & Haeupler 1998) BfN (Wisskirchen & Haeupler 1998)      0
     BEGRUENDUN IN_QUELLE_ AUTONYM ELTER_1 ELTER_2 ELTER_3 EDITSTATUS
3529       <NA>       <NA>    <NA>    <NA>    <NA>    <NA>        BfN
```

As stated in the beginning the care about the taxonomic integrity of your database should stay be the beginning of your vegetation analyses. For Turboveg databases with taxonomic reference list GermanSL (versions 0.9, 1.0 or 1.1) this can be done semi-automatic.

To run the taxonomic adjustments of the example dataset use `tv.taxval()`

```
> obs <- tv.taxval(db1, obs)
```

```
Original number of taxa: 20

 4 Synonyms found in dataset, adapted
     SPECIES_NR                              ABBREVIAT Freq_Member VALID_NR
5230      27309                 Armeria bottendorfensis           1    20585
7609      20096     Achillea millefolium subsp. collina           1       29
7763      25203                         Abies alpestris           2     4269
9853      20583 Armeria maritima subsp. bottendorfensis           1    20585
                          VALID_NAME Freq_Agg
5230 Armeria maritima subsp. halleri        0
7609                Achillea collina        0
7763                     Picea abies        0
9853 Armeria maritima subsp. halleri        0

 1 Variants, forms, subspecies etc. found also at higher level in dataset, combined at higher level
     SPECIES_NR                           ABBREVIAT Freq_Member AGG             AGG_NAME
1830         33 Achillea millefolium subsp. sudetica           1  31 Achillea millefolium
     Freq_Agg
1830        1

 3 members of occurring aggregates in dataset, aggregated:
      SPECIES_NR            ABBREVIAT Freq_Member   AGG                  AGG_NAME
1828          31 Achillea millefolium           2    27 Achillea millefolium agg.
12032       2923  Hieracium pilosella           1 12273 Hieracium subg. Pilosella
12188         29     Achillea collina           1    27 Achillea millefolium agg.
      Freq_Agg
1828         1
12032        1
12188        1

 1 Monotypic taxa found in dataset, species converted to lower rank.
    AGG_NR        AGG_NAME AGG_RANG MEMBER_NR    MEMB_NAME MEMB_RANG
966  66142 Acoraceae spec.      FAM     61329 Acorus spec.       GAT

 1 Monotypic taxa found in dataset, species converted to lower rank.
    AGG_NR     AGG_NAME AGG_RANG MEMBER_NR      MEMB_NAME MEMB_RANG
851  61329 Acorus spec.      GAT        69 Acorus calamus       SPE

 Undetermined genera and above preserved!

 Number of taxa after validation: 13


 Warning: Critical Pseudonym(s) in dataset, please check
           to_check checknr check against SPECIES_NR VALID_NR SYNONYM
4876 Galium mollugo    2555          <NA>      27395     2549    TRUE
                           NACHWEIS
4876 BfN (Wisskirchen & Haeupler 1998)

 Warning: Critical species in dataset, please check
                to_check checknr check against SPECIES_NR VALID_NR SYNONYM
12097 Dactylis glomerata    1843          <NA>      26585     1842    TRUE
12052     Galium mollugo    2555          <NA>      26777     2548    TRUE
                            NACHWEIS
12097 BfN (Wisskirchen & Haeupler 1998)
12052 BfN (Wisskirchen & Haeupler 1998)
```

Have a look at ?tv.taxval or args(tv.taxval) to change standard options.

Taxonomic evaluation of vegetation data sets can only be performed with checklists containing appropriate taxonomic information (see tax.dbf and monotypic-D.dbf for GermanSL 1.1, Jansen & Dengler (2008).

If your database is not referenced with GermanSL you can not use tv.taxval() and you have to execute tv.veg() with option tax=FALSE or convert your database to GermanSL (Export to XML in Turboveg and re-import choosing the new GermanSL) assuming you have a central european database.

German SL is based upon the **taxon views** (Berendsohn (1995) of available checklists for Germany but contains more than 16,000 synonyms which can be used to switch between different taxon views.

To deal with a different taxonomic concept than the one used in GermanSL, you can use the option **concept**. For this a file is necessary indicating the new synonymy status, valid names and new aggregation. Within the package only a small example list (**korneck1996.dbf**) for the taxonomic view of *Armeria maritima* from (Korneck *et al.*, 1996) is implemented. Please compare the following examples.

```
> tv.taxval("taxatest")
> tv.taxval("taxatest", concept = "korneck1996")
```

3.3.2 Cover values

Cover is coded in Turboveg as an alphanumeric code. Different codes can be combined by using the mean cover percentage per cover class. Function tv.coverperc() will do this job according to the definitions in *Turboveg/Popup/tvscale.dbf*.

```
> obs <- tv.coverperc(db1, obs)
```

```
 Cover code used:  Braun/Blanquet (old)
code        r        +        1        2        3        4        5
perc         1         2         3        13        38        68        88

 Cover code used:  Braun/Blanquet (new)
code        r        +        1        2m        2a        2b        3        4        5
perc         1         2         3         4         8        18        38        68        88
```

```
> head(obs)
```

```
  RELEVE_NR SPECIES_NR COVER_CODE LAYER DET_CERT SEASON MICROREL FLOWER COVERSCALE
1         2         27         2b     0        0      0 Schlenke      0         02
2         2       4685          4     1        0      0 Schlenke      0         02
3         2       4685          1     2        1      0 Schlenke      0         02
4         2       4685          1     6        0      0     <NA>     10         02
5         1         27          3     6        0      0     <NA>      0         01
6         1         27          +     6        0      0 Schlenke      1         01
  COVER_PERC
1         18
2         68
3          3
4          3
5         38
6          2
```

3.3.3 Pseudo-species, layer combinations and vegetation matrix

tv.veg() is a wrapper for the above mentioned functions and produces a vegetation matrix with releves as rows and species as columns. Additionally care about species-plot attribute differentiation and combination, the inflation of a vegetation matrix and the handling of species codes is provided.

If we have more than one occurrence of the same species in a plot, e.g. because tree species growing as young stands and adult specimens were differentiated according to growth hight classes we have to create either pseudo-species which differntiate the occurrences in the resulting vegetation matrix or to combine species occurrences from different layers. For the latter we can use different calculations i.e. mean, max, min or first value. If we assume an independent occurrence of a species in different layers, a tree with a cover of 50% in tree layer and 50% in herb layer can be accounted with an overall cover of 75%. This is done with option lc = 'layer , the default.
If you want to differentiate species according to layer or other species-plot attributes you can specify which attributes should be used for differentiation, and how pseudo-species should be labelled (e.g. speciesname.layercode). Two example data frames for layer differentiation are included in the package. lc.0 uses all Turboveg layers (0 to 9) for pseudo-species differentiation. lc.1 combines tree layers and shrub layers to a maximum of three pseudo-species per taxon.

```
> lc.1

   LAYER  COMB
1      0     0
2      1  Tree
3      2  Tree
4      3  Tree
5      4 Shrub
6      5 Shrub
7      6     0
8      7     0
9      8     0
10     9     0
```

```
> veg <- tv.veg(db1, lc = "sum", comb = list(lc.1, c("LAYER")), dec = 1,
+     quiet = TRUE)
```

```
> veg[, 1:7]

  ACERPSE ACERPSE.Shrub ACHI#MI ACHISPE ACOUCAL ADONAES AGRTS;P
1       3            13      43       3       0       3       3
2       0             0      18       0       0       0       0
3       0             0       0       0       3       0       0
```

If you want to use only presence/absence information in your analyses you can do:

```
> veg[veg > 0] <- 1
```

3.4 Additional functions

syntab() produces a relative or absolute frequency table of a vegetation table classification with the possibility to filter according to threshold values. To exemplify the function we use the second dataset implemented the package. It is the demonstration dataset from (Leyer & Wesche, 2007), a selection of grasland relevés from the floodplains of the river Elbe.

```
> data(elbaue)
```

```
> cluster <- rep(NA, nrow(site))
> cluster[elbaue.env$MGL < -100] <- "dry"
> cluster[elbaue.env$MGL < -25 & elbaue.env$MGL >= -100] <- "wet"
> cluster[elbaue.env$MGL >= -25] <- "very.wet"
```

```
> syntab(elbaue, cluster, limit = 30, sort = c("dry", "wet", "very.wet"),
+     relfr = TRUE)
```

```
 Number of clusters:  3
Cluster frequency 13 6 14
```

Use help(package='vegdata') for a complete list of available functions and data sets in vegdata.

At http://geobot.botanik.uni-greifswald.de/download/ a development version of the package vegdata is available with additional functionalities (but less stability).

The package vegdata serves only as a helper for further analysis of vegetation data which can already be done by powerful R packages like vegan. But with the functions shown above we are now ready to execute all kinds of analyses in the wide area of vegetation analyses.

3.5 Vegetation analyses

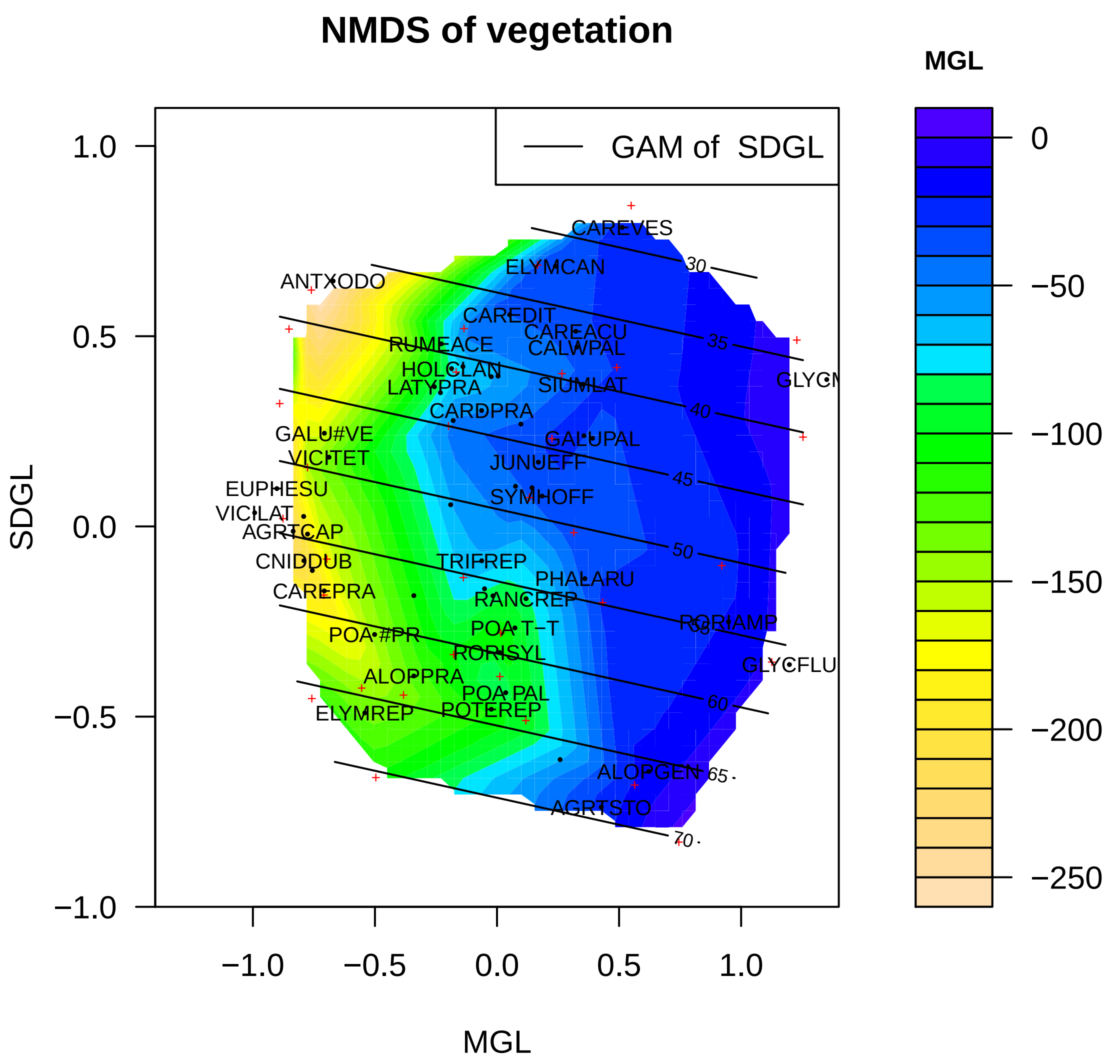
For instance we can do a "Nonmetric Multidimensional Scaling with Stable Solution from Random Starts Axis Scaling and Species Scores" which is a wrapper for Kruskal's Non-metric Multidimensional Scaling (Cox & Cox, 1994, 2001) from Jari Oksanen (Oksanen *et al.*, 2008).

```
> library(vegan)
> veg.nmds <- metaMDS(elbaue, distance = "bray", trymax = 5, autotransform = FALSE,
+     noshare = 1, expand = TRUE, trace = 2)
> plot(veg.nmds)
```

To show the result in comparison with environmental measurements in a nice graphic we do some magic.

```
> library(labdsv)
> library(akima)
> color = function(x) rev(topo.colors(x))
> nmds.plot <- function(ordi, site, var1, var2, disp, ...) {
+     lplot <- nrow(ordi$points)
+     lspc <- nrow(ordi$species)
+     filled.contour(interp(ordi$points[, 1], ordi$points[, 2], site[,
+         var1]), ylim = c(-1, 1.1), xlim = c(-1.4, 1.4), color.palette = color,
+         xlab = var1, ylab = var2, main = paste("NMDS of vegetation"),
+         key.title = title(main = var1, cex.main = 0.8, line = 1, xpd = NA),
+         plot.axes = {
+             axis(1)
+             axis(2)
+             points(ordi$points[, 1], ordi$points[, 2], xlab = "", ylab = "",
+                 cex = 0.5, col = 2, pch = "+")
+             points(ordi$species[, 1], ordi$species[, 2], xlab = "",
+                 ylab = "", cex = 0.2, pch = 19)
+             ordisurf(ordi, site[, var2], col = "black", choices = c(1,
+                 2), add = TRUE)
+             orditorp(ordi, display = disp, pch = " ")
+             legend("topright", paste("GAM of ", var2), col = "black",
+                 lty = 1)
+         }, ...)
+ }
```

```
> print(nmds.plot(veg.nmds, elbaue.env, disp = "species", var1 = "MGL",
+     var2 = "SDGL"))
```



The first axis of our NMDS plot show the influence of mean groundwater level on the patterns of the dataset. *Glyceria maxima* is marking the wet side of the gradient, whereas *Cnidium dubium Agrostis capillaris* or *Galium verum agg,* occur only at low mean groundwater level. The second axis can be assigned to the fluctuation of water levels measured as standard deviation of mean groundwater level. Species indicating high water fluctuation are *Agrostis stolonifera* or *Alopecurus geniculatus* whereas *Carex vesicaria* occurrs only at more balanced situations.

References

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