Vegetation data access and taxonomic harmonization version 0.9.7

Florian Jansen

November 5, 2019

Abstract

An example session to show functionality and usage of R library `vegdata`.
After installation of `vegdata` you can invoke this PDF with
vignette('vegdata')

1 Preliminary notes

Some `vegdata` functions expect an installation, or more precisely the main directory structure, of the vegetation database program Turboveg for Windows (see `'http://www.synbiosys.alterra.nl/turboveg/'` and Hennekens and Schaminee [2001]. If the package can not find a Turboveg installation it will use the directory within the package installation path. If you want to use function `taxval` for taxonomic harmonization you will need to have GermanSL or an equally structured reference list. If you do not specify any, the most recent version of GermanSL will be used and if it can not be found within the specified path, it will be downloaded from `https://germansl.infinitenature.org/GermanSL/latest/GermanSL.zip`.

Turboveg uses dBase database format for storage. The package tries to deal with the limitations of that format but it is essential, that you use "Database -¿ Reindex" in Turboveg every time you delete something in your Turboveg database. Otherwise it will not be deleted immediately in the dBase file, instead it is only marked for deletion, i.e. it is still there when you access this file with R and will not be recognized as deleted until you reindex your Turboveg database.

2 Provided functionality

2.1 Taxonomic harmonisation

One of the most important steps in using vegetation data (from different sources) for statistical analysis is to take care about the taxonomic content of the names existing in the database. 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 [Jansen and Dengler, 2010]. The package offers the function `taxval` with different options for the adjustment of synonyms, monotypic taxa, taxonomic levels, members of aggregates and undetermined species.

2.2 Database access

vegdata (will) provide direct access to different vegetation database formats:

Turboveg is a desktop program, written in VisualBasic. It provides basic functions to enter, import, maintain and export vegetation data. From the 2 000 000 vegetation plots registered in `http://www.GIVD.info` approximately 1.5 million are stored in Turboveg databases format.

vegetweb is the German national vegetation database. vegetweb is accessible at `https://www.vegetweb.de`. Data can be selected, open access data can be downloaded directly, other data after clearance from the owners.

VegX is an international exchange standard. An R package with a S4 implementation of the standard is in development

2.3 Cover standardization

Turboveg provides different abundance codes and all kinds of user defined cover codes can easily be added. For vegetation analysis a unique species performance platform is needed which will in most cases be the percentage cover of the observed plot area. Therefore, 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.

2.4 Layer aggregation

The most frequently used sample unit in vegetation science is a plot based vegetation relevé [Dengler et al., 2011]. A Braun-Blanquet relevé is a sample of names and coverage (abundance) of species in a specified area (usually between 1 and 1000 m^2) at a specific time. It contains (at least is intended to contain) a *complete* list of photo-autotrophic 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 is wanted. In Turboveg one additional column for the most widespread attribute is included by 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, flowering status etc.) or the month of survey in a multi-seasonal survey could also be of interest and can be added in Turboveg. For analysis you may want to differentiate species with different species-plot attributes (e.g. growing in different layers). Function `tv.veg` provides possibilities for species-plot attribute handling.

2.5 Vegetation matrix

Turboveg stores relevés as a dataframe of occurrences (s. below) but almost all functions and programs for vegetation analyses use plot-species cross-tables 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 letter-codes (default) or full names (with underscores instead of blanks to match the R naming conevntions).

3 Preparations

The best way to introduce the functionalities of the package is a session with example code.

We load the library as usual into our R environment.

```
library(vegdata)
```

Several functions of this package use the directory structure of Turboveg. The first time such a function is called, the internal function `tv.home` tries to find your Turboveg installation path. Depending on whether you have Turboveg installed on your computer or not, it will give you a message (and an invisible return) about the Turboveg installation path or the path to the Turboveg directory structure of package vegdata.

```
tv_home <- tv.home()
```

If you want to change this, declare manually by setting option "tv_home":

```
options(tv_home="path_to_your_Turboveg_root_directory")
```

4 Service functions

```
tv.db()

[1] "./elbaue"   "./taxatest"
```

will give you a list of available Turboveg database names (directories within the Turboveg *Data directory*).

```
tv.refl()

[1] "GermanSL 1.4"
```

GermanSL is the default Taxonomic reference list in package `vegdata`. However, whenever you use a Turboveg database name in a function, the Reference list will be read from the database configuration file "tvwin.set" if possible. If you want to change the default reference list:

```
tv.refl('your_preferred_list')
```

will change option *tv.refl* which will be used whenever db or refl is not given.

Package vegdata contains several service functions to query the taxonomic information contained in the reference list.

```
tax('Brachythecium rutabulum')

Reference list used:GermanSL 1.4
Taxonomic reference list file /tmp/Rtmp1IYXQL/Species/GermanSL 1.4/species.dbf does not exist.

Taxonomic list (species.dbf) of reflistGermanSL 1.4 not available.

      TaxonUsageID LETTERCODE                              TaxonName
22887        80422    BRATRUT                Brachythecium rutabulum
27110        90370    BRAT#AG            Brachythecium rutabulum agg.
31360        99979    BRATR;R Brachythecium rutabulum var. rutabulum
      VernacularName SYNONYM TaxonConceptID
22887           <NA>   FALSE          80422
27110           <NA>   FALSE          90370
31360           <NA>    TRUE          80422
```

The GermanSL is not included in vegdata to keep the R package small. Instead the reference list will be automatically downloaded into the tv_home directory (see `tv.home()`) or a temporary folder, if it is not installed but needed. If you want to use a different list, specify `refl=<Name of your list>` according to the directory name in the Turboveg directory *Species*. Function `tax` can use the given species name (with option strict=FALSE also name parts), or 7 letter abbreviation or the TaxonUsageID (called SPECIES_NR in Turboveg) to look for all (partially) matching species names within the reference list.

In GermanSL versions 1.1 to 1.3 additional information for every taxon is stored in an extra file (tax.dbf) which could be used with option *detailed = TRUE*. Since version 1.4 all information is included in the normal Turboveg file *species.dbf*.

tax will give you all matching names by default. If you set option *strict=TRUE*, only the species with exact match to the given character string will be returned.

syn will give you all taxon names within the swarm of synonyms. The valid name is marked in column SYNONYM with FALSE.

```
tax('Elytrigia repens')$TaxonName

Reference list used:GermanSL 1.4
```

```
[1] "Elytrigia repens subsp. arenosa"  "Elytrigia repens"
[3] "Elytrigia repens var. caesia"     "Elytrigia repens var. littoralis"
[5] "Elytrigia repens var. repens"

syn('Elytrigia repens')

Name swarm of Elytrigia repens :
      TaxonUsageID                         TaxonName SYNONYM
4154          6541   Agropyron repens subsp. caesium    TRUE
4157          6544 Elymus repens subsp. repens s. l.    TRUE
4906         10260      Elymus repens subsp. caesium    TRUE
8891         20143                 Agropyron caesium    TRUE
8909         20167    Agropyron repens subsp. repens    TRUE
10071        21639                  Elytrigia repens    TRUE
12261        24393                   Triticum repens    TRUE
14208        27778                     Elymus repens   FALSE
14301        27914                  Agropyron repens    TRUE
           EDITSTATUS
4154  BfN Wisskirchen
4157        Korrektur
4906  BfN Wisskirchen
8891  BfN Wisskirchen
8909  BfN Wisskirchen
10071 BfN Wisskirchen
12261 BfN Wisskirchen
14208 BfN Wisskirchen
14301 BfN Wisskirchen
```

The reference list contains information about the taxonomic hierarchy which can be used with *childs* or *parents*.

```
child(27, quiet=TRUE)$TaxonName
parent('ACHIMIL')
```

If you want to learn more about the taxonomic reference list *GermanSL* for Germany, please look at Jansen and Dengler [2008]. You can download the list manually from `'http://geobot.botanik.uni-greifswald.de/portal/reflist'`.

5 Load data from Turboveg

Care about the taxonomic content of the datasets is crucial for every analysis. Some of these steps can be automated with an appropriate taxonomic reference. For background and details see [Jansen and Dengler, 2010].

```
db <- 'taxatest'
```

Defines the vegetation database name according to the name of the Turboveg database directory name

```
tv.metadata(db)
```

Metainformation, i.e. information about the kind of available information should always be given for every database. Since Turboveg does not ask and provide such information, write a simple text file called metainfo.txt and save it within the database folder. Turboveg does not provide any metadata handling. Database `taxatest` is an artificial dataset to show functionalities and necessary steps for taxonomic harmonization.

Let's have a look at the Turboveg data structure.

```
getOption('tv_home')

[1] "/tmp/Rtmp1IYXQL"
```

```
obs.tax <- tv.obs(db)
# Adding species names
species <- tax('all', refl=tv.refl(db=db))
obs.tax$TaxonName <-  species$TaxonName[match(obs.tax$TaxonUsageID, species$TaxonUsageID)]
head(obs.tax[,c('RELEVE_NR','TaxonUsageID','COVER_CODE','LAYER','TaxonName')])

  RELEVE_NR TaxonUsageID COVER_CODE LAYER
1         2           27         2b     0
2         2         4685          4     1
3         2         4685          1     2
4         2         4685          1     6
5         1           31          3     6
6         1        20096          +     6
                           TaxonName
1           Achillea millefolium agg.
2                       Quercus robur
3                       Quercus robur
4                       Quercus robur
5                Achillea millefolium
6 Achillea millefolium subsp. collina
```

This condensed format shows only presences of species observations. Every species observation is stored in one row and the membership to a specific vegetation plot is given in column *RELEVE_NR*.

5.1 Taxonomic harmonisation - function taxval

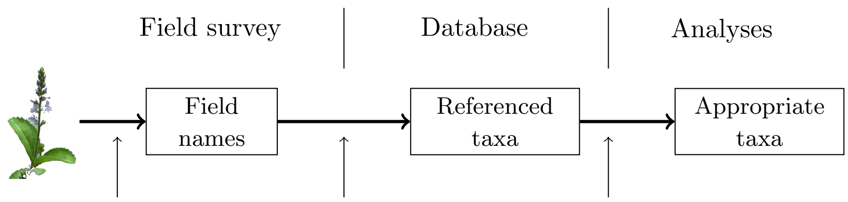
We are using the taxonomic reference list GermanSL [Jansen and Dengler, 2008] which contains not only information about synonymy of species names, but also about the taxonomic hierarchy. This enables several semi-automatic enhancements of the taxonomic information stored in your vegetation database. If your database is not referenced to GermanSL (and can not be converted), you have to dismiss function `taxval` (option tax=FALSE in `tv.veg`) and do the taxonomic harmonization by hand (function `comb.species`).

```
obs.taxval <- taxval(obs.tax, db=db, maxtaxlevel='AGG', interactive=FALSE, check.critical = TRUE)

Original number of names: 20
4 Synonyms found in dataset. Changed to valid names.
2 taxa higher than AG1 found. Deleted!
1 monotypic taxa found in dataset.  Will be set to species rank if possible.
4 conflicting child taxa found in dataset.
[1] "Achillea collina"
[2] "Achillea millefolium"
[3] "Achillea millefolium subsp. sudetica"
[4] "Hieracium pilosella"
Number of taxa after harmonisation: 11
Warning: Potential pseudonyms in dataset, please check.
       to_check check_No        check against TaxonUsageID
 Galium mollugo     2555 Galium mollugo auct.        27395
                       AccordingTo
 BfN(Wisskirchen u. Haeupler 1998)
Warning: Critical species in dataset, please check
           to_check check_No            check against TaxonUsageID
 Dactylis glomerata     1843 Dactylis glomerata s. l.        26585
     Galium mollugo     2555     Galium mollugo s. l.        26777
                       AccordingTo
 BfN(Wisskirchen u. Haeupler 1998)
 BfN(Wisskirchen u. Haeupler 1998)
```

The database contains 20 different names in the beginning.

Synonyms First the number of species names which are synonyms are given. They are transferred to accepted taxon names, respectively numbers (see option syn='adapt'). If you want to preserve synonyms, choose option syn = 'conflict' or 'preserve'.



1. Field interpretation
   - document your source(s) of taxonomic interpretation (Flora)
   - specify determination certainty
   - collect herbarium specimen
2. Database entry
   - document field records / original literature
   - reference as conservative as possible to a taxonomic reference list with all relevant taxa (synonyms, field aggregates, horticultural plants, ...)
   - document your interpretations
3. Preparation for analyses
   - standardize taxon name parts (rank abbreviations, genus sex, y versus i etc.)
   - convert synonyms
   - summarize monotypic taxa
   - clean up nested taxa
   - clean up taxonomic ranks
   - ...

Three steps of taxonomic interpretation

- need of appropriate tools (software, reference lists)
- standards
- threefold attention

Figure 1: Steps of taxonomic interpretation

Monotypic species within the area Monotypic taxa are valid taxa which are the only child of their next higher taxonomic rank within the survey area. By default they will be converted by `taxval` to the higher rank. For instance *Poa trivialis* is in Germany only represented by *Poa trivialis subspecies trivialis*. Both taxa are valid, but for most analysis only one name for these identical entities must be used. By default a list of monotypic taxa within the GermanSL (whole Germany) is considered (see `tv.mono('GermanSL 1.4')`). The default is to set all monotypic species to the higher rank (because many monotypic subspecies can occur in vegetation databases).
If necessary, the procedure has to be repeated through the taxonomic

Trimming the hierarchy If your database contains the taxon *Asteraceae spec.*, the taxval code explained in the next chapter will aggregate occurrences of all your *Asteracea* to the family level. To prevent this you can delete all observations above a certain taxonomic level. The default is not to trim the hierarchy (ROOT = "Greenish something" is the toplevel).

Solving the nestedness If your database contains *Achillea millefolium* but also *Achillea millefolium agg.* for most analysis it will be necessary to coarsen the first (option ag='conflict') because *A. millefolium agg.* will probably include further occurrences of *Achillea millefolium*.
The procedure has to be repeated until all occurring taxonomical levels are considered.
Especially with aggregates and their members the coarsening to the higher level can be a sad fate. If you have 100 occurrences of *Achillea millefolium* but a single one with *A. mill. agg.* you might want to clean your observational dataframe beforehand or do the aggregation afterwards manually with tv.veg(db, ag='preserve') and a manual correction with function comb.species (see below).

I confess that it is a strange and complete artificial example. Starting with 20 names in the beginning only 11 names survived the valuation. All others had to be converted to give only information about consistent taxon concepts.

```
obs.taxval$OriginalName <- obs.taxval$TaxonName
obs.taxval$TaxonName <-  species$TaxonName[match(obs.taxval$TaxonUsageID, species$TaxonUsageID)]
obs.taxval[!duplicated(obs.taxval$OriginalName),c('RELEVE_NR', 'COVER_CODE', 'TaxonName', 'OriginalName')]

   RELEVE_NR COVER_CODE                           TaxonName
1          2         2b           Achillea millefolium agg.
2          2          4                       Quercus robur
5          1          3           Achillea millefolium agg.
6          1          +           Achillea millefolium agg.
8          1          1                 Acer pseudoplatanus
10         1          1                         Picea abies
11         1          1           Achillea millefolium agg.
12         3          1     Armeria maritima subsp. halleri
13         3          1    Armeria maritima subsp. elongata
14         3          1     Armeria maritima subsp. halleri
17         1          1                      Galium mollugo
18         1          1                  Dactylis glomerata
19         1          1                   Adonis aestivalis
20         1          1 Agrostis stolonifera var. palustris
21         2          1           Hieracium subg. Pilosella
22         2          3     Armeria maritima subsp. halleri
23         3          1           Hieracium subg. Pilosella
24         2          1                         Picea abies
                          OriginalName
1              Achillea millefolium agg.
2                          Quercus robur
5                   Achillea millefolium
6      Achillea millefolium subsp. collina
8                    Acer pseudoplatanus
10                      Abies alpestris
11    Achillea millefolium subsp. sudetica
12 Armeria maritima subsp. bottendorfensis
13        Armeria maritima subsp. elongata
14         Armeria maritima subsp. halleri
17                        Galium mollugo
```

```
18                     Dactylis glomerata
19                      Adonis aestivalis
20     Agrostis stolonifera var. palustris
21                   Hieracium pilosella
22               Armeria bottendorfensis
23             Hieracium subg. Pilosella
24                           Picea abies
```

Critical Pseudonyms Taxon misapplication is maybe the greatest danger in using survey data. Known misapplications of names (.auct) are embedded within GermanSL. Please pay attention, if these might also be relevant for your dataset.
Completely independent from the questions of correct taxonomic naming of a specific specimen, the boundary of a taxon interpretation can differ much Jansen and Dengler [see 2010]. This should be adequately solved during data entry. Nevertheless these warnings gives you a last chance to rethink the correctness of your taxon assignments.

Coarsening to a specific taxonomic level If you want only taxa of e.g. level "species" in your analyses but no other taxonomic level, use `taxval(obs, ag='adapt', rank='SPE')`. All hierarchical levels below the species level (including the above specified monotypic subspecies) are set to species level in this case.

```
obs.tax$OriginalName <-obs.tax$TaxonName
tmp <- taxval(obs.tax, db=db, ag='adapt', maxtaxlevel = 'ROOT', rank='FAM', check.critical = FALSE)
tmp$newTaxon <- tax(tmp$TaxonUsageID, db=db)$TaxonName

Reference list used:GermanSL 1.4
```

```
head(tmp[,c('OriginalName','newTaxon')], 10)

                          OriginalName    newTaxon
1            Achillea millefolium agg.  Asteraceae
2                         Quercus robur    Fagaceae
3                         Quercus robur    Fagaceae
4                         Quercus robur    Fagaceae
5                  Achillea millefolium  Asteraceae
6  Achillea millefolium subsp. collina  Asteraceae
7                              Achillea  Asteraceae
8                   Acer pseudoplatanus Sapindaceae
9                   Acer pseudoplatanus Sapindaceae
10                      Abies alpestris    Pinaceae
```

Check `?taxval` and `args(taxval)` for more options.

6 Vegetation data

At the moment there exists no widely accepted formal class for vegetation data in R. But most functions in `vegan`, `ade4` or other packages expect vegetation data to be stored in a matrix with species in columns and plots in rows. Therefore, we need to inflate the Turboveg format (where zero occurrences are missing) to such a 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, and the handling of species codes is provided.

6.1 XML

6.2 Performance measures

At least in Europe most vegetation plots have information about the performance of a species within the survey area, often given in some kind of alphanumeric code for cover percentage within the survey plot.

Different code systems are combined by using the mean cover percentage per cover code class. Function `tv.coverperc` will do this job according to the definitions in *Turboveg/Popup/tvscale.dbf* and the entries in the header data column `COVERSCALE`.

```
obs <- tv.obs(db)
# obs <- tv.coverperc(db, obs)
tail(obs)

   RELEVE_NR TaxonUsageID COVER_CODE LAYER DET_CERT SEASON MICROREL FLOWER
19         1           76          1     6        0      0     Bult      0
20         1        10024          1     6        0      0 Schlenke      0
21         2         2923          1     0        0      0     <NA>      0
22         2        27309          3     6        0      0     <NA>      0
23         3        12273          1     6        0      0     <NA>      0
24         2         4269          1     1        0      0     <NA>      0
```

A few simple possibilities for percentage cover transformations are directly included in the `tv.veg` code, e.g. to use only presence-absence information you can choose option `cover.transform = 'pa'`.

6.3 Pseudospecies

How to account for different vegetation layers or other kinds of species differentiation?

The next step is the separation of pseudo-species. "Pseudo-species" are all kind of taxa split according to species-plot information beyond the performance measure which will be used within the matrix. At this point you have to decide which information should be preserved and which should be aggregated. For instance layer separation must be defined at this step. The default is to differentiate tree, shrub and herb layers but to combine finer layer specifications within them.

If you 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 height classes, you have to create either pseudo-species which differentiate the occurrences in the resulting vegetation matrix or to combine species occurrences from different layers. For the latter you can use different calculations e.g. to sum up all cover percentages of different layers `lc='sum'` or the maximum value (`lc='max'`), mean value (`lc='mean'`). If you assume an independent occurrence of a species in different vertical layers, you can do the calculations with option lc = 'layer' (the default). This results in a probability sum: A species covering 50% in tree layer 1 and 50% in herb layer will get a combined cover of 75% because both layers will overlap 50% (1 - 0.5*0.5).

If you want to specify pseudo-species by other species-plot differentiation you can define a combination dataframe. Two example dataframes are included in the package (`lc.0` and `lc.1`). Option comb has to be given as a list with first element naming the column name holding the grouping variable and as second element the name of the combination dataframe. Try

```
data(lc.0)
obs <- tv.obs(db)
tv.veg(db, pseudo = list(lc.0, c("LAYER")), lc = "layer")
```

and check the column names:

```
tmp <- tv.veg(db, tax=FALSE, pseudo = list(lc.0, "LAYER"), lc = "layer", quiet=TRUE)

Reading tvabund.dbf
Taxonomic reference list:  GermanSL 1.4
Reading tvhabita.dbf

1 releves without date.  Not converted from factor to date format.

converting cover code ...
creating pseudo-species ...
combining occurrences using type LAYER and creating vegetation matrix ...
replacing species numbers with  short  names ...
```

```
names(tmp)

 [1] "AGRCS;P.6" "HIER$P.6"  "ACERPSE.5" "ACERPSE.6" "DACTGLO.6" "ACHICOL.6" "ARMEIAR"   "ARMEAAR"
 [9] "ARMEIAR.1" "PICEABI.2" "PICEABI.3" "GALCMOL.6" "ACHIMIL.6" "ACHIUIL.6" "ACHI-SP.6" "ACO.6"
[17] "ADONAES.6"
```

Separated by dots and layer numbers you can see the preserved layers. For meaning of layer numbers see Turboveg help.
Check (`data(lc.1)`) for the default layer combination.

Beside layers you can use any kind of species-plot attributes to distinguish between occurrences, for instance in a multi-temporal survey.

```
comb <- list(data.frame(SEASON=0:4, COMB=c(0,'Spring','Summer','Autumn','Winter')),'SEASON')
names(tv.veg(db, tax=FALSE, pseudo=comb, quiet=TRUE))

Reading tvabund.dbf
Taxonomic reference list:  GermanSL 1.4
Reading tvhabita.dbf

1 releves without date.  Not converted from factor to date format.

converting cover code ...
creating pseudo-species ...
combining occurrences using type LAYER and creating vegetation matrix ...
replacing species numbers with  short  names ...
 [1] "AGRCS;P"        "HIER$P"         "ACERPSE.Spring" "ACERPSE.Summer" "DACTGLO"        "ACHICOL"
 [7] "ARMEIAR"        "ARMEAAR"        "ARMEIAR.1"      "PICEABI"        "GALCMOL"        "ACHIMIL"
[13] "ACHIUIL"        "ACHI-SP"        "ACO"            "ADONAES"
```

```
data(lc.1)
veg <- tv.veg(db, lc = "sum", pseudo = list(lc.1, 'LAYER'), dec = 1, check.critical = FALSE)

1 releves without date.  Not converted from factor to date format.

veg[,1:10]
```

6.4 Combine species manually

Beside semi-automatic taxon harmonization with function `taxval` there are two possibilities to change Taxonomy manually. If you decide to interpret a certain species name in your database different than stored in the standard view of the taxonomic reference you can replace species numbers within the observational dataframe and run `taxval` later on.

```
obs.tax$TaxonUsageID[obs.tax$TaxonUsageID == 27] <- 31
```

will replace all occurrences of *Achillea millefolium agg.* with *Achillea millefolium* which might be adequate for your survey and will prevent a too coarse taxon grouping. For a longer list of replacements you can use a dataframe.

```
taxon.repl <- data.frame(old=c(27), new=c(31))
obs.tax$TaxonUsageID <- replace(obs.tax$TaxonUsageID,
                                match(taxon.repl$old, obs.tax$TaxonUsageID), taxon.repl$new)
```

The second possibility is to use function `comb.species` on vegetation matrices.

```
comb.species(veg, sel=c('QUERROB','QUERROB.Tree'))
```

will use the first name ('QUERROB') for the replacement column with the cover sums of the selected columns.

7 Site conditions

Vegetation data should come with information about date, place, plot size as well as overarching properties of the plant community and site conditions, plot measurements etc. `tv.site` will load the Turboveg site (header) data and does some basic checks necessary because of the Turboveg dBase format.

```
site <- tv.site(db)

1 releves without date.  Not converted from factor to date format.
Some columns contain no data and are omitted.

 [1] TABLE_NR   NR_IN_TAB  PROJECT    AUTHOR     SYNTAXON   UTM        ALTITUDE   EXPOSITION MOSS_IDENT
[10] LICH_IDENT EPSG

Some numeric columns contain only 0 values and are omitted.

 [1] COV_TOTAL  COV_TREES  COV_SHRUBS COV_HERBS  COV_MOSSES COV_LICHEN COV_ALGAE  COV_LITTER COV_WATER
[10] COV_ROCK   TREE_HIGH  TREE_LOW   SHRUB_HIGH SHRUB_LOW  HERB_HIGH  HERB_LOW   HERB_MAX   CRYPT_HIGH

Some numeric fields contain 0 values:

[1] X_COORD Y_COORD

Please check if these are really meant as 0 or if they are erroneously assigned because of DBase restrictions.
If so, use something like:
site$Column_name[site$Column_name==0] <- NA
```

The function is quite straightforward. After loading the file *tvhabita.dbf* from the specified database folder, warnings are given for plots without specified relevé area or date and 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.

8 Additional functions

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

8.1 Frequency tables

`syntab` produces a relative or absolute frequency table of a classified vegetation table with the possibility to filter according to threshold values. To exemplify the function we use the second dataset implemented in the package. It is the demonstration dataset from Leyer and Wesche [2007], a selection of grassland relevés from the floodplains of the river Elbe.

```
elbaue <- tv.veg('elbaue', check.critical = FALSE)
elbaue.env <- tv.site('elbaue')

Some columns contain no data and are omitted.
Some numeric columns contain only 0 values and are omitted.
Some numeric fields contain 0 values:
Please check if these are really meant as 0 or if they are erroneously assigned because of DBase restrictions.
If so, use something like:
site$Column_name[site$Column_name==0] <- NA
```

```
clust <- vector('integer', nrow(elbaue.env))
clust[elbaue.env$MGL < -50 & elbaue.env$SDGL < 50] <- 1         # dry sites, low deviation
clust[elbaue.env$MGL < -50 & elbaue.env$SDGL >= 50] <- 2        # dry sites, high deviation
clust[elbaue.env$MGL >= -50 & elbaue.env$SDGL >= 50] <- 3       # wet sites, high deviation
clust[elbaue.env$MGL >= -50 & elbaue.env$SDGL < 50] <- 4        # wet sites, low deviation
levels(clust) <- c('dry.ld','dry.hd', 'wet.hd','wet.ld')
```

We can e.g. look at the relative frequency of all species with more than 40% at least in one column, according to the height of the groundwater table (low or high) and the amplitude of the groundwater table fluctuations (high or low deviations from the mean). Additionally you can use the affiliation of species to abiotic clusters with the help of package `indicspecies`, which calculates species indicator values for one or several cluster [De Cáceres et al., 2010] to order the syntaxonical table. Together with Ellenberg indicator values with will get a comprehensive view into our data.

```
require(indicspecies)

Loading required package:  indicspecies
Loading required package:  permute

mu <- multipatt(elbaue, clust)
veg <- elbaue; dec=0
st <- syntab(elbaue, clust, 'rel', mupa=mu)

 Number of clusters:  4
 Cluster frequency 7 10 5 11

# Print Ellenberg indicator values for soil moisture and nutrient demand
traits <- tv.traits()
trait <- traits[traits$LETTERCODE %in% names(elbaue), ]
rownames(trait) <- trait$LETTERCODE
trait <- trait[,c('OEK_F', 'OEK_N')]
print(st, limit=30, trait=trait)

 Number of clusters:  4
 Cluster frequency 7 10 5 11
        dry.ld dry.hd wet.hd wet.ld index      stat p.value OEK_F OEK_N
CIRSARV     43      .      .      9     1 0.6411939   0.015    NA     7
DESCCES     57      .      .     18     1 0.7229440   0.005     7     3
EUPHESU     43      .      .      .     1 0.6546537   0.025     4    NA
GALCVAG     71     20      .      .     1 0.8287419   0.005     4     3
VICITET     57     10      .      .     1 0.7079923   0.010     5     5
ALOPGEN      .     20     60      9     3 0.6474857   0.020     8     7
RORIAMP      .      .     60      9     3 0.7711677   0.005    10     8
CALTPAL      .      .      .     36     4 0.6030227   0.035     9     6
AGRCCAN      .      .      .     36     4 0.6030227   0.045     9     2
CAREVES      .      .      .     55     4 0.7385489   0.020     9     5
CARECCU     14      .     40     82     4 0.8742008   0.005     9     4
RANUFLA      .      .      .     55     4 0.7385489   0.005     9     2
CAREORA     43     70      .      .     5 0.7669650   0.005     3     4
ELYMREP     57     90      .      .     5 0.8744746   0.005    NA     7
ALOPPRA     71     90     20     36     5 0.8830871   0.005     6     7
RUMETHY     43     60      .      .     5 0.7276069   0.025     3     4
TARAEEE     57     60      .     18     5 0.7173843   0.025     5     8
CARDPRA     43     10      .     55     7 0.6869033   0.040     6    NA
GLYCMAX      .      .     80     45    10 0.7500000   0.030    10     9
SIUMLAT      .      .     40     45    10 0.6614378   0.030    10     7
```

9 Vegetation analyses

The package *vegdata* serves mostly as a helper for the analysis of vegetation data. Several powerful R packages like *vegan* and others exist, to provide a very broad range of possibilities.

9.1 Multivariate Ordinations

With the functions shown above we are now ready to do some example analyses in the wide area of vegetation analyses.

We can do, for instance, 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 and Cox, 1994, 2001] from Jari Oksanen [Oksanen et al., 2008].

```
## Data analyses
library(vegan)

Loading required package:  lattice
This is vegan 2.5-6

veg.nmds <- metaMDS(elbaue, distance = "bray", trymax = 5, autotransform =FALSE,
                    noshare = 1, expand = TRUE, trace = 2)
#eco <- tv.traits()
#eco£OEK_F <- as.numeric(eco£OEK_F)
F <- isc(elbaue, trait.db = 'ecodbase.dbf', ivname = 'OEK_F', method = 'mean')
N <- isc(elbaue, trait.db = 'ecodbase.dbf', ivname = 'OEK_N', method = 'mean')
env <- envfit(veg.nmds, env = data.frame(F, N))
```

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

```
library(labdsv)

Loading required package:  mgcv
Loading required package:  nlme
This is mgcv 1.8-30.  For overview type 'help("mgcv-package")'.
This is labdsv 2.0-1
convert existing ordinations with as.dsvord()

Attaching package:  'labdsv'
The following object is masked from 'package:stats':
        density

library(akima)
color = function(x)rev(topo.colors(x))
nmds.plot <- function(ordi, site, var1, var2, disp, plottitle =  'NMDS', env = NULL, ...) {
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 = plottitle,
           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= .5, col = 2, pch = '+')
             points(ordi$species[, 1], ordi$species[, 2], xlab = "", ylab = "", cex=.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)
             if(!is.null(env)) plot(env, col='red')
           }
           ,...)
}
```

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* occurs only in more balanced situations.

References

Stephan M. Hennekens and Johannes Hendrikus Jacques Schaminee. Turboveg, a comprehensive data base management system for vegetation datasoftware package for input, processing, and presentation of phytosociological data. *Journal of Vegetation Science*, 12:589–591, 2001.

Florian Jansen and Juergen Dengler. Plant names in vegetation databases - a neglected source of bias.

```r
nmds.plot(veg.nmds, elbaue.env, disp='species', var1="MGL", var2="SDGL", env=env, plottitle = 'Elbaue floodplain dataset')
```

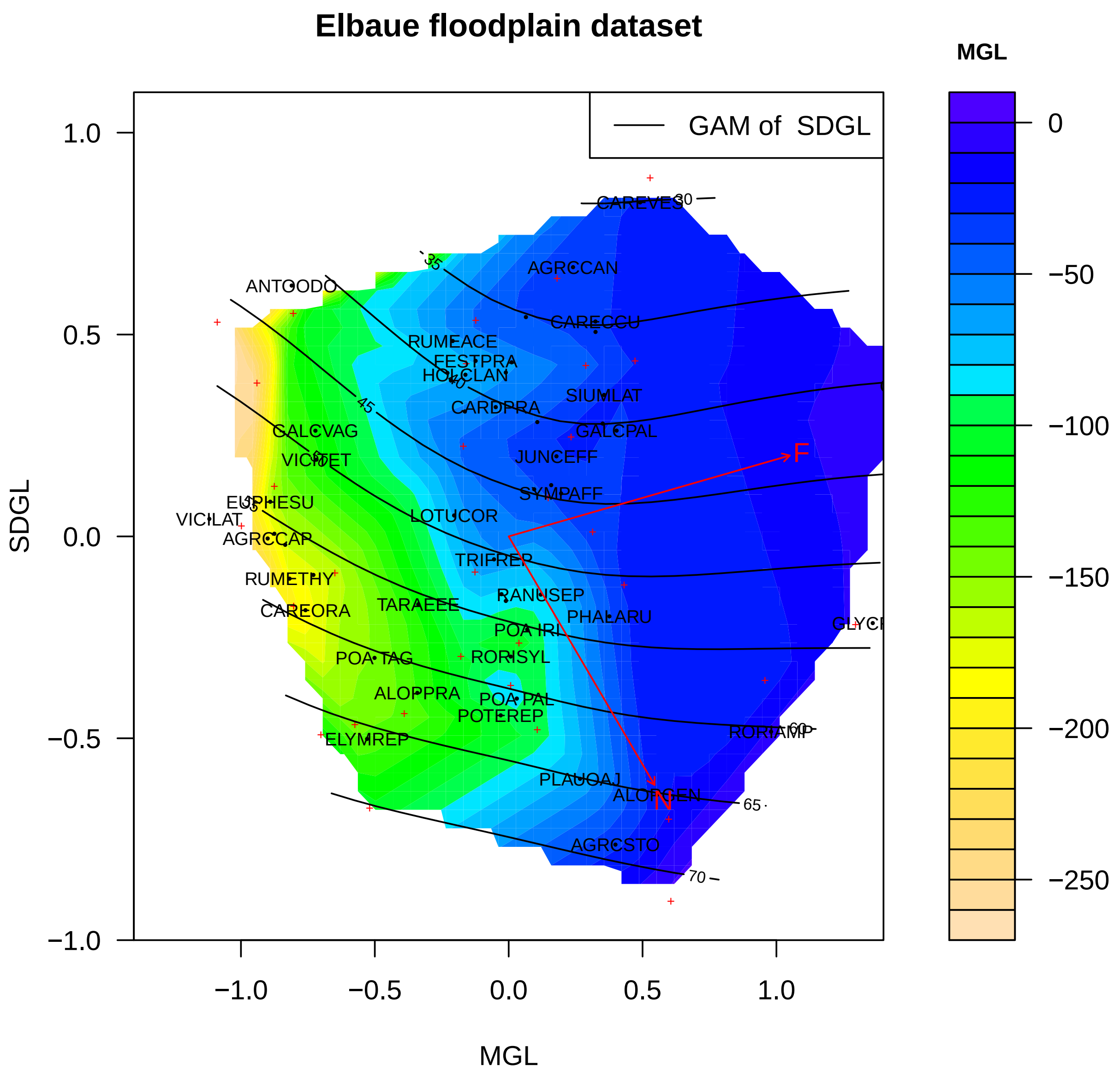


Figure 2: Non-metric multidimensional scaling of the elbaue vegetation data with an overlay of mean groundwater table (colors) and standard deviation of groundwater level fluctuations (GAM lines). Arrows show direction of increasing mean Ellenberg F (soil water) resp. N (nutrient availability).

Journal of Vegetation Science, 21(6):1179–1186, Aug 2010. doi: 10.1111/j.1654-1103.2010.01209.x. URL http://doi.wiley.com/10.1111/j.1654-1103.2010.01209.x.

Jürgen Dengler, Florian Jansen, Falko Glöckler, R.K. Peet, Miquel De Cáceres, M. Chytrý, Jörg Ewald, Jens Oldeland, G. Lopez-Gonzalez, Manfred Finckh, and Others. The Global Index of Vegetation-Plot Databases (GIVD): a new resource for vegetation science. *Journal of Vegetation Science*, 22(4):582–597, 2011. doi: 10.1111/j.1654-1103.2011.01265.x. URL http://onlinelibrary.wiley.com/doi/10.1111/j.1654-1103.2011.01265.x/full.

Florian Jansen and Juergen Dengler. Germansl - eine universelle taxonomische referenzliste fuer vegetationsdatenbanken. *Tuexenia*, 28:239–253, 2008.

Ilona Leyer and Karsten Wesche. *Multivariate Statistik in der Oekologie*. Springer, Berlin, 2007.

Miquel De Cáceres, Pierre Legendre, and Marco Moretti. Improving indicator species analysis by combining groups of sites. *Oikos*, 119(10):1674–1684, October 2010. ISSN 00301299. doi: 10.1111/j.1600-0706.2010.18334.x. URL http://doi.wiley.com/10.1111/j.1600-0706.2010.18334.x.

T. F. Cox and M. A. A. Cox. *Multidimensional Scaling*. Chapman & Hall, 1994, 2001.

Jari Oksanen, Roeland Kindt, Pierre Legendre, Bob O'Hara, Gavin L. Simpson, and M. Henry H. Stevens. *vegan: Community Ecology Package*, 2008. URL http://cran.r-project.org/,http://vegan.r-forge.r-project.org/.