Vegetation data access and taxonomic harmonization
Version 0.4

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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 **?**. 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 `http://geobot.botanik.uni-greifswald.de/reflist`.

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 Database access

At the moment vegdata provides direct access to two 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 plot 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 developed as a MySQL-Server database at the Federal Agency for Nature Conservation (BfN) and can used via a PHP framework at `http://www.floraweb.de/vegetation/vegetweb/RechercheView.php`.

2.2 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 (**?**). The package offers the function `taxval` with different options for the adjustment of synonyms, monotypic taxa, taxonomic levels, members of aggregates and undetermined species.

2.3 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 (**?**). 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).

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)
```

Many functions use the directory structure of Turbowin. The first time such a function is called, 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 about the Turboveg installation path or the path to the Turboveg directory structure of package vegdata.

```
> tv.home()
```

```
############################################################
Turboveg root directory is set to /home/florian/.wine/drive_c/Turbowin
If you want to change this use: options(tv_home="<path_to_your_Turbowin_root>")
############################################################
```

If you want to change this use:

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

4 Service functions

```
> tv.db()

[1] ""          "elbaue"   "taxatest"
```

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

```
> tv.refl()

[1] "GermanSL 1.2"
```

GermanSL 1.2 is the default Taxonomic reference list in the actual vegdata package 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.

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

```
> tax("Achillea millefolium")

Taxonomic evaluation list ( species.dbf ) of version GermanSL 1.2 not available.
I will try to download the reference now.

      SPECIES_NR LETTERCODE                                ABBREVIAT
18            27     ACHI#MI               Achillea millefolium agg.
20            31     ACHIMIL                    Achillea millefolium
21            32     ACHIM-M Achillea millefolium subsp. millefolium
22            33     ACHIM-S    Achillea millefolium subsp. sudetica
8678       20096     ACHICOL     Achillea millefolium subsp. collina
8679       20097     ACHIPAN   Achillea millefolium subsp. pannonica
8680       20098     ACHIPAN        Achillea millefolium var. lanata
13219      26082     ACHIMIL         Achillea millefolium var. firma
26247      90019     ACHI*AB     Achillea millefolium agg. x nobilis
26248      90020     ACHIM*P        Achillea millefolium x pannonica
                                NATIVENAME SYNONYM VALID_NR
18           Artengruppe Wiesen-Schafgarbe   FALSE       27
20           Gewöhnliche Wiesen-Schafgarbe   FALSE       31
21    Gewöhnliche Wiesen-Schafgarbe i.e.S.   FALSE       32
22                Sudeten-Wiesenschafgarbe   FALSE       33
8678                                  <NA>    TRUE       29
8679                                  <NA>    TRUE       34
8680                                  <NA>    TRUE       34
13219                                 <NA>    TRUE       31
26247                                 <NA>    TRUE    90028
26248                                 <NA>   FALSE    90020
```

”GermanSL 1.2” is not included in vegdata to keep the R package small. Instead the reference list will be automatically downloaded into the tv_home directory, if it is not installed but needed. If you want to use a different list, specify `refl=<Name of your list>`. Function `tax` will use the given character string to look for all (partially) matching species names within the reference list

```
> tax("Achillea millefolium", strict = TRUE, verbose = TRUE)

   SPECIES_NR LETTERCODE            ABBREVIAT AUTHOR SYNONYM VALID_NR           VALID_NAME
20         31    ACHIMIL Achillea millefolium     L.   FALSE       31 Achillea millefolium
                          NATIVENAME GRUPPE RANG AGG                  AGG_NAME
20 Gew\u0094hnliche Wiesen-Schafgarbe      S  SPE  27 Achillea millefolium agg.
                           NACHWEIS                          SECUNDUM HYBRID BEGRUEND EDITSTATUS
20 BfN(Wisskirchen u. Haeupler 1998) BfN(Wisskirchen u. Haeupler 1998)   <NA>     <NA>        BfN
```

Additional to the Turboveg standard fields comprehensive information for every taxon is stored in an extra file (tax.dbf). If you set option strict=TRUE, only the species with exact match to the given character string will be returned.

```
> tax("Elytrigia repens")$ABBREVIAT

[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 :
      SPECIES_NR                         ABBREVIAT SYNONYM                          SECUNDUM
4076        6541   Agropyron repens subsp. caesium    TRUE BfN(Wisskirchen u. Haeupler 1998)
4079        6544 Elymus repens subsp. repens s. l.    TRUE BfN(Wisskirchen u. Haeupler 1998)
4789       10260      Elymus repens subsp. caesium    TRUE BfN(Wisskirchen u. Haeupler 1998)
8712       20143                 Agropyron caesium    TRUE BfN(Wisskirchen u. Haeupler 1998)
8730       20167    Agropyron repens subsp. repens    TRUE BfN(Wisskirchen u. Haeupler 1998)
9888       21639                  Elytrigia repens    TRUE BfN(Wisskirchen u. Haeupler 1998)
12063      24393                   Triticum repens    TRUE BfN(Wisskirchen u. Haeupler 1998)
13913      27778                     Elymus repens   FALSE BfN(Wisskirchen u. Haeupler 1998)
14005      27914                  Agropyron repens    TRUE BfN(Wisskirchen u. Haeupler 1998)
      EDITSTATUS
4076         BfN
4079   Korrektur
4789         BfN
8712         BfN
8730         BfN
9888         BfN
12063        BfN
13913        BfN
14005        BfN

> childs(27, quiet = TRUE)$ABBREVIAT

 [1] "Achillea collina"                       "Achillea millefolium"
 [3] "Achillea pannonica"                     "Achillea roseoalba"
 [5] "Achillea setacea"                       "Achillea pratensis"
 [7] "Achillea lanulosa"                      "Achillea collina x millefolium"
 [9] "Achillea collina x pannonica"           "Achillea collina x pratensis"
[11] "Achillea collina x roseoalba"           "Achillea collina x setacea"
[13] "Achillea millefolium x pannonica"       "Achillea pratensis x roseoalba"
[15] "Achillea millefolium subsp. millefolium" "Achillea millefolium subsp. sudetica"

> parents("ACHIMIL")

Parents of Achillea millefolium ( 31 ):
      SPECIES_NR                ABBREVIAT                          SECUNDUM RANG GENERATION
18            27   Achillea millefolium agg. BfN(Wisskirchen u. Haeupler 1998)  AGG          1
20641      60728            Achillea species BfN(Wisskirchen u. Haeupler 1998)  GAT          2
20471      60463          Asteraceae species      Wisskirchen u. Haeupler 1998  FAM          3
20445      60415           Asterales species      Wisskirchen u. Haeupler 1998  ORD          4
20324      60079           Asteridae species      Wisskirchen u. Haeupler 1998  UKL          5
```

```
20318       60071       Magnoliopsida species      Wisskirchen u. Haeupler 1998  KLA          6
20309       60049     Magnoliophytina species      Wisskirchen u. Haeupler 1998  UAB          7
20283       60000       Spermatophyta species      Wisskirchen u. Haeupler 1998  ABT          8
29376       94419 "Gef\u0084ápflanze" species      [ad-hoc-Taxon fÃ¼r GermanSL]  AG2          9
10              0     "Gr\u0081nliches etwas"      [ad-hoc-Taxon fÃ¼r GermanSL] ROOT         10
      EDITSTATUS
18           BfN
20641        BfN
20471  Korrektur
20445        BfN
20324        BfN
20318  Korrektur
20309  Korrektur
20283  Korrektur
29376 Ergaenzung
10    Ergaenzung
```

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

5 Taxonomic harmonisation

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 (?).

```
> db <- "taxatest"
```

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

```
> tv.metainfo(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.

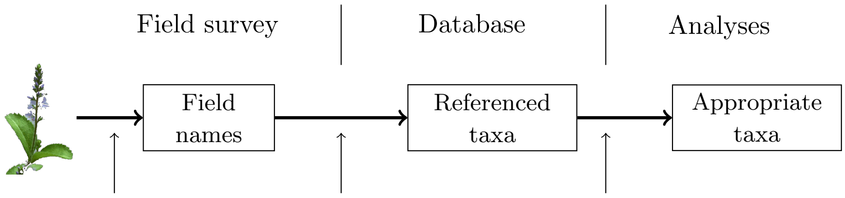
```
> obs.tax <- tv.obs(db)

reading observations ...

> species <- tax("all", syn = TRUE)
> obs.tax$Name <- species$ABBREVIAT[match(obs.tax$SPECIES_NR, species$SPECIES_NR)]
> head(obs.tax[, 1:4])

  RELEVE_NR SPECIES_NR 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
```

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`.



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
   - 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

5.1 Explaining function taxval

We are using the taxonomic reference list GermanSL (see Jansen & Dengler 2008, Tuexenia) 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, mono = "lower")
```

```
Original number of names: 25

 5 Synonyms found in dataset, adapted
 SPECIES_NR                               ABBREVIAT Freq.1 VALID_NR                       VALID_NAME
      20010    Cardamine pratensis subsp. pratensis      1    15133              Cardamine pratensis
      20096     Achillea millefolium subsp. collina      1       29                 Achillea collina
      20583 Armeria maritima subsp. bottendorfensis      1    20585 Armeria maritima subsp. halleri
      25203                         Abies alpestris      2     4269                      Picea abies
      27309                 Armeria bottendorfensis      1    20585 Armeria maritima subsp. halleri
 Freq.2
      0
      0
      0
      0
      0

 1 monotypic taxa found in dataset, set to lower rank.
 AGG_NR          AGG_NAME AGG_RANG MEMBER_NR      MEMB_NAME MEMB_RANG
  66142 Acoraceae species      FAM     61329 Acorus species       GAT

 1 monotypic taxa found in dataset, set to lower rank.
 AGG_NR       AGG_NAME AGG_RANG MEMBER_NR      MEMB_NAME MEMB_RANG
  61329 Acorus species      GAT        69 Acorus calamus       SPE

No taxa higher than ROOT found.

 8 child taxa found in dataset, adapted
 SPECIES_NR                            ABBREVIAT Freq.1   AGG                 AGG_NAME Freq.2
         29                     Achillea collina      1    27 Achillea millefolium agg.      1
         31                 Achillea millefolium      1    27 Achillea millefolium agg.      1
         33 Achillea millefolium subsp. sudetica      1    31      Achillea millefolium      1
         27            Achillea millefolium agg.      1 60728          Achillea species      1
       2923                  Hieracium pilosella      1 12273 Hieracium subg. Pilosella      1
      15133                  Cardamine pratensis      2  1105  Cardamine pratensis agg.      1
      20945                    Cardamine dentata      1  1105  Cardamine pratensis agg.      1
       1105             Cardamine pratensis agg.      1 60845         Cardamine species      1

 3 child taxa found in dataset, adapted
 SPECIES_NR                ABBREVIAT Freq.1   AGG                  AGG_NAME Freq.2
         27 Achillea millefolium agg.      1 60728          Achillea species      1
         31      Achillea millefolium      1    27 Achillea millefolium agg.      1
       1105  Cardamine pratensis agg.      1 60845         Cardamine species      1

 1 child taxa found in dataset, adapted
 SPECIES_NR                ABBREVIAT Freq.1   AGG         AGG_NAME Freq.2
         27 Achillea millefolium agg.      1 60728 Achillea species      1

Number of taxa after validation: 13
```

```
Warning: Critical Pseudonym(s) in dataset, please check
       to_check check_No        check against SPECIES_NR                          SECUNDUM
 Galium mollugo     2555 Galium mollugo auct.      27395 BfN(Wisskirchen u. Haeupler 1998)

Warning: Critical species in dataset, please check
           to_check check_No           check against SPECIES_NR                          SECUNDUM
 Dactylis glomerata     1843 Dactylis glomerata s. l.      26585 BfN(Wisskirchen u. Haeupler 1998)
     Galium mollugo     2555     Galium mollugo s. l.      26777 BfN(Wisskirchen u. Haeupler 1998)
```

The database contains 25 different names in the beginning.

Synonyms 5 of the species names are synonyms and are therefore transfered to legal taxon names, respectively numbers (see option syn='adapt'). If you want to preserve synonyms, choose option syn='conflict' or 'preserve'.

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 1.2')`). 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 to follow would 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 25 names in the beginning only 13 taxa survived the valuation. All others had to be converted.

```
> obs.taxval$Taxon <- species$ABBREVIAT[match(obs.taxval$SPECIES_NR, species$SPECIES_NR)]
> obs.taxval[order(obs.taxval$Name), c("Name", "Taxon")]
```

```
                                          Name                              Taxon
10                             Abies alpestris                        Picea abies
15                             Abies alpestris                        Picea abies
8                            Acer pseudoplatanus                Acer pseudoplatanus
9                            Acer pseudoplatanus                Acer pseudoplatanus
5                           Achillea millefolium                   Achillea species
1                      Achillea millefolium agg.                   Achillea species
6        Achillea millefolium subsp. collina                   Achillea species
11      Achillea millefolium subsp. sudetica                   Achillea species
7                               Achillea species                   Achillea species
16                            Acoraceae species                     Acorus calamus
```

```
19                          Adonis aestivalis                       Adonis aestivalis
20     Agrostis stolonifera var. palustris Agrostis stolonifera var. palustris
22                    Armeria bottendorfensis     Armeria maritima subsp. halleri
12 Armeria maritima subsp. bottendorfensis     Armeria maritima subsp. halleri
13          Armeria maritima subsp. elongata   Armeria maritima subsp. elongata
14           Armeria maritima subsp. halleri     Armeria maritima subsp. halleri
25                          Cardamine dentata                   Cardamine species
27                        Cardamine pratensis                   Cardamine species
26                   Cardamine pratensis agg.                   Cardamine species
28   Cardamine pratensis subsp. pratensis                   Cardamine species
29                          Cardamine species                   Cardamine species
18                         Dactylis glomerata                  Dactylis glomerata
17                             Galium mollugo                      Galium mollugo
21                        Hieracium pilosella          Hieracium subg. Pilosella
23                  Hieracium subg. Pilosella          Hieracium subg. Pilosella
24                                Picea abies                         Picea abies
2                                Quercus robur                       Quercus robur
3                                Quercus robur                       Quercus robur
4                                Quercus robur                       Quercus robur
```

Critical Pseudonyms Taxon misapplication is maybe the greatest danger in using survey data. Known misapplications of names (.auct) are embedded in the 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 **?**. This should be adequately solved during data entry. Nevertheless these warnings gives you a last chance to rethink the correctness of your taxon assignments.

5.2 Coarsening to a specific taxonomic level

If you want only species in your analyses and 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.

```
> tmp <- taxval(obs.tax, maxtaxlevel = "FAM", ag = "adapt", rank = "FAM")

Original number of names: 25

 5 Synonyms found in dataset, adapted
 SPECIES_NR                              ABBREVIAT Freq.1 VALID_NR                         VALID_NAME
      20010    Cardamine pratensis subsp. pratensis      1    15133                Cardamine pratensis
      20096     Achillea millefolium subsp. collina      1       29                   Achillea collina
      20583 Armeria maritima subsp. bottendorfensis      1    20585 Armeria maritima subsp. halleri
      25203                         Abies alpestris      2     4269                        Picea abies
      27309                 Armeria bottendorfensis      1    20585 Armeria maritima subsp. halleri
 Freq.2
      0
      0
      0
      0
      0

No taxa higher than FAM found.

Number of taxa after validation: 10

> tmp$Taxon <- species$ABBREVIAT[match(tmp$SPECIES_NR, species$SPECIES_NR)]
> tmp[order(tmp$Taxon), 9:10]
```

```
                                       Name                  Taxon
8                        Acer pseudoplatanus      Aceraceae species
9                        Acer pseudoplatanus      Aceraceae species
16                         Acoraceae species      Acoraceae species
1                   Achillea millefolium agg.    Asteraceae species
5                       Achillea millefolium     Asteraceae species
6      Achillea millefolium subsp. collina     Asteraceae species
7                           Achillea species     Asteraceae species
11    Achillea millefolium subsp. sudetica     Asteraceae species
21                       Hieracium pilosella     Asteraceae species
23                  Hieracium subg. Pilosella     Asteraceae species
25                         Cardamine dentata   Brassicaceae species
26                   Cardamine pratensis agg.   Brassicaceae species
27                       Cardamine pratensis   Brassicaceae species
28    Cardamine pratensis subsp. pratensis   Brassicaceae species
29                         Cardamine species   Brassicaceae species
2                              Quercus robur       Fagaceae species
3                              Quercus robur       Fagaceae species
4                              Quercus robur       Fagaceae species
10                           Abies alpestris       Pinaceae species
15                           Abies alpestris       Pinaceae species
24                               Picea abies       Pinaceae species
12 Armeria maritima subsp. bottendorfensis Plumbaginaceae species
13        Armeria maritima subsp. elongata Plumbaginaceae species
14         Armeria maritima subsp. halleri Plumbaginaceae species
22                 Armeria bottendorfensis Plumbaginaceae species
18                        Dactylis glomerata        Poaceae species
20     Agrostis stolonifera var. palustris        Poaceae species
19                         Adonis aestivalis  Ranunculaceae species
17                            Galium mollugo      Rubiaceae species
```

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

5.3 Implementing another taxon view

If you wish to use another taxonomic concept than the default, you can use a conversion table to change synonymy etc. to catch your needs.

6 Vegetation matrices

At the moment there exist no 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 Performance measures

At least in Europe most vegetation plots have some information about the cover of a species within the survey area, often given in some kind of alphanumeric code. Different codes systems can be 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*.

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

```
reading observations ...

> obs <- tv.coverperc(db, 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 COVER_PERC
1         2         27         2b     0        0      0 Schlenke      0         02         18
2         2       4685          4     1        0      0 Schlenke      0         02         68
3         2       4685          1     2        1      0 Schlenke      0         02          3
4         2       4685          1     6        0      0     <NA>     10         02          3
5         1         31          3     6        0      0     <NA>      0         01         38
6         1      20096          +     6        0      0 Schlenke      1         01          2
```

If option `convcode = TRUE` (the default) the covercodes used in the Turboveg database (see file tvscale.dbf) are converted to (mean) percentage values according to the entries in the Turboveg Popup list "TVScale". For visual control the translated values will be printed on the screen.

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

6.2 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 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 height classes, we 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 we 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 we assume an independent occurrence of a species in different vertical layers, we 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)
> tv.veg(db, pseudo = list(lc.0, c("LAYER")), lc = "layer")
```

and check the column names:

```
reading observations ...
Taxonomic reference list:  GermanSL 1.2

 converting cover code ...

 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

 creating pseudo-species ...

 combining occurrences using type LAYER and creating vegetation matrix ...

 replacing species numbers with  short  names ...


 [1] "AGRTS;P.6" "CARD#PR.6" "HIERSUG.6" "CARDPRA.6" "ACERPSE.5" "ACERPSE.6" "DACYGLO.6" "CARDPRA.6"
 [9] "ACHICOL.6" "ARMEM-H"   "ARMEM-E"   "ARMEM-H"   "CARDDEN.6" "PICEABI.2" "PICEABI.3" "GALUMOL.6"
[17] "ACHI#MI"   "ARMEM-H.6" "HIERPIO"   "ACHIMIL.6" "ACHIM-S.6" "PICEABI.1" "QUERROB.1" "QUERROB.2"
[25] "QUERROB.6" "ACHI-SP.6" "CARD-SP.6" "ACOR-SP.6" "ADONAES.6"
```

Separated by dots and layer numbers you can see the preserved layers. For meaning of layer numbers see Turboveg Help.
Check cover aggregation 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")
> tv.veg(db, tax = FALSE, pseudo = comb)
```

```
reading observations ...
Taxonomic reference list:  GermanSL 1.2

 converting cover code ...

 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

 creating pseudo-species ...

 combining occurrences using type LAYER and creating vegetation matrix ...

 replacing species numbers with  short  names ...
  AGRTS;P CARD#PR HIERSUG CARDPRA ACERPSE.Spring ACERPSE.Summer DACYGLO CARDPRA ACHICOL ARMEM-H
1       3       0       0       0              3             13       3       0       2       0
2       0       0       0       0              0              0       0       0       0       0
```

```
3        0        3        3        3              0              0        0        3        0        3
  ARMEM-E ARMEM-H CARDDEN PICEABI GALUMOL ACHI#MI ARMEM-H HIERPIO ACHIMIL ACHIM-S PICEABI QUERROB
1       0       0       0       6       3       0       0       0      38       3       0       0
2       0       0       0       0       0      18      38       3       0       0       3      70
3       3       3       3       0       0       0       0       0       0       0       0       0
  ACHI-SP CARD-SP ACOR-SP ADONAES
1       3       0       0       3
2       0       0       0       0
3       0       3       3       0
```

```
> data(lc.1)
> veg <- tv.veg(db, lc = "sum", pseudo = list(lc.1, "LAYER"), dec = 1, quiet = TRUE)
```

```
> veg[, 1:10]
```

```
  AGRTS;P HIERSUG ACERPSE ACERPSE.Shrub DACYGLO ARMEM-E ARMEM-H GALUMOL PICEABI.Tree QUERROB
1       3       0       3            13       3       0       0       3            6       0
2       0       3       0             0       0       0      38       0            3       3
3       0       3       0             0       0       3       6       0            0       0
```

6.3 Combine species by hand

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$SPECIES_NR[obs.tax$SPECIES_NR == 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$SPECIES_NR <- replace(obs.tax$SPECIES_NR, match(taxon.repl$old, obs.tax$SPECIES_NR),
+     taxon.repl$new)
```

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

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

```
 The following names are combined to new name QUERROB
[1] "QUERROB"      "QUERROB.Tree"
  AGRTS;P HIERSUG ACERPSE ACERPSE.Shrub DACYGLO ARMEM-E ARMEM-H GALUMOL PICEABI.Tree ACHI-SP
1       3       0       3            13       3       0       0       3            6      46
2       0       3       0             0       0       0      38       0            3      18
3       0       3       0             0       0       3       6       0            0       0
  CARD-SP ACOR-SP ADONAES QUERROB
1       0       0       3       0
2       0       0       0      74
3      15       3       0       0
```

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

7 Site data

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

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

```
 The following columns contain no data and are omitted
 [1] REFERENCE  TABLE_NR   NR_IN_TAB  PROJECT    AUTHOR     SYNTAXON   UTM        ALTITUDE
 [9] 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  COV_LITTER
 [9] COV_WATER  COV_ROCK   TREE_HIGH  TREE_LOW   SHRUB_HIGH SHRUB_LOW  HERB_HIGH  HERB_LOW
[17] 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 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 VegetWeb, the National German vegetation plot repository

I have written functions, which provide the possibility to access the data stored in VegetWeb, the German national vegetation database. VegetWeb is realised as MySQL database without API to access data directly. Therefore we need package RMySQL to make queries. Unfortunately there are no binary versions of RMySQL on CRAN any more. If you are working under Linux please install RMySQL with something like sudo apt-get install r-cran-rmysql. If you work with MS Windows you have to install RTools and the MySQL headers before you can compile RMySQL from source:

1. Install RTools from (`http://www.murdoch-sutherland.com/Rtools/`
2. Install MySQL Connector C with installation option "full" from `http://dev.mysql.com/downloads/connector/c/` and copy the file libmysql.dll from the directory debug to the bin directory. Alternatively you can install a complete MySQL Server.
3. create a file Renviron.site in your R installation path in directory etc/ and add the correct path to your MySQL Connector installation e.g.:

   ```
   MYSQL_HOME=C:/PROGRAMME/MySQL/MySQL Connector C 6.0.2
   ```

4. open R and type
   install.packages('RMySQL', type='source')

If you run into trouble see `http://biostat.mc.vanderbilt.edu/wiki/Main/RMySQL`.

```
> library(RMySQL)
```

To prevent incompatibilities with Windows users who want to use Turboveg data but no VegetWeb data and who are not able or willing to install RMySQL, I excluded the VegetWeb function from package vegdata, but they can be downloaded from my site:

```
> source("http://geobot.botanik.uni-greifswald.de/download/r_package/vegetweb.r")
```

```
> vw.site()
```

```
 No query string specified.
 You can select vegetation plots from VegetWeb with queries like
          query="Projekt='T271'"
 This will select all releves from project T271, i.e Dengler 2007 Tuexenia.
 If you want to see which selection parameters are available, try:
 con <- vw.con()
 dbListFields(con, "beobachtung")
 summary(dbGetQuery(con, "SELECT pH FROM beobachtung"))
 dbGetQuery(con, "SELECT * FROM projekt")
 etc.
```

`vw.site` and `veg` are the user interface to retrieve data from VegetWeb respectively an open access mirror of the original BfN Server at the University of Greifswald (mirrored every Sunday).

```
> con <- vw.con()
> dbListTables(con)
> url.show("http://planto.de/OekoArt/ModellLog.php")
```

Get names of VegetWeb tables and look for the Entity Relationship Diagram.

```
> con <- vw.con()
> dbListFields(con, "beobachtung")
```

```
 [1] "Beobachtungs_ID"                "Beobachtungscode"                "Plotcode"
 [4] "Vorbeobachtung"                 "Projekt"                         "DatumVon"
 [7] "Datum"                          "Moosidentifikation"              "Flechtenidentifikation"
[10] "Deckungsmethode"                "Deckungsmethode2"                "Nutzung"
[13] "Anteil Streuschicht"            "Anteil offene Wasserfl\xe4che" "Anteil Fels"
[16] "Anteil Skelett"                 "Anteil offener Boden"            "Deckung Baumschicht"
[19] "Deckung Strauchschicht"         "Deckung Feldschicht"             "Deckung Kryptogamenschicht"
[22] "Deckung Schwimmblattschicht"    "Deckung Wasserpflanzenschicht" "H\xf6he Baumschicht"
[25] "H\xf6he Strauchschicht"         "H\xf6he Feldschicht"             "H\xf6he Kryptogamenschicht"
[28] "Tiefe Wasserpflanzen"           "Bemerkung"                       "Erheber"
[31] "Digitalisierer"                 "Zitat"                           "Zitattabelle"
[34] "Zitataufnahme"                  "Verband"                         "Assoziation"
[37] "Gesellschaftsbezeichnung"       "Subassoziation"                  "Sukzessionsstatus"
[40] "Bestandsalter"                  "Bioz\xf6notische Aspekte"        "Hydrologie"
[43] "Grundwasserflurabstand"         "Uferentfernung"                  "Bodenart"
[46] "Bodentyp"                       "Humusform"                       "pH"
[49] "Phosphor"                       "Kalium"                          "Magnesium"
[52] "N-Gehalt"                       "Biotoptyp"                       "Pflegema\xdfnahmen"
[55] "D\xfcngung"                     "Schutz"                          "Temperatur"
[58] "User"                           "Modified"
```

```
> dbGetQuery(con, "SELECT * FROM projekt")[1:2]
```

```
   Projekt                                                      Projektname
1     Bohn                      Vegetationsaufnahmen bodensaurer Buchenw\xe4lder
2     BgWd                                                Bergwald - Datenbank
3     T252                                                T\xfcxenia 25 Becker
4     T251                                                       T\xfcxenia 25
5     T253                                           T\xfcxenia 25 B\xfcltmann
6     T262                                                       T\xfcxenia 26
7     T264                                                       T\xfcxenia 26
8     T254                                                 T\xfcxenia 25 Fuchs
9     T255                                               T\xfcxenia 25 Gehlken
10    T269                                                       T\xfcxenia 26
11    T261                                                       T\xfcxenia 26
12    T268                                                       T\xfcxenia 26
13    T256                                         T\xfcxenia 25 Otte und Maul
14    T265                                                       T\xfcxenia 26
15    T266                                                       T\xfcxenia 26
16    T282                                 Die Schwermetall-Vegetation des Harzes
17    T292      Populationsstruktur und Vergesellschaftung von Dictamnus albus L.
18    T275                                                T\xfcxenia 27 Huntke
19    T274                               T\xfcxenia 27 Kr\xe4mer u. Fartmann
20    T273                                               T\xfcxenia 27 Brandes
21    T272                                                T\xfcxenia 27 Klauck
22    T271                                               T\xfcxenia 27 Dengler
23    T263                                                       T\xfcxenia 26
24    T276                                                T\xfcxenia 27 Becker
25    T281                    Die Allmendeweide \x84NSG Kanzelstein bei Eibach\x93
26    T291 Verbreitung, Vergesellschaftung und \xd6kologie von Lathraea squamaria
27    T293           Trittgesellschaften der nordrhein-westf\xe4lischen D\xf6rfer
28    T294                     Succession and management of calcareous dry grasslands
29  SYPF10                          Synopsis der Pflanzengesellschaften Deutschlands
30    vNWR                                           Naturwaldreservate Bayerns
31   LANUV  LINFOS-Daten Landesamt f\xfcr Natur, Umwelt und Verbraucherschutz NRW
32    T302                                         T\xfcxenia 30 Schmitt et al.
```

```
> query <- "Projekt='T302'"
```

Since several years all authors of **Tuexenia** are committed to give their published data to VegetWeb. Therefore we can quite easily download the data from e.g.:
Schmitt, Fartmann, Hoelzel 2010 Phytosociology and ecology of *Gladiolus palustris* in southern Bavaria, Tuexenia 30, p. 105-128.

```
> site <- vw.site(query)
> site.coord <- site[!is.na(site$"Geografische Breite"), ]
```

9 Additional functions

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

9.1 Combine different taxonomic reference lists

If you have to combine different taxonomic reference lists, functions `tv.compRefl` might be a starting point, comparing species numbers and/or species names of both lists.

```
> tv.compRefl("taxref1", "taxref2")
```

9.2 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 ?, a selection of grassland relevés from the floodplains of the river Elbe.

```
> data(elbaue)
```

```
> clust <- vector("integer", nrow(elbaue.env))
> clust[elbaue.env$MGL < -50 & elbaue.env$SDGL < 50] <- 1
> clust[elbaue.env$MGL < -50 & elbaue.env$SDGL >= 50] <- 2
> clust[elbaue.env$MGL >= -50 & elbaue.env$SDGL >= 50] <- 3
> clust[elbaue.env$MGL >= -50 & elbaue.env$SDGL < 50] <- 4
> 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).

```
> syntab(elbaue, clust, limit = 40)
```

```
 Number of clusters:  4
Cluster frequency 7 10 5 11
        dry.ld dry.hd wet.hd wet.ld
AGRTCAP     57     30      .     18
ALOPGEN      .     20     60      9
ALOPPRA     71     90     20     36
ANTXODO     43     10      .     27
CARDPRA     43     10      .     55
CAREACU     14      .     40     82
CAREPRA     43     70      .      .
CAREVES      .      .      .     55
CIRSARV     43      .      .      9
DESCCES     57      .      .     18
ELYMREP     57     90      .      .
EUPHESU     43      .      .      .
GALUPAL     29     30     60     64
GALU#VE     71     20      .      .
GLYCMAX      .      .     80     45
HOLCLAN     43      .      .     36
JUNUEFF     14      .     20     45
LATYPRA     43      .      .      9
PHALARU     14     40     80     64
POA PAL     29     60     20     45
POA #PR     57     60     20     27
POA T-T     14     30     20     45
RANCFLA      .      .      .     55
RANCREP     29     60     40     73
RORIAMP      .      .     60      9
RUMEACE     43      .      .     27
RUMETHY     43     60      .      .
SIUMLAT      .      .     40     45
STELPAU     14     20      .     64
TARA/AN     57     60      .     18
VICICRA     43     10      .     18
VICITET     57     10      .      .
```

Or we can calculate the affiliation of species to abiotic clusters with the help of package `indicspecies`, which calculates species indicator values for one or several cluster (**?**).

```
> syntab(elbaue, clust, mupa = TRUE, fullnames = TRUE)

 Number of clusters:  4
Cluster frequency 7 10 5 11
                                dry.ld dry.hd wet.hd wet.ld  cl
Cirsium arvense                     43      .      .      9   1
Deschampsia cespitosa               57      .      .     18   1
Euphorbia esula                     43      .      .      .   1
Galium verum agg.                   71     20      .      .   1
Lathyrus pratensis                  43      .      .      9   1
Vicia tetrasperma                   57     10      .      .   1
Alopecurus geniculatus               .     20     60      9   3
Rorippa amphibia                     .      .     60      9   3
Caltha palustris                     .      .      .     36   4
Carex gracilis                      14      .     40     82   4
Carex vesicaria                      .      .      .     55   4
Agropyron caninum                    .      .      .     36   4
Ranunculus flammula                  .      .      .     55   4
Alopecurus pratensis                71     90     20     36 1+2
Carex praecox agg.                  43     70      .      . 1+2
Agropyron repens subsp. caesium     57     90      .      . 1+2
Rumex thyrsiflorus                  43     60      .      . 1+2
Taraxacum officinale agg.           57     60      .     18 1+2
Cardamine nemorosa                  43     10      .     55 1+4
Glyceria maxima                      .      .     80     45 3+4
Sium latifolium                      .      .     40     45 3+4
```

10 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.

10.1 Plot coordinates of vegetation relevés into an interactive Google Map

```
> library(googleVis)
> site.coord$loc <- paste(site.coord[, 29], site.coord[, 28], sep = ":")
```

If you do not have geodesic coordinates as used in Google Earth (EPSG-Code 4326), you can convert coordinates with R packages rgdal.

```
> library(rgdal)
> coord <- data.frame(HW = as.numeric(site.coord$Nordkoordinate), RW = as.numeric(site.coord$Ostkoordinate))
> coordinates(coord) <- c("RW", "HW")
> proj4string(coord) <- CRSargs(CRS("+init=epsg:31468"))
> coord <- spTransform(coord, CRS("+init=epsg:4326"))
> site.coord$long <- coordinates(coord)[, 1]
> site.coord$lat <- coordinates(coord)[, 2]
> site.coord$loc <- paste(site.coord$lat, site.coord$long, sep = ":")
```

To give some information we will create Tips:

```
> site.coord$tip <- paste(paste("Releve_NR:", site.coord$RELEVE_NR), paste("Table:",
+     site.coord$TABLE_NR), paste("Nr. in table:", site.coord$NR_IN_TAB), site.coord$DATE,
+     landuse = site.coord$NUTZUNG, site.coord$Assoziation, site.coord$Erheber,
+     paste("Locality:", site.coord[, 26]), paste("Longitude:", site.coord[, 28]),
+     paste("Latitude:", site.coord[, 29]), sep = "<BR>")
```

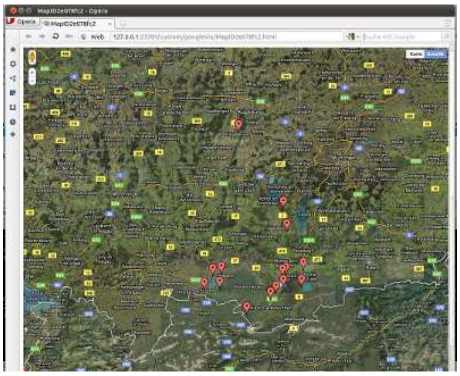


Figure 2: Spatial distribution of vegetation plots from a VegetWeb project. The map is interactive and zoomable.

and the produced map will be open in your standard web browser.

```
> places <- gvisMap(site.coord, "loc", "tip", options = list(showTip = TRUE, showLine = FALSE,
+     enableScrollWheel = TRUE, mapType = "hybrid", useMapTypeControl = TRUE,
+     width = 1000, height = 800))
> plot(places)
```

10.2 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 (**?**) from Jari Oksanen (**?**).

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

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

```
> library(labdsv)
> library(akima)
> color = function(x) rev(topo.colors(x))
> nmds.plot <- function(ordi, site, var1, var2, disp, plottitle = "NMDS", ...) {
+     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 = 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)
+         }, ...)
+ }
```

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 at more balanced situations.

```
> print(nmds.plot(veg.nmds, elbaue.env, disp = "species", var1 = "MGL", var2 = "SDGL",
+     plottitle = "NMDS of Elbaue floodplain vegetation"))
```

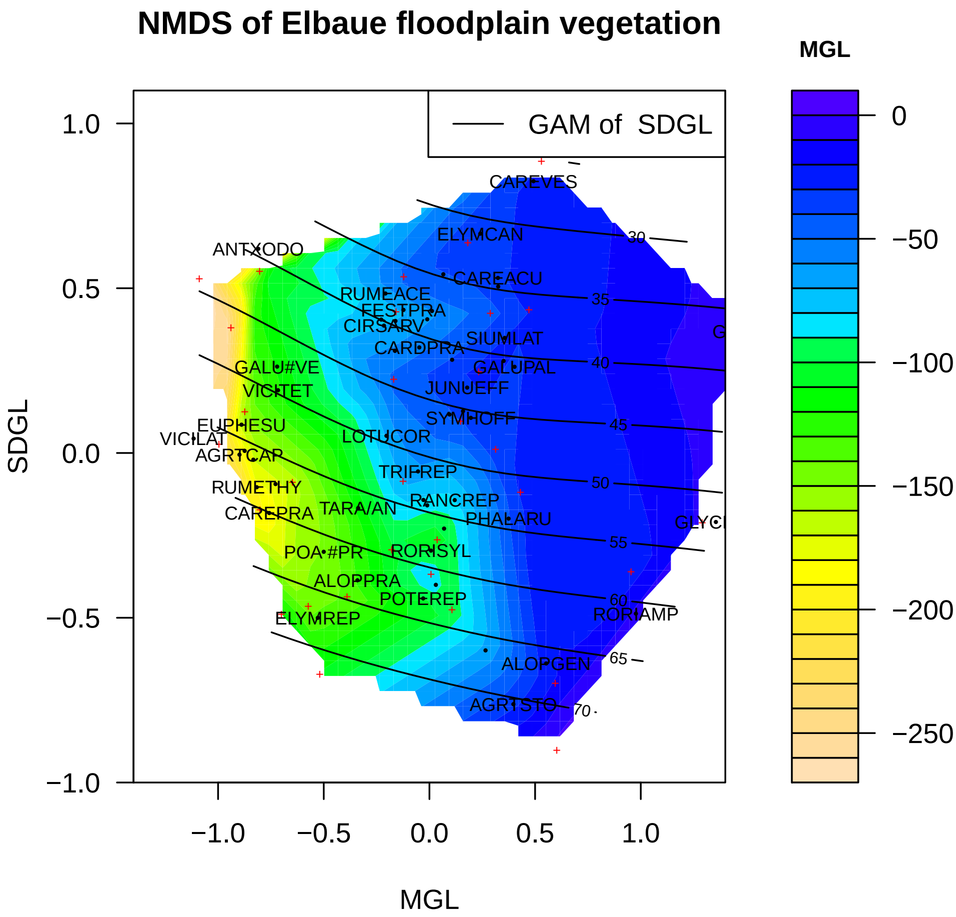


Figure 3: Non-metric multidimensional scaling of the elbaue vegetation data with an overlay of mean groundwater table (colors) and standard deviation of groundwater level fluctuations (lines).