**TABLEFIT v. 3.0 & v.4, programs for the identification of vegetation types according to the British National Vegetation Classification**

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1. General introduction
   1. Purpose of TABLEFIT

TABLEFIT is a program to identify vegetation types. Given a list of species, together with their frequency and/or abundance, the program will assign the assemblage to a vegetation community based on phytosociological or other tables. In its present form, it has been written specially to identify the vegetation types described in *British Plant Communities* (Rodwell 1991a,b, 1992, 1995, 2000). The communities and sub-communities recognized in *British Plant Communities* are called NVC types where NVC is an abbreviation referring to the National Vegetation Classification. With small modifications, it could be used to identify vegetation types described from other regions by other authors.

The basic idea of the program was first outlined by Hill (1989). Essentially, it takes data from a sample of vegetation and calculates a goodness-of-fit measure against the expected species composition of a previously-described community (here a NVC community or sub-community). The vegetation type allocated to any sample is the one with the highest goodness-of-fit. The goodness-of-fit measure used is similar to that outlined by Hill (1989). More detail is given in the section ‘Definition of goodness-of-fit values’ below.

* 1. Historical development

TABLEFIT was conceived and written by M O Hill and was first released in 1993 and was compiled in DOS, taking advantage of the Microsoft Fortran compiler for DOS. This had very limited storage space, so that the association tables had to be compressed. An updated version v1.0, including open vegetation types (OV communities) was issued in 1996. The NVC communities and sub-communities, essentially a British classification, were cross-referenced to the CORINE habitats classification (Moss & Wyatt 1994), thus providing compatibility with this EU classification system.

In 2011, the program was recompiled using the GNU Fortran G77 v0.5.25 compiler for Windows XP (Free Software Foundation, 1999). At this point, error trapping was improved. The relatively relaxed file handling also allowed these programs to run more freely and the ability to vary the number of matched communities was added.

In 2015 v.2.0 was produced which updated species nomenclature, i.e.:

1. Vascular plants, current names such as *Helminthotheca echioides* and *Schedonorus pratensis* were available to the program.
2. Bryophytes, conformed to the names in the current checklist (Hill *et al.*, 2008).
3. Lichens and algae, using data on the NBN Gateway https://data.nbn.org.uk/, accessed in May 2015.

It was still possible to use the older names for example, old names such as *Festuca pratensis* and *Agrostis tenuis* were still in the dictionary.

At this point the NVC communities were also cross-referenced to EUNIS, which had superseded the CORINE habitat classification (Devillers *et al.*, 1991; (European Environment Agency, 2007). This cross-referencing drew heavily on the account of EUNIS habitats in Scotland by Strachan (2015), to which the reader is referred for further information. NVC types and EUNIS habitats are logically-distinct entities. A NVC vegetation type can occur in more than one habitat (e.g. NVC type SD3 can occur both on dunes and on shingle). Likewise, a habitat can support several types of vegetation. A NVC vegetation type is defined completely by its plant species composition. EUNIS habitats are defined primarily by their ecosystem (woodland, dune, swamp, etc.), though the definitions may contain elements of vegetation composition and land-use.

There is often a close relation between vegetation types and habitats. Indeed, many of the semi-natural EUNIS habitats are defined in terms of their vegetation. Mires, however, are defined by physical features. Thus raised bogs and blanket bogs are treated as distinct EUNIS habitats, even though they can have almost identical vegetation. Many man-made habitats are defined by land-use. Thus arable fields and urban allotment gardens are treated as different EUNIS habitats, even where they support very similar weed communities.

NVC and EUNIS are cross-referenced in data files supplied with the TABELFIT programs (Fig. 1).

TABLEFIT is still in regular use by ecologists; it has been downloaded 513 times between 2015 and April 2019 (CEH download statistics).

1.3. Improvements in versions 3 and 4

## In early versions of TABLEFIT, it was easiest to run in single-sample mode with direct keyboard entry; the batch handling system was cumbersome and although it worked reasonable well had three major drawbacks for “industrial-scale” use, these were:

# The number of samples that could be handled in any one run was restricted to 9,999; larger studies with more than this number required multiple runs. This was an inconvenience.

# The sample name was restricted to 8 characters.

# The output files were awkward to handle in Spreadsheets and specifically they did not read easily into the standard input requirements for statistical packages without considerable post-processing.

With time there is the inevitable fourth problem:

1. New community descriptions have been produced since the NVC volumes were created and since TABLEFIT was first produced, most notably for wet grasslands (Floodplain Meadows Partnership, 2016). The description of these additional communities are provided in Appendix Table A.0.

Accordingly, two new programs (TABLEFITv3 and TABLEFITv4) have been produced by Michael Jones of Dart Computing. These were both written in C# using modern computer coding protocols; this will make it much easier for future updating, for example by adding any new communities.

Both programs now have an upper limit of 100,000 samples, a restriction on sample name size of 30 characters and an option to have the data output either as (a) the original TABLEFIT v2 output style, or (b) what we hope is a better output style (in .csv format) that provides much more information in an easy to use format.

1.4. Why two programs

The justification for producing the two programs are as follow:

* TABLEFITv3: this is essentially a faithful reproduction of v2 in C#, but modified to account for (a) and (b) above. It uses the same compressed data files as v2.
* TABLEFITv4: this is an enhanced version based on TABLEFITv3, but has the additional information on the new wet grassland communities, i.e. (c) above.

Moreover, the associated data files have been modified into more user-friendly versions which synchronize with the data files used in MAVIS v2 (**M**odular **A**nalysis of **V**egetation **I**nformation **S**ystem (<https://www.ceh.ac.uk/services/modular-analysis-vegetation-information-system-mavis>), Smart *et al*., 2016).

Hence, it is now easy to upgrade both TABLEFIT v4 and MAVIS v2 program simultaneously, should there be a need for future amendments or if new communities are described, i.e. like the wet grassland ones.

Note that an impending new release of MAVIS will now include the TABLEFIT v4 fitting algorithm enabling results to be produced for both NVC matching methods: The input option choices for TABLEFIT v4 within MAVIS are fixed as:

* All species to be included in the analysis
* Species cover (%)
* Mixed compositions and cover
* Max frequency =5
* Number of Fits=10

We argue that where compatibility is required with previous TABLEFIT community classifications then TABLEFITv3 should be used. In this way, classifications will be carried out using the same community association tables without complications from the new added communities.

For new assessments, TABLEFITv4 should be used as it:

* Covers a wider range of plant communities than TABLEFITv3.
* Includes additional possibilities for mesotrophic grassland communities and sub-communities (NVC MG communities).
  1. Setting up in TABLEFIT in WINDOWS

After extracting the downloaded .ZIP file you should have a TABLEFIT directory with two sub directories (Table YY), one labelled TABLEFIT.v3 the other TABLEFIT.v4. The executable file or TABLEFIT and their associated data files are in the appropriate sub-directories (Fig. 1). The associated data fields must be in the same sub-folder as the appropriate executable files and we suggest that you put data and results files in these directories also.

In each sub-directory there is test example data file ULM\_MEAD.txt, which is a meadows dataset from in the Danube valley near Ulm, published by Mueller-Dombois & Ellenberg (1974). The output from this file is presented from a TABLEFIT run of these data are also presented in each sub-directory as ULM\_MEAD.v3.results.csv and ULM\_MEAD.v4.results.csv respectively.

|  |  |
| --- | --- |
| **TABLEFIT** | |
| TABLEFIT.v3.V4.MANUAL | WORD file – the Manual |
| Species\_Convertor.xlsx | EXCEL file to assist with changing species names TABLEFIT short names |
| Data\_Convertor\_Spp\_As\_Rows | WORD files with R code to convert data from EXCEL .csv files to TABLEFIT format .txt files |
| Data\_Convertor\_Spp\_As\_Cols |
| Book11.csv and Book22.csv | Test files for Data\_Convertor.docx |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **TABLEFITv3** | |  | **TABLEFITv4** | |
| Tablefit.v3 | Compiled version for Windows |  | Tablefit.V4 | Compiled version for Windows |
| SPECDICT.TXT | Dictionary of plant names/code numbers |  | SPECDICT3 | Dictionary of plant names/code numbers |
| NVCTYPES.TXT | List of vegetation types /names |  | TablefitNVCDef3..TXT | List of vegetation types /names |
| ASSOCTAB.TXT | Association tables (highly condensed) |  | TablefitNVCData3.TXT | Association tables (highly condensed) |
| ULM\_MEAD.txt | Test Dataset |  | ULM\_MEAD.txt | Test Dataset |
| ULM\_MEAD.v3.results.csv | Results from Test Dataset |  | ULM\_MEAD.v4.results.csv | Results from Test Dataset |

**Fig 1.**  TABLEFIT Directory and Sub-directory structure with the component files.

2. Data entry

If you are not familiar with the program, try running it with the default options and the data in Table 1. These are selected by pressing the <RETURN> key after each question until the program starts to read in the dictionary. When the program asks you for the number of number of fitted communities to output, answer 5. When the program asks you for a sample name press <RETURN> again, and enter the following data when prompted to enter the species.

When entering data, either by keyboard or data file, there has to be a space between the genus and specific name codes and the quantitative data.

2.1. Basic Data entry

Data should be entered exactly as shown in the shaded part of Table 1. If entering data in a file exactly the same format should be used to input the data.

A blank line is used to separate the samples.

Please note tab characters must be removed from the data files.

**Table 1.** Keyboard data entry format for a test example and its meaning; just input the data in the shaded column into TABLEFIT.

|  |  |  |  |
| --- | --- | --- | --- |
| Data as input | What it means | | |
|  |  | Species | Cover value (%) |
| quer robu 100 |  | Much oak | 100 |
| pter aqui 20 | *et seq.* | Some bracken | 20 |
| holc moll 20 |  | Some creeping soft grass | 20 |
| hyac non‑ 20 |  | Some (English) bluebell | 20 |
|  |  | Blank line to end sample |  |
| Names and data separated by a space |  |  |  |

Data files for batch data entry follow the same format as Table 1 with a blank line between each sample.

2.2. Basic Data output

With the test data in Table 1, you should get the output shown in Table 2, this is accompanied by some other information. This uses the default setting of fitting the top five community types.

**Table 2. Example output from the data presented in Table 1.**

|  |
| --- |
| Sample SAMPL 1 Parameters = All sp Cover% Sp & c  G1.A11 W10 68 |63 100 73 100| Que rob‑Pte aqu‑Rub fru  F3.131 W25a 59 |59 100 97 48| Pte aq‑Rub fr underscb Hyacinth non‑sc  G1.A11 W10a 56 |54 100 62 78| Que rob‑Pte aqu‑Rub fru Typical  F3.131 W25 54 |65 85 86 37| Pte aq‑Rub fr underscb  G1.A11 W10b 51 |47 88 56 93| Que rob‑Pte aqu‑Rub fru Anemone nemoros |

To aid intrepretation here is the same table presented in an improved tabular format (Table 3).

**Table 3.** The raw output from Table 2 has been expanded; (a) the sample name “SAMPL1“, along with a record of the TABLEFIT parameters used in the analysis, and (b) the information for the five best fits (Fit#) to the NVC communities.

|  |  |
| --- | --- |
| (a) |  |
|  | Sample SAMPL1 Parameters = All sp Cover% Sp & c |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| (b) |  |  |  |  |  |
| Fit# | Eunis community code | NVC community/ sub-community type | Mean GoF | Four component GoF values | NVC community/sub-community name |
| 1 | G1.A11 | W10 | 68 | |63 100 73 100| | Que rob‑Pte aqu‑Rub fru |
| 2 | F3.131 | W25a | 59 | |59 100 97 48| | Pte aq‑Rub fr underscb Hyacinth non‑sc |
| 3 | G1.A11 | W10a | 56 | |54 100 62 78| | Que rob‑Pte aqu‑Rub fru Typical |
| 4 | F3.131 | W25 | 54 | |65 85 86 37| | Pte aq‑Rub fr underscb |
| 5 | G1.A11 | W10b | 51 | |47 88 56 93| | Que rob‑Pte aqu‑Rub fru Anemone nemoros |

What this tells you is that the best diagnosis is oak-bracken-bramble woodland (W10) with a goodness-of-fit of 68. This corresponds to EUNIS type G1.A11, Atlantic oakwood with bluebell (see Strachan (2015) for more detail).

2.3. Output from batch files

There are now two options for the output of results in TABLEFIT v3 and v4. You will be prompted to make a choice at the start of the program, i.e.

First, you are asked to type in a file name for answers, we suggest that you input a .csv filename.

The next question is as follows:

Type 0 for output in new CSV format

Type 1 for output in original tabulated text format

Existing value is 0.

Press <RETURN> to retain it, or type new value

This choice allows the option to continue to use the old style format (input 1) or the choose the new format (input 0 – this is the default).

2.3.1. The old style format

The output from a data file with more than one sample looks exactly the same as Table 0.1 but with the additional samples added in sequence at the bottom.

2.3.2. New-style format

The new style format is shown along with explanations in Table 4. This new format as a comma-delimited (.csv) file reads directly into EXCEL or other spreadsheets and is in columnar format so can be cut and pasted or read in to most statistical packages. Moreover, each line in the dataset has an unique set of identification variables.

Additional information on the species are also present as follows:

* 1. Species that were in both the sample and the NVC community/sub-community type.
  2. Species that were only in the sample.
  3. Species that were only in the NVC community/sub-community type.

**Table 4.** New improved output in TABLEFIT v3 and v4. The results are output as a comma-delimited file (.csv format), making it very easy to transfer the information in a readily-useable columnar format to an EXCEL spreadsheet or statistical package (e.g. R). Results) are provided for one sample based on fitting the five top communities (Fit#, this is under user control, the default =5). The output is organised in two parts:

1. **NVC fits (here in Dark green):** This is the standard TABLEFIT output for each Fit#, i.e. the EUNIS community code plus name, NVC community and where allocated a NVC sub-community, along with the mean Goodness-of-fit and its component parts (GoF\_1, GoF\_2, GoF\_3, GoF\_4). The parameters under which the run was performed, and the cover scale used, are also output on each line for information and ease of data handling.
2. **Species information (here in Red):** This is additional information that has not been presented in TABLEFIT before. For each of the fits information on the number (column 6) and identity (column 7) of species are presented in the following groups:
   1. Species that were in both the sample and the NVC community/sub-community type (NVC\_&\_Sample).
   2. Species that were only in the sample (NVC\_only).
   3. Species that were only in the NVC community/sub-community type (NVC\_only).

The red and green data can be easily separated by filtering or sorting on the Analysis\_type field (column 2) for further calculations.

Note each line of data has an unique set of identification variables based on Sample/Analysis\_type /Fit#

The identity of species (column 7) is in semi-colon (;) delimited list form for simplification of the output, these can be easily converted in EXCEL using the “text to columns” utility. In this example not all species are illustrated – hence **et seq.**

**Table 4 continued**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample** | **Analysis\_Type** | **Fit#** | **Eunis\_Comm** | **NVC\_Comm** | **Mean\_GoF** | **GoF\_1** | **GoF\_2** | **GoF\_3** | **GoF\_4** | **NVC\_Comm\_Name** | **NVC\_Sub\_Name** | **Eunis\_Name** | **Vasc\_Param** | **Cover\_Scale** | **Anal\_Param** |
| **Sample.#1** | **Results** | **1** | **F2.25** | **H18a** | **58** | **97** | **52** | **58** | **68** | **Vacc\_myr-Desc\_fle\_heath** | **Hyl\_spl-Rhy\_lor** | **Boreo-alpine\_heath** | **All\_sp** | **Cover\_Scale** | **Sp\_&\_cov** |  |  |  |
| **Sample.#1** | **Results** | **2** | **F2.25** | **H20d** | **54** | **86** | **42** | **68** | **61** | **Vacc\_myr-Raco\_lan\_heath** | **Rhy\_lor-Hyl\_spl** | **Boreo-alpine\_heath** | **All\_sp** | **Cover%** | **Sp\_&\_cov** |  |  |  |
| **Sample.#1** | **Results** | **3** | **F2.25** | **H20** | **52** | **89** | **54** | **47** | **64** | **Vacc\_myr-Raco\_lan\_heath** |  | **Boreo-alpine\_heath** | **All\_sp** | **Cover%** | **Sp\_&\_cov** |  |  |  |
| **Sample.#1** | **Results** | **4** | **F2.25** | **H18** | **50** | **96** | **43** | **54** | **60** | **Vacc\_myr-Desc\_fle\_heath** |  | **Boreo-alpine\_heath** | **All\_sp** | **Cover%** | **Sp\_&\_cov** |  |  |  |
| **Sample.#1** | **Results** | **5** | **E5.5** | **U16** | **50** | **100** | **45** | **53** | **52** | **Luzul\_sylv-Vaccin\_myrt** |  | **Subalp\_tall-herb/fern** | **All\_sp** | **Cover%** | **Sp\_&\_cov** |  |  |  |
| **Sample.#1** | **Analysis** | **1** | **H18a** | **NVC\_&\_Sample** | **20** | **alch alpi;anth odor;blec spic;care bige;desc flex;gali saxa;luzu sylv;mela prat;nard stri; et seq.** | | | | | | | | | | | | | | | | | | | | | | | | | |
| **Sample.#1** | **Analysis** | **1** | **H18a** | **Sample\_only** | **12** | **caly fiss;cetr isla;clad bell;clad carn; et seq.** | | | | | | | | | | | | | | | | | | |  |  |  |  |  |  |  |
| **Sample.#1** | **Analysis** | **1** | **H18a** | **NVC\_only** | **13** | **agro cani;agro capi;call vulg;cham suec;empe nigr;fest fili;oxal acet; et seq.** | | | | | | | | | | | | | | | | | | |  |  |  |  |  |  |  |
| **Sample.#1** | **Analysis** | **2** | **H20d** | **NVC\_&\_Sample** | **15** | **alch alpi;care bige;desc flex;empe herm;gali saxa;nard stri;vacc myrt;hylo sple; et seq.** | | | | | | | | | | | | | | | | | | | | |  |  |  |  |  |
| **Sample.#1** | **Analysis** | **2** | **H20d** | **Sample\_only** | **17** | **anth odor;blec spic;caly fiss;clad bell;clad carn;clad cocc;dicr fusc;dicr maju;isot myos;luzu sylv;mela prat; et seq.** | | | | | | | | | | | | | | | | | | | | | | |  |  |  |
| **Sample.#1** | **Analysis** | **2** | **H20d** | **NVC\_only** | **8** | **agro cani;fest fili;vacc viti;dicr scop;hypn cupr;poly alpi;anas orca;ptil cili; et seq.** | | | | | | | | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| **Sample.#1** | **Analysis** | **3** | **H20** | **NVC\_&\_Sample** | **16** | **alch alpi;care bige;desc flex;empe herm;gali saxa;nard stri;pote erec;vacc myrt;vacc ulig; et seq.** | | | | | | | | | | | | | | | | | | | | | |  |  |  |  |
| **Sample.#1** | **Analysis** | **3** | **H20** | **Sample\_only** | **16** | **anth odor;blec spic;caly fiss;clad bell;clad carn;clad cocc;dicr fusc;dicr maju;isot myos;luzu sylv;l et seq.** | | | | | | | | | | | | | | | | | | | | | | |  |  |  |
| **Sample.#1** | **Analysis** | **3** | **H20** | **NVC\_only** | **21** | **agro cani;agro capi;call vulg;care pilu;fest fili;diph alpi;hupe sela;succ prat;thym poly;vacc viti;viol reic; et seq.** | | | | | | | | | | | | | | | | | | | | | | | | | |
| **Sample.#1** | **Analysis** | **4** | **H18** | **NVC\_&\_Sample** | **15** | **alch alpi;anth odor;blec spic;care bige;desc flex;gali saxa;nard stri;pote erec;vacc myrt; et seq.** | | | | | | | | | | | | | | | | | | | | | |  |  |  |  |
| **Sample.#1** | **Analysis** | **4** | **H18** | **Sample\_only** | **17** | **caly fiss;cetr isla;clad bell;clad carn;clad cocc;clad unci;dicr fusc;dicr maju;empe herm; et seq.** | | | | | | | | | | | | | | | | | | | | | | |  |  |  |
| **Sample.#1** | **Analysis** | **4** | **H18** | **NVC\_only** | **13** | **agro cani;agro capi;call vulg;camp rotu;care pilu;empe nigr;fest fili;luzu camp; et seq.** | | | | | | | | | | | | | | | | | | |  |  |  |  |  |  |  |
| **Sample.#1** | **Analysis** | **5** | **U16** | **NVC\_&\_Sample** | **15** | **alch alpi;anth odor;blec spic;desc flex;gali saxa;luzu sylv;nard stri;pote erec;vacc myrt; et seq.** | | | | | | | | | | | | | | | | | | | | | |  |  |  |  |
| **Sample.#1** | **Analysis** | **5** | **U16** | **Sample\_only** | **17** | **caly fiss;care bige;cetr isla;clad arbu;clad bell;clad carn;clad cocc;clad unci;dicr fusc; et seq.** | | | | | | | | | | | | | | | | | | | | | | |  |  |  |
| **Sample.#1** | **Analysis** | **5** | **U16** | **NVC\_only** | **15** | **agro cani;agro capi;care bine;desc cesp;dryo dila;fest fili;oxal acet;rume acsa;dicr scop et seq.** | | | | | | | | | | | | | | | | | | | | | |  |  |  |  |

3. Preparing the data for entry – the options

3.1. Data entry

Data specifying the composition of a vegetation sample can be entered from the keyboard, or can be submitted as a data file with the name SAMPLES.TAB, or a user-determined filename can be used (filename.txt). Note make sure any tab spaces are removed.

The form of data input is designed to be as intelligible as possible. A basic example of data input form is shown in Table 5.

**Table 5.** Data entry format and its meaning; the data input to TABLEFIT is in the format of the shaded column.

|  |  |  |  |
| --- | --- | --- | --- |
| Data as input | What it means | | |
| EXAMPLE1 | Sample code | Species | Cover value (%) |
| nard stri 40 |  | *Nardus stricta* | 40% |
| fest ovin 40 | *et seq.* | *Festuca ovina* | 40% |
| agro vine 5 |  | *Agrostis vinealis* | 5% |
| poly comm 5 |  | *Polytrichum commune* | 5% |
| care bine |  | *Carex binervis* | <1% |
| vacc myrt 15 |  | *Vaccinium myrtillus* | 15% |
| call vulg |  | *Calluna vulgaris* | <1% |
|  |  | Blank line to end sample |  |

The data for the sample ends with a blank line, and a new sample begins. There are no requirements for formatting or for using upper or lower case. For example

Nardus stricta 4 and nard stri 40

are both interpreted the same way by the program. TABLEFIT converts everything to lower case and truncates names to 4-letter genus and 4-letter species. This creates a few problems with ambiguous names (see below).

3.2. Species names

Vascular plant names are those of Stace’s floras (1991, 2010) and Rodwell (1991a,b, 1992, 1995, 2000), with a few extra synonyms included for convenience. If you have forgotten the modern name of a species, type the name of the genus, e.g.

poly 40

The program then prompts you with a list of names starting with poly (e.g. *Polygala*, *Polypodium*, *Polystichum*, *Polytrichum*). Plant names are listed in spreadsheet Plant\_names.xls. Note that in this case the menu will not list *Polypodium vulgare* or *Polygala vulgaris*. That is because these could be confused, and are therefore abbreviated as polp vulg and polg vulg respectively. Bryophyte names include those in recent floras (Atherton *et al.*, 2010, Smith, 2004) and checklists (Blockeel & Long, 1998, Hill *et al.*, 2008).

3.3. Woody species and layered vegetation

Woody species can occur in differing layers of vegetation and may be entered separately for each layer (as in the association tables of *British Plant Communities*. The tree stratum is denoted by \*\*, the shrub and sapling stratum by \*. The position of \* or \*\* on the line does not matter. The following data signify vegetation from a wood. In this case a tree with no stars denotes a seedling of that species. In making its diagnosis, the program merely adds up the total cover (after it automatically converts to % cover from Domin or Braun-Blanquet scales if these are used) and treats the occurrence as a single one. An example of a layered-woodland sample is presented in Table 6.

**Table 6.** Data entry format and its meaning for layered woody vegetation; the data input to TABLEFIT is in the format of the shaded column.

|  |  |  |  |
| --- | --- | --- | --- |
| Data as input | What it means | | |
| EXAMPLE2 | Sample code | Species | Cover value (%) |
| quer robu\*\* 50 |  | *Quercus robur* trees | 50 |
| frax exce\*\* 40 | *et seq.* | *Fraxinus excelsior* trees | 40 |
| cory avel\* 20 |  | *Corylus avellana* shrub | 20 |
| acer camp\* 20 |  | *Acer campestre* shrub | 20 |
| frax exce\* 5 |  | *Fraxinus excelsior* sapling | 5 |
| quer robu |  | *Quercus robur* seedling | <1 |
| care pend 20 |  | [*Carex pendula* | 20 |
| desc cesp 20 |  | *Deschampsia cespitosa* | 20 |
|  |  | Blank line to end sample |  |

3.4. Frequency data

3.4.1. Samples with both frequency and cover data

Some vegetation data are obtained by recording several quadrats and recording species frequencies. In this case, the maximum possible frequency is indicated following a \* at the end of the sample name (Table 7).

**Table 7.** Data entry format and its meaning for samples where there are both frequency and cover data; the data input to TABLEFIT is in the format of the shaded column.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Data as input | What it means | | | |
| EXAMPLE3 \* 100 | Sample code \* max frequency | Species | Frequency (%) | Cover value (%) |
| erio vagi 80 20 | erio vagi | 80 | 20 |
| call vulg 100 60 | *et seq.* | call vulg | 100 | 60 |
| *etc* |  |  |  |  |
|  |  | Blank line to end sample | | |

3.4.2. Samples with frequency data for which cover values are lacking

Where information from several nearby quadrats is available, they can be entered in the obvious way (Table 8). No cover data are available, so diagnosis should be by species frequency only, i.e. Analysis parameter (see below) = 2.]

**Table 8.** Data entry format illustrating data where cover data rare lacking but frequency data are available; the data input to TABLEFIT is in the format of the shaded column.

|  |  |  |  |
| --- | --- | --- | --- |
| Data as input | What it means | | |
| EXAMPLE4\*5 | Sample code | Species | Frequency |
| arme mari 5 |  | *Armeria maritima* | in 5 out of 5 quadrats |
| plan mari 3 | *et seq.* | *Plantago maritima* | in 3 out of 5 quadrats |
| plan coro 3 |  | *Plantago coronopus* | in 3 out of 5 quadrats |
| fest rubr 1 |  | *Festuca rubra* | in 1 out of 5 quadrats |
|  |  | Blank line to end sample |  |

3.5. Simplified data entry

Simplified data entry can only be used for keyboard entry; it will not work for data entered in a data file. For simplified entry. species can be entered by their first two letters. This may be useful if you are not a fluent typist, i.e.

EXAMPLE5

c p 20

If this form of data entry is used, list of names of species whose genus begins with c and species begins with p will be supplied. The user then must identify the species by the number in the list. The program automatically picks up all names that it does not recognize and asks you if you have made a mistake.

3.6. Correcting wrongly-entered data

Wrongly-entered data can be corrected in two ways/ First, if a species is repeated, the quantitative data for that species is overwritten. Second, if data are re-entered with a -1 (or any negative number), then the species is omitted from the sample (Table 9).

**Table 9.** Data entry format illustrating how data entry can be modified to correct for wrongly-entered data; the data input to TABLEFIT is in the format of the shaded column. The values in column 2 are equivalent to those in columns 4 and 5.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Row | Data as input | What it means | | |
| 1 | EXAMPLE6 | Sample code | Species | Cover value (%) |
| 2 | care aren 10 |  | fest rubr | 10 |
| 3 | fest rubr 50 |  | ammo aren | 10 |
| 4 | ammo aren 10 |  |  |  |
| 5 | fest rubr 10 | Overwrites previous value –row 3 |  |  |
| 6 | care aren -1 | -1 removes care aren – row 2 |  |  |
|  |  | Blank line to end sample |  |  |

3.7. Data for which quantitative information is lacking

Sometimes only a species list is available. Good identification of the vegetation type is still often possible, although there is a greater chance of misidentifications.

Here a list of species is given without cover values (Table 10). In this case you need to change the value of analysis parameter from the default 1 (Mixed composition and cover) to 2 (Species composition only). The method of changing this parameter is clearly indicated by the menu ‘Set parameter to determine type of analysis’ in the program itself.

**Table 10.** Data entry format illustrating data with a simple species lit without quantitative information; the data input to TABLEFIT is in the format of the shaded column.

|  |  |
| --- | --- |
| Data as input | What it means |
| EXAMPLE7 | Sample code |
| arme mari  plan mari  plan coro  fest rubr |  |
|  | Blank line to end sample |

3.8. Storing the input and output

By default, the sample data that you type in are retained in a file SAMP.txt. If a file with this name already exists, the program will store the new data to SAMP01.txt and so on. If a name is input that has already been used, the program prompts you for another name.

The standard output file for answers is TABLOUT.txt or derivatives such as TABLOUT01.txt.

However, it is good practice to keep a record of TABLEFIT runs using user-friendly file names and text files (.txt) are recommended for input files, and the old TABLEFIT output files, but comma-delimited files (.csv) are recommended for the new improved output format.

1. Setting the Parameters

There are three decisions that need to be made to run TABLEFIT, these are to determine:

1. The species groups to be included; the cryptogam parameter.
2. The cover sale used in the analysis; the cover-scale parameter.
3. The types of data to be used in the analysis. The analysis parameter.

4.1. The cryptogam parameter

This is selected at the following stage:

Type 0 for all species to be included in analysis

Type 1 for vascular plants and bryophytes (excluding lichens and algae)

Type 2 to include only vascular plants

In general, you are advised at this point to type 0 (or merely press <RETURN>, which is equivalent). Cryptogams are important in recognizing some bog and moorland types. If you have a cryptogam-rich upland or mire community but cannot identify cryptogams, then you may try for a list of likely possibilities under option 2. If you do not use this option, then the cryptogam-rich communities will all give you a poor fit.

The main use of the no-cryptogam or no-lichen options is not so much to improve diagnosis but to give a better indication of goodness-of-fit when cryptogams are not recorded. The goodness-of-fit of a properly-recorded quadrat or series of quadrats is quite informative. If the best fit is poor, then the observed vegetation does not well match any of the vegetation types described in *British Plant Communities*.

* 1. The cover-scale parameter

The cover-scale parameter allows you to enter sample data with cover values on any of three scales, and is selected at this stage:

Set cover-abundance scale for samples

Possible values of scale parameter are

1= % cover

2= Braun-Blanquet scale

3= Domin scale

Existing value is 1

Press <RETURN> to retain it, or type new value

Internally, the program works with % cover and the other two scales are converted to % values before a sample is analysed. Domin values are converted by the formula due to Currall (1987), namely

cover % = Domin\*\*2.6 / 4.0

Braun-Blanquet values are converted using the formula in Table 11.

**Table. 11**. Conversion of Braun-Blanquet (BB) codes to cover (%)

|  |  |
| --- | --- |
| Test criterion | Cover (%) |
| if bb < 1.0 | 0 |
| if 1.0 <bb <2.0 | cover % = 15\*(bb-1) |
| if 2.0 <bb | cover % = 25\*bb-35 |

Samples entered using TABLEFIT are marked with their cover-scale parameter. If you subsequently try to run the data through the program with the parameter set differently, the program will notice this and ask you whether you wish to change the parameter to the correct value.

4.3. The analysis parameter

The analysis parameter allows you to use different types of input data and is set at the following point:

Set parameter to determine type of analysis

Possible values of analysis parameter are:

1= Mixed composition and cover

2= Species composition only.

3= Species cover only.

4= Incomplete species list only.

5= Top few spp, descending abundance, no quantitative information available.

If you have a reasonably good species list with some information on species cover you should set the analysis parameter to 1 (the default option). Overall goodness-of-fit is derived by averaging two separate measures, one for species composition and one for species cover. It is nearly (but not quite; see below) the average of the two values that you would get from options 2 and 3.

If data on abundance is lacking, then the quality should be assessed according to the data quality criteria presented in Table 12 and used to select the correct option.

**Table 12.** Data quality criteria to select the most suitable option for TABLEFIT runs when species data are lacking.

|  |  |
| --- | --- |
| **Data quality criteria** | **Option** |
| Data on abundance are lacking, | 2 |
| An incomplete species list is available but the species with cover greater than about 5% are listed | 3 |
| Only an incomplete species list | 4 |
| If only the top few most abundant species are known. | 5, list the species without cover values in descending order of abundance |

1. Interpreting the output
   1. Names and numbers of communities

The names and numbers of plant communities are provided in the files accompanying each program (Fig. 1).

* 1. Information on which identifications are based

Diagnoses made with TABLEFIT are no better than the information on which they are based. TABLEFIT bases its identifications on: (a) the species list that you supply and (b) the association tables published in *British Plant Communities* (Rodwell,1991a,b, 1992, 1995 2000)and for TABLEFITv.4 the additional tables from the Floodplain Meadows Partnership (2016), which are already included in MAVIS v1.04 (Smart *et al.,* 2016).

Diagnoses made with TABLEFIT should always be treated with caution, especially if they are based on incomplete species lists for quadrats. Check the community descriptions in *British Plant Communities* (Rodwell,1991a,b, 1992, 1995 2000; Floodplain Meadows Partnership, 2016; Smart *et al*, 2016).

## Goodness-of-fit ratings

The “correct community”, if there is one, will almost always be one of the top five listed. If goodness-of-fit is very poor (< 50), then you should probably not assign your vegetation to any NVC type unless you know that your vegetation sample was incomplete. A few man-made vegetation types and semi-natural communities are not included in the NVC types available to TABLEFIT. Obviously these will not get high goodness-of-fit ratings. Goodness-of-fit ratings are meant only as a rough guide (Table 13). The interpretation of Goodness-of-Fit scores is an area of active research and these ranking should be used with caution. A new method to evaluate Goodness-of-Fit will be in available in MAVIS v2.0 in due course.

**Table 13.** Interpretation of the Mean Goodness-of-Fit values (from Hill, 2015).

|  |  |
| --- | --- |
| **Goodness-of-fit** | **Interpretation** |
| 80-100 | Very good |
| 70-79 | Good |
| 60-69 | Fair |
| 50-59 | Poor |
| 0-49 | Very poor |

If you get a ‘very good’ rating, your sample has an essentially perfect fit to the description. However, beware of treating the diagnosis as indisputable even in this case. Remember that if you have incomplete information about the quadrat or set of quadrats the diagnosis is always somewhat doubtful, because the missing information may conflict with what you already know. For example, if cover values are not available, a community may have the composition of one type but may in reality have quite a poor fit because the dominance is wrong. TABLEFIT does the best it can on the available information.

* 1. Equal or nearly equal goodness-of-fit values

The best-fitting vegetation types may frequently have nearly equal overall goodness-of-fit values. Several possibilities are outlined in Table 14, along with their suggested interpretation.

**Table 14.** Scenarios where there may be difficulties in interpreting the outcomes from TABLEFIT results, along with suggestions for interpreting the outcome.

|  |  |  |
| --- | --- | --- |
| **Case** | **Outcomes** | **Interpretation** |
| 1 | The sample is intermediate between two or more distinct NVC types | TABLEFIT is particularly useful, indicating the intermediate status of the sample |
| 2 | The sample has the dominance of one type and composition of another | Can be recognized by inspection of the four separate goodness-of-fit values (see below). |
| 3 | The sample is a poor fit to any type | Can be recognized by low overall goodness-of-fit values |
| 4 | The two types are a community and one of its sub-communities | Hardly presents a problem, because if a sample belongs to a sub-community then it ought by rights also to belong to the main community. The correct interpretation is that it belongs to the sub-community. |
| 5 | The two types are a community and a sub-community of another | This is the hardest to interpret. Compare samples that fall into this category with community descriptions or re-diagnose using TABLEFIT with other parameter settings to find out which is most consistently correct |

* 1. Definition of goodness-of-fit values

As noted above (under ‘Analysis parameter’), the overall goodness-of-fit, G, is the average of up to 4 individual goodness-of-fit values, G1, G2, G3, G4. These are printed out for each of the best-fitting types as Table 25. The meaning of each of the goodness-of-fit values is then explained.

**Table 15**. Example of output exactly as it appears in the basic output format for a test example.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **NVC community**  **Sub-community** | **G** | **|** | **G1** | **G2** | **G3** | **G4** | **|** |
| **H4a** | 77 | | | 50 | 100 | 59 | 100| | | |
| **H8a** | 73 | | | 52 |  | 86 | 69 | | |
| **H8c** | 73 | | | 18 | 100 | 76 | 98 | | |
| **H8b** | 73 | | | 25 | 100 | 67 | 98 | | |
| **H8** | 72 | | | 32 | 100 | 62 | 96 | | |

* + 1. G1 ‘Compositional Satisfaction’

G1 is measured nearly as in Hill (1989), but with greater weight given to the higher constancy classes. A high value (max = 100) indicates that sample composition contains all the necessary species. Specifically, it means is that a sufficient number of constancy class V, IV, III or II species is present. Obviously one does not expect all the class III species to be present, but about half of them should be. If more than the expected number are present, then G1 sticks at 100.

* + 1. G2 ‘Mean Constancy’

G2 is the mean constancy (for that type) of species in the sample, as a proportion of what would be expected. G2 is also weighted to emphasize the higher constancy classes. A low value means that the sample contains many species that ought to be rare or absent in that vegetation type. It is adjusted so that the expected value, if a typical constancy-class composition is present, is 100. For species-poor samples, G2 will tend to be high and G1 low. For species-poor types, G1 will tend to be high and G2 low. G2 was not used by Hill (1989), but has been included to prevent a tendency to assign too many samples to species-poor types.

* + 1. G3 ‘Dominance Satisfaction’

G3 measures whether those species that would be expected to have high abundance in the type are actually present with high abundance. G3 is roughly as defined in Hill (1989), but the thresholds for calculating how abundant the species ‘ought’ to be are different. For types with a single dominant, G3 can be high if and only if that species is present with high abundance.

* + 1. **G4 ‘Weighted Mean Constancy’**

G4 is the weighted mean constancy, which was called the ‘Dominance Constancy’ by Hill (1989). The system of weights is here slightly different. In fact, each species is weighted by the 0.75 power of its % cover value.

* + 1. **Overall Goodness-of-Fit**

The overall goodness-of-fit value is an average of the separate values, calculated as follows:

G = c1\*G1'+ c2\*G2' + c3\*G3'+ c4\*G4'

The meaning of the individual goodness-of-fit values is explained below. The values of c1, c2, c3, c4 for the 5 possible parameter values are outline in Table 16.

**Table 16.** The value for the four constants (c1-c4) used to calculate the overall Goodness-of-Fit for each of the five Analysis Parameters.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Parameter | Appropriate data type/Analysis parameter | c1 | c2 | c3 | c4 |
| 1 | Mixed composition and cover | 0.25 | 0.25 | 0.25 | 0.25 |
| 2 | Species composition only | 0.5 | 0.5 | 0 | 0 |
| 3 | Species cover only | 0 | 0.25 | 0.5 | 0.25 |
| 4 | Incomplete species list only | 0 | 1.00 | 0 | 0 |
| 5 | Top few spp, descending | 0 | 0.25 | 0.5 | 0.25 |

For analysis parameters 4 and 5, G1' and G3' are simply goodness-of-fit values. However, for the other values (including the default value of 1) they are defined as

G1' = G1 \* (2-G2/100)\*G2/100

G2' = min (G1',G2)

G3' = G3 \* (2-G4/100)\*G4/100

G4' = min (G3', G4).

Fortunately, you do not have to calculate these values yourself.

1. The Species dictionary

6.1. Names and numbers of species

The dictionary, in a file called SPECDICT.txt, is not seen explicitly during execution of the program, but is listed in the data files provided for each program (Fig. 1)) to allow you to check on nomenclature. It is a list of names and corresponding numbers. It is in strictly alphabetical order of 9-letter short names, and must always be kept in that order, as it is not sorted into order by TABLEFIT.

For vascular plants, the numbering is basically that employed by the Biological Records Centre (BRC) at Wallingford used and on recording cards of the Botanical Society of Britain and Ireland. The numbering of bryophytes is obtained by adding 3000 to standard BRC numbers. Other numbers are arbitrary. Numbers denote taxonomic categories as follows:

1 - 2999 Vascular plants

3000 - 3999 Bryophytes

4000 - 4999 Lichens

5000 - 5999 Algae

Species names, with modern equivalents (Current\_name) are also listed in SPECDICT.xls.

## 

6.2. Synonyms

Several common synonyms such as:

agro capi/agro tenu

elym repe/elyt repe

scir cesp/tric cesp

are included in the dictionary. They can be recognized as synonyms because they have the same Tablefit\_code although the names differ.

In some cases, distinct species are given the same number, e.g.:

agro cani/agro vine

viol reic/viol rivi

This is because they are not distinguished in NVC tables. The red sphagna are also treated as synonymous for the same reason, i.e.:

spha capi/spha quin/spha rube

6.3. Ambiguous names

To avoid ambiguities, a few abbreviated names such as rume acet (which could be *Rumex acetosella* or *R. acetosa*) have been excluded from the dictionary. If you are entering data at the keyboard, you do not normally need to know these exclusions because, when you type an ambiguous name, the program will prompt you for what to do. A full list of ambiguous names and other nonstandard names is given in SPECDICT.xls.

Note that it is necessary to get the abbreviations right if data are entered from pre-existing files. For this purpose, you should run TABLEFIT once to get a report, in which unrecognized names (which may be ambiguous names) are enumerated. Ambiguous names must then be changed to their standard forms to disambiguate. A list of ambiguous names and their substitutes is given in Appendix Table A.1. Other non-standard names are listed in Appendix Table A.2.

6.4. Assistance in input file preparation

Getting the species names correct is very important yet can be quite problematic. It is important to spend time getting it correct at the start as mistakes means you have to return to the beginning again, which is very frustrating. Hence we have produced two utilities to assist in this process; but even using these you need to take care to correct mistakes and add shrub and tree values if needed. We suggest a four step process:

6.4.1. Step 1: Create a dataset in an EXCEL worksheet

There are two ways of doing this, either as a:

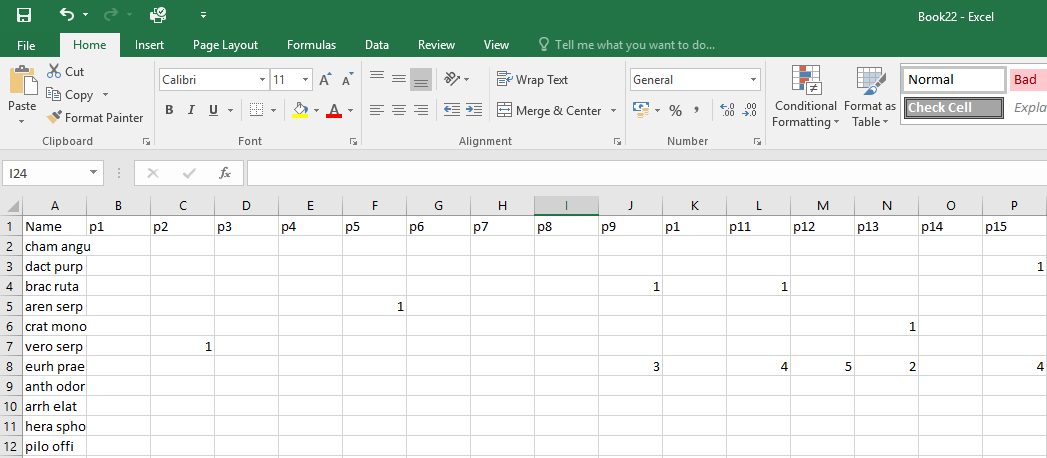
1. Species (rows) x samples (columns) matrix (Fig. 2a), or as a
2. Samples (rows) x species (columns) matrix (Fig. 2b.

It doesn’t matter which you use, but for very large datasets, the latter is preferred because you are likely to run out of columns if the sample number is very large. You are very unlikely to run out of columns by having too many species.

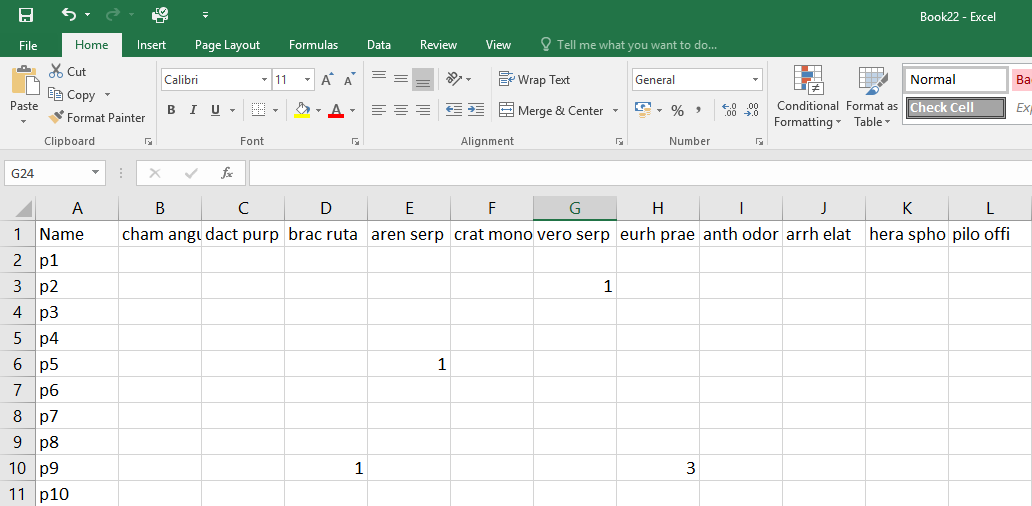
The EXCEL sheet should have blank cells rather than zero; the utilities do work with zeros but they create excessively large output files. So for brevity use blank cells.

Save the spreadsheet as a .csv file.

(a)

****

(b)

****

**Fig. 2.** Examples of the two ways data are often collected in plant community studies in a format that is suitable for easy transfer into TABLEFIT: (a) Species names in column 1 and samples in rows, and (b) Species names as column headers and samples in rows. Both should be saves as .csv files and note that where a species is absent the cell is left empty**.**

6.4.2. Step 2: Convert the species Latin names to TABLEFIT codes

This step is unnecessary if the species names are already in TABLEFIT format. GOTO Step 3.

If the species names are not in TABLEFIT format the steps for processing the species names are as follows, note your just need to use the Red>Amber>Green columns:

1. Open the EXCEL file Species\_Convertor.xlsx
2. Open the data file created at step 1 and copy the column or row containing the species Latin names.
3. Go to the Species\_Convertor.xlsx
4. If the species Latin names were copied from an EXCEL column, then paste directly into the red INPUT column [cell A3).
5. If the species Latin names were copied from an EXCEL row, then paste into the red INPUT column [cell A3) but use PASTE SPECIAL and the Transpose option.
6. If you have shrub or tree canopy codes associated with your species names, these must be coded as \* and \*\* respectively; these should then be separated from the species names and pasted into a different column. It is advised to trim spaces form the species names using the TRIM function.
7. Find the bottom row of column A
8. Move cursor over to the amber TRANSITION column C and then CTRL up arrow, move it to cell c3 and then copy the formula down to the bottom of the dataset using CTRL D.
9. This will provide the TABLEFIT codes for most of the species in the list within the amber TRANSITION column [column C].
10. Copy column C and paste it using PASTE SPECIAL with the VALUES option into the Green OUTPUT column E, this removes the formula and returns a value.
11. A “#N/A” value indicates no fit and these species have to be handled manually.
12. If \* and \*\* codes for the shrub and woodland layers were used then they need to be merged back into the species column using the CONCATENATE function.
13. Once corrected the TABLEFIT codes can be cut from the green OUTPUT column (E) and pasted back into the original file, overwriting the original species names with the Transpose option if necessary.
14. The EXCEL file should then be saved as a comma-delimited file (.csv).

6.4.3. Step 3: Convert the data from matrix format into TABLEFIT input format

Here, we have created two convertor files; they both contain some R-code which needs to be edited and then cut and pasted into the R statistical program (R Core Team, 2018). A copy of R can be downloaded free of charge from the CRAN website (<https://cran.r-project.org/>), and this needs to be installed first.

Thereafter, the program needs to be edited by the user for each run, the points where editing is needed are highlighted in yellow and the things that need edits are highlighted in green. Essentially for both programs you need to:

1. In section #1 set the working directory; i.e. replace the filename in green with your data input file.
2. In section #2, edit the line that reads your data in (read.csv line) replace the filename in green with your data input file.
3. In section 6, edit the line that outputs your results (write.table line), replace the filename in green with your data output file name. Here, make sure it is a .txt file.
4. Cut and paste the entire code within the file into R, it should run automatically.
5. The resultant output file should be able to be read into TABLEFIT v3 and v4.
6. Acknowledgements

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Appendices

**Table A.0.** New Wet Grassland communities that have been added in TABLEFIT v3: Enhanced. These Tables were MG13v2, MG8v2 and MG4v2 are all expanded constancy tables that have been added in but without replacing the original NVC community. This means users can compare matches against the old and new synoptic tables. MG6d is an accepted new sub-community of MG6. MG8v2 and MG4v2 now have 4 sub-communities each. MG14 and MG15 are new communities with 2 sub-communities each and MG16 is another new community.

|  |  |  |
| --- | --- | --- |
| NVC code | Community name | Sub-community name |
| MG4v2 | *Alopecurus pratensis-Sanguisorba officinalis* grassland |  |
| MG4a | *Alopecurus pratensis-Sanguisorba officinalis* grassland | *Dactylis glomerata*  sc |
| MG4b | *Alopecurus pratensis-Sanguisorba officinalis* grassland | Typical sc |
| MG4c | *Alopecurus pratensis-Sanguisorba officinalis* grassland | *Holcus lanatus*  sc |
| MG4d | *Alopecurus pratensis-Sanguisorba officinalis* grassland | *Agrostis stolonifera*  sc |
| MG6d | *Lolium perenne-Cynosurus cristatus* grassland |  |
| MG8v2 | *Cynosurus cristatus-Carex panicea-Caltha palustris* grassland |  |
| MG8a | *Cynosurus cristatus-Carex panicea-Caltha palustris* grassland | *Sanguisorba officinalis*  sc |
| MG8b | *Cynosurus cristatus-Carex panicea-Caltha palustris* grassland | Typical sc |
| MG8c | *Cynosurus cristatus-Carex panicea-Caltha palustris* grassland | *Carex nigra-Ranunculus flammula*  sc |
| MG8d | *Cynosurus cristatus-Carex panicea-Caltha palustris* grassland | *Caltha palustris-Bellis perennis*  sc |
| MG13v2 | *Agrostis stolonifera-Alopecurus pratensis* grassland |  |
| MG14 | *Carex nigra-Agrostis stolonifera-Senecio aquaticus* grassland |  |
| MG14a | *Carex nigra-Agrostis stolonifera-Senecio aquaticus* grassland, | Typical sc |
| MG14b | *Carex nigra-Agrostis stolonifera-Senecio aquaticus* grassland, | *Anthoxanthum odoratum-Trifolium repens*  sc |
| MG15 | *Alopecurus pratensis-Poa trivialis-Cardamine pratensis* grassland |  |
| MG15a | *Alopecurus pratensis-Poa trivialis-Cardamine pratensis* grassland. | *Agrostis stolonifera*  sc |
| MG15b | *Alopecurus pratensis-Poa trivialis-Cardamine pratensis* grassland. | *Lolium perenne-Ranunculus acris*  sc |
| MG16 | *Agrostis stolonifera-Eleocharis palustris* community |  |

**Table A.1.** List of species with ambiguous names; with one exception (cldo sp.) they correspond to the cases where the 4-4 abbreviation of two taxa is identical. Table A1. Here the ambiguous names are denoted as “To\_avoid” and their substitutes “Short\_name” should be used.

|  |  |  |  |
| --- | --- | --- | --- |
| Tablefit\_code | Short\_name | To\_avoid | Full\_name |
| 341 | care acfm | care acut | Carex acutiformis |
| 340 | care acta | care acut | Carex acuta |
| 367 | care dsti | care dist | Carex disticha |
| 366 | care dstn | care dist | Carex distans |
| 400 | care pcea | care pani | Carex panicea |
| 401 | care pnic | care pani | Carex paniculata |
| 4013 | clad ci-c | clad cili | Cladonia ciliata var. ciliata |
| 4035 | clad ci-t | clad cili | Cladonia ciliata var. tenuis |
| 4031 | clad rfrm | clad rang | Cladonia rangiformis |
| 4032 | clad rina | clad rang | Cladonia rangiferina |
| 5007 | cldo sp. | clad sp. | Cladophora sp. (not Cladonia sp.) |
| 1050 | junc acfl | junc acut | Juncus acutiflorus |
| 1052 | junc acus | junc acut | Juncus acutus |
| 3459 | plth undu | plag undu | Plagiothecium undulatum |
| 3395 | pmni undu | plag undu | Plagiomnium undulatum |
| 1515 | polg vulg | poly vulg | Polygala vulgaris |
| 1544 | polp vulg | poly vulg | Polypodium vulgare |
| 1673 | rese lola | rese lute | Reseda luteola |
| 1672 | rese ltea | rese lute | Reseda lutea |
| 3527 | rhbr rose | rhod rose | Rhodobryum roseum |
| 1882 | rhoi rose | rhod rose | Rhodiola rosea |
| 1735 | rume acel | rume acet | Rumex acetosella |
| 1734 | rume acsa | rume acet | Rumex acetosa |
| 1768 | sagn sagi | sagi sagi | Sagina saginoides |
| 1771 | sagt sagi | sagi sagi | Sagittaria sagittifolia |
| 2242 | salc frag | sali frag | Salicornia fragilis |
| 1793 | salx frag | sali frag | Salix fragilis |
| 1798 | sali myes | sali myrs | Salix myrsinites |
| 1797 | sali myrf | sali myrs | Salix myrsinifolia |
| 3618 | synt rfrm | synt rura | Syntrichia ruralis var. ruraliformis |
| 3619 | synt rlis | synt rura | Syntrichia ruralis var. ruralis |
| 3618 | tort rfrm | tort rura | Tortula ruralis var. ruraliformis |
| 3619 | tort rlis | tort rura | Tortula ruralis var. ruralis |

**Nomenclature notes:**

There are other non-standard names, mostly of hybrids, but also of taxa that are not recognized as species in current floras (Table A.2). The first five had species rank in the NVC tables, but have subsequently been sunk. *Persicaria nodosa* is treated by Stace (2010) as a full synonym of *P. lapathifolia.* The name is retained here (in a single NVC type, which also has *P. lapathifolia*) although it now serves no useful purpose. The last two non-standard names are informal entities. The rest are hybrids.

If you run the Ellenberg meadow test dataset ULM\_MEAD.txt through TABLEFIT, you will find numerous names that are not in the TABLEFIT dictionary. The first five are:

cent jace

cera caes

koel pyra

ranu acer

rume acet

These include non-British species such as *Koeleria pyramidata*, species not appearing with frequency II or more in NVC tables (*Centaurea jacea*), variant spellings (*Ranunculus acer*), and outdated names of British species (*Cerastium caespitosum* = *C. fontanum*). *Rumex acetosa* appears here as rume acet, which should be corrected to rume acsa if the program is to interpret it correctly.

**Table A2**. Non-standard names that are not ambiguous. Again the user should use substitute “Short\_name”.

|  |  |  |  |
| --- | --- | --- | --- |
| Tablefit\_code | Short\_name | To\_avoid | Full\_name |
| 163 | aren lept | aren serp | Arenaria serpyllifolia subsp. leptoclados |
| 683 | empe herm | empe nigr | Empetrum nigrum subsp. hermaphroditum |
| 5014 | fucu volu | fucu vesi | Fucus vesiculosus var. volubilis |
| 1536 | pers nodo | pers lapa | Persicaria lapathifolia |
| 2238 | zost sten | zost mari | Zostera marina var. stenophylla |
| 2997 | sali phae |  | Salix x phaeophylla - not traced |
| 2989 | betu aura |  | Betula pendula x pubescens (B. x aurata) |
| 512 | circ inte |  | Circaea alpina x lutetiana (C. x intermedia) |
| 2984 | crat medi |  | Crataegus laevigata x monogyna (C. x media) |
| 935 | glyc pedi |  | Glyceria fluitans x notata (G. x pedicellata) |
| 2690 | heli sulp |  | Helianthemum apenninum x nummularium (H. x sulphureum) |
| 1582 | pota angu |  | Potamogeton gramineus x lucens (P. x angustifolius) |
| 1571 | pota nite |  | Potamogeton gramineus x perfoliatus (P. x nitens) |
| 1606 | prim poly |  | Primula veris x vulgaris (P. x polyantha) |
| 1639 | quer rosa |  | Quercus petraea x robur (Q. x rosacea) |
| 2996 | sali boyd |  | Salix lapponum x reticulata (S. x boydii) |
| 815 | sche loli |  | Schedonorus pratensis x Lolium perenne (x Schedolium loliaceum) |
| 2065 | tili eur |  | Tilia cordata x platyphyllos (T. x europaea) |
| 205 | aste disc |  | Aster tripolium (unrayed) |