ReadMe - V_meadow_vascular_plant_abundance_experimental

Dataset responsible: Kari Anne Bråthen and Hanna Böhner
(kari.brathen@uit.no, hanna.bohner@uit.no)

18.02.2021

1 Protocol

Plant abundance in all herbivore and large herbivore exlosures as well as control plots has been measured using point intercept frequency following the COAT protocol 'protocol_plant_measurements_heath_and_meadow_varanger.'

Large herbivore exclosures were set up and sampled for the first time in 2018. All herbivore exlosures were set up and sampled for the first time in 2019.

2 Description of the dataset

The dataset includes three different types of files and all files are saved as ;-separated txt-files:

- One data file per year (`_YEAR.txt`)
- One coordinate file with coordinates of all sites (`_coordinates.txt`)
- One auxiliary file with information about which sites are included in the study design (`_aux.txt`)

2.1 V_meadow_vascular_plant_abundance_experimental_YEAR.txt

These files contain point intercept data of the following functional groups and species which can be converted to biomass estimates:

```
 [1] "Betula nana"                   "Broad leaved grasses"
 [3] "Calamagrostis phragmitoides"   "Deciduous dwarf shrubs"
 [5] "Deciduous vascular cryptogams" "Deschampsia cespitosa"
 [7] "Empetrum nigrum"               "Equisetum sp"
 [9] "Evergreen dwarf shrubs"        "Evergreen non woody"
[11] "Green willows"                 "Grey willows"
[13] "Hemiparasites"                 "Nardus stricta"
[15] "Narrow leaved grasses"         "Prostrate willows"
[17] "Rumex acetosa"                 "Salix herbacea"
[19] "Sedges and rushes"             "Small forbs"
[21] "Tall forbs"                    "Vaccinium myrtillus"
```
* Information about which species are combined to functional groups can be found in the protocol.

Example of the first rows of the data files:

```
  sn_region     sn_locality     sn_section sc_type_of_sites_ecological
1 varanger vestre_jakobselv bearalveaijohka                     meadow
2 varanger vestre_jakobselv bearalveaijohka                     meadow
3 varanger vestre_jakobselv bearalveaijohka                     meadow
   sn_site      sc_plot_treatment sn_plot t_year t_date v_observer
1 vj_be_m_a all_herbivore_exclosure       1   2018   <NA>       <NA>
2 vj_be_m_a all_herbivore_exclosure       1   2018   <NA>       <NA>
3 vj_be_m_a all_herbivore_exclosure       1   2018   <NA>       <NA>
  v_number_of_pins v_functional_group v_plant_part v_abundance
1               NA            bet_nan reproductive          NA
2               NA            bet_nan   vegetative          NA
3               NA            bet_nan         wood          NA
                          v_comment
1 all_herbivore_exclosures started in 2019
2 all_herbivore_exclosures started in 2019
3 all_herbivore_exclosures started in 2019
```

Description of the columns included in the data files:

Column name	Description	Possible values
sn_region	Study region	varanger
sn_locality	Locality (within region)	vestre_jakobselv
sn_section	Section (within locality)	bearalveaijohka, torvhaugdalen
sc_type_of_sites_ecological	Habitat type	meadow
sn_site	Unique Site ID	e.g. vj_be_m_a, vj_be_m_e, NA, NA
sc_plot_treatment	Plot treatment	all_herbivore_exclosure, control, large_herbivore_exclosure
sn_plot	Point frequency plot	1-16
t_year	Sampling year	e.g. 2019
t_date	Sampling date	YYYY-MM-DD
v_observer	Initials of observer	e.g. kab (Kari Anne Bråthen)
v_number_of_pins	Number of pins per PF plot	NA, 3, 24

v_functional_group	Functional group or species	bet_nan, broad_leaved_grasses, cal_phr, deciduous_dwarf_shrubs, deciduous_vascular_cryptogams, des_ces, emp_nig, equ_sp, evergreen_dwarf_shrubs, evergreen_non_woody, green_willows, grey_willows, hemiparasites, nar_str, narrow_leaved_grasses, prostrate_willows, rum_ace, sal_her, sedges_rushes, small_forbs, tall_forbs, vac_myr
v_plant_part	Plant part	reproductive, vegetative, wood
v_abundance	Number of point intercepts	[numeric]
v_comment	Comments	[character]

2.2 V_meadow_vascular_plant_abundance_experimental_coordinates.txt

This file contains the coordinates of all sites included in the study desgin. Coordinates are given in decimal degrees and UTM 33 (WGS 84).

Example of the first rows of coordinate files:

```
    sn_site     e_dd     n_dd e_utm33 n_utm33
1 vj_to_m_a 29.06932 70.31760 1024739 7862330
2 vj_to_m_b 29.07217 70.31538 1024901 7862113
3 vj_to_m_c 29.08576 70.30800 1025589 7861427
```

2.3 V_meadow_vascular_plant_abundance_experimental_aux.txt

This file contains further information about the dataset such as the years when sites were first included in the study design and when sites were excluded from the study design.

Example of the first rows of auxiliary-files:

```
  sn_region      sn_locality      sn_section    sn_site
1  varanger vestre_jakobselv bearalveaijohka vj_be_m_a
2  varanger vestre_jakobselv bearalveaijohka vj_be_m_a
3  varanger vestre_jakobselv bearalveaijohka vj_be_m_a
        sc_plot_treatment year_first year_last v_comment
1                 control       2018        NA        NA
2 large_herbivore_exclosure     2018        NA        NA
3   all_herbivore_exclosure     2019        NA        NA
```
* year_last is NA if the site is still included in the study design

3 Data cleaning and formatting

Rawdata is cleaned and formatted in three steps:

1. Data cleaning: All rawdata files entered in excel-templates are cleaned and saved as txt-files using the scripts `01_check_and_reformat_point_frequency_fieldsheets_all_herbivore_exclosures.R`, `01_check_and_reformat_point_frequency_fieldsheets_large_herbivore_exclosures.R` and `01_check_and_reformat_point_frequency_fieldheets_observational.R`. The scripts check for correct spelling, correct format, outliers and missing observations, adds other necessary columns (e.g. region, locality and habitat) and saves the data as txt-files. Each file is processed separately and possible mistakes are corrected in the scripts.

In particular the scripts check for:

- **sn_site:** Correct spelling of all site names and missing observation. Missing observations will be included with NA for abundance.
- **t_date:** Correct format (yyyy-mm-dd), dates in other formats are reformatted.
- **v_observer:** Correct format (initials and lowercase letters), observer is reformatted e.g. if full names were used.
- **Species and functional group names:** Correct spelling, all species names will be converted to abbreviations (e.g. vac_myr).
- **v_abundance:** Outliers in abundance, 'x' will be replaced with 0.1, empty cells will be filled with 0 and weird entries (e.g. if there was a problem with the keybaord) will be corrected.
- **v_comment:** Correct spelling and format (lowercase letters and english). Comments are edited or translated if necessary.
- The columns **sn_region, sn_locality, sn_section, t_year** and **t_season** are added.

A comment is added if corrections go beyond simple typing mistakes and lead to differences between rawdata and cleaned data.

2. Data formatting: All cleaned files are compiled and formatted using the script `02_make_datafiles_from_point_frequency_experimental.R`. The script formats the data according to the requirements of the COAT dataprotal and produces one file for each dataset derived from observational plant measurements in heath and meadow sites:

- `V_meadow_vascular_plant_abundance_experimental_YEAR.txt`
  (point intercepts on functional group level in meadow sites)
- `V_meadow_plant_species_composition_experimental_YEAR.txt`
  (presence and abundance data of all vascular plant species in meadow sites)
- `V_meadow_ground_cover_experimental_YEAR.txt`
  (abundance of for example Litter, Mosses, Lichen and small rodent activity in meadow sites)
- `V_meadow_shrub_height_experimental_YEAR.txt`
  (height of thicket forming *Salix sp.* and *Betula nana* in meadow sites)
- `V_heath_vascular_plant_abundance_experimental_YEAR.txt`
  (point intercepts on functional group level in heath sites)
- `V_heath_plant_species_composition_experimental_YEAR.txt`
  (presence and abundance data of all vascular plant species in heath sites)

- `V_heath_ground_cover_experimental_YEAR.txt`
  (abundance of for example Litter, Mosses, Lichen and small rodent activity in heath sites)

- `V_heath_shrub_height_experimental_YEAR.txt`
  (height of thicket forming *Salix sp.* and *Betula nana* in heath sites)

3. Quality check: A final quality check is performed on each dataset. All variables are checked and observations are plotted together with the years before.

4   Calculation of state variables

Point intercepts can be converted to biomass esatimates. Contact Kari Anne Bråthen for more information about the conversion factors.