

ReadMe - V_heath_vascular_plant_abundance_experimental

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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 exlosures 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_heath_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  bearylveaijohka      heath_near
2  varanger  vestre_jakobselv  bearylveaijohka      heath_near
3  varanger  vestre_jakobselv  bearylveaijohka      heath_near
      sn_site      sc_plot_treatment  sn_plot  t_year  t_date  v_observer
1  vj_be_hn_a  all_herbivore_exclosure      1    2018    <NA>    <NA>
2  vj_be_hn_a  all_herbivore_exclosure      1    2018    <NA>    <NA>
3  vj_be_hn_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	heath_near
sn_site	Unique Site ID	e.g. vj_be_hn_a, vj_be_hn_e2, 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, de- ciduous_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_heath_vascular_plant_abundance_experimental_coordinates.txt

This file contains the coordinates of all sites included in the study design. 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_hn_c 29.08530 70.30827 1025566 7861453
2 vj_to_hn_d 29.11366 70.30286 1026747 7861110
3 vj_be_hn_a 28.95137 70.28681 1021193 7857958

```

2.3 V_heath_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_hn_a
2 varanger vestre_jakobselv bearalveaijohka vj_be_hn_a
3 varanger vestre_jakobselv bearalveaijohka vj_be_hn_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_fieldsheets_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 keyboard) 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)
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(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 estimates. Contact Kari Anne Bråthen for more information about the conversion factors.