Abundance and beta-diversity of bumble bees and wildflowers in the Berchtesgadener Alps

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DATA FILES

1. floral_tax.csv

Description: Supplies family-level taxonomy for the floral taxa in our study.

Columns:

- 1. plant.sp = plant species
- 2. plant.genus = plant genus
- 3. plant.family = plant family

2. network.csv

Description: Bumble- bee-wildflower visitation data used in all analyses of (1) bumble bee abundance, (2) bumble bee beta-diversity, and (3) interaction beta-diversity.

Columns:

- 1. year = year
- 2. dayofyear = day of year since January 1
- 3. site = site name
- 4. snowcover = whether site was snow-covered
- 5. plant.sp = full plant species name
- 6. plant.genus = plant genus name
- 7. flower cover = flower cover in m^2 to the nearest 0.01 m^2
- 8. day = day of month
- 9. month = month
- 10. date = date

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floral_survey.csv

Description: Floral survey data used in all analysis of (1) floral abundance and (2) floral beta-diversity.

Columns:

```
year = year
dayofyear = day of year since January 1
site = site name
trap.time = time interaction was observed
caste = bumble bee caste (queen, male, worker, NA = parasitic Psithryus)
pollen = whether the bee had visible pollen loads
bb.sp = abbreviated bumble bee species name
bb.sp.lat = full bumble bee species name
plant.sp.abb = abbreviated plant species name
plant.sp = full plant species name
plant.genus = plant genus name
day = day of month
month = month
date = date
```

4. site_data.csv

Description: Site data including elevation, management, and geographic coordinates.

Columns:

```
site = site name
elev.class = elevation category (oben, mitte, unten)
management = site management (mowing, grasing, none)
temp.mean = mean temperature recorded with iButton devices
elev.mean = mean elevation
transect = transect name
slope.calc = slope calculated from min and max elevation
slope.est = estimated slope
elev.min = minimum elevation within site
elev.max = maximum elevation within site
lat = latitude (decimal degrees)
lon = longitude (decimal degrees)
elev.class2 = alternative elevation binning
tree_line = whether a site was above or below the tree line; only for sites included in analysis (hence NAs)
```

CODE FILES

1. ms1_abundance.Rmd

Description: R script for running abundance analyses.

2. ms1_beta_diversity.Rmd

Description: R script for running beta-diversity analyses.