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

Katharina Kallnik¹, Johanna Sieger³, Fabrice Requier², Douglas B. Sponsler^{1*}, Alice Claßen¹, A. Fabien

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. trap.time = time interaction was observed
- 5. caste = bumble bee caste (queen, male, worker, NA = parasitic Psithryus)
- 6. pollen = whether the bee had visible pollen loads
- 7. bb.sp = abbreviated bumble bee species name
- 8. bb.sp.lat = full bumble bee species name
- 9. plant.sp.abb = abbreviated plant species name
- 10. plant.sp = full plant species name
- 11. plant.genus = plant genus name
- 12. day = day of month

 $^{^{1}}$ Department of Animal Ecology and Tropical Biology, Biocenter, University of Würzburg, Würzburg, Germany

 $^{^2}$ Université Paris-Saclay, CNRS, IRD, UMR Évolution, Génomes, Comportement et Écologie, 91198, Gifsur-Yvette, France

³ Naturpark Frankenhöhe, Ansbach, Germany

^{*} Corresponding author: douglas.sponsler@uni-wuerzburg.de

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13. month = month
14. 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
    snowcover = whether site was snow-covered
    plant.sp = full plant species name
    plant.genus = plant genus name
    flower cover = flower cover in m² to the nearest 0.01 m²
    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)
```

4. bb_traits.csv

Description: Bumble bee trait data

Clade and subgenus classifications are based on Williams et al (2008).

Tongue length data are from Arbetman et al. (2017), Obeso (1992), and Durieux (2000)

Columns:

- 1. clade = bumble bee clade: LF = long faced, SH = short faced, M = Mendacibombus
- 2. subgenus = bumble bee subgenus
- 3. bb.sp.lat = full bumble bee species name
- 4. bb.sp = abbreviated bumble bee species name
- 5. pbl.w = worker tongue length based primarily on Arbetman et al. (2017) and supplemented where necessary from Durieux (2000) and Obeso (1992)
- 6. pbl.w.class = discretized worker tongue length
- 7. pbl.w.class2 = simplified discretized worker tongue length
- 8. pbl.w.ref = reference from which pbl.w was gathered
- 9. Notes = notes on pbl.w
- 10. pbl.w.durieux = alternative set of tongue length based primarily on Durieux (2000) and supplemented where necessary from Arbetman et al. (2017) and Obeso (1992)
- 11. notes_durieux = notes on pbl.w.durieux

5. fl_traits.csv

Description: Kugler's (1970) floral morphotype classification for floral species

For a description of Kugler's morphotype codes, see kugler_key.tsv.

Data were accessed in April 2020 via the Bioflor plant trait database (Klotz et al. 2002). Missing data were manually supplemented as described in fl trait proc.R.

Columns:

- 1. plant.sp = plant species
- 2. plant.genus = plant genus
- 3. plant.family = plant family
- 4. k.type = Kugler morphotype
- 5. k.type.s = Kugler morphotype simplified to 1 decimal place
- 6. k.type.ss = Kugler morphotype simplified to 0 decimal places

6. kugler_key.tsv

Description: A verbal description of Kugler's (1970) floral morphotype classification

Data were accessed in April 2020 via the Bioflor plant trait database (Klotz et al. 2002).

Columns:

- 1. code = Morphotype code
- $2. \ {\tt description} = Morphotype \ description$

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.

2. fl_trait_proc.R

Description: R script for processing raw BIOFLOR trait data and adding traits for missing species.

References

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Durieux E-A. 2000. Etude des choix floraux des bourdons (Hymenoptera, Apidae) de la commune d'eyne (france, Pyrénées-Orientales). PhD thesis, Université de Mons-Hainaut.

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