

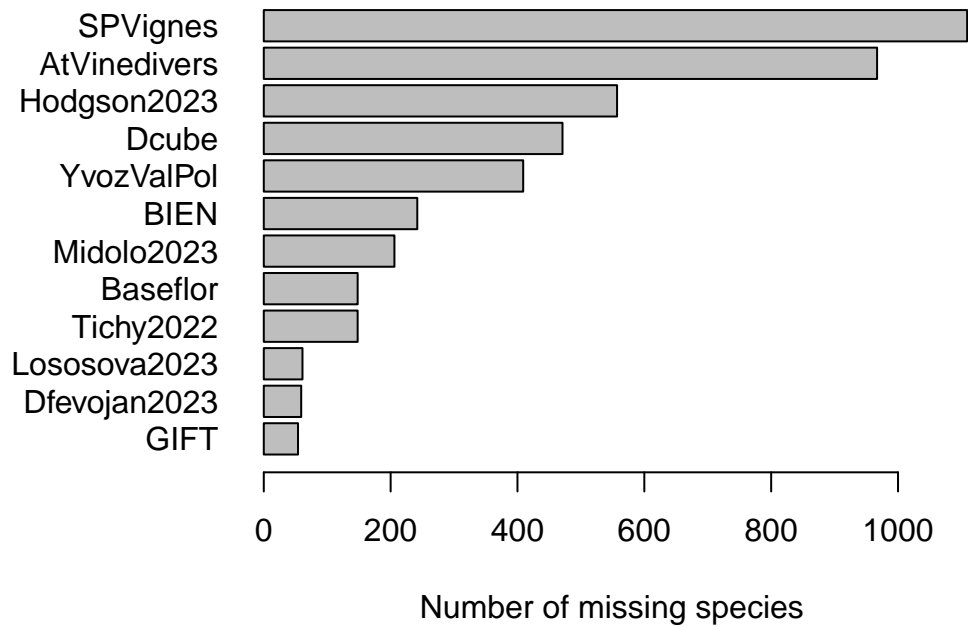
Exploration of FELLOW trait dataset

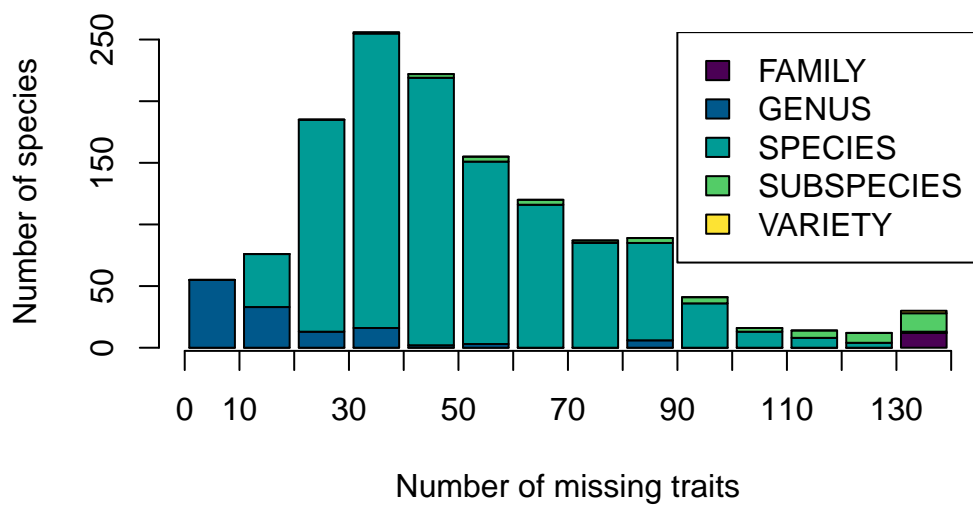
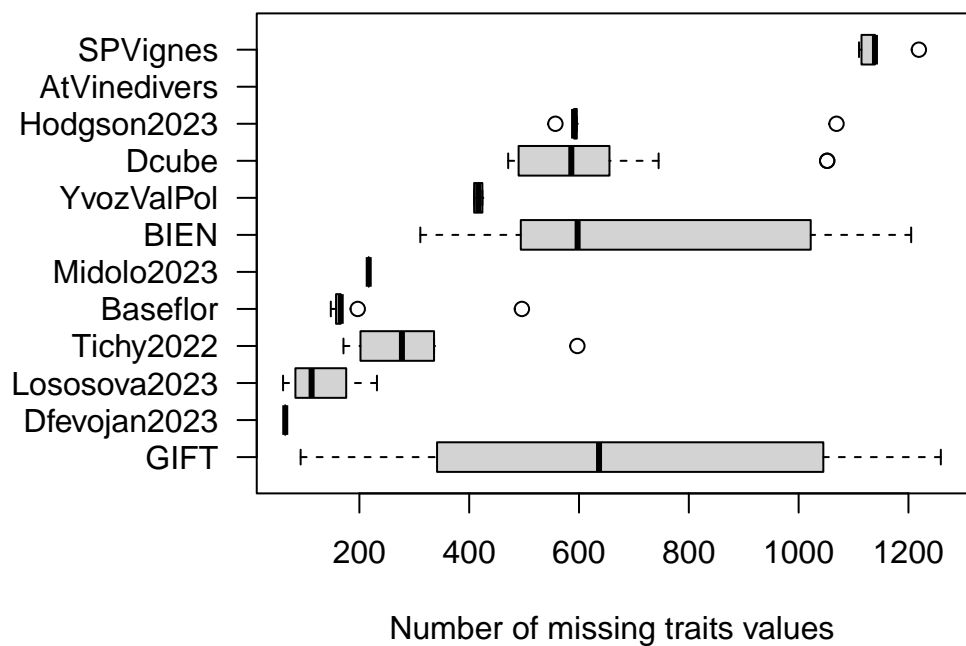
The objective of this document is to:

- visually explore the trait database
- understand trait coverage / data gaps
- check for possible inconsistencies

Description of trait databases

So far, we compiled 135 traits for 1358 taxa gathered from 12 trait databases. But there are many missing values.





Taxa with no or limited trait information (N=30).

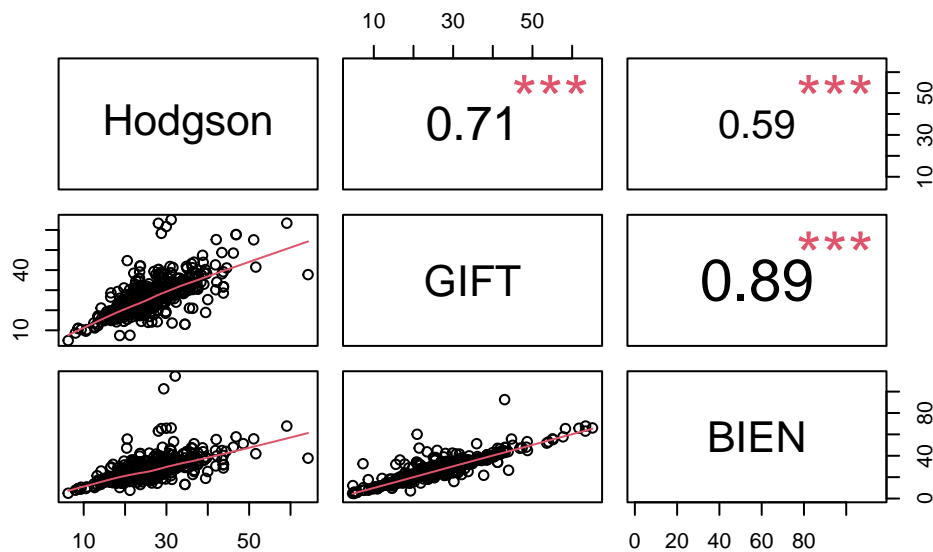
- [1] "Aethusa cynapium subsp. cynapium"
- [2] "Aremonia agrimonoides agrimonoides"
- [3] "Anthemis arvensis subsp. arvensis"
- [4] "Apiaceae"
- [5] "Arrhenatherum elatius subsp. elatius"
- [6] "Asparagaceae"
- [7] "Asteraceae"
- [8] "Brassicaceae"
- [9] "Bromus commutatus subsp. decipiens"
- [10] "Caryophyllaceae"
- [11] "Amaranthaceae"
- [12] "Crepis foetida subsp. rhoeadifolia"
- [13] "Fabaceae"
- [14] "Hordeum murinum subsp. murinum"
- [15] "Lamiaceae"
- [16] "Liliaceae"
- [17] "Nigella hispanica var. hispanica"
- [18] "Nigella hispanica var. intermedia"
- [19] "Ononis viscosa subsp. viscosa"
- [20] "Pastinaca sativa subsp. urens"
- [21] "Pisum sativum subsp. sativum"
- [22] "Pisum sativum subsp. sativum"
- [23] "Poaceae"
- [24] "Rosaceae"
- [25] "Rubiaceae"
- [26] "Sonchus arvensis subsp. uliginosus"
- [27] "Vicia lutea subsp. lutea"
- [28] "Vicia dasycarpa"
- [29] "Viola tricolor subsp. tricolor"
- [30] "Xanthium orientale subsp. orientale"

Open question: **How to deal with families or subspecies/varieties taxa?**

Comparison

SLA

There are three sources of information for Specific leaf area (SLA) : Hodgson et al. 2023 (in mm²/mg), GIFT (in cm²/g) and BIEN (in m²/kg = mm²/mg).



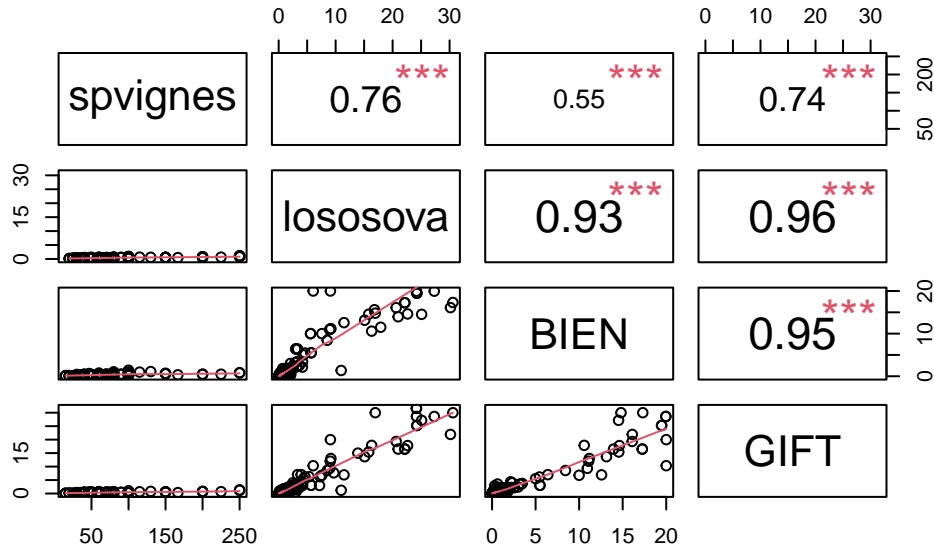
Values are highly correlated, so we could imagine filling the missing values (using preferred data sources or averaging them).

Number of NAs:

Hodgson	GIFT	BIEN	filled
591	583	583	306

Plant height

There are four sources of information for plant height.



Not sure what is the unit of Plant_Height in SPVignes (cm?), and why it is limited to only small plants (<1m). Yet we could potentially fill the height trait values.

Number of NAs:

spvignes	lososova	BIEN	GIFT	filled
1219	120	508	370	81