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Automatic report
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Study ID: Thijs_Fijen_Allium_porrum_France_2016

Contact: thijs.fijen@wur.nl

Credit: Thijs Fijen

Publication: NA

Number of sites: 18

Year of sampling: 2016

Crop: Allium porrum

Variety: There are missing varieties (given 0 out of 18).

Location: There are missing locations (given 0 out of 18).

Country: There are no locations to check.

Field size: There are missing field sizes (given 0 out of 18).

Management: Full information.

Sampling period: Full information.

Richness: Full information.

species groups considered: No taxa restrictions have been identified.

Abundance: Full information.

Visitation rate units: visits per 100 flowers and hour

Visitation rate: There are missing values (given 17 out of 18).

Yield units: z-score Seeds produced (average of female lines)

Yield: Full information.

Alternative yield units: z-score Seed set (%, average of female lines)

Alternative yield: Full information.

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Queries
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Instructions: Please, edit this file and answer the
following queries within the document, one by one.
Then send the edited 'Summary_report_and_queries'
(with your comments) and your 'Data_ownership' (excel)
file to alfonso.allen.perkins+observdataset@gmail.com
before the 20th of July.
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- Please check that credit information is correct and add the corresponding affiliations and acknowledgements/funding information in your 'Data_ownership' (excel) file.

- If your study is already published, please check that its DOI is correct.

- If possible, please provide the names of missing crop varieties.

- If possible, please provide the area of each field [in hectares].

- If possible, please provide the latitude and longitude of the missing locations [in decimal degrees].

- There are sites without visitation rate records. Please, check that such information is correct. See also the information about OBServ data processing in your 'First read me - General report' pdf file.

- Please check that our information about the species groups considered is correct.

- Please, check that the brief description of your methodology (in your insect_sampling file) is correct.

- When processing your raw data, we aggregated the measurements of the different female lines (i.e., yield, abundance, etc.). Is it correct?