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Automatic report
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Study ID: Johan_Ekroos_Vicia_faba_Sweden_2016
Contact: johan.ekroos@cec.lu.se
Credit: Johan Ekroos & Henrik Smith (Lund University)
Publication: NA
Number of sites: 16
Year of sampling: 2016
Crop: Vicia faba
Variety: There are missing varieties (given 0 out of 16).
Location: Full information.
Country: Reported countries may contain errors.
Field size: There are missing field sizes (given 0 out of 16).
Management: Full information.
Sampling period: There are missing sampling periods.
Richness: Full information.
species groups considered: only bumblebees
Abundance: Full information.
Visitation rate units: NA
Visitation rate: There are missing values (given 0 out of 16).
Yield units: NA
Yield: NA
Alternative yield units: NA
Alternative yield: NA

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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+observeddataset@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 sampling start month and sampling end month for each field, respectively, and use a numeric format (for example, 1 for January, 2 for February and so on).
- If possible, check the latitude and longitude that were included in your `field_level_data` (csv) file. According to our automatic tests, some locations do not belong to the reported country/countries.
- 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 the brief description of your methodology (in your `insect_sampling` file) is correct.