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Automatic report
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Study ID: Maj_Rundlof_Brassica_napus_Sweden_2011

Contact: Maj.Rundlof@biol.lu.se

Credit: Maj Rundlof

Publication: NA

Number of sites: 16

Year of sampling: 2011

Crop: Brassica napus

Variety: There are missing varieties (given 0 out of 16).

Location: There are missing locations (given 0 out of 16).

Country: There are no locations to check.

Field size: There are missing field sizes (given 0 out of 16).

Management: Full information.

Sampling period: Full information.

Richness: There is not enough taxonomic resolution to estimate richness.

species groups considered: NA

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+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.

- According to our raw data, there is not enough taxonomic resolution to estimate richness. 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.