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Automatic report
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Study ID: Michael_Garratt_Malus_domestica_UK_2011

Contact: m.p.garratt@reading.ac.uk

Credit: Michael Garratt (University of Reading)

Publication: unpublished, Garratt et al. 2014a,b

Number of sites: 8

Year of sampling: 2011

Crop: Malus domestica

Variety: There are missing varieties (given 0 out of 8).

Location: UTM zone is needed. There are missing locations (given 0 out of 8).

Country: There are no locations to check.

Field size: There are missing field sizes (given 0 out of 8).

Management: Full information.

Sampling period: There are missing sampling periods.

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

species groups considered: NA

Abundance: Full information.

Visitation rate units: visits per 100 flowers and hour

Visitation rate: Full information.

Yield units: % fruit set

Yield: Full information.

Alternative yield units: seeds per apple

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

- 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.