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Automatic report
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Study ID: Rachel_Mallinger_Malus_domestica_USA_2013

Contact: rachel.mallinger@ars.usda.gov

Credit: Rachel Mallinger, USDA-ARS

Publication: 10.1111/1365-2664.12377

Number of sites: 19

Year of sampling: 2013

Crop: Malus domestica

Variety: There are missing varieties (given 0 out of 19).

Location: UTM zone is needed. There are missing locations (given 0 out of 19).

Country: There are no locations to check.

Field size: Full information.

Management: Full information.

Sampling period: There are missing sampling periods.

Richness: Full information.

species groups considered: only bees. Data was obtained by using pantraps

Abundance: Full information.

Visitation rate units: NA

Visitation rate: There are missing values (given 0 out of 19).

Yield units: percentage fruit set (100 number of fruits/number of open flowers)

Yield: Full information.

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 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].
- 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.