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Automatic report
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Study ID: Jessica_D_Petersen_Cucurbita_pepo_USA_2011

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Credit: Jessica D. Petersen and Brian A. Nault

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Number of sites: 24

Year of sampling: 2011

Crop: Cucurbita pepo

Variety: Full information.

Location: There are missing locations (given 0 out of 24).

Country: There are no locations to check.

Field size: There are missing field sizes (given 0 out of 24).

Management: There are missing results for management (given 0 out of 24).

Sampling period: Full information.

Richness: Full information.

species groups considered: Only bees

Abundance: There are missing values (given 0 out of 24).

Visitation rate units: visits per 100 flowers and hour

Visitation rate: Full information.

Yield units: Fruit weight per plant

Yield: There are missing values (given 21 out of 24).

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 area of each field [in hectares].
 - If possible, please assign a management category [organic, IPM, conventional] to each field.
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- If possible, please provide the latitude and longitude of the missing locations [in decimal degrees].
- There are sites without abundance 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.
- There are sites without yield. Please, check that such information is correct. If possible, please provide the missing values (or the corresponding z-scores).
- Please, check that the brief description of your methodology (in your insect_sampling file) is correct.