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Automatic report
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Study ID: Natacha_Chacoff_Citrus_paradisi_Argentina_2002
Contact: nchacoff@gmail.com
Credit: Natacha Chacoff (Instituto de Ecologia Regional. CONICET UNT)
Publication: 10.1111/j.1365-2664.2005.01116.x,10.1098/rspb.2007.1547
Number of sites: 4
Year of sampling: 2002
Crop: Citrus paradisi
Variety: Full information.
Location: Full information.
Country: All reported countries are OK.
Field size: There are missing field sizes (given 0 out of 4).
Management: Full information.
Sampling period: There are missing sampling periods.
Richness: Full information.
species groups considered: No taxa restrictions have been identified.
Abundance: There are missing values (given 0 out of 4).
Visitation rate units: (average number of) visits per 100 flowers and hour
Visitation rate: Full information.
Yield units: fruit set (%)
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+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 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).
- 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.
- Please check that our information about the species groups considered is correct.
- Please, check that the brief description of your methodology (in your insect_sampling file) is correct.
- When processing your raw data, we aggregated the measurements at different distances within each site. Is it correct?