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Automatic report
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Study ID: Juliana_Hipólito_Mangifera_indica_Brazil_2005

Contact: jhdsousa@yahoo.com

Credit: Juliana Hipólito de Sousa, Camila Magalhães Pigozzo & Blandina Felipe Viana

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Number of sites: 4

Year of sampling: 2005

Crop: Mangifera indica

Variety: Full information.

Location: There are missing locations (given 0 out of 4).

Country: There are no locations to check.

Field size: There are missing field sizes (given 0 out of 4).

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 4).

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 area of each field [in hectares].
• If possible, please provide the latitude and longitude of the missing locations [in decimal degrees].
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- 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.