
Automatic report

Study ID: Katherine_LW_Burns_Malus_domestica_Ireland_2018

 $Contact: \ katherine.burns@ucdconnect.ie$

Credit: Katherine LW Burns & Dara A Stanley

Publication: NA
Number of sites: 16
Year of sampling: 2018
Crop: Malus domestica
Variety: Full information.
Location: Full information.

Country: All reported countries are OK.

Field size: Full information.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: visits per 100 flowers and hour

Visitation rate: Full information.

Yield units: Fruit set (%) Yield: Full information.

Alternative yield units: Mean weight per apple (g per apple)

Alternative yield: Full information.

Queries

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.

- 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.
- 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.

Comments

- 1. I have added the email address of my co-author, Dara A Stanley, and have added our affiliation and funding information in the Data ownership file
- 2. Our study has not yet been published, so the DOI is NA
- 3. The information on taxonomic richness is correct I understand that less than 75% of the observed insects in our study were identified to species or morphospecies, meaning that richness could not be calculated
- 4. I checked my previously recorded description of my methodology and it is correct