

Metadata

Overview

Type in all data in a Google Sheet. Like that, R can be used to easily blank-correct the measurements and normalize the chlorophyll concentration and Symbioniniaceae counts on the coral surface.

[Here](#) is an empty metadata sheet, please copy it before entering data.

There are three tabs:

1. **Overview&Chl:** Information on the samples itself and the chlorophyll measurements
2. **Counts:** Information on Symbioniniaceae counts
3. **Area:** Information on area measurements

To ensure that the R Script is working correctly:

- Do not rename columns or tab names.
- Columns in grey are filled in automatically, do not edit them.
- Some entries area directly verified to ensure the correct format (see below).
- Each column is explained in comments in the column name but here are some additional information.

Tab 1: Overview&Chl

- **sampleID:** The sample ID, e.g. 1EDAL005P.
- **bag number:** The number written on the bag.
- **type:** The type of the sample. Select either `blank` or `sample`. For blanks, leave `sampleID` empty. In the photometer software, the order of blanks and samples is pre-defined, but in case something goes wrong (e.g. 3 measurements of blank instead of 2), it is important to keep track on where samples are saved.
- **date_extraction:** The date when the sample was extracted. Double click for calender view. As format, DD/MM/YYYY is expected. There will be a warning if the entry is not a correctly-formatted date.
- **w_slurry1:** The weight of the tissue slurry in g (after airbrushing). There will be a warning if something else than a number was entered. Leave cells corresponding to blank measurements empty.
- **w_slurry2:** The weight of the liquid in the falcon tube in g. There will be a warning if something else than a number was entered. Leave cells corresponding to blank measurements empty.

- **date_chl_measurement:** The date when the chlorophyll concentration of the sample was measured. Double click for calendar view. As format, DD/MM/YYYY is expected. There will be a warning if the entry is not a correctly-formatted date.
- **m1** and **m2:** The position in the plate layout of the two measurements (e.g. A1 and A2). It is important that this information is correct because it will be used to extract the corresponding measurements from the photometer file. You can copy the position names from the tab **positions**.
- **filename:** The exact file name of the chlorophyll measurements, e.g. 2024_11_19_chl_adaptome_1.txt.
- **comment:** If anything is unclear or happened to the sample, describe it here.

Tab 2: Counts

- **sampleID, bag number, and type:** These columns will be filled out automatically for rows in which sample was selected as type in the tab **1.Overview&Chl**. Do not edit these columns.
- **Date of counts:** The date of the symbiont counts. Double click for calendar view. As format, DD/MM/YYYY is expected. There will be a warning if the entry is not a correctly-formatted date.
- **V_zoox:** The volume of sample in mL. There will be a warning if something else than a number was entered.
- **V_sw:** The volume of added seawater in mL. There will be a warning if something else than a number was entered.
- **c1 to c6:** The Symbiodiniaceae counts. There will be a warning if something else than a number was entered.
- **mean count per sample:** The mean of Symbiodiniaceae counts will be automatically calculated based on the c# columns and the dilution (V_zoox and V_sw).
- **comment:** If anything is unclear or happened to the sample, describe it here.

Tab 3: Area

- **sampleID, bag number, and type:** These columns will be filled out automatically for rows in which sample was selected as type in the tab **1.Overview&Chl**. Do not edit these columns.
- **w1_scratched:** The weight of the fragment after the the wax of parts without tissue was removed. There will be a warning if something else than a number was entered.
- **w2_scratched:** The weight of the fragment after the the wax of the second dip of parts without tissue was removed. There will be a warning if something else than a number was entered.
- **comment:** If anything is unclear or happened to the sample, describe it here.